

DISSERTATION

FLEXIBILITY AND CONSTRAINT IN THE EVOLUTION OF GENE EXPRESSION AND
BEHAVIOR

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Eva Kristin Fischer

Department of Biology

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Doctoral Committee:

Advisor: Kim L. Hoke

Cameron K. Ghalambor

Shane T. Hentges

Rachel L. Mueller

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ABSTRACT

FLEXIBILITY AND CONSTRAINT IN THE EVOLUTION OF GENE EXPRESSION AND BEHAVIOR

Our understanding of how underlying molecular, neural, and physiological mechanisms contribute to phenotypic evolvability remains limited. Central to understanding the evolutionary potential of phenotypes is an understanding of the extent to which the mechanisms underlying phenotypic differences are flexible versus constrained. My dissertation takes advantage of the unique evolutionary history of Trinidadian guppies (*Poecilia reticulata*) to explore patterns of flexibility and constraint at three levels.

In the first study of my dissertation, I examined genetic and developmental influences on variation and covariation in a suite of behavioral traits to understand whether correlations among traits constrain adaptation to novel environments. I reared guppies from high- and low-predation source populations in environments with and without predators to mimic native and novel environmental conditions and characterized differences in a suite of 21 behaviors measured in four behavioral assays. I found that behavioral variance and covariance structure were altered in novel environments in a manner that likely shaped subsequent selection. My findings suggest that divergence in a novel environment was not constrained by trait correlations in the native environment, and that plastic changes in covariance structure may in fact influence the form of adaptation.

In the second study of my dissertation I examined associations between gene expression (transcriptomic) differences and behavior to understand how underlying transcriptional

mechanisms mediate behavioral flexibility across developmental and evolutionary timescales. I reared guppies and assayed behavior as before, and quantified whole-brain gene expression from each individual. My dataset allowed me to relate changes in the expression of single genes and gene networks to behavior across genetic backgrounds and rearing environments. I found that conserved gene networks had flexible relationships with behavior, suggesting that alternative transcriptional solutions may give rise to similar behavioral phenotypes across timescales. I propose that this combination of conservation and flexibility balances phenotypic robustness and evolvability in novel environments.

Recent studies have considered whether similar phenotypes also share underlying mechanisms, but data are conflicting. In the third study of my dissertation, I compared gene expression signatures associated with adaptation in two distinct evolutionary lineages to ask whether parallel, independent evolutionary events rely on shared mechanisms. I used transcriptomic approaches to quantify genetic and developmental differences in brain gene expression in two high- and low-predation guppy population pairs that represent distinct evolutionary lineages. I found evidence for both shared and distinct transcriptional mechanisms associated with adaptation. Moreover, I demonstrated that expression differences are more likely to evolve in genes that were highly connected to other genes in a gene network. Application of network analyses to transcriptomic data is in its infancy, and an influence of network position on expression divergence has not been previously demonstrated.

In summary, I used novel, integrative approaches to study mechanisms of behavioral divergence at multiple levels and found evidence for a combination of conservation and flexibility across levels of biological organization and timescales.

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I have been lucky to be a part of the Hunk (Hoke-Funk) lab family during my time at CSU. The many members of the lab make it the supportive, stimulating, and just plain fun

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DEDICATION

For my family.

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1. INTRODUCTION

In his landmark 1963 paper, Nikolaas Tinbergen outlined four questions in ethology. He argued that understanding animal behavior would require exploration of causation (mechanism), ontogeny (development), adaptive value (function), and evolution (Tinbergen, 1963). These four questions consider both proximate (mechanism and development) and ultimate (function and evolution) causes, and have guided ethological research over the last 50 years. However, studies examining proximate and ultimate mechanisms of complex phenotypes have typically been conducted by distinct groups of researchers (Hofmann *et al.*, 2014). While studies specifically examining mechanisms of behavior and their evolutionary origins remain sparse, technological advances are making these studies increasingly possible (Hofmann *et al.*, 2014; Rittschof & Robinson, 2014). Indeed, while Tinbergen defined his four questions in an ethological context, the elucidation of mechanisms by which phenotypes evolve is a fundamental goal of integrative biology. My dissertation examines genetic and environmental influences on behavior and its underlying mechanisms to understand forces facilitating and constraining behavioral evolution.

Central to understanding evolutionary potential of behavioral phenotypes is an understanding of the extent to which the mechanisms underlying behavioral differences are flexible versus constrained. In other words, are there many possible mechanistic solutions for a given adaptive problem, or are systems constrained such that solutions are limited? Conservation of the neural circuitry mediating behavior across vertebrates is well documented (Nieuwenhuys *et al.*, 1998; Striedter, 2005), and some studies have argued for even more phylogenetically widespread conservation of the nervous system across animal taxa (e.g. Arendt & Nübler-Jung, 1996; Strausfeld & Hirth, 2013). Conservation is also apparent at the molecular level. Shared

molecular substrates regulate similar behaviors from mice to fish to bees (Rittschof *et al.*, 2014), and give rise to the idea that evolution repeatedly targets similar substrates to build similar behaviors (Rittschof & Robinson, 2014; Hofmann *et al.*, 2014). Yet how can widespread conservation of neural, physiological, and molecular mechanisms account for the incredible behavioral diversity we observe across species and even individuals? In contrast to patterns of widespread overlap, there is evidence that distinct mechanisms may give rise to shared phenotypes in closely related species, populations, or even among individuals of the same population (Abouheif & Wray, 2002; Hoekstra *et al.*, 2006; Crawford & Oleksiak, 2007; Goillard *et al.*, 2009; Grashow *et al.*, 2009; Rosenblum *et al.*, 2010; Manceau *et al.*, 2010; Verster *et al.*, 2014).

Reconciling patterns of constraint and flexibility is particularly interesting in an ethological context, as behavioral traits are inherently flexible. Most behaviors have some genetic basis, but are also environmentally labile, both at developmental and immediate timescales. Examining genetic and developmental influences on behavior and its underlying mechanisms is key to understanding behavioral evolution, as both environmentally induced plasticity and genetic divergence may facilitate adaptation (West-Eberhard, 2003; Ghalambor *et al.*, 2007). The role of plasticity in evolution continues to be vigorously debated in the literature (e.g. de Jong, 2005; Pigliucci *et al.*, 2006; Ghalambor *et al.*, 2007), yet empirical studies remain sparse, and studies examining underlying mechanisms are almost completely absent (but see Scoville & Pfrender, 2010; Scott McCairns & Bernatchez, 2010; Morris *et al.*, 2014). Exploring mechanistic patterns of flexibility and constraint at evolutionary and developmental timescales will shed light on how alternative behavioral mechanisms arise and how interactions between genetic and environmental influences shape evolutionary trajectories.

My dissertation work takes advantage of the unique evolutionary history of Trinidadian guppies to explore patterns of flexibility and constraint in gene expression and behavior. The Trinidadian guppy (*Poecilia reticulata*) is a small, live-bearing, freshwater fish species native to Trinidad & Tobago, and the adjacent South American mainland. Guppies have become a model system in ecology and evolutionary biology due to their ability to rapidly adapt to novel environments. Although guppies have been spread to tropical streams and pet stores worldwide, in Trinidad they exist in a natural laboratory that has made them a focus of scientific study since the 1950's (reviewed in Magurran, 2005). In the Northern Range Mountains of Trinidad guppies naturally occur in high- and low-predation sites. In downstream, high-predation sites, guppies are subject to intense predation by a range of piscivorous predators. Major predators are excluded from upstream environments by waterfall barriers, but guppies have managed to colonize upstream, low-predation environments. In low-predation sites guppies co-occur only with the minor predator, *Rivulus hartii*, which preys primarily on juveniles (Endler, 1980; 1995). Guppies from high-predation sites have repeatedly and independently colonized low-predation environments (Barson *et al.*, 2009; Willing *et al.*, 2010; Fraser *et al.*, 2015) leading to parallel evolution in life-history traits, morphology, and behavior (Reznick *et al.*, 1990; Endler, 1995; Reznick *et al.*, 1997; Magurran, 2005). Although additional environmental factors differ between high- and low-predation sites, and among river drainages (Grether *et al.*, 2001; Reznick *et al.*, 2001; e.g. Zandonà *et al.*, 2011; Fitzpatrick *et al.*, 2014), predation pressure is a major driver of adaptation in this system (reviewed in Houde, 1997; Magurran, 2005).

While there is extensive work on many phenotypes and their adaptive value in guppies (reviewed in Houde, 1997; Magurran, 2005), underlying neural, molecular, and physiological mechanisms remain virtually unexplored (but see Fischer *et al.*, 2014; Kolluru *et al.*, 2015).

Moreover, genetic and developmental contributions to adaptive phenotypes are only just beginning to be disentangled (Torres-Dowdall *et al.*, 2012; Ruehl *et al.*, 2013; Handelsman *et al.*, 2013; Fischer *et al.*, 2013; 2014; Handelsman *et al.*, 2014). To separate these influences, we rear fish from high- and low-predation populations in environments with and without predator chemical cues. Because individuals from the same population share a similar genetic background, this design allows us to distinguish environmental effects of predation (by comparing genetically similar fish from the same population under different rearing conditions) from genetic effects (by comparing genetically differentiated populations under the same rearing conditions). For my doctoral work, I have taken advantage of this experimental design and the rich literature on guppy evolutionary ecology and behavior to explore fundamental questions in neuroethology.

My dissertation encompasses three studies that examine patterns of flexibility and constraint at three levels. The first study characterizes genetic and environmental differences in behavioral trait correlations to understand how correlations among behaviors shape evolutionary trajectories. Behavioral correlations are expected to place limits on adaptation when changes in one behavior lead to unfavorable changes in correlated behaviors. However, patterns in one population or environment will only limit evolution if the relationships among traits are constrained such that correlations among them cannot be altered. If the correlations themselves are flexible in response to genetic and/or environmental perturbations correlations observed in one environment will not predict limits on evolution in another.

In the second study I examine genetic and environmental influences on transcriptomic patterns associated with behavior to understand how biological systems balance robustness and evolvability in novel and changing environments. My dataset for this second study includes

sufficient data on individual level variation in behavior and gene expression to allow me to associate behavioral variation with transcriptomic patterns. I examine associations between individual genes, gene coexpression networks, and multiple behaviors to ask whether mechanisms associated with variation in behavior are flexible across levels of biological organization and across evolutionary and developmental timescales. This study complements the first by linking flexibility in behavior to patterns in underlying molecular processes.

The third study compares gene expression signatures associated with adaptation in two evolutionary lineages to ask whether parallel, independent evolutionary events rely on shared transcriptional mechanisms. Again, I ask this question at the level of single genes as well as gene networks. In addition, I take advantage of the multivariate nature of transcriptomic data to ask how relationships among genes may influence their evolutionary potential. While the importance of gene-gene relationships for evolution of gene expression has been examined in other contexts, this type of analysis has not been applied to transcriptomic data.

Using novel, integrative approaches these studies provide evidence for a combination of constraint and flexibility across behavioral phenotypes, behavioral mechanisms, and repeated evolutionary events. My findings point to the important influence of flexibility on evolutionary potential and underline that, in our effort to understand behavioral diversity, examining differences is as important as characterizing similarities.

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2. PLASTICITY AND EVOLUTION IN CORRELATED SUITES OF TRAITS

Summary

Strongly correlated traits cannot evolve independently, and trait correlations may thus restrict evolutionary trajectories. This assessment relies on the assumption that correlations among traits are stable in the face of genetic and environmental perturbations; however, mounting evidence suggests that correlations among traits vary across time and space. To better predict how trait correlations shape evolutionary outcomes, we need a better understanding of how environmentally induced plasticity in novel environments alters trait correlations. We examined genetic and developmental influences on variation and covariation in a suite of behavioral traits to understand whether correlations among traits constrain adaptation to novel environments. We tested the role of genetic and environmental influences on trait correlations by comparing Trinidadian guppies (*Poecilia reticulata*) historically adapted to high- and low-predation environments reared under native and non-native environmental conditions. We found that overall behavioral variance and covariance structure among behaviors differed based on genetic background and rearing environment. Both high- and low-predation fish exhibited reduced behavioral variance when reared under native versus non-native environmental conditions. Furthermore, covariance structure was plastic and rearing in the non-native environment shifted the major axis of variation in the direction observed in native fish. Our findings suggest that divergence in a novel environment was not constrained along the major axis of trait variation in the native environment.

Introduction

When organisms are faced with novel environments, a central challenge is coordinating adaptive shifts in not a single, but many different, phenotypic traits. As a result, a species' ability to adapt to novel environments depends not only on variability in single traits, but also on the strength and structure of relationships among traits. Strongly correlated traits cannot evolve independently, and trait correlations may thus influence evolutionary potential (Lande, 1979; Lande & Arnold, 1983; Roff, 1997). Correlations among traits may therefore constrain evolution if they give rise to pleiotropic trade-offs, i.e. if the selection gradients for correlated traits are in opposing directions (J. Endler, 1995; Schluter, 1996). In this case, trait correlations may slow the rate of evolution or even restrict evolutionary outcomes. Alternatively, correlations among traits may facilitate evolution if changes in one trait lead to favorable changes in another, i.e. if the selection gradients for correlated traits are in the same direction (Merilä & Björklund, 2004). Our ability to infer what effects trait correlations will have on evolutionary trajectories depends on whether correlations are themselves stable or labile.

The direct and indirect effects of selection on correlated traits can be characterized by the genetic variance-covariance matrix, or G-matrix, and its phenotypic counterpart, the phenotypic variance-covariance matrix, or P-matrix (e.g. Cheverud, 1988; Roff, 1997; Lynch & Walsh, 1998). While it is generally assumed that trait correlations are stable across time and space (Lande, 1979; Lande & Arnold, 1983; Falconer & Mackay, 1996; Lynch & Walsh, 1998), evidence is accumulating that this is often not the case. Indeed, the structure of G- and P-matrices can change across environments (Lande, 1979; Lande & Arnold, 1983; Stearns *et al.*, 1991; Waitt & Levin, 1993; R. A. Newman, 1994; Roff, 1997; Sgrò & Hoffmann, 2004; Bell & Sih, 2007; Moretz *et al.*, 2007; Dingemanse *et al.*, 2012; Handelsman *et al.*, 2014) due to

environmentally induced changes (i.e. phenotypic plasticity) or evolved differences that alter the correlations among traits (Steppan *et al.*, 2002; Sgrò & Hoffmann, 2004; Eroukhmanoff & Svensson, 2009). Despite growing recognition of environmental influences on G- and P-matrix structure, the evolutionary consequences of these shifts remain largely unexplored. In particular, it is not clear how plastic changes in the structure of trait correlations shape responses to selection (Service & Rose, 1985; J. Endler, 1995; Schluter, 1996; Parsons & Robinson, 2006). While there is long-standing interest in the role of phenotypic plasticity in evolution (e.g. Baldwin, 1896; Waddington, 1959; Pigliucci, 1996; West-Eberhard, 2003; Ghalambor *et al.*, 2007), few studies have considered how plasticity in the relationships among traits contributes to evolutionary potential (but see Spitze & Sadler, 1996). In the present study, we examine genetic and environmental influences on variance and covariance in a suite of behavioral traits in guppies to address whether correlations among traits do indeed restrict adaptation to novel environments.

Environmental influences and evolution in Trinidadian guppies

The Trinidadian guppy (*Poecilia reticulata*) is a well-established model system in ecology and evolutionary biology due to its ability to rapidly evolve to changing environmental pressures. Trinidadian guppies are small, freshwater fish native to the island nation of Trinidad and Tobago and the adjacent South American mainland. In the Northern Range Mountains of Trinidad, guppies naturally occur in high-predation and low-predation environments. In downstream, high-predation environments guppies co-occur with a number of piscivorous fish that prey intensely on them. Predators are excluded from upstream sites by waterfall barriers, but guppies have managed to colonize upstream environments, giving rise to low-predation sites at

higher elevations. Here guppies co-occur only with minor predators that prey primarily on juveniles (J. Endler, 1980; 1995). Although other environmental factors also differ between high- and low-predation sites (Grether *et al.*, 2001; Reznick *et al.*, 2001; e.g. Zandonà *et al.*, 2011; Fitzpatrick *et al.*, 2014), predation pressure appears to be the major driver of adaptive divergence in this system. As with life-history (Torres-Dowdall *et al.*, 2012), morphology (Torres-Dowdall *et al.*, 2012; Fischer *et al.*, 2013; Ruell *et al.*, 2013; Handelsman *et al.*, 2014), and physiology (Handelsman *et al.*, 2013; Fischer *et al.*, 2014), behavioral traits are known to be influenced by both genetic (Seghers, 1974; Breden *et al.*, 1987; Magurran & Seghers, 1991) and environmental (Abrahams & Dill, 1989; Magurran & Seghers, 1990; Houde, 1997; Huizinga *et al.*, 2009; e.g. Torres-Dowdall *et al.*, 2012) factors.

Here, we examine genetic and environmental influences on a suite of behavioral traits in guppies to test whether (1) divergence between populations is constrained along the major axis of variation in correlated traits, and (2) plastic changes in covariance structure predict divergence between populations. We first examine differences in single behaviors based on evolutionary history with predators and lifetime exposure to predator cues. We then characterize the influence of these same factors on covariance structure to address whether trait correlations are flexible or constrained in novel environments.

Methods

Fish collection and rearing

We collected fish from the Aripo high-predation locality (HP) and the adjacent Naranjo low-predation (LP) locality in 2012 (Gilliam *et al.*, 1993). We established 20 – 25 unique family

lines from wild-caught gravid females captured from each population. First-generation lab-born fish from each wild-caught female were separated by sex and kept in isolated tanks under identical conditions. First-generation fish were then uniquely crossed (i.e. only a single male and female from each family were used, each partnered with one unrelated first-generation fish) to generate the second generation of lab-born fish used in this study. This breeding design maintains the genetic variation of the original wild-caught females while minimizing environmental and maternal effects, such that differences observed between populations reared in a common lab environment presumably reflect genetic differences (see details in Reznick and Bryga, 1987). At birth, we split second-generation siblings into rearing environments with (pred+) or without (pred-) predator chemical cues (as in Torres-Dowdall *et al.*, 2012), and they remained in these treatments until the completion of the experiment. In the pred- treatment, fish were housed in tanks in a recirculating water system containing only conditioned water (i.e. sterilized and carbon-filtered tap water that was treated to have a pH, hardness, temperature, and chemistry similar to natural streams). In the pred+ treatment, a natural predator, the pike cichlid *Crenicichla frenata*, was housed in the sump tank of the recirculating system and fed live guppies daily. Previous work demonstrates that guppies show a range of plastic responses to the presence of predator chemical cues (Nordell, 1998; Dzikowski *et al.*, 2004; Gosline & Rodd, 2008; Torres-Dowdall *et al.*, 2012; Ruell *et al.*, 2013; Fischer *et al.*, 2014), and this design allows us to discern developmental effects of predator cues from genetic effects (Fig. 2.1).

All guppies were individually housed in 1.5 liter tanks on a 12:12 hour light cycle (lights on 7:00am to 7:00pm) at Colorado State University. Fish were fed measured amounts of Tetramin™ tropical fish flake paste and hatched *Artemia* cysts on an alternating basis once a day

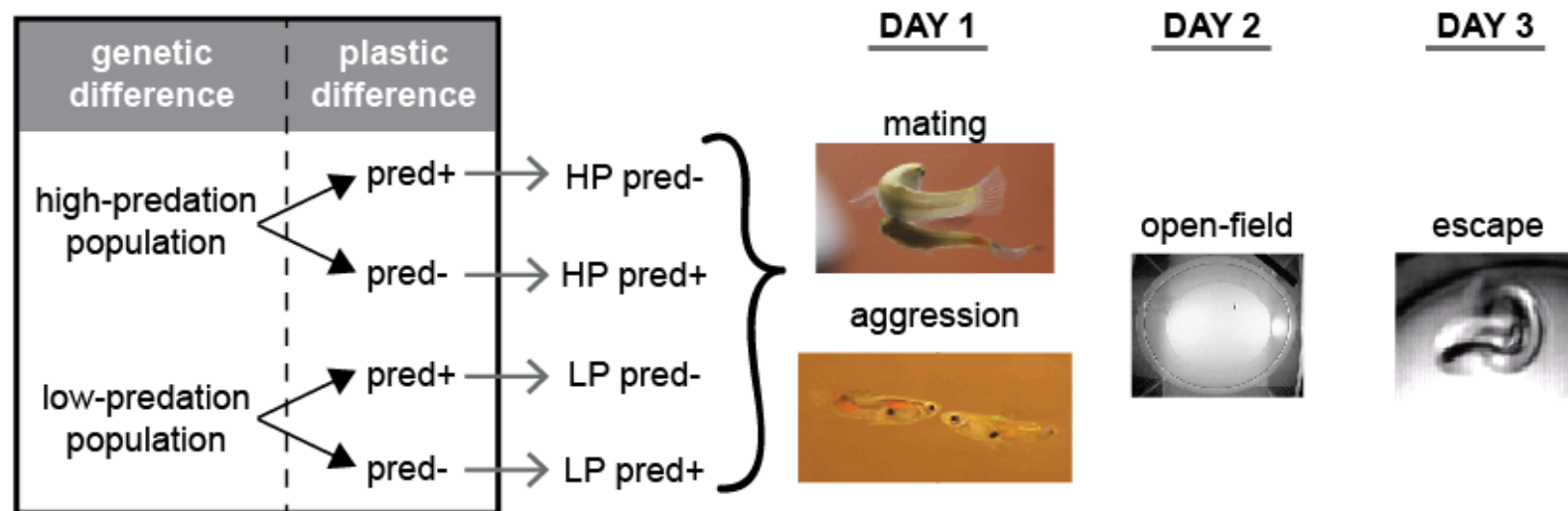


Figure 2.1. Overview of experimental design. Our breeding design allows us to discern genetic differences (contrast between populations in the same environment) from developmental plasticity (contrast between fish from the same population in different rearing conditions). We collected behavioral data for mature males in four contexts on three subsequent days. Mating and aggression behavior on day 1, open-field behavior on day 2, and escape behavior on day 3.

between 8:00am and 10:00am. Food levels were adjusted each week following previous protocols based on age and size of fish (Reznick, 1982; Reznick *et al.*, 2004). We used only mature males in this study because the courtship and aggression behaviors we were interested in are exhibited only by males. To ensure that we captured the range of genetic and behavioral variation present in the population, focal fish used for behavioral assays were evenly distributed among families. All experimental methods were approved by the Colorado State University Animal Care and Use Committee (Approval #12-3818A).

Behavior

We conducted four behavioral assays: mating, aggression, open-field, and escape. For a given individual, behavioral assays were conducted on three subsequent days; mating and aggression on the first day, open-field on the second day, and escape on the third day. Figure 2.1 presents an overview of this experimental design. We conducted behavioral experiments in the same manner for each fish in order to facilitate comparison of both group and individual differences. Fish were run together in balanced groups of four fish per week, with a representative from each population and rearing environment whenever possible and representatives from each population when not. This allowed us to control for random differences between weeks, without confounding these effects with population and/or rearing effects. All behavioral assays were run in water without predator cues as we were interested in developmental rather than acute environmental effects of predator cues. We collected water-borne hormone samples from all individuals during the week prior to behavioral data collection, and these findings are reported elsewhere. Sample sizes varied among groups due to differences in survival and the availability of a greater number of pred- fish (HP pred-: n=39; HP pred+: n=14; LP pred-: n=34; LP pred+: n=15).

Mating

We assessed mating behavior in one-on-one trials between a single male and a single female. We used virgin females to control for differences in females' reproductive status and matched males and females from the same population and rearing environment for these trials. To minimize differences in male mating behavior related to experience, we gave all males 36 hours of experience with a non-virgin female two days prior to the trial. Each focal male experienced a single trial lasting 30 minutes. At the start of the trial, the focal male and a virgin female were simultaneously added to a 9.4 liter experimental tank. The experimental tank was lit from above and placed behind a screen, such that fish could not see the observers. We gave each pair 15 minutes acclimation time followed by 15 minutes of behavioral observations. During the trial we recorded nine behaviors: the number of overt courtship displays (sigmoid displays), the duration of each courtship display, the number of sneaky copulation attempts (when males attempt to inseminate females), the number of gonopodial swings, the number of aggressive physical contacts (biting, body slamming, tail slapping), and the number of posturing incidents (when fish line up 'nose-to-nose'). We counted behaviors only when performed by the focal male. We recorded all behaviors using JWatcher software (JWatcher 1.0). All trials were watched live by two independent observers to account for inter-observer variability. We calculated the intra-class correlation (ICC) to examine variability among observers (Hallgren, 2012), and found the ICC for all behaviors measured in the mating context was 0.917 (95% CI: 0.892 – 0.937; $p < 0.0001$). We summed, rather than averaged, data from both observers to preserve the nature of the count data, and this summed value was used in all further analyses. To control for diel changes in mating behavior we conducted all mating trials in the morning between 9:00am and 11:00am when guppies have been shown to be most reproductively active

(reviewed in Houde, 1997). We replaced the water between each mating trial to eliminate the presence of chemical signals from fish in a previous trial. After completion of the trial, we removed the female and left the focal male undisturbed in the experimental tank until the aggression trial.

Aggression

We assessed aggression in one-on-three trials. Each focal male experienced a single trial lasting 10 minutes. At the start of the trial, three unfamiliar males were introduced into the 9.4 liter experimental tank previously occupied only by the focal male. Trials occurred on the same day and in the same tank in which mating trials had previously taken place. Focal males spent at least five and no more than six hours in the tank alone prior to aggression trials. Pilot tests demonstrated that allowing focal males to establish ‘residency’ in the tank, using unfamiliar non-focal fish, and beginning behavioral observations immediately on introduction of non-focal males increased the probability of aggressive displays among males, which occur only sporadically in guppies (Houde, 1997). The experimental tank was lit from above and placed behind a screen, such that fish could not see the observers. Data collection began immediately following introduction of the non-focal fish. During the trial we recorded seven behaviors: the number of lateral displays (similar to sigmoid displays, but between two males who are broad-side to one another), the duration of each lateral display, the number of gonopodial thrusts (similar to a copulation attempt, performed as an aggressive display when directed at other males), the number of gonopodial swings, the number of aggressive physical contacts (biting, body slamming, tail slapping), the number of chases, and the number of posturing incidents. We counted behaviors only when performed by the focal male. We again recorded all behaviors

using JWatcher software (JWatcher 1.0, USA) and all trials were watched live by two independent observers to control for inter-observer variability. The ICC for all behaviors measured in the aggression context was 0.795 (95% CI: 0.746 – 0.836; $p < 0.0001$). We again summed observations from the two observers and this summed value was used in all further analyses. To control for any unknown diel changes in aggression, we conducted all aggression trials between 2:00pm and 4:00pm. After completion of the trial, the focal male was returned to his home tank.

Open-field

An open-field test is generally considered to be a measure of anxiety, exploratory behavior, and activity (Hall, 1936). This test was initially designed for rodent models, but has been successfully applied in fish, including guppies (Warren & Callaghan, 1975; 1976; Budaev, 1997; Smith & Blumstein, 2010). Open-field assays across taxa follow the same basic design: animals are placed in an empty, circular arena, and overall activity as well as the amount of time spent at edges versus in the center of the arena is quantified. The interpretation is that animals that spend relatively more time in the center of the arena than at the edges are less anxious/fearful and more exploratory/bold.

We conducted open-field tests in a 40 cm diameter circular arena filled with water to a depth of 10 cm. The sides of the tank were opaque, while the bottom of the tank was clear. The arena was lit from above, with an opaque plastic barrier placed on top of the tank to evenly diffuse the light. We filmed behavior from below using a microvideo camera (SuperCircuits, Austin, TX, USA) connected to a computer running WinTV recording software (Hauppauge Computer Works, Hauppauge, NY, USA). We introduced males to the tank and immediately

began filming. Each trial lasted 10 minutes. Using JWatcher software (JWatcher 1.0, USA), we recorded the time the focal fish spent in the outer versus inner region of the tank, and the total time the focal fish spent moving versus stationary. We defined the outer region as the outer 7 cm of the circular tank (approximately four body lengths or less from the side of the tank). The inner region comprised the inner 26 cm diameter circle. To control for diel changes in activity, we conducted all open-field trials between 1:00pm and 3:00pm.

Escape

Visual and mechanical stimuli are commonly used to elicit fast-start responses in guppies and other fish (e.g. Ghalambor & Reznick, 2004; Preuss, 2006; Dadda *et al.*, 2010). However, we chose auditory stimuli here because stimulus intensity is directly correlated with response probability and thus easily controlled and manipulated (e.g. Neumeister *et al.*, 2010). We selected a stimulus amplitude that evoked intermediate response probabilities, allowing us to detect differences in response probability among groups (Fischer *et al.*, 2015). We used a 2 millisecond 200 Hz sine wave tone made in CoolEdit (Adobe Systems, San Jose, CA, USA) as an auditory stimulus.

We conducted escape trials in 10 cm diameter circular arenas with opaque sides. Four 10 cm arenas were housed inside a 60 cm tank, such that focal fish could be run in groups of four but stimuli could be delivered to them in an identical manner. The arena was lit from above, with an opaque plastic barrier placed on top of the tank to evenly diffuse the light. We filmed behavior from below using a Fastec troubleshooter HR high-speed camera (model TSHRMS, Fastec Imaging, San Diego, CA, USA) connected to a computer running Midas software (Xcitex, Woburn, MA, USA). We delivered auditory stimuli from an underwater speaker outside of the

small arenas, but inside the larger tank. The speaker was connected to an amplifier that was also connected to an LED light (RadioShack, Fort Worth, TX, USA) that could be seen in the video. We used the light in the video to determine stimulus onset down to the millisecond and quantify response latency. Each trial consisted of 20 auditory stimuli presented with variable inter-stimulus intervals to prevent fish from anticipating stimulus presentation. Intervals between stimuli in the startle stimulus train were randomized between 3 and 12 minutes, and the same stimulus train was used for all fish to facilitate comparisons across individuals and groups.

We allowed fish to acclimate for 15 minutes in the arena prior to the start of the trial. We recorded escape responses at 1,000 frames/second and subsequently analyzed all videos using the Midas software also used for recording. We scored escape responses as binary (startle or no startle), with the criteria that fish had to exhibit the characteristic c-startle escape response within 30 ms of stimulus presentation. When fish responded, we also recorded response latency and whether or not the fish was at the surface of the water column (i.e. if their escape response broke the water surface). We were interested in the position of the fish in the water column as guppies are known to change their position in the water column in response to predator cues (Torres-Dowdall *et al.*, 2012). We calculated response probability, minimum response latency, and proportion of responses at the surface for each fish. Escape trials were conducted between 1:00pm and 5:00pm. We immediately returned focal males to their home tank after the completion of the trial.

Statistical analysis

We tested the effects of genetic background and rearing environment on single behaviors within each context using generalized linear mixed model analyses. We modeled our data using a

negative binomial distribution appropriate for count data with an uneven variance distribution. We included population of origin (HP/LP), rearing environment (pred-/pred+) and their interaction as fixed effects. Because fish were run in groups of four per week, we included week as a random effect in all analyses. We tested for an effect of body size on behavior, but did not ultimately include this as a covariate as it was not a significant predictor in any of our analyses. Mixed models were run in SAS (SAS Statistical Software 9.4, SAS Institute).

Analyses of differences in correlations among behaviors required data with a Gaussian distribution, so we normalized our count data using a square-root transformation. We examined distributions of the data following transformation and excluded those behaviors that still did not follow an approximately normal distribution (average sigmoid duration, latency to feed, proportion of startles at the surface, startle latency). In addition, we standardized the data by centering values to the grand mean for each behavior and dividing them by the standard deviation. This standardization does not alter the relative values within a behavioral metric but controls for differences in measurement scale.

To visually examine relationships among behaviors within and among behavioral assays we calculated all pair-wise Pearson correlation coefficients. To test for differences in variance and covariance among behaviors, we conducted P-matrix comparisons. Matrices can vary in a diversity of characteristics, and we used multiple tests to examine complementary aspects of correlational structure (Roff *et al.*, 2012; Handelsman *et al.*, 2014). These comparisons allowed us to address whether and how matrices differed based on genetic background and rearing environment. We used the modified Mantel test to ask whether matrices were proportional (Goodnight & Schwartz, 1997), the jump-up approach of the Flury method to determine whether matrices were equal, proportional and/or shared principal components (Phillips & Arnold, 1999;

Roff & Mousseau, 2005), Bartlett's test to test for differences in overall variance among matrices (Goodnight & Schwartz, 1997), and the Jackknife-eigenvalue test to compare overall covariance structure among matrices (Kirkpatrick, 2009; Roff *et al.*, 2012). These matrix comparisons can only be conducted in a pair-wise fashion and so we ran four analyses to compare relevant pairs: We compared different populations in the same environment (HP pred- vs LP pred- and HP pred+ vs LP pred+) and rearing environments within the same population (HP pred- vs HP pred+ and LP pred- vs LP pred+). Taken together these four comparisons allowed us to understand the influence of genetic background and developmental plasticity on behavioral variance and covariance. P-matrix analyses were performed using custom scripts (Roff *et al.*, 2012) in R (R 3.1.2, The R Foundation for Statistical Computing).

Finally, we conducted between-group analyses (BGA) to test for genetic and rearing differences in multiple behaviors simultaneously. BGA is a multivariate discriminant approach in which group means are ordinated and individual samples are then projected onto orthogonal axes resulting from this ordination procedure. This allows one to apply ordination procedures – such as the principal component analysis used here – that cannot be directly applied to raw values. This approach is appropriate here as (1) it can be applied when the number of cases is relatively small compared to the number of variables, and (2) BGA is insensitive to differences in correlational structure among groups because group means, rather than values from individual fish, are used in ordination. We used mixed models to examine population and rearing differences in the eigenvalues for the principal components produced by BGA. We included population of origin (HP/LP), rearing environment (pred-/pred+) and their interaction as fixed effects. BGA analysis was performed using the *ade4* package (Thioulouse *et al.*, 1997) in R (R

3.1.2, The R Foundation for Statistical Computing) and mixed models were run in SAS (SAS Statistical Software 9.4, SAS Institute).

Results

Single behaviors

We found few differences in single behaviors based on genetic background, rearing environment, or their interaction. In the open-field assay, high-predation fish and fish reared with predator cues spent relatively more time in the center of the arena (population: $F_{1,70} = 14.05$, $p = 0.0004$; rearing: $F_{1,70} = 60.06$, $p = 0.0163$) and relatively less time moving (population: $F_{1,70} = 6.53$, $p = 0.0128$; rearing: $F_{1,70} = 17.64$, $p < 0.0001$) than their counterparts. The reduction in movement in fish reared with predators was more pronounced in the low-predation fish (population*rearing: $F_{1,70} = 10.34$, $p = 0.0020$). In escape behavior assays, the proportion of startle responses performed at the surface of the water column was greater in low-predation fish and fish reared with predator cues (population: $F_{1,61.18} = 5.23$, $p = 0.0256$; rearing: $F_{1,67.01} = 10.94$, $p = 0.0015$). There was also a marginally significant population by rearing interaction effect for startle probability (population*rearing: $F_{1,66.69} = 3.54$, $p = 0.0643$), as low-predation fish reared without predators were more likely to startle than low-predation fish reared with predators or high-predation fish from either rearing environment. Significant behavioral differences are depicted in Figure 2.2 and estimates for all behaviors are in Table 2.1.

Table 2.1. Average (s.e.) raw values for all behaviors recorded in each behavioral assay.					
		HP pred-	HP pred+	LP pred-	LP pred+
mating	sigmoid display	51.8 (6.08)	40.3 (7.88)	32.3 (5.82)	45.0 (9.09)
	ave display duration (s)	5.1 (0.34)	5.4 (0.59)	5.2 (0.33)	5.03 (0.65)
	sneaky copulation	14.8 (1.94)	19.9 (5.8)	14.6 (2.27)	17.8 (3.7)
	gonopodial swing	39.8 (3.76)	40.9 (5.38)	27.9 (3.53)	33.8 (5.65)
	contact	8.3 (1.95)	8.3 (4.99)	6.2 (1.51)	7.0 (1.66)
	posturing				
aggression	lateral display	13.0 (2.60)	6.6 (2.81)	12.6 (2.60)	13.2 (3.28)
	ave display duration (s)	7.2 (1.99)	3.8 (0.61)	4.6 (0.38)	4.4 (0.53)
	gonopodial thrust	22.5 (2.95)	24.7 (3.84)	21.0 (3.58)	22.2 (5.28)
	gonopodial swing	26.8 (2.34)	25.2 (3.18)	21.5 (2.37)	25.4 (4.06)
	contact	11.7 (2.50)	7.6 (1.31)	15.8 (3.91)	6.54 (1.33)
	chase	8.5 (1.53)	9.6 (1.84)	8.8 (1.52)	15.6 (8.23)
	posturing				
	latency to feed (s)	165.16 (25.5)	176.8 (40.0)	178.4 (28.5)	182.8 (39.2)
open-field	time in center (s)	207.9 (16.6)	262.4 (14.7)	126.6 (15.6)	179.8 (34.6)
	time moving (s)	527.2 (12.8)	506.1 (19.1)	540.7 (9.5)	390.2 (47.0)
escape	startle probability	0.325 (0.041)	0.328 (0.055)	0.464 (0.042)	0.335 (0.054)
	prop startles at surface	0.216 (0.046)	0.525 (0.091)	0.408 (0.056)	0.685 (0.076)
	min latency (ms)	6.5 (0.65)	4.7 (0.40)	4.5 (0.26)	4.8 (0.30)

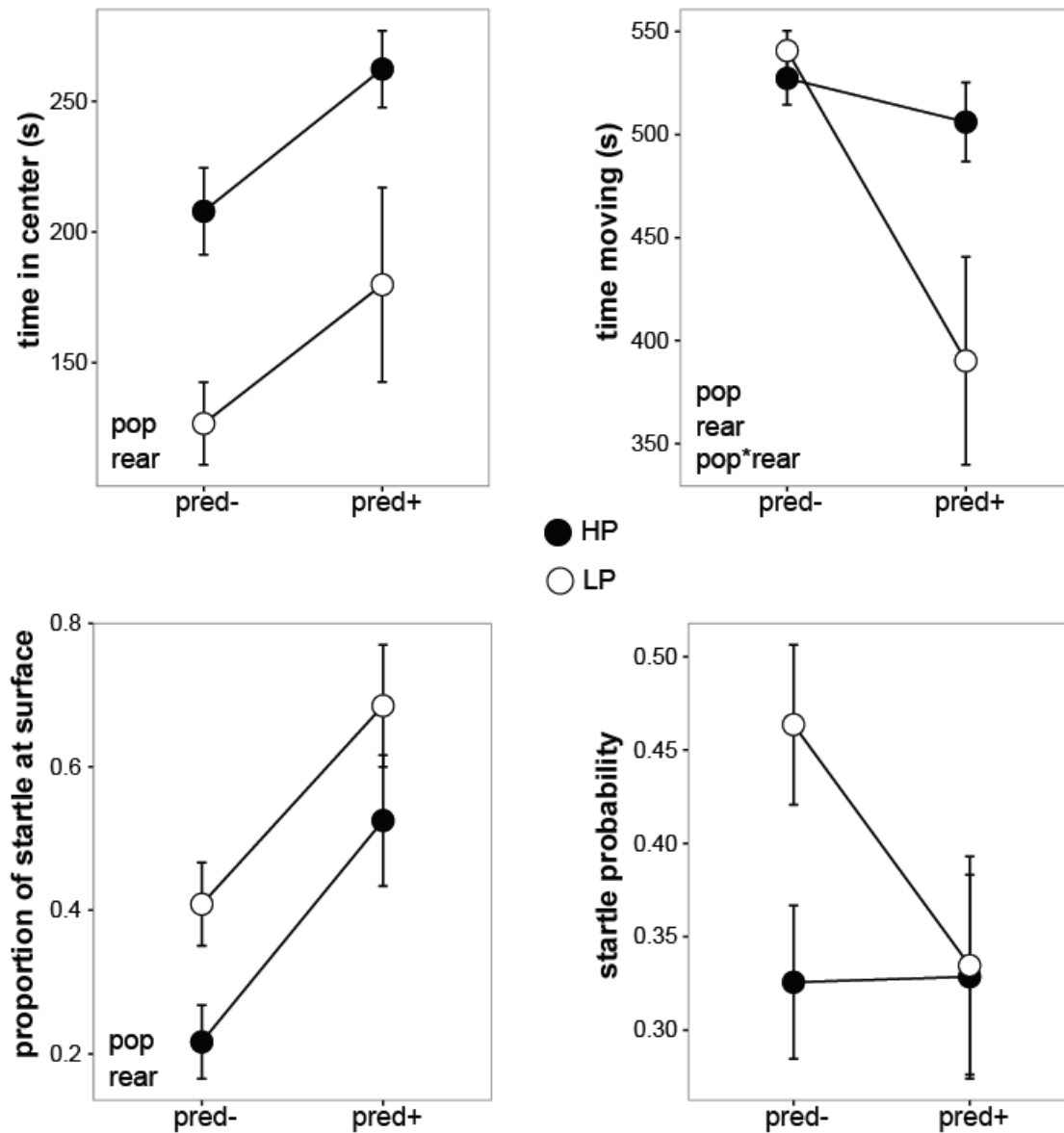


Figure 2.2. Genetic and rearing influences on behavior. Plots are shown in a traditional reaction norm format with rearing environment on the x-axis. High-predation fish and those reared with predators spent more time in the center, but less total time moving, during open-field trials. The reduction in total movement time in the open-field in response to rearing with predators was more pronounced in the low-predation population. Low-predation fish and fish reared with predator cues performed more startles at the surface of the water column. The interaction between population of origin and rearing environment had a marginally significant effect on startle response probability. Significant effects of population of origin (pop), rearing environment (rear) and their interaction (pop*rear) are shown in the bottom left corner of each plot. HP = high-predation (black); LP = low-predation (white), pred- = reared without predator cues; pred+ = reared with predator cues.

Behavioral correlations

All behaviors measured in the mating assay were highly correlated with one another (Fig. 2.3; average Pearson correlation = 0.52, range = 0.30 – 0.77), and similarly in the aggression assay (Fig. 2.3; average Pearson correlation = 0.34, range = 0.06 – 0.59). In the open-field assay, time in the center of the arena and time moving were not correlated (Pearson correlation = 0.05) indicating that the time fish spent in the center of the arena did not increase as a byproduct of increased movement. In addition to correlations within assays, we observed that behaviors in the mating and aggressive assays were more strongly correlated with one another than with behaviors performed in the open-field or escape assays. In general, we found overwhelmingly positive correlations among behaviors. Only 5/66 correlations were in the negative direction and of these four were weaker than -0.05 (Fig. 2.3).

In addition to these general patterns, we found variation in correlational structure among groups (Fig. 2.4 and Fig. S1.1 in Appendix 1). We used four methods to compare matrix structure among populations and rearing environments. We found that genetic background and rearing environment altered the overall variance (Table 2.2; Bartlett's test) and correlational structure (Table 2.2; Jackknife eigenvalue test) of the matrices. In addition, differences induced by rearing environment altered the 'shape' of the matrices such that they were no longer proportional (Table 2.2; modified Mantel test). By examining the sum of all estimated eigenvalues (the eigensum) we obtained an estimate of the total phenotypic variance in each group (Kirkpatrick, 2009). From this we saw that pred- fish were more phenotypically variable than pred+ fish in the high-predation population (HP pred- eigensum=10.99, se=1.05; HP pred+ eigensum=10.24, se=2.03), but this pattern was reversed in the low-predation population (LP

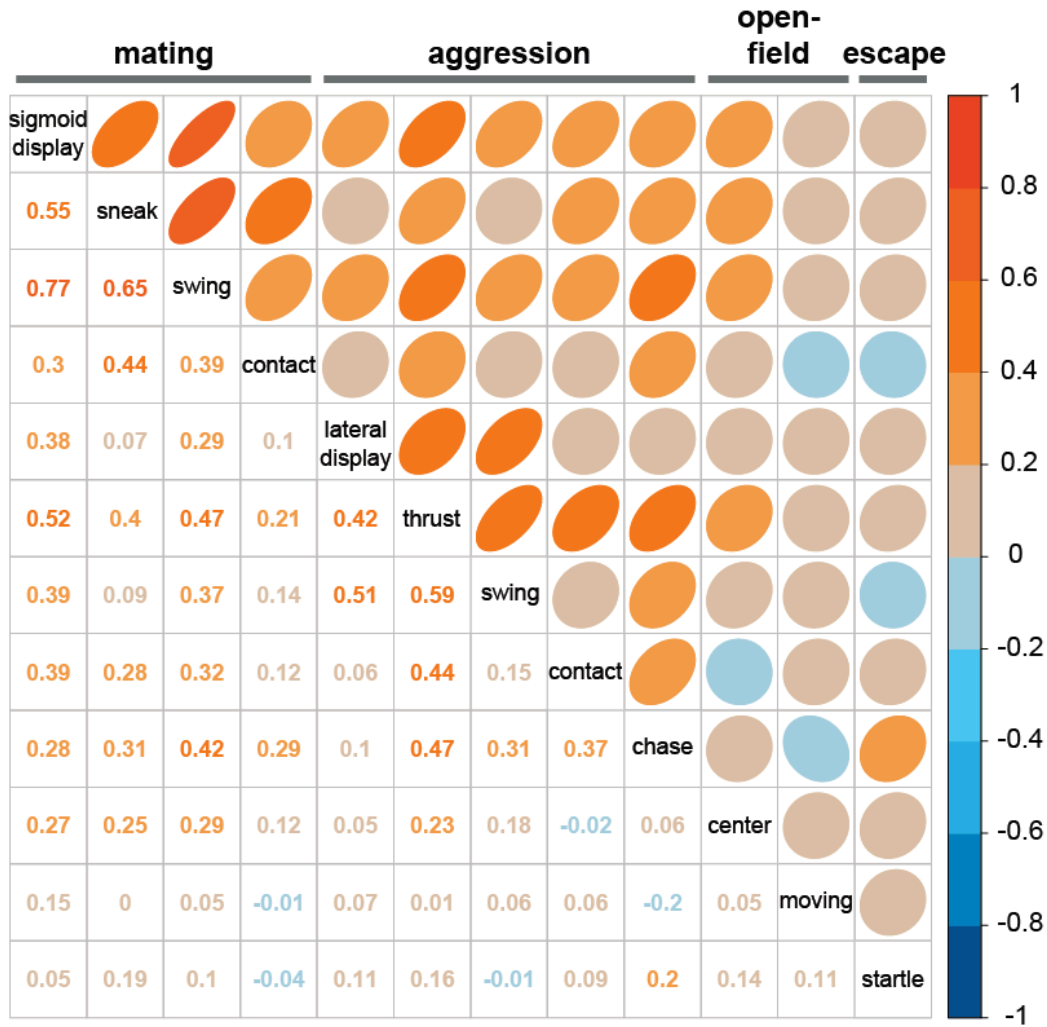


Figure 2.3. Mating and aggression behaviors, but not open-field and escape behaviors, are correlated within and among behavioral contexts. Behaviors are listed along the diagonal and behavioral contexts in which they were measured are along the top of the plot. Correlations are graphically depicted in the upper half of the plot. Correlation strength is indicated by shape (stronger correlations are more oblong) and strength and direction - from +1 to -1 - are indicated by color and shape (red, right-leaning = positive; blue, left-leaning = negative). Pearson correlations are listed in the lower half of the plot. Mating and aggressive behaviors are correlated with one another both within and between contexts (darker, oblong ellipses), but not with open-field or escape behaviors (lighter, circular ellipses). Correlations are overwhelmingly positive (orange, right-leaning ellipses).

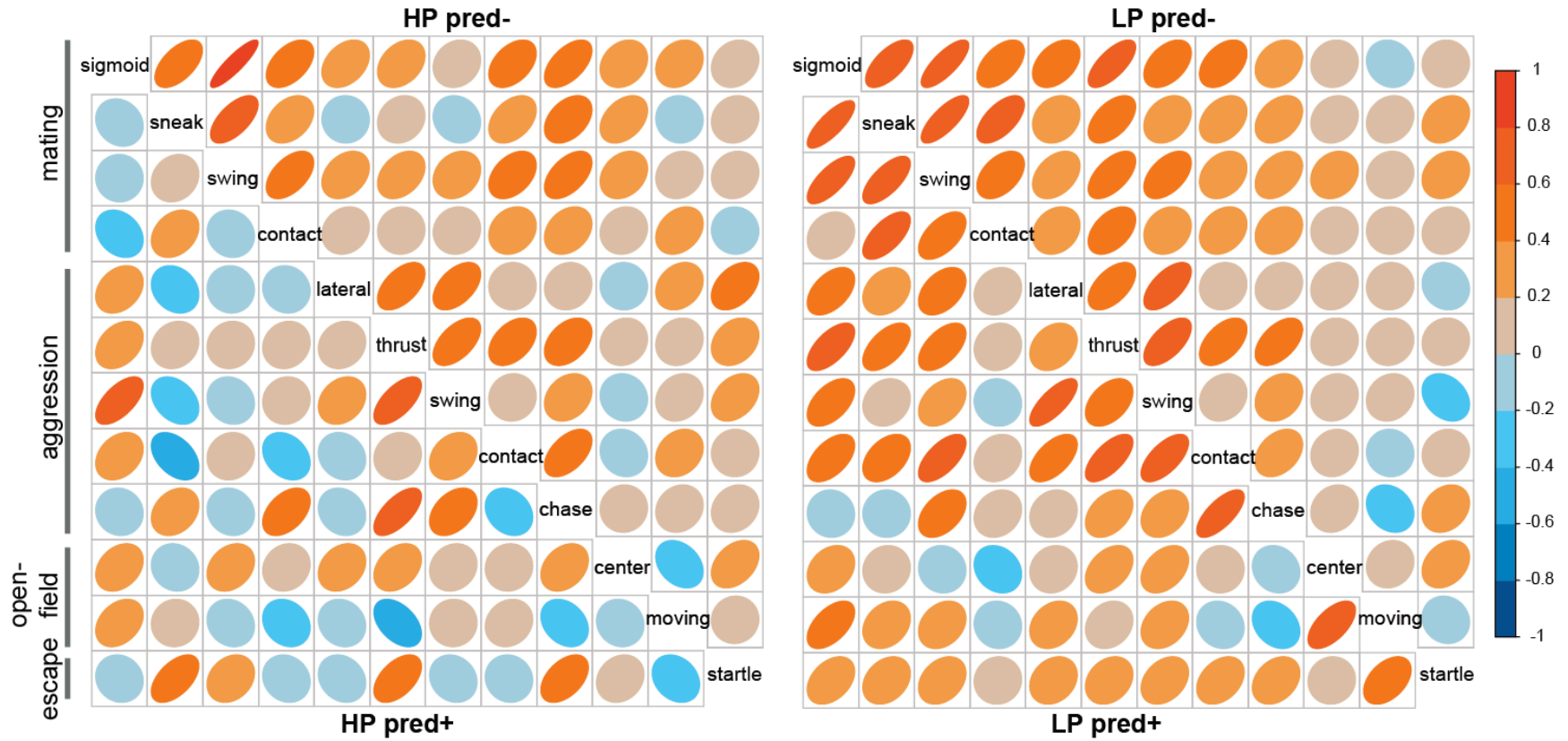


Figure 2.4. Correlational structure varies among groups. Individual behaviors are along the diagonal and associated behavioral contexts along the right side of the plot. Correlation strength is indicated by shape (stronger correlations are more oblong) and strength and direction - from +1 to -1 - are indicated by color and shape (red, right-leaning = positive; blue, left-leaning = negative). Patterns for the high-predation population (HP) are on the left and for low-predation population (LP) are on the right. The top half of the plots show correlations in rearing environments without predators (pred-) and the bottom half show correlational structure in rearing environments with predators (pred+). Correlation values are in Figure S1.1 in Appendix 1.

Table 2.2. Summary of results for P-matrix comparisons.

	Flury hierarchy			Modified Mantel test		Bartlett's test			Jackknife-eigenvalue test		
	equal (p)	prop* (p)	CPC** (p)	Obs. M	p	χ^2	df	p	Wilk's λ	df	p
HP pred- vs LP pred-	0.247	0.261	0.187	0.779	0.536	96.33	78	0.0788	0.657	12, 59	0.0084
HP pred+ vs LP pred+	0.180	0.173	0.174	0.337	0.117	125.6	78	0.0005	0.137	12,14	0.0004
HP pred- vs HP pred+	0.514	0.314	0.324	0.505	0.066	107.3	78	0.0154	0.436	12,40	0.0002
LP pred- vs LP pred+	0.262	0.130	0.084	0.429	0.032	145.2	78	<.0001	0.301	12,33	<.0001

* proportional matrices

** common principal components

pred- eigensum=10.60, se=0.99; LP pred+ eigensum=15.81, se=3.52). In other words, rearing in the non-native environment increased phenotypic variance.

To examine population- and rearing-induced shifts in collections of behaviors, we used multivariate between-group principal components analysis. Three major axes explained 95% of the variation in behavior. PC1 explained 55% of the variation in our suite of behaviors and had strong positive loadings (>0.25) for most behaviors, especially those in the mating and aggressive contexts (Table 2.3). This pattern was unsurprising given that we found strong, positive correlations among mating and aggressive behaviors. PC2 explained 21% of the variation and had strong positive loadings for several behaviors, notably those associated with the open-field context (Table 2.3). PC3 explained an additional 19% of the variation and differentiated some behaviors within mating and aggressive contexts (e.g. negative loading for sigmoid displays and positive loading for sneaky copulation attempts) as well as having a strong positive loading for escape behavior. Fish reared with predators had higher PC1 values ($F_{1,95}=26.29$, $p<0.0001$) and there was a significant population of origin by rearing environment interaction on PC2 ($F_{1,95}=7.96$, $p=0.0058$), as rearing with predators increased values in high-predation fish, but decreased values in low-predation fish (Fig. 2.5). While PC3 explained 19% of overall behavioral variance, we did not observe any differences among populations or rearing environments, indicating that this variation was not group dependent. Plots of PC eigenvalues with significant group effects corroborate conclusions from matrix analyses indicating that rearing in the non-native environment increased phenotypic variance along the dominant axis of variation (Fig. 2.5). Furthermore, while environmental effects (i.e. comparison between pred- and pred+ fish from different populations) did not shift groups in the direction of the dominant eigenvector, genetic divergence (i.e. comparison between high- and low-predation fish in the

Table 2.3. Principal component (PC) loadings and variance explained.				
		PC1	PC2	PC3
mating	sigmoid display	0.244	0.040	- 0.298
	sneaky copulation	0.305	0.024	0.343
	gonopodial swing	0.348	0.215	0.059
	contact	0.246	0.112	0.107
aggression	lateral display	0.028	- 0.391	- 0.351
	gonopodial thrust	0.276	0.112	0.297
	gonopodial swing	0.355	0.022	- 0.013
	contact	- 0.024	0.049	0.332
	chase	0.246	- 0.133	0.369
open-field	time in center	0.385	0.488	- 0.277
	time moving	- 0.442	0.715	0.012
escape	startle probability	- 0.237	-0.065	0.493
variance explained		55%	21%	19%

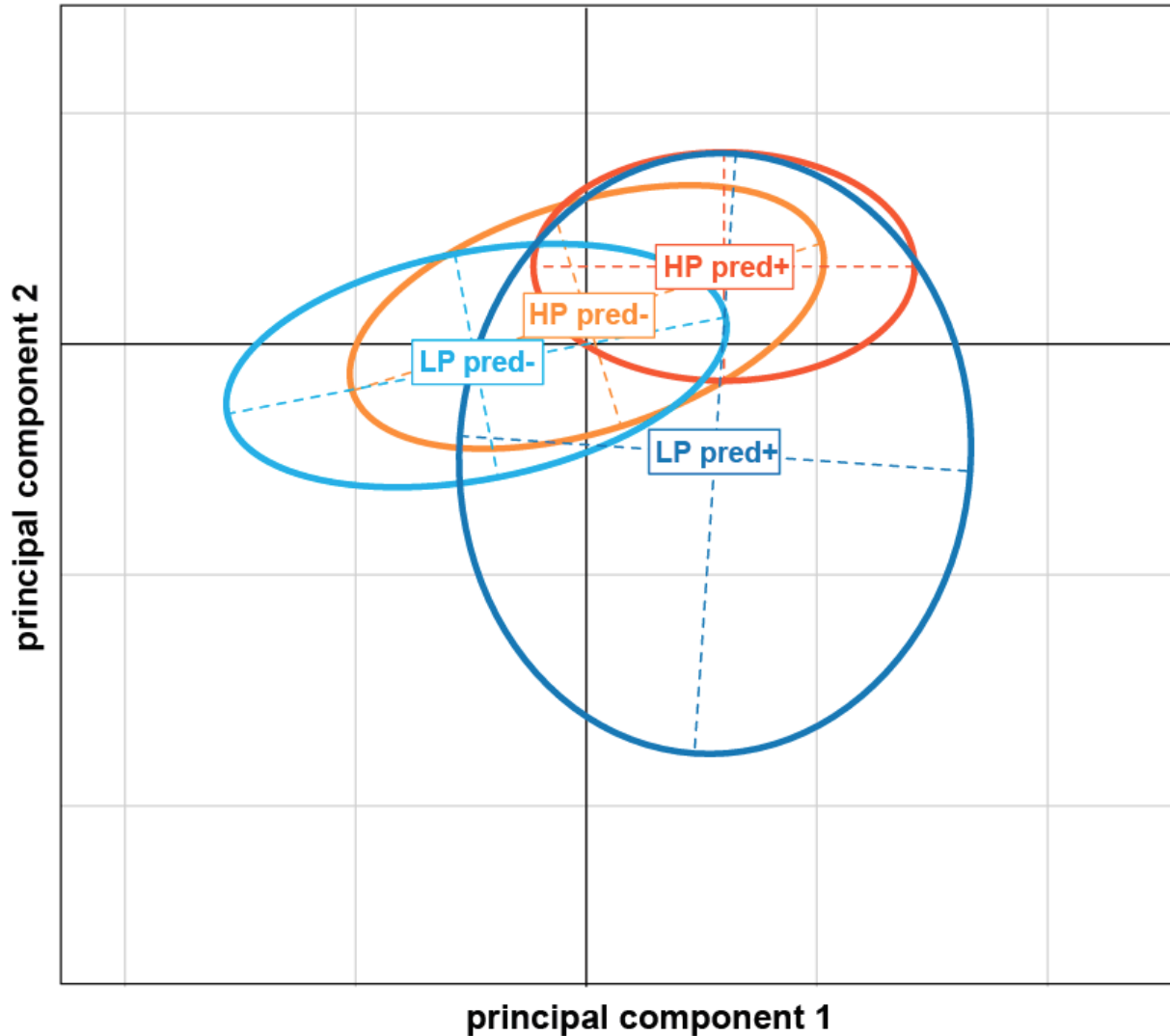


Figure 2.5. Genetic and environmental differences in multivariate trait analyses. Plots of the relationship between principal component 1 (55% of variance) and principal component 2 (21% of variance) from BGA analysis. Ellipses encompass 95% of the data for each group. Differences in ellipse size and shape indicate differences in overall behavioral variance (size) and covariance (shape) structure. Principal component 1 (x-axis) separates groups based on rearing environmental differences, while principal component 2 (y-axis) separates populations with rearing differences based on population of origin. In addition, there is a population by rearing environment interaction in principal component 2, as rearing with predators increases values in high-predation fish, but decreases values in low-predation fish. HP = high-predation (orange); LP = low-predation (blue), pred- = reared without predator cues (lighter colors); pred+ = reared with predator cues (darker colors).

pred- environment) did occur in the direction of the dominant eigenvector, i.e. along phenotypic lines of least resistance (*sensu* Schluter, 1996).

Discussion

The pattern of genetic variance and covariance among traits is thought to impose constraints on responses to selection. Yet, the degree to which G- and P-matrices impose constraints on evolutionary trajectories in novel environments depends on their stability. We found that developmental plasticity altered patterns of behavioral variance and covariance in guppies. We interpret our data as representing responses to novel environments at two timescales: evolutionary (i.e. genetic) adaptation of guppies to low-predation environments, and developmentally plastic (i.e. environmentally mediated) responses to rearing environments distinct from the native environments to which populations are adapted. Rearing with predator cues decreased overall variance in collections of correlated behaviors in high-predation fish, but increased overall variance in low-predation fish. In addition, rearing in the non-native environment altered correlational structure, shifting the major axis of behavioral variation in the direction observed in native fish. Taken together, our findings provide evidence for developmental and evolutionary flexibility in trait correlations. We propose that divergence in a novel environment – rather than being constrained by genetic trait correlations – may in fact be shaped by plastic changes in covariance structure.

Differences in single behaviors

Given previous work on behavioral traits in guppies (reviewed in Houde, 1997; Magurran, 2005), we expected to find behavioral differences based on population of origin and rearing environment. Counter to our prediction, we found few significant group differences in single behavioral metrics, with a notable absence of differences in any social behaviors. Social behaviors in guppies are highly sensitive to immediate environmental cues including light levels (J. A. Endler, 1987), social group structure (Rodd & Sokolowski, 1995), acute predator presence (Elvidge *et al.*, 2014), and predator type (Botham *et al.*, 2008). Thus, differences in immediate environmental context – rather than genetic or developmental differences – may dominate variation in these behaviors, and thus group differences may become apparent under environmental conditions different from those we considered (Brown *et al.*, 2010). We thus limit our inference that these populations did not differ in social behaviors using our behavioral assays and breeding design.

In the open-field context, high-predation fish and fish reared with predators spent relatively more time in the center of the arena, but relatively less time moving. Studies in a variety of species document genetic (Candland & Nagy, 1969; Harrington, 1972; Rebouças & Schmidek, 1997; Schmitt & Hiemke, 1998; Dingemanse *et al.*, 2002) and environmental (Crabbe, 1986; Rebouças & Schmidek, 1997; Schmitt & Hiemke, 1998; Archard *et al.*, 2012) differences (including predation; Brown *et al.*, 2007; Archard *et al.*, 2012) in open-field behavior and demonstrates that this variation can be selected upon (DeFries *et al.*, 1978; Wong *et al.*, 2012). Although population differences in open-field behavior have not previously been examined in guppies, repeated measures of guppies from the same population found that overall movement decreased as time in the center increased (Warren & Callaghan, 1976) suggesting a

negative relationship between these metrics. Warren and Callaghan (1976) interpreted increased time in the center with repeated sampling as indicating a reduction in fear responses and an increase in exploratory behavior. Extending this reasoning to the population and rearing differences we observe here, we conclude that high-predation fish and those reared with predators are less fearful and more exploratory. These interpretations are consistent with observations that, while high-predation guppies and guppies exposed to predator cues modify their behavior to reduce conspicuousness (J. A. Endler, 1987; Magurran & Seghers, 1990; Fischer *et al.*, 2015), they generally exhibit more exploratory, more ‘bold’ behaviors (Magurran & Seghers, 1994; Harris *et al.*, 2010; Elvidge *et al.*, 2014).

In addition to differences in open-field behavior, we observed differences in water column use during escape behavior. We found that fish reared with predator cues were more likely to startle at the surface of the water column. Given that spending time at the surface of the water column is tactic to avoid predators attacking from below (Torres-Dowdall *et al.*, 2012), our observation that low-predation fish spent more time at the surface again supports the idea that these populations exhibit more fearful behavior (Magurran & Seghers, 1994; Harris *et al.*, 2010; Elvidge *et al.*, 2014). In sum, the differences we observed in single behaviors are consistent with previous data and lend support to the idea that high-predation guppies and those reared with predator cues exhibit more exploratory, less fearful behavioral types. This combination of behavioral traits may help fish survive in a high-risk environment where guppies must balance trade-offs between predator avoidance and profitable behaviors, such as mating and feeding (reviewed in Magurran, 2005).

Social behavioral correlations

When we examined relationships among behaviors, a number of patterns emerged. First, behaviors performed in the mating and aggression assays were correlated within and across assays. In contrast, open-field and escape behaviors were not correlated with mating and aggression or with one another. Social behaviors – including mating and aggression – are known to share underlying neural (S. W. Newman, 1999; e.g. O'Connell & Hofmann, 2011) and physiological (e.g. E. D. Ketterson & Nolan, 1999; McGlothlin & E. Ketterson, 2008) substrates, and correlations among mating and courtship behaviors may thus arise from reliance on shared mechanisms. Second, for those behaviors that were correlated, we found overwhelmingly positive correlations, implying that certain fish were more behaviorally active than others. Thus, fish that performed more overt courtship and sneaky copulation attempts in the mating assay also interacted more with other males in the aggression assay. Importantly, this social behavioral activity appeared to be independent of generalized physical activity, and perhaps more reflective of social behavioral motivation than a consequence of overall differences in activity or energy. These observations are concordant with predictions that exposure to novel environments (i.e. adaptation to or rearing in a non-native environment) should produce primarily positive correlations among traits (Service & Rose, 1985; Parsons & Robinson, 2006), thereby influencing responses to selection (Merilä & Björklund, 2004).

Despite extensive recent interest in behavioral correlations and the intuitive link between mating and aggression, we found surprisingly few studies relating differences in mating or courtship behavior to differences in aggression. Studies that did examine both aggression and mating/courtship behavior fell primarily into two categories. First, those using an immediate choice paradigm, where trade-offs can arise due to time budgeting (Ballin, 1973; e.g. Farr, 1980),

and second, studies linking aggression to reproductive fitness. In the latter category, negative relationships between aggression and reproductive fitness were primarily the product of aggressive spillover, giving rise to aggressive acts misdirected at mates and – more frequently – offspring (Johnson & Sih, 2005; e.g. Duckworth, 2006). Among the few studies that did relate differences in mating or courtship to differences in aggression, some found positive correlations (Rowland, 1984; Reaney & Backwell, 2007; Snekser *et al.*, 2008), while others found no correlation (Houde, 1988; Wilson *et al.*, 2009). In sum, while correlations between mating and aggression seem intuitive, empirical evidence is somewhat equivocal. In guppies, we observed overall positive correlations between these behaviors, however, given the overall flexibility we observe in trait correlations in this species (see below) and the lack of consensus in the literature, we emphasize the importance of considering potential species- and context-specific influences on these relationships when attempting to predict the evolutionary consequences of correlations among traits.

Genetic and environmental influences on behavioral variance and covariance

We found significant population and rearing differences in correlational structure among behaviors. Overall behavioral variance and behavioral covariance structure differed among groups, with rearing-induced differences dependent on genetic background. These differences in correlational structure among groups influence our understanding of past evolutionary events and have important implications for future evolutionary trajectories. The potential for environmental influences to impact behavioral variation and covariation has been considered in the context of environmental stressors in general, and predation pressure in particular (Bell and Sih 2007; Dingemanse *et al.* 2009; Dingemanse *et al.* 2012). Predictions are contrasting, with arguments

for both the idea that stressors should increase (West-Eberhard 2003; Badyaev 2005) and decrease (Schlichting, 1989; Pigliucci, 2004; Luttbeg & Sih, 2010) behavioral variation. We found that high-predation fish adapted to environments with predators exhibited decreased behavioral variance when reared with predators as compared to high-predation fish reared without predators. In contrast, low-predation fish reared with predators exhibited increased behavioral variance as compared to low-predation fish reared without predators. In other words, both high- and low-predation fish exhibited reduced variance when reared under native environmental conditions (i.e. environments more similar to those they are adapted to in the wild). These results are consistent with the hypothesis that stabilizing selection reduces variance within the native rearing environment, and that novel environments (i.e. environments where selection has not had an opportunity to act) result in the expression of increased cryptic genetic variation (Gibson & Dworkin, 2004; Schlichting, 2008; McGuigan & Sgrò, 2009; McGuigan *et al.*, 2010). Our results also emphasize the importance of considering evolutionary history when interpreting environmentally induced differences, because novel – rather than stressful – environments are likely the most important determinants of variance (Schlichting, 2008) as, overtime, populations can adapt, even to stressful environmental conditions.

Along with an increase in behavioral variance, fish reared in non-native environments displayed weaker covariance among behaviors. Weaker covariance among traits could result from the release of cryptic genetic variation described above, and may allow selection to act on behaviors more independently, thereby minimizing trade-offs (McGuigan, 2006). Moreover, if traits can be fairly readily coupled and decoupled from one another, then correlations observed in one population or environment will not predict evolutionary trajectories (Sinn *et al.*, 2009; Smith & Blumstein, 2010). For example, under acute predation risk, a mating strategy trade-off exists

between sigmoid displays and sneaky copulations, as the former lead to higher reproductive success but also make males more conspicuous to predators (reviewed in Magurran, 2005). In contrast, in low-predation environments, it may be favorable to maximize mating effort by performing both sigmoid displays and sneaky matings. Given this trade-off, there could be selection against a positive correlation between sigmoid displays and sneaky copulations in environments with predators, and a lack of selection against, or even selection for, a positive correlation between these behaviors in predator-free environments. Indeed, we find that the correlation between sigmoid displays and sneaky matings is non-significant in high-predation fish reared with predators, but positive in all other groups (Fig. 2.4). Additional work is necessary to test the adaptive value of differential trait correlations explicitly; however, our findings here demonstrate that covariance structure is flexible and this flexibility in trait correlations influences evolutionary trajectories.

