Supplemental Materials

Transcriptomic analysis reveals sex-dependent expression patterns in the basolateral amygdala of dominant and subordinate animals after acute social conflict

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De novo assembly and transcriptome optimization

RNA samples (n=18; 2 animals pooled for each sample (see *Methods*)) were measured on the Agilent Bioanalyzer before they were sent for sequencing. RNA integrity numbers (all over 9 out of a maximum value of 10) and sample concentrations are listed in Supplemental Table 1. Sequence quality analysis (FastQC) was completed after sequencing, and all base scores fell in the highest quality range (Supplemental Figure 2). The *de novo* assembly using Trinity revealed 1,244,719 Trinity 'genes'. Raw reads were then aligned back to the assembly revealing that proper pairs (left and right reads aligned to same contig) accounted for 80.78%, improper pairs (left and right reads align but to different contigs due to fragmentation) for 13.81%, left-only reads for 3.57%, and right-only reads for 1.84%.

The initial *de novo* assembly generated 1.2M possible genes, many more than are truly represented in the hamster amygdala. To control for any sequences that were assembled incorrectly during the *de novo* assembly process, we first optimized the assembly using TransDecoder to determine the number of probable coding sequences within the assembly. A schematic of the assembly optimization process is shown in Supplemental Figure 3. Complete coding sequences accounted for 528,193 of the 887,774 open reading frames. The remainder of the sequences were 5-prime partial (206,792), 3-prime partial (117,384), or internal (35,405). Because the sequencing protocol had a 3-prime bias, all sequences that were either complete or 5-prime partial were retained for the optimized assembly, as these were the sequences that were most likely to code for actual genes (Senatore et al., 2015; McCann et al., 2017). We also filtered the full assembly through BLASTx (Uniprot-rodent database, 1/21/16) to match the hamster sequences to known rodent gene sequences, returning 1,319,393 matches. Many of these were at low confidence parameters, thus only those with an E-value of ≤1e-10 and a percent identification match of ≥50 were included (148,726). These stringent parameters provide enhanced confidence in the quality of the optimized and annotated transcriptome (MacManes and Lacey, 2012; Feng et al., 2015; McCann et al., 2017). We then merged the data from TransDecoder and BLASTx, leaving 120,003 transcripts matching 14,493 unique BLAST identifiers. These numbers are consistent with our previous data from hamster whole brain (McCann et al., 2017), as well as data in humans and mice (Hastie et al., 1976; Venter et al., 2001; Su et al., 2004; Carninci et al., 2005).

References

Carninci P, Kasukawa T, Katayama S, Gough J, Frith M, Maeda N, Oyama R, Ravasi T, Lenhard B, Wells C (2005). The transcriptional landscape of the mammalian genome. Science 309 (5740):1559-1563

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Hastie ND, Bishop JO (1976). The expression of three abundance classes of messenger RNA in mouse tissues. Cell 9 (4 PT 2):761-774

MacManes MD, Lacey EA (2012). The social brain: transcriptome assembly and characterization of the hippocampus from a social subterranean rodent, the colonial tuco-tuco (Ctenomys sociabilis). PloS one 7(9):e45524. doi:10.1371/journal.pone.0045524

McCann KE, Sinkiewicz DM, Norvelle A, Huhman KL (2017). De novo assembly, annotation, and characterization of the whole brain transcriptome of male and female Syrian hamsters. Scientific Reports 7:40472. doi:10.1038/srep40472

Senatore A, Edirisinghe N, Katz PS (2015). Deep mRNA sequencing of the Tritonia diomedea brain transcriptome provides access to gene homologues for neuronal excitability, synaptic transmission and peptidergic signalling. PloS one 10(2):e0118321. doi:10.1371/journal.pone.0118321

Su AI, Wiltshire T, Batalov S, Lapp H, Ching KA, Block D, Zhang J, Soden R, Hayakawa M, Kreiman G (2004). A gene atlas of the mouse and human protein-encoding transcriptomes. Proceedings of the National Academy of Sciences of the United States of America 101(16):6062-6067

Venter JC, Adams MD, Myers EW, Li PW, Mural RJ, Sutton GG, Smith HO, Yandell M, Evans CA, Holt RA (2001). The sequence of the human genome. Science 291 (5507):1304-1351

Supplemental Figure Legends

Supplemental Figure 1: Dominant (left) and subordinate (right) males and females display similar behavioral patterns across each trial. (a) Timeline of experimental design. **(b)** During Trial 1, there was a significant interaction in dominant animals ($F(3,36)=4.988$, $p=0.0054$, left panel). Dominant males exhibited significantly more non-social behavior than did dominant females ($*p=0.0291$). There were no significant sex differences observed in other behaviors in dominant hamsters nor in any behavior in subordinate hamsters (right panel). Due to a technical malfunction, one behavioral pair was not fully recorded during Trial 1, and thus was not included in Trial 1 analyses. **(c-d)** There were no differences in behavior between males and females during **(c)** Trial 2 or **(d)** Trial 3. There was a significant main effect of behavior for each trial, with dominant animals displaying primarily aggression and subordinates displaying almost exclusively submission (Trial 1 dominants: $F(3,36)=24.89$, $p<0.0001$; Trial 1 subordinates: $F(3,36)=184.9$, $p<0.0001$; Trial 2 dominants: $F(3,40)=36.43$, $p<0.0001$; Trial 2 subordinates: $F(3,40)=423.5$, $p<0.0001$; Trial 3 dominants: $F(3,40)=21.63$, $p<0.0001$; Trial 3 subordinates: $F(3,40)=439$, $p<0.0001$).

Supplemental Figure 2: FASTQC analysis revealed that all reads were of high quality. Left and right reads all fell in the good quality (green) range for each base.

Supplemental Figure 3: Schematic of assembly optimization process. The optimization revealed 120,003 transcripts that mapped to 14,493 unique genes.

Supplemental Figure 4: RRHO analysis of all transcripts in the hamster amygdala. There was no correlation in **(a, b)** dominant males and females or **(c, d)** subordinate males and females when all transcripts were compared using rank rank hypergeometric overlap (RRHO). RRHO ranks the transcripts with the significantly increased transcripts first (bottom left) and the significantly decreased transcripts last (top right) on each panel (a and c). The heatmaps **(b, d)** show the $\log_{10}$ transformed p-values of the overlapping transcripts in males and females according to the hypergeometric distribution. Higher (reds) values indicate transcripts that overlap more than expected by chance while lower (blues) values indicate lower than expected overlap. RRHO analysis reveals that the most highly expressed transcripts overlap the most (bottom left, red) between sexes (within status).

Supplemental Figure 5: Top GO Terms represented in hamster amygdala. (a) Molecular Functions, (b) Biological Processes, and (c) Protein Classes represented when all transcripts are analyzed. The numbers of transcripts in each category are shown in parentheses.

Supplemental Figure 6: Top 40 pathways from GO analysis represented in the hamster amygdala.

Supplemental Figure 7: WGCNA divided the BLA transcripts into 138 distinct modules. On the left, the color designation of the module, as randomly assigned by

WGNCA. Within each square, the correlation and the p-value for each group are listed. The modules that were significantly correlated with subordinate status or with dominant status are highlighted in Figure 6.

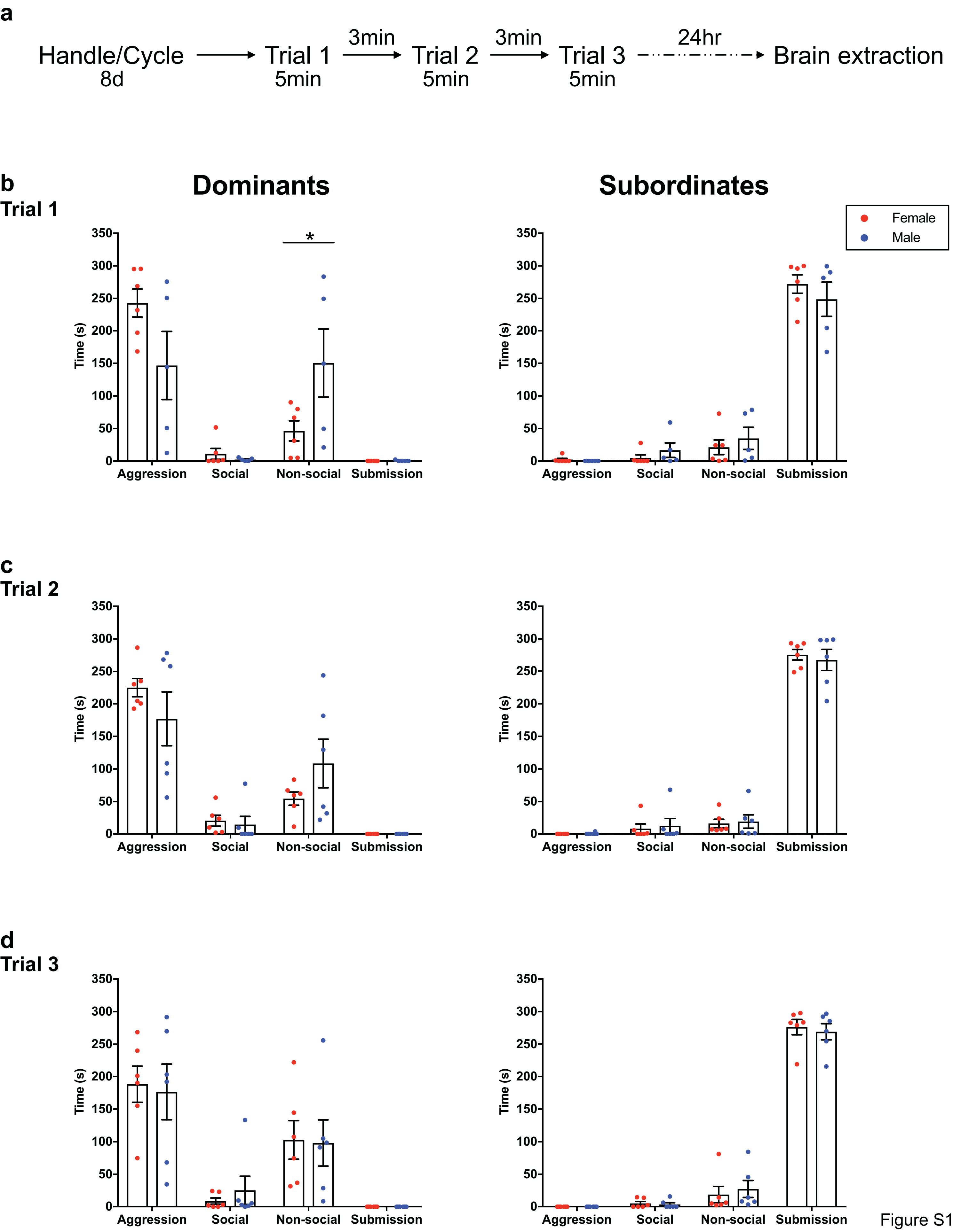

a
Handle/Cycle
8d
Trial 1
5min
3min
Trial 2
5min
3min
Trial 3
5min
24hr
Brain extraction
b
Dominants
Subordinates
Trial 1
Female
Male
*
c
Trial 2
d
Trial 3
Time (s)
0
50
100
150
200
250
300
350
Aggression
Social
Non-social
Submission

Figure S1

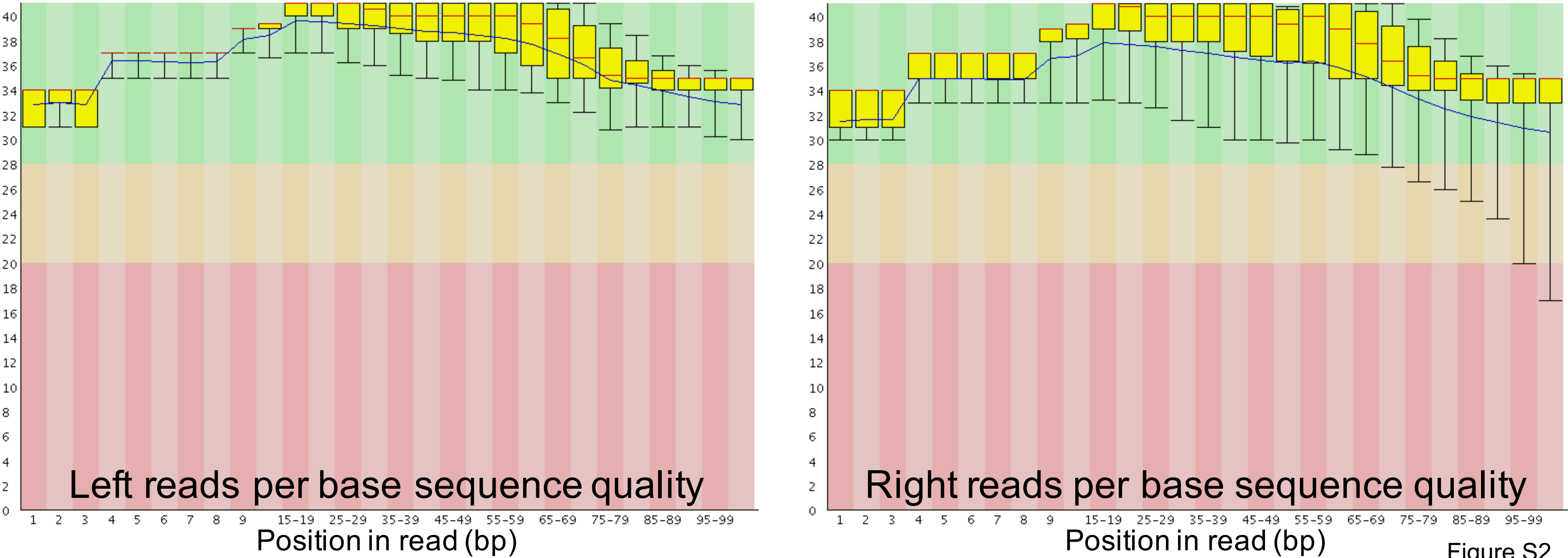

Left reads per base sequence quality
Right reads per base sequence quality
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
1
2
3
4
5
6
7
8
9
15-19
25-29
35-39
45-49
55-59
65-69
75-79
85-89
95-99
Position in read (bp)
Position in read (bp)

Figure S2

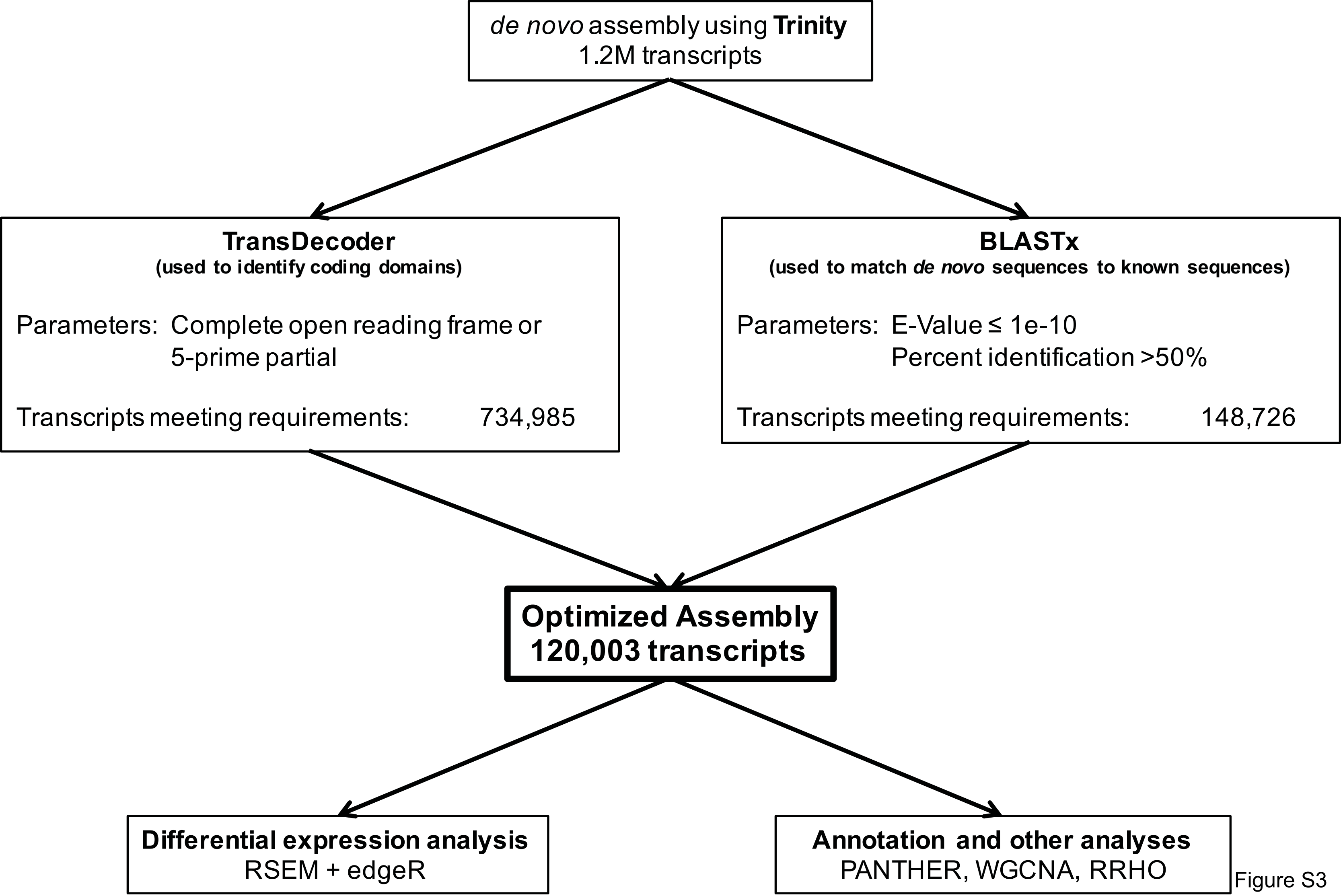

de novo assembly using **Trinity**
1.2M transcripts
TransDecoder
(used to identify coding domains)
Parameters: Complete open reading frame or 5-prime partial
Transcripts meeting requirements: 734,985
BLASTx
(used to match *de novo* sequences to known sequences)
Parameters: E-Value ≤ 1e-10
Percent identification >50%
Transcripts meeting requirements: 148,726
Optimized Assembly
120,003 transcripts
Differential expression analysis
RSEM + edgeR
Annotation and other analyses
PANTHER, WGCNA, RRHO