Although certain behavioral correlations may only be favorable under specific environmental conditions, the overall flexibility and variability we observe in covariance structure has important evolutionary implications in and of itself. Patterns in the ancestral environment will not predict evolutionary constraints if environmental shifts change trait variance and covariance. We highlight two ways in which developmental plasticity in trait correlations may shape the force of selection and potentially shape adaptation (Fig. 2.6). First, when high-predation fish were reared in non-native, predator-free environments the major axis of phenotypic variation was shifted in line with that of low-predation fish reared in predator free environments. This pattern replicates the evolutionary scenario in the wild, in which high-predation fish have repeatedly colonized and adapted to low-predation environments, and

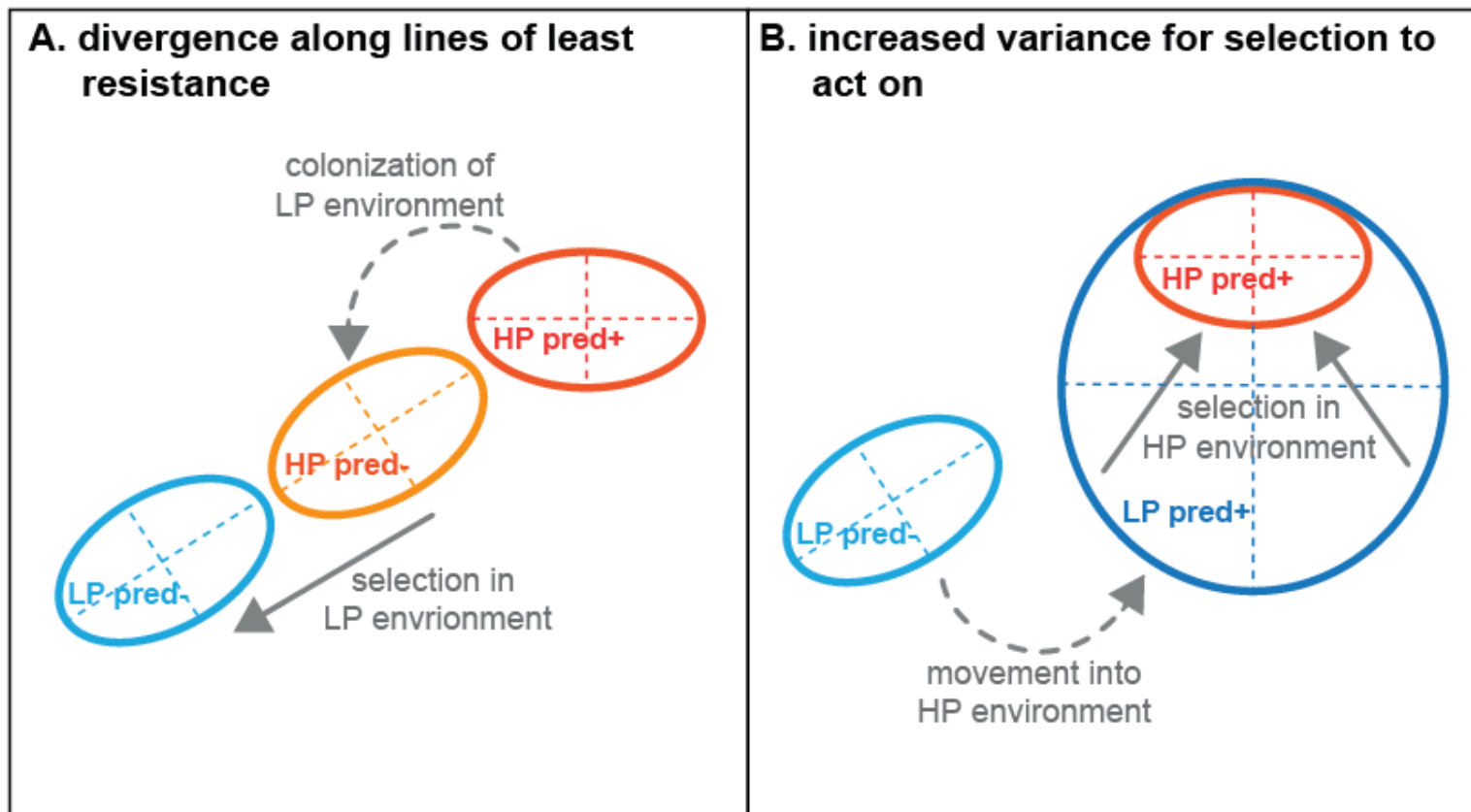


Figure 2.6. Conceptual summary of how developmental plasticity in trait correlations may facilitate evolution. (A) In high-predation guppies reared in non-native, predator-free environments (i.e. mimicking colonization of low-predation environments) the major axis of phenotypic variation is shifted in line with that of low-predation populations adapted to this environment, facilitating genetic divergence along lines of least resistance. (B) In low-predation fish reared in environments with predators (i.e. mimicking fish washed downstream) phenotypic variance is greatly increased, generating variation for selection to act upon to facilitate adaptation. The increased variance in low-predation fish completely encompasses the range of behavioral variance exhibited by high-predation fish adapted to this environment and the major axis of phenotypic variation is also shifted in line with that of the high-predation fish reared with predators. Grey arrows indicate plastic (dashed lines) and evolutionary (solid lines) directions of change. HP = high-predation (orange), LP = low-predation (blue), pred+ = reared with predators (darker colors), pred- = reared without predators (lighter colors)

suggests that evolution has occurred along environmentally contingent phenotypic lines of least resistance (Fig. 2.6A; Schluter, 1996).

Second, while changes in trait variance and covariance induced by a novel environment may not initially be adaptive – as is presumably the case in low-predation fish reared with predators – increased behavioral variance and decreased covariance may shape evolutionary trajectories by strengthening selection on these traits (Gibson & Dworkin, 2004; Ghalambor *et al.*, 2007; Schlichting, 2008; McGuigan *et al.*, 2010). Indeed, we note that the marked increase in behavioral variance in low-predation fish reared with predators completely encompasses the presumably adaptive range exhibited by high-predation fish reared with predators (Fig. 2.5). Moreover, rearing under non-native environmental conditions shifted the major axes of phenotypic variation in low-predation fish in line with that of high-predation fish adapted to environments with predators. In the wild, low-predation fish are regularly washed downstream into high-predation environments and, although there is little empirical data on this phenomenon (but see Weese *et al.*, 2011), the ability of low-predation fish to produce presumably advantageous high-predation phenotypes in response to predator cues has been observed in a number of traits (Torres-Dowdall *et al.*, 2012; Handelsman *et al.*, 2013; Fischer *et al.*, 2013) and may enable survival in this context (Fig. 2.6B; Gibson & Dworkin, 2004).

Conclusions

We found striking differences in behavioral correlations based on population of origin and genetic background. Counter to classical predictions, rigid trait correlations do not appear to constrain behavioral adaptation in this system, and exposure to novel environments altered trait variance and covariance in a manner we suggest shaped adaptation to these environments. Given

recent evidence that – like other traits – behaviors are highly heritable (Bell *et al.*, 2009) and map well onto phylogenies (de Queiroz & Wimberger, 1993; Kamilar & Cooper, 2013) the phenomena we demonstrate here likely apply to phenotypic traits generally. While there is extensive theoretical debate on the importance of developmental plasticity in evolution (e.g. West-Eberhard, 2003; Ghalambor *et al.*, 2007; Pigliucci, 2009), these ideas have rarely been considered in a multivariate context (but see Spitze & Sadler, 1996). Our findings here suggest that plasticity in the relationships among traits, rather than constraining evolutionary potential, may play an important role in shaping evolutionary trajectories.

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3. FLEXIBILITY IN TRANSCRIPTIONAL MECHANISMS OF BEHAVIOR

Summary

When organisms are faced with novel or rapidly changing environments, their developmental, physiological, molecular and neural systems must be sufficiently flexible to effect favorable phenotypic shifts, while simultaneously being sufficiently robust to prevent detrimental outcomes. Balancing robustness and evolvability is thus a fundamental challenge for biological systems. To understand the forces shaping phenotypic evolvability and robustness, we examined patterns of flexibility and constraint in associations between transcriptional mechanisms and multiple behaviors in Trinidadian guppies (*Poecilia reticulata*). In particular, we compared patterns across genetic and developmental timescales to address the role of mechanistic flexibility in adaptation to novel environments. We compared these relationships between transcriptional mechanisms and behavior at both the level of single genes and gene networks, to also address how signatures of flexibility and constraint differed across hierarchical levels of organization. Patterns of flexibility and constraint are intimately tied to the hierarchical organization of biological systems, as a diversity of lower level patterns may nonetheless give rise to similar higher-level output. We found that conserved gene networks had flexible relationships with behavior, suggesting that alternative transcriptional ‘solutions’ may give rise to similar behavioral phenotypes. We suggest that this combination of network stability and flexibility in gene expression patterns balances the maintenance of favorable trait constellations with the generation of phenotypic diversity during adaptation to novel environments.

Introduction

How biological systems balance robustness and evolvability, and whether these phenomena are conflicting or complementary, is a focus of theoretical and empirical debate (e.g. de Visser *et al.*, 2003; Wagner, 2005; Lenski *et al.*, 2006; McBride *et al.*, 2008; Draghi & Wagner, 2009; Raman & Wagner, 2011). On the one hand, underlying mechanisms must be robust enough to withstand environmental perturbations that may otherwise lead to phenotypic instability and reduced survival. On the other hand, flexibility in these same mechanisms is what generates novel phenotypic diversity that allows animals to survive and populations to adapt. To maximize evolvability - broadly defined as the ability to access evolutionary innovation (Wagner, 2005) – developmental, physiological, molecular, and neural mechanisms must be sufficiently flexible to effect favorable phenotypic shifts while being sufficiently robust to prevent detrimental changes (Kirschner & Gerhart, 1998; Lenski *et al.*, 2006).

Central to understanding phenotypic evolvability and robustness is an understanding of the extent to which the mechanisms underlying complex phenotypes are flexible versus constrained (Ketterson & Nolan, 1999; Merilä & Björklund, 2004). Are systems *flexible* such that many possible mechanisms can give rise to a given phenotypic shift, or *constrained* such that solutions are limited, and how do these patterns influence evolutionary potential? Our understanding of how underlying mechanisms shape phenotypic evolution remains limited. We know relatively little about how interspecific (i.e. longer evolutionary timescales) and intraspecific (i.e. shorter evolutionary timescales) mechanistic differences relate to one another (but see Stern & Orgogozo, 2009), and even less about how patterns of environmentally induced change (i.e. developmental plasticity) in underlying mechanisms shapes evolutionary trajectories. Furthermore, patterns of flexibility and constraint are intimately tied to the hierarchical

organization of biological systems: genes exist in regulatory networks and single neurons act as elements of neural circuits, and different patterns may emerge at different levels in the hierarchy (Prinz *et al.*, 2004; Marder & J. Goaillard, 2006; Crawford & Oleksiak, 2007; Toth *et al.*, 2010). Thus, flexibility at different levels of hierarchical biological networks may have distinct consequences for the evolutionary potential of the phenotypes they influence (Masel & Trotter, 2010).

We outline three potential scenarios that differ in the relative level of flexibility and constraint exhibited by networks and network elements, and discuss how patterns across levels of mechanistic network structure may shape evolutionary potential. First, network structure (i.e. the interactions among network elements) may be conserved, and phenotypic variation may consistently be mediated by a restricted set of elements across individuals, populations, and even species (Fig. 3.1A). For example, the nonapeptides arginine vasopressin, oxytocin, and their non-mammalian homologues are implicated in affiliative behavior across vertebrates (e.g. Insel & Young, 2000; Keverne & Curley, 2004; Heinrichs *et al.*, 2009; Goodson & Kingsbury, 2011; Godwin & Thompson, 2012). A limited suite of mechanistic options could arise from a lack of genetic diversity (e.g. Stern & Orgogozo, 2008; Rosenblum *et al.*, 2014), rigidity in developmental processes giving rise to network structure and dynamics (Katz, 2011; Jiménez *et al.*, 2015), and/or the repeated targeting of elements that minimize functional or developmental constraints (Rosenblum *et al.*, 2010; e.g. Stern, 2013; Rosenblum *et al.*, 2014). Conservation of networks and network elements may thus maximize organisms' ability to maintain favorable phenotypes and minimize tradeoffs; however, this consistency may limit the production of selectable variation and thereby restrict evolvability (Ancel & Fontana, 2000; Ance Meyers, 2005).

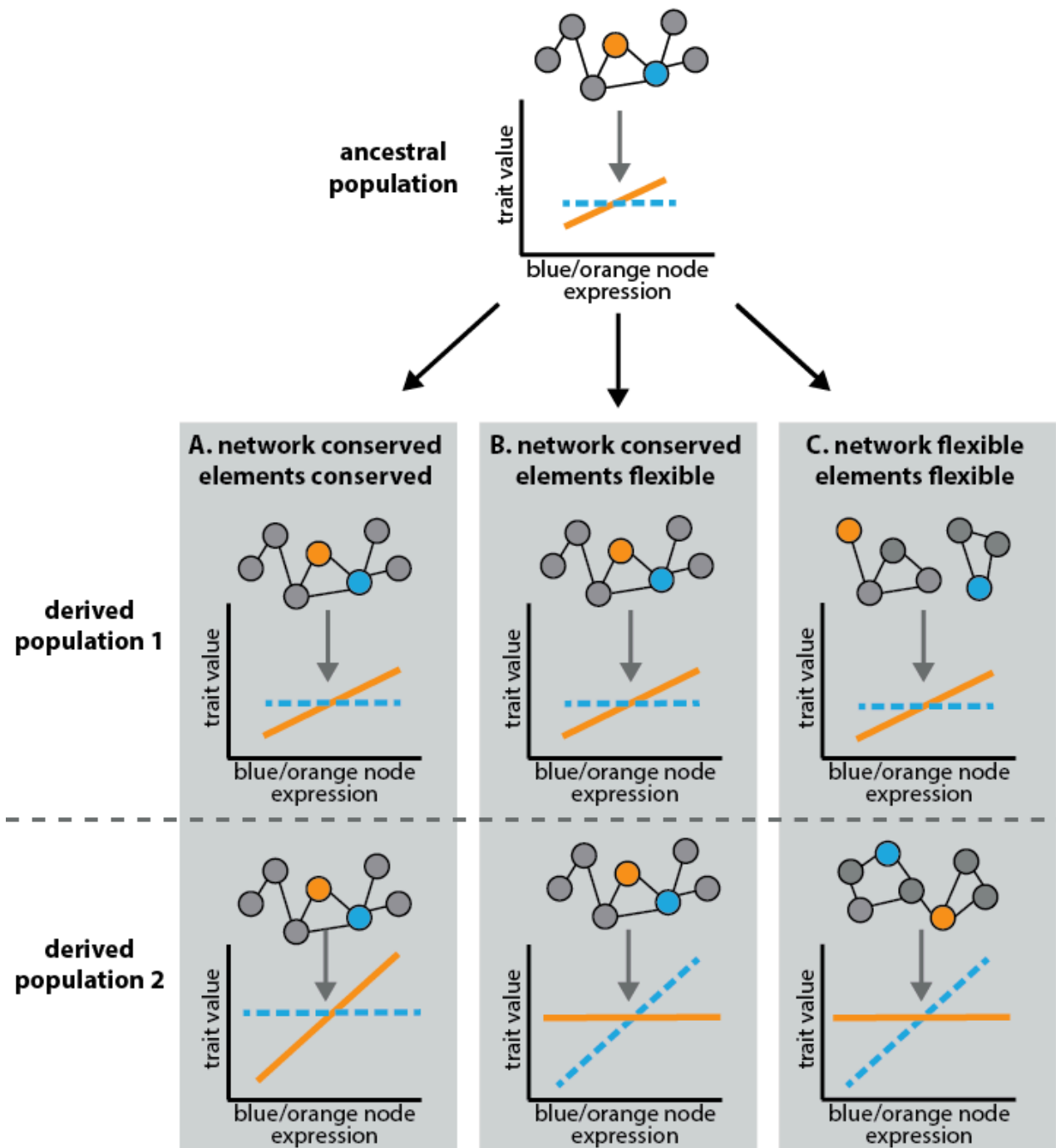


Figure 3.1. Alternative hypothesis for patterns of flexibility and constraint in networks mediating complex phenotypes. A simplified network is shown with dots representing network elements/nodes (e.g. proteins or neurons) and lines representing the connections between them (e.g. biochemical interactions or synapses). The relationships between the expression of two network nodes (blue and orange) and a single phenotypic trait is depicted by color-coded lines on the graphs. In the ancestral population, the orange node influences the trait value (sloped line), but the blue node does not (flat line). The range of trait values in derived populations is expanded to varying degrees, however the underlying mechanisms mediating these trait changes differ. (A) Network structure is conserved and the influence of network elements on the phenotype is conserved. Expanding the expression of the same element (orange) mediates the greater range of trait values in both derived population. (B) Network structure is conserved, but elements are flexible. Trait values have evolved to the same degree as in (A), but phenotypic changes are mediated by different elements in different populations (orange node in population 1 versus blue node in population 2). (C) Networks are flexible and elements are flexible. Again, derived populations express larger ranges of trait values, but elements are flexible unlike situation (A) and networks are flexible unlike in (B). While relationships with only a single trait are shown, we note that, when expanded to a multi-trait context, scenarios (B) and (C) allow for the expression of ancestrally correlated traits to be decoupled, i.e. associated with distinct mechanisms.

Alternatively, network structure may be conserved, while network elements are flexible and differentially affect organismal phenotypes (Fig. 3.1B). For example, Crawford and Oleksiak (2007) found that, among individuals from the same population of *Fundulus heteroclitus*, similar patterns of glucose metabolism were mediated by gene expression levels in distinct sets of metabolic genes, demonstrating that consistent network output may be generated by alternative expression patterns in network elements. Constraints in network structure in concert with flexibility in underlying elements may increase evolutionary potential by (1) facilitating homeostatic and compensatory changes that buffer organisms from environmental pressures (Badyaev, 2005; Scott *et al.*, 2009; Oleksiak & Crawford, 2012; Zayed & Robinson, 2012), (2) generating selectable variation in traits and/or mechanisms (Larsen, 2005; Draghi & Wagner, 2009), or (3) allowing alternative mechanisms to take over regulation of distinct traits when reliance on shared mechanisms gives rise to unfavorable correlations among them (Sinervo &

Svensson, 2002; J. C. Johnson & Sih, 2005; Tanay *et al.*, 2005; Duckworth, 2006; Ketterson *et al.*, 2009). In brief, a combination of flexibility and constraint across levels of biological organization may balance phenotypic robustness with phenotypic versatility (e.g. Kirschner & Gerhart, 1998; Masel & Trotter, 2010; Katz, 2011).

Finally, flexibility may be evident at the network level, such that existing networks can be rearranged or entirely different networks can assume control of a given phenotype (Fig. 3.1C), in a process akin to developmental systems drift, in which phenotypes are maintained with their underlying mechanisms change (e.g. True & Haag, 2001; Wang *et al.*, 2008; Verster *et al.*, 2014). For example, Wang and Sommer (2011) demonstrated that distinct developmental pathways control vulval induction in closely related species of nematodes. Flexibility may increase evolvability for any of the reasons discussed above, and this more extensive flexibility encompassing network structure may facilitate increased divergence by giving rise to an even wider array of mechanistic alternatives. The potential cost of extensive flexibility is that it may increase the likelihood of negative pleiotropic effects (Klingenberg, 2005) or make systems overly sensitive to environmental perturbations (Dewitt *et al.*, 1998; West-Eberhard, 2003; Auld *et al.*, 2010).

These three alternatives balance robustness and evolvability in different ways and demonstrate how mechanistic network structure may shape evolutionary trajectories. Empirical evidence exists for all three alternatives, but work is largely limited to morphological traits and has rarely considered mechanisms at both developmental and evolutionary timescales. How mechanistic networks shape phenotypes may depend on developmental rearing conditions, as we expect selection to produce robust mechanisms and well-adapted phenotypes only in environments commonly encountered by organisms. Novel environmental conditions may

enhance mechanistic flexibility by uncovering cryptic mechanistic diversity (de Visser *et al.*, 2003; Raman & Wagner, 2011; Wagner, 2013), and the form of this diversity will shape evolutionary trajectories as organisms colonize new environments. To understand how constraint and flexibility in underlying mechanisms mediate phenotypic evolvability, we must relate patterns of divergence in individual elements, network structure, and phenotypes across genetic backgrounds and rearing environments.

In the present study, we examine patterns of flexibility and constraint in the transcriptional mechanisms mediating behavioral variation in Trinidadian guppies (*Poecilia reticulata*). The Trinidadian guppy is a well-established model system in ecology and evolutionary biology due to guppies' ability to rapidly adapt to novel environments. In Trinidad, guppies naturally occur in high-predation and low-predation environments, in which they are subject to intense predation versus minimal predation, respectively (Haskins *et al.*, 1961; Endler, 1980; 1995). Although other environmental factors such as food availability also differ between high- and low-predation sites (Grether *et al.*, 2001; Reznick *et al.*, 2001; e.g. Zandonà *et al.*, 2011; Fitzpatrick, Torres-Dowdall, *et al.*, 2014), predation pressure is the major driver of adaptation in this system (reviewed in Magurran, 2005). Moreover, both genetic and environmental factors associated with predation shape life-history (Torres-Dowdall *et al.*, 2012), morphology (Torres-Dowdall *et al.*, 2012; Fischer *et al.*, 2013; Ruell *et al.*, 2013; Handelsman *et al.*, 2014), physiology (Handelsman *et al.*, 2013; Fischer *et al.*, 2014), and behavior (Huizinga *et al.*, 2009; Torres-Dowdall *et al.*, 2012), making guppies an ideal system in which to explore mechanistic flexibility and constraint at developmental and evolutionary timescales.

In the present study, we examine genetic and environmental influences on the relationship between large-scale gene expression (i.e. transcriptomic) differences and multiple

behaviors to understand patterns of flexibility and constraint in behavioral mechanisms. We take a novel approach and, rather than examining transcriptional responses to a single behavioral context as is the most common current approach, we link baseline transcriptional differences to differences in multiple behaviors for each individual. We interpret our data as representing differences in the transcriptional milieu that influence behavioral propensities at two timescales: evolutionary (i.e. genetic) adaptation of guppies to low-predation environments, and developmentally plastic (i.e. environmentally mediated) responses to rearing environments distinct from those of the population's native environment. We first ask whether gene coexpression networks are conserved across genetic backgrounds and rearing conditions that mimic ancestral and derived environmental conditions. We then examine associations between expression in individual genes, gene networks, and multiple behaviors and ask whether these relationships are altered by genetic and environmental influences. Our dataset includes sufficient individual level data to link continuous behavioral variation to continuous variation in gene expression and thus compare the relationships between gene expression and behavior among groups, rather than simply describing concordant group differences in gene expression and behavior. Together these analyses address whether mechanisms associated with behavioral variation are flexible on evolutionary and developmental timescales and whether patterns differ across levels of biological organization.

Methods

Fish collection and rearing

As described previously (see chapter 2), we established unique family lines from fish collected from the Aripo high-predation (HP) locality and the adjacent Naranjo low-predation (LP) locality in 2012 (Gilliam *et al.*, 1993). At birth, we split siblings from second-generation families used in this study into rearing environments with (pred+) or without (pred-) predator chemical cues (Torres-Dowdall *et al.*, 2012). In the pred- environment, fish were housed in tanks in a re-circulating water system containing only conditioned water (i.e. sterilized and carbon filtered tap water treated to have a pH, hardness, temperature, and chemistry similar to natural streams). In the pred+ environment, a natural guppy predator, the pike cichlid *Crenicichla frenata*, was housed in the sump tank of the re-circulating system and fed live guppies daily. Thus, guppies in the pred+ environment were constantly exposed to kairomones from the predator as well as conspecific alarm pheromones from guppies consumed by the predator. All fish used in this study were housed in their respective rearing environments from birth until the completion of the experiment, and removed only during behavioral trials conducted after sexual maturity. This design allows us to discern lifetime environmental effects of predation (contrast between genetically similar fish from the same population in different rearing conditions) from genetic effects (contrast between genetically differentiated populations in a shared lab environment).

Prior to the experiment, all guppies were individually housed in 1.5 liter tanks on a 12:12 hour light cycle (lights on 7:00am to 7:00pm). Fish were fed measured amounts of Tetramin™ tropical fish flake paste and hatched *Artemia* cysts on an alternating basis, once daily between 9:00am and 11:00am. We adjusted food levels following previous protocols based on age and

size of fish (Reznick, 1982; Reznick *et al.*, 2004). To maximize the range of genetic variation captured among focal fish, we selected all males in a given experimental group (i.e. population and rearing environment) were from distinct families. All experimental methods were approved by the Colorado State University Animal Care and Use Committee (Approval #12-3818A).

Behavior

Detailed methods for behavioral data collection are described elsewhere (see chapter 2). Briefly, we used a series of behavioral assays to quantify mating, aggressive, open-field, and escape behaviors. Behavioral data for each individual was collected on three subsequent days. We assayed mating and aggression behavior on the first day, open-field behavior on the second day, and escape behavior on the third day. Fish were run together in balanced groups of four fish per week, with a representative from each population and rearing environment. All behavioral assays were run in water without predator cues as we were interested in developmental plasticity in behavior rather than acute environmental effects of predator cues on behavior. Brain tissue was collected at lights-on two days after the completion of behavioral testing. We conducted behavioral trials and tissue collection in the same manner for each fish in order to facilitate comparison of both group and individual differences. An overview of our experimental design is in Figure 3.2.

Although we collected data on a variety of behaviors within each context, we used only a single value to represent each assay here. Because individual behaviors in the mating and aggression context were positively correlated (see chapter 2), we combined behaviors within these contexts into aggression and mating indices. For mating, we summed sigmoid (overt courtship) displays, sneaky copulation attempts (when males attempt to fertilize females without

their consent), physical contacts, and gonopodial swings. For aggression, we summed lateral displays (similar to sigmoid displays), sneaky copulation attempts (used as an aggressive display in this context), physical contacts, gonopodial swings, and chases. We summed, rather than averaged, these values to preserve the non-normal count distribution of the data. For open-field, we used time in the center of the arena as an index, because this was our primary behavior of interest in this assay and was not correlated with other behaviors assessed in this assay. For escape, we used startle probability as an index, as this go/no-go behavioral decision is not influenced by muscular performance nor was it correlated with other behaviors measured in this context. We refer to these indices simply as mating, aggression, open-field, and escape throughout the remainder of the text.

Tissue collection and processing

Brains were collected two days after the completion of behavioral trials. Fish were anesthetized by immersion in ice water followed by rapid decapitation. Whole brains were removed, flash frozen in liquid nitrogen, and stored at -80 °C until further processing. Tissue collection took <2 minutes, rapid enough to minimize changes in gene expression. To standardize any effects of circadian rhythms on gene expression we collected brains at lights-on each morning. We interpret our transcriptional data as baseline, in the sense that we assume fish were minimally stimulated prior to tissue collection and expression differences among individuals represent primarily stable genetic and developmental differences that may shape behavioral propensities, rather than representing responses to recent experiences and environmental conditions.

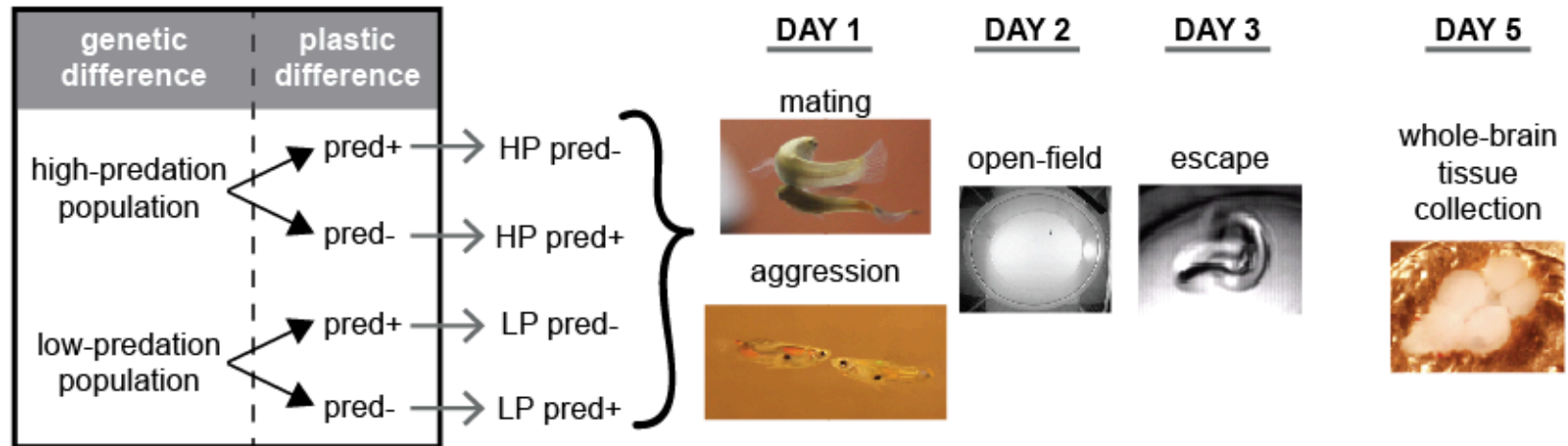


Figure 3.2. Overview of experimental design. (A) Our breeding design allows us to discern genetic differences (contrast between populations in the same environment) from developmental plasticity (contrast between fish from the same population in different rearing conditions). (B) Overview of behavioral assays. We collected data on behavior in four assays on three subsequent days. Whole-brain tissue was collected two days after the completion of behavioral testing. HP = high-predation, LP = low-predation, pred- = reared without predators, pred+ = reared with predators.

We extracted total RNA from individual brains using the Qiagen RNeasy Lipid Tissue Mini Kit (Qiagen, Germany) following manufacturer guidelines, including an optional, on-column DNase treatment. We prepared a separate sequencing library for each individual fish using the NEBNext Ultra RNA Library Prep Kit for Illumina (New England Biolabs, Massachusetts, USA) following manufacturer instructions. Libraries were sequenced on an Illumina HiSeq 2000 at the Florida State University College of Medicine Translational Science Laboratory in May 2014. In total 40 samples (n=10 per group) were sequenced in five lanes with eight samples per lane. We counterbalanced samples during RNA extraction, library construction, and sequencing to maintain the block structure (i.e. four fish per week) in which behavioral trials were conducted.

Transcriptome construction and sample mapping

We received 465 million 100-bp paired-end reads that passed the HiSeq quality filter (~11 million reads per individual). We used Trinity platform software (Grabherr *et al.*, 2011; Haas *et al.*, 2013) to construct a reference transcriptome from all reads. Reads were trimmed for high-quality sequence and normalized in-silico prior to assembly. Our initial assembly contained 121,170 transcripts (N50 = 1,488). To improve assembly quality, we filtered the initial assembly by clustering overlapping transcripts and retaining only those transcripts with an FPKM >1 and a length >300 base pairs. Our final assembly contained 72,104 transcripts (N50 = 3,173). Using default parameters and an e-value cutoff of 10^{-10} , we annotated our assembly by blastx queries against SwissProt (downloaded Aug 8, 2014) and a custom SwissProt database containing only chordate proteins (downloaded Aug 27, 2014).

To remove any non-chordate sequences from our assembly, we retained only the 65,424 transcripts that were annotated using our chordate-only database and performed all further analyses using this chordate-only assembly. We aligned our reads to the transcriptome and estimated their abundance using Trinity, which supports Bowtie (1.0.0) for read alignment and RSEM (1.2.15) for abundance estimation. On average, ~70% of sequences per individual mapped to our chordate-only reference transcriptome. Trinity identified the 65,424 transcripts in our chordate-only assembly as representing isoforms of 16,340 unique transcripts (i.e. presumptive genes), and we used these unique transcripts in all further analyses. We removed one LP pred- individual from further analysis due to problems with sequencing and two individuals (one HP pred-, one LP pred-) whose samples were contaminated with retinal tissue. We identified contamination with retinal tissue from the extreme overrepresentation (~1,000 fold greater than other samples) of genes that were annotated as retina related. This left us with a final sample size of N=37 individuals. We performed differential expression analysis on these data independently of behavioral data and these results are reported elsewhere (see chapter 4).

WGCNA

Given the size and scope of transcriptional data sets, analyzing emergent properties of transcriptional networks in addition to the expression of individual transcripts is a powerful approach, in particular when trying to link transcriptional differences to multiple traits. We constructed weighted gene correlation networks using the WGCNA package in R (Langfelder & Horvath, 2008). WGCNA has been successfully applied to a range of studies exploring relationships between gene expression and a diversity of traits (Weston *et al.*, 2008; J. A. Miller

et al., 2010; Drnevich *et al.*, 2012), including behavior (Drnevich *et al.*, 2012; Hilliard, J. E. Miller, Fraley, Horvath, & White, 2012a; Malki *et al.*, 2014), and has a number of distinct advantages. First, WGCNA mitigates issues of interpretation associated with correlated expression among genes by grouping coexpressed transcripts (Zhang & Horvath, 2005; Oldham *et al.*, 2006; Zhao *et al.*, 2010; Hilliard, J. E. Miller, Fraley, Horvath, & White, 2012a). Second, because network construction is unsupervised and does not require previous knowledge of gene-gene relationships, WGCNA presents an unbiased approach for data exploration and hypothesis generation (Langfelder & Horvath, 2008; Zhao *et al.*, 2010). Third, the fact that networks are constructed independently of trait information facilitates subsequent analysis of associations between module expression and trait data (including continuous trait data) eliminating circularity in evaluating network-trait relationships (Langfelder & Horvath, 2008; Zhao *et al.*, 2010). Finally, exploring relationships between traits and gene expression at the level of expression coexpression networks reduces statistical issues of interpretation associated with multiple hypothesis testing and biological issues of interpretation associated with considering tens of thousands of genes in isolation. In concert, these advantages allow for identification of subtle changes in gene expression and coexpression important for behavior (Oldham *et al.*, 2006; Weston *et al.*, 2008; Zhao *et al.*, 2010; J. A. Miller *et al.*, 2010).

WGCNA constructs gene expression modules based on weighted coexpression among transcripts. A statistically determined threshold for coexpression strength is used to assign genes to unique modules such that the expression of genes within the same module is more highly correlated than the expression of genes assigned to distinct modules. Module expression for each individual can then be summarized using the first principal component of the module, the module eigengene (Langfelder & Horvath, 2008). As recommended by the authors (Langfelder

& Horvath, 2008), we used variance-stabilized count data extracted from the DESeq2 program (Love *et al.*, 2014) in R to construct modules. We discarded 19 transcripts that had zero counts for multiple individuals, leaving 16,321 transcripts for module construction. We used built-in functions of the program to determine the approximate scale-free topology of the network and, given this output, used a soft thresholding power of seven for network construction. We first constructed modules using data from all individuals (n=37) and then superimposed these modules onto the groups, using a built-in function in WGCNA to test for module preservation (i.e. consistency of coexpression patterns among genes). This method uses multiple tests to assess module preservation among groups and outputs a single preservation z-score summary value that represents overall preservation of the module based on multiple metrics (Langfelder *et al.*, 2011). We performed GO term enrichment analysis for each module using annotation information for Biological Processes in the topGO package (Alexa & Rahnenfuhrer 2010) in R.

Statistical analysis of transcript and module relationships with behavior

We used generalized linear mixed models to examine relationships between transcript abundance and behavior. Prior to these analyses, raw transcript counts were variance-stabilized, normalized by library size, and mean-centered. Population of origin, rearing environment, adjusted counts and their interactions predicted variation in behavioral indices in the models. As group differences in behavior are reported elsewhere (see chapter 2), we were not directly interested in the effects of population and rearing environment here, but included them in the model to control for variation in behavior based on these factors. Models were fitted separately for each behavioral index and transcript. We modeled behaviors using a negative binomial distribution, which is appropriate for count data with unequal variances. We corrected p-values

for multiple hypothesis tests for each effect and behavior separately using the Benjamini-Hochberg procedure.

Similarly, we used generalized linear mixed models to examine relationships between module expression and behavior. The module eigengene values represented our estimates of module expression in all analyses. We included population of origin, rearing environment, module expression, and their interactions as predictors of behavior. We conducted this analysis separately for each behavior and again corrected for multiple hypothesis testing for each effect and behavior separately using the Benjamini-Hochberg procedure. All mixed models were run in SAS (SAS Statistical Software 9.4, SAS Institute), and except where noted, all other statistical tests were performed in R base packages (version 3.1.2, The R Foundation for Statistical Computing).

Results

Transcript abundance and behavior

We first examined whether relationships between transcript abundance and behavior were consistent across groups or depended on population of origin and/or rearing environment. After correction for multiple hypothesis testing, we found 19 transcripts that predicted mating behavior in a group-independent manner, and no transcripts that predicted mating behavior in a group-dependent manner. Similarly, we found 53 transcripts that predicted aggression behavior in a group-independent manner, and no transcripts that predicted mating behavior in a group-dependent manner. For open-field behavior, we found 20 transcripts with a group-independent relationship, 51 with a relationship dependent on population of origin, 51 with a relationship

dependent on rearing environment, and 22 whose relationship with behavior depended on an interaction between genetic background and rearing environment. We found no transcripts significantly associated with escape behavior. Of all the transcripts that had significant associations with behavior, only a single transcript was overlapping between those associated with mating and aggression behavior, and no other transcripts were overlapping among any behaviors. Complete annotation information for significant transcripts is in Tables S2.1-S2.7 in Appendix 2.

Module expression and behavior

We took advantage of weighted gene correlation network analysis (WGCNA) to identify modules of coexpressed genes and examine their relationships with behavior. WGCNA constructs gene expression modules based on weighted coexpression measures among transcripts. Genes are ordered into a dendrogram based on these coexpression values and modules are defined by cutting the dendrogram at a statistically determined threshold. The level of module expression for each individual is then summarized by the module eigengene (Langfelder & Horvath, 2008). To differentiate modules, each module is assigned a color. Our analysis yielded 19 unique modules with an average module size of 503 (range: 79 – 1,377) and one ‘unassigned’ module (grey), that contained the 9,060 transcripts whose coexpression levels were not high enough to pass stringent criteria for assignment to a single module (Fig. 3.3A).

All modules were preserved among groups (Fig. 3.3B) indicating that relationships among genes within a given module were consistent across genetic backgrounds and rearing environments. Modules with a z-summary preservation scores >2 are considered moderately preserved and >10 are considered highly preserved. The average preservation score across groups was 47.47 (range

of module averages: 20.90 – 100.84). Because of these high preservation scores, we included all modules in further analyses. Summary information for all modules is in Table 3.1 and GO annotation information is in Table S2.8 in Appendix 2.

We used generalized linear models to examine relationships between module expression and behavior, followed by Benjamini-Hochberg correction for multiple hypothesis testing. We discuss both uncorrected and corrected results. A summary of significant results is in Table 3.2 and complete information for statistical results is in the supplemental materials (Tables S2.9-S2.12 in Appendix 2). For mating behavior, we found two modules whose expression predicted mating behavior in a consistent manner across populations and rearing environments before and after multiple test correction (Fig. 3.4; blue, magenta). We found a single module whose expression predicted mating behavior in a group-dependent fashion, and this relationship was marginally significant after multiple test correction (Fig. 3.4; yellow). For aggression, we found three modules with group-independent effects before multiple test correction (Fig. 3.4; blue, lightgrey, yellow), one of which remained significant (yellow) and one of which remained marginally significant (blue) after correction. We found three modules whose expression predicted aggressive behavior in group-dependent fashion (Fig. 3.4; midnightblue, purple, yellow), one of which remained significant after multiple test correction (purple). A single module had a significant group-dependent association with open-field behavior before and after multiple test correction (Fig. 3.4; cyan). Group-dependent associations for all behaviors arose from a significant interaction between genetic background and rearing environment. We found no modules whose expression was significantly associated with escape behavior (Fig. 3.4). With a few exceptions, those modules that were significantly associated with behavior contained more significantly behavior-associated transcripts than expected by chance (Table 3.3). The single

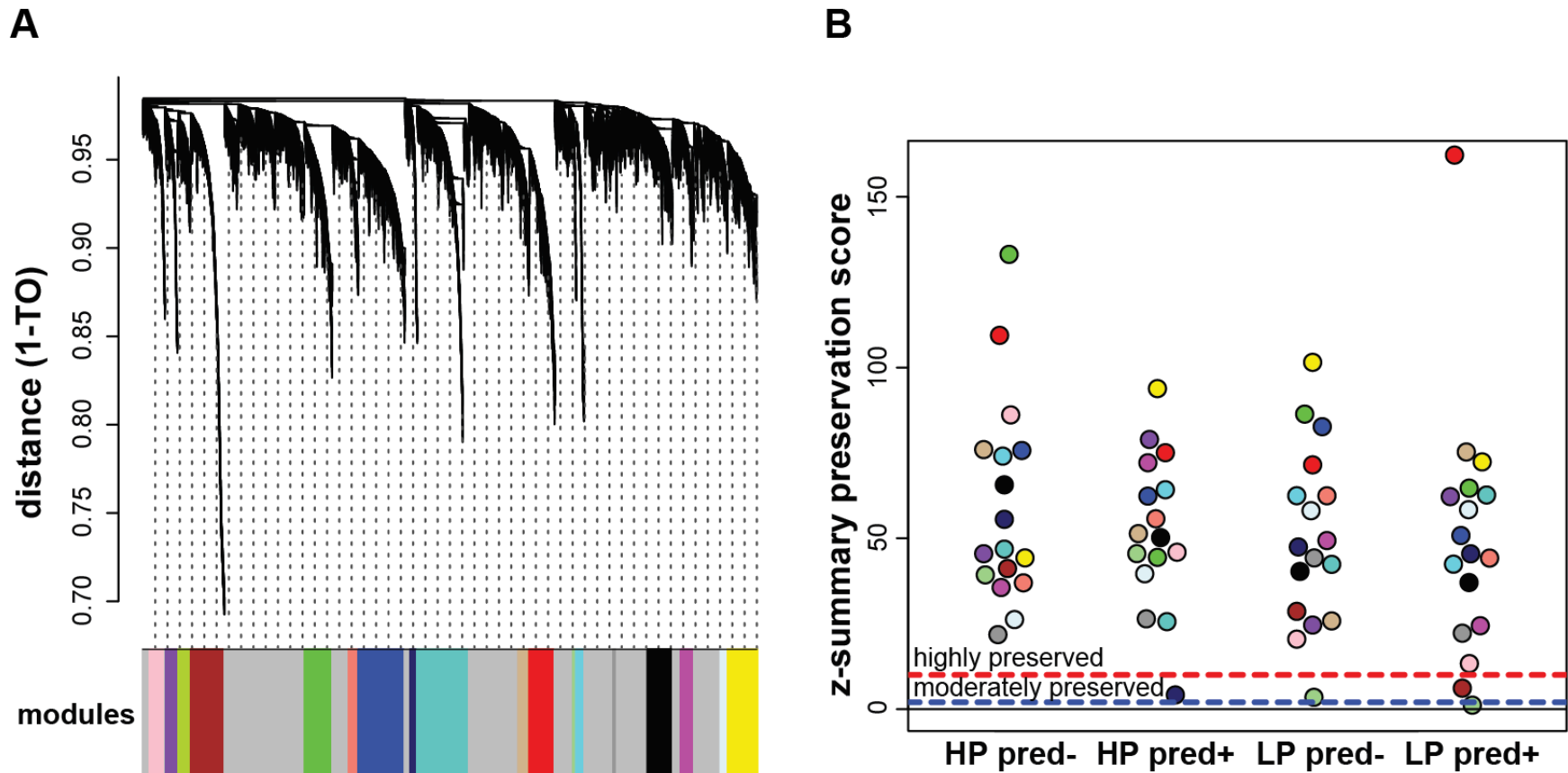


Figure 3.3. Modules are preserved across genetic backgrounds and rearing environments. (A) Dendrogram of gene coexpression with modules indicated by color blocks below. “Leaves” along the dendrogram tree represent individual transcripts. The y-axis represents coexpression ‘distance’ as defined by $1 - \text{topological overlap}$, a measure of coexpression. Values near 0 represent high expression similarity and values near 1 represent low expression similarity. Modules are defined by ‘cutting’ the tree into clusters. (B) Coexpression modules are preserved across genetic backgrounds and rearing environments. Modules with z-summary scores greater than 10 (dashed red line) are considered highly preserved, and modules with z-summary scores greater than 2 (dashed blue line) are considered moderately preserved. Colors reflect module assignment from (A). HP = high-predation, LP = low-predation, pred- = reared without predators, pred+ = reared with predators.

Table 3.1. Module summary information.

module	size (# of transcripts)	ave z-score
black	674	46.04
blue	1231	64.85
brown	896	61.51
cyan	212	57.76
green	724	78.27
greenyellow	322	39.05
lightcyan	184	44.93
lightgreen	79	21.30
lightgrey	91	20.90
magenta	342	43.55
midnightblue	184	35.01
pink	397	39.01
purple	336	50.23
red	682	100.84
salmon	271	48.14
tan	284	54.77
turquoise	1377	42.67
yellow	774	74.55
grey (unassigned)	7261	NA

Table 3.2. Summary of significant results for relationships between module expression and behaviors. Asterisks indicate modules significant after multiple hypothesis test correction.

	module		module*population		module*rearing		module*pop*rear	
	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p
mating								
blue	8.55	0.0066*			8.55	0.0273		
magenta	15.55	0.0005*			5.43	0.0269		
yellow	15.76	0.0004*					9.71	0.0041
aggression								
blue	8.21	0.0077						
lightgrey			7.58	0.0368				
midnightblue							5.89	0.0216
purple							17.50	0.0002*
yellow	28.00	<0.0001*					7.05	0.0128
open-field								
cyan	12.92	0.0012*	11.92	0.0017*	5.10	0.0317		

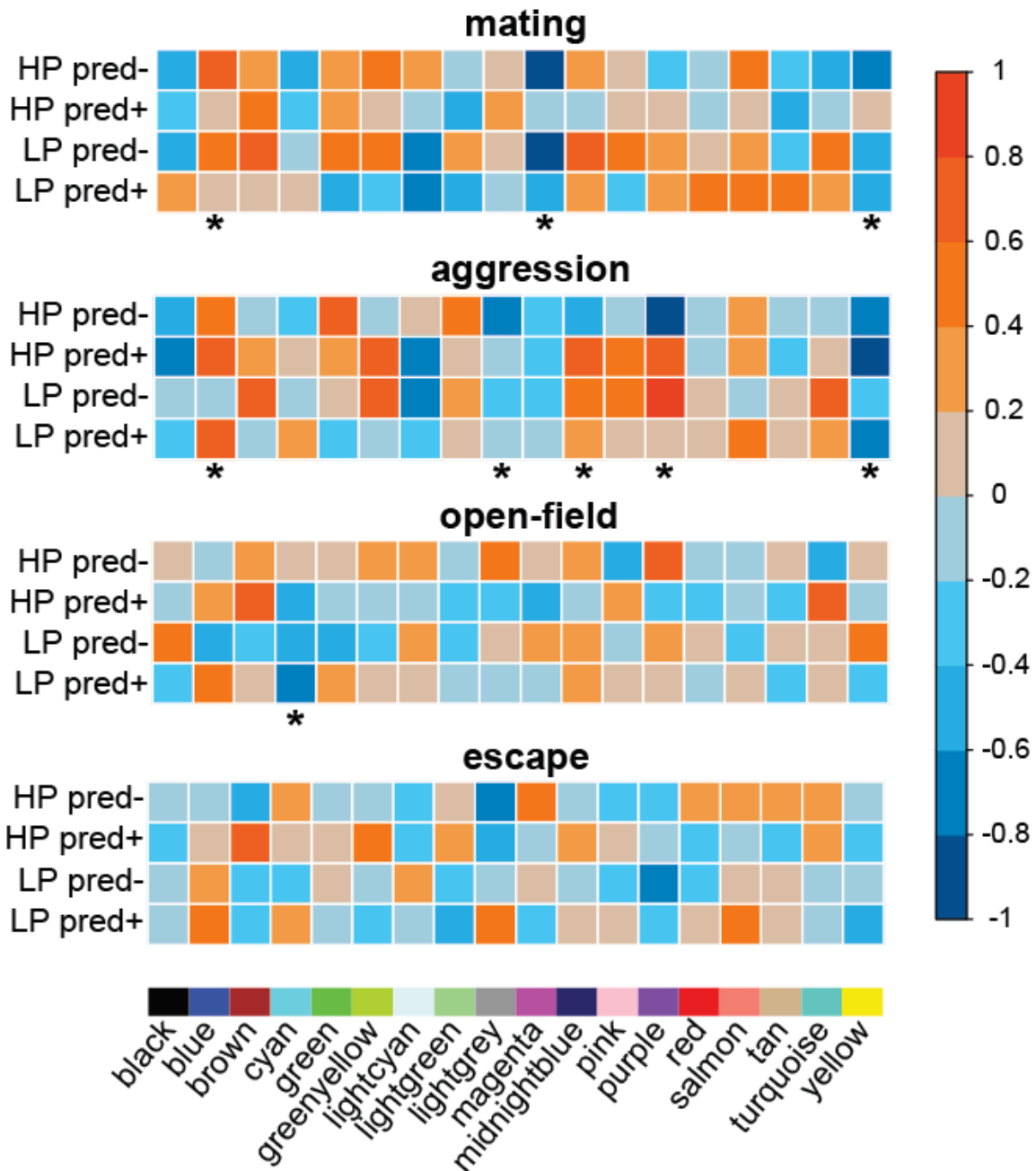


Figure 3.4. Module-behavior relationships vary by group and behavior. Pearson correlations between module expression and behavior (normalized values) are shown by group for each behavior. Correlation strengths, ranging from +1 to -1, are indicated by color (red to blue, scale bar at right). Each column represents correlation with a single module. Module identity (color) is indicated below the heatmaps. Modules in which expression was significantly correlated with behavior are indicated by asterisks below the plots. Details of significant module-behavior relationships can be found in Table 3.2. HP = high-predation, LP = low-predation, pred- = reared without predators, pred+ = reared with predators.

transcript that was significantly associated with both mating and aggression behavior was in the yellow module, which was significantly associated with both behaviors.

Of those modules with a significant association with behavior, two were overlapping between mating and aggression behaviors (blue, yellow). Both these modules were enriched for genes associated with metabolic processes, transcription and translation, and the yellow module was also enriched for genes associated with neuromodulation, among others (Table S2.8 in Appendix 2). We also note that two of the significant modules uniquely associated with aggression (midnight blue and purple) were enriched for immune response related genes, among others (Table S2.8 in Appendix 2). Of the significant modules, none were overlapping between open-field and either courtship or aggression.

Discussion

We compared the relationships between transcript expression, module expression and behavior across guppies from two populations of origin and rearing environments to understand how the mechanisms mediating behavioral variation in novel environments differed across evolutionary and developmental timescales. We found that preserved gene networks had flexible relationships with behavior, suggesting that alternative transcriptional ‘solutions’ may give rise to similar behavioral phenotypes. We suggest that this combination of network preservation and gene expression flexibility balances robustness and evolvability and thus has important implications for evolutionary potential.

Table 3.3. Distribution of behavior associated transcripts in coexpression modules. Asterisks indicate modules significantly enriched with behavior-associated transcripts and grey boxes indicate behavior-associated modules.

module	mating	aggression	open-field	open-field*group
black		1	1	8
blue	9*	16*		7
brown			1	3
cyan			9*	2
green	2*	1	2	7
greenyellow			1	3
lightcyan				1
lightgreen				
lightgrey				
magenta	3*			2
midnightblue			1	2
pink			1	1
purple				1
red				5
salmon	1	1		3
tan				3
turquoise		1		11
yellow	3*	28*		6
grey (unassigned)	1	5*	4*	57

Preserved networks regulate behavior

We found little evidence for differences in network structure using weighted gene correlation network analysis (WGCNA). Modules were preserved (i.e. had similar coexpression structure) among groups, indicating that relationships among transcripts were stable in response to genetic and environmental differences. This pattern is consistent with data from other studies that have found substantial module preservation both within (Hilliard, J. E. Miller, Fraley, Horvath, & White, 2012a; Wong *et al.*, 2014) and among (Stuart *et al.*, 2003; Snel, 2004; Oldham *et al.*, 2006) species (but see Li & A. D. Johnson, 2010). Module preservation allowed us to compare relationships between module expression (i.e. module eigenvalue values) and behavior across populations and rearing environments, a comparison that would not have been informative if the modules themselves were diverging.

We predicted that rearing in a novel environment (i.e. different from the native environment to which populations are adapted) might lead to increased mechanistic flexibility by altering developmental systems to reveal mechanistic diversity, or in other words, by uncovering cryptic mechanistic variation (Raman & Wagner, 2011). If this were indeed the case, we would expect to find decreased module preservation in fish reared in a non-native versus native environments; however, we found no evidence for this in our data (Fig. 3.3). Instead, modules were on average highly preserved. The fact that modules were preserved while phenotypes diverged lends support to the idea that transcriptional networks are robust, and trait changes proceed primarily via changes in the expression of network elements (Fig. 3.1A or 3.1B), rather than via changes in structure of the networks themselves (Fig. 3.1C).

Interpreting differences in transcripts in light of behavior

At present, studies exploring the relationships between transcript abundance and phenotypic variation among individuals remain sparse (e.g. Cummings *et al.*, 2008; Hilliard, J. E. Miller, Fraley, Horvath, & White, 2012b). Sufficient data at the individual level is often lacking or not examined (Golowasch *et al.*, 2002; Crawford & Oleksiak, 2007; Marder, 2011), particularly in behavioral studies where labor intensive data collection and destructive tissue (i.e. brain) sampling make relating brain traits to multiple behavioral phenotypes challenging. In addition, studies using transcriptomic approaches often have small sample sizes, limiting their power to relate individual differences in gene expression to continuous phenotypic variation. Despite these hurdles, studies examining transcriptional mechanisms of behavior are critical for our understanding of how behavioral phenotypes arise, are maintained, and evolve.

In contrast to many studies, we designed our experiment to examine genetic and environmental influences on baseline gene expression in order to link transcriptomic patterns to variation in multiple behaviors. Currently, the majority of studies linking transcript abundance to behavioral differences examine transcriptional responses ~30-60 minutes following performance of a specific behavior (e.g. comparing animals that had an aggressive encounter versus those that did not). Our inferences about such transcriptional responses remain limited by an incomplete understanding of how transcriptomic responses to recent contexts relate to previous neural activity patterns and influence subsequent behaviors at different timescales (Hodgins-Davis & Townsend, 2009; Drnevich *et al.*, 2012). In contrast, our approach is designed not to pinpoint acute transcriptional responses to recent experience, but to identify differences in the transcriptional milieu that may influence a variety of behavioral propensities. While the use of this approach remains limited, studies examining phenotypic differences – including behavioral

differences – in eusocial insects have used a similar approach to successfully identify global transcriptomic signatures associated with caste differences in behavior (Toth *et al.*, 2010; Chandrasekaran *et al.*, 2011). In sum, ours and similar approaches have proven fruitful and we hope that these and additional studies will shed light on how baseline gene expression patterns predict individual differences in behavior.

One caveat of our experimental design is that, as we were interested in developmental plasticity in behavior rather than acute environmental effects of predator cues, we conducted all behavioral assays in water without predator cues. Thus, those fish reared with predators experienced an acute environmental change during behavioral assays that may have affected their behavior. In this case, we might expect to find weaker evidence for associations between baseline gene expression and behavior in fish reared with predators or to overestimate mechanistic flexibility on developmental timescales if acute behavioral changes altered the relationships we observe between gene expression and behavior (see below). While we cannot exclude this possibility, we did not find evidence for weaker associations or increased mechanistic flexibility in fish reared with predators.

A second caveat of our experimental design is our use of whole-brain measures, which make our findings conservative. Transcriptional signatures differ by brain region (e.g. Evans *et al.*, 2003; Pfenning *et al.*, 2014) and these differences are linked to behavior (Sanogo *et al.*, 2012; Hilliard, J. E. Miller, Fraley, Horvath, & White, 2012a). Whole-brain estimates are generally considered conservative because they may swamp out differential expression patterns in individual brain regions. Given that escape behavior is mediated primarily by two large, paired brainstem neurons functioning within a small neural circuit (Eaton *et al.*, 2001; Korn & Faber, 2005), this swamping effect is likely particularly strong in the case of escape behavior, and may

be the reason we were unable to detect expression differences associated with escape. We chose whole-brain samples here due to a lack of information on connections between neurophysiology and behavior in guppies that could have guided an informed choice of one or more focal brain regions. Moreover, single brain regions contain heterogeneous cell types, and we felt that our power of inference would be limited even with the use of region-specific analyses. Measuring gene expression in relevant homogenous cell groups would likely identify more behavior-associated transcripts and could clarify specific behavior mechanisms, but we cannot envision a scenario that upends our positive results indicating flexibility in behavioral mechanisms.

Flexibility and constraint in gene expression and behavior

We found evidence for both consistency and flexibility in the relationships between transcripts, modules, and behavior for mating, aggression and open-field behaviors; however the patterns we observed differed among behaviors and levels of analysis. For open-field behavior, we found similar patterns in single transcripts and coexpression modules. At both levels, relationships between behavior and mRNA levels of some genes were consistent and some relationships differed based on population of origin, rearing environment, or their interaction. While consistent relationships among groups at both the transcript and module level suggest mechanistic constraints, group-dependent relationships in transcripts and/or modules indicate mechanistic flexibility, i.e. that alternative mechanisms may give rise to similar behaviors (Fig 3.1B). Thus, for open-field behavior we found flexibility in the relationships between gene expression and behavior at both developmental and evolutionary timescales.

For mating and aggression behavior, we found transcripts whose expression was associated with behavior, but no transcripts in which these associations differed among groups.

In contrast, at the level of module expression, we found both consistent relationships with behavior and relationships that differed by group. When module-behavior relationships were group-dependent, they differed based on an interaction between population of origin and rearing environment. In other words, not only did the relationships between module expression and behavior evolve (i.e. differences among populations), but developmental plasticity in module-behavior relationships also evolved (i.e. population by rearing environment interactions). Thus, in contrast to open-field behavior, flexibility in the relationships between gene expression and mating and aggression behaviors was apparent only at the level of coexpression modules. Group-dependent relationships at the level of coexpression modules but not individual transcripts suggest that module function is an emergent property of transcriptional differences, such that the expression balance among transcripts with consistent transcript-behavior relationships can give rise to group differences in module-behavior relationships (a multivariate extension of Fig. 3.1B in which the balance among multiple elements influences network output).

While we did not find significant overlap in behavior-associated transcripts among any behaviors, the modules associated with mating and aggression did overlap, and their expression tended to be in the same direction (Fig. 3.4). We have previously demonstrated that mating and aggressive behaviors are more highly correlated with one another than with open-field or escape behaviors, and that correlations between mating and aggression are dependent on genetic and environmental influences (see chapter 2). Our data here suggest that flexibility in behavioral correlations may be related to mechanistic flexibility that enables changes in behavioral correlations and thus helps maintain favorable trait combinations in novel environments.

Given that we find evidence for both consistency and flexibility, how might these patterns arise? The consistency we observe in relationships between mating and aggression

behaviors and transcript expression may result from: (1) selection for conservation of existing mechanisms, (2) a lack of selection to alter existing mechanisms, or (3) as a function of developmental, functional, or genetic constraints (Arthur, 2001; West-Eberhard, 2003; Gompel & Prud'homme, 2009). We cannot differentiate between these alternatives in our dataset, but note that – regardless of why it arises – consistency may influence evolutionary potential. On the one hand, mechanisms that are robust to genetic and environmental changes may enable organisms to maintain consistent phenotypes in novel or changing environments (Badyaev, 2005; Scott *et al.*, 2009; Oleksiak & Crawford, 2012; Zayed & Robinson, 2012). On the other hand, constrained mechanisms may slow adaptation by restricting phenotypic change (Ancel & Fontana, 2000; Ancel Meyers, 2005). In the latter case, selection on trait means is still possible via shifts in existing mechanisms, but selection on alternative mechanisms to decouple unfavorable trait combinations and minimize trade-offs is restricted (Fig. 3.1A).

The flexibility we observe in the relationships between open-field behavior and transcript expression, as well as all module-behavior associations, may arise if alternative patterns of transcript expression give rise to consistent output at the level of coexpression modules (Fig. 3.1B). Alternatively – given that our data are from brain tissue – flexibility in transcript or module expression may also arise if multiple neural circuit mechanisms give rise to similar behavioral phenotypes or if neural mechanisms remain constant but transcript levels differentially reflect the abundance of functional proteins or different molecular configurations that yield similar circuit physiology (J.-M. Goillard *et al.*, 2009; Grashow *et al.*, 2009). Any of these sources of flexibility may promote evolvability. On the one hand, the availability of multiple transcriptional mechanisms with stable gene or neural circuit output may enable compensatory or homeostatic changes in transcription that allow the production of consistent

phenotypes in the face of environmental perturbations and thus facilitate survival in novel environments until favorable mutations arise and can be selected upon (Kirschner & Gerhart, 1998; e.g. Masei & Trotter, 2010; Garfield *et al.*, 2013). Alternatively, flexibility in how neural circuits shape behavior offers more options for adaptive evolution in new habitats and may provide a means of decoupling behavioral traits from one another to minimize non-adaptive trade-offs that arise from behavioral correlations (Sinervo & Svensson, 2002; J. C. Johnson & Sih, 2005; Duckworth, 2006; Ketterson *et al.*, 2009). In sum, mechanistic flexibility may contribute to both consistency and variability at the phenotypic level, thereby increasing evolvability (Kirschner & Gerhart, 1998).

Conclusions

We took advantage of our unique individual level data on brain transcriptomic profiles and multiple behaviors to explore genetic and environmental influences on the relationships between single transcripts, gene coexpression networks, and behavior. The flexibility we observe in the relationships between gene expression and behavior indicates that multiple transcriptional mechanisms may give rise to similar behavioral phenotypes at both evolutionary and developmental timescales. While recent transcriptomic comparisons of similar behaviors across broad taxonomic scales have focused on identifying similarities in the transcriptomic mechanisms underlying behavior, our data suggest that mechanistic flexibility is an important characteristic of the mechanisms underlying intraspecific variation in behavior. In particular, we suggest that the combination of robustness and flexibility we observe in transcriptional mechanisms help maintain favorable trait constellations while also facilitating phenotypic diversity in the face of novel or changing environments.

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4. CONVERGENCE AND DIVERGENCE IN MECHANISMS OF REPEATED EVOLUTION

Summary

Recent research into whether similar phenotypes share underlying mechanisms across individuals, populations, and species has provided examples of both extreme convergence and divergence in mechanisms associated with similar phenotypes, providing conflicting views of phenotypic flexibility. What can patterns of convergent (shared) versus divergent (distinct) mechanisms associated with repeated evolutionary events tell us about the role of flexibility and constraint in mechanisms associated with adaptation to novel environments? We used transcriptomic approaches to determine whether repeated independent evolutionary events are associated with shared transcriptomic signatures in Trinidadian guppies (*Poecilia reticulata*). We combined single gene and gene network analyses to understand how relationships among genes influence their adaptive potential. We found evidence for both shared and distinct transcriptional signatures associated with adaptive divergence across drainages, indicating that a combination of consistent and alternative mechanisms may give rise to similar adaptive phenotypes across independent evolutionary events. Moreover, we demonstrated that more highly connected genes that occupy central network positions were more likely to show evolved expression divergence. Application of network analyses to transcriptomic data is in its infancy and, to our knowledge, increased expression divergence in highly connected genes has not been previously demonstrated using these approaches.

Introduction

Naturalists have long recognized that similar phenotypic solutions arise in response to similar adaptive challenges. More recently, it has been recognized that some such repeated evolutionary events also share underlying mechanisms, even across widely divergent taxa. For example, the nonapeptides arginine vasopressin and oxytocin (along with their non-mammalian homologues) are implicated in the evolution of affiliative behavior across vertebrates (Insel & Young, 2000; Keverne & Curley, 2004; Heinrichs *et al.*, 2009; Goodson & Kingsbury, 2011; Godwin & Thompson, 2012; Knobloch, 2014). In contrast to this pattern of shared mechanisms across divergent species is evidence that different mechanisms may give rise to shared phenotypes in closely related species, populations, or even individuals (e.g. Goodson & Bass, 2001; Abouheif & Wray, 2002; Crawford & Oleksiak, 2007; Donaldson & Young, 2008; Grashow *et al.*, 2009; Rosenblum *et al.*, 2010; Verster *et al.*, 2014; Albers, 2015). These patterns have been described as parallel and/or convergent evolution, with the distinction based primarily on the assumption that more closely related species should be more likely to evolve similar phenotypes via shared mechanisms (see Rosenblum *et al.*, 2014 for a recent review). While there has been considerable semantic debate concerning the use of these terms (Arendt & Reznick, 2008; Wake *et al.*, 2011; Losos, 2011; Rosenblum *et al.*, 2014) our understanding of the extent to which shared (i.e. convergent, *sensu* Arendt & Reznick, 2008) versus distinct (i.e. divergent) molecular processes mediate repeated evolution remains limited. As variation among individuals is the raw material for evolution, examining patterns within and among populations will shed light on how shared and distinct mechanisms emerge and evolve.

A prevailing view is that shared underlying mechanisms underlying convergent phenotypic changes reflect evolutionary constraints. Pleiotropic effects and developmental

constraints may cause evolutionary events to repeatedly target similar mechanistic substrates (e.g. Arthur, 2001; West-Eberhard, 2003; Gompel & Prud'homme, 2009). Even if different mechanistic solutions originally arose due to, for example, differences in standing genetic variation, such differences may disappear as the funneling effects of selection eliminate those mechanisms with relatively higher pleiotropic load (Stern & Orgogozo, 2008; Gompel & Prud'homme, 2009). Different mechanistic solutions among individuals and populations may also arise because differences in standing genetic variation determine which potential mechanisms are possible (Barrett & Schluter, 2008); but again such differences may be eliminated over time as more favorable mutations arise and are selected.

Distinct mechanisms that are associated with similar phenotypes indicate mechanistic flexibility. Such mechanistic flexibility could arise for a number of reasons. First, selection may minimize pleiotropic and developmental constraints by altering regulatory relationships, rather than selecting for alternative molecular substrates. Changes in regulatory relationships may couple or decouple the expression of genes from one another and/or alter the timing and location of gene expression in a manner that minimizes maladaptive pleiotropic effects (e.g. Stern & Orgogozo, 2009; Pavlicev & Wagner, 2012; Martin & Orgogozo, 2013). Over time, rearrangements in the interactions among genes could thus give rise to differences in the molecular networks underlying similar phenotypes, a process akin to developmental systems drift, in which phenotypes are maintained while mechanisms diverge (True & Haag, 2001), although this process can also occur under non-adaptive scenarios (Lynch, 2007). Second, patterns at higher order levels of biological organization may be an emergent property of phenomena at lower levels, such that a diversity of patterns at lower levels may nonetheless give rise to consistent higher-level output. In this case, underlying mechanisms will exhibit varying

degrees of flexibility across different levels of biological organization (Marder & J. Goillard, 2006; Crawford & Oleksiak, 2007; Toth *et al.*, 2010). Importantly, identifying mechanistic flexibility is difficult in studies that consider only single candidate genes, because changes in the relationships among interacting genes can only be detected when many genes are examined simultaneously (True & Haag, 2001). Studies of protein networks have revealed that interactions among genes influence their evolutionary potential, however, data are limited and conflicting (Hahn, 2005; Lemos, 2005; e.g. Alvarez-Ponce *et al.*, 2011; Luisi *et al.*, 2012) and these analyses are generally restricted to a small number of well-defined networks.

To explore mechanisms underlying phenotypic diversity, comparative studies are increasingly using large-scale gene expression (transcriptomic) approaches; however application of network analyses to these datasets remains limited. One critical consideration is that studies in transcriptional and other biological networks have demonstrated that diverse patterns in underlying components can give rise to stable network output (Prinz *et al.*, 2004; Crawford & Oleksiak, 2007; J.-M. Goillard *et al.*, 2009; Grashow *et al.*, 2009). In other words, network behavior may arise from a balance of activity in its underlying elements, rather than being a property of a single element. Furthermore, connections among genes in a network likely influence their propensity for expression divergence, but have only been explored indirectly in transcriptomic datasets (Alaux *et al.*, 2009; Chandrasekaran *et al.*, 2011; Ament *et al.*, 2012). Selection on central, well-connected ‘hub-genes’ may facilitate evolutionary responses by shifting expression in large collections of genes simultaneously. However, shifts in the expression of highly connected genes may increase the probability of deleterious pleiotropic effects (Klingenberg, 2005). Thus, even when genes are a part of the same network, their evolutionary potential may differ depending on their position in the network (Arendt & Reznick,

2008; Olson-Manning *et al.*, 2012). Consideration of gene expression changes in a network framework takes advantage of the expansive nature of transcriptomic datasets and provides insights into forces shaping evolution across biological levels of organization.

Intraspecific divergence and adaptation in Trinidadian guppies

The Trinidadian guppy is a model system in ecology and evolutionary biology due to its ability to rapidly adapt to novel environments, and patterns of repeated evolution in its native range. Much of the adaptive divergence observed in wild populations of guppies is associated with variation in predation pressure (Haskins *et al.*, 1961; Endler, 1995; Reznick *et al.*, 2001). In lower elevation reaches of rivers across Trinidad, guppies are found in high-predation environments where they are subject to intense predation from piscivorous predators (Endler, 1980; 1995). Major predators are excluded from upstream localities by waterfall barriers, resulting in low-predation sites at higher elevations where guppies co-occur only with minor predators. In each river drainage, high-predation guppies have independently colonized and adapted to upstream low-predation environments resulting in parallel changes in life history traits, morphology, and behavior (Reznick *et al.*, 1990; Endler, 1995; Reznick *et al.*, 1997; 2001; Magurran, 2005) that have been shown to increase survival and fitness in their respective environments (reviewed in Magurran, 2005). Genetic analyses have confirmed that different drainages have unique genetic signatures and that low-predation populations are derived from downstream high-predation populations in the same drainage, rather than from low-predation populations in other drainages (Barson *et al.*, 2009; Willing *et al.*, 2010; Fraser *et al.*, 2015). Thus, concordant adaptive differences between high- and low-predation population pairs from different drainages represent repeated evolution in independent lineages. Comparisons of high-

and low-predation populations in the same drainage allow identification of the transcriptional mechanisms involved in adaptation to low-predation environments, and comparisons across drainages reveal whether mechanisms are shared across repeated evolutionary events.

In the present study, we take advantage of repeated evolution in independent guppy lineages to examine brain transcriptomic differences associated with repeated adaptation to predator free environments. To understand whether adaptations relies on similar transcriptional substrates across repeated evolutionary events, we perform these analyses in two independent river drainages. We first analyze genetic influences on gene expression and ask to what extent shared transcriptional mechanisms are associated with adaptation across lineages. We then construct gene coexpression networks and ask to what extent gene coexpression patterns are preserved across lineages. Finally, to understand how interactions among genes contribute to patterns of gene expression divergence, we examine whether genes with expression divergence between high- and low-predation populations occupy central, more highly connected positions in coexpression networks. To our knowledge, an effect of connectivity among genes on their propensity for expression divergence has not been previously demonstrated using transcriptomic data.

Methods

Fish collection and rearing

We established lab populations from fish collected from the Guanapo and Aripo river drainages in the Northern Range Mountains of Trinidad (Gilliam *et al.*, 1993). Fish were collected from the Guanapo high-predation and Taylor low-predation localities in the Guanapo

drainage in March of 2009. Fish from the Aripo high-predation and Naranjo low-predation localities in the Aripo drainage were collected in March of 2012. To maintain the genetic variation of the original wild-caught fish, we established 20 – 30 unique family lines from for each population (i.e. for each generation a single female from each family was crossed to a single male from another family; Reznick and Bryga, 1987). To control as much as possible for environmental and maternal effects, we used second-generation lab born fish from these unique family lines in this study. At birth, we split second-generation siblings into rearing environments with (pred+) or without (pred-) predator chemical cues, and they remained in these environments until the completion of the experiment. In the pred- environment, fish were housed in tanks in a re-circulating water system containing only conditioned water. In the pred+ environment, a natural guppy predator, the pike cichlid *Crenicichla frenata*, was housed in the sump tank of the re-circulating system and fed live guppies daily. We used only mature males in this study. To maximize the range of genetic variation captured among focal fish, all males in a given experimental group (i.e. population and rearing environment) were from distinct families. An overview of our experimental design and interpretation of comparisons is in Figure 4.1.