Figure S3

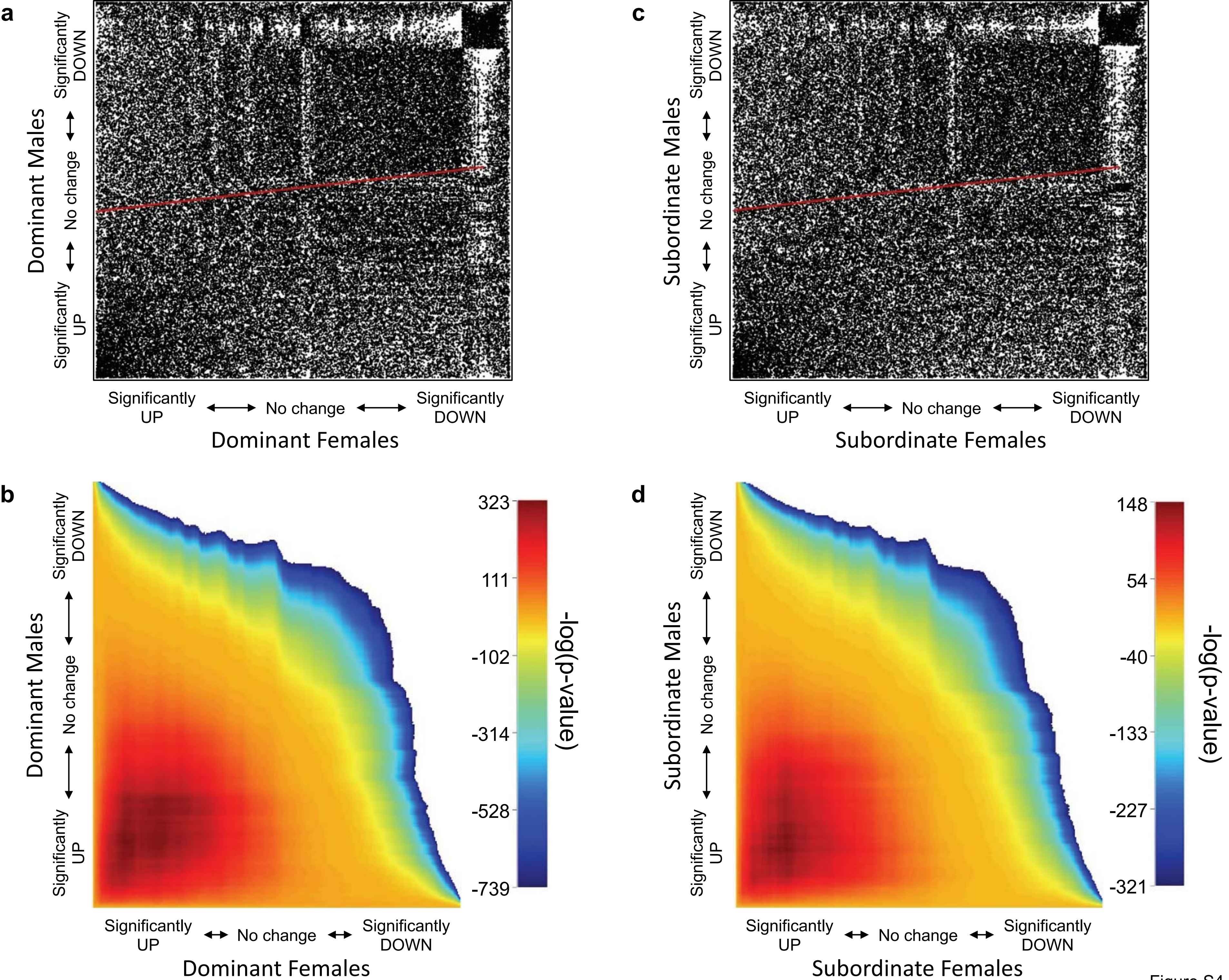
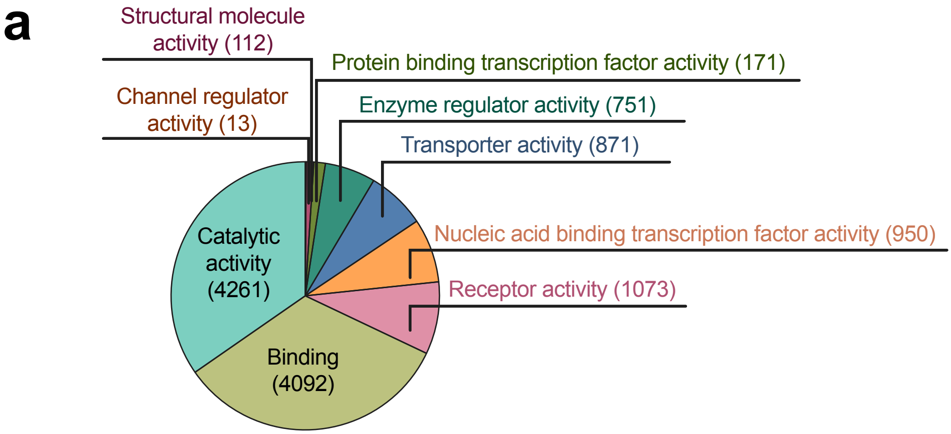
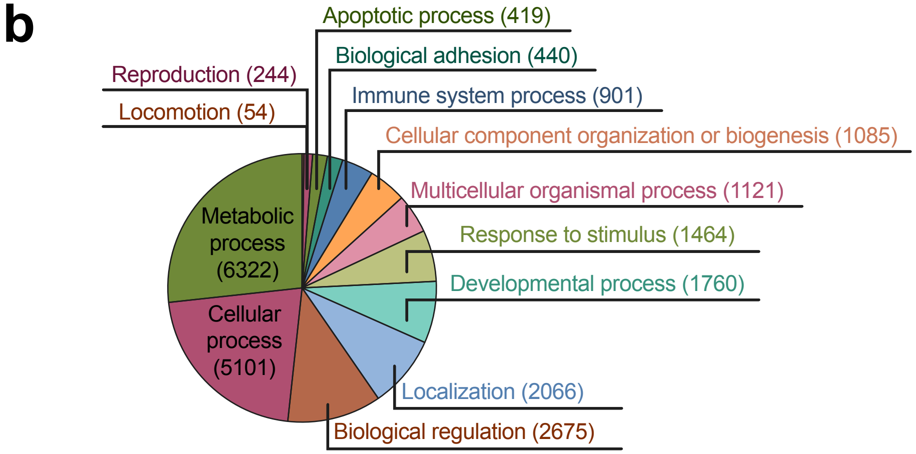

a
Dominant Males
Significantly DOWN
No change
Significantly UP
Significantly UP
No change
Significantly DOWN
Dominant Females
c
Subordinate Males
Significantly DOWN
No change
Significantly UP
Significantly UP
No change
Significantly DOWN
Subordinate Females
b
Dominant Males
Significantly DOWN
No change
Significantly UP
Significantly UP
No change
Significantly DOWN
Dominant Females
323
111
-102
-314
-528
-739
-log(p-value)
d
Subordinate Males
Significantly DOWN
No change
Significantly UP
Significantly UP
No change
Significantly DOWN
Subordinate Females
148
54
-40
-133
-227
-321
-log(p-value)

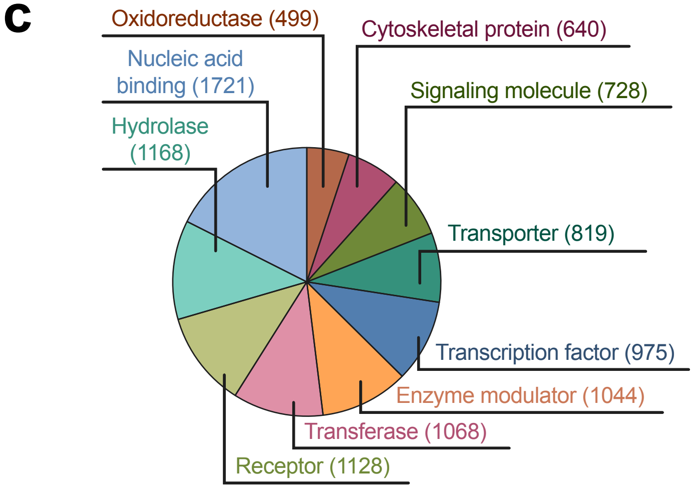
Figure S4



Molecular Function



Biological Process



Protein Class

Figure S5

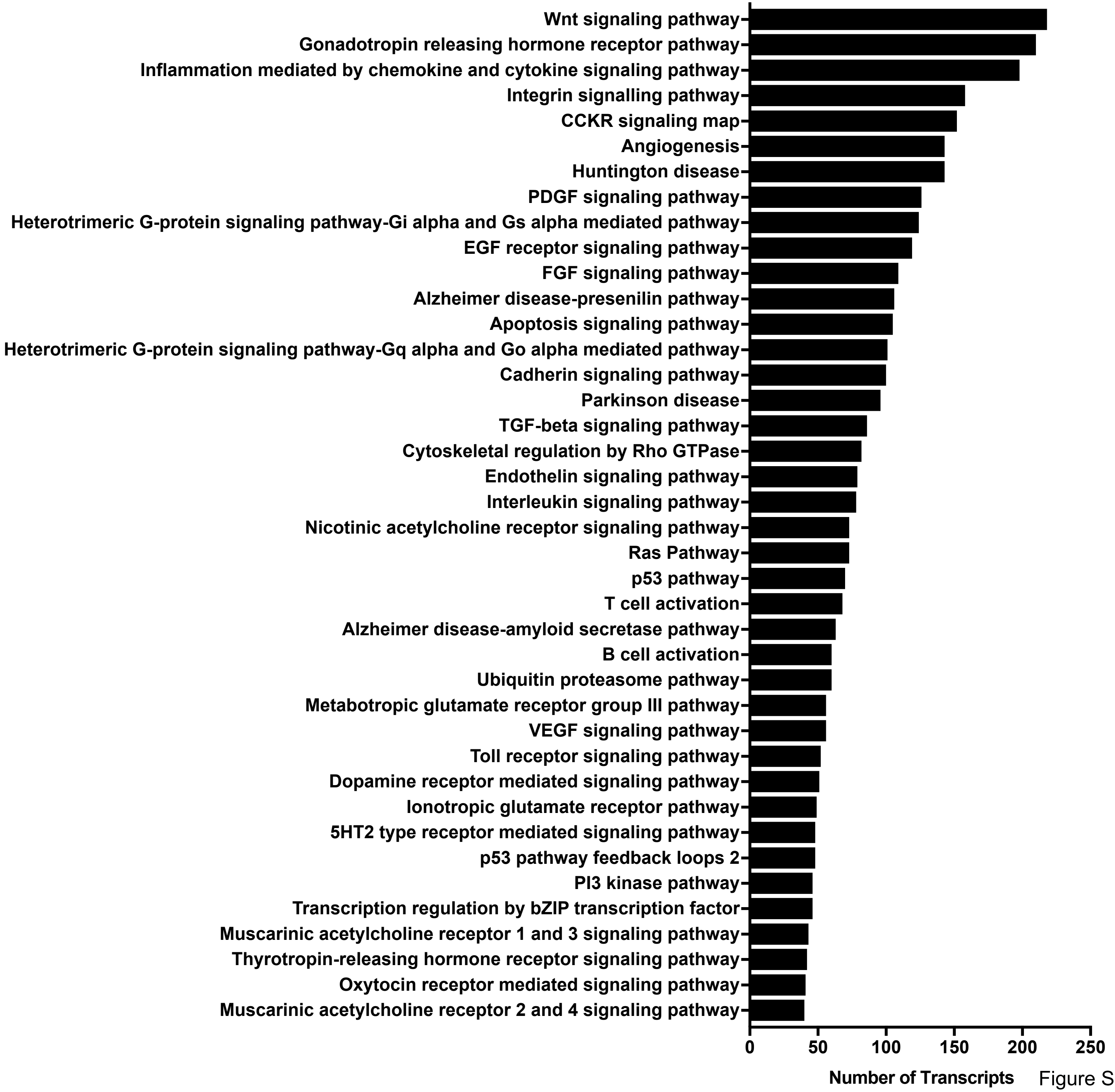

Wnt signaling pathway
Gonadotropin releasing hormone receptor pathway
Inflammation mediated by chemokine and cytokine signaling pathway
Integrin signalling pathway
CCKR signaling map
Angiogenesis
Huntington disease
PDGF signaling pathway
Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway
EGF receptor signaling pathway
FGF signaling pathway
Alzheimer disease-presenilin pathway
Apoptosis signaling pathway
Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway
Cadherin signaling pathway
Parkinson disease
TGF-beta signaling pathway
Cytoskeletal regulation by Rho GTPase
Endothelin signaling pathway
Interleukin signaling pathway
Nicotinic acetylcholine receptor signaling pathway
Ras Pathway
p53 pathway
T cell activation
Alzheimer disease-amyloid secretase pathway
B cell activation
Ubiquitin proteasome pathway
Metabotropic glutamate receptor group III pathway
VEGF signaling pathway
Toll receptor signaling pathway
Dopamine receptor mediated signaling pathway
Ionotropic glutamate receptor pathway
5HT2 type receptor mediated signaling pathway
p53 pathway feedback loops 2
PI3 kinase pathway
Transcription regulation by bZIP transcription factor
Muscarinic acetylcholine receptor 1 and 3 signaling pathway
Thyrotropin-releasing hormone receptor signaling pathway
Oxytocin receptor mediated signaling pathway
Muscarinic acetylcholine receptor 2 and 4 signaling pathway
0
50
100
150
200
250
Number of Transcripts

Figure S6

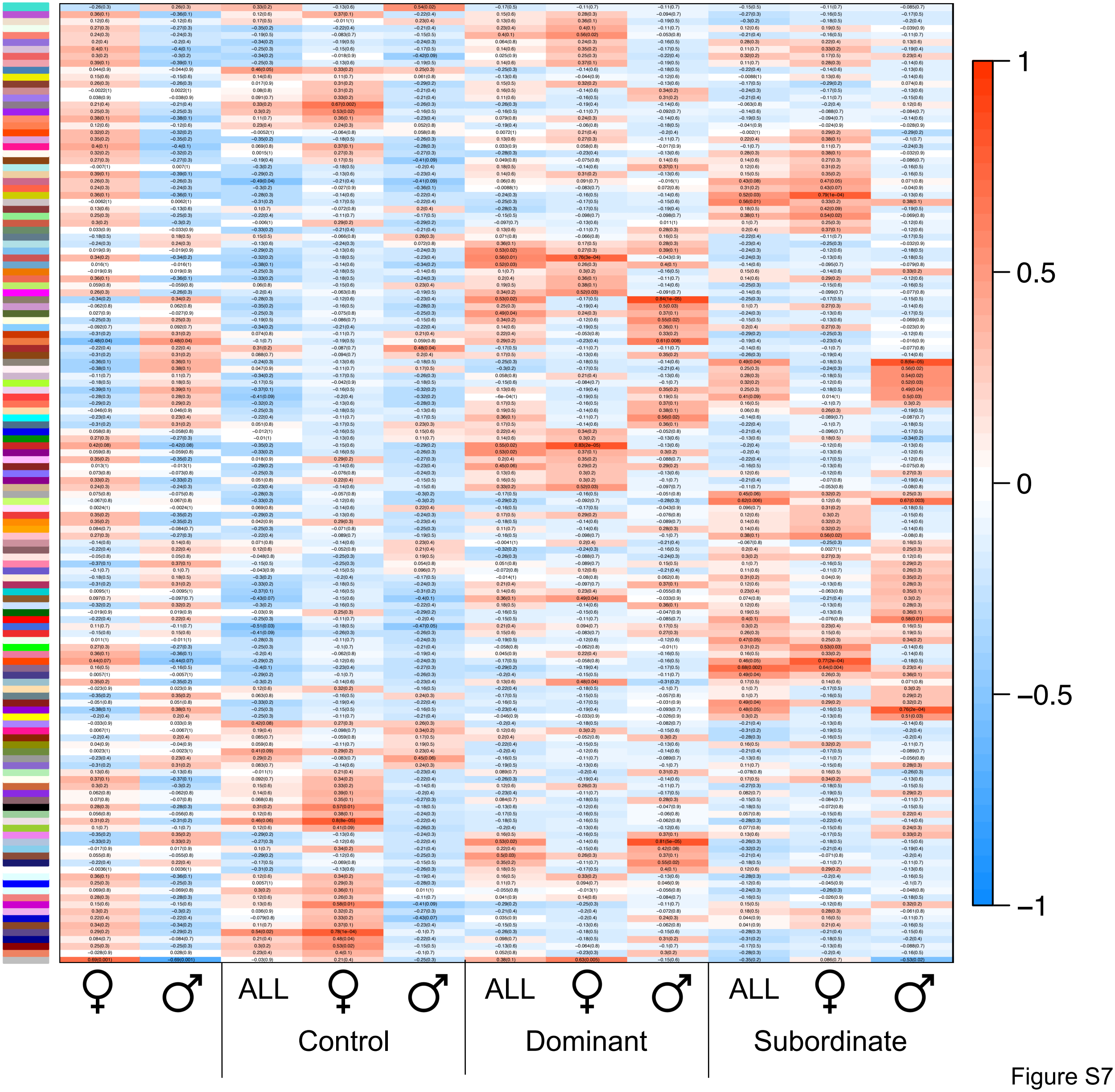


Figure S7

Supplemental Tables

Transcriptomic analysis reveals sex-dependent expression patterns in the basolateral amygdala of dominant and subordinate animals after acute social conflict

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Supplemental Table 1: RNA Integrity Numbers (RIN) and concentrations for each sample used for RNA-Seq

Sample	RNA integrity number (RIN)	Concentration (ng/µl)
Female Control A	9.1	191
Female Control B	9.1	228
Female Control C	9.2	127
Male Control A	9.2	67
Male Control B	9.1	137
Male Control C	9.0	195
Female Subordinate A	9.2	173
Female Subordinate B	9.0	185
Female Subordinate C	9.2	101
Male Subordinate A	9.1	295
Male Subordinate B	9.0	155
Male Subordinate C	9.1	254
Female Dominant A	9.3	210
Female Dominant B	9.0	75
Female Dominant C	9.1	164
Male Dominant A	9.1	214
Male Dominant B	9.2	127
Male Dominant C	9.1	183

Supplemental Table 2: Top 20 most highly expressed genes in the amygdala of male and female hamsters. * Indicates genes that were also among the top 20 genes in the hamster brain (McCann et al., 2017).

Gene ID	Gene	Uniprot ID
MT-CO2	Cytochrome c oxidase subunit 2	COX2_MICNA
Mtnd2	NADH-ubiquinone oxidoreductase chain 2	NU2M_MOUSE
Eef1a1*	Elongation factor 1-alpha 1	EF1A1_RAT
Scd2*	Acyl-CoA desaturase 2	ACOD2_MOUSE
Cpe	Carboxypeptidase E	CBPE_MOUSE
Map1a*	Microtubule-associated protein 1A	MAP1A_MOUSE
GNAS	Guanine nucleotide-binding protein G(s) subunit alpha	GNAS_MESAU
Calm1	Calmodulin	CALM_RAT
Atp1b1	Sodium/potassium-transporting ATPase subunit beta-1	AT1B1_RAT
Hsp90aa1*	Heat shock protein HSP 90-alpha	HS90A_MOUSE
NSF	Vesicle-fusing ATPase	NSF_CRIGR
Gapdh*	Glyceraldehyde-3-phosphate dehydrogenase	G3P_CRIGR
Actg1	Actin, cytoplasmic 2	ACTG_RAT
Camk2a	Calcium/calmodulin-dependent protein kinase type II subunit alpha	KCC2A_RAT
Sparcl1	SPARC-like protein 1	SPRL1_RAT
Slc1a3	Excitatory amino acid transporter 1	EAA1_RAT
Ywhaz	14-3-3 protein zeta/delta	1433Z_RAT
Prickle3	Prickle-like protein 3	PRIC3_MOUSE
Gpm6b	Neuronal membrane glycoprotein M6-b	GPM6B_RAT
Tspan7	Tetraspanin-7	TSN7_MOUSE

Supplemental Table 3: Differentially expressed transcripts between animals of different social status and their expression patterns in females and males.
Trinity Transcript ID = Transcript identification number assigned during *de novo* assembly; Uniprot ID = Identification to be used at uniport.org
Sub = Subordinate; Dom = Dominant; Con = Socially neutral control; log2FC = log2 fold change; FDR = false discovery rate

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR234744|c0_g3_i12	2A5G_MOUSE	Down in Sub v. Con (-8.28; 0.0174)	No change in males	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform
TR282126|c10_g3_i4	4EBP2_MOUSE	No change in females	Down in Dom v. Con (-10.34; 1.91e-05) Down in Dom v. Sub (-10.68; 0.0026)	Eukaryotic translation initiation factor 4E-binding protein 2
TR622108|c5_g2_i4	A4_RAT	Up in Dom v. Con (6.24; 0.04)	No change in males	Amyloid-beta A4 protein
TR478913|c8_g1_i10	ABCD3_MOUSE	No change in females	Up in Sub v. Con (8.65; 0.0266)	ATP-binding cassette sub-family D member 3
TR442240|c3_g1_i14	ABHD6_RAT	Up in Dom v. Con (9.41; 0.0475) Up in Dom v. Sub (9.33; 0.0467)	No change in males	Monoacylglycerol lipase ABHD6
TR20067|c5_g1_i4	ACADV_RAT	No change in females	Up in Sub v. Dom (8.46; 0.0084)	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial
TR602200|c9_g2_i2	ACD10_MOUSE	Up in Sub v. Dom (9.29; 0.0488)	No change in males	Acyl-CoA dehydrogenase family member 10
TR686210|c5_g2_i2	ACM2_RAT	Down in Sub v. Con (-8.54; 0.0034)	No change in males	Muscarinic acetylcholine receptor M2
TR209240|c6_g6_i20	ACOX1_RAT	No change in females	Up in Sub v. Dom (8.34; 0.0201)	Peroxisomal acyl-coenzyme A oxidase 1
TR534467|c17_g4_i15	ACSL6_MOUSE	No change in females	Up in Sub v. Dom (8.02; 0.0456)	Long-chain-fatty-acid--CoA ligase 6
TR354883|c8_g4_i7	ACSM5_MOUSE	No change in females	Up in Dom v. Con (8.67; 0.0254)	Acyl-coenzyme A synthetase ACSM5, mitochondrial
TR166210|c2_g3_i4	ACYP2_MOUSE	No change in females	Up in Dom v. Con (10.14; 0.023) Up in Sub v. Con (10.11; 0.0284)	Acylphosphatase-2
TR82040|c4_g1_i9	ADA12_MOUSE	Up in Dom v. Con (8.90; 0.0014)	No change in males	Disintegrin and metalloproteinase domain-containing protein 12
TR634973|c5_g1_i8	ADCY3_RAT	No change in females	Down in Dom v. Con (-8.62; 0.023)	Adenylate cyclase type 3
TR250569|c4_g2_i18	ADK_CRIGR	Up in Dom v. Sub (9.50; 6.03e-05)	No change in males	Adenosine kinase
TR175064|c1_g1_i4	AKAP5_MOUSE	No change in females	Down in Sub v. Con (-9.65; 0.0425) Down in Sub v. Dom (-9.30; 0.0004)	A-kinase anchor protein 5

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR170024|c2_g1_i13	AKNA_MOUSE	Up in Dom v. Sub (8.44; 0.0058)	Up in Sub v. Dom (8.89; 0.0009)	AT-hook-containing transcription factor
TR746326|c3_g3_i4	AL1A1_MESAU	No change in females	Down in Dom v. Con (-10.01; 0.0037)	Retinal dehydrogenase 1
TR410667|c2_g3_i7	ANK3_RAT	Down in Sub v. Con (-10.86; 4.20e-06) Down in Sub v. Dom (-10.75; 0.0022)	No change in males	Ankyrin-3
TR685188|c7_g6_i2	ANKR6_MOUSE	No change in females	Down in Dom v. Con (-10.93; 0.0059) Down in Dom v. Sub (-10.93; 0.0015)	Ankyrin repeat domain-containing protein 6
TR79130|c9_g3_i5	ANM7_CRILO	Up in Dom v. Con (6.26; 1.41e-05)	No change in males	Protein arginine N-methyltransferase 7
TR674922|c12_g4_i11	ANS1A_MOUSE	No change in females	Up in Dom v. Sub (8.69; 0.0016)	Ankyrin repeat and SAM domain-containing protein 1A
TR87184|c1_g1_i7	AP1B1_MOUSE	Down in Sub v. Con (-9.32; 0.0415)	No change in males	AP-1 complex subunit beta-1
TR643243|c6_g2_i10	AP1G1_MOUSE	Up in Dom v. Sub (7.06; 0.0009)	No change in males	AP-1 complex subunit gamma-1
TR759306|c12_g2_i10	AP1S2_MOUSE	Up in Sub v. Con (9.03; 0.029) Up in Sub v. Dom (8.96; 0.0382)	No change in males	AP-1 complex subunit sigma-2
TR395328|c1_g3_i4	APBB1_MOUSE	Down in Sub v. Con (-9.28; 0.0445)	No change in males	Amyloid-beta A4 precursor protein-binding family B member 1
TR232380|c7_g1_i2	APC2_MOUSE	Up in Dom v. Con (11.64; 5.44e-17) Up in Sub v. Con (10.6; 0.0023)	No change in males	Adenomatous polyposis coli protein 2
TR247634|c14_g1_i13	API5_MOUSE	No change in females	Down in Dom v. Con (-6.88; 0.029)	Apoptosis inhibitor 5
TR640930|c13_g1_i11	AREL1_MOUSE	No change in females	Up in Sub v. Dom (9.45; 1.3e-05)	Apoptosis-resistant E3 ubiquitin protein ligase 1
TR242953|c1_g2_i1	ARHG4_MOUSE	No change in females	Up in Sub v. Con (8.74; 0.0245)	Rho guanine nucleotide exchange factor 4
TR309220|c6_g4_i10	ARHGB_RAT	No change in females	Up in Dom v. Con (8.7; 0.0273)	Rho guanine nucleotide exchange factor 11
TR500495|c2_g1_i1	ARI5B_MOUSE	Up in Dom v. Con (9.06; 0.0005)	No change in males	AT-rich interactive domain-containing protein 5B
TR218070|c0_g1_i7	ASPG_RAT	No change in females	Down in Dom v. Con (-9.01; 0.0038) Down in Sub v. Con (-8.93; 0.0062)	N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR23184|c8_g2_i2	ASTN1_MOUSE	Up in Dom v. Sub (9.15; 0.0033)	No change in males	Astrotactin-1
TR443187|c0_g1_i3	ASXL3_MOUSE	No change in females	Up in Sub v. Con (8.45; 0.0302)	Putative Polycomb group protein ASXL3
TR245325|c7_g1_i2	AT8A2_MOUSE	No change in females	Up in Dom v. Con (8.49; 0.029)	Phospholipid-transporting ATPase IB
TR158276|c6_g4_i13	ATG2B_MOUSE	No change in females	Up in Dom v. Sub (9.33; 0.0459)	Autophagy-related protein 2 homolog B
TR702298|c1_g2_i17	ATL1_MOUSE	Down in Sub v. Con (-8.27; 0.0274)	No change in males	ADAMTS-like protein 1
TR193800|c13_g3_i2	ATLA1_RAT	No change in females	Up in Dom v. Con (9.76; 6.00e-05) Up in Sub v. Con (9.2; 0.0007)	Atlastin-1
TR535735|c4_g2_i3	ATR_MOUSE	No change in females	Up in Dom v. Con (8.81; 0.015)	Serine/threonine-protein kinase ATR
TR575223|c0_g1_i3	BACE2_MOUSE	No change in females	Up in Dom v. Sub (5.46; 0.011)	Beta-secretase 2
TR306564|c5_g5_i4	BARD1_MOUSE	Up in Sub v. Con (8.17; 0.0273)	No change in males	BRCA1-associated RING domain protein 1
TR159651|c4_g2_i5	BARD1_RAT	Down in Sub v. Con (-9.76; 0.0184)	No change in males	BRCA1-associated RING domain protein 1
TR615201|c6_g3_i6	BCORL_MOUSE	Down in Sub v. Con (-8.32; 0.018)	No change in males	BCL-6 corepressor-like protein 1
TR615201|c6_g3_i7	BCORL_MOUSE	Up in Sub v. Con (8.71; 0.0274)	No change in males	BCL-6 corepressor-like protein 1
TR67576|c1_g2_i6	BMR1A_MOUSE	Down in Sub v. Con (-9.9; 0.0174)	No change in males	Bone morphogenetic protein receptor type-1A
TR560446|c0_g1_i3	BMR1B_MOUSE	No change in females	Up in Dom v. Con (8.35; 0.0365)	Bone morphogenetic protein receptor type-1B
TR496126|c7_g2_i22	CA2D2_MOUSE	Up in Dom v. Con (8.42, 0.0089) Up in Sub v. Con (9.36; 0.035)	No change in males	Voltage-dependent calcium channel subunit alpha-2/delta-2
TR424497|c7_g2_i7	CAB45_MOUSE	Down in Dom v. Con (-2.98; 0.0068)	No change in males	45 kDa calcium-binding protein
TR519843|c18_g4_i28	CABIN_RAT	No change in females	Up in Sub v. Dom (8.21; 0.0201)	Calcineurin-binding protein cabin-1
TR94552|c4_g2_i11	CABYR_MOUSE	No change in females	Up in Dom v. Sub (8.29; 0.0156)	Calcium-binding tyrosine phosphorylation-regulated protein
TR694532|c3_g2_i13	CAC1E_RAT	Down in Dom v. Con (-9.66; 0.0289)	Down in Dom v. Con (-10.46; 2.02e-08) Down in Sub v. Con (-10.37; 3.67e-08)	Voltage-dependent R-type calcium channel subunit alpha-1E