All guppies were individually housed in 1.5 liter tanks on a 12:12 hour light cycle (lights on 7:00am to 7:00pm) at Colorado State University. Fish were fed a measured food diet twice daily, once in the morning between 8:00am and 10:00am and once in the afternoon between 4:00pm and 6:00pm. In the morning, fish received measured amounts of Tetramin™ tropical fish flake paste, and in the afternoon fish received measured amounts of hatched *Artemia* cysts. Food levels were adjusted each week based on age and size of fish (Reznick, 1982; Reznick *et al.*, 2004). Prior to tissue collection for this study, behavioral and hormone data were collected for the males from the Aripo high-predation and Naranjo low-predation populations, and these

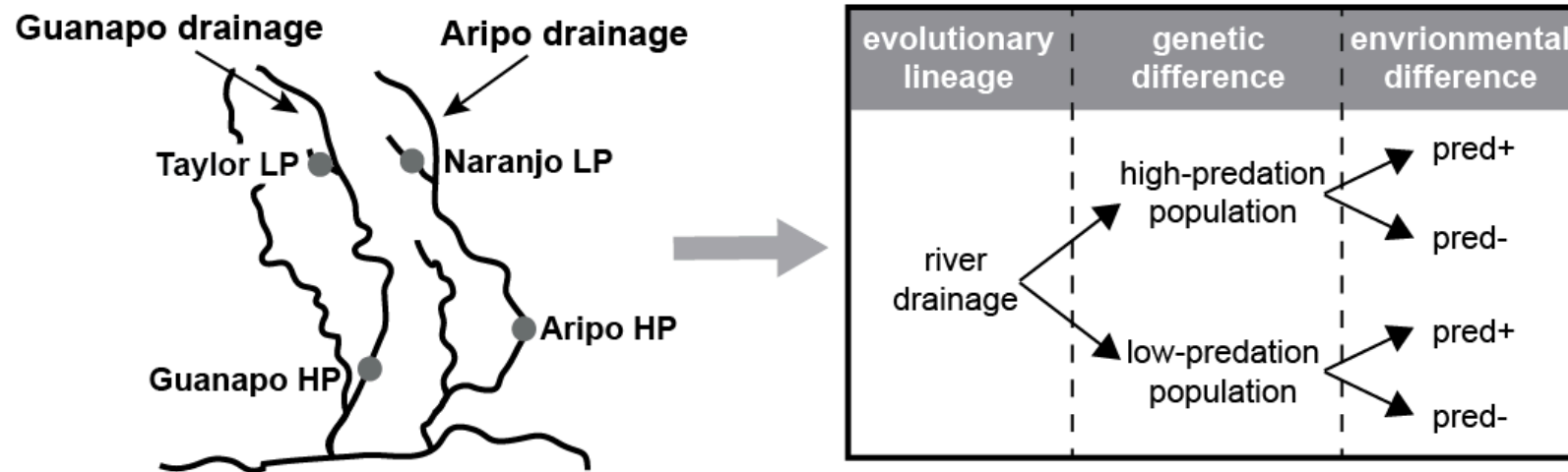


Figure 4.1. Overview of experimental design and interpretation. Lab populations were established from high-predation (HP) and low-predation (LP) population pairs from the Guanapo and Aripo river drainages in Trinidad (left side). Colonization of low-predation environments by high-predation ancestors in each drainage represent independent adaptive evolutionary events. To distinguish genetic from environmental effects of predation across lineages, we reared second-generation fish from both drainages in environments with (pred+) and without (pred-) predators.

results are reported elsewhere (see chapter 2). All experimental methods were approved by the Colorado State University Animal Care and Use Committee (Approval #12-3818A).

Tissue collection and processing

We collected tissue from high- and low-predation population pairs in the Guanapo and Aripo drainage in an identical manner in 2010 and 2013, respectively. We collected brain tissue because we were particularly interested in behavioral divergence. We collected whole brains at lights-on in the morning to standardize any effects of experience, behavior, and circadian rhythm on gene expression. We interpret our transcriptional data as baseline, in the sense that we assume fish were minimally stimulated prior to tissue collection and thus expression levels represent primarily genetic background and developmental experience, rather than responses to immediate environmental context. Fish were anesthetized by immersion in ice water followed by rapid decapitation. Whole-brains were removed, flash frozen in liquid nitrogen, and stored at -80° C until further processing. Tissue collection took <2 minutes, rapid enough to minimize changes in gene expression. We extracted total RNA from brain tissue using the Qiagen RNeasy Lipid Tissue Mini Kit (Qiagen, Germany). We followed manufacturer guidelines, including an optional, on-column DNase treatment.

For the Guanapo drainage populations, samples contained multiple brains pooled from two full siblings. At the time of library preparation, we had to pool brains to ensure sufficient amounts of RNA for sequencing. We pooled full siblings to minimize variation in pooled tissue. Sequencing libraries were constructed for each sample and sequenced on three lanes of an Illumina HiSeq 2000 with eight samples per lane at the HudsonAlpha Genomic Services

Laboratory (Huntsville, Alabama) in April 2012 (samples sizes: N=5 for HP pred+ and pred -; N=4 for LP pred+; N=2 pred-).

For the Aripo drainage populations, we prepared a separate sequencing library for each individual using the NEBNext Ultra RNA Library Prep Kit for Illumina (New England Biolabs, Massachusetts, USA) following manufacturer instructions. Libraries were sequenced on an Illumina HiSeq 2000 at the Florida State University College of Medicine Translational Science Laboratory (Tallahassee, Florida) in May 2014. In total 40 samples (N=10 per group) were sequenced in five lanes with eight samples per lane.

Transcriptome construction and sample mapping

Due to differences in library construction and sequencing between the Guanapo and Aripo datasets, we did not combine transcripts from both datasets for reference transcriptome construction. Because of the more extensive nature of the Aripo dataset, we used only this dataset for transcriptome assembly. We received 465 million 100-bp paired-end reads that passed the HiSeq quality filter, averaging 11 million reads per sample. We constructed a reference transcriptome using the Trinity platform (Grabherr *et al.*, 2011; Haas *et al.*, 2013). Reads were trimmed for high-quality sequence and normalized in-silico prior to assembly. Our initial assembly contained 121,170 transcripts (N50 = 1,488). To improve assembly quality, we filtered the initial assembly by clustering overlapping transcripts and retained only those transcripts with an FPKM >1 and a length >300bp. After filtering, our final assembly contained 72,104 transcripts (N50 = 3,173). Transcripts were annotated by blastx queries against SwissProt (downloaded Aug 8, 2014) and a custom SwissProt database containing only chordate sequences

(downloaded Aug 27, 2014). We used default parameters for our blastx queries, with an e-value cutoff of 10^{-10} .

To remove any non-chordate sequences from our assembly, we retained only the 65,424 transcripts that were annotated using our chordate database. All further analyses were performed using this chordate only assembly. We aligned reads from both datasets to our chordate only assembly and estimated their abundance using Trinity, which supports Bowtie (1.0.0) for read alignment and RSEM (1.2.15) for abundance estimation with default parameters. On average, 70% of sequences per individual mapped to our chordate-only reference transcriptome. Prior to analysis, we removed any transcripts that had less than one count per million in half or more of the samples. Trinity identified the collection of all transcripts as representing isoforms of 16,340 unique transcripts (i.e. presumptive genes), and we used these transcripts in all further analyses. In the Aripo drainage dataset, we removed one individual from further analysis due to problems with sequencing and two individuals whose samples were contaminated with retinal tissue. Similarly, in the Guanapo drainage dataset we removed two individuals due to contamination with retinal tissue. We identified contamination with retinal tissue from the extreme overrepresentation (~1,000 fold greater) of genes annotated as retina related in these samples. The final sample size in Aripo dataset was N=37 and in the Guanapo dataset was N=14.

Weighted gene correlation network analysis

We constructed weighted gene correlation networks using the WGCNA package in R (Langfelder & Horvath, 2008). WGCNA constructs gene expression modules based on weighted correlations among transcripts. Genes are ordered into a dendrogram based on coexpression values and modules are defined by cutting the dendrogram at a statistically determined threshold.

Module expression can then be summarized using the first principal component of the module, the module eigengene (Zhang & Horvath, 2005; Langfelder & Horvath, 2008). Modules are assigned a color to differentiate them verbally and graphically. We used variance stabilized count data generated using the DESeq2 program in R (Love *et al.*, 2014) to construct modules and discarded eight transcripts which had zero counts for multiple individuals (Langfelder & Horvath, 2008). This left us with 16,332 transcripts for module construction. We used built-in functions of the WGCNA program to determine the approximate scale-free topology of the network and, given this data, used a soft thresholding power of seven and a deepsplit value of one for network construction.

We first constructed modules using only data from the Aripo drainage dataset. We chose this dataset as our reference because its larger size gave us substantially more power for module construction. We then superimposed these modules onto the Guanapo drainage dataset and used a built in function in WGCNA to test for module preservation (i.e. consistency of coexpression patterns among genes within a module) across drainages. The module preservation function uses multiple tests to assess module preservation among datasets and summarizes outputs from these tests as a single module preservation z-score (Langfelder *et al.*, 2011).

Statistical analysis

We analyzed differential gene expression using the DESeq2 package in R (Love *et al.*, 2014). We included population of origin, rearing environment, and their interaction in the model and used contrast statements to examine the effects of population of origin on gene expression. While we were not directly interested in the effects of rearing environment here, we include rearing environment in the model to control for differences based on developmental

environment. We adjusted p-values for multiple hypothesis tests using the Benjamini-Hochberg procedure and called all genes with an adjusted p-value <0.1 differentially expressed (DE). To ask whether similar mechanisms were involved in divergence in gene expression across independent evolutionary events, we examined overlap in DE genes between the two datasets using a chi-square test of independence with Yates continuity correction for large samples. Due to the high rate of false negatives in differential expression analysis after multiple hypothesis testing, we also evaluated overlap in gene expression changes between datasets using a rank-based technique that is independent of p-value cutoff. This technique, rank-rank hypergeometric overlap (RRHO), steps through two lists of genes ranked based on differential expression and calculates the statistical significance of the number of overlapping genes to identify areas of significant overlap and non-overlap (Plaisier *et al.*, 2010). A Benjamini-Yekutieli correction is applied to control for multiple, dependent comparisons among lists. The output of the program is a graphical representation of the strength and direction of the hypergeometric overlap between expression profiles in the two datasets.

We compared average connectivity in DE versus non-DE genes to determine whether interactions among genes influenced gene expression divergence. We obtained pairwise gene-by-gene connectivity values for all transcripts from the WGCNA package. Using these values, we calculated a range of percentiles for connectivity values of each transcript. These percentiles thus represent each transcript's connectivity with different numbers of 'nearest neighbors' (i.e. transcripts with the most correlated expression). We focused our analysis on the 98th percentile connectivity and above, as this cutoff represents coexpression between each transcript and the collection of its ~ 325 nearest neighbors, a set of transcripts similar in size to the median module size. An overview of these methodologies is in Figure 4.2. We compared connectivity values at a

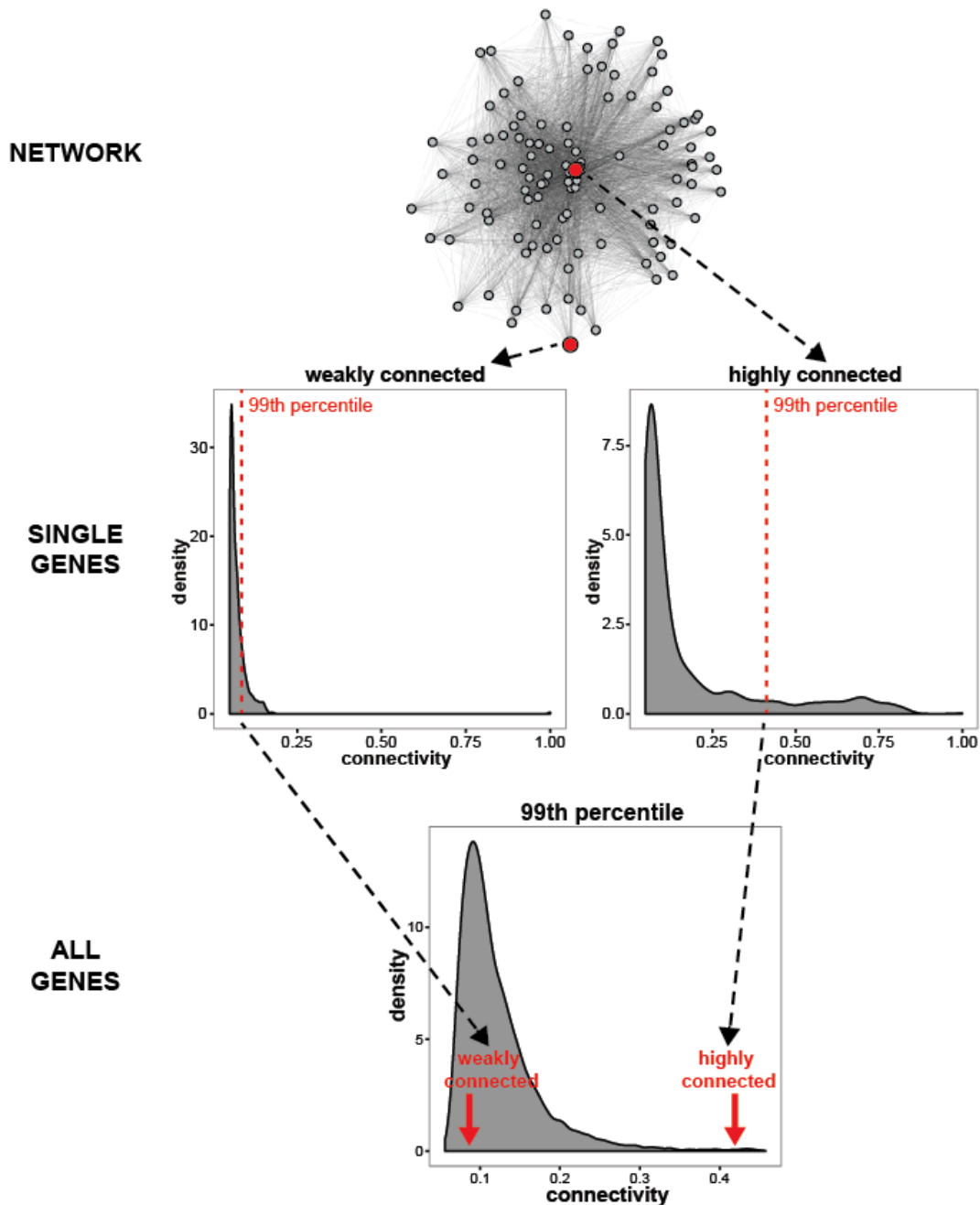


Figure 4.2. Conceptual and methodological overview of connectivity analyses. On the top is a representation of a coexpression network. Nodes (grey circles) represent genes and the distance between them indicates expression similarity. The relative network position for example highly and weakly connected genes is shown in red. Plots of connectivity values for these representative genes are shown below the network with the 99th percentile values for each example gene indicated by a dashed red line. Note, the x-axes are on the same scale, but the 99th percentile connectivity value is very different for the weakly versus highly connected gene. On the bottom is a plot of the distribution of 99th percentile connectivity values for the collection of all genes with the relative values of the two example genes from above indicated by red arrows.

range of percentiles at and above this cutoff using a two-sample Kolmogorov-Smirnov test. We chose this test as it is non-parametric and controls for unequal variances among groups, and sets of DE and non-DE genes were non-normally distributed with very different sample sizes. As this analysis was not contingent on module assignment, we performed this analysis in the same manner in both datasets. We note, however, that sample size in the Guanapo drainage dataset is small.

We performed GO term enrichment analysis for both DE transcripts and modules using annotation information for ‘Biological Processes’ in the topGO package (Alexa & Rahnenfuhrer 2010) in R. Except where noted, all statistical tests were performed in R (version 3.1.2, The R Foundation for Statistical Computing).

Results

Differential transcript expression

We found similar patterns of differential transcript expression in the Aripo and Guanapo drainages. In the Aripo drainage, fish from high- and low-predation populations differed in expression of 621 transcripts, and, in the Guanapo drainage, high- and low-predation fish differed in expression of 975 transcripts. Complete annotation information for all DE transcripts is in Tables S3.1 and S3.2 in Appendix 3. Of all differentially expressed (DE) genes in both datasets, 74 were overlapping. Of these, 52 had expression differences in the same direction based on predation level, more than expected by chance (Fig. 4.3; $\chi^2=8.78$, $p=0.003$). We call these genes concordantly differentially expressed (CDE), and propose that these genes are likely under direct selection in both lineages because they serve similar adaptive functions, or are under

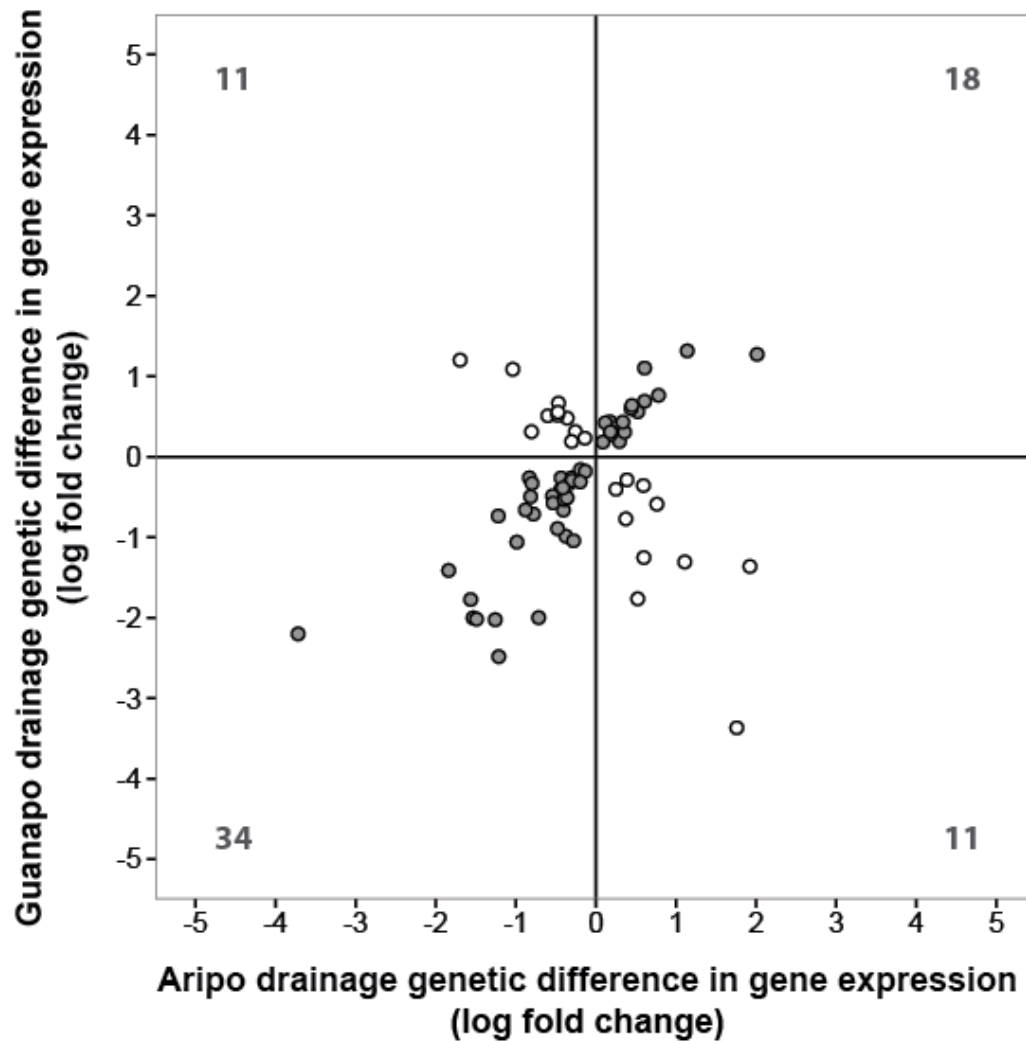


Figure 4.3. Concordant versus non-concordant expression in DE transcripts overlapping between lineages. Top right and bottom left quadrants represent concordantly differentially expressed transcripts (i.e. overlapping DE transcripts for which expression differences were in the same direction in both datasets; grey circles). Conversely, top left and bottom right quadrants represent non-concordantly differentially expressed transcripts (i.e. overlapping DE transcripts for which expression differences were in opposite directions between datasets; white circles). 2/3 of overlapping transcripts were concordantly differentially expressed. The numbers of genes in each category are indicated by numbers in the corners of the quadrants.

similar indirect selection in both lineages if expression changes arise as correlated responses to selection on linked genes. CDE transcripts were enriched for genes associated with DNA integration, biosynthetic processes, and cellular chemical homeostasis (Table S3.3 and S3.4 in Appendix 3).

We wanted to examine more broadly the extent to which changes in gene expression were similar across lineages. Due to the necessity of assigning a hard threshold for differential expression and correcting for large numbers of hypothesis tests, analysis of transcriptomic data is prone to false negatives (Rice *et al.*, 2008). To assess a possible influence of false negatives on our interpretation of overlap versus non-overlap, we compared lists of genetically DE transcripts between datasets using a rank-rank hypergeometric overlap approach that allows for comparison of overlapping gene sets independent of p-value cutoff. This analysis revealed strong overlap among the most differentially expressed transcripts between datasets, in particular for those genes that were down regulated in low-predation as compared to high-predation populations (Fig. 4.4). Conversely, we observed that transcripts that were highly up regulated in one low-predation population were rarely down regulated in the other low-predation population (Fig. 4.4), indicating that the most differentially expressed genes tended not to be differentially expressed in opposite directions between lineages. From rank based analyses, we conclude that the degree of overlap (and conversely non-overlap) we observed was not an artifact of false negatives.

Weighted gene correlation network analysis

We took advantage of weighted gene correlation network analysis (WGCNA) to account for non-independence of expression among transcripts and to assess coexpression similarities across datasets. WGCNA constructs gene expression modules based on weighted correlations

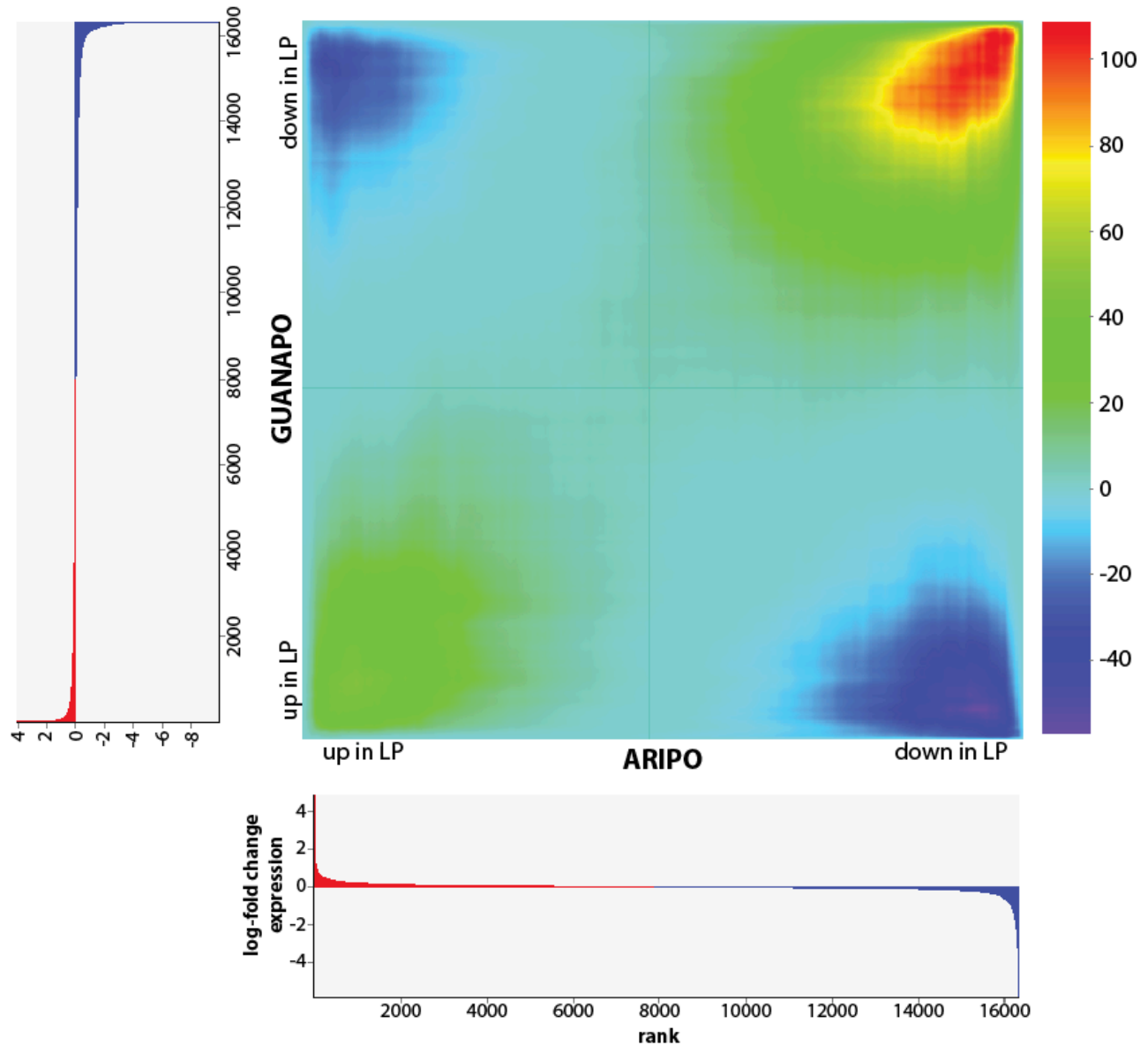


Figure 4.4. Significant overlap among the most differentially expressed transcripts between datasets. Heatmap is of rank-rank hypergeometric overlap between datasets. Axes of the heatmap show transcripts ranked from those most up regulated in low-predation (LP) populations (bottom left corner) to those most down regulated in LP populations (top right corner). The boxes below and to the left indicate rank number and log-fold change numerically and graphically. Color scale at right indicates the degree of statistically significant overlap between the two ranked lists from strong overlap (red) to strong non-overlap (blue). Numbers are direction-signed log10-transformed hypergeometric p-values. We observe significant overlap between datasets among those transcripts most down regulated in both LP populations (red area in top right corner) and weaker overlap among the most up regulated transcripts (green area in bottom left corner). Conversely, those genes that tended to be up regulated in one low-predation population were not down regulated in the other (blue areas in top left and bottom right corners).

among transcripts. Module expression can then be summarized using the first principal component of the module, the module eigengene (Zhang & Horvath, 2005; Langfelder & Horvath, 2008). Modules are assigned a color to differentiate them verbally and graphically. Our analysis yielded 20 unique modules with an average module size of 500 (range: 79 - 1636) and one unassigned module (grey module) comprised of the 6,332 transcripts that did not meet stringent criteria for definitive assignment to a module (Fig. 4.5A). We initially constructed modules using the larger Aripo dataset and then tested for preservation (i.e. similar covariance structure) of these modules in the Guanapo dataset. We found that eight modules were highly preserved (Fig. 4.5B; z-score >10; black, cyan, lightcyan, midnightblue, salmon, tan, turquoise, yellow), nine modules were moderately preserved (Fig. 4.5B; z-score >2; blue, green, greenyellow, lightgreen, magenta, pink, purple, red, royalblue), and three modules were non-preserved (Fig. 4.5B; brown, lightgrey, lightyellow). In addition, we note that module preservation was not strictly a byproduct of module size (Fig. 4.5B). Summary information for all modules is in Tables 4.1 and module annotation information is in Table S3.5 in Appendix 3.

We next asked whether DE genes had higher connectivity (i.e. correlated expression) with their nearest neighbors than non-DE genes. To address this question, we examined connectivity in DE versus non-DE genes at a range of percentiles representing collections of genes of varying sizes. We focused our analysis on the 98th percentile connectivity and above as this cutoff represents connections between a given transcript and its ~ 325 nearest neighbors, and thus reflects a set of transcripts similar in size to the median module size. We found that DE genes had higher connectivity at and above this cutoff (representative plot of 99th percentile in Fig. 4.6). In the Aripo drainage this pattern was driven in part by the presence of a substantial number of extremely highly connected DE genes (red arrow in Fig. 4.6).

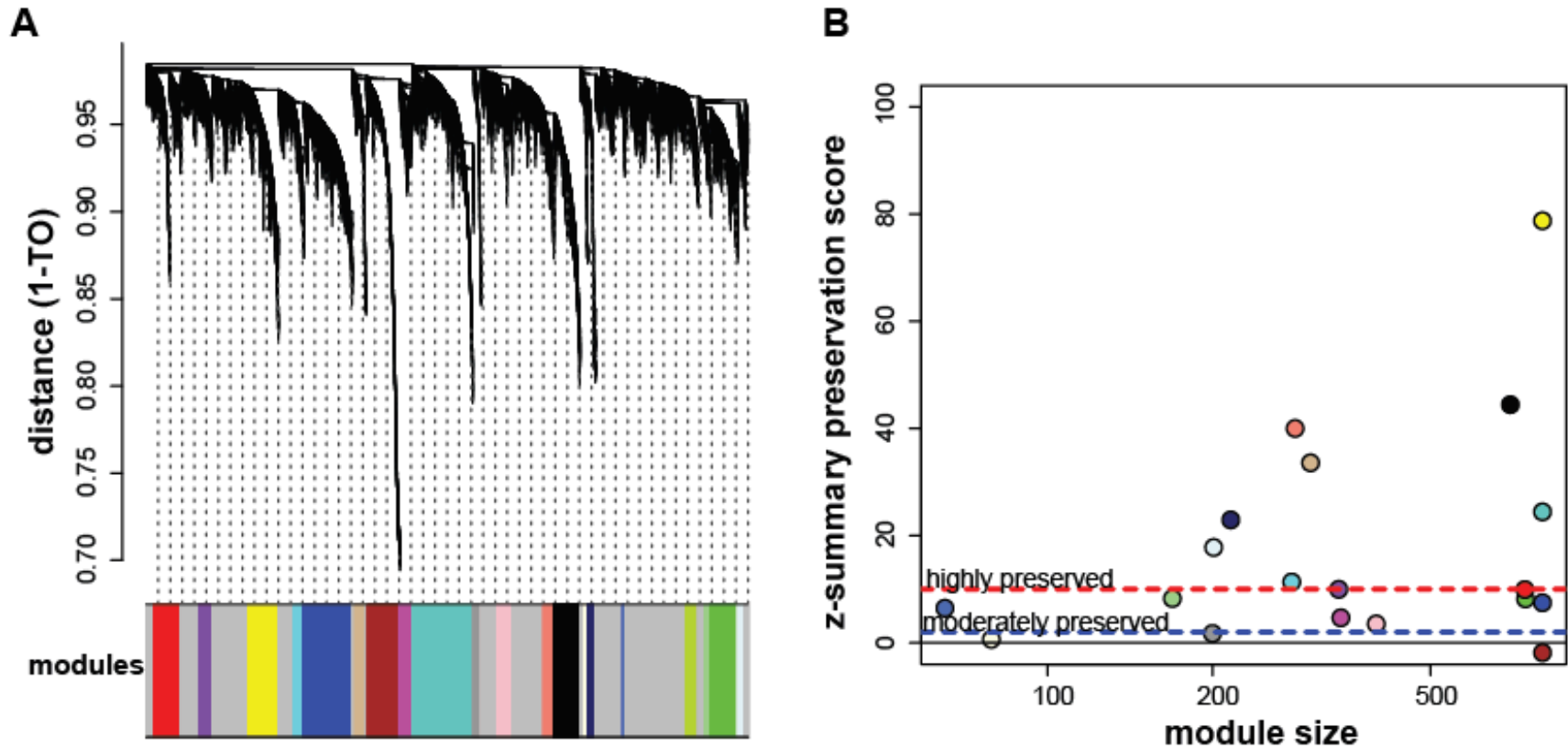


Figure 4.5. (A) Dendrogram of gene coexpression in the Aripa dataset with uniquely defined modules indicated by color blocks below. “Leaves” along the dendrogram tree represent individual transcripts. The y-axis represents coexpression ‘distance’ as defined by $1 - \text{topological overlap}$, a measure of coexpression. Values near 0 represent high expression similarity and values near 1 represent low expression similarity. Modules are defined by ‘cutting’ the tree into clusters. (B) Coexpression modules are preserved across datasets independent of size. Preservations scores are calculated by superimposing modules from Aripa dataset in (A) onto the Guanapo dataset. Modules with z-summary scores >10 (dashed red line) are considered highly preserved, and modules with z-summary scores > 2 (dashed blue line) are considered moderately preserved. Colors reflect module assignment from (A).

Table 4.1. Module summary information.

module	size	z-score summary	# DE genes in module	
			Aripo	Guanapo
black	699	44.4	2	62
blue	1315	7.5	17	89
brown	858	-1.9	96	60
cyan	279	11.3	0	30
green	745	8.2	20	63
greenyellow	329	7.0	6	11
lightcyan	201	17.8	0	14
lightgreen	169	8.3	0	9
lightgrey	200	1.7	22	13
lightyellow	79	0.6	2	5
magenta	343	4.7	4	26
midnightblue	216	22.9	13	6
pink	398	3.5	2	18
purple	340	10.0	5	12
red	743	9.9	29	51
royalblue	65	6.4	2	1
salmon	283	40.0	1	5
tan	302	33.6	2	6
turquoise	1636	24.4	129	82
yellow	800	78.7	6	38
grey (unassigned)	6332	NA	263	374

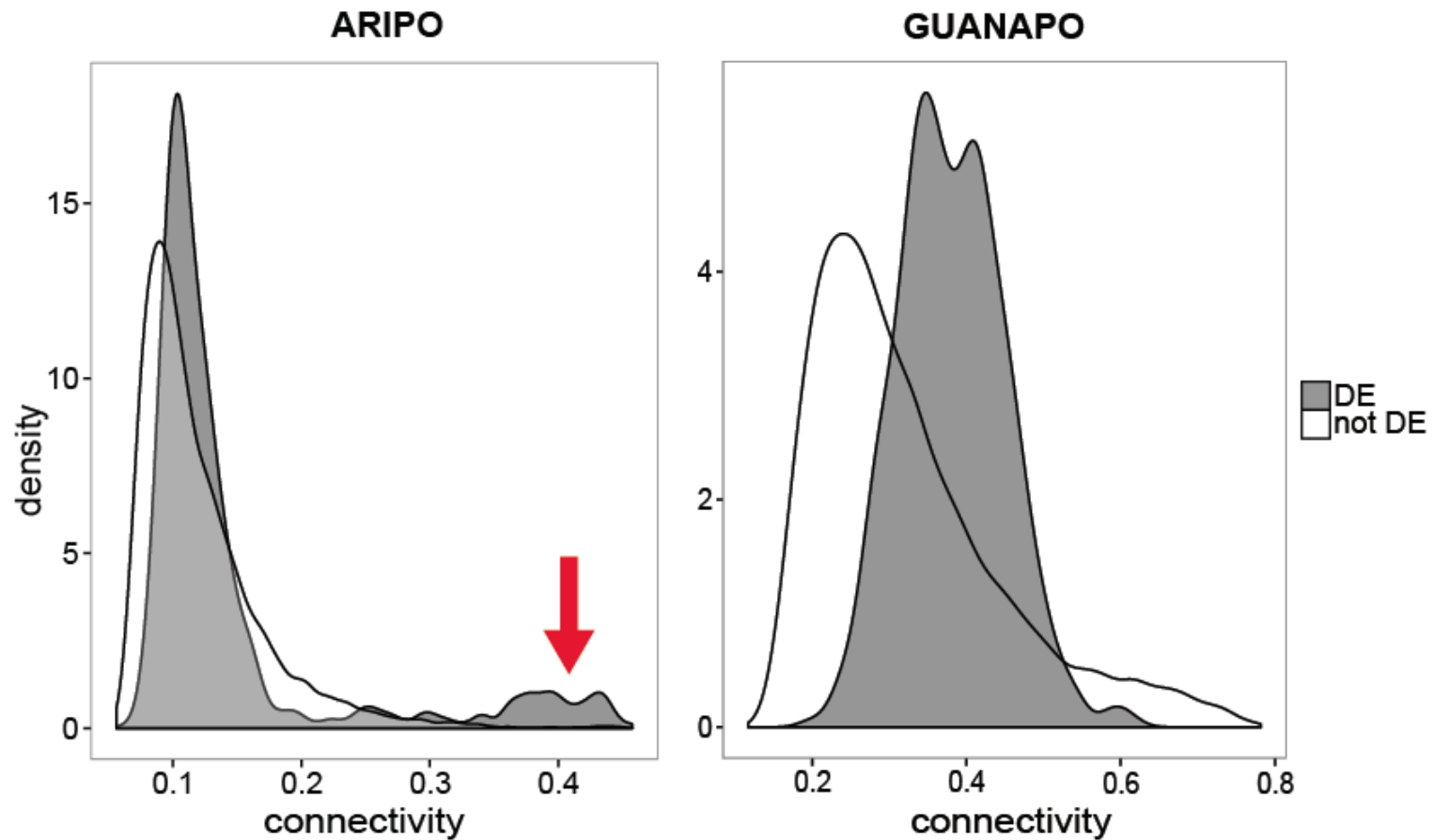


Figure 4.7. DE genes have an overrepresentation of highly connected transcripts. Representative plots of 99th percentile connectivity of DE versus non-DE transcripts in the Aripo and Guanapo datasets. As samples size for DE versus non-DE transcripts were vastly different, the density of transcripts with a given connectivity value is plotted. DE transcripts have higher connectivity in collections of genes similar in size to median module size and smaller. In the Aripo drainage, this pattern is driven in part by the presence of a small percentage of very highly connected genes (red arrow, left panel).

Discussion

We examined transcriptomic differences associated with adaptive divergence across repeated, independent evolutionary events in guppies. Significant overlap in differentially expressed (DE) transcripts between drainages indicated that some shared mechanisms underlie repeated adaptation across lineages in guppies. However, we also found evidence for substantial non-overlap in DE genes, suggesting some distinct mechanisms as well. We discuss the potential significance of shared versus distinct transcripts associated with divergence. We next considered patterns at the level of gene networks. We found substantial preservation of gene expression networks across lineages, demonstrating that coexpression patterns among transcripts were largely stable. Moreover, we demonstrated that network position influenced adaptive potential: more highly connected, central genes were more likely to show expression divergence between high- and low-predation populations in both lineages. This finding highlights the potential value of network type analyses as a means of revealing forces shaping patterns of differential expression.

Shared versus distinct transcriptomic signatures associated with adaptation

When we compared collections of DE transcripts with evolved differences, ~10% of differentially expressed transcripts were overlapping between evolutionary lineages, and 2/3 of these were differentially expressed in the same direction, i.e. concordantly differentially expressed (CDE). Concordant differential expression across lineages and signatures of overlap in rank-based analyses suggest that expression differences in these transcripts are associated with repeated, adaptive divergence. The abundance of concordantly differentially expressed genes suggests that some mechanisms are indeed shared across repeated, independent evolutionary

events. These transcripts are excellent candidates for future work in guppies, as well as additional work linking patterns of intra- and inter-specific divergence associated with differences in predation pressure. Indeed, the enrichment for metabolism related genes that we observe in CDE genes has been observed in other studies examining brain gene expression differences linked to predation (Mommer & Bell, 2014) and behavior (Rittschof *et al.*, 2014).

While we found more overlap than expected by chance, only ~7% of differentially expressed genes in either dataset were concordantly differentially expressed between lineages. In the context of the extensive literature on parallel evolution in life-history, morphology, and behavior in Trinidadian guppies (reviewed in Magurran, 2005), these observations suggest that, while some mechanisms are shared, multiple transcriptional mechanisms may also give rise to some repeatedly evolved phenotypes. Multiple transcriptional mechanisms could arise if a diversity of transcriptional patterns can give rise to consistent output at the level of transcriptional and/or neural networks. In this case, transcriptional mechanisms may be flexible while mechanisms at higher orders of biological organization remain constrained (Prinz *et al.*, 2004; e.g. Crawford & Oleksiak, 2007). Indeed, we find that gene coexpression networks are largely preserved (see below), and, given that our transcriptomic data come from brain tissue, gene expression links to neural circuit physiology may be more flexible than neural circuit influences on behavior (e.g. J.-M. Goillard *et al.*, 2009; Grashow *et al.*, 2009). Some non-concordant transcriptional differences may also reflect homeostatic changes that arise to maintain consistent network output. While the possibility that closely related populations or species rely on shared mechanisms to evolve similar phenotypes seems intuitive (e.g. Rosenblum *et al.*, 2014), our findings here contribute to the mounting evidence that distinct mechanisms may

underlying similar phenotypes among closely related populations or even individuals (Crawford & Oleksiak, 2007; Kaeuffer *et al.*, 2012).

While concordant differential expression among drainages suggests gene expression differences are adaptive, both adaptive and non-adaptive processes may contribute to transcriptional differences restricted to a single lineage. First, high- and low-predation populations in different drainages are genetically distinct (Barson *et al.*, 2009; Willing *et al.*, 2010), and differences in standing genetic variation may influence which mechanisms are available for selection to act on (Barrett & Schluter, 2008). Second, differential expression in non-overlapping transcripts may represent adaptive responses to drainage- or site-specific environmental factors (Zandonà *et al.*, 2011; Kaeuffer *et al.*, 2012; Fitzpatrick, Torres-Dowdall, *et al.*, 2014). Third, low-predation populations are typically established by a very small number of individuals (Barson *et al.*, 2009; Willing *et al.*, 2010; Fraser *et al.*, 2015) and founder effects in these populations may make them more susceptible to influences of genetic drift and inbreeding. We cannot distinguish which non-concordant expression differences are the result of adaptive versus non-adaptive processes, yet their sheer number (90% of all DE genes in our dataset) suggests that distinct mechanisms have contributed to repeated, adaptive evolution in some phenotypes. Moreover, even non-adaptive expression divergence is relevant for a complete understanding of evolution in novel environments, as any divergence – be it adaptive, non-adaptive, or neutral – will shape evolutionary trajectories (Lynch, 2007). Given their rarity, the subset of transcripts differentially regulated in opposite directions among lineages may serve as particularly interesting starting points for exploring drainage-specific divergence. In light of the expansive nature of transcriptomic datasets, understanding transcriptomic signatures associated with repeated phenotypic evolution will require consideration not only of the role of a usually

relatively small number of overlapping transcripts, but also of non-overlapping patterns of differential expression. We suggest that the preponderance of unique DE genes in our dataset points to flexibility as a major factor in evolution.

Module preservation across evolutionary lineages

We took advantage of weighted gene coexpression network analysis (WGCNA) to examine expression patterns in a multivariate context. We found that modules were overall preserved between datasets, demonstrating that relationships among transcripts are stable across independent evolutionary lineages. This is in accordance with data from other studies that have found substantial module preservation both within (Hilliard *et al.*, 2012; Wong *et al.*, 2014) and among (Stuart *et al.*, 2003; Snel, 2004; Oldham *et al.*, 2006) species (but see Li & Johnson, 2010). The fact that modules are preserved while phenotypes diverge lends support to the idea that trait changes proceed primarily via changes in the expression of preserved transcriptional networks, rather than via changes in network structure.

As pleiotropic trade-offs arising from interactions among genes in a network may influence their propensity for expression divergence, we asked whether position in a network (i.e. connectivity with other genes) might influence patterns of differential expression. When we considered collections of genes similar in size to median module size, DE genes had relatively higher connectivity than non-DE genes. Highly connected genes may show a greater propensity for differential expression because they present a larger target for selection, either because their central position in the network allows them to most effectively shift overall module function, or conversely, because their central position makes them likely to exhibit correlated responses when other genes in the module are targeted by selection (Olson-Manning *et al.*, 2012). In either case,

the ability of central genes to facilitate changes in network function likely trades off with a higher pleiotropic load. The evidence we find for divergence in highly connected genes implies that selection on genes that shift network function is favorable, despite a potential increase in pleiotropic effects (Klingenberg, 2005). On the one hand, pleiotropic effects may be weak compared to beneficial changes, perhaps because they are mitigated by compensatory changes. On the other hand, pleiotropic effects could also be reduced if subsequent selection on gene-gene interactions gives rise to changes in network structure. The existence of some WGCNA modules with lower module preservation scores could reflect either adaptive evolution to reduce pleiotropic load or non-adaptive forms of developmental systems drift (True & Haag, 2001). Building on our understanding of how correlations among phenotypic traits may constrain (Endler, 1995; Schluter, 1996) or facilitate (Merilä & Björklund, 2004) evolution, our findings here provide evidence that highly connected genes have greater evolutionary potential than weakly connected genes.

Conclusions

We found evidence for shared mechanisms of evolution across two independent evolutionary lineages. Yet, the preponderance of non-overlapping transcriptional mechanisms associated with similar adaptive patterns across drainages highlights that alternative mechanisms may also give rise to similar adaptive phenotypes across independent evolutionary events in a single species. Furthermore, we provide evidence that highly connected genes may have greater adaptive potential. Application of network analyses to transcriptomic data remains uncommon, but this finding highlights the potential importance of these analyses in revealing how mechanistic phenomena may shape evolutionary patterns. We suggest that emergent properties

of transcriptional networks facilitate both robustness and evolutionary flexibility in transcriptional mechanisms.

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5. CONCLUSIONS AND SYNTHESIS

The goal of my dissertation was to study forces facilitating and constraining behavioral evolution, and in particular to explore interactions between developmental plasticity and evolutionary divergence in this context. To address these questions I conducted three studies examining patterns of flexibility and constraint in the evolution of behavior and its underlying mechanisms in Trinidadian guppies, *Poecilia reticulata*. The results of my dissertation research provide insights into how transcriptional mechanisms shape behavioral evolution and contribute to our understanding of how animals respond to novel and changing environments. While my work focused primarily on behavioral traits, recent evidence demonstrates that – like other traits – behaviors are heritable (e.g. Bell *et al.*, 2009) and can be used to estimate phylogenies (e.g. de Queiroz & Wimberger, 1993; Kamilar & Cooper, 2013), suggesting that the phenomena I demonstrate here likely apply to phenotypic traits generally.

In the first study, I characterized variation in a suite of behavioral traits based on differences in evolutionary history with and lifetime exposure to predators. I found that trait correlations were flexible in response to environmental differences at both developmental and evolutionary timescales, and that this flexibility influenced evolutionary trajectories. Evolutionary biologist, ethologists, and animal breeders have long been interested in understanding evolutionary constraints imposed by correlations among traits, and this question has recently received growing attention specifically in regards to behavior under the headings of behavioral syndromes and animal personality. Contrary to classical predictions, I showed that trait correlations observed in one population or environment did not predict evolutionary constraints in another, and that flexibility in trait correlations played an important role in shaping

evolutionary trajectories. Recognition of the fact that trait correlations are not stable across space and time will help inform both theoretical predictions and empirical studies of adaptation.

Given evidence for flexibility at the level of behavior, I next asked how such flexibility might be reflected by flexibility in underlying transcriptional mechanisms. My experimental approaches for this second study are notable for two reasons. First, rather than examining transcriptional responses to a single behavioral context, as is the most common current approach, I choose to link baseline transcriptional differences to differences in multiple behaviors. Second, my study included sufficient samples to link individual variation in behavior to individual variation in gene expression. Using this design, I examined relationships between gene expression and the same set of behaviors examined in the first study at both the level of single transcripts and gene coexpression networks. I found evidence for both consistency and flexibility in the associations between gene expression and behavior, with genetic background and rearing environment interacting to alter the relationships between transcript abundance and behavioral measures. This study complements the conclusions of the first by demonstrating flexibility in the transcriptional mechanisms associated with behavior. Specifically, I observed flexibility across timescales (i.e. relationships between gene expression and behavior depended on genetic and developmental differences) and levels of biological organization (i.e. patterns differed when I considered relationships between behavior and single transcripts versus coexpression networks). Importantly, I observed flexibility at the transcriptional level despite a similar range of variation at the behavioral level, suggesting that mechanistic flexibility does indeed reflect alternative transcriptional ‘solutions’ for similar phenotypes. The outcomes of this second study have both practical and theoretical implications. On a practical level, my work serves as a model for future studies that link baseline gene expression patterns to behavior as a means of understanding the

maintenance and evolution of both group and individual differences in behavior. On a theoretical level, I suggest that flexibility at the transcriptional level may increase evolutionary potential by balancing the maintenance of favorable trait constellations with the generation of phenotypic diversity during adaptation to novel environments.

If mechanisms are generally flexible, as I showed in the first and second studies, then we can expect distinct solutions to give rise to similar phenotypes among species, populations, and even individuals. In contrast, shared mechanisms that underlie similar phenotypes across parallel evolutionary events are generally considered evidence for functional or developmental constraints (e.g. Arthur, 2001; West-Eberhard, 2003; Gompel & Prud'homme, 2009). To expand my characterization of flexibility and constraints to include broader evolutionary patterns, in the third study of my dissertation I took advantage of the unique attributes of the guppy system to compare gene expression signatures associated with adaptation across two independent evolutionary lineages. I found evidence for both shared and distinct transcriptional mechanisms associated with repeated phenotypic evolution. This combination of consistency and flexibility across evolutionary lineages is similar to that observed across genetic backgrounds and rearing environments in the second study. Moreover, findings of this third study provide indirect support for a role for mechanistic flexibility in evolutionary potential; the existence of alternative mechanisms associated with similar patterns of trait divergence may allow for the generation and maintenance of cryptic variation that can be released and selected upon when environmental conditions change (Gibson & Dworkin, 2004; Schlichting, 2008; McGuigan & Sgrò, 2009; Paaby & Rockman, 2014). In concert, data from the second and third studies demonstrate how mechanistic flexibility may enable selection to build and maintain biological systems that are

simultaneously robust and flexible, thereby shedding light on longstanding questions concerning the mechanistic basis of evolvability.

In this third study I also showed that highly connected genes are more likely to evolve expression divergence than weakly connected genes. Notably, population differences in expression of highly connected genes were not accompanied by corresponding changes in overall network expression, speaking to a role for transcriptional flexibility in enabling compensatory transcriptional changes that maintain stable network output. To my knowledge, no other studies have addressed how a gene's propensity for expression divergence may be influenced by its connectivity with other genes. My findings here suggest that, while emergent properties of transcriptional networks may enable alternative gene expression patterns to give rise to similar phenotypes, coexpression patterns among genes may nonetheless be important predictors of a gene's evolutionary potential. While additional work is needed to determine the generality of these results, they highlight how underlying mechanisms may potentiate phenotypic divergence and adaptation.

In this dissertation research I found evidence for striking flexibility across behavioral phenotypes, behavioral mechanisms, and repeated evolutionary events. Guppies are known for being particularly rapidly adapting, and it remains to be seen whether the flexibility I find here is exceptional in this and other rapidly adapting species, or is a general principle explaining how biological systems balance robustness and evolvability. Our understanding of how differences in underlying mechanisms influence phenotypic evolution is still limited, but I suggest that mechanistic flexibility increases evolutionary potential. A deeper understanding of patterns of flexibility and constraint will ultimately inform our understanding of the forces limiting and potentiating adaptive evolution.

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APPENDIX 1

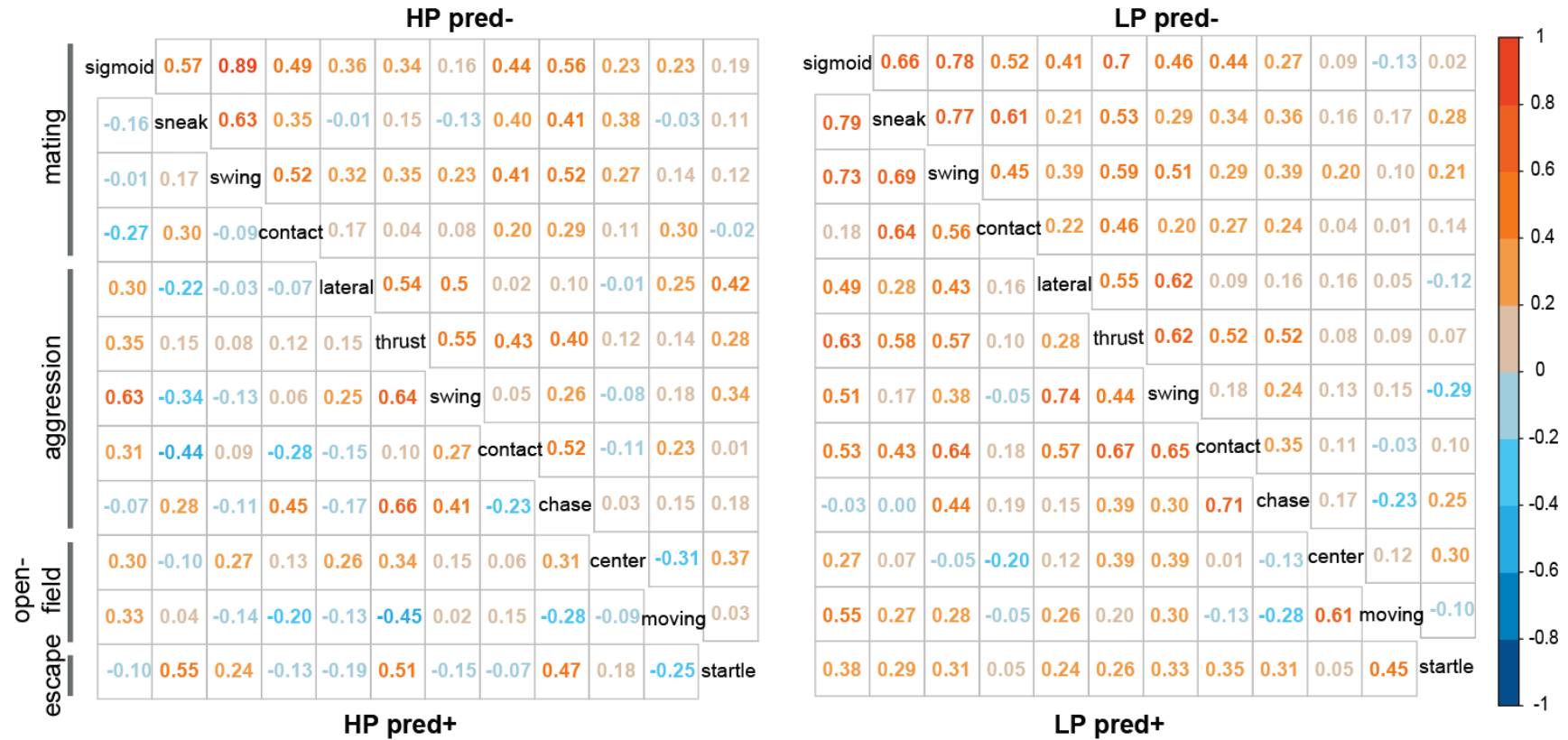


Figure S1.1. Correlational structure varies among groups. Individual behaviors are along the diagonal and associated behavioral contexts along the right side of the plot. Correlation values are shown and correlation strength and direction - form +1 to -1 – are indicated by color. Patterns for the high-predation population (HP) are on the left and for low-predation population (LP) are on the right. The top half of the plots show correlations in rearing environments without predators (pred-) and the bottom half show correlational structure in rearing environments with predators (pred+).

APPENDIX 2

Table S2.1. Annotation information for transcripts significantly associated with courtship behavior.

contig	module	SwissProt ID	SwissProt entry name	Protein name	Organism
c57781_g1	grey	Q499Z4	ZN672_HUMAN	Zinc finger protein 672	Homo sapiens (Human)
c83926_g2	yellow	P32392	ARP3_DROME	Actin-related protein 3 (Actin-2) (Actin-like protein 3) (Actin-like protein 66B)	Drosophila melanogaster (Fruit fly)
c84383_g2	blue	Q91VH1	ADR1_MOUSE	Adiponectin receptor protein 1	Mus musculus (Mouse)
c84440_g6	magenta	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	Homo sapiens (Human)
c86028_g1	blue	Q5R5Y7	ZN436_PONAB	Zinc finger protein 436	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c89322_g4	green	Q6UUV9	CRTC1_HUMAN	CREB-regulated transcription coactivator 1 (Mucoepidermoid carcinoma translocated protein 1) (Transducer of regulated cAMP response element-binding protein 1) (TORC-1) (Transducer of CREB protein 1)	Homo sapiens (Human)
c91145_g3	yellow	Q3MHN0	PSB6_BOVIN	Proteasome subunit beta type-6 (EC 3.4.25.1)	Bos taurus (Bovine)
c91247_g1	blue	Q9XSZ4	S4A4_RABIT	Electrogenic sodium bicarbonate cotransporter 1 (Sodium bicarbonate cotransporter) (Na(+)/HCO3(-) cotransporter) (Solute carrier family 4 member 4)	Oryctolagus cuniculus (Rabbit)
c93054_g3	magenta	Q5RD23	ATPO_PONAB	ATP synthase subunit O, mitochondrial (Oligomycin sensitivity conferral protein) (OSCP)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c93094_g7	blue	Q2T9W1	SNX20_BOVIN	Sorting nexin-20	Bos taurus (Bovine)
c93408_g1	salmon	Q12933	TRAF2_HUMAN	TNF receptor-associated factor 2 (EC 6.3.2.-) (E3 ubiquitin-protein ligase TRAF2) (Tumor necrosis factor type 2 receptor-associated protein 3)	Homo sapiens (Human)

c93513_g2	blue	Q9Z0V1	KCND3_MOUSE	Potassium voltage-gated channel subfamily D member 3 (Voltage-gated potassium channel subunit Kv4.3)	Mus musculus (Mouse)
c93571_g3	blue	P62870	ELOB_RAT	Transcription elongation factor B polypeptide 2 (Elongin 18 kDa subunit) (Elongin-B) (EloB) (RNA polymerase II transcription factor SIII subunit B) (SIII p18)	Rattus norvegicus (Rat)
c94640_g2	blue	Q6ZPY5	ZN507_MOUSE	Zinc finger protein 507	Mus musculus (Mouse)
c94844_g1	blue	Q6PEH9	S39AA_DANRE	Zinc transporter ZIP10 (Solute carrier family 39 member 10) (Zrt- and Irt-like protein 10) (ZIP-10)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94983_g1	yellow	Q6DFM1	SNF5_XENTR	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c95197_g3	green	O95948	ONEC2_HUMAN	One cut domain family member 2 (Hepatocyte nuclear factor 6-beta) (HNF-6-beta) (One cut homeobox 2) (Transcription factor ONECUT-2) (OC-2)	Homo sapiens (Human)
c95548_g7	magenta	Q9D3D9	ATPD_MOUSE	ATP synthase subunit delta, mitochondrial (F-ATPase delta subunit)	Mus musculus (Mouse)
c96577_g2	blue	P08548	LIN1_NYCCO	LINE-1 reverse transcriptase homolog (EC 2.7.7.49)	Nycticebus coucang (Slow loris)

Table S2.2. Annotation information for transcripts significantly associated with aggression behavior.

contig	module	SwissProt ID	SwissProt entry name	Protein name	Organism
c46561_g1	yellow	P49715	CEBPA_HUMAN	CCAAT/enhancer-binding protein alpha (C/EBP alpha)	Homo sapiens (Human)
c67560_g1	yellow	P70066	RS15_XIPMA	40S ribosomal protein S15 (RIG protein)	Xiphophorus maculatus (Southern platyfish) (Platyopocilus maculatus)
c83002_g1	yellow	O43526	KCNQ2_HUMAN	Potassium voltage-gated channel subfamily KQT member 2 (KQT-like 2) (Neuroblastoma-specific potassium channel subunit alpha KvLQT2) (Voltage-gated potassium channel subunit Kv7.2)	Homo sapiens (Human)
c83014_g1	grey	Q5R5B0	HERP1_PONAB	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c83926_g2	yellow	P32392	ARP3_DROME	Actin-related protein 3 (Actin-2) (Actin-like protein 3) (Actin-like protein 66B)	Drosophila melanogaster (Fruit fly)
c84393_g1	yellow	Q6P0D5	WBP11_DANRE	WW domain-binding protein 11 (WBP-11)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85256_g4	yellow	P97500	MYT1L_MOUSE	Myelin transcription factor 1-like protein (MyT1-L) (MyT1L) (Neural zinc finger factor 1) (NZF-1) (Postmitotic neural gene 1 protein) (Zinc finger protein Png-1)	Mus musculus (Mouse)
c85900_g8	blue	P18729	ZG57_XENLA	Gastrula zinc finger protein XICGF57.1 (Fragment)	Xenopus laevis (African clawed frog)
c86590_g1	grey	Q6P963	GLO2_DANRE	Hydroxyacylglutathione hydrolase, mitochondrial (EC 3.1.2.6) (Glyoxalase II) (Glx II)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87352_g5	blue	P62824	RAB3C_RAT	Ras-related protein Rab-3C	Rattus norvegicus (Rat)
c87423_g4	blue	Q9P2E7	PCD10_HUMAN	Protocadherin-10	Homo sapiens (Human)
c87752_g1	blue	Q9BWQ8	LFG2_HUMAN	Protein lifeguard 2 (Fas apoptotic inhibitory molecule 2) (Neural membrane protein 35) (Transmembrane BAX inhibitor motif-containing protein 2)	Homo sapiens (Human)
c88588_g2	yellow	Q9H8E8	CSR2B_HUMAN	Cysteine-rich protein 2-binding protein (CSRP2-binding protein) (ADA2A-containing complex subunit 2) (ATAC2)	Homo sapiens (Human)

c88658_g6	turquoise	Q90953	CSPG2_CHICK	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Large fibroblast proteoglycan) (PG-M)	Gallus gallus (Chicken)
c88717_g2	grey	Q6PA97	TPPC9_XENLA	Trafficking protein particle complex subunit 9 (NIK- and IKBKB-binding protein homolog)	Xenopus laevis (African clawed frog)
c89309_g6	blue	NA			
c89339_g3	yellow	Q5R6L5	CAND1_PONAB	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated and neddylation-dissociated protein 1) (p120 CAND1)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c89379_g7	blue	Q29397	SV2A_BOVIN	Synaptic vesicle glycoprotein 2A (p87)	Bos taurus (Bovine)
c89784_g3	blue	Q5R9T5	SPTC1_PONAB	Serine palmitoyltransferase 1 (EC 2.3.1.50) (Long chain base biosynthesis protein 1) (LCB 1) (Serine-palmitoyl-CoA transferase 1) (SPT 1) (SPT1)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c90188_g6	yellow	Q9NQ29	LUC7L_HUMAN	Putative RNA-binding protein Luc7-like 1 (Putative SR protein LUC7B1) (SR+89)	Homo sapiens (Human)
c90481_g2	grey	Q96EE4	CC126_HUMAN	Coiled-coil domain-containing protein 126	Homo sapiens (Human)
c91173_g2	grey	A3KGV1	ODFP2_MOUSE	Outer dense fiber protein 2 (84 kDa outer dense fiber protein) (Cenexin) (Outer dense fiber of sperm tails protein 2)	Mus musculus (Mouse)
c91354_g1	yellow	NA			
c91373_g7	blue	Q5R9Z6	ELAV2_PONAB	ELAV-like protein 2	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c92193_g1	black	A4QN56	NAGT1_DANRE	Sodium-dependent glucose transporter 1	Danio rerio (Zebrafish)
c92655_g4	yellow	Q6DGH9	OTBP_DANRE	Homeobox protein orthopedia B	(Brachydanio rerio) Danio rerio (Zebrafish)
c92824_g1	blue	NA			
c93263_g2	yellow	Q96KQ4	ASPP1_HUMAN	Apoptosis-stimulating of p53 protein 1 (Protein phosphatase 1 regulatory subunit 13B)	Homo sapiens (Human)
c93743_g5	blue	A6QLJ3	GUF1_BOVIN	Translation factor GUF1, mitochondrial (EC 3.6.5.-) (Elongation factor 4 homolog) (EF-4) (GTPase GUF1) (Ribosomal back-translocase)	Bos taurus (Bovine)
c93886_g7	yellow	Q1LVE8	SF3B3_DANRE	Splicing factor 3B subunit 3	Danio rerio (Zebrafish) (Brachydanio rerio)

c93946_g1	yellow	Q0IHI6	MED30_XENLA	Mediator of RNA polymerase II transcription subunit 30 (Mediator complex subunit 30)	Xenopus laevis (African clawed frog)
c94084_g4	yellow	Q8N6I4	TM251_HUMAN	Transmembrane protein 251	Homo sapiens (Human)
c94150_g3	blue	Q14318	FKBP8_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP8 (PPlase FKBP8) (EC 5.2.1.8) (38 kDa FK506-binding protein) (38 kDa FKBP) (FKBP-38) (hFKBP38) (FK506-binding protein 8) (FKBP-8) (FKBPR38) (Rotamase)	Homo sapiens (Human)
c94211_g5	blue	Q9DAX9	APBP2_MOUSE	Amyloid protein-binding protein 2 (Amyloid beta precursor protein-binding protein 2) (APP-BP2)	Mus musculus (Mouse)
c94330_g7	yellow	Q5XPI4	RN123_HUMAN	E3 ubiquitin-protein ligase RNF123 (EC 6.3.2.-) (Kip1 ubiquitination-promoting complex protein 1) (RING finger protein 123)	Homo sapiens (Human)
c94699_g5	yellow	Q63ZW7	INADL_MOUSE	InaD-like protein (Inadl protein) (Channel-interacting PDZ domain-containing protein) (Pals1-associated tight junction protein) (Protein associated to tight junctions)	Mus musculus (Mouse)
c94773_g7	yellow	P18700	TBB_STRPU	Tubulin beta chain (Beta-tubulin) (Fragment)	Strongylocentrotus purpuratus (Purple sea urchin)
c94909_g3	yellow	O94889	KLH18_HUMAN	Kelch-like protein 18	Homo sapiens (Human)
c95113_g4	yellow	P62263	RS14_HUMAN	40S ribosomal protein S14	Homo sapiens (Human)
c95309_g3	blue				
c95353_g1	yellow	Q7Z401	MYCPP_HUMAN	C-myc promoter-binding protein (DENN domain-containing protein 4A)	Homo sapiens (Human)
c95478_g1	salmon	Q91044	NTRK3_CHICK	NT-3 growth factor receptor (EC 2.7.10.1) (Neurotrophic tyrosine kinase receptor type 3) (TrkC tyrosine kinase) (Trk-C)	Gallus gallus (Chicken)
c95521_g1	yellow	O15550	KDM6A_HUMAN	Lysine-specific demethylase 6A (EC 1.14.11.-) (Histone demethylase UTX) (Ubiquitously-transcribed TPR protein on the X chromosome) (Ubiquitously-transcribed X chromosome tetratricopeptide repeat protein)	Homo sapiens (Human)
c95576_g7	yellow	P37727	RAE1_RAT	Rab proteins geranylgeranyltransferase component A 1 (Choroideremia protein homolog) (Rab escort protein 1) (REP-1)	Rattus norvegicus (Rat)
c95809_g6	blue	Q9JJV2	PROF2_MOUSE	Profilin-2 (Profilin II)	Mus musculus (Mouse)

c96180_g3	yellow	O00750	P3C2B_HUMAN	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta (PI3K-C2-beta) (PtdIns-3-kinase C2 subunit beta) (EC 2.7.1.154) (C2-PI3K) (Phosphoinositide 3-kinase-C2-beta)	Homo sapiens (Human)
c96342_g2	blue	Q8NHE4	VA0E2_HUMAN	V-type proton ATPase subunit e 2 (V-ATPase subunit e 2) (Lysosomal 9 kDa H(+)-transporting ATPase V0 subunit e2) (Vacuolar proton pump subunit e 2)	Homo sapiens (Human)
c96405_g3	yellow	Q8NFD5	ARI1B_HUMAN	AT-rich interactive domain-containing protein 1B (ARID domain-containing protein 1B) (BRG1-associated factor 250b) (BAF250B) (BRG1-binding protein hELD/OSA1) (Osa homolog 2) (hOsa2) (p250R)	Homo sapiens (Human)
c96613_g6	blue	Q5RD78	HECD2_PONAB	Probable E3 ubiquitin-protein ligase HECTD2 (EC 6.3.2.-) (HECT domain-containing protein 2)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c96820_g7	green	Q05AL2	PPM1H_DANRE	Protein phosphatase 1H (EC 3.1.3.16)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96862_g5	yellow	P70399	TP53B_MOUSE	Tumor suppressor p53-binding protein 1 (53BP1) (p53-binding protein 1) (p53BP1)	Mus musculus (Mouse)
c96905_g3	yellow	Q569Z5	DDX46_MOUSE	Probable ATP-dependent RNA helicase DDX46 (EC 3.6.4.13) (DEAD box protein 46)	Mus musculus (Mouse)
c97011_g6	yellow	P43686	PRS6B_HUMAN	26S protease regulatory subunit 6B (26S proteasome AAA-ATPase subunit RPT3) (MB67-interacting protein) (MIP224) (Proteasome 26S subunit ATPase 4) (Tat-binding protein 7) (TBP-7)	Homo sapiens (Human)

Table S2.3. Annotation information for transcripts significantly associated with open-field behavior.

contig	module	SwissProt ID	SwissProt entry name	Protein name	Organism
c80935_g2	cyan	P06398	TNNT3_COTJA	Troponin T, fast skeletal muscle isoforms	Coturnix coturnix japonica (Japanese quail) (Coturnix japonica)
c81233_g2	brown	O42583	PRPH2_XENLA	Peripherin-2 (Retinal degeneration slow protein) (xRDS38)	Xenopus laevis (African clawed frog)
c84235_g1	midnightblue	Q5ZM55	FEM1B_CHICK	Protein fem-1 homolog B (FEM1b) (FEM1-beta)	Gallus gallus (Chicken)
c85325_g3	cyan	Q90339	MYSS_CYPKA	Myosin heavy chain, fast skeletal muscle	Cyprinus carpio (Common carp)
c86598_g3	cyan	P00504	AATC_CHICK	Aspartate aminotransferase, cytoplasmic (cAspAT) (EC 2.6.1.1) (EC 2.6.1.3) (Cysteine aminotransferase, cytoplasmic) (cCAT) (Glutamate oxaloacetate transaminase 1) (Transaminase A)	Gallus gallus (Chicken)
c88143_g1	cyan	NA			
c88364_g6	cyan	P81660	TNNC2_ANGAN	Troponin C, skeletal muscle (TNC)	Anguilla anguilla (European freshwater eel) (Muraena anguilla)
c88380_g1	cyan	Q90339	MYSS_CYPKA	Myosin heavy chain, fast skeletal muscle	Cyprinus carpio (Common carp)
c88564_g3	grey	NA			
c89633_g4	green	Q6GLR7	CAPS1_XENLA	Calcium-dependent secretion activator 1 (Calcium-dependent activator protein for secretion 1) (CAPS-1)	Xenopus laevis (African clawed frog)
c91377_g1	cyan	Q90339	MYSS_CYPKA	Myosin heavy chain, fast skeletal muscle	Cyprinus carpio (Common carp)
c91377_g3	cyan	Q90339	MYSS_CYPKA	Myosin heavy chain, fast skeletal muscle	Cyprinus carpio (Common carp)
c91696_g6	grey	Q6IQH6	LPPR1_DANRE	Lipid phosphate phosphatase-related protein type 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c93049_g1	grey	NA			
c93448_g2	cyan	Q95L39	LOXL1_BOVIN	Lysyl oxidase homolog 1 (EC 1.4.3.-) (Lysyl oxidase-like protein 1)	Bos taurus (Bovine)

c93910_g2	green	Q5RCU4	SOX6_PONAB	Transcription factor SOX-6	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c94207_g7	black	Q202B1	AT1B4_XENLA	Protein ATP1B4 (X,K-ATPase subunit beta-m) (X/potassium-transporting ATPase subunit beta-m)	Xenopus laevis (African clawed frog)
c95539_g4	grey	NA			
c95599_g3	pink	P11369	LORF2_MOUSE	LINE-1 retrotransposable element ORF2 protein (ORF2p) (Long interspersed element-1) (L1) (Retrovirus-related Pol polyprotein LINE-1)	Mus musculus (Mouse)
c96530_g8	greenyellow	Q3SZX0	PLM_BOVIN	Phospholemman (FXVD domain-containing ion transport regulator 1)	Bos taurus (Bovine)

Table S2.4. Annotation information for transcripts with a population dependent relationship with open-field behavior.

contig	module	SwissProt ID	SwissProt entry name	Protein name	Organism
c67973_g1	midnightblue	Q2M385	MPEG1_HUMAN	Macrophage-expressed gene 1 protein (Macrophage gene 1 protein) (Mpg-1)	Homo sapiens (Human)
c77052_g1	yellow	O57592	RL7A_TAKRU	60S ribosomal protein L7a (Surfeit locus protein 3)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c77109_g1	grey	Q6ZM63	GPN3_DANRE	GPN-loop GTPase 3 (ATP-binding domain 1 family member C)	Danio rerio (Zebrafish) (Brachydanio rerio)
c79099_g1	grey	P30404	PPIF_BOVIN	Peptidyl-prolyl cis-trans isomerase F, mitochondrial (PPIase F) (EC 5.2.1.8) (Cyclophilin D) (CyP-D) (CypD) (Cyclophilin F) (Rotamase F)	Bos taurus (Bovine)
c80815_g2	grey	Q9WU49	CHSP1_RAT	Calcium-regulated heat stable protein 1 (Calcium-regulated heat-stable protein of 24 kDa) (CRHSP-24)	Rattus norvegicus (Rat)
c81102_g1	grey	Q1LXI5	RM54_DANRE	39S ribosomal protein L54, mitochondrial (L54mt) (MRP-L54)	Danio rerio (Zebrafish) (Brachydanio rerio)
c82412_g3	magenta	P48201	AT5G3_HUMAN	ATP synthase F(0) complex subunit C3, mitochondrial (ATP synthase lipid-binding protein) (ATP synthase proteolipid P3) (ATP synthase proton-transporting mitochondrial F(0) complex subunit C3) (ATPase protein 9) (ATPase subunit c)	Homo sapiens (Human)
c82568_g1	grey	P13716	HEM2_HUMAN	Delta-aminolevulinic acid dehydratase (ALADH) (EC 4.2.1.24) (Porphobilinogen synthase)	Homo sapiens (Human)
c82751_g1	grey	Q7Z5K2	WAPL_HUMAN	Wings apart-like protein homolog (Friend of EBNA2 protein)	Homo sapiens (Human)
c84958_g2	greenyellow	Q60898	SLAP1_MOUSE	Src-like-adaptor (Src-like-adaptor protein 1) (SLAP-1) (mSLAP)	Mus musculus (Mouse)
c85141_g1	grey	Q4R4C9	ARFG3_MACFA	ADP-ribosylation factor GTPase-activating protein 3 (ARF GAP 3)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c85871_g3	grey	NA			
c85871_g4	green	P20700	LMNB1_HUMAN	Lamin-B1	Homo sapiens (Human)

c85909_g4	grey	Q5R7K9	EDIL3_PONAB	EGF-like repeat and discoidin I-like domain-containing protein 3	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii) Mus musculus (Mouse)
c86290_g1	blue	P23359	BMP7_MOUSE	Bone morphogenetic protein 7 (BMP-7) (Osteogenic protein 1) (OP-1)	
c86985_g8	grey	Q16394	EXT1_HUMAN	Exostosin-1 (EC 2.4.1.224) (EC 2.4.1.225) (Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Multiple exostoses protein 1) (Putative tumor suppressor protein EXT1)	Homo sapiens (Human)
c87095_g2	purple	Q8R5M0	GIPC3_MOUSE	PDZ domain-containing protein GIPC3 (Regulator of G-protein signaling 19-interacting protein 3)	Mus musculus (Mouse)
c87097_g10	grey	Q14721	KCNB1_HUMAN	Potassium voltage-gated channel subfamily B member 1 (Delayed rectifier potassium channel 1) (DRK1) (h-DRK1) (Voltage-gated potassium channel subunit Kv2.1)	Homo sapiens (Human)
c87108_g3	tan	P17426	AP2A1_MOUSE	AP-2 complex subunit alpha-1 (100 kDa coated vesicle protein A) (Adaptor protein complex AP-2 subunit alpha-1) (Adaptor-related protein complex 2 subunit alpha-1) (Alpha-adaptin A) (Alpha1-adaptin) (Clathrin assembly protein complex 2 alpha-A large chain) (Plasma membrane adaptor HA2/AP2 adaptin alpha A subunit)	Mus musculus (Mouse)
c88564_g11	grey	Q90W33	HIC2_DANRE	Hypermethylated in cancer 2 protein	Danio rerio (Zebrafish) (Brachydanio rerio)
c88627_g1	grey	P81127	SNAG_BOVIN	Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-sensitive factor attachment protein gamma)	Bos taurus (Bovine)
c88651_g8	grey	Q9WVC1	SLIT2_RAT	Slit homolog 2 protein (Slit-2) (Fragment)	Rattus norvegicus (Rat)
c88783_g7	grey	O43933	PEX1_HUMAN	Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)	Homo sapiens (Human)
c88817_g3	blue	P08548	LIN1_NYCCO	LINE-1 reverse transcriptase homolog (EC 2.7.7.49)	Nycticebus coucang (Slow loris)
c88820_g2	grey	Q1LWL8	MCL1B_DANRE	Protein L-Myc-1b	Danio rerio (Zebrafish) (Brachydanio rerio)

c89015_g5	grey	Q17QD9	CSEN_BOVIN	Calsenilin (A-type potassium channel modulatory protein 3) (Kv channel-interacting protein 3) (KChIP3)	Bos taurus (Bovine)
c89035_g3	grey	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A (YPT1-related protein)	Homo sapiens (Human)
c90079_g4	green	Q02357	ANK1_MOUSE	Ankyrin-1 (ANK-1) (Erythrocyte ankyrin)	Mus musculus (Mouse)
c90354_g11	yellow	P53992	SC24C_HUMAN	Protein transport protein Sec24C (SEC24-related protein C)	Homo sapiens (Human)
c90365_g5	pink				
c90741_g2	grey	Q5RAA9	NPS3A_PONAB	Protein NipSnap homolog 3A (NipSnap3A)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c91810_g5	grey	Q6NYL5	ALAT2_DANRE	Alanine aminotransferase 2-like (ALT2) (EC 2.6.1.2) (Glutamate pyruvate transaminase 2) (GPT 2) (Glutamic--alanine transaminase 2) (Glutamic--pyruvic transaminase 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91812_g1	purple	P39061	COIA1_MOUSE	Collagen alpha-1(XVIII) chain [Cleaved into: Endostatin]	Mus musculus (Mouse)
c92102_g7	grey	Q9HAT8	PELI2_HUMAN	E3 ubiquitin-protein ligase pellino homolog 2 (Pellino-2) (EC 6.3.2.-)	Homo sapiens (Human)
c92266_g4	grey	Q8BZT9	LACC1_MOUSE	Laccase domain-containing protein 1	Mus musculus (Mouse)
c93389_g3	black	O95372	LYPA2_HUMAN	Acyl-protein thioesterase 2 (APT-2) (EC 3.1.2.-) (Lysophospholipase II) (LPL-II) (LysoPLA II)	Homo sapiens (Human)
c93483_g1	turquoise	Q96KQ7	EHMT2_HUMAN	Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (EC 2.1.1.43) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Lysine N-methyltransferase 1C) (Protein G9a)	Homo sapiens (Human)
c93522_g2	black	Q9NT68	TEN2_HUMAN	Teneurin-2 (Ten-2) (Protein Odd Oz/ten-m homolog 2) (Tenascin-M2) (Ten-m2) (Teneurin transmembrane protein 2) [Cleaved into: Ten-2, soluble form; Ten-2 intracellular domain (Ten-2 ICD)]	Homo sapiens (Human)
c93819_g2	brown	P53452	DRD1L_TAKRU	D(1)-like dopamine receptor	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c93872_g7	grey	Q91XL9	OSBL1_MOUSE	Oxysterol-binding protein-related protein 1 (ORP-1) (OSBP-related protein 1)	Mus musculus (Mouse)

c94338_g2	blue	Q8IY84	NIM1_HUMAN	Serine/threonine-protein kinase NIM1 (EC 2.7.11.1) (NIM1 serine/threonine-protein kinase)	Homo sapiens (Human)
c94538_g10	grey	P35813	PPM1A_HUMAN	Protein phosphatase 1A (EC 3.1.3.16) (Protein phosphatase 2C isoform alpha) (PP2C-alpha) (Protein phosphatase 1A)	Homo sapiens (Human)
c95201_g2	grey	Q64GL0	EVL_XENLA	Ena/VASP-like protein (Ena/vasodilator-stimulated phosphoprotein-like)	Xenopus laevis (African clawed frog)
c95491_g5	black	Q08BI9	MCU_DANRE	Calcium uniporter protein, mitochondrial (Coiled-coil domain-containing protein 109A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95950_g1	grey	Q96JB2	COG3_HUMAN	Conserved oligomeric Golgi complex subunit 3 (COG complex subunit 3) (Component of oligomeric Golgi complex 3) (Vesicle-docking protein SEC34 homolog) (p94)	Homo sapiens (Human)
c95995_g4	grey	P31409	VATB_DROME	V-type proton ATPase subunit B (V-ATPase subunit B) (V-ATPase 55 kDa subunit) (Vacuolar proton pump subunit B)	Drosophila melanogaster (Fruit fly)
c96011_g4	grey	Q5NCY0	KDM6B_MOUSE	Lysine-specific demethylase 6B (EC 1.14.11.-) (JmjC domain-containing protein 3) (Jumonji domain-containing protein 3)	Mus musculus (Mouse)
c96066_g4	grey	Q80U12	SGSM2_MOUSE	Small G protein signaling modulator 2 (RUN and TBC1 domain-containing protein 1)	Mus musculus (Mouse)
c96071_g7	salmon	Q6P2L7	CASC4_MOUSE	Protein CASC4 (Cancer susceptibility candidate gene 4 protein homolog)	Mus musculus (Mouse)
c96943_g6	turquoise	Q90ZK6	ACVR1_CHICK	Activin receptor type-1 (EC 2.7.11.30) (Activin receptor type I) (Type I TGF B receptor)	Gallus gallus (Chicken)
c97040_g4	grey	Q6DIC0	SMCA2_MOUSE	Probable global transcription activator SNF2L2 (EC 3.6.4.-) (ATP-dependent helicase SMARCA2) (BRG1-associated factor 190B) (BAF190B) (Protein brahma homolog) (SNF2-alpha) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 2)	Mus musculus (Mouse)

Table S2.5. Annotation information for transcripts with a rearing dependent relationship with open-field behavior.

contig	module	SwissProt ID	SwissProt entry name	Protein name	Organism
c76628_g1	yellow	P41115	RS11_XENLA	40S ribosomal protein S11	Xenopus laevis (African clawed frog)
c78151_g1	magenta	Q5TYQ3	COA7_DANRE	Cytochrome c oxidase assembly factor 7 (Beta-lactamase hcp-like protein) (Sel1 repeat-containing protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c79370_g1	grey	Q2KIR1	SNRPA_BOVIN	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	Bos taurus (Bovine)
c80657_g2	grey	Q9NUS5	AP5S1_HUMAN	AP-5 complex subunit sigma-1 (Adaptor-related protein complex 5 sigma subunit) (Sigma5)	Homo sapiens (Human)
c80735_g1	grey	Q8QFQ9	TRH_ONCNE	Pro-thyrotropin-releasing hormone-A (Pro-TRH-A) (Prothyroliberin type A) [Cleaved into: Thyrotropin-releasing hormone (TRH) (Protirelin) (TSH-releasing factor) (Thyroliberin) (Thyrotropin-releasing factor) (TRF)]	Oncorhynchus nerka (Sockeye salmon) (Salmo nerka)
c82186_g9	cyan	P13637	AT1A3_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-3 (Na(+)/K(+) ATPase alpha-3 subunit) (EC 3.6.3.9) (Na(+)/K(+) ATPase alpha(III) subunit) (Sodium pump subunit alpha-3)	Homo sapiens (Human)
c82728_g1	grey	O95237	LRAT_HUMAN	Lecithin retinol acyltransferase (EC 2.3.1.135) (Phosphatidylcholine--retinol O-acyltransferase)	Homo sapiens (Human)
c83835_g1	grey	Q5FVJ5	CP045_RAT	Uncharacterized protein C16orf45 homolog	Rattus norvegicus (Rat)
c84551_g4	tan	Q8BRB7	KAT6B_MOUSE	Histone acetyltransferase KAT6B (EC 2.3.1.48) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 4) (MYST-4) (Protein querkopf)	Mus musculus (Mouse)
c86127_g3	grey	Q90854	KCNJ3_CHICK	G protein-activated inward rectifier potassium channel 1 (GIRK-1) (Inward rectifier K(+) channel Kir3.1) (Potassium channel, inwardly rectifying subfamily J member 3)	Gallus gallus (Chicken)
c86243_g4	green	Q5VUJ6	LRCH2_HUMAN	Leucine-rich repeat and calponin homology domain-containing protein 2	Homo sapiens (Human)
c86316_g4	grey	Q62889	NLGN3_RAT	Neuroigin-3 (Gliotactin homolog)	Rattus norvegicus (Rat)
c86413_g6	grey	Q99MD9	NASP_MOUSE	Nuclear autoantigenic sperm protein (NASP)	Mus musculus (Mouse)

c87282_g9	grey	Q7Z3F1	GP155_HUMAN	Integral membrane protein GPR155 (G-protein coupled receptor PGR22)	Homo sapiens (Human)
c87402_g9	red	P54731	FAF1_MOUSE	FAS-associated factor 1	Mus musculus (Mouse)
c87926_g2	green	P19493	GRIA4_RAT	Glutamate receptor 4 (GluR-4) (GluR4) (AMPA-selective glutamate receptor 4) (GluR-D) (Glutamate receptor ionotropic, AMPA 4) (GluA4)	Rattus norvegicus (Rat)
c88052_g3	turquoise	Q06AU5	RAB32_PIG	Ras-related protein Rab-32	Sus scrofa (Pig)
c88052_g7	turquoise	Q13255	GRM1_HUMAN	Metabotropic glutamate receptor 1 (mGluR1)	Homo sapiens (Human)
c88466_g1	grey	O43347	MSI1H_HUMAN	RNA-binding protein Musashi homolog 1 (Musashi-1)	Homo sapiens (Human)
c88663_g6	grey	Q91309	F26_LITCT	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (6PF-2-K/Fru-2,6-P2ase) (PFK/FBPase) (6PF-2-K/Fru-2,6-P2ase liver/muscle isozymes) [Includes: 6-phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)]	Lithobates catesbeiana (American bullfrog) (Rana catesbeiana)
c89193_g2	yellow	Q6P5L3	RL19_DANRE	60S ribosomal protein L19	Danio rerio (Zebrafish) (Brachydanio rerio)
c89501_g2	grey	NA			
c89528_g7	grey	Q6ZWJ1	STXB4_HUMAN	Syntaxin-binding protein 4 (Syntaxin 4-interacting protein) (STX4-interacting protein) (Synip)	Homo sapiens (Human)
c89650_g5	turquoise	O94933	SLIK3_HUMAN	SLIT and NTRK-like protein 3	Homo sapiens (Human)
c89681_g3	purple	NA			
c89735_g2	grey	Q9NYT6	ZN226_HUMAN	Zinc finger protein 226	Homo sapiens (Human)
c89892_g7	red	P11730	KCC2G_RAT	Calcium/calmodulin-dependent protein kinase type II subunit gamma (CaM kinase II subunit gamma) (CaMK-II subunit gamma) (EC 2.7.11.17)	Rattus norvegicus (Rat)
c89913_g5	turquoise	Q68Y21	GRID2_DANRE	Glutamate receptor ionotropic, delta-2 (GluD2) (GluR delta-2 subunit)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90484_g1	turquoise	Q80UN9	MOD5_MOUSE	tRNA dimethylallyltransferase, mitochondrial (EC 2.5.1.75) (Isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPP transferase) (IPPT) (tRNA isopentenyltransferase) (IPTase)	Mus musculus (Mouse)
c90928_g5	blue	Q5PR61	LMBD1_DANRE	Probable lysosomal cobalamin transporter (LMBR1 domain-containing protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)

c91208_g2	grey	O55166	VPS52_RAT	Vacuolar protein sorting-associated protein 52 homolog (SAC2 suppressor of actin mutations 2-like protein)	Rattus norvegicus (Rat)
c91234_g2	black	O15068	MCF2L_HUMAN	Guanine nucleotide exchange factor DBS (DBL's big sister) (MCF2-transforming sequence-like protein)	Homo sapiens (Human)
c91819_g1	grey	Q9ULH0	KDIS_HUMAN	Kinase D-interacting substrate of 220 kDa (Ankyrin repeat-rich membrane-spanning protein)	Homo sapiens (Human)
c91930_g5	tan	Q80TG9	LRFN2_MOUSE	Leucine-rich repeat and fibronectin type-III domain-containing protein 2	Mus musculus (Mouse)
c92082_g7	grey	Q9UHD2	TBK1_HUMAN	Serine/threonine-protein kinase TBK1 (EC 2.7.11.1) (NF-kappa-B-activating kinase) (T2K) (TANK-binding kinase 1)	Homo sapiens (Human)
c92648_g7	salmon	NA			
c92853_g4	salmon	P50607	TUB_HUMAN	Tubby protein homolog	Homo sapiens (Human)
c93171_g4	red	O75410	TACC1_HUMAN	Transforming acidic coiled-coil-containing protein 1 (Gastric cancer antigen Ga55) (Taxin-1)	Homo sapiens (Human)
c93891_g4	blue	Q8QZZ7	TPRKB_MOUSE	EKC/KEOPS complex subunit Tprkb (TP53RK-binding protein)	Mus musculus (Mouse)
c94262_g4	grey	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	Homo sapiens (Human)
c94302_g1 0	grey	P37285	KLC1_RAT	Kinesin light chain 1 (KLC 1)	Rattus norvegicus (Rat)
c94633_g1 3	grey	Q6DGH9	OTBP_DANRE	Homeobox protein orthopedia B	Danio rerio (Zebrafish) (Brachydanio rerio)
c94689_g1	grey	O00763	ACACB_HUMAN	Acetyl-CoA carboxylase 2 (EC 6.4.1.2) (ACC-beta) [Includes: Biotin carboxylase (EC 6.3.4.14)]	Homo sapiens (Human)
c94974_g3	grey	P15306	TRBM_MOUSE	Thrombomodulin (TM) (Fetomodulin) (CD antigen CD141)	Mus musculus (Mouse)
c95127_g1 0	turquoise	D2I3C6	DCLK2_AILME	Serine/threonine-protein kinase DCLK2 (EC 2.7.11.1) (CaMK-like CREB regulatory kinase 2) (CL2) (CLICK-II) (CLICK2) (Doublecortin-like and CAM kinase-like 2) (Doublecortin-like kinase 2)	Ailuropoda melanoleuca (Giant panda)

c95142_g4	black	Q5SFM8	RBM27_MOUSE	RNA-binding protein 27 (Peri-implantation stem cell protein 1) (RNA-binding motif protein 27)	Mus musculus (Mouse)
c95689_g2	yellow	Q80YV3	TRRAP_MOUSE	Transformation/transcription domain-associated protein (Tra1 homolog)	Mus musculus (Mouse)
c96291_g7	cyan	P14618	KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	Homo sapiens (Human)
c96391_g1	black	Q99676	ZN184_HUMAN	Zinc finger protein 184	Homo sapiens (Human)
c96420_g2	brown	Q90487	HBA_DANRE	Hemoglobin subunit alpha (Alpha-globin aa1) (Hemoglobin alpha chain)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96761_g4	turquoise	Q5VWQ0	RSBN1_HUMAN	Round spermatid basic protein 1	Homo sapiens (Human)

Table S2.6. Annotation information for transcripts with a population by rearing dependent relationship with open-field behavior.

contig	module	SwissProt ID	SwissProt entry name	Protein name	Organism
c71493_g1	greenyellow	Q8K342	RASF9_MOUSE	Ras association domain-containing protein 9 (PAM COOH-terminal interactor protein 1) (P-CIP1) (Peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor)	Mus musculus (Mouse)
c79001_g1	red	Q9JKF8	RASD1_RAT	Dexamethasone-induced Ras-related protein 1	Rattus norvegicus (Rat)
c80516_g1	yellow	Q14511	CASL_HUMAN	Enhancer of filamentation 1 (hEF1) (CRK-associated substrate-related protein) (CAS-L) (CasL) (Cas scaffolding protein family member 2) (Neural precursor cell expressed developmentally down-regulated protein 9) (NEDD-9) (Renal carcinoma antigen NY-REN-12) (p105) [Cleaved into: Enhancer of filamentation 1 p55]	Homo sapiens (Human)
c81296_g1	grey	Q9H307	PININ_HUMAN	Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Desmosome-associated protein) (Domain-rich serine protein) (DRS protein) (DRSP) (Melanoma metastasis clone A protein) (Nuclear protein SDK3) (SR-like protein)	Homo sapiens (Human)
c83730_g2	midnightblue	A4IFE9	TM9S1_BOVIN	Transmembrane 9 superfamily member 1	Bos taurus (Bovine)
c85868_g1	grey	Q9TRY0	FKBP4_BOVIN	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (FK506-binding protein 4) (FKBP-4) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	Bos taurus (Bovine)
c86812_g3	green	O62305	KCC2D_CAEEL	Calcium/calmodulin-dependent protein kinase type II (CaM kinase II) (EC 2.7.11.17) (Uncoordinated protein 43)	Caenorhabditis elegans
c87537_g1	blue	Q9HC56	PCDH9_HUMAN	Protocadherin-9	Homo sapiens (Human)

c89067_g1	turquoise	O95602	RPA1_HUMAN	DNA-directed RNA polymerase I subunit RPA1 (RNA polymerase I subunit A1) (EC 2.7.7.6) (A190) (DNA-directed RNA polymerase I largest subunit) (Homo sapiens (Human)
c89211_g4	turquoise	Q9HAV0	GBB4_HUMAN	Guanine nucleotide-binding protein subunit beta-4 (Transducin beta chain 4)	Homo sapiens (Human)
c89249_g5	greenyellow	P56199	ITA1_HUMAN	Integrin alpha-1 (CD49 antigen-like family member A) (Laminin and collagen receptor) (VLA-1) (CD antigen CD49a)	Homo sapiens (Human)
c89674_g2	brown	Q0V898	NELFE_BOVIN	Negative elongation factor E (NELF-E) (RNA-binding protein RD)	Bos taurus (Bovine)
c90763_g4	grey	Q1LUT1	EDC4_DANRE	Enhancer of mRNA-decapping protein 4	Danio rerio (Zebrafish) (Brachydanio rerio)
c92235_g3	green	Q9BYP7	WNK3_HUMAN	Serine/threonine-protein kinase WNK3 (EC 2.7.11.1) (Protein kinase lysine-deficient 3) (Protein kinase with no lysine 3)	Homo sapiens (Human)
c92873_g2	lightcyan	Q9YH16	LMO3_XENLA	LIM domain only protein 3 (LMO-3) (LIM domain only protein 1) (LMO-1) (xLMO1)	Xenopus laevis (African clawed frog)
c93624_g7	blue	O70404	VAMP8_MOUSE	Vesicle-associated membrane protein 8 (VAMP-8) (Endobrevin) (Edb)	Mus musculus (Mouse)
c93833_g5	red	P18265	GSK3A_RAT	Glycogen synthase kinase-3 alpha (GSK-3 alpha) (EC 2.7.11.26) (Factor A) (FA) (Serine/threonine-protein kinase GSK3A) (EC 2.7.11.1)	Rattus norvegicus (Rat)
c94298_g5	green	Q01815	CAC1C_MOUSE	Voltage-dependent L-type calcium channel subunit alpha-1C (Calcium channel, L type, alpha-1 polypeptide, isoform 1, cardiac muscle) (MELC-CC) (Mouse brain class C) (MBC) (Voltage-gated calcium channel subunit alpha Cav1.2)	Mus musculus (Mouse)
c94744_g2	grey	B2RWS6	EP300_MOUSE	Histone acetyltransferase p300 (p300 HAT) (EC 2.3.1.48) (E1A-associated protein p300)	Mus musculus (Mouse)
c96010_g8	black	Q9P2R6	RERE_HUMAN	Arginine-glutamic acid dipeptide repeats protein (Atrophin-1-like protein) (Atrophin-1-related protein)	Homo sapiens (Human)
c96937_g6	grey	O88420	SCN8A_RAT	Sodium channel protein type 8 subunit alpha (Peripheral nerve protein type 4) (PN4) (Sodium channel 6) (NaCh6) (Sodium channel protein type VIII subunit alpha) (Voltage-gated sodium channel subunit alpha Nav1.6)	Rattus norvegicus (Rat)

c96970_g4	black	P20237	GBRA4_BOVIN	Gamma-aminobutyric acid receptor subunit alpha-4 (GABA(A) receptor subunit alpha-4)	Bos taurus (Bovine)
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Table S2.7. Significantly ($p < 0.05$) enriched GO terms in each coexpression module

module	GO terms
black	metabolic process, ephrin receptor signaling pathway, cyclic nucleotide metabolic process, intracellular protein transport
blue	DNA-templated transcription initiation, nucleoside metabolic process, transcription from RNA polymerase II, RNA processing, protein glycosylation, protein folding, cellular protein complex assembly, small GTPase mediated signal transduction, translation initiation, DNA repair, organelle fission
brown	steroid hormone mediated signaling pathway, termination of G-protein coupled receptor signaling, amino acid transmembrane transport, protein phosphorylation, G-protein coupled receptor signaling pathway, Notch signaling pathway, metabolic process
cyan	carbohydrate metabolic process, glycolytic process, metabolic process, calcium ion transmembrane transport, protein modification by small protein conjugation; coenzyme biosynthetic process, nucleotide catabolic process, nucleotide metabolic process, purine nucleotide biosynthetic process
green	ion transport, transmembrane transport, transport, ephrin receptor signaling pathway, single organism signaling, inorganic anion transport, calcium ion transmembrane transport, G-protein coupled receptor signaling pathway, protein homooligomerization, cell communication, potassium ion transport, cellular process, signal transduction
greenyellow	proteolysis, cell redox homeostasis, lipid metabolic process, regulation of cytoskeleton organization, regulation of biological quality, cell adhesion, localization, carbohydrate metabolic process
lightcyan	DNA-templated regulation of transcription, hemophilic cell adhesion
lightgreen	oxidation-reduction process, cellular amino acid catabolic process, protein-DNA complex assembly
lightgrey	protein dephosphorylation, protein phosphorylation, DNA-templated regulation of transcription, neuropeptide signaling pathway, metabolic process, tRNA aminoacylation for protein translation, biosynthetic process, multicellular organismal development, protein glycosylation, protein folding, oxidation-reduction process, nucleobase-containing compound metabolic process, DNA repair, ubiquitin-dependent protein catabolic process

magenta	ATP metabolic process, proteolysis involved in cellular protein catabolic process, hydrogen ion transmembrane transport, purine ribonucleoside monophosphate biosynthesis, GTP catabolic process, ATP hydrolysis coupled proton transport, purine ribonucleoside triphosphate biosynthesis, protein polymerization, generation of precursor metabolites and energy, oxidation-reduction process, cellular protein metabolic process, purine ribonucleoside biosynthetic process, DNA conformation change, DNA replication, purine ribonucleotide biosynthetic process, DNA recombination, DNA repair, metabolic process, translational initiation, primary metabolic process, cellular nitrogen compound biosynthetic process, regulation of catabolic process, Golgi vesicle transport, nucleobase-containing compound metabolic process, chromatin assembly or disassembly, protein-DNA complex assembly, carbohydrate metabolic process, protein complex assembly, glucose metabolic process, NADP metabolic process
midnightblue	antigen processing and presentation, exocytosis, immune response, lipopolysaccharide biosynthetic process
pink	fatty acid biosynthetic process, nucleobase-containing compound catabolic process, immune response, DNA integration, regulation of gene expression, actin cytoskeleton organization, regulation of biological quality, regulation of apoptotic process, positive regulation of cellular process, antigen processing and presentation, proteolysis, inorganic ion transmembrane transport, regulation of cytoskeleton organization, translational elongation, regulation of cellular protein metabolic process, regulation of protein metabolic process regulation of hydrolase activity, protein transport
purple	regulation of cell growth, immune response, oxidation-reduction process, maintenance of protein location in cell, dicarboxylic acid transport, proteolysis, sulfur compound metabolic process, DNA-templated regulation of transcription
red	regulation of small GTPase mediated signal transduction, G-protein coupled receptor signaling pathway, protein phosphorylation, signal transduction, intracellular signal transduction, regulation of ARF protein signal transduction, cell communication, regulation of Rho protein signal transduction, small GTPase mediated signal transduction, response to biotic stimulus, filopodium assembly, cyclic nucleotide biosynthetic process
salmon	G-protein coupled receptor signaling pathway, phosphatidylinositol metabolic process
tan	microtubule-based movement, vesicle-mediated transport, intracellular protein transport, proton transport, neuropeptide signaling pathway, protein catabolic process
turquoise	signal transduction, nucleocytoplasmic transport, protein import, ubiquitin-dependent protein catabolic process, Wnt signaling pathway, DNA-templated regulation of transcription, glycolytic process, hexose metabolic process, cell projection organization, response to external stimulus, protein dephosphorylation, regulation of cell cycle, autophagy, establishment of protein localization nucleus, cellular component movement
yellow	translation, cellular protein metabolic process, translational elongation, protein polymerization, RNA processing, Golgi vesicle transport, GTP catabolic process, tRNA aminoacylation for protein translation, neuropeptide signaling pathway, nucleoside phosphate catabolic process

Table S2.8. Complete statistical information for relationships between coexpression modules and mating behavior.

module			module*population		module*rear		module*population*rearing	
module	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p
black	1.85	0.1840	0.00	0.9446	2.78	0.1064	0.56	0.4616
blue	8.55	0.0066	2.04	0.1641	5.40	0.0273	2.61	0.1173
brown	0.48	0.4924	0.11	0.7398	0.05	0.8210	0.00	0.9640
cyan	2.56	0.1202	2.66	0.1138	2.55	0.1212	1.16	0.2910
green	0.58	0.4518	0.30	0.5866	0.43	0.5175	1.19	0.2834
greenyellow	0.17	0.6849	0.24	0.626	0.67	0.4183	0.05	0.8305
lightcyan	0.93	0.3438	2.40	0.1322	0.45	0.5073	0.02	0.8758
lightgreen	0.18	0.6725	0.02	0.8864	1.26	0.2708	1.02	0.3209
lightgrey	0.01	0.9404	0.02	0.8969	0.03	0.8535	0.13	0.7182
magenta	15.55	0.0005	0.03	0.8534	5.43	0.0269	2.78	0.1063
midnightblue	0.00	0.9739	0.14	0.7066	0.12	0.7298	0.05	0.8226
pink	0.13	0.7259	0.06	0.8068	0.61	0.4416	0.53	0.4710
purple	0.17	0.6876	1.37	0.2521	0.00	0.9586	0.57	0.4550
red	0.11	0.7451	0.45	0.5099	0.10	0.7496	0.09	0.7710
salmon	2.52	0.1233	0.16	0.6881	0.04	0.8359	0.89	0.3525
tan	0.05	0.8328	1.12	0.2983	0.39	0.5396	1.36	0.2527
turquoise	0.92	0.3463	3.89	0.0583	0.94	0.3404	1.16	0.2905
yellow	15.76	0.0004	3.34	0.0778	9.08	0.0053	9.71	0.0041

Table S2.9. Complete statistical information for relationships between coexpression modules and aggression behavior.

module			module*population		module*rear		module*population*rearing	
module	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p
black	2.80	0.1052	0.77	0.3876	0.13	0.7252	0.00	0.9484
blue	8.21	0.0077	0.50	0.4862	0.64	0.4304	3.30	0.0796
brown	0.08	0.7835	0.08	0.7763	0.34	0.5639	0.55	0.4635
cyan	0.31	0.5824	1.07	0.3097	2.13	0.1548	0.01	0.9330
green	1.85	0.1842	2.98	0.0952	1.81	0.1885	0.07	0.7863
greenyellow	0.63	0.4334	0.35	0.5562	0.66	0.4227	3.40	0.0755
lightcyan	3.67	0.0654	0.13	0.7227	2.10	0.1576	2.01	0.1669
lightgreen	0.46	0.5025	0.21	0.6533	0.36	0.5526	0.19	0.6686
lightgrey	4.79	0.0368	2.66	0.1137	2.95	0.0967	2.92	0.0980
magenta	1.56	0.2212	0.12	0.7315	0.37	0.5468	0.01	0.9123
midnightblue	3.96	0.0561	2.72	0.1100	5.20	0.0301	5.89	0.0216
pink	0.56	0.4606	0.11	0.7427	0.13	0.7191	0.97	0.3328
purple	0.09	0.7614	11.08	0.0024	1.68	0.2055	17.5	0.0002
red	0.01	0.9046	0.25	0.6240	0.01	0.9323	0.01	0.9061
salmon	1.95	0.1727	0.02	0.8951	0.62	0.4387	1.24	0.2737
tan	0.03	0.8633	1.00	0.3246	0.05	0.8197	0.05	0.8165
turquoise	0.95	0.3373	0.25	0.6193	0.07	0.7952	0.83	0.3708
yellow	28.00	0.00001	6.70	0.0149	1.27	0.2695	7.05	0.0128

Table S2.10. Complete statistical information for relationships between coexpression modules and open-field behavior.

module			module*population		module*rear		module*population*rearing	
module	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p
black	0.00	0.9847	0.01	0.9348	1.51	0.2290	0.98	0.3316
blue	0.59	0.4485	0.72	0.4043	2.64	0.1147	1.34	0.2570
brown	0.22	0.6410	0.00	0.9801	0.21	0.6513	0.59	0.4496
cyan	12.92	0.0012	11.92	0.0017	5.10	0.0317	1.98	0.1698
green	0.11	0.7405	0.26	0.6172	0.99	0.3285	1.86	0.1826
greenyellow	0.18	0.6735	0.30	0.5904	0.00	0.9614	0.93	0.3427
lightcyan	0.70	0.4109	0.08	0.7840	0.74	0.3971	0.25	0.6215
lightgreen	0.27	0.6047	0.15	0.7061	0.20	0.6601	0.18	0.6761
lightgrey	0.14	0.7123	0.20	0.6610	0.76	0.3907	0.12	0.7272
magenta	0.01	0.9209	0.01	0.9381	0.39	0.5368	0.00	0.9701
midnightblue	0.03	0.8533	0.03	0.8689	0.00	0.9604	0.02	0.8808
pink	0.00	0.9809	0.34	0.5646	0.77	0.3885	0.00	0.9809
purple	1.95	0.1728	0.00	0.9765	1.04	0.3161	0.54	0.4689
red	0.07	0.7975	0.00	0.9596	0.1	0.7586	0.03	0.8572
salmon	0.11	0.7393	0.01	0.9329	0.15	0.6984	0.13	0.7236
tan	0.03	0.8637	0.00	0.9753	0.54	0.4682	0.08	0.7834
turquoise	0.00	0.9894	0.05	0.8200	0.73	0.3986	1.19	0.2839
yellow	0.09	0.7704	0.03	0.8539	0.89	0.3524	0.16	0.6885

Table S2.11. Complete statistical information for relationships between coexpression modules and escape behavior.

module			module*population		module*rear		module*population*rearing	
module	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p	F _{1,29}	p
black	1.13	0.2962	0.00	0.9774	0.94	0.3410	0.00	0.9994
blue	2.49	0.1258	1.45	0.2380	1.95	0.1733	0.56	0.4610
brown	3.09	0.0893	1.81	0.1892	0.52	0.4759	2.42	0.1303
cyan	0.09	0.7684	0.06	0.8090	0.17	0.6835	0.91	0.3473
green	0.04	0.8470	0.06	0.8108	0.12	0.7294	0.10	0.7521
greenyellow	0.00	0.9773	2.14	0.1545	0.37	0.5460	2.34	0.1370
lightcyan	0.80	0.3785	1.89	0.1802	0.00	0.9627	0.35	0.5604
lightgreen	2.19	0.1500	2.84	0.1024	0.36	0.5527	0.44	0.5137
lightgrey	1.19	0.2845	6.58	0.0157	1.68	0.2049	0.57	0.4572
magenta	0.00	0.9820	0.80	0.3790	2.50	0.1249	0.22	0.6391
midnightblue	0.81	0.3743	0.92	0.3454	1.09	0.3062	0.67	0.4201
pink	0.02	0.8956	0.01	0.9135	1.05	0.3140	0.24	0.6266
purple	5.42	0.0271	2.02	0.1663	0.12	0.7360	0.01	0.9312
red	0.11	0.7431	0.01	0.9220	0.37	0.5464	1.46	0.2360
salmon	1.83	0.1868	0.98	0.3295	0.26	0.6162	2.11	0.1575
tan	0.00	0.9787	0.15	0.7023	0.68	0.4170	0.13	0.7206
turquoise	0.38	0.5449	0.62	0.4372	0.09	0.7672	0.01	0.9059
yellow	2.67	0.1130	0.05	0.8214	1.04	0.3161	0.44	0.5114

APPENDIX 3

Table S3.1. Annotation information for differentially expressed transcripts in the Aripo drainage dataset.

contig	SwissProt ID	SwissProt entry name	Protein name	Organism
c119484_g1	P80961	AFP4_MYOOC	Type-4 ice-structuring protein LS-12 (ISP LS-12) (Antifreeze protein LS-12)	Myoxocephalus octodecemspinosus (Longhorn sculpin) (Cottus octodecemspinosus)
c138604_g1	P48303	S1PR1_RAT	Sphingosine 1-phosphate receptor 1 (S1P receptor 1) (S1P1) (Endothelial differentiation G-protein coupled receptor 1) (Sphingosine 1-phosphate receptor Edg-1) (S1P receptor Edg-1) (CD antigen CD363)	Rattus norvegicus (Rat)
c38121_g1	P19632	PHOS_BOVIN	Phosducin (PHD) (33 kDa phototransducing protein) (Protein MEKA)	Bos taurus (Bovine)
c55991_g1	Q6PBN4	CQ10X_DANRE	Coenzyme Q-binding protein COQ10 homolog, mitochondrial	Danio rerio (Zebrafish) (Brachydanio rerio)
c63589_g1	P47804	RGR_HUMAN	RPE-retinal G protein-coupled receptor	Homo sapiens (Human)
c66577_g1	P63210	GBG1_CANFA	Guanine nucleotide-binding protein G(T) subunit gamma-T1 (Transducin gamma chain)	Canis familiaris (Dog) (Canis lupus familiaris)
c66965_g1	Q49HM9	GRK7A_DANRE	G-protein-coupled receptor kinase 7A (EC 2.7.11.14) (EC 2.7.11.16) (G protein-coupled receptor kinase 7-1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c72092_g1	P87366	OPSG_ORYLA	Green-sensitive opsin (Green cone photoreceptor pigment) (KFH-G)	Oryzias latipes (Medaka fish) (Japanese ricefish)
c72940_g1	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	Homo sapiens (Human)
c72950_g1	O88382	MAGI2_RAT	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 (Atrophin-1-interacting protein 1) (AIP-1) (Membrane-associated guanylate kinase inverted 2) (MAGI-2) (Synaptic-scaffolding molecule) (S-SCAM)	Rattus norvegicus (Rat)

c73901_g1	O88759	KCNS3_RAT	Potassium voltage-gated channel subfamily S member 3 (Delayed-rectifier K(+) channel alpha subunit 3) (Voltage-gated potassium channel subunit Kv9.3)	Rattus norvegicus (Rat)
c74239_g1	P79848	OPSD_POERE	Rhodopsin	Poecilia reticulata (Guppy) (Acanthophaelus reticulatus)
c75004_g2	O55175	CNCG_SPETR	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma (GMP-PDE gamma) (EC 3.1.4.35)	Spermophilus tridecemlineatus (Thirteen-lined ground squirrel) (Ictidomys tridecemlineatus)
c76445_g1	Q6VTH5	RSPH1_CYPCA	Radial spoke head 1 homolog (Meichroacidin homolog) (Meichroacidin-like sperm-specific axonemal protein) (Testis-specific gene A2-like protein)	Cyprinus carpio (Common carp)
c76786_g1	Q13541	4EBP1_HUMAN	Eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1) (eIF4E-binding protein 1) (Phosphorylated heat- and acid-stable protein regulated by insulin 1) (PHAS-I)	Homo sapiens (Human)
c76990_g1	Q6PBW5	RP65A_DANRE	Retinoid isomerohydrolase (EC 3.1.1.64) (All-trans-retinylester 11-cis isomerohydrolase A) (Retinal pigment epithelium-specific 65 kDa protein homolog A) (RPE56a)	Danio rerio (Zebrafish) (Brachydanio rerio)
c77142_g1	O97564	GBGT2_CANFA	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-T2 (G gamma-C) (Tgamma c)	Canis familiaris (Dog) (Canis lupus familiaris)
c77423_g1	P87366	OPSG_ORYLA	Green-sensitive opsin (Green cone photoreceptor pigment) (KFH-G)	Oryzias latipes (Medaka fish) (Japanese ricefish)
c77979_g2	Q13886	KLF9_HUMAN	Krueppel-like factor 9 (Basic transcription element-binding protein 1) (BTE-binding protein 1) (GC-box-binding protein 1) (Transcription factor BTEB1)	Homo sapiens (Human)
c78334_g2	Q14192	FHL2_HUMAN	Four and a half LIM domains protein 2 (FHL-2) (LIM domain protein DRAL) (Skeletal muscle LIM-protein 3) (SLIM-3)	Homo sapiens (Human)
c78397_g1	Q7Z628	ARHG8_HUMAN	Neuroepithelial cell-transforming gene 1 protein (Proto-oncogene p65 Net1) (Rho guanine nucleotide exchange factor 8)	Homo sapiens (Human)
c78602_g5	P11778	MYH7_PAPHA	Myosin-7 (Myosin heavy chain 7) (Myosin heavy chain slow isoform) (MyHC-slow) (Myosin heavy chain, cardiac muscle beta isoform) (MyHC-beta) (Fragment)	Papio hamadryas (Hamadryas baboon)
c78709_g1	Q3U5Q7	CMPK2_MOUSE	UMP-CMP kinase 2, mitochondrial (EC 2.7.4.14) (Nucleoside-diphosphate kinase) (EC 2.7.4.6) (Thymidylate kinase LPS-inducible member) (TYKi)	Mus musculus (Mouse)
c79323_g1	Q9NYR8	RDH8_HUMAN	Retinol dehydrogenase 8 (EC 1.1.1.300) (Photoreceptor outer segment all-trans retinol dehydrogenase)	Homo sapiens (Human)
c79469_g1	P10286	CALCA_CHICK	Calcitonin gene-related peptide (CGRP)	Gallus gallus (Chicken)

c79977_g1	B5DGM7	ALDOA_SALSA	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (allergen Sal s 3.0101)	Salmo salar (Atlantic salmon)
c80369_g1	Q90952	PON2_CHICK	Serum paraoxonase/arylesterase 2 (PON 2) (EC 3.1.1.2) (EC 3.1.8.1) (Aromatic esterase 2) (A-esterase 2) (Serum arylalkylphosphatase 2)	Gallus gallus (Chicken)
c80458_g1	Q1LZ79	GEMI8_BOVIN	Gem-associated protein 8 (Gemin-8)	Bos taurus (Bovine)
c80619_g1	Q13541	4EBP1_HUMAN	Eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1) (eIF4E-binding protein 1) (Phosphorylated heat- and acid-stable protein regulated by insulin 1) (PHAS-I)	Homo sapiens (Human)
c80645_g1	P87365	OPSB_ORYLA	Blue-sensitive opsin (Blue cone photoreceptor pigment) (KFH-B)	Oryzias latipes (Medaka fish) (Japanese ricefish)
c80765_g1	A2CES0	NEUFC_DANRE	Neuferricin (Cytochrome b5 domain-containing protein 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c81126_g1	P62881	GBB5_MOUSE	Guanine nucleotide-binding protein subunit beta-5 (Gbeta5) (Transducin beta chain 5)	Mus musculus (Mouse)
c81179_g1	P08168	ARRS_BOVIN	S-arrestin (48 kDa protein) (Retinal S-antigen) (S-AG) (Rod photoreceptor arrestin) [Cleaved into: S-arrestin short form]	Bos taurus (Bovine)
c81220_g1	Q04650	LMX1A_MESAU	LIM homeobox transcription factor 1-alpha (LIM/homeobox protein LMX1A) (LIM/homeobox protein 1) (LMX-1)	Mesocricetus auratus (Golden hamster)
c81220_g4	O88609	LMX1B_MOUSE	LIM homeobox transcription factor 1-beta (LIM/homeobox protein 1.2) (LMX-1.2) (LIM/homeobox protein LMX1B)	Mus musculus (Mouse)
c81249_g1	P52293	IMA1_MOUSE	Importin subunit alpha-1 (Importin alpha P1) (Karyopherin subunit alpha-2) (Pendulin) (Pore targeting complex 58 kDa subunit) (PTAC58) (RAG cohort protein 1) (SRP1-alpha)	Mus musculus (Mouse)
c81324_g3	Q9NP86	CABP5_HUMAN	Calcium-binding protein 5 (CaBP5)	Homo sapiens (Human)
c81335_g1	P53447	ALDOB_SPAAU	Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase)	Sparus aurata (Gilthead sea bream)
c81363_g1	B0BNG2	TM6S2_RAT	Transmembrane 6 superfamily member 2	Rattus norvegicus (Rat)
c81484_g1	P00375	DYR_MOUSE	Dihydrofolate reductase (EC 1.5.1.3)	Mus musculus (Mouse)
c81536_g1	Q8R205	ZC3HA_MOUSE	Zinc finger CCCH domain-containing protein 10	Mus musculus (Mouse)
c81546_g1	Q05922	DUS2_MOUSE	Dual specificity protein phosphatase 2 (EC 3.1.3.16) (EC 3.1.3.48) (Dual specificity protein phosphatase PAC-1)	Mus musculus (Mouse)
c81588_g1	Q5RFR0	TTPAL_PONAB	Alpha-tocopherol transfer protein-like	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c81628_g1	Q9QW08	PHOS_MOUSE	Phosducin (PHD) (33 kDa phototransducing protein) (Rod photoreceptor 1) (RPR-1)	Mus musculus (Mouse)
c81782_g1	Q9NZJ4	SACS_HUMAN	Sacsin (DnaJ homolog subfamily C member 29) (DNAJC29)	Homo sapiens (Human)

c81782_g3	Q9NZJ4	SACS_HUMAN	Sacsin (DnaJ homolog subfamily C member 29) (DNAJC29)	Homo sapiens (Human)
c81791_g1	Q96C10	DHX58_HUMAN	Probable ATP-dependent RNA helicase DHX58 (EC 3.6.4.13) (Probable ATP-dependent helicase LGP2) (Protein D11Lgp2 homolog) (RIG-I-like receptor 3) (RLR-3) (RIG-I-like receptor LGP2) (RLR)	Homo sapiens (Human)
c81793_g1	P51482	ARRC_LITPI	Arrestin-C (Cone arrestin)	Lithobates pipiens (Northern leopard frog) (Rana pipiens)
c81855_g2	Q9D531	NXNL2_MOUSE	Nucleoredoxin-like protein 2 (Rod-derived cone viability factor 2) (RdCVF2)	Mus musculus (Mouse)
c81896_g4	P17182	ENOA_MOUSE	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Enolase 1) (Non-neural enolase) (NNE)	Mus musculus (Mouse)
c82077_g1	Q1LZ71	LFG2_BOVIN	Protein lifeguard 2 (Fas apoptotic inhibitory molecule 2)	Bos taurus (Bovine)
c82098_g1	Q8K3K9	GIMA4_RAT	GTPase IMAF family member 4 (Immunity-associated nucleotide 1 protein) (IAN-1) (Immunity-associated protein 4)	Rattus norvegicus (Rat)
c82305_g1	P79881	GUC1B_CHICK	Guanylyl cyclase-activating protein 2 (GCAP 2) (Guanylate cyclase activator 1B)	Gallus gallus (Chicken)
c82353_g2	Q9BQQ7	RTP3_HUMAN	Receptor-transporting protein 3 (Transmembrane protein 7)	Homo sapiens (Human)
c82364_g1	O02776	PARG_BOVIN	Poly(ADP-ribose) glycohydrolase (EC 3.2.1.143)	Bos taurus (Bovine)
c82425_g1	P79881	GUC1B_CHICK	Guanylyl cyclase-activating protein 2 (GCAP 2) (Guanylate cyclase activator 1B)	Gallus gallus (Chicken)
c82444_g1	B5FX50	CT027_TAEGU	UPF0687 protein C20orf27 homolog	Taeniopygia guttata (Zebra finch) (Poephila guttata)
c82568_g1	P10518	HEM2_MOUSE	Delta-aminolevulinic acid dehydratase (ALADH) (EC 4.2.1.24) (Porphobilinogen synthase)	Mus musculus (Mouse)
c82639_g1	Q9Y255	PRLD1_HUMAN	PRELI domain-containing protein 1, mitochondrial (25 kDa protein of relevant evolutionary and lymphoid interest) (Px19-like protein)	Homo sapiens (Human)
c82821_g1	Q13956	CNCG_HUMAN	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma (GMP-PDE gamma) (EC 3.1.4.35)	Homo sapiens (Human)
c82856_g1	Q5ZMD2	ANKY2_CHICK	Ankyrin repeat and MYND domain-containing protein 2	Gallus gallus (Chicken)
c82926_g1	Q8NBN7	RDH13_HUMAN	Retinol dehydrogenase 13 (EC 1.1.1.-)	Homo sapiens (Human)
c82942_g2	Q15937	ZNF79_HUMAN	Zinc finger protein 79 (ZNFpT7)	Homo sapiens (Human)
c82971_g2	Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 (Inactive ubiquitin-specific peptidase 39) (SAD1 homolog) (U4/U6.U5 tri-snRNP-associated 65 kDa protein) (65K)	Homo sapiens (Human)

c82997_g1	Q8VD31	TPSNR_MOUSE	Tapasin-related protein (TAPASIN-R) (TAP-binding protein-like) (TAP-binding protein-related protein) (TAPBP-R) (Tapasin-like)	Mus musculus (Mouse)
c83020_g1	Q9ULS6	KCNS2_HUMAN	Potassium voltage-gated channel subfamily S member 2 (Delayed-rectifier K(+)) channel alpha subunit 2) (Voltage-gated potassium channel subunit Kv9.2)	Homo sapiens (Human)
c83280_g2	Q8TD55	PKHO2_HUMAN	Pleckstrin homology domain-containing family O member 2 (PH domain-containing family O member 2) (Pleckstrin homology domain-containing family Q member 1) (PH domain-containing family Q member 1)	Homo sapiens (Human)
c83329_g1	Q6PBN5	AUP1_DANRE	Ancient ubiquitous protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c83330_g1	O14893	GEMI2_HUMAN	Gem-associated protein 2 (Gemin-2) (Component of gems 2) (Survival of motor neuron protein-interacting protein 1) (SMN-interacting protein 1)	Homo sapiens (Human)
c83616_g1	P40692	MLH1_HUMAN	DNA mismatch repair protein Mlh1 (MutL protein homolog 1)	Homo sapiens (Human)
c83715_g4	Q2V2M9	FHOD3_HUMAN	FH1/FH2 domain-containing protein 3 (Formactin-2) (Formin homolog overexpressed in spleen 2) (hFHOS2)	Homo sapiens (Human)
c83744_g1	P35815	PPM1B_RAT	Protein phosphatase 1B (EC 3.1.3.16) (Protein phosphatase 2C isoform beta) (PP2C-beta)	Rattus norvegicus (Rat)
c83835_g3	Q96MC5	CP045_HUMAN	Uncharacterized protein C16orf45	Homo sapiens (Human)
c83845_g1	P43091	HEM1_OPSTA	5-aminolevulinate synthase, nonspecific, mitochondrial (ALAS-H) (EC 2.3.1.37) (5-aminolevulinic acid synthase 1) (Delta-ALA synthase 1) (Delta-aminolevulinate synthase 1)	Opsanus tau (Oyster toadfish) (Gadus tau)
c83990_g1	P23280	CAH6_HUMAN	Carbonic anhydrase 6 (EC 4.2.1.1) (Carbonate dehydratase VI) (Carbonic anhydrase VI) (CA-VI) (Salivary carbonic anhydrase) (Secreted carbonic anhydrase)	Homo sapiens (Human)
c84000_g2	P0C7U4	C3AR_DANRE	C3a anaphylatoxin chemotactic receptor (C3AR) (C3a-R)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84158_g4	Q6NWF6	K2C8_DANRE	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84186_g3	NA			
c84255_g2	Q96H78	S2544_HUMAN	Solute carrier family 25 member 44	Homo sapiens (Human)
c84278_g1	A2VDT1	TP4A3_BOVIN	Protein tyrosine phosphatase type IVA 3 (EC 3.1.3.48) (Protein-tyrosine phosphatase 4a3)	Bos taurus (Bovine)
c84336_g2	Q9Y2E4	DIP2C_HUMAN	Disco-interacting protein 2 homolog C (DIP2 homolog C)	Homo sapiens (Human)
c84347_g1	Q3ZC84	CNDP2_BOVIN	Cytosolic non-specific dipeptidase (EC 3.4.13.18) (CNDP dipeptidase 2)	Bos taurus (Bovine)

c84384_g2	Q9JJC6	RIPL1_MOUSE	RILP-like protein 1 (Rab-interacting lysosomal-like protein 1)	Mus musculus (Mouse)
c84467_g1	Q5XJK9	CMS1_DANRE	Protein CMSS1 (Cms1 ribosomal small subunit homolog)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84508_g6	P51641	CNTFR_CHICK	Ciliary neurotrophic factor receptor subunit alpha (CNTF receptor subunit alpha) (CNTFR-alpha) (Growth-promoting activity receptor subunit alpha) (GPA receptor subunit alpha) (GPAR-alpha)	Gallus gallus (Chicken)
c84563_g5	Q801X6	PHAR1_CHICK	Phosphatase and actin regulator 1	Gallus gallus (Chicken)
c84588_g1	Q8BM65	NYAP2_MOUSE	Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 2	Mus musculus (Mouse)
c84598_g1	P79101	CPSF3_BOVIN	Cleavage and polyadenylation specificity factor subunit 3 (EC 3.1.27.-) (Cleavage and polyadenylation specificity factor 73 kDa subunit) (CPSF 73 kDa subunit) (mRNA 3'-end-processing endonuclease CPSF-73)	Bos taurus (Bovine)
c84599_g6	Q7ZUV2	KTNB1_DANRE	Katanin p80 WD40 repeat-containing subunit B1 (Katanin p80 subunit B1) (p80 katanin)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84680_g9	Q80TB7	ZSWM6_MOUSE	Zinc finger SWIM domain-containing protein 6	Mus musculus (Mouse)
c84703_g2	Q9H3F6	BACD3_HUMAN	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3 (hBACURD3) (BTB/POZ domain-containing protein KCTD10) (Potassium channel tetramerization domain-containing protein 10)	Homo sapiens (Human)
c84706_g1	Q32PA4	PHP14_BOVIN	14 kDa phosphohistidine phosphatase (EC 3.1.3.-) (Phosphohistidine phosphatase 1)	Bos taurus (Bovine)
c84731_g2	O95985	TOP3B_HUMAN	DNA topoisomerase 3-beta-1 (EC 5.99.1.2) (DNA topoisomerase III beta-1)	Homo sapiens (Human)
c84732_g4	Q5ZHV1	RB33B_CHICK	Ras-related protein Rab-33B	Gallus gallus (Chicken)
c84765_g8	Q13409	DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 (Cytoplasmic dynein intermediate chain 2) (Dynein intermediate chain 2, cytosolic) (DH IC-2)	Homo sapiens (Human)
c84843_g6	Q28EM7	OTX5_XENTR	Homeobox protein otx5 (Orthodenticle homolog 5)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c84843_g7	Q28EM7	OTX5_XENTR	Homeobox protein otx5 (Orthodenticle homolog 5)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c84983_g4	Q9NRJ7	PCDBG_HUMAN	Protocadherin beta-16 (PCDH-beta-16) (Protocadherin-3X)	Homo sapiens (Human)
c85125_g2	Q9NX07	TSAP1_HUMAN	tRNA selenocysteine 1-associated protein 1 (SECp43) (tRNA selenocysteine-associated protein 1)	Homo sapiens (Human)

c85204_g4	Q9H9J4	UBP42_HUMAN	Ubiquitin carboxyl-terminal hydrolase 42 (EC 3.4.19.12) (Deubiquitinating enzyme 42) (Ubiquitin thioesterase 42) (Ubiquitin-specific-processing protease 42)	Homo sapiens (Human)
c85232_g6	P63033	RHES_RAT	GTP-binding protein Rhes (Ras homolog enriched in striatum) (SE6C)	Rattus norvegicus (Rat)
c85237_g1	Q96ME1	FXL18_HUMAN	F-box/LRR-repeat protein 18 (F-box and leucine-rich repeat protein 18)	Homo sapiens (Human)
c85257_g1	Q9Y487	VPP2_HUMAN	V-type proton ATPase 116 kDa subunit a isoform 2 (V-ATPase 116 kDa isoform a2) (Lysosomal H(+)-transporting ATPase V0 subunit a2) (TJ6) (Vacuolar proton translocating ATPase 116 kDa subunit a isoform 2)	Homo sapiens (Human)
c85322_g5	Q17QD9	CSEN_BOVIN	Calsenilin (A-type potassium channel modulatory protein 3) (Kv channel-interacting protein 3) (KChIP3)	Bos taurus (Bovine)
c85340_g5	Q08E27	STRBP_BOVIN	Spermatid perinuclear RNA-binding protein	Bos taurus (Bovine)
c85425_g2	Q9P0X4	CAC1I_HUMAN	Voltage-dependent T-type calcium channel subunit alpha-1I (Voltage-gated calcium channel subunit alpha Cav3.3) (Ca(v)3.3)	Homo sapiens (Human)
c85442_g3	Q1JPZ3	SRC_DANRE	Proto-oncogene tyrosine-protein kinase Src (EC 2.7.10.2) (Proto-oncogene c-Src) (pp60c-src) (p60-Src)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85443_g6	Q5W8I7	VGL2B_DANRE	Vesicular glutamate transporter 2.2 (Solute carrier family 17 member 6-A) (Vesicular glutamate transporter 2-B)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85450_g7	Q499R4	YRDC_RAT	YrdC domain-containing protein, mitochondrial (Ischemia/reperfusion-inducible protein homolog)	Rattus norvegicus (Rat)
c85510_g5	B6RSP1	PKHA7_DANRE	Pleckstrin homology domain-containing family A member 7 (PH domain-containing family A member 7) (Heart adapter protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85572_g1	P04574	CPNS1_PIG	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	Sus scrofa (Pig)
c85619_g1	Q13287	NMI_HUMAN	N-myc-interactor (Nmi) (N-myc and STAT interactor)	Homo sapiens (Human)
c85654_g1	O00506	STK25_HUMAN	Serine/threonine-protein kinase 25 (EC 2.7.11.1) (Ste20-like kinase) (Sterile 20/oxidant stress-response kinase 1) (SOK-1) (Ste20/oxidant stress response kinase 1)	Homo sapiens (Human)
c85675_g2	O00294	TULP1_HUMAN	Tubby-related protein 1 (Tubby-like protein 1)	Homo sapiens (Human)
c85708_g1	Q08BA6	ALKB5_DANRE	RNA demethylase ALKBH5 (EC 1.14.11.-) (Alkylated DNA repair protein alkB homolog 5) (Alpha-ketoglutarate-dependent dioxygenase alkB homolog 5)	Danio rerio (Zebrafish) (Brachydanio rerio)

c85815_g4	Q32L22	RPAC1_BOVIN	DNA-directed RNA polymerases I and III subunit RPAC1 (DNA-directed RNA polymerase I subunit C) (RNA polymerases I and III subunit AC1)	Bos taurus (Bovine)
c86004_g2	Q2TV84	TRPM1_MOUSE	Transient receptor potential cation channel subfamily M member 1 (Long transient receptor potential channel 1) (LTrpC1) (Melastatin-1)	Mus musculus (Mouse)
c86032_g3	P02401	RLA2_RAT	60S acidic ribosomal protein P2	Rattus norvegicus (Rat)
c86037_g4	P08548	LIN1_NYCCO	LINE-1 reverse transcriptase homolog (EC 2.7.7.49)	Nycticebus coucang (Slow loris)
c86037_g6	Q68EL2	DTD2_DANRE	Probable D-tyrosyl-tRNA(Tyr) deacylase 2 (EC 3.1.-.-) (D-tyrosyl-tRNA deacylase 2)	Danio rerio (Zebrafish)
c86057_g8	Q8QFX1	RIMB2_CHICK	RIMS-binding protein 2 (RIM-BP2)	(Brachydanio rerio)
c86107_g1	P62312	LSM6_HUMAN	U6 snRNA-associated Sm-like protein LSM6	Gallus gallus (Chicken)
c86138_g2	P58005	SESN3_HUMAN	Sestrin-3	Homo sapiens (Human)
c86151_g5	P97434	MPRIP_MOUSE	Myosin phosphatase Rho-interacting protein (Rho-interacting protein 3) (RIP3) (p116Rip)	Mus musculus (Mouse)
c86168_g4	O15397	IPO8_HUMAN	Importin-8 (Imp8) (Ran-binding protein 8) (RanBP8)	Homo sapiens (Human)
c86178_g2	Q6LD29	FXA1A_XENLA	Forkhead box protein A1-A (FoxA1a) (Fork head domain-related protein 7) (xFD-7) (Hepatocyte nuclear factor 3-alpha homolog A) (HNF3alpha homolog A) (xHNF3alpha-A)	Xenopus laevis (African clawed frog)
c86182_g3	Q61142	SPIN1_MOUSE	Spindlin-1 (30000 Mr metaphase complex) (SSEC P) (Spindlin1)	Mus musculus (Mouse)
c86191_g5	Q575T0	CYGB1_ORYLA	Cytoglobin-1	Oryzias latipes (Medaka fish)
c86196_g1	Q96HN2	SAHH3_HUMAN	Putative adenosylhomocysteinase 3 (AdoHcyase 3) (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase 3) (S-adenosylhomocysteine hydrolase-like protein 2)	(Japanese ricefish)
c86255_g8	O95180	CAC1H_HUMAN	Voltage-dependent T-type calcium channel subunit alpha-1H (Low-voltage-activated calcium channel alpha1 3.2 subunit) (Voltage-gated calcium channel subunit alpha Cav3.2)	Homo sapiens (Human)
c86328_g4	Q4R550	SYCC_MACFA	Cysteine--tRNA ligase, cytoplasmic (EC 6.1.1.16) (CysteinyI-tRNA synthetase) (CysRS)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c86339_g1	P20290	BTF3_HUMAN	Transcription factor BTF3 (Nascent polypeptide-associated complex subunit beta) (NAC-beta) (RNA polymerase B transcription factor 3)	Homo sapiens (Human)

c86343_g3	P28652	KCC2B_MOUSE	Calcium/calmodulin-dependent protein kinase type II subunit beta (CaM kinase II subunit beta) (CaMK-II subunit beta) (EC 2.7.11.17)	Mus musculus (Mouse)
c86401_g4	P02628	PRVA_ESOLU	Parvalbumin alpha (Parvalbumin III) (Parvalbumin pl 5.0) (Parvalbumin-3)	Esox lucius (Northern pike)
c86478_g4	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin) (Tubulin H2-alpha) (Tubulin alpha-1 chain)	Homo sapiens (Human)
c86495_g1	A2AKY4	Z804A_MOUSE	Zinc finger protein 804A	Mus musculus (Mouse)
c86530_g2	Q6NXX7	DPP10_MOUSE	Inactive dipeptidyl peptidase 10 (Dipeptidyl peptidase X) (DPP X)	Mus musculus (Mouse)
c86576_g1	Q5DRE0	PCDB1_PANTR	Protocadherin beta-1 (PCDH-beta-1)	Pan troglodytes (Chimpanzee)
c86589_g3	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c86591_g1	A1L244	SAC1A_DANRE	Phosphatidylinositol phosphatase SAC1-A (EC 3.1.3.-) (Suppressor of actin mutations 1-like protein A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86604_g4	B1AZ99	OTUD3_MOUSE	OTU domain-containing protein 3 (EC 3.4.19.12)	Mus musculus (Mouse)
c86632_g1	Q15937	ZNF79_HUMAN	Zinc finger protein 79 (ZNFpT7)	Homo sapiens (Human)
c86644_g6	Q98875	DLX1A_DANRE	Homeobox protein Dlx1a (DLX-1) (Distal-less homeobox gene 1a)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86692_g1	Q96CN4	EVI5L_HUMAN	EVI5-like protein (Ecotropic viral integration site 5-like protein)	Homo sapiens (Human)
c86710_g1	Q7T292	MFRN2_DANRE	Mitoferrin-2 (Mitochondrial iron transporter 2) (Solute carrier family 25 member 28)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86736_g3	Q91513	PRLR_ORENI	Prolactin receptor (PRL-R)	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)
c86824_g3	P29374	ARI4A_HUMAN	AT-rich interactive domain-containing protein 4A (ARID domain-containing protein 4A) (Retinoblastoma-binding protein 1) (RBBP-1)	Homo sapiens (Human)
c86824_g5	P29374	ARI4A_HUMAN	AT-rich interactive domain-containing protein 4A (ARID domain-containing protein 4A) (Retinoblastoma-binding protein 1) (RBBP-1)	Homo sapiens (Human)
c86832_g6	Q6PFP3	PDPFA_DANRE	Pancreatic progenitor cell differentiation and proliferation factor A (Exocrine differentiation and proliferation factor A) (Exocrine differentiation and proliferation factor)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86845_g1	Q5VU43	MYOME_HUMAN	Myomegalin (Cardiomyopathy-associated protein 2) (Phosphodiesterase 4D-interacting protein)	Homo sapiens (Human)
c86858_g2	Q5XI46	CJ088_RAT	Uncharacterized protein C10orf88 homolog	Rattus norvegicus (Rat)
c86890_g1	H0YL14	CI069_HUMAN	Protein C9orf69 (Herpes virus UL25-binding protein)	Homo sapiens (Human)

c86901_g3	Q6P4W7	RIC8A_XENTR	Synembryn-A (Protein Ric-8A)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c86961_g5	Q0IHT3	CRTC3_XENTR	CREB-regulated transcription coactivator 3 (Transducer of regulated cAMP response element-binding protein 3) (TORC-3) (Transducer of CREB protein 3)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c86967_g1	P47736	RPGP1_HUMAN	Rap1 GTPase-activating protein 1 (Rap1GAP) (Rap1GAP1)	Homo sapiens (Human)
c86973_g1	Q5RFZ7	F167A_DANRE	Protein FAM167A	Danio rerio (Zebrafish) (Brachydanio rerio)
c86985_g6	Q5IGR6	EXT1C_DANRE	Exostosin-1c (EC 2.4.1.224) (EC 2.4.1.225) (Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase 1c) (Multiple exostoses protein 1 homolog c)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87042_g1	P54613	2AAB_PIG	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (PP2A subunit A isoform PR65-beta) (PP2A subunit A isoform R1-beta) (Fragment)	Sus scrofa (Pig)
c87074_g5	Q1JQA3	AP3S2_BOVIN	AP-3 complex subunit sigma-2 (AP-3 complex subunit sigma-3B) (Adaptor-related protein complex 3 subunit sigma-2) (Sigma-3B-adaptin) (Sigma3B-adaptin) (Sigma-adaptin 3b)	Bos taurus (Bovine)
c87147_g1	P29401	TKT_HUMAN	Transketolase (TK) (EC 2.2.1.1)	Homo sapiens (Human)
c87149_g7	Q64487	PTPRD_MOUSE	Receptor-type tyrosine-protein phosphatase delta (Protein-tyrosine phosphatase delta) (R-PTP-delta) (EC 3.1.3.48)	Mus musculus (Mouse)
c87162_g8	Q9D0F9	PGM1_MOUSE	Phosphoglucomutase-1 (PGM 1) (EC 5.4.2.2) (Glucose phosphomutase 1) (Phosphoglucomutase-2)	Mus musculus (Mouse)
c87211_g6	Q5F4B2	SWP70_CHICK	Switch-associated protein 70 (SWAP-70)	Gallus gallus (Chicken)
c87235_g4	Q8IZN3	ZDH14_HUMAN	Probable palmitoyltransferase ZDHHC14 (EC 2.3.1.225) (NEW1 domain-containing protein) (NEW1CP) (Zinc finger DHHC domain-containing protein 14) (DHHC-14)	Homo sapiens (Human)
c87237_g1	Q6ZMT1	STAC2_HUMAN	SH3 and cysteine-rich domain-containing protein 2 (24b2/STAC2) (Src homology 3 and cysteine-rich domain-containing protein 2)	Homo sapiens (Human)
c87295_g6	B3F211	IBP2B_DANRE	Insulin-like growth factor-binding protein 2-B (IGF-binding protein 2-B) (IGFBP-2-B) (IGFBP-2b)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87348_g8	Q05AL2	PPM1H_DANRE	Protein phosphatase 1H (EC 3.1.3.16)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87376_g3	P57772	SELB_HUMAN	Selenocysteine-specific elongation factor (Elongation factor sec) (Eukaryotic elongation factor, selenocysteine-tRNA-specific)	Homo sapiens (Human)

c87379_g9	Q62233	SIX3_MOUSE	Homeobox protein SIX3 (Sine oculis homeobox homolog 3)	Mus musculus (Mouse)
c87394_g11	Q4R380	DPLL2_MOUSE	DNA polymerase lambda (Pol Lambda) (EC 2.7.7.7) (EC 4.2.99.-)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c87483_g1	O00743	PPP6_HUMAN	Serine/threonine-protein phosphatase 6 catalytic subunit (PPP6C) (EC 3.1.3.16) [Cleaved into: Serine/threonine-protein phosphatase 6 catalytic subunit, N-terminally processed]	Homo sapiens (Human)
c87488_g3	Q7ZW47	STAU2_DANRE	Double-stranded RNA-binding protein Staufen homolog 2	Danio rerio (Zebrafish) (Brachydanio rerio)
c87509_g4	P0C7T6	ATX1L_MOUSE	Ataxin-1-like (Brother of ataxin-1)	Mus musculus (Mouse)
c87664_g3	Q9N1F2	FLVC1_FELCA	Feline leukemia virus subgroup C receptor-related protein 1	Felis catus (Cat) (Felis silvestris catus)
c87717_g1	P79147	GBB3_CANFA	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 (Transducin beta chain 3)	Canis familiaris (Dog) (Canis lupus familiaris)
c87733_g6	P35350	ACKR4_BOVIN	Atypical chemokine receptor 4 (C-C chemokine receptor type 11) (C-C CKR-11) (CC-CKR-11) (CCR-11) (CC chemokine receptor-like 1) (Protein PPR1) (Putative gustatory receptor type B)	Bos taurus (Bovine)
c87770_g5	P28828	PTPRM_MOUSE	Receptor-type tyrosine-protein phosphatase mu (Protein-tyrosine phosphatase mu) (R-PTP-mu) (EC 3.1.3.48)	Mus musculus (Mouse)
c87811_g4	Q9H0Q0	FA49A_HUMAN	Protein FAM49A	Homo sapiens (Human)
c87817_g6	Q90435	PO4F3_DANRE	POU domain, class 4, transcription factor 3 (Brain-specific homeobox/POU domain protein 3.1) (Brain-3.1) (zfbBrn-3.1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87848_g1	Q8WN57	TYRP1_BOVIN	5,6-dihydroxyindole-2-carboxylic acid oxidase (DHICA oxidase) (EC 1.14.18.-) (Tyrosinase-related protein 1) (TRP-1) (TRP1)	Bos taurus (Bovine)
c87853_g1	Q6NW52	MSRB2_DANRE	Methionine-R-sulfoxide reductase B2, mitochondrial (MsrB2) (EC 1.8.4.-)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87934_g4	Q0P4A4	NAT14_DANRE	N-acetyltransferase 14 (EC 2.3.1.-)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87988_g2	Q3UDW8	HGNAT_MOUSE	Heparan-alpha-glucosaminide N-acetyltransferase (EC 2.3.1.78) (Transmembrane protein 76)	Mus musculus (Mouse)
c88004_g2	Q9Y263	PLAP_HUMAN	Phospholipase A-2-activating protein (PLA2P) (PLAP)	Homo sapiens (Human)
c88029_g3	Q05655	KPCD_HUMAN	Protein kinase C delta type (EC 2.7.11.13) (Tyrosine-protein kinase PRKCD) (EC 2.7.10.2) (nPKC-delta) [Cleaved into: Protein kinase C delta type regulatory subunit; Protein kinase C delta type catalytic subunit (Sphingosine-dependent protein kinase-1) (SDK1)]	Homo sapiens (Human)