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR694532|c3_g2_i14	CAC1E_RAT	Up in Dom v. Sub (11.14; 9.01e-19)	No change in males	Voltage-dependent R-type calcium channel subunit alpha-1E
TR694532|c3_g2_i10	CAC1E_RAT	Up in Sub v. Dom (2.54; 0.0107)	No change in males	Voltage-dependent R-type calcium channel subunit alpha-1E
TR604362|c7_g3_i6	CAC1H_RAT	Up in Sub v. Dom (8.5; 0.0058)	Up in Sub v. Con (9; 0.0037)	Voltage-dependent T-type calcium channel subunit alpha-1H
TR748348|c15_g2_i4	CACB4_MOUSE	No change in females	Down in Sub v. Con (-10.53; 0.0462)	Voltage-dependent L-type calcium channel subunit beta-4
TR719666|c4_g1_i6	CAN15_MOUSE	Down in Sub v. Con (-9.79; 0.0173)	No change in males	Calpain-15
TR517507|c15_g2_i1	CASC4_MOUSE	No change in females	Down in Dom v. Con (-7.66; 5.53e-07)	Protein CASC4
TR277565|c5_g1_i15	CB068_MOUSE	No change in females	Up in Dom v. Sub (8.1; 0.0297)	UPF0561 protein C2orf68 homolog
TR85002|c0_g3_i11	CBLB_RAT	No change in females	Up in Dom v. Con (9.85; 0.0423)	E3 ubiquitin-protein ligase CBL-B
TR113925|c8_g2_i5	CCD92_MOUSE	Down in Sub v. Con (-4.24; 0.029)	No change in males	Coiled-coil domain-containing protein 92
TR157408|c3_g1_i23	CCM2_MOUSE	Up in Dom v. Con (8.61; 0.0046) Up in Dom v. Sub (8.53; 0.0053)	No change in males	Cerebral cavernous malformations protein 2 homolog
TR633248|c7_g1_i8	CCNL1_MOUSE	Up in Dom v. Con (8.27; 0.0193) Up in Sub v. Con (8.92; 0.0006)	No change in males	Cyclin-L1
TR239215|c4_g1_i8	CCSE2_MOUSE	No change in females	Up in Dom v. Con (10.21; 7.80e-07)	Serine-rich coiled-coil domain-containing protein 2
TR190655|c14_g1_i10	CDK5_MOUSE	Up in Dom v. Con (9.83; 0.0184) Up in Sub v. Con (10.5; 8.68e-13)	No change in males	Cyclin-dependent-like kinase 5
TR190655|c14_g1_i8	CDK5_MOUSE	Up in Dom v. Con (10.51; 0.0043) Up in Sub v. Con (11.22; 6.30e-16)	No change in males	Cyclin-dependent-like kinase 5
TR576923|c1_g3_i12	CELR3_MOUSE	Up in Dom v. Sub (8.53; 0.0111)	No change in males	Cadherin EGF LAG seven-pass G-type receptor 3
TR659894|c2_g1_i6	CENPC_MOUSE	Up in Sub v. Con (5.13; 0.274)	No change in males	Centromere protein C
TR483264|c6_g2_i13	CF089_RAT	No change in females	Down in Dom v. Con (-9.07; 0.0029) Down in Dom v. Sub (-8.2; 0.0341)	Bombesin receptor-activated protein C6orf89 homolog

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR544530|c12_g5_i3	CF106_MOUSE	Up in Sub v. Con (9.32; 6.32e-06)	No change in males	Uncharacterized protein C6orf106 homolog
TR327832|c0_g1_i7	CGAT1_MOUSE	Up in Sub v. Con (8.22; 0.0274)	No change in males	Chondroitin sulfate N-acetylgalactosaminyltransferase 1
TR355755|c5_g1_i2	CH033_MOUSE	Up in Dom v. Con (8.52; 0.0343)	No change in males	UPF0488 protein C8orf33 homolog
TR738415|c2_g2_i2	CHSS3_MOUSE	Down in Dom v. Con (-8.83; 0.0039)	No change in males	Chondroitin sulfate synthase 3
TR234188|c12_g4_i14	CIP2A_MOUSE	Up in Dom v. Con (5.94; 0.0015)	No change in males	Protein CIP2A
TR727494|c14_g1_i2	CNOT6_RAT	No change in females	Up in Sub v. Dom (7.29; 0.0004)	CCR4-NOT transcription complex subunit 6
TR752730|c3_g5_i11	CNTN1_MOUSE	No change in females	Down in Sub v. Con (-8.81; 0.0332)	Contactin-1
TR488658|c6_g7_i17	COGA1_MOUSE	No change in females	Down in Dom v. Con (-8.62; 0.02)	Collagen alpha-1(XVI) chain
TR113730|c7_g2_i13	CP250_MOUSE	Down in Dom v. Con (-8.38; 0.0391) Down in Sub v. Con (-8.37; 0.0299)	No change in males	Centrosome-associated protein CEP250
TR29058|c4_g1_i11	CPEB1_MOUSE	No change in females	Up in Dom v. Sub (9.1; 0.0002)	Cytoplasmic polyadenylation element-binding protein 1
TR213815|c3_g1_i4	CPSF7_MOUSE	No change in females	Up in Dom v. Sub (8.49; 0.0155)	Cleavage and polyadenylation specificity factor subunit 7
TR220715|c12_g1_i31	CSF1R_MOUSE	No change in females	Up in Sub v. Dom (9.31; 1.76e-05)	Macrophage colony-stimulating factor 1 receptor
TR224107|c4_g1_i12	CSKI1_RAT	No change in females	Up in Sub v. Dom (8.35; 0.011)	Caskin-1
TR108616|c11_g7_i2	CT194_MOUSE	Down in Sub v. Con (-8.24; 0.0184)	No change in males	Uncharacterized protein C20orf194 homolog
TR194016|c0_g1_i3	CUL3_RAT	Down in Dom v. Con (-9.66; 0.004)	Down in Dom v. Con (-11.38; 1.17e-09) Down in Dom v. Sub (-10.24; 0.0103)	Cullin-3
TR417587|c6_g2_i29	CUL9_MOUSE	Down in Sub v. Con (-3.87; 0.0415)	No change in males	Cullin-9
TR417587|c6_g2_i22	CUL9_MOUSE	Up in Sub v. Dom (8.58; 0.0175)	No change in males	Cullin-9
TR379494|c3_g4_i1	CX056_MOUSE	No change in females	Up in Dom v. Con (8.97; 0.0052)	UPF0428 protein CXorf56 homolog
TR139846|c14_g1_i6	CXAR_MOUSE	Down in Dom v. Con (-8.93; 0.0004)	No change in males	Coxsackievirus and adenovirus receptor homolog
TR690572|c15_g1_i5	CYBP_MOUSE	Up in Dom v. Sub (9.49; 0.034)	No change in males	Calcyclin-binding protein

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TR162|c4_g1_i10	CYTSB_MOUSE	Up in Dom v. Sub (8.67; 0.0023)	No change in males	Cytospin-B
TR728257|c0_g1_i2	CYYR1_MOUSE	No change in females	Down in Dom v. Con (-6.68; 0.0022)	Cysteine and tyrosine-rich protein 1
TR703960|c6_g2_i3	DAPK3_MOUSE	Down in Sub v. Con (-9.79; 0.0002)	No change in males	Death-associated protein kinase 3
TR485954|c1_g1_i4	DCC_MOUSE	No change in females	Up in Dom v. Sub (9.59; 0.0219)	Netrin receptor DCC
TR485954|c1_g1_i2	DCC_RAT	No change in females	Up in Dom v. Con (9.47; 0.0004) Up in Dom v. Sub (9.68; 2.22e-06)	Netrin receptor DCC
TR485954|c1_g1_i7	DCC_RAT	Up in Dom v. Con (9.3; 0.0002) Up in Sub v. Con (9.25; 0.0486)	No change in males	Netrin receptor DCC
TR609750|c14_g1_i1	DCE2_RAT	No change in females	Up in Dom v. Con (9.33; 0.0097)	Glutamate decarboxylase 2
TR324823|c20_g5_i9	DDX58_MOUSE	Up in Sub v. Con (8.17; 0.0262)	No change in males	Probable ATP-dependent RNA helicase DDX58
TR674200|c5_g4_i16	DEN4C_MOUSE	Up in Sub v. Dom (8.54; 0.0382)	No change in males	DENN domain-containing protein 4C
TR447485|c3_g4_i23	DGKB_MOUSE	No change in females	Up in Sub v. Dom (10.6; 1.16e-11)	Diacylglycerol kinase beta
TR447485|c3_g4_i9	DGKB_MOUSE	No change in females	Up in Sub v. Dom (11.61; 3.03e-19)	Diacylglycerol kinase beta
TR447485|c3_g4_i27	DGKB_RAT	No change in females	Down in Dom v. Con (-9.83; 0.0399) Down in Dom v. Sub (-11.15; 1.12e-17)	Diacylglycerol kinase beta
TR447485|c3_g4_i1	DGKB_RAT	No change in females	Up in Dom v. Sub (4.93; 0.0234)	Diacylglycerol kinase beta
TR309424|c5_g2_i22	DGKZ_RAT	No change in females	Up in Dom v. Sub (8.06; 0.0411)	Diacylglycerol kinase zeta
TR608511|c3_g1_i7	DHDDS_MOUSE	No change in females	Up in Dom v. Con (8.6; 0.0141)	Dehydrodolichyl diphosphate synthase complex subunit Dhdds
TR407735|c6_g1_i14	DHX9_MOUSE	Down in Dom v. Con (-9.55; 0.0348)	No change in males	ATP-dependent RNA helicase A
TR299047|c6_g1_i10	DICER_CRIGR	No change in females	Up in Dom v. Con (8.6; 0.0471)	Endoribonuclease Dicer
TR496829|c10_g2_i8	DNAI1_MOUSE	No change in females	Up in Sub v. Con (9.71; 0.0001) Up in Sub v. Dom (10.02; 2.54e-09)	Dynein intermediate chain 1, axonemal

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TR293624|c1_g1_i7	DNJC5_RAT	No change in females	Up in Dom v. Con (8.43; 0.0472)	DnaJ homolog subfamily C member 5
TR726665|c3_g2_i13	DPOG1_RAT	Up in Sub v. Dom (9.2; 6.90e-05)	No change in males	DNA polymerase subunit gamma-1
TR84647|c0_g2_i40	DYH17_MOUSE	Up in Dom v. Con (8.77; 0.002)	No change in males	Dynein heavy chain 17, axonemal
TR408305|c8_g3_i4	DYH7_RAT	Up in Sub v. Dom (9.27; 2.69e-05)	No change in males	Dynein heavy chain 7, axonemal
TR234188|c12_g4_i7	DZIP3_MOUSE	Down in Dom v. Con (-9.03; 0.0003)	No change in males	E3 ubiquitin-protein ligase DZIP3
TR743368|c3_g1_i13	E41L1_RAT	Up in Sub v. Con (9.61; 0.0246)	No change in males	Band 4.1-like protein 1
TR281012|c3_g1_i4	E41L2_MOUSE	Up in Sub v. Con (8.14; 0.0262)	No change in males	Band 4.1-like protein 2
TR54670|c7_g4_i3	E41LB_RAT	No change in females	Up in Dom v. Con (9.54; 0.0011)	Band 4.1-like protein 4B
TR278365|c5_g1_i3	EFC14_MOUSE	No change in females	Up in Dom v. Con (9.66; 0.0471)	EF-hand calcium-binding domain-containing protein 14
TR719571|c0_g3_i1	EHD4_MOUSE	Up in Dom v. Con (8.65; 0.0042)	No change in males	EH domain-containing protein 4
TR121574|c6_g1_i18	EME2_MOUSE	No change in females	Up in Sub v. Con (9.35; 0.0006)	Probable crossover junction endonuclease EME2
TR479052|c4_g2_i11	EPHAA_MOUSE	No change in females	Up in Dom v. Con (8.91; 0.0092)	Ephrin type-A receptor 10
TR229077|c4_g3_i10	EPS8_MOUSE	Up in Dom v. Con (8.06; 0.0475)	No change in males	Epidermal growth factor receptor kinase substrate 8
TR534844|c5_g7_i8	EPT1_MOUSE	No change in females	Down in Sub v. Con (-8.99; 0.0048)	Ethanolaminephosphotransferase 1
TR2061|c7_g3_i8	EVI5_MOUSE	Up in Dom v. Con (9.45; 0.0446) Up in Sub v. Con (9.86; 0.0147)	No change in males	Ecotropic viral integration site 5 protein
TR258166|c0_g1_i3	EXPH5_MOUSE	Up in Dom v. Sub (8.67; 0.0031)	No change in males	Exophilin-5
TR430745|c4_g1_i3	F102A_MOUSE	No change in females	Down in Dom v. Con (-8.76; 0.0076)	Protein FAM102A
TR343457|c9_g2_i1	F117B_MOUSE	Up in Sub v. Con (8.93; 0.0004)	No change in males	Protein FAM117B
TR501071|c2_g2_i2	F179B_MOUSE	No change in females	Down in Dom v. Con (-7.7; 0.0047) Down in Dom v. Sub (-6.83; 0.0109)	TOG array regulator of axonemal microtubules protein 1
TR235840|c10_g2_i4	F196B_MOUSE	No change in females	Up in Dom v. Con (8.33; 0.0423)	Protein FAM196B

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TR186263|c6_g1_i5	FA57A_MOUSE	No change in females	Up in Dom v. Con (8.57; 0.0274)	Protein FAM57A
TR372268|c7_g2_i9	FA69B_RAT	Up in Dom v. Sub (9.02; 0.0007)	No change in males	Protein FAM69B
TR550033|c16_g1_i4	FA76B_MOUSE	Up in Sub v. Con (8.06; 0.0415)	No change in males	Protein FAM76B
TR743817|c1_g3_i7	FAIM1_RAT	No change in females	Up in Dom v. Sub (8.22; 0.0196)	Fas apoptotic inhibitory molecule 1
TR31372|c0_g1_i13	FAS_RAT	No change in females	Down in Dom v. Con (-8.51; 0.023) Down in Dom v. Sub (-8.72; 0.0051)	Fatty acid synthase
TR278137|c6_g3_i11	FBW1B_MOUSE	No change in females	Up in Dom v. Con (8.86; 0.0188) Up in Sub v. Con (8.96; 0.003)	F-box/WD repeat-containing protein 11
TR227061|c2_g1_i4	FBX31_MOUSE	No change in females	Up in Dom v. Sub (8.08; 2.62e-15)	F-box only protein 31
TR672334|c3_g2_i10	FBX41_MOUSE	Down in Sub v. Con (-11.42; 2.10e-18) Down in Sub v. Dom (-9.31; 0.0005)	No change in males	F-box only protein 41
TR593350|c4_g1_i9	FBXL2_MOUSE	No change in females	Up in Dom v. Con (10.42; 0.0127)	F-box/LRR-repeat protein 2
TR35243|c5_g1_i6	FBXL5_MOUSE	No change in females	Down in Sub v. Con (-8.54; 0.0289)	F-box/LRR-repeat protein 5
TR123327|c5_g2_i10	FCSD2_MOUSE	No change in females	Up in Dom v. Con (8.71; 0.0141)	F-BAR and double SH3 domains protein 2
TR308572|c6_g5_i1	FGD1_MOUSE	Down in Dom v. Con (-8.69; 0.0024)	No change in males	FYVE, RhoGEF and PH domain-containing protein 1
TR308572|c6_g5_i10	FGD1_MOUSE	Up in Dom v. Con (8.72; 0.0026)	No change in males	FYVE, RhoGEF and PH domain-containing protein 1
TR690274|c3_g3_i7	FGF12_RAT	No change in females	Up in Dom v. Sub (12.7; 0.002)	Fibroblast growth factor 12
TR362729|c6_g3_i3	FLNB_MOUSE	Up in Dom v. Con (10.3; 2.97e-08) Up in Sub v. Con (9.53; 0.0275)	No change in males	Filamin-B
TR641946|c0_g1_i23	FLT3_MOUSE	Up in Dom v. Sub (8.37; 0.0124)	No change in males	Receptor-type tyrosine-protein kinase FLT3
TR693275|c10_g2_i15	FND3A_MOUSE	No change in females	Up in Dom v. Sub (8.17; 0.0219)	Fibronectin type-III domain-containing protein 3A
TR693275|c10_g2_i13	FND3A_MOUSE	Up in Sub v. Con (10.14; 0.0077)	No change in males	Fibronectin type-III domain-containing protein 3A

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TR95663|c5_g3_i6	FRS2_MOUSE	Up in Dom v. Con (8.7; 0.0032)	No change in males	Fibroblast growth factor receptor substrate 2
TR372268|c4_g1_i7	FXL17_MOUSE	Up in Dom v. Con (8.46; 9.29e-21) Up in Sub v. Con (7.83; 0.0054)	No change in males	F-box/LRR-repeat protein 17
TR644939|c6_g1_i16	G6PD_CRIGR	No change in females	Up in Dom v. Con (9.96; 7.15e-06) Up in Sub v. Con (10.12; 2.49e-05)	Glucose-6-phosphate 1-dehydrogenase
TR374171|c6_g4_i20	GANC_MOUSE	No change in females	Up in Sub v. Dom (8.57; 0.012)	Neutral alpha-glucosidase C
TR741316|c0_g1_i4	GBRA4_MOUSE	No change in females	Up in Dom v. Sub (9.45; 0.0342)	Gamma-aminobutyric acid receptor subunit alpha-4
TR336063|c11_g1_i2	GD1L1_MOUSE	No change in females	Up in Sub v. Dom (9.37; 4.03e-05)	Ganglioside-induced differentiation-associated protein 1-like 1
TR709728|c2_g2_i8	GGACT_RAT	Down in Sub v. Con (-9.48; 5.35e-06)	No change in males	Gamma-glutamylaminecyclotransferase
TR709728|c2_g2_i1	GGACT_RAT	Up in Sub v. Con (9.55; 5.61e-06)	No change in males	Gamma-glutamylaminecyclotransferase
TR237061|c5_g1_i3	GHR_RAT	Down in Sub v. Con (-4.97; 0.0459)	No change in males	Growth hormone receptor
TR532823|c10_g6_i12	GPBL1_RAT	Up in Sub v. Con (8.28; 0.02)	No change in males	Vasculin-like protein 1
TR49785|c4_g8_i7	GPCP1_MOUSE	No change in females	Down in Dom v. Con (-9.05; 0.0023)	Glycerophosphocholine phosphodiesterase GPCPD1
TR651284|c1_g1_i1	GPR45_MOUSE	No change in females	Up in Dom v. Con (8.33; 0.0409)	Probable G-protein coupled receptor 45
TR648315|c14_g3_i2	GPSM1_RAT	No change in females	Down in Dom v. Con (-8.98; 0.0069)	G-protein-signaling modulator 1
TR737628|c5_g1_i9	GPT11_MOUSE	No change in females	Up in Sub v. Dom (8.36; 0.012)	G patch domain-containing protein 11
TR525908|c6_g2_i4	GRAM3_MOUSE	No change in females	Up in Sub v. Dom (9.18; 0.0002)	GRAM domain-containing protein 2B
TR563386|c9_g2_i4	GRDN_MOUSE	No change in females	Up in Sub v. Con (4.24; 0.0116)	Girdin
TR345044|c11_g4_i14	GRIA2_MOUSE	No change in females	Up in Dom v. Con (9.73; 0.0001) Up in Sub v. Con (9.02; 0.0043)	Glutamate receptor 2
TR613585|c8_g2_i11	GSE1_MOUSE	No change in females	Up in Dom v. Sub (8.06; 0.0411)	Genetic suppressor element 1
TR617876|c13_g2_i13	GT2D1_MOUSE	No change in females	Up in Sub v. Con (8.46; 0.0448)	General transcription factor II-I repeat domain-containing protein 1

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TR617876|c13_g2_i10	GT2D1_MOUSE	No change in females	Up in Sub v. Con (9.09; 0.0079)	General transcription factor II-I repeat domain-containing protein 1
TR63596|c8_g3_i11	GT2D2_MOUSE	No change in females	Up in Dom v. Con (8.56; 0.0168)	General transcription factor II-I repeat domain-containing protein 2
TR620641|c13_g10_i3	HA1L_MOUSE	Up in Dom v. Con (8.26; 0.0204)	No change in males	H-2 class I histocompatibility antigen, L-D alpha chain
TR361687|c9_g1_i4	HDAC6_MOUSE	No change in females	Up in Sub v. Dom (9.76; 4.55e-08)	Histone deacetylase 6
TR615411|c14_g3_i2	HEBP1_MOUSE	Down in Dom v. Con (-9.09; 0.0002) Down in Sub v. Con (-9.07; 0.0001)	No change in males	Heme-binding protein 1
TR77719|c2_g7_i20	HECW1_MOUSE	No change in females	Up in Dom v. Con (8.23; 0.0463)	E3 ubiquitin-protein ligase HECW1
TR68087|c1_g1_i10	HELZ2_MOUSE	Down in Sub v. Con (-8.04; 0.0357)	No change in males	Helicase with zinc finger domain 2
TR625626|c0_g1_i3	HINT3_RAT	Up in Sub v. Dom (9.94; 9.40e-09)	Up in Sub v. Dom (10.26; 8.09e-12)	Histidine triad nucleotide-binding protein 3
TR660169|c1_g1_i3	HMMR_RAT	No change in females	Up in Dom v. Con (8.31; 0.0367) Up in Dom v. Sub (8.53, 0.0046)	Hyaluronan-mediated motility receptor
TR198219|c16_g6_i2	HNRDL_MOUSE	Up in Dom v. Con (5.19; 0.0254) Up in Dom v. Sub (9.79; 2.47e-07)	No change in males	Heterogeneous nuclear ribonucleoprotein D-like
TR594542|c8_g2_i12	HPCA_RAT	Up in Sub v. Con (8.16; 0.0241) Up in Sub in Dom (8.1; 0.0304)	No change in males	Neuron-specific calcium-binding protein hippocalcin
TR607386|c5_g5_i3	HS12A_MOUSE	No change in females	Up in Dom v. Sub (9.39; 0.0332)	Heat shock 70 kDa protein 12A
TR152480|c1_g2_i13	HTR5A_MOUSE	No change in females	Up in Dom v. Con (9.04; 0.0213)	HEAT repeat-containing protein 5A
TR154660|c8_g2_i2	HTR5B_MOUSE	Up in Sub v. Con (9.53; 4.48e-06)	No change in males	HEAT repeat-containing protein 5B
TR550516|c13_g2_i5	IF4E_RAT	No change in females	Up in Dom v. Sub (7.38; 0.0001)	Eukaryotic translation initiation factor 4E
TR88466|c1_g4_i11	IFG15_MOUSE	Up in Dom v. Sub (9.43; 3.35e-05)	No change in males	Torsin-1A-interacting protein 2, isoform IFRG15
TR88466|c1_g4_i9	IFG15_MOUSE	Up in Sub v. Con (8.68; 0.0275) Up in Sub v. Dom (8.62; 0.0382)	No change in males	Torsin-1A-interacting protein 2, isoform IFRG15

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TR88466|c1_g4_i8	IFG15_MOUSE	Up in Sub v. Dom (8.23; 0.0382)	No change in males	Torsin-1A-interacting protein 2, isoform IFRG15
TR704361|c0_g3_i6	IGS11_MOUSE	No change in females	Down in Dom v. Con (-9.04; 0.0471)	Immunoglobulin superfamily member 11
TR273156|c0_g1_i17	IGSF1_MOUSE	No change in females	Up in Dom v. Sub (8.01; 0.0416)	Immunoglobulin superfamily member 1
TR192311|c5_g3_i17	IKZF4_MOUSE	No change in females	Up in Sub v. Con (8.87; 0.0216)	Zinc finger protein Eos
TR371089|c0_g2_i5	IL1R1_RAT	No change in females	Up in Dom v. Sub (8.7; 0.0083)	Interleukin-1 receptor type 1
TR371089|c0_g2_i1	IL1R1_RAT	No change in females	Up in Sub v. Dom (8.26; 0.0233)	Interleukin-1 receptor type 1
TR98898|c0_g1_i4	IMDH2_CRIGR	Up in Dom v. Sub (10.15; 4.77e-09)	No change in males	Inosine-5'-monophosphate dehydrogenase 2
TR98898|c0_g1_i3	IMDH2_MOUSE	Down in Sub v. Con (-9.86; 0.0175) Down in Sub v. Dom (-10.06; 1.27e-08)	No change in males	Inosine-5'-monophosphate dehydrogenase 2
TR737239|c13_g3_i8	IP6K2_MOUSE	Down in Sub v. Con (-9.36; 0.0366)	No change in males	Inositol hexakisphosphate kinase 2
TR260068|c11_g2_i15	IPO9_MOUSE	No change in females	Up in Sub v. Con (8.81; 0.009)	Importin-9
TR776756|c11_g7_i1	IRS1_MOUSE	Up in Sub v. Dom (9.19; 0.0013)	No change in males	Insulin receptor substrate 1
TR233613|c0_g1_i3	ITM2C_RAT	Down in Sub v. Con (-7.36; 0.0044)	Up in Dom v. Con (9.18; 0.0003) Up in Sub v. Con (9.23; 4.15e-05)	Integral membrane protein 2C
TR233613|c0_g1_i4	ITM2C_RAT	Up in Dom v. Con (10.25; 0.0018)	Up in Dom v. Con (7.01; 0.0063)	Integral membrane protein 2C
TR495590|c6_g1_i12	ITSN2_MOUSE	Down in Dom v. Con (-9.42; 1.41e-05) Down in Dom v. Sub (-10.19; 6.52e-11)	No change in males	Intersectin-2
TR463575|c11_g2_i10	JPH1_MOUSE	Down in Sub v. Con (-9.63; 1.31e-06)	Up in Sub v. Dom (5.59; 0.0407)	Junctophilin-1
TR220853|c0_g1_i7	K2022_MOUSE	No change in females	Up in Sub v. Con (8.61; 0.0245)	Neurite extension and migration factor
TR220853|c0_g1_i2	K2022_MOUSE	Up in Dom v. Con (9.16; 0.0002)	No change in males	Neurite extension and migration factor
TR148994|c0_g2_i6	KAD4_RAT	Down in Sub v. Con (-9.41; 0.0328) Down in Sub v. Dom (-9.41; 0.0395)	No change in males	Adenylate kinase 4, mitochondrial

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR750954|c3_g3_i3	KALRN_MOUSE	No change in females	Up in Sub v. Dom (9.01; 0.0003)	Kalirin
TR130077|c10_g2_i15	KBTB4_MOUSE	Up in Dom v. Con (8.11; 0.0423) Up in Sub v. Con (9.09; 0.0001)	Down in Dom v. Con (-9.22; 0.0021)	Kelch repeat and BTB domain-containing protein 4
TR339072|c3_g3_i12	KCNA2_RAT	Up in Sub v. Dom (9.52; 1.41e-05)	No change in males	Potassium voltage-gated channel subfamily A member 2
TR73160|c7_g1_i7	KCNH3_RAT	No change in females	Down in Sub v. Con (-8.45; 0.0459)	Potassium voltage-gated channel subfamily H member 3
TR12653|c6_g2_i17	KCNT2_RAT	No change in females	Up in Sub v. Dom (9.72; 0.0162)	Potassium channel subfamily T member 2
TR580703|c5_g1_i2	KCTD7_MOUSE	No change in females	Up in Dom v. Con (9.08; 0.0027) Up in Sub v. Con (9.19; 0.0019)	BTB/POZ domain-containing protein KCTD7
TR10245|c6_g2_i22	KDM3A_MOUSE	Down in Dom v. Con (-8.35; 0.0147) Down in Dom v. Sub (-8.68; 0.0032)	No change in males	Lysine-specific demethylase 3A
TR214512|c7_g2_i21	KDM6B_MOUSE	No change in females	Up in Sub v. Con (9.24; 0.0008)	Lysine-specific demethylase 6B
TR214512|c7_g2_i22	KDM6B_MOUSE	Up in Sub v. Con (8.33; 0.0179) Up in Sub v. Dom (8.27; 0.0221)	No change in males	Lysine-specific demethylase 6B
TR621495|c1_g3_i2	KI13A_MOUSE	Down in Sub v. Con (-9.05; 0.0017)	No change in males	Kinesin-like protein KIF13A
TR20782|c12_g5_i12	KIFC3_MOUSE	Up in Dom v. Con (8.09; 0.0446)	No change in males	Kinesin-like protein KIFC3
TR67005|c18_g1_i10	KLC1_RAT	No change in females	Up in Sub v. Dom (9.75; 0.0159)	Kinesin light chain 1
TR67005|c18_g1_i27	KLC1_RAT	No change in females	Up in Sub v. Dom (10.52; 0.003)	Kinesin light chain 1
TR383901|c2_g1_i19	KLH17_RAT	No change in females	Up in Dom v. Sub (7; 0.0016)	Kelch-like protein 17
TR463198|c6_g4_i11	KMT2A_MOUSE	Up in Dom v. Sub (8.11; 0.0382)	No change in males	Histone-lysine N-methyltransferase 2A
TR277869|c4_g1_i3	KMT2D_MOUSE	No change in females	Up in Dom v. Sub (9.5; 0.0281)	Histone-lysine N-methyltransferase 2D
TR335446|c0_g2_i19	KPYM_RAT	No change in females	Up in Dom v. Con (9.11; 0.0141)	Pyruvate kinase PKM
TR335446|c0_g2_i2	KPYM_RAT	Up in Dom v. Con (6.2; 0.039)	No change in males	Pyruvate kinase PKM

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TR100414|c0_g2_i2	KRCC1_MOUSE	No change in females	Up in Sub v. Con (8.74; 0.0481)	Lysine-rich coiled-coil protein 1
TR480375|c2_g1_i7	LAMA1_MOUSE	Down in Sub v. Con (-9.83; 0.0155)	No change in males	Laminin subunit alpha-1
TR480375|c2_g1_i5	LAMA1_MOUSE	No change in females	Up in Sub v. Con (8.57; 0.0459)	Laminin subunit alpha-1
TR101141|c1_g2_i8	LAMA2_MOUSE	Down in Dom v. Con (-9.23; 0.0007) Down in Dom v. Sub (-8.2; 0.0204)	No change in males	Laminin subunit alpha-2
TR180895|c4_g3_i10	LDLR_CRIGR	No change in females	Down in Dom v. Con (-9.3; 0.006)	Low-density lipoprotein receptor
TR323008|c0_g3_i1	LGI3_MOUSE	Up in Sub v. Dom (8.6; 0.0031)	No change in males	Leucine-rich repeat LGI family member 3
TR68341|c0_g1_i3	LIPL_RAT	No change in females	Up in Sub v. Con (8.95; 0.0047)	Lipoprotein lipase
TR99902|c1_g2_i24	LMTK1_MOUSE	No change in females	Up in Dom v. Sub (8.89; 0.0004)	Serine/threonine-protein kinase LMTK1
TR390042|c1_g3_i9	LONF3_MOUSE	Down in Sub v. Con (-12.15; 2.07e-13) Down in Sub v. Dom (-9.71; 0.0266)	No change in males	LON peptidase N-terminal domain and RING finger protein 3
TR376100|c10_g2_i2	LPPR4_MOUSE	No change in females	Down in Dom v. Con (-9.02; 0.0049)	Phospholipid phosphatase-related protein type 4
TR198870|c12_g4_i7	LRCH1_MOUSE	No change in females	Up in Sub v. Con (9.56; 0.0002)	Leucine-rich repeat and calponin homology domain-containing protein 1
TR198870|c12_g4_i12	LRCH1_MOUSE	Up in Sub v. Dom (6.67; 0.0169)	No change in males	Leucine-rich repeat and calponin homology domain-containing protein 1
TR181123|c0_g1_i6	LRCH4_MOUSE	Up in Dom v. Con (8.47; 0.0361)	No change in males	Leucine-rich repeat and calponin homology domain-containing protein 4
TR35563|c2_g2_i7	LRFN5_MOUSE	Up in Dom v. Con (9.19; 0.0003)	No change in males	Leucine-rich repeat and fibronectin type-III domain-containing protein 5
TR5357|c9_g3_i3	LSM8_MOUSE	No change in females	Down in Dom v. Con (-9.75; 0.042)	U6 snRNA-associated Sm-like protein LSm8
TR5357|c9_g3_i11	LSM8_MOUSE	No change in females	Up in Dom v. Sub (9.7; 0.019)	U6 snRNA-associated Sm-like protein LSm8
TR372441|c0_g3_i5	M3K6_MOUSE	No change in females	Up in Dom v. Con (8.37; 0.0286)	Mitogen-activated protein kinase kinase kinase 6
TR671122|c6_g9_i31	MAGI2_MOUSE	Up in Sub v. Con (8.73; 0.0262)	No change in males	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2
TR707668|c3_g1_i4	MAP1S_MOUSE	No change in females	Down in Sub v. Con (-12.16; 0.0014)	Microtubule-associated protein 1S
TR707668|c3_g1_i6	MAP1S_MOUSE	No change in females	Down in Sub v. Con (-10.91; 0.0123)	Microtubule-associated protein 1S