c88030_g2	B2RRF6	Z518A_MOUSE	Zinc finger protein 518A	Mus musculus (Mouse)
c88060_g3	O57594	SURF6_TAKRU	Surfeit locus protein 6 homolog	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c88062_g1	Q6P0E8	PPAC3_DANRE	Probable lipid phosphate phosphatase PPAPDC3 (EC 3.1.3.-) (Phosphatidic acid phosphatase type 2 domain-containing protein 3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88111_g1	Q7M733	HPS6_RAT	Hermansky-Pudlak syndrome 6 protein homolog (Ruby-eye protein homolog) (Ruby-eye-like protein) (Ru)	Rattus norvegicus (Rat)
c88143_g5	P84335	TPM1_LIZAU	Tropomyosin alpha-1 chain (Alpha-tropomyosin) (Tropomyosin-1)	Liza aurata (Golden grey mullet)
c88145_g1	P79147	GBB3_CANFA	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 (Transducin beta chain 3)	Canis familiaris (Dog) (Canis lupus familiaris)
c88161_g2	Q8WYP3	RIN2_HUMAN	Ras and Rab interactor 2 (Ras association domain family 4) (Ras inhibitor JC265) (Ras interaction/interference protein 2)	Homo sapiens (Human)
c88206_g1	Q90617	LAMP2_CHICK	Lysosome-associated membrane glycoprotein 2 (LAMP-2) (Lysosome-associated membrane protein 2)	Gallus gallus (Chicken)
c88207_g3	P08548	LIN1_NYCCO	LINE-1 reverse transcriptase homolog (EC 2.7.7.49)	Nycticebus coucang (Slow loris)
c88249_g3	Q66H98	SDPR_RAT	Serum deprivation-response protein (Cavin-2) (Phosphatidylserine-binding protein)	Rattus norvegicus (Rat)
c88318_g1	Q7SYN4	5NT3_DANRE	Cytosolic 5'-nucleotidase 3 (EC 3.1.3.5) (Cytosolic 5'-nucleotidase III) (cN-III)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88344_g2	Q4R7U0	TMC7_MACFA	Transmembrane channel-like protein 7	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c88404_g6	Q9EQ60	CAC1H_RAT	Voltage-dependent T-type calcium channel subunit alpha-1H (Voltage-gated calcium channel subunit alpha Cav3.2)	Rattus norvegicus (Rat)
c88424_g11	Q6P2P2	ANM9_HUMAN	Putative protein arginine N-methyltransferase 9 (Putative protein arginine N-methyltransferase 10) (EC 2.1.1.-)	Homo sapiens (Human)
c88428_g5	Q6P371	HOT_XENTR	Hydroxyacid-oxoacid transhydrogenase, mitochondrial (HOT) (EC 1.1.99.24) (Alcohol dehydrogenase iron-containing protein 1) (ADHFe1)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c88469_g3	O43663	PRC1_HUMAN	Protein regulator of cytokinesis 1	Homo sapiens (Human)
c88498_g4	Q07002	CDK18_HUMAN	Cyclin-dependent kinase 18 (EC 2.7.11.22) (Cell division protein kinase 18) (PCTAIRE-motif protein kinase 3) (Serine/threonine-protein kinase PCTAIRE-3)	Homo sapiens (Human)
c88513_g2	Q502B3	B3GL2_DANRE	UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2 (Beta-1,3-GalNAc-T2) (EC 2.4.1.-) (Beta-1,3-N-acetylgalactosaminyltransferase II)	Danio rerio (Zebrafish) (Brachydanio rerio)

c88525_g1	O22347	TBA1_ELEIN	Tubulin alpha-1 chain (Alpha-1-tubulin)	Eleusine indica (Goosegrass) (Cynosurus indicus)
c88551_g9	Q9JKS4	LDB3_MOUSE	LIM domain-binding protein 3 (Protein cypher) (Protein oracle) (Z-band alternatively spliced PDZ-motif protein)	Mus musculus (Mouse)
c88557_g4	Q8BHJ5	TBL1R_MOUSE	F-box-like/WD repeat-containing protein TBL1XR1 (Nuclear receptor corepressor/HDAC3 complex subunit TBLR1) (TBL1-related protein 1) (Transducin beta-like 1X-related protein 1)	Mus musculus (Mouse)
c88574_g1	Q2NL16	FBX28_BOVIN	F-box only protein 28	Bos taurus (Bovine)
c88589_g1	Q78T81	F102A_MOUSE	Protein FAM102A	Mus musculus (Mouse)
c88589_g3	Q6GNM6	F102A_XENLA	Protein FAM102A	Xenopus laevis (African clawed frog)
c88652_g2	A1A5X5	ADIPL_DANRE	Adipolin (Adipose-derived insulin-sensitizing factor) (Complement C1q tumor necrosis factor-related protein 12)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88658_g3	Q5ZMP3	T184C_CHICK	Transmembrane protein 184C (Transmembrane protein 34)	Gallus gallus (Chicken)
c88663_g2	Q16877	F264_HUMAN	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4 (6PF-2-K/Fru-2,6-P2ase 4) (PFK/FBPase 4) (6PF-2-K/Fru-2,6-P2ase testis-type isozyme) [Includes: 6-phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)]	Homo sapiens (Human)
c88692_g2	Q9Y5I4	PCDC2_HUMAN	Protocadherin alpha-C2 (PCDH-alpha-C2)	Homo sapiens (Human)
c88713_g1	B2RX14	TUT4_MOUSE	Terminal uridylyltransferase 4 (TUTase 4) (EC 2.7.7.52) (Zinc finger CCHC domain-containing protein 11)	Mus musculus (Mouse)
c88713_g3	B2RX14	TUT4_MOUSE	Terminal uridylyltransferase 4 (TUTase 4) (EC 2.7.7.52) (Zinc finger CCHC domain-containing protein 11)	Mus musculus (Mouse)
c88727_g2	Q7SZI7	RET3_XENLA	Retinol-binding protein 3 (Interphotoreceptor retinoid-binding protein) (IRBP) (xIRBP) (Interstitial retinol-binding protein)	Xenopus laevis (African clawed frog)
c88727_g4	P08938	PURP_CHICK	Purpurin	Gallus gallus (Chicken)
c88727_g5	P48441	IDUA_MOUSE	Alpha-L-iduronidase (EC 3.2.1.76)	Mus musculus (Mouse)
c88756_g1	Q14108	SCRB2_HUMAN	Lysosome membrane protein 2 (85 kDa lysosomal membrane sialoglycoprotein) (LGP85) (CD36 antigen-like 2) (Lysosome membrane protein II) (LIMP II) (Scavenger receptor class B member 2) (CD antigen CD36)	Homo sapiens (Human)
c88770_g8	A3KMV1	SHKB1_BOVIN	SH3KBP1-binding protein 1	Bos taurus (Bovine)
c88785_g1	Q9I8C7	ACH10_CHICK	Neuronal acetylcholine receptor subunit alpha-10 (Alpha 10 nAChR) (Nicotinic acetylcholine receptor subunit alpha-10) (NACHR alpha-10)	Gallus gallus (Chicken)

c88792_g6	Q4R495	MFS11_MACFA	UNC93-like protein MFSD11 (Major facilitator superfamily domain-containing protein 11)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c88811_g11	P46896	GTR1_CHICK	Solute carrier family 2, facilitated glucose transporter member 1 (Glucose transporter type 1) (GLUT-1) (GT1)	Gallus gallus (Chicken)
c88867_g7	Q8C8N3	VWC2_MOUSE	Brorin (Brain-specific chordin-like protein) (CR (chordin-like cysteine-rich) domain-containing adhesive protein) (Cradin) (von Willebrand factor C domain-containing protein 2)	Mus musculus (Mouse)
c88894_g6	B5X3C4	LIS1B_SALSA	Lissencephaly-1 homolog B	Salmo salar (Atlantic salmon)
c88906_g4	O15524	SOCS1_HUMAN	Suppressor of cytokine signaling 1 (SOCS-1) (JAK-binding protein) (JAB) (STAT-induced STAT inhibitor 1) (SSI-1) (Tec-interacting protein 3) (TIP-3)	Homo sapiens (Human)
c88910_g5	Q9C0G0	ZN407_HUMAN	Zinc finger protein 407	Homo sapiens (Human)
c88922_g1	Q28EW0	TM87A_XENTR	Transmembrane protein 87A	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c88937_g2	Q3T0X9	DPOD4_BOVIN	DNA polymerase delta subunit 4 (DNA polymerase delta subunit p12)	Bos taurus (Bovine)
c88939_g3	O42122	WNT5B_ORYLA	Protein Wnt-5b	Oryzias latipes (Medaka fish) (Japanese ricefish)
c88939_g4	O42122	WNT5B_ORYLA	Protein Wnt-5b	Oryzias latipes (Medaka fish) (Japanese ricefish)
c88971_g2	Q6PDK8	DTX4_MOUSE	E3 ubiquitin-protein ligase DTX4 (EC 6.3.2.-) (Protein deltex-4) (Deltex4)	Mus musculus (Mouse)
c88987_g6	Q5U3N0	PKHA8_DANRE	Pleckstrin homology domain-containing family A member 8 (PH domain-containing family A member 8)	Danio rerio (Zebrafish) (Brachydanio rerio)
c89003_g1	O75689	ADAP1_HUMAN	Arf-GAP with dual PH domain-containing protein 1 (Centaurin-alpha-1) (Cnt-a1) (Putative MAPK-activating protein PM25)	Homo sapiens (Human)
c89012_g3	Q28EW0	TM87A_XENTR	Transmembrane protein 87A	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c89016_g4	Q66HX8	GDAP2_DANRE	Ganglioside-induced differentiation-associated protein 2	Danio rerio (Zebrafish) (Brachydanio rerio)
c89026_g5	Q5BK43	ESIP1_RAT	Epithelial-stromal interaction protein 1	Rattus norvegicus (Rat)
c89048_g8	G3XA57	RFIP2_MOUSE	Rab11 family-interacting protein 2 (Rab11-FIP2)	Mus musculus (Mouse)
c89106_g11	B9TQX3	UCMA_DICLA	Unique cartilage matrix-associated protein [Cleaved into: Unique cartilage matrix-associated protein C-terminal fragment (Ucma-C) (Gla-rich protein) (GRP)]	Dicentrarchus labrax (European seabass) (Morone labrax)
c89131_g1	Q803M5	SAAL1_DANRE	Protein saal1	Danio rerio (Zebrafish) (Brachydanio rerio)

c89163_g1	B2RX14	TUT4_MOUSE	Terminal uridylyltransferase 4 (TUTase 4) (EC 2.7.7.52) (Zinc finger CCHC domain-containing protein 11)	Mus musculus (Mouse)
c89180_g5	Q50L44	LIGO1_CHICK	Leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 1 (cLINGO-1)	Gallus gallus (Chicken)
c89184_g2	Q8WXD5	GEMI6_HUMAN	Gem-associated protein 6 (Gemin-6) (SIP2)	Homo sapiens (Human)
c89211_g5	P52848	NDST1_HUMAN	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 (EC 2.8.2.8) (Glucosaminyl N-deacetylase/N-sulfotransferase 1) (NDST-1) (N-heparan sulfate sulfotransferase 1) (N-HSST 1) ([Heparan sulfate]-glucosamine N-sulfotransferase 1) (HSNST 1) [Includes: Heparan sulfate N-deacetylase 1 (EC 3.-.-.); Heparan sulfate N-sulfotransferase 1 (EC 2.8.2.-.)]	Homo sapiens (Human)
c89214_g1	Q7TNF8	RIMB1_MOUSE	Peripheral-type benzodiazepine receptor-associated protein 1 (PRAX-1) (Peripheral benzodiazepine receptor-interacting protein) (PBR-IP) (RIMS-binding protein 1) (RIM-BP1)	Mus musculus (Mouse)
c89224_g2	P35520	CBS_HUMAN	Cystathionine beta-synthase (EC 4.2.1.22) (Beta-thionase) (Serine sulfhydryase)	Homo sapiens (Human)
c89233_g2	Q86VZ4	LRP11_HUMAN	Low-density lipoprotein receptor-related protein 11 (LRP-11)	Homo sapiens (Human)
c89253_g5	Q5ZIL4	STRBP_CHICK	Spermatid perinuclear RNA-binding protein	Gallus gallus (Chicken)
c89263_g2	Q8C0V0	TLK1_MOUSE	Serine/threonine-protein kinase tousled-like 1 (EC 2.7.11.1) (Tousled-like kinase 1)	Mus musculus (Mouse)
c89284_g1	NA			
c89296_g8	Q9EQJ9	MAGI3_MOUSE	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 (Membrane-associated guanylate kinase inverted 3) (MAGI-3)	Mus musculus (Mouse)
c89346_g1	Q6TN15	MX_SINCH	Interferon-induced GTP-binding protein Mx (Interferon-inducible Mx protein)	Siniperca chuatsi (Mandarin fish)
c89346_g2	Q2KTC2	MX_DICLA	Interferon-induced GTP-binding protein Mx (Interferon-inducible Mx protein)	Dicentrarchus labrax (European seabass) (Morone labrax)
c89412_g5	P20612	GNAT1_MOUSE	Guanine nucleotide-binding protein G(t) subunit alpha-1 (Transducin alpha-1 chain)	Mus musculus (Mouse)
c89457_g4	Q5T9S5	CCD18_HUMAN	Coiled-coil domain-containing protein 18 (Sarcoma antigen NY-SAR-24)	Homo sapiens (Human)
c89528_g9	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89552_g1	P47709	RP3A_RAT	Rabphilin-3A (Exophilin-1)	Rattus norvegicus (Rat)
c89562_g4	O88751	CABP1_RAT	Calcium-binding protein 1 (CaBP1) (Caldendrin)	Rattus norvegicus (Rat)

c89565_g6	Q66H42	LYPD1_RAT	Ly6/PLAUR domain-containing protein 1	Rattus norvegicus (Rat)
c89590_g1	Q9BW60	ELOV1_HUMAN	Elongation of very long chain fatty acids protein 1 (EC 2.3.1.199) (3-keto acyl-CoA synthase ELOVL1) (ELOVL fatty acid elongase 1) (ELOVL FA elongase 1) (Very-long-chain 3-oxoacyl-CoA synthase 1)	Homo sapiens (Human)
c89599_g3	O60336	MABP1_HUMAN	Mitogen-activated protein kinase-binding protein 1 (JNK-binding protein 1) (JNKBP-1)	Homo sapiens (Human)
c89605_g3	Q6P121	HYCCI_DANRE	Hyccin (Protein FAM126A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c89648_g8	Q6AYR4	TOR2A_RAT	Torsin-2A (Torsin family 2 member A)	Rattus norvegicus (Rat)
c89704_g7	O46606	DDHD1_BOVIN	Phospholipase DDHD1 (EC 3.1.1.-) (DDHD domain-containing protein 1) (Phosphatidic acid-preferring phospholipase A1) (PA-PLA1)	Bos taurus (Bovine)
c89734_g2	Q86UW9	DTX2_HUMAN	Probable E3 ubiquitin-protein ligase DTX2 (EC 6.3.2.-) (Protein deltex-2) (Deltex2) (hDTX2) (RING finger protein 58)	Homo sapiens (Human)
c89737_g1	Q1LZD3	TSSC4_BOVIN	Protein TSSC4	Bos taurus (Bovine)
c89776_g4	Q8BNQ3	G137B_MOUSE	Integral membrane protein GPR137B (Transmembrane 7 superfamily member 1 protein)	Mus musculus (Mouse)
c89776_g6	O60478	G137B_HUMAN	Integral membrane protein GPR137B (Transmembrane 7 superfamily member 1 protein)	Homo sapiens (Human)
c89788_g9	Q5PR73	DIRA2_MOUSE	GTP-binding protein Di-Ras2 (Distinct subgroup of the Ras family member 2)	Mus musculus (Mouse)
c89807_g4	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89807_g5	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89807_g6	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89822_g1	P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1- α /beta (Transcription factor ISGF-3 components p91/p84)	Homo sapiens (Human)
c89824_g1	P32745	SSR3_HUMAN	Somatostatin receptor type 3 (SS-3-R) (SS3-R) (SS3R) (SSR-28)	Homo sapiens (Human)
c89842_g1	A1L2F6	TM205_DANRE	Transmembrane protein 205	Danio rerio (Zebrafish) (Brachydanio rerio)
c89972_g5	A2CG49	KALRN_MOUSE	Kalirin (EC 2.7.11.1) (Protein Duo) (Serine/threonine-protein kinase with Dbl- and pleckstrin homology domain)	Mus musculus (Mouse)

c90030_g2	Q15835	RK_HUMAN	Rhodopsin kinase (RK) (EC 2.7.11.14) (G protein-coupled receptor kinase 1)	Homo sapiens (Human)
c90030_g5	Q15835	RK_HUMAN	Rhodopsin kinase (RK) (EC 2.7.11.14) (G protein-coupled receptor kinase 1)	Homo sapiens (Human)
c90052_g4	Q08CZ6	NAKD2_XENTR	NAD kinase 2, mitochondrial (EC 2.7.1.23) (NAD kinase domain-containing protein 1, mitochondrial)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c90061_g2	Q9Y226	S22AD_HUMAN	Solute carrier family 22 member 13 (Organic cation transporter-like 3) (ORCTL-3)	Homo sapiens (Human)
c90092_g8	Q80TT8	CUL9_MOUSE	Cullin-9 (CUL-9) (p53-associated parkin-like cytoplasmic protein)	Mus musculus (Mouse)
c90146_g2	Q5ZJ58	PI51B_CHICK	Phosphatidylinositol 4-phosphate 5-kinase type-1 beta (PIP5K1-beta) (PtdIns(4)P-5-kinase 1 beta) (EC 2.7.1.68) (Phosphatidylinositol 4-phosphate 5-kinase type I beta) (PIP5K1beta) (Type I phosphatidylinositol 4-phosphate 5-kinase beta)	Gallus gallus (Chicken)
c90167_g1	Q6Q629	DPP10_RAT	Inactive dipeptidyl peptidase 10 (Dipeptidyl peptidase X) (DPP X) (Kv4 potassium channel auxiliary subunit)	Rattus norvegicus (Rat)
c90217_g3	Q8WW59	SPRY4_HUMAN	SPRY domain-containing protein 4	Homo sapiens (Human)
c90220_g1	P31153	METK2_HUMAN	S-adenosylmethionine synthase isoform type-2 (AdoMet synthase 2) (EC 2.5.1.6) (Methionine adenosyltransferase 2) (MAT 2) (Methionine adenosyltransferase II) (MAT-II)	Homo sapiens (Human)
c90267_g1	Q8CDU6	HECD2_MOUSE	Probable E3 ubiquitin-protein ligase HECTD2 (EC 6.3.2.-) (HECT domain-containing protein 2)	Mus musculus (Mouse)
c90277_g6	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c90284_g1	Q9H6B4	CLMP_HUMAN	CXADR-like membrane protein (Adipocyte adhesion molecule) (Coxsackie- and adenovirus receptor-like membrane protein) (CAR-like membrane protein)	Homo sapiens (Human)
c90320_g7	O13166	TLE2_DANRE	Protein groucho-2 (Groucho-related Grg2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90323_g7	Q24K03	THUM1_BOVIN	THUMP domain-containing protein 1	Bos taurus (Bovine)
c90341_g1	Q071E0	SET8A_DANRE	N-lysine methyltransferase SETD8-A (EC 2.1.1.-) (Histone-lysine N-methyltransferase SETD8-A) (EC 2.1.1.43) (SET domain-containing protein 8-A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90369_g6	P82013	VDAC2_MELGA	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (Outer mitochondrial membrane protein porin 2)	Meleagris gallopavo (Common turkey)
c90374_g1	P46844	BIEA_RAT	Biliverdin reductase A (BVR A) (EC 1.3.1.24) (Biliverdin-IX alpha-reductase)	Rattus norvegicus (Rat)

c90392_g2	B5DGH9	EIF3E_SALSA	Eukaryotic translation initiation factor 3 subunit E (eIF3e) (Eukaryotic translation initiation factor 3 subunit 6)	Salmo salar (Atlantic salmon)
c90432_g5	P10123	RLBP1_BOVIN	Retinaldehyde-binding protein 1 (Cellular retinaldehyde-binding protein)	Bos taurus (Bovine)
c90442_g3	Q8BQU7	TMM74_MOUSE	Transmembrane protein 74	Mus musculus (Mouse)
c90460_g5	Q15678	PTN14_HUMAN	Tyrosine-protein phosphatase non-receptor type 14 (EC 3.1.3.48) (Protein-tyrosine phosphatase pez)	Homo sapiens (Human)
c90527_g11	Q13275	SEM3F_HUMAN	Semaphorin-3F (Sema III/F) (Semaphorin IV) (Sema IV)	Homo sapiens (Human)
c90539_g5	P29374	ARI4A_HUMAN	AT-rich interactive domain-containing protein 4A (ARID domain-containing protein 4A) (Retinoblastoma-binding protein 1) (RBBP-1)	Homo sapiens (Human)
c90545_g2	Q2M3D2	EX3L2_HUMAN	Exocyst complex component 3-like protein 2 (HBV X-transactivated gene 7 protein) (HBV XAg-transactivated protein 7)	Homo sapiens (Human)
c90585_g6	Q63HN8	RN213_HUMAN	E3 ubiquitin-protein ligase RNF213 (EC 6.3.2.-) (ALK lymphoma oligomerization partner on chromosome 17) (Mysterin) (RING finger protein 213)	Homo sapiens (Human)
c90598_g3	Q6PHN7	TM164_MOUSE	Transmembrane protein 164	Mus musculus (Mouse)
c90624_g1	P11260	LORF1_MOUSE	LINE-1 retrotransposable element ORF1 protein (L1ORF1p) (LINE retrotransposable element 1) (LINE1 retrotransposable element 1) (Transposase element L1Md-A101/L1Md-A102/L1Md-A2)	Mus musculus (Mouse)
c90631_g4	Q02817	MUC2_HUMAN	Mucin-2 (MUC-2) (Intestinal mucin-2)	Homo sapiens (Human)
c90661_g2	P07224	PROS_BOVIN	Vitamin K-dependent protein S	Bos taurus (Bovine)
c90668_g5	Q3U0L2	AN33B_MOUSE	Ankyrin repeat domain-containing protein 33B	Mus musculus (Mouse)
c90675_g3	P17810	PRPH2_BOVIN	Peripherin-2 (Retinal degeneration slow protein)	Bos taurus (Bovine)
c90675_g9	O42281	PRPH2_CHICK	Peripherin-2 (CRDS1) (Photoreceptor outer segment membrane glycoprotein 1) (Retinal degeneration slow protein)	Gallus gallus (Chicken)
c90691_g6	Q9Y5Y6	ST14_HUMAN	Suppressor of tumorigenicity 14 protein (EC 3.4.21.109) (Matriptase) (Membrane-type serine protease 1) (MT-SP1) (Prostamin) (Serine protease 14) (Serine protease TADG-15) (Tumor-associated differentially-expressed gene 15 protein)	Homo sapiens (Human)
c90725_g5	P58369	ANKH_TETNG	Progressive ankylosis protein homolog (ANK)	Tetraodon nigroviridis (Spotted green pufferfish) (Chelonodon nigroviridis)
c90740_g5	Q9I8D1	MYO6_CHICK	Unconventional myosin-VI (Unconventional myosin-6)	Gallus gallus (Chicken)

c90844_g4	P35219	CAH8_HUMAN	Carbonic anhydrase-related protein (CARP) (Carbonic anhydrase VIII) (CA-VIII)	Homo sapiens (Human)
c90847_g2	P55006	RDH7_RAT	Retinol dehydrogenase 7 (EC 1.1.1.105) (Retinol dehydrogenase type III) (RODH III)	Rattus norvegicus (Rat)
c90876_g3	Q92900	RENT1_HUMAN	Regulator of nonsense transcripts 1 (EC 3.6.4.-) (ATP-dependent helicase RENT1) (Nonsense mRNA reducing factor 1) (NORF1) (Up-frameshift suppressor 1 homolog) (hUpf1)	Homo sapiens (Human)
c90958_g2	O60701	UGDH_HUMAN	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) (EC 1.1.1.22)	Homo sapiens (Human)
c90983_g8	P07949	RET_HUMAN	Proto-oncogene tyrosine-protein kinase receptor Ret (EC 2.7.10.1) (Cadherin family member 12) (Proto-oncogene c-Ret) [Cleaved into: Soluble RET kinase fragment; Extracellular cell-membrane anchored RET cadherin 120 kDa fragment]	Homo sapiens (Human)
c90995_g2	Q5SYY0	Z322B_HUMAN	Deleted.	0
c90997_g4	Q6DHL5	LRC57_DANRE	Leucine-rich repeat-containing protein 57	Danio rerio (Zebrafish) (Brachydanio rerio)
c91011_g3	Q9H5L6	THAP9_HUMAN	DNA transposase THAP9 (EC 2.7.7.-) (THAP domain-containing protein 9) (hTh9)	Homo sapiens (Human)
c91019_g6	P78363	ABCA4_HUMAN	Retinal-specific ATP-binding cassette transporter (ATP-binding cassette sub-family A member 4) (RIM ABC transporter) (RIM protein) (RmP) (Stargardt disease protein)	Homo sapiens (Human)
c91045_g1	Q6Q0C0	TRAF7_HUMAN	E3 ubiquitin-protein ligase TRAF7 (EC 6.3.2.-) (RING finger and WD repeat-containing protein 1) (RING finger protein 119) (TNF receptor-associated factor 7)	Homo sapiens (Human)
c91058_g2	Q9ERS6	IRPL2_MOUSE	X-linked interleukin-1 receptor accessory protein-like 2 (IL-1 receptor accessory protein-like 2) (IL-1-RAPL-2) (IL-1RAPL-2) (IL1RAPL-2) (IL1RAPL-2-related protein) (Three immunoglobulin domain-containing IL-1 receptor-related 1) (TIGIRR-1)	Mus musculus (Mouse)
c91077_g1	Q6ZM28	HRG1B_DANRE	Heme transporter hrg1-B (Heme-responsive gene 1 protein homolog B) (HRG-1B) (Solute carrier family 48 member 1-A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91108_g7	Q8BJU2	TSN9_MOUSE	Tetraspanin-9 (Tspan-9) (Tetraspan NET-5)	Mus musculus (Mouse)
c91135_g6	Q9ESG8	ZDHC16_MOUSE	Probable palmitoyltransferase ZDHC16 (EC 2.3.1.225) (Ablphilin-2) (Zinc finger DHHC domain-containing protein 16) (DHHC-16)	Mus musculus (Mouse)

c91179_g5	A4IHK1	MFHA1_XENTR	Malignant fibrous histiocytoma-amplified sequence 1 homolog	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c91179_g6	O57415	RREB1_CHICK	Ras-responsive element-binding protein 1 (RREB-1)	Gallus gallus (Chicken)
c91181_g4	P06180	HIBN_XENLA	Histone-binding protein N1/N2	Xenopus laevis (African clawed frog)
c91213_g1	P23610	F8I2_HUMAN	Factor VIII intron 22 protein (CpG island protein)	Homo sapiens (Human)
c91232_g2	Q3KR56	GRM1A_RAT	GRAM domain-containing protein 1A (EG1RVC)	Rattus norvegicus (Rat)
c91248_g1	Q5R5M0	MTCH2_PONAB	Mitochondrial carrier homolog 2	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c91268_g4	A0AUR5	F188A_DANRE	Protein FAM188A (Protein CARP)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91271_g2	Q6RFY2	PHAR3_RAT	Phosphatase and actin regulator 3 (Scaffold-associated PP1-inhibiting protein) (Scapinin)	Rattus norvegicus (Rat)
c91286_g8	A0JME2	MCAF1_DANRE	Activating transcription factor 7-interacting protein 1 (MBD1-containing chromatin-associated factor 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91312_g1	P36915	GNL1_HUMAN	Guanine nucleotide-binding protein-like 1 (GTP-binding protein HSR1)	Homo sapiens (Human)
c91313_g3	Q5VU43	MYOME_HUMAN	Myomegalin (Cardiomyopathy-associated protein 2) (Phosphodiesterase 4D-interacting protein)	Homo sapiens (Human)
c91323_g2	P41440	S19A1_HUMAN	Folate transporter 1 (FOLT) (Intestinal folate carrier 1) (IFC-1) (Placental folate transporter) (Reduced folate carrier protein) (RFC) (Solute carrier family 19 member 1)	Homo sapiens (Human)
c91332_g1	Q13873	BMPR2_HUMAN	Bone morphogenetic protein receptor type-2 (BMP type-2 receptor) (BMPR-2) (EC 2.7.11.30) (Bone morphogenetic protein receptor type II) (BMP type II receptor) (BMPR-II)	Homo sapiens (Human)
c91342_g3	P29692	EF1D_HUMAN	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	Homo sapiens (Human)
c91361_g4	O60229	KALRN_HUMAN	Kalirin (EC 2.7.11.1) (Huntingtin-associated protein-interacting protein) (Protein Duo) (Serine/threonine-protein kinase with Dbl- and pleckstrin homology domain)	Homo sapiens (Human)
c91382_g5	Q2T9I9	F208A_XENLA	Protein FAM208A	Xenopus laevis (African clawed frog)
c91384_g2	Q803C9	PTSS1_DANRE	Phosphatidylserine synthase 1 (PSS-1) (PtdSer synthase 1) (EC 2.7.8.29) (Serine-exchange enzyme I)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91389_g1	Q5R685	P85A_PONAB	Phosphatidylinositol 3-kinase regulatory subunit alpha (PI3-kinase regulatory subunit alpha) (PI3K regulatory subunit alpha) (PtdIns-3-kinase regulatory subunit alpha) (Phosphatidylinositol 3-kinase 85 kDa regulatory subunit alpha) (PI3-kinase subunit p85-alpha)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)

c91396_g4	P26196	DDX6_HUMAN	Probable ATP-dependent RNA helicase DDX6 (EC 3.6.4.13) (ATP-dependent RNA helicase p54) (DEAD box protein 6) (Oncogene RCK)	Homo sapiens (Human)
c91402_g3	C6K2K4	NETO2_RAT	Neuropilin and tolloid-like protein 2 (Brain-specific transmembrane protein containing 2 CUB and 1 LDL-receptor class A domains protein 2)	Rattus norvegicus (Rat)
c91472_g6	Q01584	LIPO_BUFMA	Lipocalin	Bufo marinus (Giant toad) (Cane toad)
c91472_g7	Q7Z7G2	CPLX4_HUMAN	Complexin-4 (Complexin IV) (CPX IV)	Homo sapiens (Human)
c91527_g8	Q7SY24	KPCB_DANRE	Protein kinase C beta type (PKC-B) (PKC-beta) (EC 2.7.11.13)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91532_g6	P24406	RHOA_CANFA	Transforming protein RhoA (Rho1)	Canis familiaris (Dog) (Canis lupus familiaris)
c91595_g1	Q6Q629	DPP10_RAT	Inactive dipeptidyl peptidase 10 (Dipeptidyl peptidase X) (DPP X) (Kv4 potassium channel auxiliary subunit)	Rattus norvegicus (Rat)
c91635_g1	Q8JGW0	TSP4B_DANRE	Thrombospondin-4-B (Thbs4-B)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91693_g1	B0R0T1	VWA8_DANRE	von Willebrand factor A domain-containing protein 8	Danio rerio (Zebrafish) (Brachydanio rerio)
c91696_g4	Q29RT8	LPPR2_BOVIN	Lipid phosphate phosphatase-related protein type 2 (EC 3.1.3.4) (Plasticity-related gene 4 protein) (PRG-4)	Bos taurus (Bovine)
c91696_g6	Q6GM05	LPPR5_XENLA	Lipid phosphate phosphatase-related protein type 5 (EC 3.1.3.-)	Xenopus laevis (African clawed frog)
c91792_g2	Q7TN99	CPEB3_MOUSE	Cytoplasmic polyadenylation element-binding protein 3 (CPE-BP3) (CPE-binding protein 3) (mCPEB-3)	Mus musculus (Mouse)
c91826_g3	Q5EA55	GOGA7_BOVIN	Golgin subfamily A member 7	Bos taurus (Bovine)
c91869_g2	Q90257	ES1_DANRE	ES1 protein, mitochondrial	Danio rerio (Zebrafish) (Brachydanio rerio)
c91871_g12	Q9Y5F2	PCDBB_HUMAN	Protocadherin beta-11 (PCDH-beta-11)	Homo sapiens (Human)
c91879_g3	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c91893_g2	P49190	PTH2R_HUMAN	Parathyroid hormone 2 receptor (PTH2 receptor)	Homo sapiens (Human)
c91900_g1	Q08CX2	SH24A_XENTR	SH2 domain-containing protein 4A	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c91902_g7	Q9Y5F7	PCDGL_HUMAN	Protocadherin gamma-C4 (PCDH-gamma-C4)	Homo sapiens (Human)
c91922_g11	Q01339	APOH_MOUSE	Beta-2-glycoprotein 1 (APC inhibitor) (Activated protein C-binding protein) (Apolipoprotein H) (Apo-H) (Beta-2-glycoprotein I) (B2GPI) (Beta(2)GPI)	Mus musculus (Mouse)

c91932_g1	Q8BHY3	ANO1_MOUSE	Anoctamin-1 (Transmembrane protein 16A)	Mus musculus (Mouse)
c91964_g1	P61020	RAB5B_HUMAN	Ras-related protein Rab-5B	Homo sapiens (Human)
c91972_g7	Q8TDR2	STK35_HUMAN	Serine/threonine-protein kinase 35 (EC 2.7.11.1) (CLP-36-interacting kinase 1) (CLIK-1) (PDLIM1-interacting kinase 1) (Serine/threonine-protein kinase 35 L1)	Homo sapiens (Human)
c92018_g6	P42224	STAT1_HUMAN	Signal transducer and activator of transcription 1- alpha/beta (Transcription factor ISGF-3 components p91/p84)	Homo sapiens (Human)
c92022_g2	O14764	GBRD_HUMAN	Gamma-aminobutyric acid receptor subunit delta (GABA(A) receptor subunit delta)	Homo sapiens (Human)
c92026_g1	Q3SYV4	CAP1_BOVIN	Adenylyl cyclase-associated protein 1 (CAP 1)	Bos taurus (Bovine)
c92038_g2	Q6P9U4	SLMO2_RAT	Protein slowmo homolog 2	Rattus norvegicus (Rat)
c92048_g7	O42281	PRPH2_CHICK	Peripherin-2 (CRDS1) (Photoreceptor outer segment membrane glycoprotein 1) (Retinal degeneration slow protein)	Gallus gallus (Chicken)
c92054_g5	Q5M7W6	ITFG3_RAT	Protein ITFG3	Rattus norvegicus (Rat)
c92118_g2	Q96MT3	PRIC1_HUMAN	Prickle-like protein 1 (REST/NRSF-interacting LIM domain protein 1)	Homo sapiens (Human)
c92217_g2	P14735	IDE_HUMAN	Insulin-degrading enzyme (EC 3.4.24.56) (Abeta-degrading protease) (Insulin protease) (Insulinase) (Insulysin)	Homo sapiens (Human)
c92218_g5	P00491	PNPH_HUMAN	Purine nucleoside phosphorylase (PNP) (EC 2.4.2.1) (Inosine phosphorylase) (Inosine-guanosine phosphorylase)	Homo sapiens (Human)
c92221_g1	Q3SWZ4	EXOS9_BOVIN	Exosome complex component RRP45 (Exosome component 9)	Bos taurus (Bovine)
c92240_g7	Q4V8U5	ANO10_DANRE	Anoctamin-10 (Transmembrane protein 16K)	Danio rerio (Zebrafish) (Brachydanio rerio)
c92315_g5	O88917	LPHN1_RAT	Latrophilin-1 (Calcium-independent alpha-latrotoxin receptor 1) (CIRL-1)	Rattus norvegicus (Rat)
c92349_g4	Q9DC40	TELO2_MOUSE	Telomere length regulation protein TEL2 homolog	Mus musculus (Mouse)
c92409_g10	Q9H7Z3	NRDE2_HUMAN	Protein NRDE2 homolog	Homo sapiens (Human)
c92432_g2	Q02556	IRF8_HUMAN	Interferon regulatory factor 8 (IRF-8) (Interferon consensus sequence-binding protein) (H-ICSBP) (ICSBP)	Homo sapiens (Human)
c92481_g6	Q2KNE5	OPN4A_DANRE	Melanopsin-A (Mammalian-like melanopsin) (Melanopsin- M) (Opsin-4-A) (Opsin-4M)	Danio rerio (Zebrafish) (Brachydanio rerio)
c92573_g1	Q16352	AINX_HUMAN	Alpha-internexin (Alpha-Inx) (66 kDa neurofilament protein) (NF-66) (Neurofilament-66) (Neurofilament 5)	Homo sapiens (Human)
c92573_g2	Q08DH7	AINX_BOVIN	Alpha-internexin (Alpha-Inx)	Bos taurus (Bovine)

c92575_g4	P12271	RLBP1_HUMAN	Retinaldehyde-binding protein 1 (Cellular retinaldehyde-binding protein)	Homo sapiens (Human)
c92581_g2	O54819	TFPI1_MOUSE	Tissue factor pathway inhibitor (TFPI) (Extrinsic pathway inhibitor) (EPI) (Lipoprotein-associated coagulation inhibitor) (LACI)	Mus musculus (Mouse)
c92633_g11	Q9DCN1	NUD12_MOUSE	Peroxisomal NADH pyrophosphatase NUDT12 (EC 3.6.1.22) (Nucleoside diphosphate-linked moiety X motif 12) (Nudix motif 12)	Mus musculus (Mouse)
c92652_g1	Q5QGU6	RTP3_MOUSE	Receptor-transporting protein 3 (Transmembrane protein 7)	Mus musculus (Mouse)
c92680_g1	Q92072	DNMT1_CHICK	DNA (cytosine-5)-methyltransferase 1 (Dnmt1) (EC 2.1.1.37) (DNA methyltransferase Ggal) (DNA MTase Ggal) (M.Ggal) (MCMT)	Gallus gallus (Chicken)
c92698_g1	Q9NUV9	GIMA4_HUMAN	GTPase IMAP family member 4 (Immunity-associated nucleotide 1 protein) (IAN-1) (hIAN1) (Immunity-associated protein 4)	Homo sapiens (Human)
c92715_g1	P70297	STAM1_MOUSE	Signal transducing adapter molecule 1 (STAM-1)	Mus musculus (Mouse)
c92718_g3	Q9DBW0	CP4V2_MOUSE	Cytochrome P450 4V2 (EC 1.14.13.-)	Mus musculus (Mouse)
c92726_g3	Q96PY5	FMNL2_HUMAN	Formin-like protein 2 (Formin homology 2 domain-containing protein 2)	Homo sapiens (Human)
c92749_g3	P21329	RTJK_DROFU	RNA-directed DNA polymerase from mobile element jockey (EC 2.7.7.49) (Reverse transcriptase)	Drosophila funebris (Fruit fly)
c92787_g4	A2AQH4	BCORL_MOUSE	BCL-6 corepressor-like protein 1 (BCoR-L1) (BCoR-like protein 1)	Mus musculus (Mouse)
c92794_g2	Q6XQH0	G3ST2_MOUSE	Galactose-3-O-sulfotransferase 2 (Gal3ST-2) (EC 2.8.2.-) (Beta-galactose-3-O-sulfotransferase 2) (Gal-beta-1, 3-GalNAc 3'-sulfotransferase 2)	Mus musculus (Mouse)
c92812_g2	Q9HC58	NCKX3_HUMAN	Sodium/potassium/calcium exchanger 3 (Na(+)/K(+)/Ca(2+)-exchange protein 3) (Solute carrier family 24 member 3)	Homo sapiens (Human)
c92824_g2	P02561	TPM4_HORSE	Tropomyosin alpha-4 chain (Platelet beta tropomyosin) (Tropomyosin-4)	Equus caballus (Horse)
c92828_g2	Q99973	TEP1_HUMAN	Telomerase protein component 1 (Telomerase-associated protein 1) (Telomerase protein 1) (p240) (p80 telomerase homolog)	Homo sapiens (Human)
c92833_g4	Q8CF93	GLT13_MOUSE	Polypeptide N-acetylgalactosaminyltransferase 13 (EC 2.4.1.41) (Polypeptide GalNAc transferase 13) (GalNAc-T13) (pp-GaNTase 13) (Protein-UDP-acetylgalactosaminyltransferase 13) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 13)	Mus musculus (Mouse)

c92865_g3	Q3UPY5	GLBL2_MOUSE	Beta-galactosidase-1-like protein 2 (EC 3.2.1.-)	Mus musculus (Mouse)
c92897_g2	Q53HC0	CCD92_HUMAN	Coiled-coil domain-containing protein 92 (Limkain beta-2)	Homo sapiens (Human)
c92909_g1	Q5R685	P85A_PONAB	Phosphatidylinositol 3-kinase regulatory subunit alpha (PI3-kinase regulatory subunit alpha) (PI3K regulatory subunit alpha) (PtdIns-3-kinase regulatory subunit alpha) (Phosphatidylinositol 3-kinase 85 kDa regulatory subunit alpha) (PI3-kinase subunit p85-alpha) (PtdIns-3-kinase regulatory subunit p85-alpha)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c92933_g7	Q6GQB9	EDEM3_XENLA	ER degradation-enhancing alpha-mannosidase-like protein 3 (EC 3.2.1.113) (Alpha-1,2-mannosidase EDEM3)	Xenopus laevis (African clawed frog)
c92942_g4	P0C6R4	IFFO2_RAT	Intermediate filament family orphan 2	Rattus norvegicus (Rat)
c92967_g1	Q3SY69	AL1L2_HUMAN	Mitochondrial 10-formyltetrahydrofolate dehydrogenase (Mitochondrial 10-FTHFDH) (mtFDH) (EC 1.5.1.6) (Aldehyde dehydrogenase family 1 member L2)	Homo sapiens (Human)
c93062_g4	Q90641	IPKA_CHICK	cAMP-dependent protein kinase inhibitor alpha (PKI-alpha) (cAMP-dependent protein kinase inhibitor, kidney isoform)	Gallus gallus (Chicken)
c93117_g1	Q3U829	AP5Z1_MOUSE	AP-5 complex subunit zeta-1 (Adaptor-related protein complex 5 zeta subunit) (Zeta5)	Mus musculus (Mouse)
c93172_g6	Q96HB5	CC120_HUMAN	Coiled-coil domain-containing protein 120	Homo sapiens (Human)
c93241_g2	Q684M4	KEAP1_PIG	Kelch-like ECH-associated protein 1 (Cytosolic inhibitor of Nrf2) (INrf2)	Sus scrofa (Pig)
c93242_g3	Q6GNG3	TMX3_XENLA	Protein disulfide-isomerase TMX3 (EC 5.3.4.1) (Thioredoxin domain-containing protein 10) (Thioredoxin-related transmembrane protein 3)	Xenopus laevis (African clawed frog)
c93339_g1	Q6P1L5	F117B_HUMAN	Protein FAM117B (Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 13 protein)	Homo sapiens (Human)
c93376_g2	Q6GMI9	UXS1_DANRE	UDP-glucuronic acid decarboxylase 1 (EC 4.1.1.35) (UDP-glucuronate decarboxylase 1) (UXS-1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c93430_g2	P08582	TRFM_HUMAN	Melanotransferrin (Melanoma-associated antigen p97) (CD antigen CD228)	Homo sapiens (Human)
c93435_g1	D2XV59	GTPB1_RAT	GTP-binding protein 1	Rattus norvegicus (Rat)
c93470_g1	P58873	RHBL3_MOUSE	Rhomboid-related protein 3 (EC 3.4.21.105) (Ventroid transmembrane protein)	Mus musculus (Mouse)
c93483_g1	Q96KQ7	EHMT2_HUMAN	Histone-lysine N-methyltransferase EHMT2 (EC 2.1.1.-) (EC 2.1.1.43) (Euchromatic histone-lysine N-methyltransferase 2) (HLA-B-associated transcript 8) (Histone H3-K9 methyltransferase 3) (H3-K9-HMTase 3) (Lysine N-methyltransferase 1C) (Protein G9a)	Homo sapiens (Human)

c93487_g4	A2AX52	CO6A4_MOUSE	Collagen alpha-4(VI) chain	Mus musculus (Mouse)
c93499_g5	Q9C0I3	CCSE1_HUMAN	Serine-rich coiled-coil domain-containing protein 1 (Coiled-coil serine-rich protein 1)	Homo sapiens (Human)
c93508_g1	Q5ZKI4	CCD93_CHICK	Coiled-coil domain-containing protein 93	Gallus gallus (Chicken)
c93515_g5	P28840	NEC1_RAT	Neuroendocrine convertase 1 (NEC 1) (EC 3.4.21.93) (Prohormone convertase 1) (Proprotein convertase 1) (PC1)	Rattus norvegicus (Rat)
c93549_g1	Q8TEQ0	SNX29_HUMAN	Sorting nexin-29 (RUN domain-containing protein 2A)	Homo sapiens (Human)
c93557_g2	A2ASS6	TITIN_MOUSE	Titin (EC 2.7.11.1) (Connectin)	Mus musculus (Mouse)
c93561_g4	Q3V1V3	ESF1_MOUSE	ESF1 homolog (ABT1-associated protein)	Mus musculus (Mouse)
c93574_g1	Q7TPG7	F19A2_MOUSE	Protein FAM19A2 (Chemokine-like protein TAFA-2)	Mus musculus (Mouse)
c93600_g2	Q5JXC2	MIIP_HUMAN	Migration and invasion-inhibitory protein (IGFBP2-binding protein) (Invasion-inhibitory protein 45) (Iip45)	Homo sapiens (Human)
c93611_g2	Q16760	DGKD_HUMAN	Diacylglycerol kinase delta (DAG kinase delta) (EC 2.7.1.107) (130 kDa diacylglycerol kinase) (Diglyceride kinase delta) (DGK-delta)	Homo sapiens (Human)
c93639_g1	Q9UPQ0	LIMC1_HUMAN	LIM and calponin homology domains-containing protein 1	Homo sapiens (Human)
c93711_g2	P97952	SCN1B_MOUSE	Sodium channel subunit beta-1	Mus musculus (Mouse)
c93737_g2	Q9CQ54	NDUC2_MOUSE	NADH dehydrogenase [ubiquinone] 1 subunit C2 (Complex I-B14.5b) (CI-B14.5b) (NADH-ubiquinone oxidoreductase subunit B14.5b)	Mus musculus (Mouse)
c93744_g2	P04972	CNRG_BOVIN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma (GMP-PDE gamma) (EC 3.1.4.35)	Bos taurus (Bovine)
c93745_g3	A1A5G4	MAGI3_XENTR	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 (Membrane-associated guanylate kinase inverted 3) (MAGI-3)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c93762_g2	P35803	GPM6B_MOUSE	Neuronal membrane glycoprotein M6-b (M6b)	Mus musculus (Mouse)
c93765_g1	Q9ESZ0	XRCC1_RAT	DNA repair protein XRCC1 (X-ray repair cross-complementing protein 1)	Rattus norvegicus (Rat)
c93773_g6	A0JNK3	HTRA2_BOVIN	Serine protease HTRA2, mitochondrial (EC 3.4.21.108)	Bos taurus (Bovine)
c93796_g9	Q76LL6	FHOD3_MOUSE	FH1/FH2 domain-containing protein 3 (Formin homolog overexpressed in spleen 2) (mFHOS2)	Mus musculus (Mouse)
c93817_g5	P53413	LMX1B_CHICK	LIM/homeobox protein LMX-1.2 (Homeobox protein LMX-1) (LIM/homeobox protein 1) (LMX)	Gallus gallus (Chicken)
c93927_g1	Q6NYT3	IER5L_DANRE	Immediate early response gene 5-like protein	Danio rerio (Zebrafish) (Brachydanio rerio)

c93938_g4	Q8BRE0	RD3_MOUSE	Protein RD3	Mus musculus (Mouse)
c93997_g1	Q5ZKN1	CDK9_CHICK	Cyclin-dependent kinase 9 (EC 2.7.11.22) (EC 2.7.11.23) (Cell division protein kinase 9)	Gallus gallus (Chicken)
c94038_g6	Q7T2A3	DDA1_DANRE	DET1- and DDB1-associated protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c94040_g2	Q5U3W1	SG196_DANRE	Protein O-mannose kinase (POMK) (EC 2.7.1.183) (Protein kinase-like protein SgK196) (Sugen kinase 196)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94121_g2	A3KNL6	GGACC_DANRE	Gamma-glutamylaminecyclotransferase C (GGACT C) (EC 2.3.2.4) (AIG2-like domain-containing protein 1-C) (Gamma-glutamylamine cyclotransferase C) (Gamma-glutamylamine cyclotransferase, tandem duplicate 3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94130_g1	Q0P426	SKA2_DANRE	Spindle and kinetochore-associated protein 2 (Protein FAM33A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94140_g2	Q5RBL6	GOSR1_PONAB	Golgi SNAP receptor complex member 1 (28 kDa Golgi SNARE protein) (28 kDa cis-Golgi SNARE p28)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c94175_g1	A2ASS6	TITIN_MOUSE	Titin (EC 2.7.11.1) (Connectin)	Mus musculus (Mouse)
c94175_g2	A2ASS6	TITIN_MOUSE	Titin (EC 2.7.11.1) (Connectin)	Mus musculus (Mouse)
c94180_g2	Q6AYH2	INO80E_RAT	INO80 complex subunit E (Coiled-coil domain-containing protein 95)	Rattus norvegicus (Rat)
c94207_g7	Q202B1	AT1B4_XENLA	Protein ATP1B4 (X,K-ATPase subunit beta-m) (X/potassium-transporting ATPase subunit beta-m)	Xenopus laevis (African clawed frog)
c94301_g5	Q8JZX4	SPF45_MOUSE	Splicing factor 45 (45 kDa-splicing factor) (RNA-binding motif protein 17)	Mus musculus (Mouse)
c94308_g4	Q8BXR9	OSBL6_MOUSE	Oxysterol-binding protein-related protein 6 (ORP-6) (OSBP-related protein 6)	Mus musculus (Mouse)
c94342_g9	Q7Z5K2	WAPL_HUMAN	Wings apart-like protein homolog (Friend of EBNA2 protein)	Homo sapiens (Human)
c94378_g3	Q9Y5R2	MMP24_HUMAN	Matrix metalloproteinase-24 (MMP-24) (EC 3.4.24.-) (Membrane-type matrix metalloproteinase 5) (MT-MMP 5) (MTMMP5) (Membrane-type-5 matrix metalloproteinase) (MT5-MMP) (MT5MMP) [Cleaved into: Processed matrix metalloproteinase-24]	Homo sapiens (Human)
c94379_g2	P22122	RHO_DIPOM	Ras-like GTP-binding protein O-RHO	Diplobatis ommata (Ocellated electric ray) (Discopyge ommata)
c94386_g1	Q95LD9	AHR_DELLE	Aryl hydrocarbon receptor (Ah receptor) (AhR)	Delphinapterus leucas (Beluga whale)

c94387_g2	Q2TAF3	EMAL4_XENLA	Echinoderm microtubule-associated protein-like 4 (EMAP-4)	Xenopus laevis (African clawed frog)
c94388_g7	Q32LU1	MIRO2_DANRE	Mitochondrial Rho GTPase 2 (MIRO-2) (EC 3.6.5.-) (Ras homolog gene family member T2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94396_g2	Q925E0	SNTG2_MOUSE	Gamma-2-syntrophin (G2SYN) (Syntrophin-5) (SYN5)	Mus musculus (Mouse)
c94418_g4	P49247	RPIA_HUMAN	Ribose-5-phosphate isomerase (EC 5.3.1.6) (Phosphoriboisomerase)	Homo sapiens (Human)
c94436_g6	Q99N23	CAH15_MOUSE	Carbonic anhydrase 15 (EC 4.2.1.1) (Carbonate dehydratase XV) (Carbonic anhydrase XV) (CA-XV)	Mus musculus (Mouse)
c94466_g3	A7LCJ3	SN_PIG	Sialoadhesin (pSn) (Sialic acid-binding Ig-like lectin 1) (Siglec-1) (p210)	Sus scrofa (Pig)
c94496_g8	Q3B8N5	PROX2_HUMAN	Prospero homeobox protein 2 (Homeobox prospero-like protein PROX2) (PROX-2)	Homo sapiens (Human)
c94514_g2	O00139	KIF2A_HUMAN	Kinesin-like protein KIF2A (Kinesin-2) (hK2)	Homo sapiens (Human)
c94522_g4	Q4U116	S4A4_PIG	Electrogenic sodium bicarbonate cotransporter 1 (Sodium bicarbonate cotransporter) (Na(+)/HCO3(-) cotransporter) (Solute carrier family 4 member 4)	Sus scrofa (Pig)
c94524_g5	P83436	COG7_HUMAN	Conserved oligomeric Golgi complex subunit 7 (COG complex subunit 7) (Component of oligomeric Golgi complex 7)	Homo sapiens (Human)
c94564_g2	Q4V7E8	LRRF2_RAT	Leucine-rich repeat flightless-interacting protein 2 (LRR FLII-interacting protein 2)	Rattus norvegicus (Rat)
c94582_g2	B0FYY4	ITB1_SHEEP	Integrin beta-1 (Fibronectin receptor subunit beta) (Integrin subunit beta-1) (VLA-4 subunit beta) (CD antigen CD29)	Ovis aries (Sheep)
c94665_g3	Q99JR6	NMNA3_MOUSE	Nicotinamide mononucleotide adenylyltransferase 3 (NMN adenylyltransferase 3) (EC 2.7.7.1) (Nicotinate-nucleotide adenylyltransferase 1) (NaMN adenylyltransferase 1) (EC 2.7.7.18)	Mus musculus (Mouse)
c94720_g8	Q8JHW2	TSP3A_DANRE	Thrombospondin-3a (Thbs3a)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94733_g1	P08649	CO4_RAT	Complement C4 [Cleaved into: Complement C4 beta chain; Complement C4 alpha chain; C4a anaphylatoxin; Complement C4 gamma chain]	Rattus norvegicus (Rat)
c94766_g5	Q99J23	GHDC_MOUSE	GH3 domain-containing protein	Mus musculus (Mouse)
c94779_g5	P52731	PDE6C_CHICK	Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha' (EC 3.1.4.35) (cGMP phosphodiesterase 6C)	Gallus gallus (Chicken)
c94781_g7	Q6NVJ5	DI2BA_DANRE	Disco-interacting protein 2 homolog B-A (DIP2 homolog B-A)	Danio rerio (Zebrafish) (Brachydanio rerio)

c94826_g3	O88506	STK39_RAT	STE20/SPS1-related proline-alanine-rich protein kinase (Ste-20-related kinase) (EC 2.7.11.1) (Pancreatic serine/threonine-protein kinase) (PS/TK) (PSTK1) (Serine/threonine-protein kinase 39)	Rattus norvegicus (Rat)
c94833_g1	P08487	PLCG1_BOVIN	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 (EC 3.1.4.11) (PLC-148) (Phosphoinositide phospholipase C-gamma-1) (Phospholipase C-II) (PLC-II) (Phospholipase C-gamma-1) (PLC-gamma-1)	Bos taurus (Bovine)
c94839_g4	Q9QXG4	ACSA_MOUSE	Acetyl-coenzyme A synthetase, cytoplasmic (EC 6.2.1.1) (Acetate--CoA ligase) (Acetyl-CoA synthetase) (ACS) (AceCS) (Acyl-CoA synthetase short-chain family member 2) (Acyl-activating enzyme)	Mus musculus (Mouse)
c94843_g3	Q1LYM3	SPIR1_DANRE	Protein spire homolog 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c94846_g3	Q8R3L2	TCF25_MOUSE	Transcription factor 25 (TCF-25) (Nuclear localized protein 1)	Mus musculus (Mouse)
c94856_g1	Q6TEN6	WDR91_DANRE	WD repeat-containing protein 91	Danio rerio (Zebrafish) (Brachydanio rerio)
c94881_g5	Q6NXL6	SEN5_MOUSE	Sentrin-specific protease 5 (EC 3.4.22.68) (SUMO/Smt3-specific isopeptidase 3) (Smt3ip3) (Sentrin/SUMO-specific protease SENP5)	Mus musculus (Mouse)
c94958_g1	Q9H0M0	WWP1_HUMAN	NEDD4-like E3 ubiquitin-protein ligase WWP1 (EC 6.3.2.-) (Atrophin-1-interacting protein 5) (AIP5) (TGIF-interacting ubiquitin ligase 1) (Tiul1) (WW domain-containing protein 1)	Homo sapiens (Human)
c94965_g1	P20237	GBRA4_BOVIN	Gamma-aminobutyric acid receptor subunit alpha-4 (GABA(A) receptor subunit alpha-4)	Bos taurus (Bovine)
c94965_g2	P30191	GBRA6_RAT	Gamma-aminobutyric acid receptor subunit alpha-6 (GABA(A) receptor subunit alpha-6)	Rattus norvegicus (Rat)
c94967_g8	P0CT34	TF21_SCHPO	Transposon Tf2-1 polyprotein (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c94975_g6	P52731	PDE6C_CHICK	Cone cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha' (EC 3.1.4.35) (cGMP phosphodiesterase 6C)	Gallus gallus (Chicken)
c95004_g4	P12798	KPBB_RABIT	Phosphorylase b kinase regulatory subunit beta (Phosphorylase kinase subunit beta)	Oryctolagus cuniculus (Rabbit)
c95039_g4	Q5TZ51	MPV17_DANRE	Protein Mpv17	Danio rerio (Zebrafish) (Brachydanio rerio)
c95070_g2	P98196	AT11A_HUMAN	Probable phospholipid-transporting ATPase IH (EC 3.6.3.1) (ATPase IS) (ATPase class VI type 11A) (P4-ATPase flippase complex alpha subunit ATP11A)	Homo sapiens (Human)

c95121_g1	O14678	ABCD4_HUMAN	ATP-binding cassette sub-family D member 4 (PMP70-related protein) (P70R) (Peroxisomal membrane protein 1-like) (PXMP1-L) (Peroxisomal membrane protein 69) (PMP69)	Homo sapiens (Human)
c95122_g2	O14795	UN13B_HUMAN	Protein unc-13 homolog B (Munc13-2) (munc13)	Homo sapiens (Human)
c95129_g1	Q6DGA6	ALLC_DANRE	Allantoicase (EC 3.5.3.4) (Allantoate amidinohydrolase)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95142_g4	Q14183	DOC2A_HUMAN	Double C2-like domain-containing protein alpha (Doc2) (Doc2-alpha)	Homo sapiens (Human)
c95145_g2	P43155	CACP_HUMAN	Carnitine O-acetyltransferase (Carnitine acetylase) (EC 2.3.1.7) (Carnitine acetyltransferase) (CAT) (CrAT)	Homo sapiens (Human)
c95145_g3	P52826	CACP_COLLI	Carnitine O-acetyltransferase (Carnitine acetylase) (EC 2.3.1.7) (Carnitine acetyltransferase) (CAT) (CrAT)	Columba livia (Domestic pigeon)
c95218_g1	P51477	ARRS_XENLA	S-arrestin (Retinal S-antigen) (S-AG) (Rod photoreceptor arrestin)	Xenopus laevis (African clawed frog)
c95250_g5	Q6PCB7	S27A1_HUMAN	Long-chain fatty acid transport protein 1 (FATP-1) (Fatty acid transport protein 1) (EC 6.2.1.-) (Solute carrier family 27 member 1)	Homo sapiens (Human)
c95268_g1	O15211	RGL2_HUMAN	Ral guanine nucleotide dissociation stimulator-like 2 (RalGDS-like 2) (RalGDS-like factor) (Ras-associated protein RAB2L)	Homo sapiens (Human)
c95287_g3	Q32LP4	S4A10_BOVIN	Sodium-driven chloride bicarbonate exchanger (Solute carrier family 4 member 10)	Bos taurus (Bovine)
c95287_g5	Q32LP4	S4A10_BOVIN	Sodium-driven chloride bicarbonate exchanger (Solute carrier family 4 member 10)	Bos taurus (Bovine)
c95300_g3	Q9H013	ADA19_HUMAN	Disintegrin and metalloproteinase domain-containing protein 19 (ADAM 19) (EC 3.4.24.-) (Meltrin-beta) (Metalloprotease and disintegrin dendritic antigen marker) (MADDAM)	Homo sapiens (Human)
c95378_g3	O15344	TRI18_HUMAN	E3 ubiquitin-protein ligase Midline-1 (EC 6.3.2.-) (Midin) (Putative transcription factor XPRF) (RING finger protein 59) (RING finger protein Midline-1) (Tripartite motif-containing protein 18)	Homo sapiens (Human)
c95382_g2	Q9UMW8	UBP18_HUMAN	Ubl carboxyl-terminal hydrolase 18 (EC 3.4.19.-) (43 kDa ISG15-specific protease) (hUBP43) (ISG15-specific-processing protease) (Ubl thioesterase 18)	Homo sapiens (Human)
c95432_g11	P31647	S6A11_RAT	Sodium- and chloride-dependent GABA transporter 3 (GAT-3) (Solute carrier family 6 member 11)	Rattus norvegicus (Rat)
c95476_g7	Q6DGY7	CRGNB_DANRE	Gamma-crystallin N-B (Gamma-N-crystallin-B) (Gamma-N2-crystallin)	Danio rerio (Zebrafish) (Brachydanio rerio)

c95485_g1	A3KFX0	5NT1A_MOUSE	Cytosolic 5'-nucleotidase 1A (cN1A) (EC 3.1.3.5) (Cytosolic 5'-nucleotidase 1A) (cN-1A)	Mus musculus (Mouse)
c95511_g2	Q13451	FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5 (PPIase FKBP5) (EC 5.2.1.8) (51 kDa FK506-binding protein) (51 kDa FKBP) (FKBP-51) (54 kDa progesterone receptor-associated immunophilin) (Androgen-regulated protein 6) (FF1 antigen) (FK506-binding protein 5) (FKBP-5) (FKBP54) (p54) (HSP90-binding immunophilin) (Rotamase)	Homo sapiens (Human)
c95572_g4	Q2V2M9	FHOD3_HUMAN	FH1/FH2 domain-containing protein 3 (Formactin-2) (Formin homolog overexpressed in spleen 2) (hFHOS2)	Homo sapiens (Human)
c95599_g3	P11369	LORF2_MOUSE	LINE-1 retrotransposable element ORF2 protein (ORF2p) (Long interspersed element-1) (L1) (Retrovirus-related Pol polyprotein LINE-1) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Mus musculus (Mouse)
c95628_g3	Q8BZ20	PAR12_MOUSE	Poly [ADP-ribose] polymerase 12 (PARP-12) (EC 2.4.2.30) (ADP-ribosyltransferase diphtheria toxin-like 12) (ARTD12) (Zinc finger CCCH domain-containing protein 1)	Mus musculus (Mouse)
c95650_g4	Q99569	PKP4_HUMAN	Plakophilin-4 (p0071)	Homo sapiens (Human)
c95650_g5	Q68FH0	PKP4_MOUSE	Plakophilin-4 (Armadillo-related protein)	Mus musculus (Mouse)
c95659_g4	Q6DBU5	GMPPB_DANRE	Mannose-1-phosphate guanylyltransferase beta (EC 2.7.7.13) (GDP-mannose pyrophosphorylase B) (GTP-mannose-1-phosphate guanylyltransferase beta)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95693_g11	P70083	AT2A1_MAKNI	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (SERCA1) (SR Ca(2+)-ATPase 1) (EC 3.6.3.8) (Calcium pump 1) (Calcium-transporting ATPase sarcoplasmic reticulum type, fast twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)	Makaira nigricans (Atlantic blue marlin)
c95693_g2	Q504A5	TPMT_DANRE	Probable thiopurine S-methyltransferase (Thiopurine methyltransferase) (EC 2.1.1.67)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95694_g3	Q6PD31	TRAK1_MOUSE	Trafficking kinesin-binding protein 1	Mus musculus (Mouse)
c95731_g3	O43299	AP5Z1_HUMAN	AP-5 complex subunit zeta-1 (Adaptor-related protein complex 5 zeta subunit) (Zeta5)	Homo sapiens (Human)
c95734_g1	Q5RAN1	RBGP1_PONAB	Rab GTPase-activating protein 1 (GAP and centrosome-associated protein) (Rab6 GTPase-activating protein GAPCenA)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c95749_g2	P54289	CA2D1_HUMAN	Voltage-dependent calcium channel subunit alpha-2/delta-1 (Voltage-gated calcium channel subunit alpha-2/delta-1)	Homo sapiens (Human)
c95821_g2	Q68FK8	DHX9_XENLA	ATP-dependent RNA helicase A-like protein (EC 3.6.4.13) (DEAH box protein 9) (Nuclear DNA helicase II) (NDH II)	Xenopus laevis (African clawed frog)

c95823_g2	P62972	UBIQP_XENLA	Polyubiquitin [Cleaved into: Ubiquitin] (Fragment)	Xenopus laevis (African clawed frog)
c95827_g3	P19493	GRIA4_RAT	Glutamate receptor 4 (GluR-4) (GluR4) (AMPA-selective glutamate receptor 4) (GluR-D) (Glutamate receptor ionotropic, AMPA 4) (GluA4)	Rattus norvegicus (Rat)
c95832_g4	Q66PY1	SCUB3_MOUSE	Signal peptide, CUB and EGF-like domain-containing protein 3	Mus musculus (Mouse)
c95838_g2	A2AAE1	K1109_MOUSE	Uncharacterized protein KIAA1109 (Fragile site-associated protein homolog)	Mus musculus (Mouse)
c95879_g7	Q28ES4	S22FL_XENTR	Solute carrier family 22 member 15-like	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c95891_g3	O88286	WIZ_MOUSE	Protein Wiz (Widely-interspaced zinc finger-containing protein)	Mus musculus (Mouse)
c95937_g3	O43847	NRDC_HUMAN	Nardilysin (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C)	Homo sapiens (Human)
c95965_g4	P40692	MLH1_HUMAN	DNA mismatch repair protein Mlh1 (MutL protein homolog 1)	Homo sapiens (Human)
c95976_g6	Q5RAU7	BRE1B_PONAB	E3 ubiquitin-protein ligase BRE1B (BRE1-B) (EC 6.3.2.-) (RING finger protein 40)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c95977_g2	Q61214	DYR1A_MOUSE	Dual specificity tyrosine-phosphorylation-regulated kinase 1A (EC 2.7.12.1) (Dual specificity YAK1-related kinase) (MP86) (Protein kinase minibrain homolog) (MNBH)	Mus musculus (Mouse)
c95979_g8	A2AGL3	RYP3_MOUSE	Ryanodine receptor 3 (RYP-3) (RyR3) (Brain ryanodine receptor-calcium release channel) (Brain-type ryanodine receptor) (Type 3 ryanodine receptor)	Mus musculus (Mouse)
c96003_g1	O70318	E41L2_MOUSE	Band 4.1-like protein 2 (Generally expressed protein 4.1) (4.1G)	Mus musculus (Mouse)
c96010_g6	P25815	S100P_HUMAN	Protein S100-P (Migration-inducing gene 9 protein) (MIG9) (Protein S100-E) (S100 calcium-binding protein P)	Homo sapiens (Human)
c96029_g10	Q498T3	ING3_RAT	Inhibitor of growth protein 3	Rattus norvegicus (Rat)
c96035_g5	P25054	APC_HUMAN	Adenomatous polyposis coli protein (Protein APC) (Deleted in polyposis 2.5)	Homo sapiens (Human)
c96048_g1	Q5JV73	FRPD3_HUMAN	FERM and PDZ domain-containing protein 3	Homo sapiens (Human)
c96048_g5	Q9Z1P7	KANK3_MOUSE	KN motif and ankyrin repeat domain-containing protein 3 (Ankyrin repeat domain-containing protein 47)	Mus musculus (Mouse)
c96073_g4	Q8QFX1	RIMB2_CHICK	RIMS-binding protein 2 (RIM-BP2)	Gallus gallus (Chicken)
c96126_g4	Q96JM2	ZN462_HUMAN	Zinc finger protein 462	Homo sapiens (Human)

c96161_g6	P50143	TCPG_XENLA	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma)	Xenopus laevis (African clawed frog)
c96164_g2	Q0P5J8	STRP1_BOVIN	Striatin-interacting protein 1 (Protein FAM40A)	Bos taurus (Bovine)
c96166_g1	O60573	IF4E2_HUMAN	Eukaryotic translation initiation factor 4E type 2 (eIF-4E type 2) (eIF4E type 2) (Eukaryotic translation initiation factor 4E homologous protein) (Eukaryotic translation initiation factor 4E-like 3) (eIF4E-like protein 4E-LP) (mRNA cap-binding protein 4EHP) (mRNA cap-binding protein type 3)	Homo sapiens (Human)
c96191_g2	Q0P4D6	TEFM_DANRE	Transcription elongation factor, mitochondrial	Danio rerio (Zebrafish) (Brachydanio rerio)
c96199_g6	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c96225_g1	Q6Y1E2	PLP2_BOVIN	Proteolipid protein 2	Bos taurus (Bovine)
c96250_g1	Q96B26	EXOS8_HUMAN	Exosome complex component RRP43 (Exosome component 8) (Opa-interacting protein 2) (OIP-2) (Ribosomal RNA-processing protein 43) (p9)	Homo sapiens (Human)
c96281_g6	P51689	ARSD_HUMAN	Arylsulfatase D (ASD) (EC 3.1.6.-)	Homo sapiens (Human)
c96285_g11	Q9HCD6	TANC2_HUMAN	Protein TANC2 (Tetratricopeptide repeat, ankyrin repeat and coiled-coil domain-containing protein 2)	Homo sapiens (Human)
c96379_g1	Q6DEL7	KLH15_DANRE	Kelch-like protein 15	Danio rerio (Zebrafish) (Brachydanio rerio)
c96381_g6	Q8BXL9	IFFO1_MOUSE	Intermediate filament family orphan 1	Mus musculus (Mouse)
c96426_g1	O93297	CP2K4_ONCMY	Cytochrome P450 2K4 (EC 1.14.14.1) (CYP11K4)	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
c96445_g3	Q8IWN7	RP1L1_HUMAN	Retinitis pigmentosa 1-like 1 protein	Homo sapiens (Human)
c96448_g3	Q6PA06	ATLA2_MOUSE	Atlastin-2 (EC 3.6.5.-) (ADP-ribosylation factor-like protein 6-interacting protein 2) (ARL-6-interacting protein 2) (Aip-2)	Mus musculus (Mouse)
c96452_g1	Q8BIY1	GPTC3_MOUSE	G patch domain-containing protein 3	Mus musculus (Mouse)
c96458_g2	Q8BGW6	ST32A_MOUSE	Serine/threonine-protein kinase 32A (EC 2.7.11.1)	Mus musculus (Mouse)
c96460_g4	Q9P2N4	ATS9_HUMAN	A disintegrin and metalloproteinase with thrombospondin motifs 9 (ADAM-TS 9) (ADAM-TS9) (ADAMTS-9) (EC 3.4.24.-)	Homo sapiens (Human)
c96470_g4	P04972	CNRG_BOVIN	Retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma (GMP-PDE gamma) (EC 3.1.4.35)	Bos taurus (Bovine)