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TR504027|c3_g6_i4	MAP4_MOUSE	Down in Sub v. Con (-11.05; 0.0013) Down in Sub v. Dom (-11.72; 0.0005)	No change in males	Microtubule-associated protein 4
TR51000|c1_g4_i5	MAP6_MOUSE	No change in females	Up in Sub v. Con (9.04; 0.0027)	Microtubule-associated protein 6
TR754933|c8_g3_i8	MARE3_RAT	Down in Sub v. Con (-11.76; 0.0004) Down in Sub v. Dom (-11.94; 0.0004)	No change in males	Microtubule-associated protein RP/EB family member 3
TR351367|c3_g1_i2	MARH1_MOUSE	Down in Sub v. Con (-8.58; 0.0061)	No change in males	E3 ubiquitin-protein ligase MARCH1
TR406133|c1_g1_i5	MB12B_MOUSE	Up in Dom v. Sub (5.76; 0.0005)	No change in males	Multivesicular body subunit 12B
TR91087|c3_g4_i1	MBD1_MOUSE	Down in Dom v. Con (-8.57; 0.0141)	No change in males	Methyl-CpG-binding domain protein 1
TR209478|c7_g6_i11	MBNL2_RAT	No change in females	Down in Dom v. Con (-10.28; 8.99e-08)	Muscleblind-like protein 2
TR112862|c9_g2_i1	MDGA2_RAT	Up in Dom v. Con (10.02; 0.0152) Up in Dom v. Sub (9.94; 0.0128)	Down in Sub v. Con (-9.69; 0.04) Down in Sub v. Dom (-9.99; 0.011)	MAM domain-containing glycosylphosphatidylinositol anchor protein 2
TR449005|c6_g1_i17	MED12_MOUSE	Up in Sub v. Con (8.12; 0.0407)	No change in males	Mediator of RNA polymerase II transcription subunit 12
TR195400|c2_g1_i21	MEGF8_MOUSE	Up in Sub v. Con (9.72; 0.0184)	No change in males	Multiple epidermal growth factor-like domains protein 8
TR751996|c1_g3_i12	MEP1A_RAT	Down in Dom v. Con (-8.5; 0.0147)	Up in Sub v. Con (8.47; 0.0284)	Meprin A subunit alpha
TR525714|c1_g2_i4	METH_RAT	No change in females	Up in Dom v. Sub (9; 0.0004)	Methionine synthase
TR583033|c0_g1_i2	MFHA1_MOUSE	No change in females	Up in Sub v. Con (8.89; 0.0123)	Malignant fibrous histiocytoma-amplified sequence 1 homolog
TR109397|c8_g3_i2	MFSD6_MOUSE	Up in Dom v. Con (8.27; 0.0343)	No change in males	Major facilitator superfamily domain-containing protein 6
TR90995|c7_g1_i4	MGAP_MOUSE	Up in Sub v. Dom (8.32; 0.0111)	No change in males	MAX gene-associated protein
TR225465|c13_g3_i8	MGT5A_CRIGR	Down in Sub v. Con (-8.66; 0.0017)	No change in males	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A
TR225465|c13_g3_i2	MGT5A_CRIGR	No change in females	Up in Dom v. Sub (9.6; 0.0288)	Alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase A
TR645064|c5_g4_i19	MICA3_MOUSE	Up in Sub v. Dom (9.09; 0.0004)	No change in males	[F-actin]-monooxygenase MICAL3
TR270798|c7_g4_i12	MIO_MOUSE	No change in females	Up in Sub v. Con (9.14; 0.0011)	GATOR complex protein MIOS

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TR512995|c0_g2_i4	MK04_MOUSE	Up in Sub v. Con (10.07; 2.04e-08)	No change in males	Mitogen-activated protein kinase 4
TR113730|c6_g2_i7	MKL1_MOUSE	No change in females	Up in Dom v. Con (9.32; 0.0011)	MKL/myocardin-like protein 1
TR225339|c11_g3_i8	MO4L2_RAT	Down in Sub v. Con (-9.79; 3.36e-06) Down in Sub v. Dom (-9.9; 0.0107)	No change in males	Mortality factor 4-like protein 2
TR307270|c13_g5_i8	MTMRC_MOUSE	Down in Sub v. Con (-8.24; 0.0459)	No change in males	Myotubularin-related protein 12
TR535379|c7_g1_i1	MXI1_RAT	Down in Sub v. Con (-9.95; 4.80e-09)	No change in males	Max-interacting protein 1
TR20412|c18_g1_i9	N42L1_MOUSE	Up in Dom v. Sub (9.05; 0.0014)	Up in Dom v. Con (8.83; 0.0086)	NEDD4-binding protein 2-like 1
TR186309|c3_g1_i2	NAA50_MOUSE	Up in Dom v. Sub (8.61; 0.0172)	No change in males	N-alpha-acetyltransferase 50
TR588175|c7_g3_i3	NAB1_MESAU	Down in Sub v. Con (-9.01; 0.0004)	No change in males	NGFI-A-binding protein 1
TR399252|c3_g4_i3	NAB2_MOUSE	Up in Dom v. Con (8.2; 0.0343)	No change in males	NGFI-A-binding protein 2
TR180180|c8_g3_i13	NBEL2_MOUSE	Up in Sub v. Dom (8.84; 0.001)	No change in males	Neurobeachin-like protein 2
TR195037|c5_g1_i3	NDUAA_RAT	No change in females	Up in Dom v. Sub (9.18; 0.0003)	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial
TR389055|c11_g1_i19	NEK9_MOUSE	Up in Sub v. Dom (9.8; 1.40e-05)	No change in males	Serine/threonine-protein kinase Nek9
TR687290|c7_g2_i5	NELL2_RAT	Down in Dom v. Con (-8.66; 0.0025)	No change in males	Protein kinase C-binding protein NELL2
TR755075|c0_g1_i15	NEUL4_MOUSE	No change in females	Up in Dom v. Con (8.91; 0.0073)	Neuralized-like protein 4
TR607309|c0_g2_i3	NEUR1_MOUSE	No change in females	Down in Dom v. Con (-9.42; 0.0006)	Sialidase-1
TR545769|c4_g2_i6	NFAT5_RAT	Up in Dom v. Con (9.6; 1.24e-05)	No change in males	Nuclear factor of activated T-cells 5
TR53098|c2_g6_i13	NFYB_RAT	Down in Sub v. Con (-8.58; 0.007)	No change in males	Nuclear transcription factor Y subunit beta
TR236179|c2_g2_i3	NIPA1_MOUSE	Down in Sub v. Con (-10.91; 0.0017)	Up in Dom v. Sub (8.21; 0.0253)	Magnesium transporter NIPA1
TR607032|c0_g1_i5	NK3R_MOUSE	Up in Dom v. Sub (9.23; 2.69e-05)	No change in males	Neuromedin-K receptor
TR607032|c0_g1_i2	NK3R_MOUSE	Up in Sub v. Dom (9.18; 5.46e-05)	No change in males	Neuromedin-K receptor

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TR632261|c4_g1_i9	NKTR_MOUSE	Down in Sub v. Con (-9.49; 0.0341)	No change in males	NK-tumor recognition protein
TR524789|c1_g4_i17	NMT2_MOUSE	Up in Sub v. Dom (9.19; 0.0005)	Down in Sub v. Con (-9.02; 0.0123)	Glycylpeptide N-tetradecanoyltransferase 2
TR24607|c0_g1_i3	NOE3_RAT	Up in Dom v. Con (10.61; 0.0037) Up in Sub v. Con (9.53; 0.0264)	No change in males	Noelin-3
TR60453|c4_g2_i6	NOP14_MOUSE	Up in Dom v. Con (8.07; 0.0355)	No change in males	Nucleolar protein 14
TR60453|c4_g2_i15	NOP14_MOUSE	Up in Dom v. Con (9.14; 8.33e-05)	No change in males	Nucleolar protein 14
TR297293|c1_g3_i13	NOS3_MOUSE	No change in females	Up in Dom v. Con (8.42; 0.0255)	Nitric oxide synthase, endothelial
TR725436|c1_g2_i6	NPHP1_MOUSE	Up in Sub v. Con (9.77; 0.0174)	No change in males	Nephrocystin-1
TR411818|c1_g1_i10	NRP1_MOUSE	No change in females	Up in Dom v. Sub (10.4; 0.0035)	Neuropilin-1
TR417502|c2_g1_i5	NSMA_RAT	No change in females	Up in Sub v. Con (8.45; 0.0459)	Sphingomyelin phosphodiesterase 2
TR475792|c2_g2_i16	NU214_MOUSE	Up in Sub v. Con (8.21; 0.0288)	No change in males	Nuclear pore complex protein Nup214
TR442682|c7_g1_i8	NUP50_RAT	No change in females	Down in Sub v. Con (-9.29; 0.0015) Down in Sub v. Dom (-10.24; 0.012)	Nuclear pore complex protein Nup50
TR167074|c10_g1_i6	NUP93_RAT	Up in Sub v. Dom (8.52; 0.0436)	No change in males	Nuclear pore complex protein Nup93
TR87431|c3_g1_i2	NWD2_MOUSE	Up in Dom v. Con (10.57; 0.0037) Up in Dom v. Sub (10.49; 0.0028)	No change in males	NACHT and WD repeat domain-containing protein 2
TR508960|c3_g2_i9	ODO1_RAT	Down in Sub v. Con (-8.91; 0.0004) Down in Sub v. Dom (-8.29; 0.0304)	No change in males	2-oxoglutarate dehydrogenase, mitochondrial
TR667186|c0_g2_i4	OGFD2_MOUSE	No change in females	Up in Dom v. Con (8.39; 0.0274)	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2
TR620383|c0_g7_i9	OSBL6_MOUSE	Up in Dom v. Con (8.46; 0.0127) Up in Dom v. Sub (8.38; 0.0124)	No change in males	Oxysterol-binding protein-related protein 6
TR620383|c0_g7_i6	OSBL6_MOUSE	Up in Dom v. Sub (9.3; 0.0003)	No change in males	Oxysterol-binding protein-related protein 6

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TR620383|c0_g7_i15	OSBL6_MOUSE	Up in Sub v. Dom (9.62; 3.18e-05)	No change in males	Oxysterol-binding protein-related protein 6
TR281026|c11_g4_i16	OSBL8_MOUSE	No change in females	Up in Sub v. Dom (8.12; 0.0317)	Oxysterol-binding protein-related protein 8
TR259645|c2_g2_i4	P5CR2_MOUSE	No change in females	Up in Sub v. Dom (8.3; 0.0248)	Pyrroline-5-carboxylate reductase 2
TR134896|c6_g2_i3	PACR_MOUSE	Up in Sub v. Dom (9.91; 0.0131)	No change in males	Pituitary adenylate cyclase-activating polypeptide type I receptor
TR19880|c8_g6_i12	PAK2_RAT	Down in Sub v. Con (-9.17; 6.11e-05) Down in Sub v. Dom (-8.89; 0.0005)	No change in males	Serine/threonine-protein kinase PAK 2
TR19880|c8_g6_i8	PAK2_RAT	Up in Sub v. Con (8.19; 5.25e-08)	Up in Dom v. Sub (6.14; 0.0095)	Serine/threonine-protein kinase PAK 2
TR451580|c1_g2_i8	PAPOG_MOUSE	Down in Sub v. Con (-5.28; 0.035)	No change in males	Poly(A) polymerase gamma
TR451580|c1_g2_i6	PAPOG_MOUSE	No change in females	Up in Dom v. Sub (9.08; 0.0006)	Poly(A) polymerase gamma
TR207093|c0_g1_i28	PCD16_MOUSE	No change in females	Up in Dom v. Con (8.62; 0.015)	Protocadherin-16
TR284008|c0_g1_i4	PCX3_MOUSE	No change in females	Up in Dom v. Con (8.33; 0.0366)	Pecanex-like protein 3
TR652575|c6_g1_i4	PCY1B_RAT	Up in Dom v. Con (8.4; 0.0152)	No change in males	Choline-phosphate cytidylyltransferase B
TR50213|c1_g1_i9	PDE1B_RAT	Up in Sub v. Con (8.62; 0.0066)	No change in males	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B
TR692604|c8_g2_i21	PDE1C_RAT	No change in females	Up in Sub v. Dom (8.28; 0.0281)	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C
TR308413|c8_g3_i12	PF21A_MOUSE	Down in Dom v. Con (-9.41; 2.76e-05)	No change in males	PHD finger protein 21A
TR120662|c2_g2_i24	PFKAM_MOUSE	Down in Sub v. Con (-10.19; 3.66e-08)	Up in Sub v. Con (9.94; 3.78e-05)	ATP-dependent 6-phosphofructokinase, muscle type
TR764800|c5_g1_i25	PGP_MOUSE	Up in Sub v. Dom (8.88; 0.0005)	No change in males	Glycerol-3-phosphate phosphatase
TR78315|c7_g1_i11	PHF12_MOUSE	No change in females	Up in Dom v. Sub (8.93; 0.0003)	PHD finger protein 12
TR396488|c0_g3_i21	PHF2_MOUSE	No change in females	Up in Dom v. Con (10.02; 1.90e-05)	Lysine-specific demethylase PHF2
TR211358|c6_g5_i1	PHTF1_MOUSE	No change in females	Up in Dom v. Sub (10.09; 0.008)	Putative homeodomain transcription factor 1
TR211358|c6_g5_i7	PHTF1_MOUSE	No change in females	Up in Sub v. Dom (8.67; 0.0148)	Putative homeodomain transcription factor 1

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TR216650|c8_g4_i2	PLAP_RAT	Up in Sub v. Con (9.05; 0.0017) Up in Sub v. Dom (8.99; 0.0022)	No change in males	Phospholipase A-2-activating protein
TR79717|c0_g1_i11	PLCB1_RAT	Down in Sub v. Con (-9.76; 0.0179)	No change in males	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1
TR79717|c0_g1_i1	PLCB1_RAT	Down in Sub v. Con (-9.41; 0.0363)	No change in males	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1
TR84722|c8_g2_i17	PLEC_CRIGR	No change in females	Up in Dom v. Con (9.05; 0.0184) Up in Sub v. Con (9.54; 0.0003)	Plectin
TR84722|c8_g2_i10	PLEC_CRIGR	No change in females	Up in Sub v. Con (11.4; 3.62e-12)	Plectin
TR554121|c4_g1_i12	PLPL7_MOUSE	No change in females	Up in Dom v. Sub (8.17; 0.0462)	Patatin-like phospholipase domain-containing protein 7
TR374955|c3_g1_i8	PLPL8_MOUSE	No change in females	Up in Sub v. Con (9.42; 0.0006)	Calcium-independent phospholipase A2-gamma
TR732934|c3_g2_i19	PLXB1_MOUSE	No change in females	Up in Sub v. Dom (8.59; 0.003)	Plexin-B1
TR728427|c16_g5_i3	PP2BA_RAT	No change in females	Up in Dom v. Con (10.44; 5.10e-07)	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform
TR492399|c10_g2_i4	PP2BB_MOUSE	Up in Sub v. Con (9.31; 0.0415)	No change in males	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform
TR355760|c15_g2_i1	PPME1_RAT	No change in females	Up in Dom v. Con (8.21; 0.0471)	Protein phosphatase methylesterase 1
TR765050|c8_g1_i8	PR40A_MOUSE	No change in females	Up in Dom v. Con (9.93; 0.0059)	Pre-mRNA-processing factor 40 homolog A
TR488977|c4_g2_i4	PRGC1_RAT	Up in Dom v. Sub (10.06; 1.29e-08)	No change in males	Peroxisome proliferator-activated receptor gamma coactivator 1-alpha
TR701529|c3_g1_i2	PRKRA_MOUSE	Up in Sub v. Dom (9.65; 0.0327)	No change in males	Interferon-inducible double-stranded RNA-dependent protein kinase activator A
TR85359|c0_g1_i2	PRP4B_RAT	No change in females	Down in Dom v. Con (-10.37; 2.26e-06)	Serine/threonine-protein kinase PRP4 homolog
TR242744|c4_g6_i9	PRP6_MOUSE	Up in Sub v. Con (9.79; 3.30e-07)	No change in males	Pre-mRNA-processing factor 6
TR196275|c3_g1_i5	PRP8_MOUSE	Up in Sub v. Con (8.23; 0.0272)	No change in males	Pre-mRNA-processing-splicing factor 8
TR241967|c14_g2_i4	PSA2_RAT	Up in Dom v. Con (8.25; 0.0311)	No change in males	Proteasome subunit alpha type-2
TR186395|c11_g3_i12	PTBP2_RAT	Up in Dom v. Con (9.31; 0.0014)	No change in males	Polypyrimidine tract-binding protein 2
TR515944|c8_g3_i14	PTCD3_MOUSE	No change in females	Up in Sub v. Dom (8.57; 0.011)	Pentatricopeptide repeat domain-containing protein 3, mitochondrial