c96478_g2	A7E2Z2	EZH1_BOVIN	Histone-lysine N-methyltransferase EZH1 (EC 2.1.1.43) (Enhancer of zeste homolog 1)	Bos taurus (Bovine)
c96519_g1	A1YF22	ZHX1_GORGO	Zinc fingers and homeoboxes protein 1	Gorilla gorilla gorilla (Lowland gorilla)
c96545_g3	Q8C6K9	CO6A6_MOUSE	Collagen alpha-6(VI) chain	Mus musculus (Mouse)
c96559_g1	Q6DGP8	NRN1_DANRE	Neuritin	Danio rerio (Zebrafish) (Brachydanio rerio)
c96599_g1	O14843	FFAR3_HUMAN	Free fatty acid receptor 3 (G-protein coupled receptor 41)	Homo sapiens (Human)
c96619_g7	NA			
c96634_g4	Q6P4P2	LMD2B_DANRE	LMBR1 domain-containing protein 2-B	Danio rerio (Zebrafish) (Brachydanio rerio)
c96636_g4	Q8BGD8	COA6_MOUSE	Cytochrome c oxidase assembly factor 6 homolog	Mus musculus (Mouse)
c96643_g4	Q8TD20	GTR12_HUMAN	Solute carrier family 2, facilitated glucose transporter member 12 (Glucose transporter type 12) (GLUT-12)	Homo sapiens (Human)
c96647_g1	P37232	PPARA_XENLA	Peroxisome proliferator-activated receptor alpha (PPAR-alpha) (Nuclear receptor subfamily 1 group C member 1)	Xenopus laevis (African clawed frog)
c96648_g9	Q8QZX5	LSM10_MOUSE	U7 snRNA-associated Sm-like protein LSM10	Mus musculus (Mouse)
c96662_g1	Q6NYJ3	TE2IP_DANRE	Telomeric repeat-binding factor 2-interacting protein 1 (TERF2-interacting telomeric protein 1) (TRF2-interacting telomeric protein 1) (Repressor/activator protein 1 homolog) (RAP1 homolog)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96668_g1	P17427	AP2A2_MOUSE	AP-2 complex subunit alpha-2 (100 kDa coated vesicle protein C) (Adaptor protein complex AP-2 subunit alpha-2) (Adaptor-related protein complex 2 subunit alpha-2) (Alpha-adaptin C) (Alpha2-adaptin) (Clathrin assembly protein complex 2 alpha-C large chain) (Plasma membrane adaptor HA2/AP2 adaptin alpha C subunit)	Mus musculus (Mouse)
c96689_g5	Q96QV1	HHIP_HUMAN	Hedgehog-interacting protein (HHIP) (HIP)	Homo sapiens (Human)
c96696_g5	P27115	MGAT1_RABIT	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (EC 2.4.1.101) (N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase I) (GNT-I) (GlcNAc-T I)	Oryctolagus cuniculus (Rabbit)
c96736_g2	Q8IZN3	ZDH14_HUMAN	Probable palmitoyltransferase ZDHHC14 (EC 2.3.1.225) (NEW1 domain-containing protein) (NEW1CP) (Zinc finger DHHC domain-containing protein 14) (DHHC-14)	Homo sapiens (Human)
c96742_g3	Q5VZ66	JKIP3_HUMAN	Janus kinase and microtubule-interacting protein 3 (Neuroendocrine long coiled-coil protein 2)	Homo sapiens (Human)
c96752_g1	Q91WA3	HDA11_MOUSE	Histone deacetylase 11 (HD11) (EC 3.5.1.98)	Mus musculus (Mouse)

c96808_g2	O08585	CLCA_MOUSE	Clathrin light chain A (Lca)	Mus musculus (Mouse)
c96831_g9	Q8BHR2	ENOX1_MOUSE	Ecto-NOX disulfide-thiol exchanger 1 (Constitutive Ecto-NOX) (cNOX) [Includes: Hydroquinone [NADH] oxidase (EC 1.-.-.-); Protein disulfide-thiol oxidoreductase (EC 1.-.-.-)]	Mus musculus (Mouse)
c96841_g1	Q5DRE5	PCDA7_PANTR	Protocadherin alpha-7 (PCDH-alpha-7)	Pan troglodytes (Chimpanzee)
c96876_g2	P30931	TF_BOVIN	Tissue factor (TF) (Coagulation factor III) (CD antigen CD142)	Bos taurus (Bovine)
c97005_g3	Q6GLU8	PHAR1_XENLA	Phosphatase and actin regulator 1	Xenopus laevis (African clawed frog)
c97005_g8	Q8QGQ8	PER2_CHICK	Period circadian protein homolog 2 (cPER2) (Circadian clock protein PERIOD 2)	Gallus gallus (Chicken)
c97024_g5	P56542	DNS2A_MOUSE	Deoxyribonuclease-2-alpha (EC 3.1.22.1) (Acid DNase) (Deoxyribonuclease II alpha) (DNase II alpha) (Lysosomal DNase II)	Mus musculus (Mouse)
c97025_g2	Q8I7P9	POL5_DROME	Retrovirus-related Pol polyprotein from transposon opus [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97054_g8	Q5RHR6	BROMI_DANRE	Protein broad-minded (TBC1 domain family member 32)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97109_g4	Q8NB12	SMYD1_HUMAN	Histone-lysine N-methyltransferase SMYD1 (EC 2.1.1.43) (SET and MYND domain-containing protein 1)	Homo sapiens (Human)
c97134_g3	B5DGI7	RBM8A_SALSA	RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribonucleoprotein RBM8A)	Salmo salar (Atlantic salmon)
c97134_g6	B5DGI7	RBM8A_SALSA	RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribonucleoprotein RBM8A)	Salmo salar (Atlantic salmon)
c97152_g2	O14832	PAHX_HUMAN	Phytanoyl-CoA dioxygenase, peroxisomal (EC 1.14.11.18) (Phytanic acid oxidase) (Phytanoyl-CoA alpha-hydroxylase) (PhyH)	Homo sapiens (Human)
c97153_g4	Q9Y5F6	PCDGM_HUMAN	Protocadherin gamma-C5 (PCDH-gamma-C5)	Homo sapiens (Human)
c97160_g2	Q96DM1	PGBD4_HUMAN	PiggyBac transposable element-derived protein 4	Homo sapiens (Human)
c97161_g2	P19087	GNAT2_HUMAN	Guanine nucleotide-binding protein G(t) subunit alpha-2 (Transducin alpha-2 chain)	Homo sapiens (Human)
c97170_g1	P59222	SREC2_MOUSE	Scavenger receptor class F member 2 (Scavenger receptor expressed by endothelial cells 2 protein) (SREC-II)	Mus musculus (Mouse)
c97223_g1	A0JND4	SBNO2_BOVIN	Protein strawberry notch homolog 2	Bos taurus (Bovine)
c97246_g1	Q6DG99	KCTD6_DANRE	BTB/POZ domain-containing protein KCTD6	Danio rerio (Zebrafish) (Brachydanio rerio)

c97272_g6	Q9Y2E4	DIP2C_HUMAN	Disco-interacting protein 2 homolog C (DIP2 homolog C)	Homo sapiens (Human)
c97273_g1	Q8BHY3	ANO1_MOUSE	Anoctamin-1 (Transmembrane protein 16A)	Mus musculus (Mouse)
c97285_g2	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c97290_g3	A1L1P9	S47A1_DANRE	Multidrug and toxin extrusion protein 1 (MATE-1) (Solute carrier family 47 member 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97290_g6	A1L1P9	S47A1_DANRE	Multidrug and toxin extrusion protein 1 (MATE-1) (Solute carrier family 47 member 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97314_g1	Q5RIU9	PORED_DANRE	Polyprenol reductase (EC 1.3.1.94) (3-oxo-5-alpha-steroid 4-dehydrogenase 3) (EC 1.3.1.22) (Steroid 5-alpha-reductase 3) (S5AR 3) (SR type 3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97352_g1	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97355_g2	Q566X6	PTCD2_DANRE	Pentatricopeptide repeat-containing protein 2, mitochondrial	Danio rerio (Zebrafish) (Brachydanio rerio)
c97371_g1	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c97398_g1	O00254	PAR3_HUMAN	Proteinase-activated receptor 3 (PAR-3) (Coagulation factor II receptor-like 2) (Thrombin receptor-like 2)	Homo sapiens (Human)
c97414_g1	Q14008	CKAP5_HUMAN	Cytoskeleton-associated protein 5 (Colonic and hepatic tumor overexpressed gene protein) (Ch-TOG)	Homo sapiens (Human)
c97443_g3	Q90339	MYSS_CYPKA	Myosin heavy chain, fast skeletal muscle	Cyprinus carpio (Common carp)
c97445_g4	Q9UK61	F208A_HUMAN	Protein FAM208A (CTCL tumor antigen se89-1) (Retinoblastoma-associated protein RAP140)	Homo sapiens (Human)
c97463_g3	P49946	FRIH_SALSA	Ferritin, heavy subunit (Ferritin H) (EC 1.16.3.1)	Salmo salar (Atlantic salmon)
c97473_g1	Q5XTS1	PLPL8_RABIT	Calcium-independent phospholipase A2-gamma (EC 3.1.1.5) (Group VIB calcium-independent phospholipase A2) (Intracellular membrane-associated calcium-independent phospholipase A2 gamma) (iPLA2-gamma) (Patatin-like phospholipase domain-containing protein 8)	Oryctolagus cuniculus (Rabbit)
c97489_g1	Q9Y5I4	PCDC2_HUMAN	Protocadherin alpha-C2 (PCDH-alpha-C2)	Homo sapiens (Human)
c97493_g1	P0CT41	TF212_SCHPO	Transposon Tf2-12 polyprotein (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)

c97493_g2	Q7TN75	PEG10_MOUSE	Retrotransposon-derived protein PEG10 (Embryonal carcinoma differentiation regulated protein) (Mammalian retrotransposon-derived protein 2) (Myelin expression factor 3) (MyEF-3) (Myelin expression factor 3-like protein 1) (MEF3-like protein 1) (Paternaly expressed gene 10 protein) (Retrotransposon gag domain-containing protein 3) (Retrotransposon-derived gag-like polyprotein) (Ty3/Gypsy-like protein)	Mus musculus (Mouse)
c97495_g1	O92815	POL_WDSV	Gag-Pol polyprotein [Cleaved into: Matrix protein p10 (MA); p20; Capsid protein p25 (CA); Nucleocapsid protein p14 (NC-pol); Protease p15 (PR) (EC 3.4.23.-); Reverse transcriptase/ribonuclease H p90 (RT) (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4); Integrase p46 (IN)]	Walleye dermal sarcoma virus (WDSV)
c97504_g1	Q9NZJ4	SACS_HUMAN	Sacsin (DnaJ homolog subfamily C member 29) (DNAJC29)	Homo sapiens (Human)
c97529_g1	P33897	ABCD1_HUMAN	ATP-binding cassette sub-family D member 1 (Adrenoleukodystrophy protein) (ALDP)	Homo sapiens (Human)
c97568_g2	P10394	POL4_DROME	Retrovirus-related Pol polyprotein from transposon 412 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97570_g1	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c97572_g2	Q9NPR2	SEM4B_HUMAN	Semaphorin-4B	Homo sapiens (Human)
c97582_g1	Q03278	PO21_NASVI	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2 (Retrovirus-related Pol polyprotein from type I retrotransposable element R2) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease] (Fragment)	Nasonia vitripennis (Parasitic wasp)
c97594_g1	P35072	TCB1_CAEBR	Transposable element Tcb1 transposase (Transposable element Barney transposase)	Caenorhabditis briggsae
c97607_g2	P13264	GLSK_RAT	Glutaminase kidney isoform, mitochondrial (GLS) (EC 3.5.1.2) (K-glutaminase) (L-glutamine amidohydrolase) [Cleaved into: Glutaminase kidney isoform 68 kDa chain; Glutaminase kidney isoform 65 kDa chain]	Rattus norvegicus (Rat)
c97822_g1	P00429	CX6B1_BOVIN	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase polypeptide VII) (Cytochrome c oxidase subunit AED) (Cytochrome c oxidase subunit VIb isoform 1) (COX VIb-1)	Bos taurus (Bovine)

Table S3.2. Annotation information for differentially expressed transcripts in the Guanapo drainage dataset.

contig	SwissProt ID	SwissProt entry name	Protein name	Organism
c36462_g1	Q6PBF0	RL8_XENTR	60S ribosomal protein L8	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c38121_g1	P19632	PHOS_BOVIN	Phosducin (PHD) (33 kDa phototransducing protein) (Protein MEKA)	Bos taurus (Bovine)
c49618_g1	Q5I0R6	RL22L_XENTR	60S ribosomal protein L22-like 1	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c55639_g1	Q5CZK2	REL3_PANTR	Relaxin-3 (Prorelaxin H3) [Cleaved into: Relaxin-3 B chain; Relaxin-3 A chain]	Pan troglodytes (Chimpanzee)
c66907_g1	Q90839	DKK3_CHICK	Dickkopf-related protein 3 (Dickkopf-3) (Dkk-3) (Lens fiber protein CLFEST4)	Gallus gallus (Chicken)
c68197_g2	P61958	SUMO2_PIG	Small ubiquitin-related modifier 2 (SUMO-2) (MIF2 suppressor) (SMT3 homolog 2) (Sentrin-2) (Ubiquitin-like protein SMT3A) (Smt3A)	Sus scrofa (Pig)
c69075_g1	P48772	COX8B_MOUSE	Cytochrome c oxidase subunit 8B, mitochondrial (Cytochrome c oxidase polypeptide VIII-heart) (Cytochrome c oxidase subunit 8-1) (Cytochrome c oxidase subunit 8H)	Mus musculus (Mouse)
c70444_g2	Q96IX5	USMG5_HUMAN	Up-regulated during skeletal muscle growth protein 5 (Diabetes-associated protein in insulin-sensitive tissues) (HCV F-transactivated protein 2)	Homo sapiens (Human)
c72950_g1	O88382	MAGI2_RAT	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 (Atrophin-1-interacting protein 1) (AIP-1) (Membrane-associated guanylate kinase inverted 2) (MAGI-2) (Synaptic-scaffolding molecule) (S-SCAM)	Rattus norvegicus (Rat)
c72965_g1	Q9CPX9	APC11_MOUSE	Anaphase-promoting complex subunit 11 (APC11) (Cyclosome subunit 11)	Mus musculus (Mouse)
c75019_g1	Q7ZV82	RL27_DANRE	60S ribosomal protein L27	Danio rerio (Zebrafish) (Brachydanio rerio)
c75540_g1	Q90YP3	RS28 ICTPU	40S ribosomal protein S28	Ictalurus punctatus (Channel catfish) (Silurus punctatus)

c75863_g2	O60259	KLK8_HUMAN	Kallikrein-8 (hK8) (EC 3.4.21.118) (Neuropsin) (NP) (Ovasin) (Serine protease 19) (Serine protease TADG-14) (Tumor-associated differentially expressed gene 14 protein)	Homo sapiens (Human)
c76173_g1	Q8BH95	ECHM_MOUSE	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	Mus musculus (Mouse)
c76410_g2	P31580	HCE1_ORYLA	High choriolytic enzyme 1 (EC 3.4.24.67) (Choriolysin H 1) (HCE23) (Hatching enzyme zinc-protease subunit HCE 1)	Oryzias latipes (Medaka fish) (Japanese ricefish)
c77709_g1	O42197	B2MG ICTPU	Beta-2-microglobulin	Ictalurus punctatus (Channel catfish) (Silurus punctatus)
c78023_g1	P61805	DAD1_RAT	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 (Oligosaccharyl transferase subunit DAD1) (EC 2.4.99.18) (Defender against cell death 1) (DAD-1)	Rattus norvegicus (Rat)
c78074_g1	Q02084	A33_PLEWA	Zinc-binding protein A33	Pleurodeles waltl (Iberian ribbed newt)
c78280_g2	Q8TDV0	GP151_HUMAN	Probable G-protein coupled receptor 151 (G-protein coupled receptor PGR7) (GPCR-2037)	Homo sapiens (Human)
c78415_g1	NA			
c78631_g1	Q95204	CY561_SHEEP	Cytochrome b561 (Cytochrome b-561)	Ovis aries (Sheep)
c78982_g1	NA			
c79114_g1	Q01758	ISP2_OSMMO	Type-2 ice-structuring protein (Type II antifreeze protein) (AFP)	Osmerus mordax (Rainbow smelt) (Atherina mordax)
c79270_g3	E9PUL5	PRRT2_MOUSE	Proline-rich transmembrane protein 2 (Dispanin subfamily B member 3) (DSPB3)	Mus musculus (Mouse)
c79371_g1	A5PL98	SDHB_DANRE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) (Iron-sulfur subunit of complex II) (Ip)	Danio rerio (Zebrafish) (Brachydanio rerio)
c79371_g2	P21913	SDHB_RAT	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) (Iron-sulfur subunit of complex II) (Ip)	Rattus norvegicus (Rat)
c79448_g1	Q5XIE8	ITM2B_RAT	Integral membrane protein 2B (Immature BRI2) (imBRI2) (Transmembrane protein BRI) (Bri) [Cleaved into: BRI2, membrane form (Mature BRI2) (mBRI2); BRI2 intracellular domain (BRI2 ICD); BRI2C, soluble form; Bri23 peptide (Bri2-23) (ABri23) (C-terminal peptide) (P23 peptide)]	Rattus norvegicus (Rat)

c79813_g1	Q5XH16	NH2L1_XENLA	NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) (U4/U6.U5 tri-snRNP 15.5 kDa protein)	Xenopus laevis (African clawed frog)
c79966_g1	Q7SYU0	RS8_XENLA	40S ribosomal protein S8	Xenopus laevis (African clawed frog)
c79967_g1	P19945	RLA0_RAT	60S acidic ribosomal protein P0 (60S ribosomal protein L10E)	Rattus norvegicus (Rat)
c80095_g2	O57312	CCKN_PAROL	Cholecystokinin (CCK) [Cleaved into: Cholecystokinin-8 (CCK8)]	Paralichthys olivaceus (Bastard halibut) (Hippoglossus olivaceus)
c80151_g3	Q7T3N2	RL15_MONAL	60S ribosomal protein L15	Monopterus albus (Swamp eel)
c80448_g1	P05140	ISP2_HEMAM	Type-2 ice-structuring protein (Type II antifreeze protein) (AFP)	Hemitripterus americanus (Sea raven)
c80516_g2	Q14511	CASL_HUMAN	Enhancer of filamentation 1 (hEF1) (CRK-associated substrate-related protein) (CAS-L) (CasL) (Cas scaffolding protein family member 2) (Neural precursor cell expressed developmentally down-regulated protein 9) (NEDD-9) (Renal carcinoma antigen NY-REN-12) (p105) [Cleaved into: Enhancer of filamentation 1 p55]	Homo sapiens (Human)
c80563_g2	Q75N62	GIMA8_MOUSE	GTPase IMAP family member 8 (mGIMAP8) (Immune-associated nucleotide-binding protein 9) (IAN-9) (Immunity-associated protein 8)	Mus musculus (Mouse)
c80787_g1	Q9D3U0	PUS10_MOUSE	Putative tRNA pseudouridine synthase Pus10 (EC 5.4.99.-) (Coiled-coil domain-containing protein 139) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	Mus musculus (Mouse)
c80855_g1	P54851	EMP2_HUMAN	Epithelial membrane protein 2 (EMP-2) (Protein XMP)	Homo sapiens (Human)
c81179_g1	P08168	ARRS_BOVIN	S-arrestin (48 kDa protein) (Retinal S-antigen) (S-AG) (Rod photoreceptor arrestin) [Cleaved into: S-arrestin short form]	Bos taurus (Bovine)
c81193_g1	Q8UW64	PSB9_ORYLA	Proteasome subunit beta type-9 (EC 3.4.25.1) (Low molecular mass protein 2)	Oryzias latipes (Medaka fish) (Japanese ricefish)
c81291_g1	Q32KT5	CF136_BOVIN	Uncharacterized protein C6orf136 homolog	Bos taurus (Bovine)
c81345_g1	Q86UT8	CCD84_HUMAN	Coiled-coil domain-containing protein 84	Homo sapiens (Human)
c81373_g1	Q5DRE6	PCDA6_PANTR	Protocadherin alpha-6 (PCDH-alpha-6)	Pan troglodytes (Chimpanzee)
c81395_g1	P28648	CD63_RAT	CD63 antigen (Mast cell antigen AD1) (CD antigen CD63)	Rattus norvegicus (Rat)

c81431_g2	P17936	IBP3_HUMAN	Insulin-like growth factor-binding protein 3 (IBP-3) (IGF-binding protein 3) (IGFBP-3)	Homo sapiens (Human)
c81462_g1	Q5RII3	GINM1_DANRE	Glycoprotein integral membrane protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c81536_g1	Q8R205	ZC3HA_MOUSE	Zinc finger CCCH domain-containing protein 10	Mus musculus (Mouse)
c81542_g1	Q01841	TGM2_CHICK	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase-2) (TGase-2)	Gallus gallus (Chicken)
c81643_g1	P91791	PPIA_HEMPU	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8) (Cyclophilin) (Cyclosporin A-binding protein) (Rotamase)	Hemicentrotus pulcherrimus (Sea urchin) (Strongylocentrotus pulcherrimus)
c81643_g2	P91791	PPIA_HEMPU	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8) (Cyclophilin) (Cyclosporin A-binding protein) (Rotamase)	Hemicentrotus pulcherrimus (Sea urchin) (Strongylocentrotus pulcherrimus)
c81651_g1	Q09139	FABP7_BOVIN	Fatty acid-binding protein, brain (Brain-type fatty acid-binding protein) (B-FABP) (Fatty acid-binding protein 7)	Bos taurus (Bovine)
c81927_g1	B1AR13	CISD3_MOUSE	CDGSH iron-sulfur domain-containing protein 3, mitochondrial (Melanoma nuclear protein 13)	Mus musculus (Mouse)
c81968_g2	P97434	MPRIIP_MOUSE	Myosin phosphatase Rho-interacting protein (Rho-interacting protein 3) (RIP3) (p116Rip)	Mus musculus (Mouse)
c81985_g2	Q16644	MAPK3_HUMAN	MAP kinase-activated protein kinase 3 (MAPK-activated protein kinase 3) (MAPKAP kinase 3) (MAPKAP-K3) (MAPKAPK-3) (MK-3) (EC 2.7.11.1) (Chromosome 3p kinase) (3pK)	Homo sapiens (Human)
c82009_g2	Q63ZU3	MYADM_XENLA	Myeloid-associated differentiation marker homolog	Xenopus laevis (African clawed frog)
c82012_g2	Q7ZW16	RNF41_DANRE	E3 ubiquitin-protein ligase NRDP1 (EC 6.3.2.-) (RING finger protein 41)	Danio rerio (Zebrafish) (Brachydanio rerio)
c82053_g1	Q9YGL3	NR2E1_ORYLA	Nuclear receptor subfamily 2 group E member 1 (Nuclear receptor TLX) (Protein tailless homolog) (TII)	Oryzias latipes (Medaka fish) (Japanese ricefish)
c82103_g1	O94855	SC24D_HUMAN	Protein transport protein Sec24D (SEC24-related protein D)	Homo sapiens (Human)
c82158_g1	Q0VC68	SEPT5_BOVIN	Septin-5	Bos taurus (Bovine)
c82256_g1	Q7ZW46	S35B4_DANRE	UDP-xylose and UDP-N-acetylglucosamine transporter (Solute carrier family 35 member B4)	Danio rerio (Zebrafish) (Brachydanio rerio)
c82267_g1	Q3SX17	P2Y14_BOVIN	P2Y purinoceptor 14 (P2Y14) (UDP-glucose receptor)	Bos taurus (Bovine)

c82313_g1	Q4QQN5	SETD7_XENTR	Histone-lysine N-methyltransferase SETD7 (EC 2.1.1.43) (SET domain-containing protein 7)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c82403_g2	P45433	SSRA_ONCMY	Translocon-associated protein subunit alpha (TRAP-alpha) (Signal sequence receptor subunit alpha) (SSR-alpha)	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
c82568_g1	P10518	HEM2_MOUSE	Delta-aminolevulinic acid dehydratase (ALADH) (EC 4.2.1.24) (Porphobilinogen synthase)	Mus musculus (Mouse)
c82576_g1	P30043	BLVRB_HUMAN	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	Homo sapiens (Human)
c82691_g1	D3ZUU2	GZF1_RAT	GDNF-inducible zinc finger protein 1 (Zinc finger protein 336)	Rattus norvegicus (Rat)
c82691_g3	D3ZUU2	GZF1_RAT	GDNF-inducible zinc finger protein 1 (Zinc finger protein 336)	Rattus norvegicus (Rat)
c82755_g3	Q9P2E7	PCD10_HUMAN	Protocadherin-10	Homo sapiens (Human)
c82786_g1	Q5PRC7	SOSB2_DANRE	SOSS complex subunit B2 (Nucleic acid-binding protein 1) (Oligonucleotide/oligosaccharide-binding fold-containing protein 2A) (Sensor of single-strand DNA complex subunit B2) (Sensor of ssDNA subunit B2) (SOSS-B2) (Single-stranded DNA-binding protein 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c82863_g1	Q9D6R2	IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial (EC 1.1.1.41) (Isocitric dehydrogenase subunit alpha) (NAD(+)-specific ICDH subunit alpha)	Mus musculus (Mouse)
c82971_g2	Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 (Inactive ubiquitin-specific peptidase 39) (SAD1 homolog) (U4/U6.U5 tri-snRNP-associated 65 kDa protein) (65K)	Homo sapiens (Human)
c83025_g1	P42356	PI4KA_HUMAN	Phosphatidylinositol 4-kinase alpha (PI4-kinase alpha) (PI4K-alpha) (PtdIns-4-kinase alpha) (EC 2.7.1.67)	Homo sapiens (Human)
c83071_g1	P16330	CN37_MOUSE	2',3'-cyclic-nucleotide 3'-phosphodiesterase (CNP) (CNPase) (EC 3.1.4.37)	Mus musculus (Mouse)
c83147_g1	Q9Z2B1	I18RA_MOUSE	Interleukin-18 receptor accessory protein (IL-18 receptor accessory protein) (IL-18RAcP) (Accessory protein-like) (AcPL) (CD218 antigen-like family member B) (IL-1R accessory protein-like) (IL-1RAcPL) (Interleukin-18 receptor accessory protein-like) (Interleukin-18 receptor beta) (IL-18R-beta) (IL-18Rbeta) (CD antigen CD218b)	Mus musculus (Mouse)

c83165_g1	P91791	PPIA_HEMPU	Peptidyl-prolyl cis-trans isomerase (PPlase) (EC 5.2.1.8) (Cyclophilin) (Cyclosporin A-binding protein) (Rotamase)	Hemicentrotus pulcherrimus (Sea urchin) (Strongylocentrotus pulcherrimus) Rattus norvegicus (Rat)
c83207_g2	O35217	MINP1_RAT	Multiple inositol polyphosphate phosphatase 1 (EC 3.1.3.62) (2,3-bisphosphoglycerate 3-phosphatase) (2,3-BPG phosphatase) (EC 3.1.3.80) (Inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase) (Ins(1,3,4,5)P(4) 3-phosphatase)	
c83225_g1	Q5TJF5	DHB8_CANFA	Estradiol 17-beta-dehydrogenase 8 (EC 1.1.1.62) (17-beta-hydroxysteroid dehydrogenase 8) (17-beta-HSD 8) (3-oxoacyl-[acyl-carrier-protein] reductase) (EC 1.1.1.-) (Testosterone 17-beta-dehydrogenase 8) (EC 1.1.1.239)	Canis familiaris (Dog) (Canis lupus familiaris)
c83280_g2	Q8TD55	PKHO2_HUMAN	Pleckstrin homology domain-containing family O member 2 (PH domain-containing family O member 2) (Pleckstrin homology domain-containing family Q member 1) (PH domain-containing family Q member 1)	Homo sapiens (Human)
c83309_g1	Q6DGL2	KBR222_DANRE	NF-kappa-B inhibitor-interacting Ras-like protein 2 (I-kappa-B-interacting Ras-like protein 2) (Kappa B-Ras protein 2) (KappaB-Ras2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c83359_g4	P46777	RL5_HUMAN	60S ribosomal protein L5	Homo sapiens (Human)
c83359_g5	P15125	RL5A_XENLA	60S ribosomal protein L5-A	Xenopus laevis (African clawed frog)
c83380_g1	Q13490	BIRC2_HUMAN	Baculoviral IAP repeat-containing protein 2 (EC 6.3.2.-) (C-IAP1) (IAP homolog B) (Inhibitor of apoptosis protein 2) (IAP-2) (hIAP-2) (hIAP2) (RING finger protein 48) (TNFR2-TRAF-signaling complex protein 2)	Homo sapiens (Human)
c83386_g1	P47749	PAR1_XENLA	Proteinase-activated receptor 1 (PAR-1) (Thrombin receptor)	Xenopus laevis (African clawed frog)
c83391_g1	Q8N5H7	SH2D3_HUMAN	SH2 domain-containing protein 3C (Novel SH2-containing protein 3) (SH2 domain-containing Eph receptor-binding protein 1) (SHEP1)	Homo sapiens (Human)
c83503_g1	Q5REH1	PICK1_PONAB	PRKCA-binding protein (Protein interacting with C kinase 1) (Protein kinase C-alpha-binding protein)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c83566_g2	Q5E959	STRAP_BOVIN	Serine-threonine kinase receptor-associated protein	Bos taurus (Bovine)
c83582_g1	Q9YGL6	PALM_CHICK	Paralemmin-1 (Paralemmin)	Gallus gallus (Chicken)
c83633_g1	Q6PE25	EF1G_DANRE	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	Danio rerio (Zebrafish) (Brachydanio rerio)

c83638_g1	Q9D099	ACER3_MOUSE	Alkaline ceramidase 3 (AlkCDase 3) (Alkaline CDase 3) (EC 3.5.1.-) (Alkaline phytoceramidase) (aPHC)	Mus musculus (Mouse)
c83646_g2	Q32LP4	S4A10_BOVIN	Sodium-driven chloride bicarbonate exchanger (Solute carrier family 4 member 10)	Bos taurus (Bovine)
c83794_g1	Q8JHF0	PEN2_DANRE	Gamma-secretase subunit PEN-2 (Presenilin enhancer protein 2 homolog)	Danio rerio (Zebrafish) (Brachydanio rerio)
c83926_g1	Q641P0	ARP3B_MOUSE	Actin-related protein 3B (ARP3-beta) (Actin-like protein 3B)	Mus musculus (Mouse)
c83926_g2	O73723	ARP3_TAKRU	Actin-related protein 3 (Actin-like protein 3)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c84000_g2	P0C7U4	C3AR_DANRE	C3a anaphylatoxin chemotactic receptor (C3AR) (C3a-R)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84097_g1	P54254	ATX1_MOUSE	Ataxin-1 (Spinocerebellar ataxia type 1 protein homolog)	Mus musculus (Mouse)
c84105_g1	Q8IUZ5	AT2L2_HUMAN	5-phosphohydroxy-L-lysine phospho-lyase (EC 4.2.3.134) (Alanine--glyoxylate aminotransferase 2-like 2)	Homo sapiens (Human)
c84153_g1	Q8BKT8	HAUS7_MOUSE	HAUS augmin-like complex subunit 7 (26S proteasome-associated UCH37-interacting protein 1) (UCHL5-interacting protein)	Mus musculus (Mouse)
c84157_g3	C3KJF2	SWI5_ANOFI	DNA repair protein SWI5 homolog (Protein SAE3 homolog)	Anoplopoma fimbria (Sablefish)
c84158_g2	Q6AY85	ALG14_RAT	UDP-N-acetylglucosamine transferase subunit ALG14 homolog	Rattus norvegicus (Rat)
c84230_g1	A8C754	THADA_CHICK	Thyroid adenoma-associated protein homolog	Gallus gallus (Chicken)
c84237_g1	P62762	VISL1_RAT	Visinin-like protein 1 (VILIP) (21 kDa CABP) (Neural visinin-like protein 1) (NVL-1) (NVP-1)	Rattus norvegicus (Rat)
c84248_g1	Q5DRA4	PCDGK_PANTR	Protocadherin gamma-C3 (PCDH-gamma-C3)	Pan troglodytes (Chimpanzee)
c84256_g1	P08631	HCK_HUMAN	Tyrosine-protein kinase HCK (EC 2.7.10.2) (Hematopoietic cell kinase) (Hemopoietic cell kinase) (p59-HCK/p60-HCK) (p59Hck) (p61Hck)	Homo sapiens (Human)
c84281_g1	Q6NYR8	NPL_DANRE	N-acetylneuraminase lyase (NALase) (EC 4.1.3.3) (N-acetylneuraminase pyruvate-lyase) (N-acetylneuraminic acid aldolase) (Sialate lyase) (Sialate-pyruvate lyase) (Sialic acid aldolase) (Sialic acid lyase)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84293_g1	Q9D8U8	SNX5_MOUSE	Sorting nexin-5	Mus musculus (Mouse)
c84366_g9	Q8CHJ1	PIGU_RAT	Phosphatidylinositol glycan anchor biosynthesis class U protein (Cell division cycle protein 91-like 1) (Protein CDC91-like 1) (GPI transamidase component PIG-U) (Liver regeneration-related protein LRRGT00059)	Rattus norvegicus (Rat)

c84375_g4	O42130	TOP2A_CHICK	DNA topoisomerase 2-alpha (EC 5.99.1.3) (DNA topoisomerase II, alpha isozyme)	Gallus gallus (Chicken)
c84392_g1	P20491	FCERG_MOUSE	High affinity immunoglobulin epsilon receptor subunit gamma (Fc receptor gamma-chain) (FcRgamma) (Fc-epsilon RI-gamma) (IgE Fc receptor subunit gamma) (FceRI gamma)	Mus musculus (Mouse)
c84436_g1	Q5ZL38	SGF29_CHICK	SAGA-associated factor 29 homolog (Coiled-coil domain-containing protein 101)	Gallus gallus (Chicken)
c84532_g1	Q9Y5J1	UTP18_HUMAN	U3 small nucleolar RNA-associated protein 18 homolog (WD repeat-containing protein 50)	Homo sapiens (Human)
c84577_g1	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c84721_g2	Q6P949	PHF2_DANRE	Lysine-specific demethylase phf2 (EC 1.14.11.-) (PHD finger protein 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84746_g1	P19205	ACPH_PIG	Acylamino-acid-releasing enzyme (AARE) (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase)	Sus scrofa (Pig)
c84892_g12	Q64336	TBR1_MOUSE	T-box brain protein 1 (T-brain-1) (TBR-1) (TES-56)	Mus musculus (Mouse)
c84923_g1	O35594	IFT81_MOUSE	Intraflagellar transport protein 81 homolog (Carnitine deficiency-associated protein expressed in ventricle 1) (CDV-1)	Mus musculus (Mouse)
c84927_g1	Q5F361	TBCK_CHICK	TBC domain-containing protein kinase-like protein	Gallus gallus (Chicken)
c84934_g1	Q32PC3	RM27_BOVIN	39S ribosomal protein L27, mitochondrial (L27mt) (MRP-L27)	Bos taurus (Bovine)
c84983_g4	Q9NRJ7	PCDBG_HUMAN	Protocadherin beta-16 (PCDH-beta-16) (Protocadherin-3X)	Homo sapiens (Human)
c85036_g12	Q99784	NOE1_HUMAN	Noelin (Neuronal olfactomedin-related ER localized protein) (Olfactomedin-1)	Homo sapiens (Human)
c85041_g5	Q95JR7	GDPD4_MACFA	Glycerophosphodiester phosphodiesterase domain-containing protein 4 (EC 3.1.-.-)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c85125_g2	Q9NX07	TSAP1_HUMAN	tRNA selenocysteine 1-associated protein 1 (SECp43) (tRNA selenocysteine-associated protein 1)	Homo sapiens (Human)
c85134_g4	Q7SXC6	SLAIL_DANRE	SLAIN motif-containing protein-like	Danio rerio (Zebrafish) (Brachydanio rerio)
c85152_g2	P60604	UB2G2_HUMAN	Ubiquitin-conjugating enzyme E2 G2 (EC 6.3.2.19) (Ubiquitin carrier protein G2) (Ubiquitin-protein ligase G2)	Homo sapiens (Human)
c85210_g6	P82911	RT11_BOVIN	28S ribosomal protein S11, mitochondrial (MRP-S11) (S11mt)	Bos taurus (Bovine)

c85213_g1	Q13123	RED_HUMAN	Protein Red (Cytokine IK) (IK factor) (Protein RER)	Homo sapiens (Human)
c85232_g6	P63033	RHES_RAT	GTP-binding protein Rhes (Ras homolog enriched in striatum) (SE6C)	Rattus norvegicus (Rat)
c85252_g1	Q08CH3	MPND_DANRE	MPN domain-containing protein (EC 3.4.-.-)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85282_g2	P26325	ADH1_GADMC	Alcohol dehydrogenase 1 (EC 1.1.1.1)	Gadus morhua subsp. callarias (Baltic cod) (Gadus callarias)
c85303_g9	Q16832	DDR2_HUMAN	Discoidin domain-containing receptor 2 (Discoidin domain receptor 2) (EC 2.7.10.1) (CD167 antigen-like family member B) (Discoidin domain-containing receptor tyrosine kinase 2) (Neurotrophic tyrosine kinase, receptor-related 3) (Receptor protein-tyrosine kinase TKT) (Tyrosine-protein kinase TYRO10) (CD antigen CD167b)	Homo sapiens (Human)
c85331_g5	P32298	GRK4_HUMAN	G protein-coupled receptor kinase 4 (EC 2.7.11.16) (G protein-coupled receptor kinase GRK4) (ITI1)	Homo sapiens (Human)
c85383_g2	Q9EQ60	CAC1H_RAT	Voltage-dependent T-type calcium channel subunit alpha-1H (Voltage-gated calcium channel subunit alpha Cav3.2)	Rattus norvegicus (Rat)
c85383_g3	Q9EQ60	CAC1H_RAT	Voltage-dependent T-type calcium channel subunit alpha-1H (Voltage-gated calcium channel subunit alpha Cav3.2)	Rattus norvegicus (Rat)
c85394_g1	Q8JGR7	INT7_DANRE	Integrator complex subunit 7 (Int7)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85415_g3	Q9BY84	DUS16_HUMAN	Dual specificity protein phosphatase 16 (EC 3.1.3.16) (EC 3.1.3.48) (Mitogen-activated protein kinase phosphatase 7) (MAP kinase phosphatase 7) (MKP-7)	Homo sapiens (Human)
c85425_g4	Q9P0X4	CAC1I_HUMAN	Voltage-dependent T-type calcium channel subunit alpha-1I (Voltage-gated calcium channel subunit alpha Cav3.3) (Ca(v)3.3)	Homo sapiens (Human)
c85434_g1	O73723	ARP3_TAKRU	Actin-related protein 3 (Actin-like protein 3)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c85436_g1	P17634	FIBG_XENLA	Fibrinogen gamma chain	Xenopus laevis (African clawed frog)
c85436_g4	P86178	CSL2_ONCKE	L-rhamnose-binding lectin CSL2	Oncorhynchus keta (Chum salmon) (Salmo keta)
c85466_g4	P18724	ZG49_XENLA	Gastrula zinc finger protein XICGF49.1 (Fragment)	Xenopus laevis (African clawed frog)
c85510_g5	B6RSP1	PKHA7_DANRE	Pleckstrin homology domain-containing family A member 7 (PH domain-containing family A member 7) (Heart adapter protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)

c85572_g1	P04574	CPNS1_PIG	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	Sus scrofa (Pig)
c85575_g3	Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP)	Homo sapiens (Human)
c85671_g2	A0JN40	KIF3C_BOVIN	Kinesin-like protein KIF3C	Bos taurus (Bovine)
c85678_g1	Q921I2	KLDC4_MOUSE	Kelch domain-containing protein 4	Mus musculus (Mouse)
c85812_g7	O75170	PP6R2_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 2 (SAPS domain family member 2)	Homo sapiens (Human)
c85819_g1	P23928	CRYAB_RAT	Alpha-crystallin B chain (Alpha(B)-crystallin)	Rattus norvegicus (Rat)
c85845_g2	Q9D4V0	EKI1_MOUSE	Ethanolamine kinase 1 (EKI 1) (EC 2.7.1.82)	Mus musculus (Mouse)
c85860_g1	P15650	ACADL_RAT	Long-chain specific acyl-CoA dehydrogenase, mitochondrial (LCAD) (EC 1.3.8.8)	Rattus norvegicus (Rat)
c85883_g12	P45652	GON3_HAPBU	Progonadoliberin-3 (Progonadoliberin III) [Cleaved into: Gonadoliberin-3 (Gonadoliberin III) (Gonadotropin-releasing hormone III) (GnRH III) (Luliberin III) (Luteinizing hormone-releasing hormone III) (LH-RH III); GnRH-associated peptide 3 (GnRH-associated peptide III)]	Haplochromis burtoni (Burton's mouthbrooder)
c85917_g2	P00789	CANX_CHICK	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase) (CANP) (Calpain-1 large subunit) (Mu/M-type)	Gallus gallus (Chicken)
c85938_g1	Q5NVK4	COR1B_PONAB	Coronin-1B	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c86007_g5	Q8C190	VP9D1_MOUSE	VPS9 domain-containing protein 1 (5-day ovary-specific transcript 1 protein)	Mus musculus (Mouse)
c86067_g1	P18729	ZG57_XENLA	Gastrula zinc finger protein XICGF57.1 (Fragment)	Xenopus laevis (African clawed frog)
c86103_g2	P79457	UTY_MOUSE	Histone demethylase UTY (EC 1.14.11.-) (Male-specific histocompatibility antigen H-YDB) (Ubiquitously transcribed TPR protein on the Y chromosome) (Ubiquitously transcribed Y chromosome tetratricopeptide repeat protein)	Mus musculus (Mouse)
c86181_g5	C7A276	CIB2_SHEEP	Calcium and integrin-binding family member 2 (Fragment)	Ovis aries (Sheep)

c86195_g1	Q6P3H4	PNCB_DANRE	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 6.3.4.21) (Nicotinate phosphoribosyltransferase domain-containing protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86195_g2	Q6P3H4	PNCB_DANRE	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 6.3.4.21) (Nicotinate phosphoribosyltransferase domain-containing protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86198_g1	O73895	TPSN_CHICK	Tapasin (TPN) (TPSN) (TAP-associated protein) (TAP-binding protein)	Gallus gallus (Chicken)
c86231_g3	Q04173	GDS1_BOVIN	Rap1 GTPase-GDP dissociation stimulator 1 (Exchange factor smgGDS) (SMG GDS protein) (SMG P21 stimulatory GDP/GTP exchange protein)	Bos taurus (Bovine)
c86273_g4	Q9Y5L0	TNPO3_HUMAN	Transportin-3 (Importin-12) (Imp12) (Transportin-SR) (TRN-SR)	Homo sapiens (Human)
c86298_g3	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c86308_g1	Q91453	STXB_SYNHO	Stonustoxin subunit beta (SNTX subunit beta)	Synanceia horrida (Estuarine stonefish) (Scorpaena horrida)
c86315_g1	Q9JMD3	PCTL_MOUSE	PCTP-like protein (PCTP-L) (START domain-containing protein 10) (StARD10) (Serologically defined colon cancer antigen 28 homolog) (StAR-related lipid transfer protein 10)	Mus musculus (Mouse)
c86328_g4	Q4R550	SYCC_MACFA	Cysteine--tRNA ligase, cytoplasmic (EC 6.1.1.16) (CysteinyI-tRNA synthetase) (CysRS)	Macaca fascicularis (Crab- eating macaque) (Cynomolgus monkey)
c86328_g9	P43407	SDC2_MOUSE	Syndecan-2 (SYND2) (Fibroglycan) (Heparan sulfate proteoglycan core protein) (HSPG) (CD antigen CD362)	Mus musculus (Mouse)
c86329_g3	Q9Z254	GIPC1_RAT	PDZ domain-containing protein GIPC1 (GAIP C-terminus-interacting protein) (GLUT1 C-terminal-binding protein) (GLUT1CBP) (RGS-GAIP-interacting protein) (RGS19-interacting protein 1) (Synectin)	Rattus norvegicus (Rat)
c86367_g2	O75140	DEPD5_HUMAN	DEP domain-containing protein 5	Homo sapiens (Human)
c86368_g1	P18846	ATF1_HUMAN	Cyclic AMP-dependent transcription factor ATF-1 (cAMP-dependent transcription factor ATF-1) (Activating transcription factor 1) (Protein TREB36)	Homo sapiens (Human)
c86430_g1	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)

c86446_g2	O00273	DFFA_HUMAN	DNA fragmentation factor subunit alpha (DNA fragmentation factor 45 kDa subunit) (DFF-45) (Inhibitor of CAD) (ICAD)	Homo sapiens (Human)
c86535_g1	Q6NX31	MCM7_XENTR	DNA replication licensing factor mcm7 (EC 3.6.4.12) (CDC47 homolog) (Minichromosome maintenance protein 7)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c86537_g1	Q3MHH4	SYQ_BOVIN	Glutamine--tRNA ligase (EC 6.1.1.18) (Glutaminyl-tRNA synthetase) (GlnRS)	Bos taurus (Bovine)
c86538_g1	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c86542_g1	Q9NP74	PALMD_HUMAN	Palmdelphin (Paralemmmin-like protein)	Homo sapiens (Human)
c86543_g5	NA			
c86558_g3	A6H768	GALK1_BOVIN	Galactokinase (EC 2.7.1.6) (Galactose kinase)	Bos taurus (Bovine)
c86576_g5	Q8WTP8	AEN_HUMAN	Apoptosis-enhancing nuclease (EC 3.1.-.-) (Interferon-stimulated 20 kDa exonuclease-like 1)	Homo sapiens (Human)
c86589_g3	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c86621_g1	O75131	CPNE3_HUMAN	Copine-3 (Copine III)	Homo sapiens (Human)
c86629_g7	Q16620	NTRK2_HUMAN	BDNF/NT-3 growth factors receptor (EC 2.7.10.1) (GP145-TrkB) (Trk-B) (Neurotrophic tyrosine kinase receptor type 2) (TrkB tyrosine kinase) (Tropomyosin-related kinase B)	Homo sapiens (Human)
c86632_g1	Q15937	ZNF79_HUMAN	Zinc finger protein 79 (ZNFpT7)	Homo sapiens (Human)
c86633_g1	O93510	GELS_CHICK	Gelsolin (Actin-depolymerizing factor) (ADF) (Brevin) (Homogenin)	Gallus gallus (Chicken)
c86657_g3	Q6NU40	CTF18_XENLA	Chromosome transmission fidelity protein 18 homolog	Xenopus laevis (African clawed frog)
c86668_g1	Q80VW5	WHRN_MOUSE	Whirlin	Mus musculus (Mouse)
c86687_g5	O88751	CABP1_RAT	Calcium-binding protein 1 (CaBP1) (Caldendrin)	Rattus norvegicus (Rat)
c86694_g7	P50894	RS7_TAKRU	40S ribosomal protein S7	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c86696_g1	Q90ZY6	TLK1B_DANRE	Serine/threonine-protein kinase tousled-like 1-B (EC 2.7.11.1) (PKU-beta) (Tousled-like kinase 1-B)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86696_g16	Q9UKI8	TLK1_HUMAN	Serine/threonine-protein kinase tousled-like 1 (EC 2.7.11.1) (PKU-beta) (Tousled-like kinase 1)	Homo sapiens (Human)
c86696_g18	Q28EM7	OTX5_XENTR	Homeobox protein otx5 (Orthodenticle homolog 5)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)

c86752_g2	Q7ZWE6	DTB1A_DANRE	Dysbindin-A (Biogenesis of lysosome-related organelles complex 1 subunit 8-A) (BLOC-1 subunit 8-A) (Dystrobrevin-binding protein 1-A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c86790_g3	P11833	TBB_PARLI	Tubulin beta chain (Beta-tubulin)	Paracentrotus lividus (Common sea urchin)
c86804_g4	Q13163	MP2K5_HUMAN	Dual specificity mitogen-activated protein kinase kinase 5 (MAP kinase kinase 5) (MAPKK 5) (EC 2.7.12.2) (MAPK/ERK kinase 5) (MEK 5)	Homo sapiens (Human)
c86816_g1	Q9Z2U1	PSA5_MOUSE	Proteasome subunit alpha type-5 (EC 3.4.25.1) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (Proteasome zeta chain)	Mus musculus (Mouse)
c86818_g4	Q95209	SORL_RABIT	Sortilin-related receptor (Low-density lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding repeats) (LR11) (SorLA-1) (Sorting protein-related receptor containing LDLR class A repeats) (SorLA)	Oryctolagus cuniculus (Rabbit)
c86829_g1	Q99828	CIB1_HUMAN	Calcium and integrin-binding protein 1 (CIB) (Calcium- and integrin-binding protein) (CIBP) (Calmyrin) (DNA-PKcs-interacting protein) (Kinase-interacting protein) (KIP) (SNK-interacting protein 2-28) (SIP2-28)	Homo sapiens (Human)
c86835_g2	Q9ULV3	CIZ1_HUMAN	Cip1-interacting zinc finger protein (CDKN1A-interacting zinc finger protein 1) (Nuclear protein NP94) (Zinc finger protein 356)	Homo sapiens (Human)
c86852_g1	O95478	NSA2_HUMAN	Ribosome biogenesis protein NSA2 homolog (Hairy cell leukemia protein 1) (TGF-beta-inducible nuclear protein 1)	Homo sapiens (Human)
c86861_g2	Q14690	RRP5_HUMAN	Protein RRP5 homolog (NF-kappa-B-binding protein) (NFBP) (Programmed cell death protein 11)	Homo sapiens (Human)
c86901_g3	Q6P4W7	RIC8A_XENTR	Synembryn-A (Protein Ric-8A)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c86933_g4	Q7Z434	MAVS_HUMAN	Mitochondrial antiviral-signaling protein (MAVS) (CARD adapter inducing interferon beta) (Cardif) (Interferon beta promoter stimulator protein 1) (IPS-1) (Putative NF-kappa-B-activating protein 031N) (Virus-induced-signaling adapter) (VISA)	Homo sapiens (Human)
c86937_g1	Q8K1S5	KLF11_MOUSE	Krueppel-like factor 11 (TGFB-inducible early growth response protein 2b) (Transforming growth factor-beta-inducible early growth response protein 3) (TGFB-inducible early growth response protein 3) (TIEG-3)	Mus musculus (Mouse)

c86950_g3	P55292	DSC2_MOUSE	Desmocollin-2 (Epithelial type 2 desmocollin)	Mus musculus (Mouse)
c86973_g1	Q5RFZ7	F167A_DANRE	Protein FAM167A	Danio rerio (Zebrafish) (Brachydanio rerio)
c86980_g4	Q14684	RRP1B_HUMAN	Ribosomal RNA processing protein 1 homolog B (RRP1-like protein B)	Homo sapiens (Human)
c87042_g1	P54613	2AAB_PIG	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (PP2A subunit A isoform PR65-beta) (PP2A subunit A isoform R1-beta) (Fragment)	Sus scrofa (Pig)
c87048_g3	Q1LWL2	DS22A_DANRE	Dual specificity protein phosphatase 22-A (EC 3.1.3.16) (EC 3.1.3.48)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87051_g4	O19048	PCBP1_RABIT	Poly(rC)-binding protein 1 (Alpha-CP1) (Heterogeneous nuclear ribonucleoprotein E1) (hnRNP E1)	Oryctolagus cuniculus (Rabbit)
c87066_g1	P18715	ZG26_XENLA	Gastrula zinc finger protein XICGF26.1 (Fragment)	Xenopus laevis (African clawed frog)
c87066_g3	P18737	ZG8_XENLA	Gastrula zinc finger protein XICGF8.2DB (Fragment)	Xenopus laevis (African clawed frog)
c87109_g2	Q5ZLS3	BRE1A_CHICK	E3 ubiquitin-protein ligase BRE1A (BRE1-A) (EC 6.3.2.-) (RING finger protein 20)	Gallus gallus (Chicken)
c87133_g4	Q5RDE3	CEP70_PONAB	Centrosomal protein of 70 kDa (Cep70)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c87151_g3	O00237	RN103_HUMAN	E3 ubiquitin-protein ligase RNF103 (EC 6.3.2.-) (KF-1) (hKF-1) (RING finger protein 103) (Zinc finger protein 103 homolog) (Zfp-103)	Homo sapiens (Human)
c87167_g3	B5XFA7	LYRM2_SALSA	LYR motif-containing protein 2	Salmo salar (Atlantic salmon)
c87181_g1	Q6IN33	RCAN1_RAT	Calcipressin-1 (Down syndrome critical region protein 1 homolog) (Myocyte-enriched calcineurin-interacting protein 1) (MCIP1) (Regulator of calcineurin 1)	Rattus norvegicus (Rat)
c87206_g2	Q8BGE9	RL3R1_MOUSE	Relaxin-3 receptor 1 (RLN3 receptor 1) (G protein-coupled receptor SALPR homolog) (Relaxin family peptide receptor 3)	Mus musculus (Mouse)
c87206_g4	Q8BGE9	RL3R1_MOUSE	Relaxin-3 receptor 1 (RLN3 receptor 1) (G protein-coupled receptor SALPR homolog) (Relaxin family peptide receptor 3)	Mus musculus (Mouse)
c87211_g6	Q5F4B2	SWP70_CHICK	Switch-associated protein 70 (SWAP-70)	Gallus gallus (Chicken)
c87254_g3	O88444	ADCY1_MOUSE	Adenylate cyclase type 1 (EC 4.6.1.1) (ATP pyrophosphate-lyase 1) (Adenylate cyclase type I) (Adenylyl cyclase 1) (Ca(2+)/calmodulin-activated adenylyl cyclase)	Mus musculus (Mouse)

c87285_g5	A2VDT6	ZDH21_BOVIN	Probable palmitoyltransferase ZDHHC21 (EC 2.3.1.225) (Zinc finger DHHC domain-containing protein 21) (DHHC-21)	Bos taurus (Bovine)
c87295_g6	B3F211	IBP2B_DANRE	Insulin-like growth factor-binding protein 2-B (IGF-binding protein 2-B) (IGFBP-2-B) (IGFBP-2b)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87315_g8	P18729	ZG57_XENLA	Gastrula zinc finger protein XICGF57.1 (Fragment)	Xenopus laevis (African clawed frog)
c87316_g1	Q7ZVT5	ROGDI_DANRE	Protein rogdi homolog	Danio rerio (Zebrafish) (Brachydanio rerio)
c87319_g6	Q6NZM9	HDAC4_MOUSE	Histone deacetylase 4 (HD4) (EC 3.5.1.98)	Mus musculus (Mouse)
c87320_g2	P49760	CLK2_HUMAN	Dual specificity protein kinase CLK2 (EC 2.7.12.1) (CDC-like kinase 2)	Homo sapiens (Human)
c87320_g9	Q7SY29	SPX2_DANRE	Sugar phosphate exchanger 2 (Solute carrier family 37 member 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87331_g2	P08045	XFIN_XENLA	Zinc finger protein Xfin (Xenopus fingers protein) (Xfin)	Xenopus laevis (African clawed frog)
c87348_g4	Q00342	FLT3_MOUSE	Receptor-type tyrosine-protein kinase FLT3 (EC 2.7.10.1) (FL cytokine receptor) (Fetal liver kinase 2) (FLK-2) (Fms-like tyrosine kinase 3) (FLT-3) (Tyrosine-protein kinase receptor flk-2) (CD antigen CD135)	Mus musculus (Mouse)
c87355_g2	Q3MIF4	XYLB_RAT	Xylulose kinase (Xylulokinase) (EC 2.7.1.17)	Rattus norvegicus (Rat)
c87404_g3	A5D6R3	PLD3A_DANRE	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3-A (EC 3.1.4.11) (Phosphoinositide phospholipase C-delta-3-A) (Phospholipase C-delta-3-A) (PLC-delta-3-A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87420_g1	P97428	RGS16_MOUSE	Regulator of G-protein signaling 16 (RGS16) (A28-RGS14P) (Retinal-specific RGS) (RGS-r) (Retinally abundant regulator of G-protein signaling)	Mus musculus (Mouse)
c87428_g1	Q99KK7	DPP3_MOUSE	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl arylamidase III) (Dipeptidyl peptidase III) (DPP III) (Enkephalinase B)	Mus musculus (Mouse)
c87462_g14	O42222	GDF8_DANRE	Growth/differentiation factor 8 (GDF-8) (Myostatin) (Myostatin-1) (zfmSTN-1) (Myostatin-B)	Danio rerio (Zebrafish) (Brachydanio rerio)
c87468_g3	Q06831	SOX4_MOUSE	Transcription factor SOX-4	Mus musculus (Mouse)
c87477_g1	Q90705	EF2_CHICK	Elongation factor 2 (EF-2)	Gallus gallus (Chicken)
c87486_g4	Q5R4Q8	PRUN2_PONAB	Protein prune homolog 2 (BNIP2 motif-containing molecule at the C-terminal region 1)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)

c87486_g5	Q5BJR4	PRUN2_RAT	Protein prune homolog 2 (BNIP2 motif-containing molecule at the C-terminal region 1)	Rattus norvegicus (Rat)
c87488_g3	Q7ZW47	STAU2_DANRE	Double-stranded RNA-binding protein Staufen homolog 2	Danio rerio (Zebrafish) (Brachydanio rerio)
c87546_g3	P55262	ADK_CRIGR	Adenosine kinase (AK) (EC 2.7.1.20) (Adenosine 5'-phosphotransferase)	Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)
c87547_g3	Q99704	DOK1_HUMAN	Docking protein 1 (Downstream of tyrosine kinase 1) (p62(dok)) (pp62)	Homo sapiens (Human)
c87620_g4	P50636	RN19A_MOUSE	E3 ubiquitin-protein ligase RNF19A (EC 6.3.2.-) (Double ring-finger protein) (Dorfin) (Gametogenesis-expressed protein GEG-154) (RING finger protein 19A) (UBCM4-interacting protein 117) (UIP117) (XY body protein) (XYbp)	Mus musculus (Mouse)
c87626_g4	P47245	NRDC_RAT	Nardilysin (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C)	Rattus norvegicus (Rat)
c87685_g5	Q8C0J2	A16L1_MOUSE	Autophagy-related protein 16-1 (APG16-like 1)	Mus musculus (Mouse)
c87686_g6	Q9BUR5	APOO_HUMAN	Apolipoprotein O (Protein FAM121B)	Homo sapiens (Human)
c87736_g8	Q2NKS2	COX16_BOVIN	Cytochrome c oxidase assembly protein COX16 homolog, mitochondrial	Bos taurus (Bovine)
c87767_g4	Q5MJS3	DMP4_MOUSE	Extracellular serine/threonine protein kinase FAM20C (EC 2.7.11.1) (Dentin matrix protein 4) (DMP-4) (Golgi-enriched fraction casein kinase) (GEF-CK)	Mus musculus (Mouse)
c87778_g3	Q29960	1C16_HUMAN	HLA class I histocompatibility antigen, Cw-16 alpha chain (MHC class I antigen Cw*16)	Homo sapiens (Human)
c87787_g1	Q16891	MIC60_HUMAN	MICOS complex subunit MIC60 (Cell proliferation-inducing gene 4/52 protein) (Mitochondrial inner membrane protein) (Mitofilin) (p87/89)	Homo sapiens (Human)
c87793_g9	Q3ZBF8	CERS2_BOVIN	Ceramide synthase 2 (CerS2) (LAG1 longevity assurance homolog 2)	Bos taurus (Bovine)
c87797_g1	Q9UHC1	MLH3_HUMAN	DNA mismatch repair protein Mlh3 (MutL protein homolog 3)	Homo sapiens (Human)
c87835_g4	Q03669	AT2A2_CHICK	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (SERCA2) (SR Ca(2+)-ATPase 2) (EC 3.6.3.8) (Calcium pump 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)	Gallus gallus (Chicken)
c87846_g4	NA			

c87877_g2	P14231	AT1B2_MOUSE	Sodium/potassium-transporting ATPase subunit beta-2 (Adhesion molecule in glia) (AMOG) (Sodium/potassium-dependent ATPase subunit beta-2)	Mus musculus (Mouse)
c87885_g9	Q6PB70	ANO8_MOUSE	Anoctamin-8 (Transmembrane protein 16H)	Mus musculus (Mouse)
c87886_g1	Q3TMX7	QSOX2_MOUSE	Sulfhydryl oxidase 2 (EC 1.8.3.2) (Quiescin Q6-like protein 1)	Mus musculus (Mouse)
c87891_g2	Q91YL3	UCKL1_MOUSE	Uridine-cytidine kinase-like 1 (EC 2.7.1.-)	Mus musculus (Mouse)
c87897_g1	O08795	GLU2B_MOUSE	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	Mus musculus (Mouse)
c87899_g1	P55821	STMN2_MOUSE	Stathmin-2 (Superior cervical ganglion-10 protein) (Protein SCG10)	Mus musculus (Mouse)
c87947_g3	O76050	NEUL1_HUMAN	E3 ubiquitin-protein ligase NEURL1 (EC 6.3.2.-) (Neuralized-like protein 1A) (h-neu) (h-neuralized 1) (RING finger protein 67)	Homo sapiens (Human)
c87956_g3	Q56A04	EME2_MOUSE	Probable crossover junction endonuclease EME2 (EC 3.1.22.-)	Mus musculus (Mouse)
c87981_g2	A2A6Q5	CDC27_MOUSE	Cell division cycle protein 27 homolog	Mus musculus (Mouse)
c88025_g3	Q5F3L3	K1467_CHICK	Uncharacterized protein KIAA1467 homolog	Gallus gallus (Chicken)
c88061_g2	Q5ZIF5	TSN12_CHICK	Tetraspanin-12 (Tspan-12)	Gallus gallus (Chicken)
c88141_g7	B1B1A0	LMBL4_MOUSE	Lethal(3)malignant brain tumor-like protein 4 (L(3)mbt-like protein 4)	Mus musculus (Mouse)
c88153_g5	Q08BJ2	KHDR2_DANRE	KH domain-containing, RNA-binding, signal transduction-associated protein 2	Danio rerio (Zebrafish) (Brachydanio rerio)
c88157_g3	Q9Y2W6	TDRKH_HUMAN	Tudor and KH domain-containing protein (Tudor domain-containing protein 2)	Homo sapiens (Human)
c88187_g1	Q6YGGZ5	BMAL1_TYTAL	Aryl hydrocarbon receptor nuclear translocator-like protein 1 (Brain and muscle ARNT-like 1)	Tyto alba (Barn owl)
c88201_g4	P15651	ACADS_RAT	Short-chain specific acyl-CoA dehydrogenase, mitochondrial (SCAD) (EC 1.3.8.1) (Butyryl-CoA dehydrogenase)	Rattus norvegicus (Rat)
c88208_g3	A2CEA7	RGRF2_DANRE	Ras-specific guanine nucleotide-releasing factor 2 (Ras-GRF2) (Ras guanine nucleotide exchange factor 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88212_g13	Q98895	CNR1B_TAKRU	Cannabinoid receptor type 1B	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c88263_g5	P63043	STMN4_RAT	Stathmin-4 (Stathmin-like protein B3) (RB3)	Rattus norvegicus (Rat)
c88275_g3	Q7ZUA6	LMBR1_CHICK	Limb region 1 protein homolog	Gallus gallus (Chicken)

c88306_g2	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c88315_g9	P19103	PPR1A_RAT	Protein phosphatase 1 regulatory subunit 1A (Protein phosphatase inhibitor 1) (I-1) (IPP-1)	Rattus norvegicus (Rat)
c88324_g3	Q803C1	RNF8_DANRE	E3 ubiquitin-protein ligase RNF8 (EC 6.3.2.-) (RING finger protein 8)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88342_g3	Q58EK4	PARL_DANRE	Presenilins-associated rhomboid-like protein, mitochondrial (EC 3.4.21.105)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88344_g2	Q4R7U0	TMC7_MACFA	Transmembrane channel-like protein 7	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c88403_g4	Q9H098	F107B_HUMAN	Protein FAM107B	Homo sapiens (Human)
c88420_g1	P97799	NRSN1_MOUSE	Neurexin-1 (Neuro-p24) (Vesicular membrane protein of 24 kDa) (Vesicular membrane protein p24)	Mus musculus (Mouse)
c88435_g1	Q8JZR4	EAA5_MOUSE	Excitatory amino acid transporter 5 (Solute carrier family 1 member 7)	Mus musculus (Mouse)
c88469_g10	P97479	MYO7A_MOUSE	Unconventional myosin-VIIa	Mus musculus (Mouse)
c88469_g4	P97479	MYO7A_MOUSE	Unconventional myosin-VIIa	Mus musculus (Mouse)
c88481_g4	Q3UV71	TMTC1_MOUSE	Transmembrane and TPR repeat-containing protein 1	Mus musculus (Mouse)
c88503_g1	O60216	RAD21_HUMAN	Double-strand-break repair protein rad21 homolog (hHR23) (Nuclear matrix protein 1) (NXP-1) (SCC1 homolog)	Homo sapiens (Human)
c88526_g1	Q9P281	BAHC1_HUMAN	BAH and coiled-coil domain-containing protein 1 (Bromo adjacent homology domain-containing protein 2) (BAH domain-containing protein 2)	Homo sapiens (Human)
c88534_g3	Q8BMS1	ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial (TP-alpha) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]	Mus musculus (Mouse)
c88534_g4	Q8BMS1	ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial (TP-alpha) [Includes: Long-chain enoyl-CoA hydratase (EC 4.2.1.17); Long chain 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211)]	Mus musculus (Mouse)
c88549_g1	P11233	RALA_HUMAN	Ras-related protein Ral-A	Homo sapiens (Human)
c88552_g1	Q24JV9	L3BPA_DANRE	Galectin-3-binding protein A (Lectin galactoside-binding soluble 3-binding protein A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88575_g1	P49407	ARRB1_HUMAN	Beta-arrestin-1 (Arrestin beta-1)	Homo sapiens (Human)

c88599_g3	P05771	KPCB_HUMAN	Protein kinase C beta type (PKC-B) (PKC-beta) (EC 2.7.11.13)	Homo sapiens (Human)
c88639_g8	Q8QFX1	RIMB2_CHICK	RIMS-binding protein 2 (RIM-BP2)	Gallus gallus (Chicken)
c88642_g1	O43747	AP1G1_HUMAN	AP-1 complex subunit gamma-1 (Adaptor protein complex AP-1 subunit gamma-1) (Adaptor-related protein complex 1 subunit gamma-1) (Clathrin assembly protein complex 1 gamma-1 large chain) (Gamma1-adaptin) (Golgi adaptor HA1/AP1 adaptin subunit gamma-1)	Homo sapiens (Human)
c88658_g1	P24774	RET4A_ONCMY	Retinol-binding protein 4-A (Plasma retinol-binding protein 1) (PRBP-1) (Plasma retinol-binding protein II) (PRBP-I)	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
c88658_g3	Q5ZMP3	T184C_CHICK	Transmembrane protein 184C (Transmembrane protein 34)	Gallus gallus (Chicken)
c88669_g5	A2SWM2	SPNS2_DANRE	Protein spinster homolog 2 (Protein two of hearts)	Danio rerio (Zebrafish) (Brachydanio rerio)
c88692_g7	P28022	CRGM3_CYPCA	Gamma-crystallin M3 (Gamma-M3)	Cyprinus carpio (Common carp)
c88701_g2	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c88712_g4	Q8WUJ3	CEMIP_HUMAN	Cell migration-inducing and hyaluronan-binding protein (EC 3.2.1.35)	Homo sapiens (Human)
c88734_g3	Q86XN7	PRSR1_HUMAN	Proline and serine-rich protein 1	Homo sapiens (Human)
c88770_g8	A3KMV1	SHKB1_BOVIN	SH3KBP1-binding protein 1	Bos taurus (Bovine)
c88770_g9	O00148	DX39A_HUMAN	ATP-dependent RNA helicase DDX39A (EC 3.6.4.13) (DEAD box protein 39) (Nuclear RNA helicase URH49)	Homo sapiens (Human)
c88778_g6	P53448	ALDOC_CARAU	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain-type aldolase)	Carassius auratus (Goldfish)
c88785_g1	Q9I8C7	ACH10_CHICK	Neuronal acetylcholine receptor subunit alpha-10 (Alpha 10 nAChR) (Nicotinic acetylcholine receptor subunit alpha-10) (NACHR alpha-10)	Gallus gallus (Chicken)
c88792_g6	Q4R495	MFS11_MACFA	UNC93-like protein MFSD11 (Major facilitator superfamily domain-containing protein 11)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c88801_g1	O14490	DLGP1_HUMAN	Disks large-associated protein 1 (DAP-1) (Guanylate kinase-associated protein) (hGKAP) (PSD-95/SAP90-binding protein 1) (SAP90/PSD-95-associated protein 1) (SAPAP1)	Homo sapiens (Human)

c88809_g2	Q5R9S8	TMM43_PONAB	Transmembrane protein 43 (Protein LUMA)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c88811_g5	Q6PD24	AN13D_MOUSE	Ankyrin repeat domain-containing protein 13D	Mus musculus (Mouse)
c88821_g2	Q9R1R0	LHX6_MOUSE	LIM/homeobox protein Lhx6 (LIM homeobox protein 6) (LIM/homeobox protein Lhx6.1)	Mus musculus (Mouse)
c88827_g1	P50532	SMC4_XENLA	Structural maintenance of chromosomes protein 4 (SMC protein 4) (SMC-4) (Chromosome assembly protein XCAP-C) (Chromosome-associated protein C)	Xenopus laevis (African clawed frog)
c88906_g4	O15524	SOCS1_HUMAN	Suppressor of cytokine signaling 1 (SOCS-1) (JAK-binding protein) (JAB) (STAT-induced STAT inhibitor 1) (SSI-1) (Tec-interacting protein 3) (TIP-3)	Homo sapiens (Human)
c88908_g3	Q9NSI6	BRWD1_HUMAN	Bromodomain and WD repeat-containing protein 1 (WD repeat-containing protein 9)	Homo sapiens (Human)
c88908_g4	Q921C3	BRWD1_MOUSE	Bromodomain and WD repeat-containing protein 1 (WD repeat-containing protein 9)	Mus musculus (Mouse)
c88909_g3	Q8BFW4	TRI65_MOUSE	Tripartite motif-containing protein 65	Mus musculus (Mouse)
c88910_g3	Q92574	TSC1_HUMAN	Hamartin (Tuberous sclerosis 1 protein)	Homo sapiens (Human)
c88918_g9	Q5PQJ7	TBCEL_RAT	Tubulin-specific chaperone cofactor E-like protein (Leucine-rich repeat-containing protein 35)	Rattus norvegicus (Rat)
c88922_g1	Q28EW0	TM87A_XENTR	Transmembrane protein 87A	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c88948_g2	Q8NCC3	PAG15_HUMAN	Group XV phospholipase A2 (EC 2.3.1.-) (1-O-acylceramide synthase) (ACS) (LCAT-like lysophospholipase) (LLPL) (Lysophospholipase 3) (Lysosomal phospholipase A2) (LPLA2)	Homo sapiens (Human)
c88979_g3	P27105	STOM_HUMAN	Erythrocyte band 7 integral membrane protein (Protein 7.2b) (Stomatin)	Homo sapiens (Human)
c88991_g6	O93512	GFRA4_CHICK	GNDF family receptor alpha-4 (GNDF receptor alpha-4) (GNDFR-alpha-4) (GFR-alpha-4)	Gallus gallus (Chicken)
c89005_g3	O75131	CPNE3_HUMAN	Copine-3 (Copine III)	Homo sapiens (Human)
c89042_g3	P60983	GMFB_HUMAN	Glia maturation factor beta (GMF-beta)	Homo sapiens (Human)
c89051_g1	P51514	HTF4_RAT	Transcription factor 12 (TCF-12) (DNA-binding protein HTF4) (E-box-binding protein) (Salivary-specific cAMP response element-binding protein alpha) (SCBP-alpha) (Transcription factor HTF-4)	Rattus norvegicus (Rat)