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR186263|c7_g1_i11	PTHD2_MOUSE	No change in females	Up in Sub v. Con (8.33; 0.0471)	Protein dispatched homolog 3
TR185321|c6_g5_i12	PTN2_RAT	Up in Dom v. Con (8.31; 0.0152)	No change in males	Tyrosine-protein phosphatase non-receptor type 2
TR618188|c12_g2_i1	PTPRA_RAT	Down in Sub v. Con (-5.39; 0.0274)	No change in males	Receptor-type tyrosine-protein phosphatase alpha
TR44165|c10_g1_i9	PTPRD_MOUSE	Down in Dom v. Con (-9.9; 0.0161)	No change in males	Receptor-type tyrosine-protein phosphatase delta
TR44165|c10_g1_i4	PTPRD_MOUSE	Up in Sub v. Con (8.42; 0.0274)	No change in males	Receptor-type tyrosine-protein phosphatase delta
TR44165|c10_g1_i1	PTPRD_MOUSE	Up in Sub v. Con (8.93; 0.0263)	No change in males	Receptor-type tyrosine-protein phosphatase delta
TR117342|c9_g2_i25	PTPRS_RAT	No change in females	Up in Dom v. Sub (9.42; 0.0342)	Receptor-type tyrosine-protein phosphatase S
TR188330|c12_g1_i5	PXDN_MOUSE	No change in females	Up in Sub v. Dom (9.69; 5.05e-05)	Peroxidasin homolog
TR368474|c8_g4_i8	PYRG1_MOUSE	No change in females	Down in Dom v. Con (-9.03; 0.0066) Down in Sub v. Con (-8.94; 0.0112)	CTP synthase 1
TR607537|c9_g13_i2	QSOX2_MOUSE	No change in females	Up in Dom v. Sub (8.41; 0.012)	Sulfhydryl oxidase 2
TR75122|c11_g6_i1	R12BA_MOUSE	Up in Sub v. Con (9.49; 0.0326)	No change in males	RNA-binding protein 12B-A
TR743387|c1_g1_i17	R3HD2_MOUSE	No change in females	Down in Dom v. Con (-9.08; 0.0073) Down in Sub v. Con (-8.99; 0.0123)	R3H domain-containing protein 2
TR253589|c7_g1_i4	RA51D_MOUSE	No change in females	Up in Dom v. Sub (8.91; 0.0129)	DNA repair protein RAD51 homolog 4
TR253589|c7_g1_i3	RA51D_MOUSE	Up in Sub v. Dom (6.16; 0.0028)	Up in Dom v. Con (5.62; 0.0351)	DNA repair protein RAD51 homolog 4
TR498468|c0_g1_i2	RAB43_MOUSE	No change in females	Up in Dom v. Con (8.45; 0.0245)	Ras-related protein Rab-43
TR76607|c0_g1_i2	RAD50_RAT	Up in Dom v. Con (8.36; 0.0129)	No change in males	DNA repair protein RAD50
TR538118|c7_g11_i3	RAN_RAT	Down in Dom v. Con (-11.07; 0.0017) Down in Sub v. Con (-11.06; 0.0013)	No change in males	GTP-binding nuclear protein Ran
TR476256|c8_g2_i5	RAP1A_RAT	No change in females	Up in Sub v. Con (10.11, 0.0289)	Ras-related protein Rap-1A
TR58470|c1_g1_i1	RB6I2_MOUSE	No change in females	Up in Sub v. Dom (5.8; 0.0095)	ELKS/Rab6-interacting/CAST family member 1

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR543482|c10_g9_i9	RBGP1_MOUSE	No change in females	Up in Dom v. Con (10; 0.0267)	Rab GTPase-activating protein 1
TR205592|c14_g3_i2	RBM14_MOUSE	Up in Sub v. Con (8.7; 0.0043)	No change in males	RNA-binding protein 14
TR692274|c4_g2_i5	RECQ4_MOUSE	Up in Sub v. Dom (8.22; 0.0229)	No change in males	ATP-dependent DNA helicase Q4
TR700954|c0_g1_i12	RELN_RAT	Up in Sub v. Dom (8.68; 0.0017)	No change in males	Reelin
TR92618|c3_g2_i11	RERE_RAT	No change in females	Up in Dom v. Con (8.85; 0.0168) Up in Sub v. Con (8.65; 0.0198)	Arginine-glutamic acid dipeptide repeats protein
TR408896|c7_g2_i9	RFIP3_MOUSE	No change in females	Up in Sub v. Con (8.73; 0.0167)	Rab11 family-interacting protein 3
TR255783|c12_g1_i1	RFX4_MOUSE	Down in Sub v. Con (-8.74; 0.0027) Down in Sub v. Dom (-8.99; 0.0009)	No change in males	Transcription factor RFX4
TR84362|c5_g2_i24	RIMS1_MOUSE	Up in Sub v. Con (8.68; 0.005) Up in Sub v. Dom (8.62; 0.0064)	No change in males	Regulating synaptic membrane exocytosis protein 1
TR437166|c0_g1_i7	RL3_MOUSE	No change in females	Up in Dom v. Con (10.5; 1.82e-07)	60S ribosomal protein L3
TR175708|c4_g1_i2	RL4_MOUSE	No change in females	Up in Sub v. Dom (8.26; 0.0182)	60S ribosomal protein L4
TR516330|c10_g1_i1	RN121_MOUSE	No change in females	Up in Sub v. Con (9.63; 9.65e-05)	RING finger protein 121
TR631917|c2_g1_i14	RN123_RAT	Up in Dom v. Sub (9.91; 0.021)	No change in males	E3 ubiquitin-protein ligase RNF123
TR403545|c0_g1_i3	RN169_MOUSE	No change in females	Up in Sub v. Dom (8.28; 0.0156)	E3 ubiquitin-protein ligase RNF169
TR604819|c0_g3_i31	RN213_MOUSE	Down in Sub v. Con (-10.39; 3.55e-13)	No change in males	E3 ubiquitin-protein ligase RNF213
TR437936|c11_g1_i9	ROGDI_RAT	Down in Dom v. Con (-8.33; 0.0215)	No change in males	Protein rogdi homolog
TR34457|c7_g3_i7	RPAP3_RAT	No change in females	Up in Dom v. Sub (8.08; 0.0416)	RNA polymerase II-associated protein 3
TR411257|c1_g4_i17	RPGR1_MOUSE	No change in females	Up in Dom v. Sub (9.78; 4.90e-06)	X-linked retinitis pigmentosa GTPase regulator-interacting protein 1
TR566505|c9_g5_i4	RPKL1_MOUSE	No change in females	Down in Dom v. Con (-9.2; 0.0009) Down in Sub v. Con (-9.12; 0.0014)	Ribosomal protein S6 kinase-like 1

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR48032|c6_g1_i1	RPN2_RAT	Down in Sub v. Con (-8.24; 0.0373)	No change in males	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2
TR47678|c14_g1_i6	RRFM_RAT	No change in females	Up in Sub v. Dom (8.54; 0.0084)	Ribosome-recycling factor, mitochondrial
TR410399|c11_g4_i3	RT15_RAT	Up in Sub v. Con (8.14; 0.0415)	No change in males	28S ribosomal protein S15, mitochondrial
TR584664|c10_g2_i9	RUBIC_MOUSE	No change in females	Up in Dom v. Con (9.91; 0.029) Up in Sub v. Con (10.93; 8.42e-08)	Run domain Beclin-1-interacting and cysteine-rich domain-containing protein
TR518595|c3_g3_i3	RUFY1_MOUSE	Down in Sub v. Con (-8.55; 0.0077)	No change in males	RUN and FYVE domain-containing protein 1
TR605459|c0_g3_i4	RUSD1_MOUSE	Up in Dom v. Sub (9.94; 0.0124)	No change in males	RNA pseudouridylate synthase domain-containing protein 1
TR458627|c7_g1_i2	RXFP1_RAT	Up in Dom v. Sub (8.97; 0.0022)	No change in males	Relaxin receptor 1
TR658790|c12_g1_i5	S15A2_MOUSE	No change in females	Up in Dom v. Sub (9.83; 1.59e-08)	Solute carrier family 15 member 2
TR658790|c12_g1_i3	S15A2_MOUSE	No change in females	Up in Sub v. Con (9.75; 0.0001) Up in Sub v. Dom (4.02; 0.0083)	Solute carrier family 15 member 2
TR553895|c1_g3_i4	S22AN_MOUSE	Up in Sub v. Dom (10.24; 0.0042)	No change in males	Solute carrier family 22 member 23
TR292620|c7_g1_i10	S39AC_MOUSE	Up in Dom v. Sub (8.4; 0.0182)	No change in males	Zinc transporter ZIP12
TR93960|c6_g1_i5	S4A10_MOUSE	Down in Dom v. Con (-7.65; 0.0289) Down in Dom v. Sub (-8.86; 1.85e-26)	No change in males	Sodium-driven chloride bicarbonate exchanger
TR479334|c10_g5_i10	S61A2_MOUSE	Up in Dom v. Sub (6.9; 0.008)	No change in males	Protein transport protein Sec61 subunit alpha isoform 2
TR171712|c0_g1_i2	SARDH_MOUSE	Down in Dom v. Con (-8.34; 0.0193)	No change in males	Sarcosine dehydrogenase, mitochondrial
TR576065|c6_g1_i9	SC24A_MOUSE	Down in Sub v. Con (-9.49; 0.0395)	Up in Dom v. Sub (9.01; 0.0002)	Protein transport protein Sec24A
TR260313|c7_g4_i4	SDCG3_MOUSE	No change in females	Up in Sub v. Con (9.77; 0.0003)	Serologically defined colon cancer antigen 3 homolog
TR725493|c4_g4_i10	SE1L1_MESAU	Up in Dom v. Sub (9.4; 0.0009)	No change in males	Protein sel-1 homolog 1
TR317120|c0_g2_i1	SEM3C_MOUSE	Up in Sub v. Con (9.02; 0.0002)	No change in males	Semaphorin-3C
TR731590|c9_g2_i13	SEM4D_MOUSE	No change in females	Up in Sub v. Dom (9.76; 0.0003)	Semaphorin-4D

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR363510|c6_g3_i17	SENP6_MOUSE	No change in females	Up in Sub v. Con (8.33; 0.0494)	Sentrin-specific protease 6
TR302088|c13_g1_i9	SERC5_RAT	Up in Sub v. Dom (9.46; 0.0457)	No change in males	Serine incorporator 5
TR31238|c0_g1_i3	SET1B_MOUSE	No change in females	Up in Sub v. Dom (8.19; 0.0226)	Histone-lysine N-methyltransferase SETD1B
TR448160|c5_g1_i7	SFR19_MOUSE	No change in females	Up in Sub v. Dom (8.12; 0.0279)	Splicing factor, arginine/serine-rich 19
TR197077|c5_g1_i12	SGIP1_MOUSE	No change in females	Down in Dom v. Con (-9.92; 5.91e-06)	SH3-containing GRB2-like protein 3-interacting protein 1
TR698500|c15_g1_i3	SH3B4_MOUSE	Down in Dom v. Con (-8.81; 0.0012)	No change in males	SH3 domain-binding protein 4
TR562281|c0_g4_i9	SH3K1_MOUSE	No change in females	Up in Dom v. Sub (8.07; 0.0332)	SH3 domain-containing kinase-binding protein 1
TR124845|c7_g5_i4	SI1L2_MOUSE	No change in females	Up in Sub v. Con (8.49; 0.0387)	Signal-induced proliferation-associated 1-like protein 2
TR214033|c1_g1_i5	SLF2_MOUSE	No change in females	Up in Dom v. Sub (8.17; 0.0288)	SMC5-SMC6 complex localization factor protein 2
TR685188|c6_g1_i8	SLIK2_MOUSE	Down in Dom v. Con (-9.29; 0.0026)	No change in males	SLIT and NTRK-like protein 2
TR325443|c11_g1_i3	SMS1_RAT	Up in Sub v. Con (8.79; 0.0019)	No change in males	Phosphatidylcholine:ceramide cholinephosphotransferase 1
TR102150|c7_g3_i8	SNX30_MOUSE	Up in Sub v. Dom (9.97; 0.0094)	No change in males	Sorting nexin-30
TR44352|c8_g3_i9	SO3A1_MOUSE	No change in females	Up in Dom v. Con (10.31; 0.0141) Up in Sub v. Con (9.82; 0.0462)	Solute carrier organic anion transporter family member 3A1
TR44352|c8_g3_i6	SO3A1_MOUSE	Up in Sub v. Con (9.5; 0.0275)	No change in males	Solute carrier organic anion transporter family member 3A1
TR395659|c3_g4_i1	SOAT1_CRIGR	No change in females	Up in Dom v. Sub (8.25; 0.0196)	Sterol O-acyltransferase 1
TR411257|c1_g4_i18	SP16H_MOUSE	No change in females	Up in Sub v. Con (11.14; 4.64e-10)	FACT complex subunit SPT16
TR394431|c5_g1_i11	SPB1_MOUSE	Up in Dom v. Con (9.74; 0.0109) Up in Sub v. Con (9.79; 0.0178)	No change in males	pre-rRNA processing protein FTSJ3
TR440022|c5_g3_i8	SPIR1_MOUSE	Up in Sub v. Dom (6.78; 0.0111)	No change in males	Protein spire homolog 1
TR739932|c10_g1_i7	SPTB2_MOUSE	No change in females	Up in Dom v. Sub (9.44; 0.041)	Spectrin beta chain, non-erythrocytic 1
TR331878|c11_g3_i11	SRGEF_MOUSE	Up in Dom v. Sub (8.82; 0.0017)	No change in males	Secretion-regulating guanine nucleotide exchange factor

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR437104|c8_g1_i5	SRRT_MOUSE	No change in females	Up in Dom v. Sub (8.34; 0.0218)	Serrate RNA effector molecule homolog
TR50333|c3_g3_i8	SSH2_MOUSE	Up in Sub v. Dom (8.79; 0.001)	No change in males	Protein phosphatase Slingshot homolog 2
TR161608|c0_g1_i4	SSPO_RAT	No change in females	Up in Dom v. Con (9.19; 0.0009)	SCO-spondin
TR45260|c7_g10_i5	ST4A1_RAT	Up in Sub v. Con (9.27; 0.0489)	No change in males	Sulfotransferase 4A1
TR158450|c3_g2_i9	ST5_MOUSE	No change in females	Up in Dom v. Sub (6.95; 1.30e-08)	Suppression of tumorigenicity 5 protein
TR158450|c3_g2_i18	ST5_MOUSE	No change in females	Up in Sub v. Con (9.29; 0.0007) Up in Sub v. Dom (6.53; 9.00e-05)	Suppression of tumorigenicity 5 protein
TR618173|c6_g4_i2	STIMA_MOUSE	Up in Sub v. Dom (8.26; 0.0464)	No change in males	Store-operated calcium entry regulator STIMATE
TR131572|c5_g1_i6	STRN3_MOUSE	No change in females	Down in Sub v. Con (-10.96; 4.64e-10) Down in Sub v. Dom (-12.4; 1.31e-27)	Striatin-3
TR153049|c0_g3_i14	STXB4_MOUSE	Down in Dom v. Con (-9.56; 1.51e-06)	No change in males	Syntaxin-binding protein 4
TR153049|c0_g3_i5	STXB4_MOUSE	No change in females	Up in Sub v. Con (9.82; 6.05e-05)	Syntaxin-binding protein 4
TR153049|c0_g3_i2	STXB4_MOUSE	Up in Dom v. Con (10.36; 4.94e-12)	No change in males	Syntaxin-binding protein 4
TR544782|c12_g2_i3	STXB6_MOUSE	No change in females	Up in Dom v. Con (9.01; 0.0053)	Syntaxin-binding protein 6
TR359468|c5_g2_i14	SV2B_RAT	Up in Sub v. Con (6.75; 1.18e-08)	No change in males	Synaptic vesicle glycoprotein 2B
TR462716|c18_g1_i6	SYHM_MOUSE	Down in Sub v. Con (-9.46; 0.0328)	No change in males	Probable histidine--tRNA ligase, mitochondrial
TR287017|c8_g1_i9	SYTC_MOUSE	Up in Dom v. Sub (9.52; 0.0271)	No change in males	Threonine--tRNA ligase, cytoplasmic
TR437257|c5_g4_i5	SZT2_MOUSE	Down in Dom v. Con (-8.29; 0.0336)	No change in males	KICSTOR complex protein SZT2
TR437257|c5_g4_i18	SZT2_MOUSE	Up in Sub v. Con (10.16; 0.0083)	No change in males	KICSTOR complex protein SZT2
TR431493|c13_g1_i1	T22D4_MOUSE	Down in Sub v. Con (-8.67; 0.0043)	No change in males	TSC22 domain family protein 4
TR608582|c3_g1_i2	T2EA_MOUSE	Down in Sub v. Con (-8.29; 0.0363)	No change in males	General transcription factor IIE subunit 1
TR668226|c2_g1_i9	TAPT1_MOUSE	Up in Sub v. Dom (8.25; 0.0202)	No change in males	Transmembrane anterior posterior transformation protein 1