c89059_g1	O97492	CATA_CANFA	Catalase (EC 1.11.1.6)	Canis familiaris (Dog) (Canis lupus familiaris)
c89066_g1	A9UMS3	PHB2_XENTR	Prohibitin-2	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c89101_g2	Q5NTB3	FA11_BOVIN	Coagulation factor XI (FXI) (EC 3.4.21.27) (Plasma thromboplastin antecedent) (PTA) [Cleaved into: Coagulation factor XIa heavy chain; Coagulation factor XIa light chain]	Bos taurus (Bovine)
c89109_g7	A4QNW7	PHIPL_DANRE	Phytanoyl-CoA hydroxylase-interacting protein-like	Danio rerio (Zebrafish) (Brachydanio rerio)
c89114_g1	Q810A7	DDX42_MOUSE	ATP-dependent RNA helicase DDX42 (EC 3.6.4.13) (DEAD box protein 42)	Mus musculus (Mouse)
c89120_g1	Q6DG22	ADA_DANRE	Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Danio rerio (Zebrafish) (Brachydanio rerio)
c89128_g1	P56975	NRG3_HUMAN	Pro-neuregulin-3, membrane-bound isoform (Pro-NRG3) [Cleaved into: Neuregulin-3 (NRG-3)]	Homo sapiens (Human)
c89145_g4	Q75V66	ANO5_HUMAN	Anoctamin-5 (Gnathodiaphyseal dysplasia 1 protein) (Transmembrane protein 16E)	Homo sapiens (Human)
c89160_g12	Q7SZM9	TB1RA_XENLA	F-box-like/WD repeat-containing protein TBL1XR1-A (Nuclear receptor corepressor/HDAC3 complex subunit TBLR1-A) (TBL1-related protein 1-A) (xTBLR1)	Xenopus laevis (African clawed frog)
c89160_g7	Q8BHJ5	TBL1R_MOUSE	F-box-like/WD repeat-containing protein TBL1XR1 (Nuclear receptor corepressor/HDAC3 complex subunit TBLR1) (TBL1-related protein 1) (Transducin beta-like 1X-related protein 1)	Mus musculus (Mouse)
c89173_g3	O15127	SCAM2_HUMAN	Secretory carrier-associated membrane protein 2 (Secretory carrier membrane protein 2)	Homo sapiens (Human)
c89187_g7	O42384	5H1AB_TAKRU	5-hydroxytryptamine receptor 1A-beta (5-HT-1A-beta) (5-HT1A-beta) (F1B) (Serotonin receptor 1A-beta)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c89269_g1	Q6ZVX9	PAQR9_HUMAN	Progestin and adipoQ receptor family member 9 (Progestin and adipoQ receptor family member IX)	Homo sapiens (Human)
c89285_g4	Q28DB0	TT39B_XENTR	Tetratricopeptide repeat protein 39B (TPR repeat protein 39B)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c89296_g4	Q5SPD7	P5CR3_DANRE	Pyrroline-5-carboxylate reductase 3 (P5C reductase 3) (P5CR 3) (EC 1.5.1.2) (Pyrroline-5-carboxylate reductase-like protein)	Danio rerio (Zebrafish) (Brachydanio rerio)

c89296_g8	Q9EQJ9	MAGI3_MOUSE	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 (Membrane-associated guanylate kinase inverted 3) (MAGI-3)	Mus musculus (Mouse)
c89297_g1	A2Q0U8	RSSA_SOLSE	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40)	Solea senegalensis (Senegalese sole)
c89303_g6	Q3LGD4	RFP4A_DANRE	Rab11 family-interacting protein 4A (FIP4-Rab11) (Rab11-FIP4-A) (zRab11-FIP4-A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c89320_g7	P21531	RL3_RAT	60S ribosomal protein L3 (L4)	Rattus norvegicus (Rat)
c89324_g2	A8KB87	COA3_DANRE	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial (Coiled-coil domain-containing protein 56)	Danio rerio (Zebrafish) (Brachydanio rerio)
c89350_g10	Q08E50	GBRA5_BOVIN	Gamma-aminobutyric acid receptor subunit alpha-5 (GABA(A) receptor subunit alpha-5)	Bos taurus (Bovine)
c89365_g2	Q8BMJ7	CGRF1_MOUSE	Cell growth regulator with RING finger domain protein 1 (Cell growth regulatory gene 19 protein)	Mus musculus (Mouse)
c89425_g2	Q9WTP5	CAD22_MOUSE	Cadherin-22 (Pituitary and brain cadherin) (PB-cadherin)	Mus musculus (Mouse)
c89449_g2	Q640P2	ANGL1_MOUSE	Angiopoietin-related protein 1 (Angiopoietin-like protein 1)	Mus musculus (Mouse)
c89522_g1	P10394	POL4_DROME	Retrovirus-related Pol polyprotein from transposon 412 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c89528_g9	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89539_g2	Q8N8M0	NAT16_HUMAN	Putative N-acetyltransferase 16 (EC 2.3.1.-)	Homo sapiens (Human)
c89594_g5	Q6P950	PR3CB_DANRE	Protein phosphatase 1 regulatory subunit 3C-B	Danio rerio (Zebrafish) (Brachydanio rerio)
c89603_g2	Q9Z2V5	HDAC6_MOUSE	Histone deacetylase 6 (HD6) (EC 3.5.1.98) (Histone deacetylase mHDA2)	Mus musculus (Mouse)
c89608_g3	Q9NQV8	PRDM8_HUMAN	PR domain zinc finger protein 8 (EC 2.1.1.-) (PR domain-containing protein 8)	Homo sapiens (Human)
c89661_g2	P10820	PERF_MOUSE	Perforin-1 (P1) (Cytolysin) (Lymphocyte pore-forming protein)	Mus musculus (Mouse)
c89662_g3	P05619	ILEU_HORSE	Leukocyte elastase inhibitor (LEI) (Serpine B1)	Equus caballus (Horse)
c89671_g2	B5DE73	ASPH2_XENTR	Aspartate beta-hydroxylase domain-containing protein 2 (EC 1.14.11.-)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c89695_g2	D3Z3C6	ZFAN4_MOUSE	AN1-type zinc finger protein 4 (AN1-type zinc finger and ubiquitin domain-containing protein-like 1)	Mus musculus (Mouse)

c89704_g1	O75140	DEPD5_HUMAN	DEP domain-containing protein 5	Homo sapiens (Human)
c89707_g3	P51448	RORA_MOUSE	Nuclear receptor ROR-alpha (Nuclear receptor RZR-alpha) (Nuclear receptor subfamily 1 group F member 1) (RAR-related orphan receptor A) (Retinoid-related orphan receptor-alpha)	Mus musculus (Mouse)
c89727_g1	Q68FU4	SUCHY_RAT	Succinate--hydroxymethylglutarate CoA-transferase (EC 2.8.3.13) (SuccinylCoA:glutarate-CoA transferase)	Rattus norvegicus (Rat)
c89735_g3	Q9NQZ8	ZNF71_HUMAN	Endothelial zinc finger protein induced by tumor necrosis factor alpha (Zinc finger protein 71)	Homo sapiens (Human)
c89743_g2	P20701	ITAL_HUMAN	Integrin alpha-L (CD11 antigen-like family member A) (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (LFA-1A) (Leukocyte function-associated molecule 1 alpha chain) (CD antigen CD11a)	Homo sapiens (Human)
c89805_g1	P12928	KPYR_RAT	Pyruvate kinase PKLR (EC 2.7.1.40) (L-PK) (Pyruvate kinase isozymes L/R)	Rattus norvegicus (Rat)
c89807_g5	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89807_g6	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89810_g1	Q7SXW3	LRC40_DANRE	Leucine-rich repeat-containing protein 40	Danio rerio (Zebrafish) (Brachydanio rerio)
c89818_g5	P55058	PLTP_HUMAN	Phospholipid transfer protein (Lipid transfer protein II)	Homo sapiens (Human)
c89852_g2	P43006	EAA2_MOUSE	Excitatory amino acid transporter 2 (GLT-1) (Sodium-dependent glutamate/aspartate transporter 2) (Solute carrier family 1 member 2)	Mus musculus (Mouse)
c89881_g3	Q8WY21	SORC1_HUMAN	VPS10 domain-containing receptor SorCS1 (hSorCS)	Homo sapiens (Human)
c89884_g4	A2AV25	FBCD1_MOUSE	Fibrinogen C domain-containing protein 1	Mus musculus (Mouse)
c89891_g1	Q61627	GRID1_MOUSE	Glutamate receptor ionotropic, delta-1 (GluD1) (GluR delta-1 subunit)	Mus musculus (Mouse)
c89919_g4	Q8K363	DDX18_MOUSE	ATP-dependent RNA helicase DDX18 (EC 3.6.4.13) (DEAD box protein 18)	Mus musculus (Mouse)
c89924_g1	Q502L7	KAD8_DANRE	Adenylate kinase 8 (AK 8) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 8)	Danio rerio (Zebrafish) (Brachydanio rerio)
c89948_g7	Q2KJH5	K1430_BOVIN	UPF0501 protein KIAA1430 homolog	Bos taurus (Bovine)
c89958_g2	Q9W6I0	UQCC1_XENLA	Ubiquinol-cytochrome-c reductase complex assembly factor 1 (Basic FGF-repressed Zic-binding protein homolog) (Ubiquinol-cytochrome c reductase complex chaperone CBP3 homolog) (Zic3-binding protein)	Xenopus laevis (African clawed frog)

c89976_g4	Q3UMT1	PP12C_MOUSE	Protein phosphatase 1 regulatory subunit 12C (Protein phosphatase 1 myosin-binding subunit of 85 kDa) (Protein phosphatase 1 myosin-binding subunit p85)	Mus musculus (Mouse)
c89982_g1	Q6NYN7	S22A6_DANRE	Solute carrier family 22 member 6 (Organic anion transporter 1) (Renal organic anion transporter 1) (ROAT1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90006_g5	P31213	S5A2_HUMAN	3-oxo-5-alpha-steroid 4-dehydrogenase 2 (EC 1.3.1.22) (5 alpha-SR2) (SR type 2) (Steroid 5-alpha-reductase 2) (S5AR 2) (Type II 5-alpha reductase)	Homo sapiens (Human)
c90008_g2	Q4V328	GRAP1_HUMAN	GRIP1-associated protein 1 (GRASP-1)	Homo sapiens (Human)
c90008_g4	Q4V328	GRAP1_HUMAN	GRIP1-associated protein 1 (GRASP-1)	Homo sapiens (Human)
c90023_g1	Q5RD69	TICN3_PONAB	Testican-3 (SPARC/osteonectin, CWCV, and Kazal-like domains proteoglycan 3)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c90031_g5	P35001	NEUM_CHICK	Neuromodulin (Axonal membrane protein GAP-43) (Growth-associated protein 43)	Gallus gallus (Chicken)
c90037_g8	Q6V4S5	SDK2_MOUSE	Protein sidekick-2	Mus musculus (Mouse)
c90047_g3	P41586	PACR_HUMAN	Pituitary adenylate cyclase-activating polypeptide type I receptor (PACAP type I receptor) (PACAP-R-1) (PACAP-R1)	Homo sapiens (Human)
c90047_g7	P28840	NEC1_RAT	Neuroendocrine convertase 1 (NEC 1) (EC 3.4.21.93) (Prohormone convertase 1) (Proprotein convertase 1) (PC1)	Rattus norvegicus (Rat)
c90062_g5	Q3B7Z2	OSBP1_MOUSE	Oxysterol-binding protein 1	Mus musculus (Mouse)
c90066_g5	Q7SXV2	AEBP2_DANRE	Zinc finger protein AEBP2 (Adipocyte enhancer-binding protein 2 homolog) (AE-binding protein 2 homolog)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90089_g4	Q8N960	CE120_HUMAN	Centrosomal protein of 120 kDa (Cep120) (Coiled-coil domain-containing protein 100)	Homo sapiens (Human)
c90111_g1	B5XCB8	THAP1_SALSA	THAP domain-containing protein 1	Salmo salar (Atlantic salmon)
c90146_g2	Q5ZJ58	PI51B_CHICK	Phosphatidylinositol 4-phosphate 5-kinase type-1 beta (PIP5K1-beta) (PtdIns(4)P-5-kinase 1 beta) (EC 2.7.1.68) (Phosphatidylinositol 4-phosphate 5-kinase type I beta) (PIP5KIbeta) (Type I phosphatidylinositol 4-phosphate 5-kinase beta)	Gallus gallus (Chicken)
c90166_g3	Q28CA0	PITC1_XENTR	Cytoplasmic phosphatidylinositol transfer protein 1 (Retinal degeneration B homolog beta) (RdgBbeta)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)

c90177_g2	Q0IIY7	AJAP1_XENTR	Adherens junction-associated protein 1	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c90194_g2	Q7ZV46	METRL_DANRE	Meteorin-like protein	Danio rerio (Zebrafish) (Brachydanio rerio)
c90196_g3	P23790	SRF_XENLA	Serum response factor (SRF)	Xenopus laevis (African clawed frog)
c90216_g8	Q96N03	VTM2L_HUMAN	V-set and transmembrane domain-containing protein 2-like protein	Homo sapiens (Human)
c90217_g3	Q8WW59	SPRY4_HUMAN	SPRY domain-containing protein 4	Homo sapiens (Human)
c90238_g1	Q9JM96	BORG4_MOUSE	Cdc42 effector protein 4 (Binder of Rho GTPases 4)	Mus musculus (Mouse)
c90256_g5	Q9H7B4	SMYD3_HUMAN	Histone-lysine N-methyltransferase SMYD3 (EC 2.1.1.43) (SET and MYND domain-containing protein 3) (Zinc finger MYND domain-containing protein 1)	Homo sapiens (Human)
c90258_g1	Q503I2	TRI13_DANRE	Tripartite motif-containing 13	Danio rerio (Zebrafish) (Brachydanio rerio)
c90308_g4	Q08331	CALB2_MOUSE	Calretinin (CR)	Mus musculus (Mouse)
c90312_g2	Q1RMJ7	TSAP1_BOVIN	tRNA selenocysteine 1-associated protein 1 (tRNA selenocysteine-associated protein 1)	Bos taurus (Bovine)
c90338_g10	P02553	TBA_LYTPI	Tubulin alpha chain (Fragment)	Lytechinus pictus (Painted sea urchin)
c90338_g4	P30436	TBA_ONCKE	Tubulin alpha chain	Oncorhynchus keta (Chum salmon) (Salmo keta)
c90338_g8	P02552	TBA1_CHICK	Tubulin alpha-1 chain (Fragment)	Gallus gallus (Chicken)
c90348_g3	P61810	CD5R1_RAT	Cyclin-dependent kinase 5 activator 1 (CDK5 activator 1) (Cyclin-dependent kinase 5 regulatory subunit 1) (TPKII regulatory subunit) [Cleaved into: Cyclin-dependent kinase 5 activator 1, p35 (p35); Cyclin-dependent kinase 5 activator 1, p25 (p25) (Tau protein kinase II 23 kDa subunit) (p23)]	Rattus norvegicus (Rat)
c90348_g5	Q28199	CD5R1_BOVIN	Cyclin-dependent kinase 5 activator 1 (CDK5 activator 1) (Cyclin-dependent kinase 5 regulatory subunit 1) (TPKII regulatory subunit) [Cleaved into: Cyclin-dependent kinase 5 activator 1, p35 (p35); Cyclin-dependent kinase 5 activator 1, p25 (p25) (Tau protein kinase II 23 kDa subunit) (p23)]	Bos taurus (Bovine)
c90353_g8	P29992	GNA11_HUMAN	Guanine nucleotide-binding protein subunit alpha-11 (G alpha-11) (G-protein subunit alpha-11) (Guanine nucleotide-binding protein G(y) subunit alpha)	Homo sapiens (Human)

c90353_g9	Q28294	GNAQ_CANFA	Guanine nucleotide-binding protein G(q) subunit alpha (Guanine nucleotide-binding protein alpha-q)	Canis familiaris (Dog) (Canis lupus familiaris)
c90419_g1	Q8BLY1	SMOC1_MOUSE	SPARC-related modular calcium-binding protein 1 (SPARC-related gene protein) (Secreted modular calcium-binding protein 1) (SMOC-1)	Mus musculus (Mouse)
c90430_g1	A0AUS0	WSDU1_DANRE	WD repeat, SAM and U-box domain-containing protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c90451_g5	Q9I9R3	S40A1_DANRE	Solute carrier family 40 member 1 (Ferroportin-1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90461_g6	Q6P7E4	PDLI7_DANRE	PDZ and LIM domain protein 7	Danio rerio (Zebrafish) (Brachydanio rerio)
c90467_g3	O88444	ADCY1_MOUSE	Adenylate cyclase type 1 (EC 4.6.1.1) (ATP pyrophosphate-lyase 1) (Adenylate cyclase type I) (Adenylyl cyclase 1) (Ca(2+)/calmodulin-activated adenylyl cyclase)	Mus musculus (Mouse)
c90471_g2	Q9P0K1	ADA22_HUMAN	Disintegrin and metalloproteinase domain-containing protein 22 (ADAM 22) (Metalloproteinase-disintegrin ADAM22-3) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 2)	Homo sapiens (Human)
c90485_g1	Q9Y2M2	SSUH2_HUMAN	Protein SSUH2 homolog (Protein ssu-2 homolog)	Homo sapiens (Human)
c90517_g1	O60637	TSN3_HUMAN	Tetraspanin-3 (Tspan-3) (Tetraspanin TM4-A) (Transmembrane 4 superfamily member 8)	Homo sapiens (Human)
c90525_g3	Q3UNH4	GRIN1_MOUSE	G protein-regulated inducer of neurite outgrowth 1 (GRIN1)	Mus musculus (Mouse)
c90536_g6	Q14590	ZN235_HUMAN	Zinc finger protein 235 (Zinc finger protein 270) (Zinc finger protein 93 homolog) (Zfp-93) (Zinc finger protein HZF6)	Homo sapiens (Human)
c90553_g5	O08791	COE3_MOUSE	Transcription factor COE3 (Early B-cell factor 3) (EBF-3) (Olf-1/EBF-like 2) (O/E-2) (OE-2)	Mus musculus (Mouse)
c90590_g2	A1L253	F149B_DANRE	Protein FAM149B1	Danio rerio (Zebrafish) (Brachydanio rerio)
c90592_g2	B5DF11	ZFAN5_RAT	AN1-type zinc finger protein 5 (Zinc finger protein 216)	Rattus norvegicus (Rat)
c90593_g6	Q8BH60	GOPC_MOUSE	Golgi-associated PDZ and coiled-coil motif-containing protein (PDZ protein interacting specifically with TC10) (PIST)	Mus musculus (Mouse)
c90596_g2	Q6DBY0	NUP85_DANRE	Nuclear pore complex protein Nup85 (85 kDa nucleoporin) (Nucleoporin Nup85) (Pericentrin-1)	Danio rerio (Zebrafish) (Brachydanio rerio)

c90613_g2	B5X8M4	BRCC3_SALSA	Lys-63-specific deubiquitinase BRCC36 (EC 3.4.19.-) (BRCA1-A complex subunit BRCC36) (BRCA1/BRCA2-containing complex subunit 3) (BRCA1/BRCA2-containing complex subunit 36) (BRISC complex subunit BRCC36)	Salmo salar (Atlantic salmon)
c90633_g4	Q63259	PTPRN_RAT	Receptor-type tyrosine-protein phosphatase-like N (R-PTP-N) (105 kDa islet cell antigen) (BEM-3) (Brain-enriched membrane-associated protein tyrosine phosphatase) (ICA105) (PTP IA-2) (PTPLP)	Rattus norvegicus (Rat)
c90633_g5	P56722	PTPRN_BOVIN	Receptor-type tyrosine-protein phosphatase-like N (R-PTP-N) (Islet cell autoantigen 512) (ICA512)	Bos taurus (Bovine)
c90655_g3	Q5R903	SNX14_PONAB	Sorting nexin-14	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c90671_g1	P04574	CPNS1_PIG	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	Sus scrofa (Pig)
c90675_g3	P17810	PRPH2_BOVIN	Peripherin-2 (Retinal degeneration slow protein)	Bos taurus (Bovine)
c90675_g9	O42281	PRPH2_CHICK	Peripherin-2 (CRDS1) (Photoreceptor outer segment membrane glycoprotein 1) (Retinal degeneration slow protein)	Gallus gallus (Chicken)
c90688_g7	Q2HJ53	CISH_BOVIN	Cytokine-inducible SH2-containing protein (CIS)	Bos taurus (Bovine)
c90691_g3	Q4V328	GRAP1_HUMAN	GRIP1-associated protein 1 (GRASP-1)	Homo sapiens (Human)
c90693_g2	P0CAX4	AUGNB_DANRE	Augurin-B	Danio rerio (Zebrafish)
c90694_g3	Q6GMF8	RHDF1_DANRE	Inactive rhomboid protein 1 (iRhom1) (Rhomboid family member 1)	(Brachydanio rerio) Danio rerio (Zebrafish)
c90743_g4	Q00939	FOXG1_RAT	Forkhead box protein G1 (FoxG1) (Brain factor 1) (BF-1) (BF1) (Forkhead-related protein FKHL1)	(Brachydanio rerio) Rattus norvegicus (Rat)
c90759_g5	Q14590	ZN235_HUMAN	Zinc finger protein 235 (Zinc finger protein 270) (Zinc finger protein 93 homolog) (Zfp-93) (Zinc finger protein HZF6)	Homo sapiens (Human)
c90783_g7	O02813	NPY1R_CANFA	Neuropeptide Y receptor type 1 (NPY1-R)	Canis familiaris (Dog) (Canis lupus familiaris)
c90826_g1	Q96RE7	NACC1_HUMAN	Nucleus accumbens-associated protein 1 (NAC-1) (BTB/POZ domain-containing protein 14B)	Homo sapiens (Human)
c90826_g7	Q96RE7	NACC1_HUMAN	Nucleus accumbens-associated protein 1 (NAC-1) (BTB/POZ domain-containing protein 14B)	Homo sapiens (Human)

c90854_g10	Q08209	PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform (EC 3.1.3.16) (CAM-PRP catalytic subunit) (Calmodulin-dependent calcineurin A subunit alpha isoform)	Homo sapiens (Human)
c90865_g1	Q5RAB8	FARP1_PONAB	FERM, RhoGEF and pleckstrin domain-containing protein 1	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c90870_g11	Q9DE25	FXC1A_DANRE	Forkhead box C1-A	Danio rerio (Zebrafish) (Brachydanio rerio)
c90889_g2	C8YR32	LOXH1_MOUSE	Lipoxygenase homology domain-containing protein 1	Mus musculus (Mouse)
c90893_g1	Q9JLR9	HIG1A_MOUSE	HIG1 domain family member 1A, mitochondrial (Hypoxia-inducible gene 1 protein)	Mus musculus (Mouse)
c90931_g2	Q7L523	RRAGA_HUMAN	Ras-related GTP-binding protein A (Rag A) (RagA) (Adenovirus E3 14.7 kDa-interacting protein 1) (FIP-1)	Homo sapiens (Human)
c90936_g1	A2RV29	ZN346_DANRE	Zinc finger protein 346 (Just another zinc finger protein) (Protein jaz)	Danio rerio (Zebrafish) (Brachydanio rerio)
c90943_g4	A1L3I3	F1712_XENLA	Protein FAM171A2	Xenopus laevis (African clawed frog)
c90950_g5	Q8N0W4	NLGNX_HUMAN	Neuroigin-4, X-linked (Neuroigin X) (HNLX)	Homo sapiens (Human)
c90988_g1	Q5XJR6	ORML3_DANRE	ORM1-like protein 3	Danio rerio (Zebrafish) (Brachydanio rerio)
c90993_g5	Q0VCK9	VMP1_BOVIN	Vacuole membrane protein 1 (Transmembrane protein 49)	Bos taurus (Bovine)
c91052_g8	P0C1G7	WBP1L_RAT	WW domain binding protein 1-like (Outcome predictor in acute leukemia 1 homolog)	Rattus norvegicus (Rat)
c91053_g2	Q14094	CCNI_HUMAN	Cyclin-I	Homo sapiens (Human)
c91074_g4	Q66H20	PTBP2_RAT	Polypyrimidine tract-binding protein 2 (Neural polypyrimidine tract-binding protein) (PTB-like protein)	Rattus norvegicus (Rat)
c91102_g1	Q14590	ZN235_HUMAN	Zinc finger protein 235 (Zinc finger protein 270) (Zinc finger protein 93 homolog) (Zfp-93) (Zinc finger protein HZF6)	Homo sapiens (Human)
c91122_g4	Q99NI4	IPMK_RAT	Inositol polyphosphate multikinase (EC 2.7.1.151) (Inositol 1,3,4,6-tetrakisphosphate 5-kinase)	Rattus norvegicus (Rat)
c91145_g3	Q3MHN0	PSB6_BOVIN	Proteasome subunit beta type-6 (EC 3.4.25.1)	Bos taurus (Bovine)
c91146_g5	Q70EK8	UBP53_HUMAN	Inactive ubiquitin carboxyl-terminal hydrolase 53 (Inactive ubiquitin-specific peptidase 53)	Homo sapiens (Human)
c91150_g3	Q58T08	ISM2_DANRE	Isthmin-2	Danio rerio (Zebrafish) (Brachydanio rerio)

c91172_g7	Q9QZM6	NCKX1_RAT	Sodium/potassium/calcium exchanger 1 (Na(+)/K(+)/Ca(2+)-exchange protein 1) (Retinal rod Na-Ca+K exchanger) (Solute carrier family 24 member 1)	Rattus norvegicus (Rat)
c91188_g7	Q9Y5K8	VATD_HUMAN	V-type proton ATPase subunit D (V-ATPase subunit D) (V-ATPase 28 kDa accessory protein) (Vacuolar proton pump subunit D)	Homo sapiens (Human)
c91199_g3	O43313	ATMIN_HUMAN	ATM interactor (ATM/ATR-substrate CHK2-interacting zinc finger protein) (ASCIZ) (Zinc finger protein 822)	Homo sapiens (Human)
c91199_g4	O43313	ATMIN_HUMAN	ATM interactor (ATM/ATR-substrate CHK2-interacting zinc finger protein) (ASCIZ) (Zinc finger protein 822)	Homo sapiens (Human)
c91235_g2	Q5E9D3	MIC19_BOVIN	MICOS complex subunit MIC19 (Coiled-coil-helix-coiled-coil-helix domain-containing protein 3)	Bos taurus (Bovine)
c91288_g5	Q92753	RORB_HUMAN	Nuclear receptor ROR-beta (Nuclear receptor RZR-beta) (Nuclear receptor subfamily 1 group F member 2) (Retinoid-related orphan receptor-beta)	Homo sapiens (Human)
c91299_g5	Q32PG1	AP3B1_BOVIN	AP-3 complex subunit beta-1 (Adaptor protein complex AP-3 subunit beta-1) (Adaptor-related protein complex 3 subunit beta-1) (Beta-3A-adaptin) (Clathrin assembly protein complex 3 beta-1 large chain)	Bos taurus (Bovine)
c91302_g1	Q8K0C1	IPO13_MOUSE	Importin-13 (Imp13)	Mus musculus (Mouse)
c91324_g1	Q9Y2D8	ADIP_HUMAN	Afadin- and alpha-actinin-binding protein (ADIP) (Afadin DIL domain-interacting protein) (SSX2-interacting protein)	Homo sapiens (Human)
c91384_g2	Q803C9	PTSS1_DANRE	Phosphatidylserine synthase 1 (PSS-1) (PtdSer synthase 1) (EC 2.7.8.29) (Serine-exchange enzyme I)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91389_g4	P27986	P85A_HUMAN	Phosphatidylinositol 3-kinase regulatory subunit alpha (PI3-kinase regulatory subunit alpha) (PI3K regulatory subunit alpha) (PtdIns-3-kinase regulatory subunit alpha) (Phosphatidylinositol 3-kinase 85 kDa regulatory subunit alpha) (PI3-kinase subunit p85-alpha) (PtdIns-3-kinase regulatory subunit p85-alpha)	Homo sapiens (Human)
c91398_g8	Q28294	GNAQ_CANFA	Guanine nucleotide-binding protein G(q) subunit alpha (Guanine nucleotide-binding protein alpha-q)	Canis familiaris (Dog) (Canis lupus familiaris)
c91402_g3	C6K2K4	NETO2_RAT	Neuropilin and tolloid-like protein 2 (Brain-specific transmembrane protein containing 2 CUB and 1 LDL-receptor class A domains protein 2)	Rattus norvegicus (Rat)
c91402_g4	C6K2K4	NETO2_RAT	Neuropilin and tolloid-like protein 2 (Brain-specific transmembrane protein containing 2 CUB and 1 LDL-receptor class A domains protein 2)	Rattus norvegicus (Rat)

c91406_g2	P07197	NFM_HUMAN	Neurofilament medium polypeptide (NF-M) (160 kDa neurofilament protein) (Neurofilament 3) (Neurofilament triplet M protein)	Homo sapiens (Human)
c91434_g6	Q9NYB5	SO1C1_HUMAN	Solute carrier organic anion transporter family member 1C1 (Organic anion transporter F) (OATP-F) (Organic anion transporter polypeptide-related protein 5) (OAT-RP-5) (OATPRP5) (Organic anion-transporting polypeptide 14) (OATP-14) (Solute carrier family 21 member 14) (Thyroxine transporter)	Homo sapiens (Human)
c91453_g4	Q99LM2	CK5P3_MOUSE	CDK5 regulatory subunit-associated protein 3	Mus musculus (Mouse)
c91459_g1	Q70EK8	UBP53_HUMAN	Inactive ubiquitin carboxyl-terminal hydrolase 53 (Inactive ubiquitin-specific peptidase 53)	Homo sapiens (Human)
c91470_g2	Q9UNX4	WDR3_HUMAN	WD repeat-containing protein 3	Homo sapiens (Human)
c91472_g6	Q01584	LIPO_BUFMA	Lipocalin	Bufo marinus (Giant toad) (Cane toad)
c91475_g3	Q1RMB5	K1644_DANRE	Uncharacterized protein KIAA1644 homolog	Danio rerio (Zebrafish) (Brachydanio rerio)
c91504_g1	O88871	GABR2_RAT	Gamma-aminobutyric acid type B receptor subunit 2 (GABA-B receptor 2) (GABA-B-R2) (GABA-BR2) (GABABR2) (Gb2) (G-protein coupled receptor 51)	Rattus norvegicus (Rat)
c91504_g2	O75899	GABR2_HUMAN	Gamma-aminobutyric acid type B receptor subunit 2 (GABA-B receptor 2) (GABA-B-R2) (GABA-BR2) (GABABR2) (Gb2) (G-protein coupled receptor 51) (HG20)	Homo sapiens (Human)
c91514_g4	Q8BI55	DYRK4_MOUSE	Dual specificity tyrosine-phosphorylation-regulated kinase 4 (EC 2.7.12.1)	Mus musculus (Mouse)
c91520_g6	Q29058	LEG4_PIG	Galectin-4 (Gal-4) (L-36 lactose-binding protein) (L36LBP) (Lactose-binding lectin 4)	Sus scrofa (Pig)
c91547_g3	Q6DGX3	ANR54_DANRE	Ankyrin repeat domain-containing protein 54	Danio rerio (Zebrafish) (Brachydanio rerio)
c91573_g1	Q9P2R6	RERE_HUMAN	Arginine-glutamic acid dipeptide repeats protein (Atrophin-1-like protein) (Atrophin-1-related protein)	Homo sapiens (Human)
c91574_g6	A0JPF9	ISPD_DANRE	Isoprenoid synthase domain-containing protein (EC 2.7.7.-) (2-C-methyl-D-erythritol 4-phosphate cytidyltransferase-like protein)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91575_g2	O75131	CPNE3_HUMAN	Copine-3 (Copine III)	Homo sapiens (Human)
c91583_g4	P16970	ABCD3_RAT	ATP-binding cassette sub-family D member 3 (70 kDa peroxisomal membrane protein) (PMP70)	Rattus norvegicus (Rat)

c91601_g1	Q92055	LDHA_FUNHE	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (LDH-M)	Fundulus heteroclitus (Killifish) (Mummichog)
c91603_g2	A3KP77	OXND1_DANRE	Oxidoreductase NAD-binding domain-containing protein 1 (EC 1.-.-.-)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91604_g3	Q5R533	SERC3_PONAB	Serine incorporator 3	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c91614_g3	Q0VCQ4	RRFM_BOVIN	Ribosome-recycling factor, mitochondrial (RRF) (Ribosome-releasing factor, mitochondrial)	Bos taurus (Bovine)
c91616_g2	Q8K482	EMIL2_MOUSE	EMILIN-2 (Basilin) (Elastin microfibril interface-located protein 2) (Elastin microfibril interfacer 2)	Mus musculus (Mouse)
c91620_g3	Q2TA45	AGFG1_BOVIN	Arf-GAP domain and FG repeat-containing protein 1 (HIV-1 Rev-binding protein homolog) (Nucleoporin-like protein RIP)	Bos taurus (Bovine)
c91678_g3	Q3T093	NECP1_BOVIN	Adaptin ear-binding coat-associated protein 1 (NECAP endocytosis-associated protein 1) (NECAP-1)	Bos taurus (Bovine)
c91691_g3	Q3SZC4	NSF1C_BOVIN	NSFL1 cofactor p47 (p97 cofactor p47)	Bos taurus (Bovine)
c91696_g4	Q29RT8	LPPR2_BOVIN	Lipid phosphate phosphatase-related protein type 2 (EC 3.1.3.4) (Plasticity-related gene 4 protein) (PRG-4)	Bos taurus (Bovine)
c91696_g6	Q6GM05	LPPR5_XENLA	Lipid phosphate phosphatase-related protein type 5 (EC 3.1.3.-)	Xenopus laevis (African clawed frog)
c91717_g4	P79944	EOMES_XENLA	Eomesodermin	Xenopus laevis (African clawed frog)
c91723_g1	F1QCC6	GPC1_DANRE	Glypican-1 [Cleaved into: Secreted glypican-1]	Danio rerio (Zebrafish) (Brachydanio rerio)
c91730_g4	Q8R189	PAQRA_MOUSE	Monocyte to macrophage differentiation factor 2 (Progestin and adipoQ receptor family member X)	Mus musculus (Mouse)
c91739_g1	P10160	IF5A1_RABIT	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (eIF-4D)	Oryctolagus cuniculus (Rabbit)
c91769_g3	Q8CIV2	MBRL_MOUSE	Membralin (Transmembrane protein 259)	Mus musculus (Mouse)
c91780_g1	A2VD13	PTCD1_RAT	Pentatricopeptide repeat-containing protein 1, mitochondrial	Rattus norvegicus (Rat)
c91789_g6	Q8BKT3	GCFC2_MOUSE	GC-rich sequence DNA-binding factor 2 (GC-rich sequence DNA-binding factor) (Transcription factor 9) (TCF-9)	Mus musculus (Mouse)
c91795_g2	Q9HCE3	ZN532_HUMAN	Zinc finger protein 532	Homo sapiens (Human)
c91804_g10	Q1JQ66	S35E3_DANRE	Solute carrier family 35 member E3	Danio rerio (Zebrafish) (Brachydanio rerio)

c91806_g1	F1QAJ4	GATA_DANRE	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial (Glu-AdT subunit A) (EC 6.3.5.7) (Glutamyl-tRNA synthase-like protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91828_g6	Q6P104	QKIB_DANRE	Protein quaking-B (Quaking-related protein)	Danio rerio (Zebrafish) (Brachydanio rerio)
c91852_g1	Q8BUH1	TXN4B_MOUSE	Thioredoxin-like protein 4B	Mus musculus (Mouse)
c91866_g1	Q80TG9	LRFN2_MOUSE	Leucine-rich repeat and fibronectin type-III domain-containing protein 2	Mus musculus (Mouse)
c91866_g5	P10894	PLCB1_BOVIN	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 (EC 3.1.4.11) (PLC-154) (Phosphoinositide phospholipase C-beta-1) (Phospholipase C-beta-1) (PLC-beta-1)	Bos taurus (Bovine)
c91868_g4	Q5M9P8	ARL6_DANRE	ADP-ribosylation factor-like protein 6	Danio rerio (Zebrafish) (Brachydanio rerio)
c91873_g2	NA			
c91880_g1	Q63548	SEM3A_RAT	Semaphorin-3A (Semaphorin III) (Sema III)	Rattus norvegicus (Rat)
c91886_g3	Q92777	SYN2_HUMAN	Synapsin-2 (Synapsin II)	Homo sapiens (Human)
c91889_g4	Q5RHU7	MDM1_DANRE	Nuclear protein MDM1	Danio rerio (Zebrafish) (Brachydanio rerio)
c91902_g3	Q9Y5F6	PCDGM_HUMAN	Protocadherin gamma-C5 (PCDH-gamma-C5)	Homo sapiens (Human)
c91902_g6	Q9Y5F7	PCDGL_HUMAN	Protocadherin gamma-C4 (PCDH-gamma-C4)	Homo sapiens (Human)
c91902_g7	Q9Y5F7	PCDGL_HUMAN	Protocadherin gamma-C4 (PCDH-gamma-C4)	Homo sapiens (Human)
c91902_g8	Q9Y5F6	PCDGM_HUMAN	Protocadherin gamma-C5 (PCDH-gamma-C5)	Homo sapiens (Human)
c91940_g8	Q98UF7	PCX1_TAKRU	Pecanex-like protein 1 (Pecanex homolog)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c91981_g2	Q1LY10	FSD1_DANRE	Fibronectin type III and SPRY domain-containing protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c91987_g2	Q12873	CHD3_HUMAN	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha) (Zinc finger helicase) (hZFH)	Homo sapiens (Human)
c91999_g5	Q6NRB0	HOOK2_XENLA	Protein Hook homolog 2	Xenopus laevis (African clawed frog)
c92010_g4	NA			
c92035_g3	Q9H2S1	KCNN2_HUMAN	Small conductance calcium-activated potassium channel protein 2 (SK2) (SKCa 2) (SKCa2) (KCa2.2)	Homo sapiens (Human)

c92054_g5	Q5M7W6	ITFG3_RAT	Protein ITFG3	Rattus norvegicus (Rat)
c92056_g13	Q96RT1	LAP2_HUMAN	Protein LAP2 (Densin-180-like protein) (ErbB2-interacting protein) (Erbin)	Homo sapiens (Human)
c92102_g6	Q96FA3	PELI1_HUMAN	E3 ubiquitin-protein ligase pellino homolog 1 (Pellino-1) (EC 6.3.2.-) (Pellino-related intracellular-signaling molecule)	Homo sapiens (Human)
c92149_g3	O95201	ZN205_HUMAN	Zinc finger protein 205 (Zinc finger protein 210)	Homo sapiens (Human)
c92162_g5	D3ZC96	TT39B_RAT	Tetratricopeptide repeat protein 39B (TPR repeat protein 39B)	Rattus norvegicus (Rat)
c92178_g1	P33150	CAD13_CHICK	Cadherin-13 (Truncated cadherin) (T-cad) (T-cadherin)	Gallus gallus (Chicken)
c92179_g1	Q5XH95	SCMC2_XENTR	Calcium-binding mitochondrial carrier protein SCaMC-2 (Small calcium-binding mitochondrial carrier protein 2) (Solute carrier family 25 member 25)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c92181_g1	Q5QJE6	TDIF2_HUMAN	Deoxynucleotidyltransferase terminal-interacting protein 2 (Estrogen receptor-binding protein) (LPTS-interacting protein 2) (LPTS-RP2) (Terminal deoxynucleotidyltransferase-interacting factor 2) (TdIF2) (TdT-interacting factor 2)	Homo sapiens (Human)
c92204_g2	A2BFP5	S12A9_DANRE	Solute carrier family 12 member 9	Danio rerio (Zebrafish) (Brachydanio rerio)
c92218_g4	P00789	CANX_CHICK	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calcium-activated neutral proteinase) (CANP) (Calpain-1 large subunit) (Mu/M-type)	Gallus gallus (Chicken)
c92226_g5	O88427	CAC1H_MOUSE	Voltage-dependent T-type calcium channel subunit alpha-1H (Voltage-gated calcium channel subunit alpha Cav3.2)	Mus musculus (Mouse)
c92233_g4	Q5XXB5	MSH2_CHLAE	DNA mismatch repair protein Msh2 (MutS protein homolog 2)	Chlorocebus aethiops (Green monkey) (Cercopithecus aethiops)
c92234_g4	O54749	CP2J5_MOUSE	Cytochrome P450 2J5 (EC 1.14.14.1) (Arachidonic acid epoxidase) (CYPII5)	Mus musculus (Mouse)
c92243_g9	Q16568	CART_HUMAN	Cocaine- and amphetamine-regulated transcript protein [Cleaved into: CART(1-39); CART(42-89)]	Homo sapiens (Human)
c92253_g5	P13549	EF1A0_XENLA	Elongation factor 1-alpha, somatic form (EF-1-alpha-S)	Xenopus laevis (African clawed frog)
c92257_g3	P62700	YPEL5_MOUSE	Protein yippee-like 5	Mus musculus (Mouse)
c92289_g5	Q0V9X5	BHE22_XENTR	Class E basic helix-loop-helix protein 22 (bHLHe22) (Class B basic helix-loop-helix protein 5) (bHLHb5)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)

c92309_g12	O42584	NO29_XENLA	Nucleoplasmin-like protein NO29 (NOVA)	Xenopus laevis (African clawed frog)
c92322_g5	Q96FL9	GLT14_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 14 (EC 2.4.1.41) (Polypeptide GalNAc transferase 14) (GalNAc-T14) (pp-GaNTase 14) (Protein-UDP acetylgalactosaminyltransferase 14) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 14)	Homo sapiens (Human)
c92323_g2	O08919	NUMBL_MOUSE	Numb-like protein	Mus musculus (Mouse)
c92324_g4	Q16363	LAMA4_HUMAN	Laminin subunit alpha-4 (Laminin-14 subunit alpha) (Laminin-8 subunit alpha) (Laminin-9 subunit alpha)	Homo sapiens (Human)
c92328_g3	NA			
c92394_g7	Q502A3	UBAD2_DANRE	UBA-like domain-containing protein 2	Danio rerio (Zebrafish) (Brachydanio rerio)
c92403_g2	Q9XT62	RAD17_CHLAE	Cell cycle checkpoint protein RAD17	Chlorocebus aethiops (Green monkey) (Cercopithecus aethiops)
c92409_g13	Q9H7Z3	NRDE2_HUMAN	Protein NRDE2 homolog	Homo sapiens (Human)
c92421_g3	Q6NYE2	RCC2_DANRE	Protein RCC2 homolog	Danio rerio (Zebrafish) (Brachydanio rerio)
c92489_g4	Q8VI63	MOB2_MOUSE	MOB kinase activator 2 (Mob2 homolog) (Mps one binder kinase activator-like 2) (Ovary-specific MOB-like protein)	Mus musculus (Mouse)
c92507_g5	Q9Y5H6	PCDA8_HUMAN	Protocadherin alpha-8 (PCDH-alpha-8)	Homo sapiens (Human)
c92542_g10	Q2KJI7	AFG32_BOVIN	AFG3-like protein 2 (EC 3.4.24.-)	Bos taurus (Bovine)
c92549_g7	Q5ZMP3	T184C_CHICK	Transmembrane protein 184C (Transmembrane protein 34)	Gallus gallus (Chicken)
c92560_g4	A6QNL6	NKAI2_BOVIN	Sodium/potassium-transporting ATPase subunit beta-1-interacting protein 2 (Na(+)/K(+)-transporting ATPase subunit beta-1-interacting protein 2)	Bos taurus (Bovine)
c92564_g5	Q1LY10	FSD1_DANRE	Fibronectin type III and SPRY domain-containing protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)
c92603_g1	P51793	CLCN4_HUMAN	H(+)/Cl(-) exchange transporter 4 (Chloride channel protein 4) (ClC-4) (Chloride transporter ClC-4)	Homo sapiens (Human)
c92603_g2	P51793	CLCN4_HUMAN	H(+)/Cl(-) exchange transporter 4 (Chloride channel protein 4) (ClC-4) (Chloride transporter ClC-4)	Homo sapiens (Human)
c92634_g13	O75164	KDM4A_HUMAN	Lysine-specific demethylase 4A (EC 1.14.11.-) (JmjC domain-containing histone demethylation protein 3A) (Jumonji domain-containing protein 2A)	Homo sapiens (Human)

c92634_g2	Q8BW72	KDM4A_MOUSE	Lysine-specific demethylase 4A (EC 1.14.11.-) (JmjC domain-containing histone demethylation protein 3A) (Jumonji domain-containing protein 2A)	Mus musculus (Mouse)
c92672_g1	Q9R1M7	NMD3A_RAT	Glutamate receptor ionotropic, NMDA 3A (GluN3A) (Glutamate receptor chi-1) (N-methyl-D-aspartate receptor) (N-methyl-D-aspartate receptor subtype 3A) (NMDAR3A) (NR3A) (NMDAR-L) (NMDAR-L1)	Rattus norvegicus (Rat)
c92679_g10	Q62682	CNTN3_RAT	Contactin-3 (Brain-derived immunoglobulin superfamily protein 1) (BIG-1)	Rattus norvegicus (Rat)
c92718_g3	Q9DBW0	CP4V2_MOUSE	Cytochrome P450 4V2 (EC 1.14.13.-)	Mus musculus (Mouse)
c92723_g1	Q69ZQ1	K1161_MOUSE	Uncharacterized family 31 glucosidase KIAA1161 (EC 3.2.1.-)	Mus musculus (Mouse)
c92735_g4	P07871	THIKB_RAT	3-ketoacyl-CoA thiolase B, peroxisomal (EC 2.3.1.16) (Acetyl-CoA acyltransferase B) (Beta-ketothiolase B) (Peroxisomal 3-oxoacyl-CoA thiolase B)	Rattus norvegicus (Rat)
c92739_g2	Q7ZU13	SPNS1_DANRE	Protein spinster homolog 1 (Protein not really started) (Spinster-like protein)	Danio rerio (Zebrafish) (Brachydanio rerio)
c92749_g6	Q9D1H6	NDUF4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 (Hormone-regulated proliferation-associated protein of 20 kDa homolog)	Mus musculus (Mouse)
c92758_g5	Q14831	GRM7_HUMAN	Metabotropic glutamate receptor 7 (mGluR7)	Homo sapiens (Human)
c92761_g1	P51797	CLCN6_HUMAN	Chloride transport protein 6 (Chloride channel protein 6) (CIC-6)	Homo sapiens (Human)
c92799_g3	Q9PWR1	KCAB1_CHICK	Voltage-gated potassium channel subunit beta-1 (K(+) channel subunit beta-1) (Kv-beta-1)	Gallus gallus (Chicken)
c92823_g3	Q13905	RPGF1_HUMAN	Rap guanine nucleotide exchange factor 1 (CRK SH3-binding GNRP) (Guanine nucleotide-releasing factor 2) (Protein C3G)	Homo sapiens (Human)
c92825_g1	Q2YDR3	IMPA3_DANRE	Inositol monophosphatase 3 (IMP 3) (IMPase 3) (EC 3.1.3.25) (Inositol monophosphatase domain-containing protein 1) (Inositol-1(or 4)-monophosphatase 3) (Myo-inositol monophosphatase A3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c92827_g1	O95071	UBR5_HUMAN	E3 ubiquitin-protein ligase UBR5 (EC 6.3.2.-) (E3 ubiquitin-protein ligase, HECT domain-containing 1) (Hyperplastic discs protein homolog) (hHYD) (Progestin-induced protein)	Homo sapiens (Human)
c92828_g2	Q99973	TEP1_HUMAN	Telomerase protein component 1 (Telomerase-associated protein 1) (Telomerase protein 1) (p240) (p80 telomerase homolog)	Homo sapiens (Human)

c92844_g3	Q8BYA0	TBCD_MOUSE	Tubulin-specific chaperone D (Beta-tubulin cofactor D) (Tubulin-folding cofactor D)	Mus musculus (Mouse)
c92857_g13	Q8R431	MGLL_RAT	Monoglyceride lipase (MGL) (EC 3.1.1.23) (Monoacylglycerol lipase) (MAGL)	Rattus norvegicus (Rat)
c92876_g2	Q91560	REXO4_XENLA	RNA exonuclease 4 (EC 3.1.-.-) (Exonuclease XPMC2) (Prevents mitotic catastrophe 2 protein)	Xenopus laevis (African clawed frog)
c92878_g2	Q6ZMW2	ZN782_HUMAN	Zinc finger protein 782	Homo sapiens (Human)
c92893_g3	Q1RMR2	RU17_BOVIN	U1 small nuclear ribonucleoprotein 70 kDa (U1 snRNP 70 kDa) (U1-70K) (snRNP70)	Bos taurus (Bovine)
c92905_g1	Q5RE87	S38A4_PONAB	Sodium-coupled neutral amino acid transporter 4 (Amino acid transporter A3) (Na(+)-coupled neutral amino acid transporter 4) (Solute carrier family 38 member 4) (System A amino acid transporter 3)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c92913_g10	Q00960	NMDE2_RAT	Glutamate receptor ionotropic, NMDA 2B (GluN2B) (Glutamate [NMDA] receptor subunit epsilon-2) (N-methyl D-aspartate receptor subtype 2B) (NMDAR2B) (NR2B)	Rattus norvegicus (Rat)
c92913_g7	Q01097	NMDE2_MOUSE	Glutamate receptor ionotropic, NMDA 2B (GluN2B) (Glutamate [NMDA] receptor subunit epsilon-2) (N-methyl D-aspartate receptor subtype 2B) (NMDAR2B) (NR2B)	Mus musculus (Mouse)
c92921_g1	P18729	ZG57_XENLA	Gastrula zinc finger protein XICGF57.1 (Fragment)	Xenopus laevis (African clawed frog)
c92934_g7	P17790	BASI_CHICK	Basigin (5A11 antigen) (Blood-brain barrier HT7 antigen) (Neurothelin)	Gallus gallus (Chicken)
c92942_g3	A5A8Y8	EGFL8_PIG	Epidermal growth factor-like protein 8 (EGF-like protein 8)	Sus scrofa (Pig)
c92970_g1	Q6DN14	MCTP1_HUMAN	Multiple C2 and transmembrane domain-containing protein 1	Homo sapiens (Human)
c92971_g4	A2VDD2	TC1DB_XENLA	Tctex1 domain-containing protein 1-B (Fragment)	Xenopus laevis (African clawed frog)
c93001_g3	Q8BG21	FLOWR_MOUSE	Calcium channel flower homolog (Calcium channel flower domain-containing protein 1)	Mus musculus (Mouse)
c93028_g4	Q5H8A4	PIGG_HUMAN	GPI ethanolamine phosphate transferase 2 (EC 2.-.-.-) (GPI7 homolog) (hGPI7) (Phosphatidylinositol-glycan biosynthesis class G protein) (PIG-G)	Homo sapiens (Human)
c93047_g1	B1AK53	ESPN_HUMAN	Espin (Autosomal recessive deafness type 36 protein) (Ectoplasmic specialization protein)	Homo sapiens (Human)
c93047_g2	B1AK53	ESPN_HUMAN	Espin (Autosomal recessive deafness type 36 protein) (Ectoplasmic specialization protein)	Homo sapiens (Human)

c93048_g1	Q92956	TNR14_HUMAN	Tumor necrosis factor receptor superfamily member 14 (Herpes virus entry mediator A) (Herpesvirus entry mediator A) (HveA) (Tumor necrosis factor receptor-like 2) (TR2) (CD antigen CD270)	Homo sapiens (Human)
c93064_g1	Q03669	AT2A2_CHICK	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (SERCA2) (SR Ca(2+)-ATPase 2) (EC 3.6.3.8) (Calcium pump 2) (Calcium-transporting ATPase sarcoplasmic reticulum type, slow twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase)	Gallus gallus (Chicken)
c93078_g2	Q7ZXY0	INO1A_XENLA	Inositol-3-phosphate synthase 1-A (IPS 1-A) (EC 5.5.1.4) (Myo-inositol 1-phosphate synthase A) (MI-1-P synthase A) (MIP synthase A)	Xenopus laevis (African clawed frog)
c93079_g1	O00533	CHL1_HUMAN	Neural cell adhesion molecule L1-like protein (Close homolog of L1) [Cleaved into: Processed neural cell adhesion molecule L1-like protein]	Homo sapiens (Human)
c93079_g4	A0FKI7	ACBD5_RAT	Acyl-CoA-binding domain-containing protein 5	Rattus norvegicus (Rat)
c93125_g1	Q5H8C1	FREM1_HUMAN	FRAS1-related extracellular matrix protein 1 (Protein QBRICK)	Homo sapiens (Human)
c93134_g2	A0JPF5	F16B2_DANRE	Protein FAM160B2 (RAI16-like protein) (Retinoic acid-induced protein 16)	Danio rerio (Zebrafish) (Brachydanio rerio)
c93134_g3	A0JPF5	F16B2_DANRE	Protein FAM160B2 (RAI16-like protein) (Retinoic acid-induced protein 16)	Danio rerio (Zebrafish) (Brachydanio rerio)
c93135_g3	Q9BQQ3	GORS1_HUMAN	Golgi reassembly-stacking protein 1 (Golgi peripheral membrane protein p65) (Golgi phosphoprotein 5) (GOLPH5) (Golgi reassembly-stacking protein of 65 kDa) (GRASP65)	Homo sapiens (Human)
c93138_g3	Q9UGI6	KCNN3_HUMAN	Small conductance calcium-activated potassium channel protein 3 (SK3) (SKCa 3) (SKCa3) (KCa2.3)	Homo sapiens (Human)
c93147_g2	P01023	A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	Homo sapiens (Human)
c93181_g4	A2VDH3	LRC38_MOUSE	Leucine-rich repeat-containing protein 38 (BK channel auxiliary gamma subunit LRRC38)	Mus musculus (Mouse)
c93185_g2	O08967	CYH3_MOUSE	Cytohesin-3 (ARF nucleotide-binding site opener 3) (Protein ARNO3) (General receptor of phosphoinositides 1) (Grp1) (PH, SEC7 and coiled-coil domain-containing protein 3) (CLM3) (SEC7 homolog C) (mSec7-3)	Mus musculus (Mouse)
c93194_g1	Q6PD21	SHB_MOUSE	SH2 domain-containing adapter protein B	Mus musculus (Mouse)
c93214_g3	Q802V6	ABH2A_DANRE	Abhydrolase domain-containing protein 2-A (EC 3.1.1.-)	Danio rerio (Zebrafish) (Brachydanio rerio)

c93262_g3	Q4V8X0	TPRA1_DANRE	Transmembrane protein adipocyte-associated 1 homolog (Integral membrane protein GPR175)	Danio rerio (Zebrafish) (Brachydanio rerio)
c93264_g1	A1A4J1	PFKAL_BOVIN	ATP-dependent 6-phosphofructokinase, liver type (ATP-PFK) (PFK-L) (EC 2.7.1.11) (6-phosphofructokinase type B) (Phosphofructo-1-kinase isozyme B) (PFK-B) (Phosphohexokinase)	Bos taurus (Bovine)
c93283_g1	Q99MU5	SPAT6_RAT	Spermatogenesis-associated protein 6 (Kinesin-related protein) (Spermatogenesis-related factor 1)	Rattus norvegicus (Rat)
c93339_g1	Q6P1L5	F117B_HUMAN	Protein FAM117B (Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 13 protein)	Homo sapiens (Human)
c93339_g2	Q561P5	MCM5_XENTR	DNA replication licensing factor mcm5 (EC 3.6.4.12)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c93376_g2	Q6GMI9	UXS1_DANRE	UDP-glucuronic acid decarboxylase 1 (EC 4.1.1.35) (UDP-glucuronate decarboxylase 1) (UXS-1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c93378_g1	Q9ULJ1	ODF2L_HUMAN	Outer dense fiber protein 2-like	Homo sapiens (Human)
c93399_g3	Q5R8H3	BAP31_PONAB	B-cell receptor-associated protein 31 (BCR-associated protein 31) (Bap31)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c93441_g5	O75326	SEM7A_HUMAN	Semaphorin-7A (CDw108) (JMH blood group antigen) (John-Milton-Hargen human blood group Ag) (Semaphorin-K1) (Sema K1) (Semaphorin-L) (Sema L) (CD antigen CD108)	Homo sapiens (Human)
c93460_g2	P51523	ZNF84_HUMAN	Zinc finger protein 84 (Zinc finger protein HPF2)	Homo sapiens (Human)
c93471_g4	Q8C761	WDR60_MOUSE	WD repeat-containing protein 60	Mus musculus (Mouse)
c93490_g1	P05165	PCCA_HUMAN	Propionyl-CoA carboxylase alpha chain, mitochondrial (PCCase subunit alpha) (EC 6.4.1.3) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	Homo sapiens (Human)
c93495_g2	Q5ZI04	FA49A_CHICK	Protein FAM49A	Gallus gallus (Chicken)
c93498_g2	Q5ZM33	HP1B3_CHICK	Heterochromatin protein 1-binding protein 3	Gallus gallus (Chicken)
c93502_g3	Q7TNR6	IGS21_MOUSE	Immunoglobulin superfamily member 21 (IgSF21)	Mus musculus (Mouse)
c93549_g1	Q8TEQ0	SNX29_HUMAN	Sorting nexin-29 (RUN domain-containing protein 2A)	Homo sapiens (Human)
c93549_g3	Q8TEQ0	SNX29_HUMAN	Sorting nexin-29 (RUN domain-containing protein 2A)	Homo sapiens (Human)
c93554_g9	Q13905	RPGF1_HUMAN	Rap guanine nucleotide exchange factor 1 (CRK SH3-binding GNRP) (Guanine nucleotide-releasing factor 2) (Protein C3G)	Homo sapiens (Human)

c93555_g2	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c93561_g4	Q3V1V3	ESF1_MOUSE	ESF1 homolog (ABT1-associated protein)	Mus musculus (Mouse)
c93588_g1	Q08D69	MED16_XENTR	Mediator of RNA polymerase II transcription subunit 16 (Mediator complex subunit 16)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c93595_g5	Q8JZV4	RBM41_MOUSE	RNA-binding protein 41 (RNA-binding motif protein 41)	Mus musculus (Mouse)
c93615_g1	Q9JLH6	CK5P1_RAT	CDK5 regulatory subunit-associated protein 1 (CDK5 activator-binding protein C42)	Rattus norvegicus (Rat)
c93617_g6	P55040	GEM_HUMAN	GTP-binding protein GEM (GTP-binding mitogen-induced T-cell protein) (RAS-like protein KIR)	Homo sapiens (Human)
c93636_g2	P15586	GNS_HUMAN	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase) (G6S)	Homo sapiens (Human)
c93657_g2	O18920	ANGP1_BOVIN	Angiopoietin-1 (ANG-1)	Bos taurus (Bovine)
c93659_g2	P50538	MAD1_MOUSE	Max dimerization protein 1 (Max dimerizer 1) (Protein MAD)	Mus musculus (Mouse)
c93660_g2	Q08C72	CWC22_DANRE	Pre-mRNA-splicing factor CWC22 homolog (Nucampholin homolog)	Danio rerio (Zebrafish) (Brachydanio rerio)
c93664_g2	O42099	MK08B_CYPKA	Mitogen-activated protein kinase 8B (MAP kinase 8B) (MAPK 8B) (EC 2.7.11.24) (Stress-activated protein kinase JNKb) (c-Jun N-terminal kinase B)	Cyprinus carpio (Common carp)
c93664_g3	Q90327	MK08A_CYPKA	Mitogen-activated protein kinase 8A (MAP kinase 8A) (MAPK 8A) (EC 2.7.11.24) (Stress-activated protein kinase JNKa) (c-Jun N-terminal kinase A)	Cyprinus carpio (Common carp)
c93677_g3	P48453	PP2BB_MOUSE	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform (EC 3.1.3.16) (CAM-PRP catalytic subunit) (Calmodulin-dependent calcineurin A subunit beta isoform)	Mus musculus (Mouse)
c93698_g1	Q5DRC0	PCDGB_PANTR	Protocadherin gamma-A11 (PCDH-gamma-A11)	Pan troglodytes (Chimpanzee)
c93702_g3	Q5PPK1	BRI3_RAT	Brain protein I3	Rattus norvegicus (Rat)
c93748_g7	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]	Homo sapiens (Human)
c93815_g5	Q8TBB5	KLDC4_HUMAN	Kelch domain-containing protein 4	Homo sapiens (Human)
c93830_g1	O42386	RABP1_TAKRU	Cellular retinoic acid-binding protein 1 (Cellular retinoic acid-binding protein I) (CRABP-I)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)

c93834_g2	Q02880	TOP2B_HUMAN	DNA topoisomerase 2-beta (EC 5.99.1.3) (DNA topoisomerase II, beta isozyme)	Homo sapiens (Human)
c93912_g3	Q92845	KIFA3_HUMAN	Kinesin-associated protein 3 (KAP-3) (KAP3) (Smg GDS-associated protein)	Homo sapiens (Human)
c93946_g4	Q6NS60	FBX41_MOUSE	F-box only protein 41	Mus musculus (Mouse)
c93950_g1	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c93972_g1	A2AWA9	RBGP1_MOUSE	Rab GTPase-activating protein 1 (GAP and centrosome-associated protein) (Rab6 GTPase-activating protein GAPCenA)	Mus musculus (Mouse)
c94065_g2	P31152	MK04_HUMAN	Mitogen-activated protein kinase 4 (MAP kinase 4) (MAPK 4) (EC 2.7.11.24) (Extracellular signal-regulated kinase 4) (ERK-4) (MAP kinase isoform p63) (p63-MAPK)	Homo sapiens (Human)
c94077_g2	O43184	ADA12_HUMAN	Disintegrin and metalloproteinase domain-containing protein 12 (ADAM 12) (EC 3.4.24.-) (Meltrin-alpha)	Homo sapiens (Human)
c94119_g1	Q12872	SFSWA_HUMAN	Splicing factor, suppressor of white-apricot homolog (Splicing factor, arginine/serine-rich 8) (Suppressor of white apricot protein homolog)	Homo sapiens (Human)
c94121_g2	A3KNL6	GGACC_DANRE	Gamma-glutamylaminecyclotransferase C (GGACT C) (EC 2.3.2.4) (AIG2-like domain-containing protein 1-C) (Gamma-glutamylamine cyclotransferase C) (Gamma-glutamylamine cyclotransferase, tandem duplicate 3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94121_g6	A3KNL6	GGACC_DANRE	Gamma-glutamylaminecyclotransferase C (GGACT C) (EC 2.3.2.4) (AIG2-like domain-containing protein 1-C) (Gamma-glutamylamine cyclotransferase C) (Gamma-glutamylamine cyclotransferase, tandem duplicate 3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94138_g1	Q5XJS0	FA73A_DANRE	Protein FAM73A	Danio rerio (Zebrafish) (Brachydanio rerio)
c94141_g2	Q9N1F5	GSTO1_PIG	Glutathione S-transferase omega-1 (GSTO-1) (EC 2.5.1.18) (Glutathione S-transferase omega 1-1) (GSTO 1-1) (Glutathione-dependent dehydroascorbate reductase) (EC 1.8.5.1) (Monomethylarsonic acid reductase) (MMA(V) reductase) (EC 1.20.4.2) (S-(Phenacyl)glutathione reductase) (SPG-R)	Sus scrofa (Pig)
c94143_g6	P30490	1B52_HUMAN	HLA class I histocompatibility antigen, B-52 alpha chain (Bw-52) (HLA class I histocompatibility antigen, B-5 alpha chain) (MHC class I antigen B*52)	Homo sapiens (Human)

c94169_g2	Q15051	IQCB1_HUMAN	IQ calmodulin-binding motif-containing protein 1 (Nephrocystin-5) (p53 and DNA damage-regulated IQ motif protein) (PIQ)	Homo sapiens (Human)
c94175_g4	P15999	ATPA_RAT	ATP synthase subunit alpha, mitochondrial	Rattus norvegicus (Rat)
c94198_g4	A2RRV3	PATL1_DANRE	Protein PAT1 homolog 1 (PAT1-like protein 1) (Protein PAT1 homolog b) (Pat1b)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94214_g2	Q9P1Z9	CC180_HUMAN	Coiled-coil domain-containing protein 180	Homo sapiens (Human)
c94218_g4	A0FKG7	CAN7_PIG	Calpain-7 (EC 3.4.22.-)	Sus scrofa (Pig)
c94239_g3	Q56JX9	FABPI_BOVIN	Fatty acid-binding protein, intestinal (Fatty acid-binding protein 2) (Intestinal-type fatty acid-binding protein) (I-FABP)	Bos taurus (Bovine)
c94251_g1	Q9R080	GPSM1_RAT	G-protein-signaling modulator 1 (Activator of G-protein signaling 3)	Rattus norvegicus (Rat)
c94252_g3	Q7SYL3	SIAH2_DANRE	E3 ubiquitin-protein ligase Siah2 (EC 6.3.2.-) (Seven in absentia homolog 2-like) (Siah-2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94282_g4	Q71LX4	TLN2_MOUSE	Talin-2	Mus musculus (Mouse)
c94295_g5	A2A9C3	SZT2_MOUSE	Protein SZT2 (Seizure threshold 2 protein) (Transcript increased in glutamate resistance) (TIGR)	Mus musculus (Mouse)
c94310_g4	Q9ULW5	RAB26_HUMAN	Ras-related protein Rab-26	Homo sapiens (Human)
c94326_g1	B0UYT5	MFD6B_DANRE	Major facilitator superfamily domain-containing protein 6-B (Macrophage MHC class I receptor 2 homolog B)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94329_g3	Q9H8L6	MMRN2_HUMAN	Multimerin-2 (EMILIN-3) (Elastin microfibril interface located protein 3) (Elastin microfibril interfacer 3) (EndoGlyx-1 p125/p140 subunit)	Homo sapiens (Human)
c94352_g6	Q58DR5	SCAM3_BOVIN	Secretory carrier-associated membrane protein 3 (Secretory carrier membrane protein 3)	Bos taurus (Bovine)
c94361_g1	P70188	KIFA3_MOUSE	Kinesin-associated protein 3 (KAP-3) (KAP3)	Mus musculus (Mouse)
c94386_g1	Q95LD9	AHR_DELLE	Aryl hydrocarbon receptor (Ah receptor) (AhR)	Delphinapterus leucas (Beluga whale)
c94410_g4	Q2KIB3	TM101_BOVIN	Transmembrane protein 101	Bos taurus (Bovine)
c94420_g1	Q6AZA0	THIL_DANRE	Acetyl-CoA acetyltransferase, mitochondrial (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94427_g1	Q3ZBF8	CERS2_BOVIN	Ceramide synthase 2 (CerS2) (LAG1 longevity assurance homolog 2)	Bos taurus (Bovine)
c94460_g3	A2AAE1	K1109_MOUSE	Uncharacterized protein KIAA1109 (Fragile site-associated protein homolog)	Mus musculus (Mouse)
c94469_g1	Q8BWT5	DIP2A_MOUSE	Disco-interacting protein 2 homolog A (DIP2 homolog A)	Mus musculus (Mouse)

c94492_g3	P0C644	VIP1_RAT	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1 (EC 2.7.4.21) (EC 2.7.4.24) (Diphosphoinositol pentakisphosphate kinase 1) (Histidine acid phosphatase domain-containing protein 2A) (InsP6 and PP-IP5 kinase 1) (VIP1 homolog)	Rattus norvegicus (Rat)
c94504_g5	P52181	TGM2_PAGMA	Protein-glutamine gamma-glutamyltransferase 2 (EC 2.3.2.13) (Tissue transglutaminase) (Transglutaminase C) (TG(C)) (TGC) (TGase C) (Transglutaminase-2) (TGase-2)	Pagrus major (Red sea bream) (Chrysophrys major)
c94505_g1	Q0VA42	F188B_XENTR	Protein FAM188B	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c94539_g2	P10247	HG2A_RAT	H-2 class II histocompatibility antigen gamma chain (Ia antigen-associated invariant chain) (Ii) (MHC class II-associated invariant chain) (CD antigen CD74)	Rattus norvegicus (Rat)
c94551_g2	Q13367	AP3B2_HUMAN	AP-3 complex subunit beta-2 (Adaptor protein complex AP-3 subunit beta-2) (Adaptor-related protein complex 3 subunit beta-2) (Beta-3B-adaptin) (Clathrin assembly protein complex 3 beta-2 large chain) (Neuron-specific vesicle coat protein beta-NAP)	Homo sapiens (Human)
c94554_g2	Q5BKX0	TM248_DANRE	Transmembrane protein 248	Danio rerio (Zebrafish) (Brachydanio rerio)
c94555_g2	P49758	RGS6_HUMAN	Regulator of G-protein signaling 6 (RGS6) (S914)	Homo sapiens (Human)
c94557_g10	Q07889	SOS1_HUMAN	Son of sevenless homolog 1 (SOS-1)	Homo sapiens (Human)
c94585_g5	P19618	NCPR_SALTR	NADPH--cytochrome P450 reductase (CPR) (P450R) (EC 1.6.2.4) (Fragments)	Salmo trutta (Brown trout)
c94594_g3	P13497	BMP1_HUMAN	Bone morphogenetic protein 1 (BMP-1) (EC 3.4.24.19) (Mammalian tolloid protein) (mTld) (Procollagen C-proteinase) (PCP)	Homo sapiens (Human)
c94595_g1	Q7SZI5	RFTN1_CHICK	Raftlin (Raft-linking protein)	Gallus gallus (Chicken)
c94598_g1	P49589	SYCC_HUMAN	Cysteine--tRNA ligase, cytoplasmic (EC 6.1.1.16) (Cysteinyl-tRNA synthetase) (CysRS)	Homo sapiens (Human)
c94599_g2	Q2KJI7	AFG32_BOVIN	AFG3-like protein 2 (EC 3.4.24.-)	Bos taurus (Bovine)
c94602_g1	Q6PCJ1	DCTN1_XENLA	Dynactin subunit 1	Xenopus laevis (African clawed frog)
c94622_g2	Q1H9T6	ZBT48_MOUSE	Zinc finger and BTB domain-containing protein 48 (Krueppel-related zinc finger protein 3) (Protein HKR3)	Mus musculus (Mouse)
c94633_g13	Q6DGH9	OTBP_DANRE	Homeobox protein orthopedia B	Danio rerio (Zebrafish) (Brachydanio rerio)