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR744091|c5_g3_i8	TBA1B_RAT	No change in females	Up in Dom v. Con (9.87; 3.46e-05) Up in Dom v. Sub (10.86; 1.15e-09)	Tubulin alpha-1B chain
TR308518|c2_g1_i30	TBC24_MOUSE	No change in females	Up in Dom v. Con (8.59; 0.0411) Up in Dom v. Sub (8.81; 0.0069)	TBC1 domain family member 24
TR308518|c2_g1_i26	TBC24_MOUSE	Up in Dom v. Sub (10.23; 5.65e-10)	No change in males	TBC1 domain family member 24
TR180325|c6_g1_i5	TEN1_MOUSE	No change in females	Up in Sub v. Dom (10.36; 0.0092)	Teneurin-1
TR180325|c6_g1_i16	TEN1_MOUSE	Up in Dom v. Con (2.25; 0.0475)	No change in males	Teneurin-1
TR489754|c12_g2_i5	TENR_MOUSE	Down in Sub v. Con (-8.92; 5.04e-06)	No change in males	Tenascin-R
TR504870|c13_g1_i17	TENS3_MOUSE	Up in Dom v. Con (8.36; 0.0137)	No change in males	Tensin-3
TR260582|c0_g1_i7	TEP1_RAT	Up in Sub v. Dom (8.39; 0.0094)	No change in males	Telomerase protein component 1
TR587501|c4_g1_i39	TESK2_RAT	No change in females	Up in Dom v. Sub (8; 0.0416)	Dual specificity testis-specific protein kinase 2
TR414167|c3_g5_i8	TET3_MOUSE	Up in Sub v. Dom (8.71; 0.0014)	No change in males	Methylcytosine dioxygenase TET3
TR87292|c6_g4_i6	THOC5_MOUSE	Up in Dom v. Sub (8.49; 0.0103)	No change in males	THO complex subunit 5 homolog
TR732783|c2_g2_i5	TICN3_MOUSE	Up in Sub v. Con (10.3; 0.0043)	No change in males	Testican-3
TR320086|c15_g2_i4	TJAP1_MOUSE	No change in females	Up in Dom v. Con (9.57; 0.0003)	Tight junction-associated protein 1
TR275346|c15_g6_i7	TM2D1_MOUSE	Up in Sub v. Con (9.83; 1.76e-08) Up in Sub v. Dom (9.76; 4.84e-08)	Down in Dom v. Con (-9.62; 0.0422)	TM2 domain-containing protein 1
TR305885|c0_g2_i1	TM40L_RAT	No change in females	Up in Dom v. Sub (8.62; 0.0156)	Mitochondrial import receptor subunit TOM40B
TR291968|c10_g2_i20	TNPO1_MOUSE	No change in females	Up in Dom v. Sub (8.03; 0.039)	Transportin-1
TR726894|c16_g1_i3	TNR21_RAT	No change in females	Up in Dom v. Sub (9.95; 0.012)	Tumor necrosis factor receptor superfamily member 21
TR159288|c5_g1_i5	TRI33_MOUSE	No change in females	Down in Dom v. Con (-10.39; 0.0157)	E3 ubiquitin-protein ligase TRIM33

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR359329|c6_g4_i9	TRIM9_MOUSE	No change in females	Up in Dom v. Con (6.75; 0.0151) Up in Dom v. Sub (9.02; 0.0001)	E3 ubiquitin-protein ligase TRIM9
TR359329|c6_g4_i1	TRIM9_MOUSE	No change in females	Up in Sub v. Dom (9.31; 1.36e-05)	E3 ubiquitin-protein ligase TRIM9
TR501811|c9_g2_i10	TRM6_MOUSE	No change in females	Up in Dom v. Sub (8.19; 0.0249)	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6
TR248969|c0_g2_i5	TSN9_MOUSE	No change in females	Up in Dom v. Con (10.87; 1.78e-09) Up in Sub v. Con (10.44; 4.60e-07)	Tetraspanin-9
TR507460|c8_g3_i8	TTC14_MOUSE	Down in Dom v. Con (-8.97; 0.0003)	No change in males	Tetratricopeptide repeat protein 14
TR492995|c9_g1_i9	TTC33_MOUSE	No change in females	Down in Dom v. Con (-9.61; 0.0499)	Tetratricopeptide repeat protein 33
TR604218|c2_g2_i3	TTHY_MOUSE	No change in females	Down in Dom v. Con (-16.47; 0.0034)	Transthyretin
TR714608|c5_g2_i7	TULP4_MOUSE	Up in Sub v. Dom (10.16; 1.57e-10)	Down in Sub v. Con (-11.66; 0.0123)	Tubby-related protein 4
TR710623|c5_g3_i26	TUTLA_RAT	Down in Sub v. Con (-2.09; 0.0164)	No change in males	Protein turtle homolog A
TR747055|c11_g2_i7	U730_MOUSE	No change in females	Down in Sub v. Con (-12.91; 1.35e-20) Down in Sub v. Dom (-12.45; 2.08e-26)	Putative UPF0730 protein encoded by LINC00643 homolog
TR747055|c11_g2_i2	U730_MOUSE	No change in females	Down in Sub v. Con (-11.51; 1.48e-11) Down in Sub v. Dom (-11.83; 3.28e-26)	Putative UPF0730 protein encoded by LINC00643 homolog
TR747055|c11_g2_i10	U730_MOUSE	No change in females	Down in Sub v. Con (-6.26; 0.0099) Down in Sub v. Dom (-5.79; 0.0085)	Putative UPF0730 protein encoded by LINC00643 homolog
TR747055|c11_g2_i5	U730_MOUSE	No change in females	Up in Sub v. Con (14.04; 9.83e-28)	Putative UPF0730 protein encoded by LINC00643 homolog
TR406880|c1_g1_i3	UAP1_MOUSE	No change in females	Up in Dom v. Con (8.29; 0.038)	UDP-N-acetylhexosamine pyrophosphorylase
TR421338|c4_g2_i13	UBA6_MOUSE	No change in females	Down in Sub v. Con (-11.29; 3.17e-12) Down in Sub v. Dom (-10.79; 0.0019)	Ubiquitin-like modifier-activating enzyme 6
TR410867|c3_g3_i19	UBP40_MOUSE	No change in females	Up in Dom v. Sub (8.37; 0.0116)	Ubiquitin carboxyl-terminal hydrolase 40

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR696425|c2_g1_i14	UBP53_MOUSE	Down in Dom v. Con (-10.93; 1.93e-11)	Up in Sub v. Con (9.95; 0.0485)	Inactive ubiquitin carboxyl-terminal hydrolase 53
TR679315|c3_g4_i11	UBXN6_MOUSE	Up in Dom v. Sub (8.78; 0.0019)	No change in males	UBX domain-containing protein 6
TR258018|c2_g3_i6	USE1_MOUSE	Down in Sub v. Con (-8.47; 0.0054)	No change in males	Vesicle transport protein USE1
TR122651|c12_g2_i12	VDAC2_MOUSE	Up in Dom v. Sub (5.49; 0.0055)	No change in males	Voltage-dependent anion-selective channel protein 2
TR81700|c4_g2_i10	VP13C_MOUSE	No change in females	Up in Dom v. Con (8.79; 0.0092) Up in Sub v. Con (8.64; 0.0417)	Vacuolar protein sorting-associated protein 13C
TR43107|c13_g1_i15	VPP2_MOUSE	No change in females	Up in Dom v. Con (8.91; 0.0117) Up in Sub v. Con (8.83; 0.0123)	V-type proton ATPase 116 kDa subunit a isoform 2
TR109117|c3_g1_i16	VPS51_MOUSE	Up in Dom v. Sub (9.34; 0.0467)	No change in males	Vacuolar protein sorting-associated protein 51 homolog
TR36520|c2_g2_i7	WDR35_MOUSE	No change in females	Up in Sub v. Con (9.95; 2.49e-05)	WD repeat-containing protein 35
TR50291|c16_g2_i6	WDR76_MOUSE	Up in Dom v. Sub (9.13; 0.0004)	No change in males	WD repeat-containing protein 76
TR64740|c5_g2_i6	WNK3_MOUSE	Down in Dom v. Con (-9.37; 1.41e-05)	No change in males	Serine/threonine-protein kinase WNK3
TR64740|c5_g2_i10	WNK3_MOUSE	Down in Sub v. Con (-6.33; 0.0017) Down in Sub v. Dom (-7.69; 2.31e-06)	No change in males	Serine/threonine-protein kinase WNK3
TR64740|c5_g2_i2	WNK3_MOUSE	Up in Sub v. Dom (11.18; 1.80e-17)	No change in males	Serine/threonine-protein kinase WNK3
TR231901|c0_g1_i2	WNK4_RAT	No change in females	Up in Dom v. Con (8.77; 0.0065)	Serine/threonine-protein kinase WNK4
TR605741|c9_g2_i1	WNT5A_MOUSE	Up in Sub v. Con (8.04; 0.0415)	No change in males	Protein Wnt-5a
TR239373|c2_g2_i5	WRIP1_MOUSE	No change in females	Up in Sub v. Dom (8.21; 0.0188)	ATPase WRNIP1
TR150419|c4_g6_i12	WSCD1_MOUSE	Down in Dom v. Con (-9.54; 0.0356) Down in Sub v. Con (-9.52; 0.0274)	No change in males	WSC domain-containing protein 1
TR677393|c7_g2_i2	XCT_MOUSE	No change in females	Up in Dom v. Con (9.93; 0.029) Up in Dom v. Sub (10.15; 0.0075)	Cystine/glutamate transporter

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR677393|c7_g2_i7	XCT_MOUSE	No change in females	Up in Dom v. Con (9.75; 0.0447) Up in Dom v. Sub (9.96; 0.011)	Cystine/glutamate transporter
TR148272|c7_g2_i14	XPO2_MOUSE	No change in females	Up in Dom v. Con (5.21; 0.0471)	Exportin-2
TR733280|c3_g1_i2	XPO4_MOUSE	Up in Dom v. Sub (8.83; 0.0015)	Up in Dom v. Con (8.45; 0.047) Up in Dom v. Sub (8.67; 0.0081)	Exportin-4
TR354440|c8_g2_i14	YETS2_MOUSE	Down in Sub v. Con (-9.18; 6.57e-05)	No change in males	YEATS domain-containing protein 2
TR225190|c11_g2_i14	YIF1B_MOUSE	Up in Dom v. Con (9.47; 7.93e-05)	No change in males	Protein YIF1B
TR673677|c11_g1_i3	YTHD3_MOUSE	Down in Sub v. Con (-8.35; 0.0174)	No change in males	YTH domain-containing family protein 3
TR642349|c0_g2_i7	ZDH17_RAT	No change in females	Up in Sub v. Con (9.61; 0.0001)	Palmitoyltransferase ZDHHC17
TR434034|c15_g7_i15	ZEP2_RAT	No change in females	Up in Dom v. Con (11.02; 9.53e-09) Up in Sub v. Con (10.1; 0.0468)	Human immunodeficiency virus type I enhancer-binding protein 2 homolog
TR434034|c15_g7_i19	ZEP2_RAT	No change in females	Up in Dom v. Con (9.91; 0.0003) Up in Sub v. Con (10.36; 8.69e-05)	Human immunodeficiency virus type I enhancer-binding protein 2 homolog
TR372268|c8_g1_i13	ZEP3_MOUSE	Down in Sub v. Con (-8.26; 0.0445)	No change in males	Transcription factor HIVEP3
TR372268|c8_g1_i10	ZEP3_MOUSE	No change in females	Up in Dom v. Con (8.87; 0.0073)	Transcription factor HIVEP3
TR504036|c0_g1_i1	ZFP62_MOUSE	Up in Dom v. Con (9.2; 5.95e-05)	No change in males	Zinc finger protein 62
TR319959|c6_g4_i4	ZFY26_MOUSE	Up in Dom v. Sub (8.67; 0.0023)	No change in males	Zinc finger FYVE domain-containing protein 26
TR585004|c0_g3_i11	ZN106_MOUSE	No change in females	Down in Dom v. Con (-6.61; 0.0001)	Zinc finger protein 106
TR405877|c5_g1_i3	ZN281_MOUSE	Up in Sub v. Con (10.8; 0.0017) Up in Sub v. Dom (10.74; 0.0016)	No change in males	Zinc finger protein 281
TR235840|c9_g1_i14	ZN532_MOUSE	No change in females	Up in Dom v. Con (8.46; 0.0225) Up in Sub v. Con (8.59; 0.0459)	Zinc finger protein 532

Trinity Transcript ID	Uniprot ID	Expression Change in Females (log2FC; FDR)	Expression Change in Males (log2FC; FDR)	Gene
TR381605|c9_g2_i1	ZN775_MOUSE	Up in Sub v. Con (9.72; 0.0262) Up in Sub v. Dom (9.66; 0.0281)	No change in males	Zinc finger protein 775
TR193324|c4_g1_i14	ZO1_MOUSE	Up in Dom v. Con (8.7; 0.0079)	No change in males	Tight junction protein ZO-1
TR193324|c4_g1_i4	ZO1_MOUSE	Up in Dom v. Con (9.95; 1.89e-05)	No change in males	Tight junction protein ZO-1

Supplemental Table 4: Gene ontology terms that were significantly enriched in dominant and subordinate females compared with home cage controls (MF = molecular function; CC = cellular component; BP = biological processes)

GO Term	Ontology	FDR
Siderophore transporter activity	MF	0.004
Enterobactin transporter activity	MF	0.004
Acetylcholine receptor activator activity	MF	0.004
ErbB-2 class receptor binding	MF	0.004
Cyclin-dependent protein kinase 5 holoenzyme complex	CC	0.004
Serine phosphorylation of STAT3 protein	BP	0.004
Cerebellar cortex formation	BP	0.007
Negative regulation of synaptic plasticity	BP	0.007
Sensory perception of sour taste	BP	0.008
ErbB-3 class receptor binding	MF	0.006
Serine phosphorylation of STAT protein	BP	0.006
Detection of chemical stimulus involved in sensory perception of pain	BP	0.006
Ligand-gated sodium channel activity	MF	0.009
Acetylcholine receptor regulator activity	MF	0.041
Detection of mechanical stimulus involved in sensory perception of pain	BP	0.024
Synaptic transmission, dopaminergic	BP	0.012
Negative regulation of protein export from nucleus	BP	0.034
Cerebellar cortex development	BP	0.030
Corpus callosum development	BP	0.041
Behavioral response to cocaine	BP	0.030
Detection of temperature stimulus involved in sensory perception	BP	0.041
Detection of temperature stimulus involved in sensory perception of pain	BP	0.041
Detection of temperature stimulus	BP	0.041
Sensory perception of taste	BP	0.041
Detection of chemical stimulus involved in sensory perception	BP	0.031
Receptor activator activity	MF	0.041
Response to acidic Ph	BP	0.041
Skeletal muscle tissue development	BP	0.012
Negative regulation of nucleocytoplasmic transport	BP	0.033
Negative regulation of intracellular protein transport	BP	0.039
Negative regulation of cytoplasmic transport	BP	0.041
Striated muscle tissue development	BP	0.033
Muscle tissue development	BP	0.041