c94639_g3	A2AAE1	K1109_MOUSE	Uncharacterized protein KIAA1109 (Fragile site-associated protein homolog)	Mus musculus (Mouse)
c94664_g6	Q8BHE3	ATCAY_MOUSE	Caytaxin	Mus musculus (Mouse)
c94689_g1	O00763	ACACB_HUMAN	Acetyl-CoA carboxylase 2 (EC 6.4.1.2) (ACC-beta) [Includes: Biotin carboxylase (EC 6.3.4.14)]	Homo sapiens (Human)
c94693_g3	Q86YV5	SG223_HUMAN	Tyrosine-protein kinase Sgk223 (EC 2.7.10.2) (Sugen kinase 223)	Homo sapiens (Human)
c94699_g2	Q8NI35	INADL_HUMAN	InaD-like protein (Inadl protein) (hINADL) (Pals1-associated tight junction protein) (Protein associated to tight junctions)	Homo sapiens (Human)
c94699_g5	Q63ZW7	INADL_MOUSE	InaD-like protein (Inadl protein) (Channel-interacting PDZ domain-containing protein) (Pals1-associated tight junction protein) (Protein associated to tight junctions)	Mus musculus (Mouse)
c94709_g2	P29597	TYK2_HUMAN	Non-receptor tyrosine-protein kinase TYK2 (EC 2.7.10.2)	Homo sapiens (Human)
c94714_g5	Q96MM6	HS12B_HUMAN	Heat shock 70 kDa protein 12B	Homo sapiens (Human)
c94720_g8	Q8JHW2	TSP3A_DANRE	Thrombospondin-3a (Thbs3a)	Danio rerio (Zebrafish) (Brachydanio rerio)
c94765_g7	Q8R3Q2	PP6R2_MOUSE	Serine/threonine-protein phosphatase 6 regulatory subunit 2 (SAPS domain family member 2)	Mus musculus (Mouse)
c94785_g4	Q61091	FZD8_MOUSE	Frizzled-8 (Fz-8) (mFz8)	Mus musculus (Mouse)
c94788_g4	Q6NXX2	ZN532_MOUSE	Zinc finger protein 532	Mus musculus (Mouse)
c94798_g4	A4Q9F4	TTL11_MOUSE	Tubulin polyglutamylase TTL11 (EC 6.-.-.-) (Tubulin--tyrosine ligase-like protein 11)	Mus musculus (Mouse)
c94807_g1	Q9Y5X5	NPFF2_HUMAN	Neuropeptide FF receptor 2 (G-protein coupled receptor 74) (G-protein coupled receptor HLWAR77) (Neuropeptide G-protein coupled receptor)	Homo sapiens (Human)
c94855_g2	Q9BXS0	COPA1_HUMAN	Collagen alpha-1(XXV) chain (Alzheimer disease amyloid-associated protein) (AMY) (CLAC-P) [Cleaved into: Collagen-like Alzheimer amyloid plaque component (CLAC)]	Homo sapiens (Human)
c94897_g2	Q5W111	SPRY7_HUMAN	SPRY domain-containing protein 7 (Chronic lymphocytic leukemia deletion region gene 6 protein) (CLL deletion region gene 6 protein)	Homo sapiens (Human)
c94909_g3	O94889	KLH18_HUMAN	Kelch-like protein 18	Homo sapiens (Human)
c94919_g4	Q8BIA3	MKX_MOUSE	Homeobox protein Mohawk	Mus musculus (Mouse)
c94922_g7	P47211	GALR1_HUMAN	Galanin receptor type 1 (GAL1-R) (GALR-1)	Homo sapiens (Human)

c94935_g3	O88204	LRP3_RAT	Low-density lipoprotein receptor-related protein 3 (LRP-3) (105 kDa low-density lipoprotein receptor-related protein) (rLRp105)	Rattus norvegicus (Rat)
c94939_g2	Q6PJW8	CNST_HUMAN	Consortin	Homo sapiens (Human)
c94952_g7	Q9BXI9	C1QT6_HUMAN	Complement C1q tumor necrosis factor-related protein 6	Homo sapiens (Human)
c94958_g1	Q9H0M0	WWP1_HUMAN	NEDD4-like E3 ubiquitin-protein ligase WWP1 (EC 6.3.2.-) (Atrophin-1-interacting protein 5) (AIP5) (TGIF-interacting ubiquitin ligase 1) (Tiul1) (WW domain-containing protein 1)	Homo sapiens (Human)
c94967_g8	P0CT34	TF21_SCHPO	Transposon Tf2-1 polypeptide (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c94976_g1	Q8NEZ4	KMT2C_HUMAN	Histone-lysine N-methyltransferase 2C (Lysine N-methyltransferase 2C) (EC 2.1.1.43) (Homologous to ALR protein) (Myeloid/lymphoid or mixed-lineage leukemia protein 3)	Homo sapiens (Human)
c94976_g2	Q8NEZ4	KMT2C_HUMAN	Histone-lysine N-methyltransferase 2C (Lysine N-methyltransferase 2C) (EC 2.1.1.43) (Homologous to ALR protein) (Myeloid/lymphoid or mixed-lineage leukemia protein 3)	Homo sapiens (Human)
c94983_g2	Q80Z29	NAMPT_RAT	Nicotinamide phosphoribosyltransferase (NAmPRTase) (Nampt) (EC 2.4.2.12) (Pre-B-cell colony-enhancing factor 1 homolog) (PBEF) (Visfatin)	Rattus norvegicus (Rat)
c94984_g5	Q9H5Y7	SLIK6_HUMAN	SLIT and NTRK-like protein 6	Homo sapiens (Human)
c95008_g6	A7E2V4	ZSWM8_HUMAN	Zinc finger SWIM domain-containing protein 8	Homo sapiens (Human)
c95009_g7	Q9W6I1	RBPM5_CHICK	RNA-binding protein with multiple splicing (RBP-MS) (Heart and RRM expressed sequence) (Hermes)	Gallus gallus (Chicken)
c95009_g8	Q91880	SUH_XENLA	Suppressor of hairless protein homolog (X-Su(H))	Xenopus laevis (African clawed frog)
c95013_g4	Q91ZP3	LPIN1_MOUSE	Phosphatidate phosphatase LPIN1 (EC 3.1.3.4) (Fatty liver dystrophy protein) (Lipin-1)	Mus musculus (Mouse)
c95031_g1	P43003	EAA1_HUMAN	Excitatory amino acid transporter 1 (Sodium-dependent glutamate/aspartate transporter 1) (GLAST-1) (Solute carrier family 1 member 3)	Homo sapiens (Human)
c95041_g13	Q5TH69	BIG3_HUMAN	Brefeldin A-inhibited guanine nucleotide-exchange protein 3	Homo sapiens (Human)
c95084_g5	Q5DU56	NLRC3_MOUSE	Protein NLRC3	Mus musculus (Mouse)
c95088_g1	Q15075	EEA1_HUMAN	Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain-containing protein 2)	Homo sapiens (Human)

c95089_g2	Q62232	SIX2_MOUSE	Homeobox protein SIX2 (Sine oculis homeobox homolog 2)	Mus musculus (Mouse)
c95122_g2	O14795	UN13B_HUMAN	Protein unc-13 homolog B (Munc13-2) (munc13)	Homo sapiens (Human)
c95124_g1	Q66I22	SRRT_DANRE	Serrate RNA effector molecule homolog (Arsenite-resistance protein 2)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95127_g10	D2I3C6	DCLK2_AILME	Serine/threonine-protein kinase DCLK2 (EC 2.7.11.1) (CaMK-like CREB regulatory kinase 2) (CL2) (CLICK-II) (CLICK2) (Doublecortin-like and CAM kinase-like 2) (Doublecortin-like kinase 2)	Ailuropoda melanoleuca (Giant panda)
c95130_g9	Q8N0W4	NLGNX_HUMAN	Neurologin-4, X-linked (Neurologin X) (HNLX)	Homo sapiens (Human)
c95134_g2	A8C750	THADA_CANFA	Thyroid adenoma-associated protein homolog	Canis familiaris (Dog) (Canis lupus familiaris)
c95164_g7	Q66I12	CCD47_DANRE	Coiled-coil domain-containing protein 47	Danio rerio (Zebrafish) (Brachydanio rerio)
c95174_g4	O08838	AMPH_RAT	Amphiphysin	Rattus norvegicus (Rat)
c95176_g1	Q2VPU4	MLXIP_MOUSE	MLX-interacting protein (Transcriptional activator MondoA)	Mus musculus (Mouse)
c95187_g8	Q00361	ATP5I_BOVIN	ATP synthase subunit e, mitochondrial (ATPase subunit e)	Bos taurus (Bovine)
c95192_g3	Q811M5	CO6_RAT	Complement component C6	Rattus norvegicus (Rat)
c95204_g2	Q7SY49	CAMKV_DANRE	CaM kinase-like vesicle-associated protein (1G5z)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95208_g1	B6VA23	2ABB_CARAU	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B beta isoform (PP2A subunit B isoform B55-beta) (PP2A subunit B isoform PR55-beta) (PP2A subunit B isoform R2-beta) (PP2A subunit B isoform beta)	Carassius auratus (Goldfish)
c95229_g8	P28331	NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-75kD) (CI-75kD)	Homo sapiens (Human)
c95241_g1	Q3UJK4	GTPB2_MOUSE	GTP-binding protein 2 (GTP-binding-like protein 2)	Mus musculus (Mouse)
c95243_g14	Q7ZXF5	FACR1_XENLA	Fatty acyl-CoA reductase 1 (EC 1.2.1.n2) (Male sterility domain-containing protein 2)	Xenopus laevis (African clawed frog)
c95254_g2	Q071E0	SET8A_DANRE	N-lysine methyltransferase SETD8-A (EC 2.1.1.-) (Histone-lysine N-methyltransferase SETD8-A) (EC 2.1.1.43) (SET domain-containing protein 8-A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95285_g2	Q8R5F7	IFIH1_MOUSE	Interferon-induced helicase C domain-containing protein 1 (EC 3.6.4.13) (Helicase with 2 CARD domains) (Helicard) (Interferon induced with helicase C domain protein 1) (Melanoma differentiation-associated protein 5) (MDA-5) (RIG-I-like receptor 2) (RLR-2)	Mus musculus (Mouse)

c95334_g6	Q14435	GALT3_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 3 (EC 2.4.1.41) (Polypeptide GalNAc transferase 3) (GalNAc-T3) (pp-GaNTase 3) (Protein-UDP acetylgalactosaminyltransferase 3) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 3)	Homo sapiens (Human)
c95339_g2	Q8QFV0	KCNT1_CHICK	Potassium channel subfamily T member 1 (Sequence like a calcium-activated potassium channel subunit)	Gallus gallus (Chicken)
c95340_g4	P17085	IGF1_ONCKI	Insulin-like growth factor I (IGF-I) (Somatomedin)	Oncorhynchus kisutch (Coho salmon) (Salmo kisutch)
c95364_g1	Q5RCC5	GBRA2_PONAB	Gamma-aminobutyric acid receptor subunit alpha-2 (GABA(A) receptor subunit alpha-2)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c95371_g2	Q92614	MY18A_HUMAN	Unconventional myosin-XVIIIa (Molecule associated with JAK3 N-terminus) (MAJN) (Myosin containing a PDZ domain)	Homo sapiens (Human)
c95379_g4	Q9JI35	HRH3_CAVPO	Histamine H3 receptor (H3R) (HH3R)	Cavia porcellus (Guinea pig)
c95384_g4	Q6NRL1	AGAP1_XENLA	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1 (AGAP-1) (Centaurin-gamma-2) (Cnt-g2)	Xenopus laevis (African clawed frog)
c95391_g1	Q62415	ASPP1_MOUSE	Apoptosis-stimulating of p53 protein 1 (Protein phosphatase 1 regulatory subunit 13B)	Mus musculus (Mouse)
c95397_g1	Q5RCY9	SCAM4_PONAB	Secretory carrier-associated membrane protein 4 (Secretory carrier membrane protein 4)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c95398_g6	Q8JFF3	MKRN1_SERQU	Probable E3 ubiquitin-protein ligase makorin-1 (EC 6.3.2.-)	Seriola quinqueradiata (Five-ray yellowtail)
c95402_g1	Q6NYK8	MARH5_DANRE	E3 ubiquitin-protein ligase MARCH5 (EC 6.3.2.-) (Membrane-associated RING finger protein 5) (Membrane-associated RING-CH protein V) (MARCH-V)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95408_g3	Q02127	PYRD_HUMAN	Dihydroorotate dehydrogenase (quinone), mitochondrial (DHODEHase) (EC 1.3.5.2) (Dihydroorotate oxidase)	Homo sapiens (Human)
c95414_g4	P78559	MAP1A_HUMAN	Microtubule-associated protein 1A (MAP-1A) (Proliferation-related protein p80) [Cleaved into: MAP1A heavy chain; MAP1 light chain LC2]	Homo sapiens (Human)
c95419_g4	P01904	HA21_MOUSE	H-2 class II histocompatibility antigen, E-D alpha chain (H2-IE-alpha)	Mus musculus (Mouse)
c95426_g6	Q6ZMQ8	LMTK1_HUMAN	Serine/threonine-protein kinase LMTK1 (EC 2.7.11.1) (Apoptosis-associated tyrosine kinase) (AATYK) (Brain apoptosis-associated tyrosine kinase) (CDK5-binding protein) (Lemur tyrosine kinase 1) (p35-binding protein)	Homo sapiens (Human)

c95444_g3	Q6K1J1	UDB31_CANFA	UDP-glucuronosyltransferase 2B31 (UDPGT 2B31) (EC 2.4.1.17)	Canis familiaris (Dog) (Canis lupus familiaris)
c95447_g1	P61107	RAB14_RAT	Ras-related protein Rab-14	Rattus norvegicus (Rat)
c95452_g1	P21579	SYT1_HUMAN	Synaptotagmin-1 (Synaptotagmin I) (Sytl) (p65)	Homo sapiens (Human)
c95490_g3	Q96JG6	CC132_HUMAN	Coiled-coil domain-containing protein 132	Homo sapiens (Human)
c95510_g8	Q0PV50	TLR3_BOSTR	Toll-like receptor 3 (CD antigen CD283)	Boselaphus tragocamelus (Nilgai)
c95512_g4	A8WGA3	LFN1L_DANRE	Leucine-rich repeat and fibronectin type III domain-containing protein 1-like protein	Danio rerio (Zebrafish) (Brachydanio rerio)
c95520_g2	P21291	CSRP1_HUMAN	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP) (CRP1) (Epididymis luminal protein 141) (HEL-141)	Homo sapiens (Human)
c95535_g2	P30044	PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial (EC 1.11.1.15) (Alu corepressor 1) (Antioxidant enzyme B166) (AOEB166) (Liver tissue 2D-page spot 71B) (PLP) (Peroxiredoxin V) (Prx-V) (Peroxisomal antioxidant enzyme) (TPx type VI) (Thioredoxin peroxidase PMP20) (Thioredoxin reductase)	Homo sapiens (Human)
c95539_g4	A3KNA5	FIL1L_DANRE	Filamin A-interacting protein 1-like	Danio rerio (Zebrafish) (Brachydanio rerio)
c95548_g4	O60294	TYW4_HUMAN	tRNA wybutosine-synthesizing protein 4 (tRNA yW-synthesizing protein 4) (EC 2.1.1.290) (EC 2.3.1.231) (Leucine carboxyl methyltransferase 2) (tRNA(Phe) (7-(3-amino-3-(methoxycarbonyl)propyl)wyosine(37)-N-methoxycarbonyltransferase) (tRNA(Phe) (7-(3-amino-3-carboxypropyl)wyosine(37)-O)-methyltransferase)	Homo sapiens (Human)
c95599_g3	P11369	LORF2_MOUSE	LINE-1 retrotransposable element ORF2 protein (ORF2p) (Long interspersed element-1) (L1) (Retrovirus-related Pol polyprotein LINE-1) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Mus musculus (Mouse)
c95600_g8	Q14416	GRM2_HUMAN	Metabotropic glutamate receptor 2 (mGluR2)	Homo sapiens (Human)
c95627_g2	Q58EB4	HIBCH_DANRE	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (EC 3.1.2.4) (3-hydroxyisobutyryl-coenzyme A hydrolase) (HIB-CoA hydrolase) (HIBYL-CoA-H)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95630_g1	Q8R1B5	CPLX3_MOUSE	Complexin-3 (Complexin III) (CPX III)	Mus musculus (Mouse)
c95642_g4	O70628	PDE9A_MOUSE	High affinity cGMP-specific 3',5'-cyclic phosphodiesterase 9A (EC 3.1.4.35)	Mus musculus (Mouse)
c95649_g4	Q8WWN8	ARAP3_HUMAN	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 3 (Centaurin-delta-3) (Cnt-d3)	Homo sapiens (Human)

c95680_g5	Q9QYS2	GRM3_MOUSE	Metabotropic glutamate receptor 3 (mGluR3)	Mus musculus (Mouse)
c95686_g1	P16257	TSPO_RAT	Translocator protein (Mitochondrial benzodiazepine receptor) (PKBS) (Peripheral-type benzodiazepine receptor) (PBR)	Rattus norvegicus (Rat)
c95687_g1	A3QK15	AACS_DANRE	Acetoacetyl-CoA synthetase (EC 6.2.1.16)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95689_g2	Q80YV3	TRRAP_MOUSE	Transformation/transcription domain-associated protein (Tra1 homolog)	Mus musculus (Mouse)
c95713_g8	P43114	PE2R4_RAT	Prostaglandin E2 receptor EP4 subtype (PGE receptor EP4 subtype) (PGE2 receptor EP4 subtype) (Prostanoid EP4 receptor)	Rattus norvegicus (Rat)
c95756_g8	Q5RDE3	CEP70_PONAB	Centrosomal protein of 70 kDa (Cep70)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c95768_g2	O95544	NADK_HUMAN	NAD kinase (EC 2.7.1.23) (Poly(P)/ATP NAD kinase)	Homo sapiens (Human)
c95796_g2	NA			
c95807_g7	Q9R0M0	CELR2_MOUSE	Cadherin EGF LAG seven-pass G-type receptor 2 (Fleming homolog)	Mus musculus (Mouse)
c95822_g3	Q13905	RPGF1_HUMAN	Rap guanine nucleotide exchange factor 1 (CRK SH3-binding GNRFP) (Guanine nucleotide-releasing factor 2) (Protein C3G)	Homo sapiens (Human)
c95831_g9	P47934	CACP_MOUSE	Carnitine O-acetyltransferase (Carnitine acetylase) (EC 2.3.1.7) (Carnitine acetyltransferase) (CAT) (CrAT)	Mus musculus (Mouse)
c95850_g3	O70161	PI51C_MOUSE	Phosphatidylinositol 4-phosphate 5-kinase type-1 gamma (PIP5K1-gamma) (PtdIns(4)P-5-kinase 1 gamma) (EC 2.7.1.68) (Phosphatidylinositol 4-phosphate 5-kinase type I gamma) (PIP5KIgamma)	Mus musculus (Mouse)
c95856_g5	Q6DH86	C149B_DANRE	Coiled-coil domain-containing protein 149-B	Danio rerio (Zebrafish) (Brachydanio rerio)
c95908_g7	Q12873	CHD3_HUMAN	Chromodomain-helicase-DNA-binding protein 3 (CHD-3) (EC 3.6.4.12) (ATP-dependent helicase CHD3) (Mi-2 autoantigen 240 kDa protein) (Mi2-alpha) (Zinc finger helicase) (hZFH)	Homo sapiens (Human)
c95909_g4	Q9NVA1	UQCC1_HUMAN	Ubiquinol-cytochrome-c reductase complex assembly factor 1 (Basic FGF-repressed Zic-binding protein) (bFGF-repressed Zic-binding protein) (bFZb) (Ubiquinol-cytochrome c reductase complex chaperone CBP3 homolog)	Homo sapiens (Human)
c95935_g3	Q24K12	GPTC1_BOVIN	G patch domain-containing protein 1	Bos taurus (Bovine)

c95937_g3	O43847	NRDC_HUMAN	Nardilysin (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C)	Homo sapiens (Human)
c95948_g5	P30999	CTND1_MOUSE	Catenin delta-1 (Cadherin-associated Src substrate) (CAS) (p120 catenin) (p120(ctn)) (p120(cas))	Mus musculus (Mouse)
c95968_g1	Q90X49	CCD80_DANRE	Coiled-coil domain-containing protein 80	Danio rerio (Zebrafish) (Brachydanio rerio)
c95978_g4	Q5F488	MAGI3_CHICK	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 (Membrane-associated guanylate kinase inverted 3) (MAGI-3)	Gallus gallus (Chicken)
c95981_g2	O70352	CD82_RAT	CD82 antigen (Metastasis suppressor Kangai-1 homolog) (CD antigen CD82)	Rattus norvegicus (Rat)
c95985_g4	P35436	NMDE1_MOUSE	Glutamate receptor ionotropic, NMDA 2A (GluN2A) (Glutamate [NMDA] receptor subunit epsilon-1) (N-methyl D-aspartate receptor subtype 2A) (NMDAR2A) (NR2A)	Mus musculus (Mouse)
c95993_g2	Q5BLE8	RETST_DANRE	Putative all-trans-retinol 13,14-reductase (EC 1.3.99.23) (All-trans-13,14-dihydroretinol saturase) (RetSat)	Danio rerio (Zebrafish) (Brachydanio rerio)
c95995_g2	Q9Z0R6	ITSN2_MOUSE	Intersectin-2 (EH domain and SH3 domain regulator of endocytosis 2) (EH and SH3 domains protein 2) (SH3 domain-containing protein 1B)	Mus musculus (Mouse)
c95995_g3	P31409	VATB_DROME	V-type proton ATPase subunit B (V-ATPase subunit B) (V-ATPase 55 kDa subunit) (Vacuolar proton pump subunit B)	Drosophila melanogaster (Fruit fly)
c95999_g4	O60282	KIF5C_HUMAN	Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific 2)	Homo sapiens (Human)
c96001_g1	Q642M9	DHDH_DANRE	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase (EC 1.3.1.20) (D-xylose 1-dehydrogenase) (D-xylose-NADP dehydrogenase) (EC 1.1.1.179) (Dimeric dihydrodiol dehydrogenase)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96003_g1	O70318	E41L2_MOUSE	Band 4.1-like protein 2 (Generally expressed protein 4.1) (4.1G)	Mus musculus (Mouse)
c96005_g4	Q6P1D5	SE6L1_MOUSE	Seizure 6-like protein (Acupuncture-induced protein 1-L) (Brain-specific receptor-like protein B) (BSRP-B)	Mus musculus (Mouse)
c96007_g3	Q8CFI0	NED4L_MOUSE	E3 ubiquitin-protein ligase NEDD4-like (EC 6.3.2.-) (NEDD4.2) (Nedd4-2)	Mus musculus (Mouse)
c96013_g2	Q96AZ1	MT21B_HUMAN	Protein-lysine methyltransferase METTL21B (EC 2.1.1.-) (Hepatocellular carcinoma-associated antigen 557a) (Methyltransferase-like protein 21B)	Homo sapiens (Human)
c96041_g2	Q5VVB8	TM244_HUMAN	Transmembrane protein 244	Homo sapiens (Human)
c96042_g1	Q7ZUW2	HYOU1_DANRE	Hypoxia up-regulated protein 1	Danio rerio (Zebrafish) (Brachydanio rerio)

c96070_g5	Q6DV14	PRDX1_GECJA	Peroxiredoxin-1 (EC 1.11.1.15)	Gecko japonicus (Japanese gecko)
c96078_g9	Q9W7J1	SE3AA_DANRE	Semaphorin-3aa (Semaphorin-1A) (Semaphorin-Z1A) (Sema Z1A)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96079_g2	Q05BV3	EMAL5_HUMAN	Echinoderm microtubule-associated protein-like 5 (EMAP-5)	Homo sapiens (Human)
c96092_g1	Q9NUP7	TRM13_HUMAN	tRNA:m(4)X modification enzyme TRM13 homolog (EC 2.1.1.225) (Coiled-coil domain-containing protein 76)	Homo sapiens (Human)
c96093_g2	Q14CH7	SYAM_MOUSE	Alanine--tRNA ligase, mitochondrial (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS)	Mus musculus (Mouse)
c96097_g3	Q8R5B6	SPSB4_MOUSE	SPRY domain-containing SOCS box protein 4 (SSB-4)	Mus musculus (Mouse)
c96106_g1	Q17RM4	CC142_HUMAN	Coiled-coil domain-containing protein 142	Homo sapiens (Human)
c96141_g2	B5X1P9	F175A_SALSA	BRCA1-A complex subunit Abraxas (Coiled-coil domain-containing protein 98) (Protein FAM175A)	Salmo salar (Atlantic salmon)
c96150_g2	P49697	EM55_TAKRU	55 kDa erythrocyte membrane protein (p55) (Membrane protein, palmitoylated 1)	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c96151_g3	Q6DIC0	SMCA2_MOUSE	Probable global transcription activator SNF2L2 (EC 3.6.4.-) (ATP-dependent helicase SMARCA2) (BRG1-associated factor 190B) (BAF190B) (Protein brahma homolog) (SNF2-alpha) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 2)	Mus musculus (Mouse)
c96159_g3	Q01433	AMPD2_HUMAN	AMP deaminase 2 (EC 3.5.4.6) (AMP deaminase isoform L)	Homo sapiens (Human)
c96159_g4	Q02356	AMPD2_RAT	AMP deaminase 2 (EC 3.5.4.6) (AMP deaminase isoform L)	Rattus norvegicus (Rat)
c96174_g1	Q9NW07	ZN358_HUMAN	Zinc finger protein 358	Homo sapiens (Human)
c96175_g3	O19477	HMR1_RAT	Major histocompatibility complex class I-related gene protein (MHC class I-related gene protein)	Rattus norvegicus (Rat)
c96175_g4	P15979	HA1F_CHICK	Class I histocompatibility antigen, F10 alpha chain (B-F histocompatibility F10 antigen) (B-F-beta-IV) (B12)	Gallus gallus (Chicken)
c96180_g3	O00750	P3C2B_HUMAN	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta (PI3K-C2-beta) (PtdIns-3-kinase C2 subunit beta) (EC 2.7.1.154) (C2-PI3K) (Phosphoinositide 3-kinase-C2-beta)	Homo sapiens (Human)
c96187_g1	Q09014	NCF1_MOUSE	Neutrophil cytosol factor 1 (NCF-1) (47 kDa neutrophil oxidase factor) (NCF-47K) (Neutrophil NADPH oxidase factor 1) (p47-phox)	Mus musculus (Mouse)
c96190_g3	Q90669	AVR2A_CHICK	Activin receptor type-2A (EC 2.7.11.30) (Activin receptor type IIA) (ACTR-IIA) (ACTRIIA)	Gallus gallus (Chicken)

c96199_g6	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c96201_g1	Q6NTL4	GRP1_XENLA	RAS guanyl-releasing protein 1	Xenopus laevis (African clawed frog)
c96206_g7	P05696	KPCA_RAT	Protein kinase C alpha type (PKC-A) (PKC-alpha) (EC 2.7.11.13)	Rattus norvegicus (Rat)
c96212_g5	Q6ZSJ9	SHSA6_HUMAN	Protein shisa-6 homolog	Homo sapiens (Human)
c96223_g11	Q5RAF0	NUDT4_PONAB	Diphosphoinositol polyphosphate phosphohydrolase 2 (DIPP-2) (EC 3.6.1.52) (Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase 2) (EC 3.6.1.-) (Nucleoside diphosphate-linked moiety X motif 4) (Nudix motif 4)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c96229_g1	Q62108	DLG4_MOUSE	Disks large homolog 4 (Postsynaptic density protein 95) (PSD-95) (Synapse-associated protein 90) (SAP-90) (SAP90)	Mus musculus (Mouse)
c96244_g7	Q7ZXX1	CADM3_XENLA	Cell adhesion molecule 3 (Immunoglobulin superfamily member 4B) (IgSF4B)	Xenopus laevis (African clawed frog)
c96252_g2	Q6NUT7	SORT1_DANRE	Sortilin	Danio rerio (Zebrafish) (Brachydanio rerio)
c96271_g2	Q9WTP0	E41L1_RAT	Band 4.1-like protein 1 (Neuronal protein 4.1) (4.1N)	Rattus norvegicus (Rat)
c96281_g6	P51689	ARSD_HUMAN	Arylsulfatase D (ASD) (EC 3.1.6.-)	Homo sapiens (Human)
c96288_g4	P10394	POL4_DROME	Retrovirus-related Pol polyprotein from transposon 412 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c96293_g5	O35344	IMA4_MOUSE	Importin subunit alpha-4 (Importin alpha Q2) (Qip2) (Karyopherin subunit alpha-3)	Mus musculus (Mouse)
c96313_g2	Q99985	SEM3C_HUMAN	Semaphorin-3C (Semaphorin-E) (Sema E)	Homo sapiens (Human)
c96340_g1	P38919	IF4A3_HUMAN	Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (EC 3.6.4.13) (ATP-dependent RNA helicase DDX48) (ATP-dependent RNA helicase eIF4A-3) (DEAD box protein 48) (Eukaryotic initiation factor 4A-like NUK-34) (Eukaryotic translation initiation factor 4A isoform 3) (Nuclear matrix protein 265) (NMP 265) (hNMP 265) [Cleaved into: Eukaryotic initiation factor 4A-III, N-terminally processed]	Homo sapiens (Human)
c96342_g1	Q8AV58	SDK1_CHICK	Protein sidekick-1	Gallus gallus (Chicken)
c96370_g1	O43155	FLRT2_HUMAN	Leucine-rich repeat transmembrane protein FLRT2 (Fibronectin-like domain-containing leucine-rich transmembrane protein 2)	Homo sapiens (Human)

c96381_g3	P0C6R4	IFFO2_RAT	Intermediate filament family orphan 2	Rattus norvegicus (Rat)
c96384_g1	Q9NZJ4	SACS_HUMAN	Sacsin (DnaJ homolog subfamily C member 29) (DNAJC29)	Homo sapiens (Human)
c96389_g2	Q62415	ASPP1_MOUSE	Apoptosis-stimulating of p53 protein 1 (Protein phosphatase 1 regulatory subunit 13B)	Mus musculus (Mouse)
c96401_g11	Q6PH57	GBB1_DANRE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Transducin beta chain 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96406_g10	Q9H156	SLIK2_HUMAN	SLIT and NTRK-like protein 2	Homo sapiens (Human)
c96423_g3	A2CEQ0	SCM2B_DANRE	Calcium-binding mitochondrial carrier protein SCaMC-2-B (Small calcium-binding mitochondrial carrier protein 2-B) (Solute carrier family 25 member 25-B)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96427_g1	P47859	PFKAP_RABIT	ATP-dependent 6-phosphofructokinase, platelet type (ATP-PFK) (PFK-P) (EC 2.7.1.11) (6-phosphofructokinase type C) (Phosphofructo-1-kinase isozyme C) (PFK-C) (Phosphohexokinase)	Oryctolagus cuniculus (Rabbit)
c96442_g2	P50904	RASA1_RAT	Ras GTPase-activating protein 1 (GAP) (GTPase-activating protein) (RasGAP) (Ras p21 protein activator) (p120GAP)	Rattus norvegicus (Rat)
c96447_g5	Q1JP79	ARC1A_BOVIN	Actin-related protein 2/3 complex subunit 1A	Bos taurus (Bovine)
c96458_g2	Q8BGW6	ST32A_MOUSE	Serine/threonine-protein kinase 32A (EC 2.7.11.1)	Mus musculus (Mouse)
c96461_g1	Q8K4Y7	CANT1_RAT	Soluble calcium-activated nucleotidase 1 (SCAN-1) (EC 3.6.1.6) (Apyrase homolog)	Rattus norvegicus (Rat)
c96469_g3	P10073	ZSC22_HUMAN	Zinc finger and SCAN domain-containing protein 22 (Krueppel-related zinc finger protein 2) (Protein HKR2) (Zinc finger protein 50)	Homo sapiens (Human)
c96476_g3	Q9YGM4	CAMKV_TAKRU	CaM kinase-like vesicle-associated protein	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)
c96492_g2	Q4ZIN3	MBRL_HUMAN	Membralin (Transmembrane protein 259)	Homo sapiens (Human)
c96505_g1	Q9JJN6	CNBP1_MOUSE	Beta-catenin-interacting protein 1 (Inhibitor of beta-catenin and Tcf-4)	Mus musculus (Mouse)
c96522_g4	Q92038	ACOD_CYPCA	Acyl-CoA desaturase (EC 1.14.19.1) (Delta(9)-desaturase) (Delta-9 desaturase) (Fatty acid desaturase) (Stearoyl-CoA desaturase)	Cyprinus carpio (Common carp)
c96529_g2	A4D2P6	GRD2I_HUMAN	Delphilin (Glutamate receptor, ionotropic, delta 2-interacting protein 1)	Homo sapiens (Human)
c96540_g3	Q9JIX8	ACINU_MOUSE	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	Mus musculus (Mouse)
c96546_g4	P24524	GLRA3_RAT	Glycine receptor subunit alpha-3	Rattus norvegicus (Rat)

c96551_g11	F1QW76	BATF_DANRE	Basic leucine zipper transcriptional factor ATF-like (B-cell-activating transcription factor) (B-ATF)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96551_g12	O08849	RGS2_MOUSE	Regulator of G-protein signaling 2 (RGS2)	Mus musculus (Mouse)
c96571_g1	Q9UBC2	EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1 (Eps15-related protein) (Eps15R)	Homo sapiens (Human)
c96577_g2	P08548	LIN1_NYCCO	LINE-1 reverse transcriptase homolog (EC 2.7.7.49)	Nycticebus coucang (Slow loris)
c96584_g3	P39872	RL3_BOVIN	60S ribosomal protein L3	Bos taurus (Bovine)
c96592_g2	P46197	ANPRB_BOVIN	Atrial natriuretic peptide receptor 2 (EC 4.6.1.2) (Atrial natriuretic peptide receptor type B) (ANP-B) (ANPR-B) (NPR-B) (Guanylate cyclase B) (GC-B)	Bos taurus (Bovine)
c96601_g3	Q5RDL3	SGIP1_PONAB	SH3-containing GRB2-like protein 3-interacting protein 1 (Endophilin-3-interacting protein)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c96625_g3	Q98TZ8	FLOT2_DANRE	Flotillin-2a (Reggie-1a) (REG-1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96630_g2	P19540	FA9_CANFA	Coagulation factor IX (EC 3.4.21.22) (Christmas factor) [Cleaved into: Coagulation factor IXa light chain; Coagulation factor IXa heavy chain]	Canis familiaris (Dog) (Canis lupus familiaris)
c96636_g4	Q8BGD8	COA6_MOUSE	Cytochrome c oxidase assembly factor 6 homolog	Mus musculus (Mouse)
c96653_g4	Q15772	SPEG_HUMAN	Striated muscle preferentially expressed protein kinase (EC 2.7.11.1) (Aortic preferentially expressed protein 1) (APEG-1)	Homo sapiens (Human)
c96661_g1	A4QP73	TTC19_DANRE	Tetratricopeptide repeat protein 19, mitochondrial (TPR repeat protein 19)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96670_g2	Q8NDA8	MROH1_HUMAN	Maestro heat-like repeat-containing protein family member 1 (HEAT repeat-containing protein 7A)	Homo sapiens (Human)
c96675_g5	Q8BI06	CEMIP_MOUSE	Cell migration-inducing and hyaluronan-binding protein (EC 3.2.1.35) (Protein 12H19.01.T7)	Mus musculus (Mouse)
c96690_g2	Q9VP48	RAB26_DROME	Ras-related protein Rab-26	Drosophila melanogaster (Fruit fly)
c96690_g3	O08705	NTCP_MOUSE	Sodium/bile acid cotransporter (Na(+)/bile acid cotransporter) (Na(+)/taurocholate transport protein) (Sodium/taurocholate cotransporting polypeptide) (Solute carrier family 10 member 1)	Mus musculus (Mouse)
c96699_g2	P09849	LPH_RABIT	Lactase-phlorizin hydrolase (Lactase-glycosylceramidase) [Includes: Lactase (EC 3.2.1.108); Phlorizin hydrolase (EC 3.2.1.62)]	Oryctolagus cuniculus (Rabbit)

c96701_g3	Q9Y2Y9	KLF13_HUMAN	Krueppel-like factor 13 (Basic transcription element-binding protein 3) (BTE-binding protein 3) (Novel Sp1-like zinc finger transcription factor 1) (RANTES factor of late activated T-lymphocytes 1) (RFLAT-1) (Transcription factor BTEB3) (Transcription factor NSLP1)	Homo sapiens (Human)
c96705_g2	P0C6C1	AN34C_HUMAN	Ankyrin repeat domain-containing protein 34C	Homo sapiens (Human)
c96728_g5	O09126	SEM4D_MOUSE	Semaphorin-4D (M-Sema G) (Semaphorin-C-like 2) (Semaphorin-J) (Sema J) (CD antigen CD100)	Mus musculus (Mouse)
c96743_g3	Q8C120	SH3R3_MOUSE	SH3 domain-containing RING finger protein 3 (Plenty of SH3s 2) (SH3 multiple domains protein 4)	Mus musculus (Mouse)
c96744_g9	Q76N89	HECW1_HUMAN	E3 ubiquitin-protein ligase HECW1 (EC 6.3.2.-) (HECT, C2 and WW domain-containing protein 1) (NEDD4-like E3 ubiquitin-protein ligase 1) (hNEDL1)	Homo sapiens (Human)
c96756_g6	Q9Y3M8	STA13_HUMAN	StAR-related lipid transfer protein 13 (46H23.2) (Deleted in liver cancer 2 protein) (DLC-2) (Rho GTPase-activating protein) (START domain-containing protein 13) (StARD13)	Homo sapiens (Human)
c96757_g3	Q9HCJ2	LRC4C_HUMAN	Leucine-rich repeat-containing protein 4C (Netrin-G1 ligand) (NGL-1)	Homo sapiens (Human)
c96758_g4	Q5ZMD6	H2AZ_CHICK	Histone H2A.Z (H2A/z)	Gallus gallus (Chicken)
c96764_g6	O00408	PDE2A_HUMAN	cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic GMP-stimulated phosphodiesterase) (CGS-PDE) (cGSPDE)	Homo sapiens (Human)
c96787_g2	Q501Z5	GTPB3_DANRE	tRNA modification GTPase GTPBP3, mitochondrial (GTP-binding protein 3)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96792_g1	P35953	VLDLR_RABIT	Very low-density lipoprotein receptor (VLDL receptor) (VLDL-R)	Oryctolagus cuniculus (Rabbit)
c96797_g2	Q6P9K8	CSKI1_MOUSE	Caskin-1 (CASK-interacting protein 1)	Mus musculus (Mouse)
c96802_g2	B4DXR9	ZN732_HUMAN	Zinc finger protein 732	Homo sapiens (Human)
c96813_g5	P51121	GLNA_XENLA	Glutamine synthetase (GS) (EC 6.3.1.2) (Glutamate decarboxylase) (EC 4.1.1.15) (Glutamate--ammonia ligase)	Xenopus laevis (African clawed frog)
c96826_g7	Q15596	NCOA2_HUMAN	Nuclear receptor coactivator 2 (NCoA-2) (Class E basic helix-loop-helix protein 75) (bHLHe75) (Transcriptional intermediary factor 2) (hTIF2)	Homo sapiens (Human)
c96832_g3	Q9Y2I7	FYV1_HUMAN	1-phosphatidylinositol 3-phosphate 5-kinase (Phosphatidylinositol 3-phosphate 5-kinase) (EC 2.7.1.150) (FYVE finger-containing phosphoinositide kinase) (PIKfyve) (Phosphatidylinositol 3-phosphate 5-kinase type III) (PIPkin-III) (Type III PIP kinase)	Homo sapiens (Human)

c96834_g1	Q5MPA9	DCLK2_RAT	Serine/threonine-protein kinase DCLK2 (EC 2.7.11.1) (CaMK-like CREB regulatory kinase 2) (CL2) (CLICK-II) (CLICK2) (Doublecortin-like and CAM kinase-like 2) (Doublecortin-like kinase 2)	Rattus norvegicus (Rat)
c96838_g3	Q28085	CFAH_BOVIN	Complement factor H (H factor 1)	Bos taurus (Bovine)
c96838_g4	P08603	CFAH_HUMAN	Complement factor H (H factor 1)	Homo sapiens (Human)
c96860_g6	O55005	ROBO1_RAT	Roundabout homolog 1	Rattus norvegicus (Rat)
c96877_g2	P18910	ANPRA_RAT	Atrial natriuretic peptide receptor 1 (EC 4.6.1.2) (Atrial natriuretic peptide receptor type A) (ANP-A) (ANPR-A) (NPR-A) (Guanylate cyclase A) (GC-A)	Rattus norvegicus (Rat)
c96892_g4	P83900	RPGF5_RAT	Rap guanine nucleotide exchange factor 5 (M-Ras-regulated Rap GEF) (MR-GEF) (rMR-GEF)	Rattus norvegicus (Rat)
c96915_g2	Q5VWW1	C1QL3_HUMAN	Complement C1q-like protein 3 (C1q and tumor necrosis factor-related protein 13) (C1q/TNF-related protein 13)	Homo sapiens (Human)
c96928_g2	Q8K4G1	LTBP4_MOUSE	Latent-transforming growth factor beta-binding protein 4 (LTBP-4)	Mus musculus (Mouse)
c96966_g1	Q8JHW2	TSP3A_DANRE	Thrombospondin-3a (Thbs3a)	Danio rerio (Zebrafish) (Brachydanio rerio)
c96968_g3	P13020	GELS_MOUSE	Gelsolin (Actin-depolymerizing factor) (ADF) (Brevin)	Mus musculus (Mouse)
c96989_g4	Q9JLA3	UGGG1_RAT	UDP-glucose:glycoprotein glucosyltransferase 1 (UGT1) (rUGT1) (EC 2.4.1.-) (UDP--Glc:glycoprotein glucosyltransferase) (UDP-glucose ceramide glucosyltransferase-like 1)	Rattus norvegicus (Rat)
c96994_g3	P41585	PACA_ONCNE	Glucagon family neuropeptides [Cleaved into: Growth hormone-releasing factor (GRF) (Growth hormone-releasing hormone) (GHRH); Pituitary adenylate cyclase-activating polypeptide (PACAP)]	Oncorhynchus nerka (Sockeye salmon) (Salmo nerka)
c96997_g3	Q6UVM3	KCNT2_HUMAN	Potassium channel subfamily T member 2 (Sequence like an intermediate conductance potassium channel subunit) (Sodium and chloride-activated ATP-sensitive potassium channel Slo2.1)	Homo sapiens (Human)
c97053_g2	P01897	HA1L_MOUSE	H-2 class I histocompatibility antigen, L-D alpha chain	Mus musculus (Mouse)
c97057_g5	Q8R0N9	ZDHC1_MOUSE	Probable palmitoyltransferase ZDHHC1 (EC 2.3.1.225) (Zinc finger DHHC domain-containing protein 1) (DHHC-1)	Mus musculus (Mouse)
c97059_g2	Q7RTR2	NLRC3_HUMAN	Protein NLRC3 (CARD15-like protein) (Caterpillar protein 16.2) (CLR16.2) (Nucleotide-binding oligomerization domain protein 3)	Homo sapiens (Human)

c97066_g3	P56974	NRG2_MOUSE	Pro-neuregulin-2, membrane-bound isoform (Pro-NRG2) [Cleaved into: Neuregulin-2 (NRG-2) (Divergent of neuregulin 1) (DON-1)]	Mus musculus (Mouse)
c97119_g2	Q5VU43	MYOME_HUMAN	Myomegalin (Cardiomyopathy-associated protein 2) (Phosphodiesterase 4D-interacting protein)	Homo sapiens (Human)
c97125_g3	Q91987	NTRK2_CHICK	BDNF/NT-3 growth factors receptor (EC 2.7.10.1) (Neurotrophic tyrosine kinase receptor type 2) (TrkB tyrosine kinase) (Trk-B)	Gallus gallus (Chicken)
c97129_g1	P20825	POL2_DROME	Retrovirus-related Pol polyprotein from transposon 297 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97152_g2	O14832	PAHX_HUMAN	Phytanoyl-CoA dioxygenase, peroxisomal (EC 1.14.11.18) (Phytanic acid oxidase) (Phytanoyl-CoA alpha-hydroxylase) (PhyH)	Homo sapiens (Human)
c97153_g5	Q9Y5F6	PCDGM_HUMAN	Protocadherin gamma-C5 (PCDH-gamma-C5)	Homo sapiens (Human)
c97163_g2	Q9QXH4	ITAX_MOUSE	Integrin alpha-X (CD11 antigen-like family member C) (Leukocyte adhesion glycoprotein p150,95 alpha chain) (Leukocyte adhesion receptor p150,95) (CD antigen CD11c)	Mus musculus (Mouse)
c97188_g3	Q96BR1	SGK3_HUMAN	Serine/threonine-protein kinase Sgk3 (EC 2.7.11.1) (Cytokine-independent survival kinase) (Serum/glucocorticoid-regulated kinase 3) (Serum/glucocorticoid-regulated kinase-like)	Homo sapiens (Human)
c97190_g5	Q58A65	JIP4_MOUSE	C-Jun-amino-terminal kinase-interacting protein 4 (JIP-4) (JNK-interacting protein 4) (JNK-associated leucine-zipper protein) (JLP) (JNK/SAPK-associated protein 2) (JSAP2) (Mitogen-activated protein kinase 8-interacting protein 4) (Sperm-associated antigen 9)	Mus musculus (Mouse)
c97194_g2	O55187	CBX4_MOUSE	E3 SUMO-protein ligase CBX4 (EC 6.3.2.-) (Chromobox protein homolog 4) (Polycomb 2 homolog) (Pc2) (mPc2)	Mus musculus (Mouse)
c97210_g4	E9Q5R7	NAL12_MOUSE	NACHT, LRR and PYD domains-containing protein 12 (Monarch-1) (PYRIN-containing APAF1-like protein 7) (PYPAF7)	Mus musculus (Mouse)
c97214_g1	P70175	DLG3_MOUSE	Disks large homolog 3 (Synapse-associated protein 102) (SAP-102) (SAP102)	Mus musculus (Mouse)
c97232_g5	P48435	SOX11_CHICK	Transcription factor SOX-11 (cSox11)	Gallus gallus (Chicken)
c97234_g2	P34057	RECO_MOUSE	Recoverin (23 kDa photoreceptor cell-specific protein) (Cancer-associated retinopathy protein) (Protein CAR)	Mus musculus (Mouse)
c97255_g2	O75970	MPDZ_HUMAN	Multiple PDZ domain protein (Multi-PDZ domain protein 1)	Homo sapiens (Human)

c97266_g8	Q9HAU0	PKHA5_HUMAN	Pleckstrin homology domain-containing family A member 5 (PH domain-containing family A member 5) (Phosphoinositol 3-phosphate-binding protein 2) (PEPP-2)	Homo sapiens (Human)
c97273_g1	Q8BHY3	ANO1_MOUSE	Anoctamin-1 (Transmembrane protein 16A)	Mus musculus (Mouse)
c97276_g1	P35953	VLDLR_RABIT	Very low-density lipoprotein receptor (VLDL receptor) (VLDL-R)	Oryctolagus cuniculus (Rabbit)
c97286_g1	Q8BGS2	BOLA2_MOUSE	BolA-like protein 2	Mus musculus (Mouse)
c97290_g6	A1L1P9	S47A1_DANRE	Multidrug and toxin extrusion protein 1 (MATE-1) (Solute carrier family 47 member 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97295_g4	P10394	POL4_DROME	Retrovirus-related Pol polyprotein from transposon 412 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97339_g1	A0JM08	C170B_XENTR	Centrosomal protein of 170 kDa protein B (Centrosomal protein 170B) (Cep170B)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c97341_g1	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c97341_g2	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c97345_g1	Q9NBX4	RTXE_DROME	Probable RNA-directed DNA polymerase from transposon X-element (EC 2.7.7.49) (Reverse transcriptase)	Drosophila melanogaster (Fruit fly)
c97349_g1	P03934	TC1A_CAEEL	Transposable element Tc1 transposase	Caenorhabditis elegans
c97354_g1	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97355_g2	Q566X6	PTCD2_DANRE	Pentatricopeptide repeat-containing protein 2, mitochondrial	Danio rerio (Zebrafish) (Brachydanio rerio)
c97367_g1	O92815	POL_WDSV	Gag-Pol polyprotein [Cleaved into: Matrix protein p10 (MA); p20; Capsid protein p25 (CA); Nucleocapsid protein p14 (NC-pol); Protease p15 (PR) (EC 3.4.23.-); Reverse transcriptase/ribonuclease H p90 (RT) (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4); Integrase p46 (IN)]	Walleye dermal sarcoma virus (WDSV)
c97371_g1	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c97373_g2	O60292	SI1L3_HUMAN	Signal-induced proliferation-associated 1-like protein 3 (SIPA1-like protein 3) (SPA-1-like protein 3)	Homo sapiens (Human)

c97384_g1	O73700	CAC1D_CHICK	Voltage-dependent L-type calcium channel subunit alpha-1D (CHCACHA1D) (Voltage-gated calcium channel subunit alpha Cav1.3)	Gallus gallus (Chicken)
c97389_g2	Q92887	MRP2_HUMAN	Canalicular multispecific organic anion transporter 1 (ATP-binding cassette sub-family C member 2) (Canalicular multidrug resistance protein) (Multidrug resistance-associated protein 2)	Homo sapiens (Human)
c97399_g1	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)
c97404_g1	P0CT34	TF21_SCHPO	Transposon Tf2-1 polyprotein (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c97406_g1	Q9CPW0	CNTP2_MOUSE	Contactin-associated protein-like 2 (Cell recognition molecule Caspr2)	Mus musculus (Mouse)
c97408_g2	O14513	NCKP5_HUMAN	Nck-associated protein 5 (NAP-5) (Peripheral clock protein)	Homo sapiens (Human)
c97410_g2	P20825	POL2_DROME	Retrovirus-related Pol polyprotein from transposon 297 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97419_g4	P29804	ODPA_PIG	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (EC 1.2.4.1) (PDHE1-A type I) (Fragment)	Sus scrofa (Pig)
c97428_g1	Q1LVF0	LAMC1_DANRE	Laminin subunit gamma-1	Danio rerio (Zebrafish) (Brachydanio rerio)
c97437_g5	Q81010	VP37D_MOUSE	Vacuolar protein sorting-associated protein 37D (ESCRT-I complex subunit VPS37D) (Williams-Beuren syndrome region protein 24 homolog)	Mus musculus (Mouse)
c97441_g4	P35285	RB22A_MOUSE	Ras-related protein Rab-22A (Rab-22) (Rab-14)	Mus musculus (Mouse)
c97449_g1	Q28DA8	LETM2_XENTR	LETM1 domain-containing protein LETM2, mitochondrial (LETM1 and EF-hand domain-containing protein 2) (Leucine zipper-EF-hand-containing transmembrane protein 1-like)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c97460_g1	P08548	LIN1_NYCCO	LINE-1 reverse transcriptase homolog (EC 2.7.7.49)	Nycticebus coucang (Slow loris)
c97463_g3	P49946	FRIH_SALSA	Ferritin, heavy subunit (Ferritin H) (EC 1.16.3.1)	Salmo salar (Atlantic salmon)
c97470_g2	Q8NFT2	STEAP2_HUMAN	Metalloreductase STEAP2 (EC 1.16.1.-) (Prostate cancer-associated protein 1) (Protein up-regulated in metastatic prostate cancer) (PUMPCn) (Six-transmembrane epithelial antigen of prostate 2)	Homo sapiens (Human)

c97479_g1	B8PYG1	NSMF_DANRE	NMDA receptor synaptonuclear signaling and neuronal migration factor (Nasal embryonic luteinizing hormone-releasing hormone factor) (Nasal embryonic LHRH factor)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97493_g1	P0CT41	TF212_SCHPO	Transposon Tf2-12 polyprotein (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c97493_g2	Q7TN75	PEG10_MOUSE	Retrotransposon-derived protein PEG10 (Embryonal carcinoma differentiation regulated protein) (Mammalian retrotransposon-derived protein 2) (Myelin expression factor 3) (MyEF-3) (Myelin expression factor 3-like protein 1) (MEF3-like protein 1) (Paternaly expressed gene 10 protein) (Retrotransposon gag domain-containing protein 3) (Retrotransposon-derived gag-like polyprotein) (Ty3/Gypsy-like protein)	Mus musculus (Mouse)
c97493_g3	P0CT41	TF212_SCHPO	Transposon Tf2-12 polyprotein (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c97495_g1	O92815	POL_WDSV	Gag-Pol polyprotein [Cleaved into: Matrix protein p10 (MA); p20; Capsid protein p25 (CA); Nucleocapsid protein p14 (NC-pol); Protease p15 (PR) (EC 3.4.23.-); Reverse transcriptase/ribonuclease H p90 (RT) (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4); Integrase p46 (IN)]	Walleye dermal sarcoma virus (WDSV)
c97499_g1	Q7L775	EPMIP_HUMAN	EPM2A-interacting protein 1 (Laforin-interacting protein)	Homo sapiens (Human)
c97503_g2	A5X7A0	SOBPA_DANRE	Sine oculis-binding protein homolog (Jackson circler protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97518_g1	P04323	POL3_DROME	Retrovirus-related Pol polyprotein from transposon 17.6 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97535_g2	Q8CDN6	TXNL1_MOUSE	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	Mus musculus (Mouse)
c97544_g1	P07751	SPTN1_CHICK	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain)	Gallus gallus (Chicken)
c97560_g1	Q7RTR2	NLRC3_HUMAN	Protein NLRC3 (CARD15-like protein) (Caterpillar protein 16.2) (CLR16.2) (Nucleotide-binding oligomerization domain protein 3)	Homo sapiens (Human)
c97565_g2	P21328	RTJK_DROME	RNA-directed DNA polymerase from mobile element jockey (EC 2.7.7.49) (Reverse transcriptase)	Drosophila melanogaster (Fruit fly)
c97567_g1	Q13332	PTPRS_HUMAN	Receptor-type tyrosine-protein phosphatase S (R-PTP-S) (EC 3.1.3.48) (Receptor-type tyrosine-protein phosphatase sigma) (R-PTP-sigma)	Homo sapiens (Human)

c97568_g2	P10394	POL4_DROME	Retrovirus-related Pol polyprotein from transposon 412 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97580_g1	Q9ZZM6	COX1_SALSA	Cytochrome c oxidase subunit 1 (EC 1.9.3.1) (Cytochrome c oxidase polypeptide I)	Salmo salar (Atlantic salmon)
c97589_g2	P83606	BMTI6_RHIMP	Kunitz-type serine protease inhibitor 6 (BmTI-6) (Fragment)	Rhipicephalus microplus (Cattle tick) (Boophilus microplus)
c97592_g2	A1Z651	POL_XMRV6	Gag-Pol polyprotein (Pr180gag-pol) [Cleaved into: Matrix protein p15 (MA); RNA-binding phosphoprotein p12 (pp12); Capsid protein p30 (CA); Nucleocapsid protein p10 (NC-pol); Protease p14 (PR) (EC 3.4.23.-); Reverse transcriptase/ribonuclease H p80 (RT) (EC 2.7.7.49) (EC 2.7.7.7) (EC 3.1.26.4); Integrase p46 (IN)]	Xenotropic MuLV-related virus (isolate VP62) (XMRV)
c97594_g1	P35072	TCB1_CAEBR	Transposable element Tcb1 transposase (Transposable element Barney transposase)	Caenorhabditis briggsae
c97596_g1	Q5RCZ2	CY561_PONAB	Cytochrome b561 (Cytochrome b-561)	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)
c97603_g1	P42684	ABL2_HUMAN	Abelson tyrosine-protein kinase 2 (EC 2.7.10.2) (Abelson murine leukemia viral oncogene homolog 2) (Abelson-related gene protein) (Tyrosine-protein kinase ARG)	Homo sapiens (Human)

Table S3.3. Significantly ($p < 0.05$) enriched GO terms in DE and CDE transcripts

DE	GO terms
Aripo DE	response to chemical, cellular modified amino acid biosynthetic process, protein homooligomerization, biosynthetic process, glycolytic process, Wnt signaling pathway, inorganic ion transmembrane transport, regulation of gene expression, translational initiation
Guanapo DE	DNA integration, antigen processing and presentation, immune response, regulation of cellular component organization, protein polymerization, translation, phosphatidylinositol metabolic process, lipid metabolic process
CDE	DNA integration, glycerophospholipid biosynthetic process, cellular modified amino acid biosynthetic process, cellular chemical homeostasis

Table S3.4. Annotation information for transcripts concordantly differentially expressed in Aripa and Guanapo datasets.

contig	SwissProt ID	SwissProt entry name	Protein name	Organism
c38121_g1	P19632	PHOS_BOVIN	Phosducin (PHD) (33 kDa phototransducing protein) (Protein MEKA)	Bos taurus (Bovine)
c72950_g1	O88382	MAGI2_RAT	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 (Atrophin-1-interacting protein 1) (AIP-1) (Membrane-associated guanylate kinase inverted 2) (MAGI-2) (Synaptic-scaffolding molecule) (S-SCAM)	Rattus norvegicus (Rat)
c81536_g1	Q8R205	ZC3HA_MOUSE	Zinc finger CCCH domain-containing protein 10	Mus musculus (Mouse)
c82971_g2	Q53GS9	SNUT2_HUMAN	U4/U6.U5 tri-snRNP-associated protein 2 (Inactive ubiquitin-specific peptidase 39) (SAD1 homolog) (U4/U6.U5 tri-snRNP-associated 65 kDa protein) (65K)	Homo sapiens (Human)
c83280_g2	Q8TD55	PKHO2_HUMAN	Pleckstrin homology domain-containing family O member 2 (PH domain-containing family O member 2) (Pleckstrin homology domain-containing family Q member 1) (PH domain-containing family Q member 1)	Homo sapiens (Human)
c84000_g2	P0C7U4	C3AR_DANRE	C3a anaphylatoxin chemotactic receptor (C3AR) (C3a-R)	Danio rerio (Zebrafish) (Brachydanio rerio)
c84983_g4	Q9NRJ7	PCDBG_HUMAN	Protocadherin beta-16 (PCDH-beta-16) (Protocadherin-3X)	Homo sapiens (Human)
c85125_g2	Q9NX07	TSAP1_HUMAN	tRNA selenocysteine 1-associated protein 1 (SECp43) (tRNA selenocysteine-associated protein 1)	Homo sapiens (Human)
c85232_g6	P63033	RHES_RAT	GTP-binding protein Rhes (Ras homolog enriched in striatum) (SE6C)	Rattus norvegicus (Rat)
c85510_g5	B6RSP1	PKHA7_DANRE	Pleckstrin homology domain-containing family A member 7 (PH domain-containing family A member 7) (Heart adapter protein 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c85572_g1	P04574	CPNS1_PIG	Calpain small subunit 1 (CSS1) (Calcium-activated neutral proteinase small subunit) (CANP small subunit) (Calcium-dependent protease small subunit) (CDPS) (Calcium-dependent protease small subunit 1) (Calpain regulatory subunit)	Sus scrofa (Pig)
c86328_g4	Q4R550	SYCC_MACFA	Cysteine--tRNA ligase, cytoplasmic (EC 6.1.1.16) (CysteinyI-tRNA synthetase) (CysRS)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)

c86589_g3	P14381	YTX2_XENLA	Transposon TX1 uncharacterized 149 kDa protein (ORF 2)	Xenopus laevis (African clawed frog)
c86632_g1	Q15937	ZNF79_HUMAN	Zinc finger protein 79 (ZNFpT7)	Homo sapiens (Human)
c86901_g3	Q6P4W7	RIC8A_XENTR	Synembryn-A (Protein Ric-8A)	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c87042_g1	P54613	2AAB_PIG	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform (PP2A subunit A isoform PR65-beta) (PP2A subunit A isoform R1-beta) (Fragment)	Sus scrofa (Pig)
c87488_g3	Q7ZW47	STAU2_DANRE	Double-stranded RNA-binding protein Staufien homolog 2	Danio rerio (Zebrafish) (Brachydanio rerio)
c88658_g3	Q5ZMP3	T184C_CHICK	Transmembrane protein 184C (Transmembrane protein 34)	Gallus gallus (Chicken)
c88785_g1	Q9I8C7	ACH10_CHICK	Neuronal acetylcholine receptor subunit alpha-10 (Alpha 10 nAChR) (Nicotinic acetylcholine receptor subunit alpha-10) (NACHR alpha-10)	Gallus gallus (Chicken)
c88792_g6	Q4R495	MFS11_MACFA	UNC93-like protein MFSD11 (Major facilitator superfamily domain-containing protein 11)	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)
c88922_g1	Q28EW0	TM87A_XENTR	Transmembrane protein 87A	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
c89296_g8	Q9EQJ9	MAGI3_MOUSE	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 (Membrane-associated guanylate kinase inverted 3) (MAGI-3)	Mus musculus (Mouse)
c89807_g5	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c89807_g6	Q9UJF2	NGAP_HUMAN	Ras GTPase-activating protein nGAP (RAS protein activator-like 2)	Homo sapiens (Human)
c90146_g2	Q5ZJ58	PI51B_CHICK	Phosphatidylinositol 4-phosphate 5-kinase type-1 beta (PIP5K1-beta) (PtdIns(4)P-5-kinase 1 beta) (EC 2.7.1.68) (Phosphatidylinositol 4-phosphate 5-kinase type I beta) (PIP5KIbeta) (Type I phosphatidylinositol 4-phosphate 5-kinase beta)	Gallus gallus (Chicken)
c90217_g3	Q8WW59	SPRY4_HUMAN	SPRY domain-containing protein 4	Homo sapiens (Human)
c90675_g3	P17810	PRPH2_BOVIN	Peripherin-2 (Retinal degeneration slow protein)	Bos taurus (Bovine)
c90675_g9	O42281	PRPH2_CHICK	Peripherin-2 (CRDS1) (Photoreceptor outer segment membrane glycoprotein 1) (Retinal degeneration slow protein)	Gallus gallus (Chicken)
c91384_g2	Q803C9	PTSS1_DANRE	Phosphatidylserine synthase 1 (PSS-1) (PtdSer synthase 1) (EC 2.7.8.29) (Serine-exchange enzyme I)	Danio rerio (Zebrafish) (Brachydanio rerio)

c91402_g3	C6K2K4	NETO2_RAT	Neuropilin and tolloid-like protein 2 (Brain-specific transmembrane protein containing 2 CUB and 1 LDL-receptor class A domains protein 2)	Rattus norvegicus (Rat)
c91696_g4	Q29RT8	LPPR2_BOVIN	Lipid phosphate phosphatase-related protein type 2 (EC 3.1.3.4) (Plasticity-related gene 4 protein) (PRG-4)	Bos taurus (Bovine)
c91696_g6	Q6GM05	LPPR5_XENLA	Lipid phosphate phosphatase-related protein type 5 (EC 3.1.3.-)	Xenopus laevis (African clawed frog)
c93339_g1	Q6P1L5	F117B_HUMAN	Protein FAM117B (Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 13 protein)	Homo sapiens (Human)
c93549_g1	Q8TEQ0	SNX29_HUMAN	Sorting nexin-29 (RUN domain-containing protein 2A)	Homo sapiens (Human)
c93561_g4	Q3V1V3	ESF1_MOUSE	ESF1 homolog (ABT1-associated protein)	Mus musculus (Mouse)
c94386_g1	Q95LD9	AHR_DELLE	Aryl hydrocarbon receptor (Ah receptor) (AhR)	Delphinapterus leucas (Beluga whale)
c94958_g1	Q9H0M0	WWP1_HUMAN	NEDD4-like E3 ubiquitin-protein ligase WWP1 (EC 6.3.2.-) (Atrophin-1-interacting protein 5) (AIP5) (TGIF-interacting ubiquitin ligase 1) (Tiul1) (WW domain-containing protein 1)	Homo sapiens (Human)
c94967_g8	P0CT34	TF21_SCHPO	Transposon Tf2-1 polypeptide (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c95122_g2	O14795	UN13B_HUMAN	Protein unc-13 homolog B (Munc13-2) (munc13)	Homo sapiens (Human)
c95599_g3	P11369	LORF2_MOUSE	LINE-1 retrotransposable element ORF2 protein (ORF2p) (Long interspersed element-1) (L1) (Retrovirus-related Pol polyprotein LINE-1) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Mus musculus (Mouse)
c95937_g3	O43847	NRDC_HUMAN	Nardilysin (EC 3.4.24.61) (N-arginine dibasic convertase) (NRD convertase) (NRD-C)	Homo sapiens (Human)
c96458_g2	Q8BGW6	ST32A_MOUSE	Serine/threonine-protein kinase 32A (EC 2.7.11.1)	Mus musculus (Mouse)
c97152_g2	O14832	PAHX_HUMAN	Phytanoyl-CoA dioxygenase, peroxisomal (EC 1.14.11.18) (Phytanic acid oxidase) (Phytanoyl-CoA alpha-hydroxylase) (PhyH)	Homo sapiens (Human)
c97273_g1	Q8BHY3	ANO1_MOUSE	Anoctamin-1 (Transmembrane protein 16A)	Mus musculus (Mouse)
c97290_g6	A1L1P9	S47A1_DANRE	Multidrug and toxin extrusion protein 1 (MATE-1) (Solute carrier family 47 member 1)	Danio rerio (Zebrafish) (Brachydanio rerio)
c97355_g2	Q566X6	PTCD2_DANRE	Pentatricopeptide repeat-containing protein 2, mitochondrial	Danio rerio (Zebrafish) (Brachydanio rerio)
c97371_g1	O00370	LORF2_HUMAN	LINE-1 retrotransposable element ORF2 protein (ORF2p) [Includes: Reverse transcriptase (EC 2.7.7.49); Endonuclease (EC 3.1.21.-)]	Homo sapiens (Human)

c97463_g3	P49946	FRIH_SALSA	Ferritin, heavy subunit (Ferritin H) (EC 1.16.3.1)	Salmo salar (Atlantic salmon)
c97493_g1	P0CT41	TF212_SCHPO	Transposon Tf2-12 polyprotein (Retrotransposable element Tf2 155 kDa protein)	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)
c97493_g2	Q7TN75	PEG10_MOUSE	Retrotransposon-derived protein PEG10 (Embryonal carcinoma differentiation regulated protein) (Mammalian retrotransposon-derived protein 2) (Myelin expression factor 3) (MyEF-3) (Myelin expression factor 3-like protein 1) (MEF3-like protein 1) (Paternaly expressed gene 10 protein) (Retrotransposon gag domain-containing protein 3) (Retrotransposon-derived gag-like polyprotein) (Ty3/Gypsy-like protein)	Mus musculus (Mouse)
c97568_g2	P10394	POL4_DROME	Retrovirus-related Pol polyprotein from transposon 412 [Includes: Protease (EC 3.4.23.-); Reverse transcriptase (EC 2.7.7.49); Endonuclease]	Drosophila melanogaster (Fruit fly)
c97594_g1	P35072	TCB1_CAEBR	Transposable element Tcb1 transposase (Transposable element Barney transposase)	Caenorhabditis briggsae

Table S3.5. Significantly ($p < 0.05$) enriched GO terms in each coexpression module

module	GO terms
black	regulation of small GTPase mediated signal transduction, G-protein coupled receptor signaling pathway, protein phosphorylation signal transduction, intracellular signal transduction, regulation of ARF protein signal transduction, cell communication, small GTPase mediated signal transduction, response to biotic stimulus, ephrin receptor signaling pathway, filopodium assembly, regulation of Rho protein signal transduction, cyclic nucleotide biosynthetic process, ion transport
blue	DNA-templated transcription initiation, protein glycosylation, transcription from TNA polymerase II, RNA processing, DNA repair, cellular protein complex assembly, protein folding, small GTPase mediated signal transduction, translation initiation, vesicle docking involved in exocytosis, organelle fission, nucleoside metabolic process
brown	termination of G-protein coupled receptor signaling, amino acid transmembrane transport, steroid hormone mediated signaling pathway, G-protein coupled receptor signaling pathway, Notch signaling pathway
cyan	G-protein coupled receptor signaling pathway, phosphatidylinositol metabolic process
green	translation, translation elongation, cellular protein metabolic process, RNA processing, neuropeptide signaling pathway, nucleoside phosphate catabolic process
greenyellow	metabolic process, ubiquitin-dependent protein catabolic process, calcium ion transmembrane transport
lightcyan	ATP metabolic process, hydrogen ion transmembrane transport, purine ribonucleoside monophosphate biosynthetic process, oxidation-reduction process, purine ribonucleoside triphosphate biosynthetic process, ATP hydrolysis coupled proton transport, purine ribonucleoside biosynthetic process, generation of precursor metabolites and energy, DNA replication, metabolic process, proteolysis involved in cellular protein catabolic process, primary metabolic process, cellular nitrogen compound biosynthetic process, protein catabolic process
lightgreen	DNA-templated regulation of transcription, hemophilic cell adhesion, cell surface receptor signaling pathway
lightgrey	Antigen processing and presentation, protein oligomerization, immune response, DNA repair
lightyellow	oxidation-reduction process, cellular amino acid catabolic process, protein-DNA complex assembly
magenta	cell redox homeostasis, proteolysis, actin cytoskeleton organization, dephosphorylation, regulation of cytoskeleton organization, protein glycosylation, regulation of biological quality, localization

midnightblue	carbohydrate metabolic process, glycolytic process, metabolic process, glucose metabolic process, NADP metabolic process, calcium ion transmembrane transport, protein modification by small protein conjugation, coenzyme biosynthetic process, oxidation-reduction process, nucleotide catabolic process, nucleotide metabolic process, purine nucleotide biosynthetic process
pink	GTP catabolic process, protein polymerization, protein glycosylation, cell redox homeostasis, ferrous iron transport, single-organism cellular localization, protein localization to membrane, cellular carbohydrate biosynthetic process, glutamine metabolic process, cell morphogenesis
purple	DNA repair, multicellular organismal development, DNA-templated regulation of transcription
red	carbohydrate derivative catabolic process, positive regulation of cellular process, immune response rRNA processing, organophosphate catabolic process, regulation of apoptotic process, fatty acid biosynthetic process, regulation of gene expression, RNA metabolic process, anion transmembrane transport, inorganic ion transmembrane transport
royalblue	protein dephosphorylation, DNA-template regulation of transcription
salmon	microtubule-based movement, vesicle-mediated transport, intracellular protein transport, proton transport, neuropeptide signaling pathway, protein catabolic process
tan	regulation of cell growth, oxidation-reduction process, proteolysis, immune response, dicarboxylic acid transport, sulfur compound metabolic process, cell redox homeostasis
turquoise	DNA-templated transcription, cellular component movement, signal transduction, Wnt signaling pathway, DNA-templated regulation of transcription, glutamine metabolic process, cell projection organization response to external stimulus, hexose metabolic process, protein dephosphorylation, autophagy
yellow	ion transport, transmembrane transport, ephrin receptor signaling pathway, transport, protein homooligomerization, single organism signaling, hemophilic cell adhesion, inorganic anion transport, calcium ion transmembrane transport, potassium ion transport, cyclic nucleotide biosynthetic process, steroid hormone mediated signaling pathway, G-protein coupled receptor signaling pathway, cell communication, cellular process