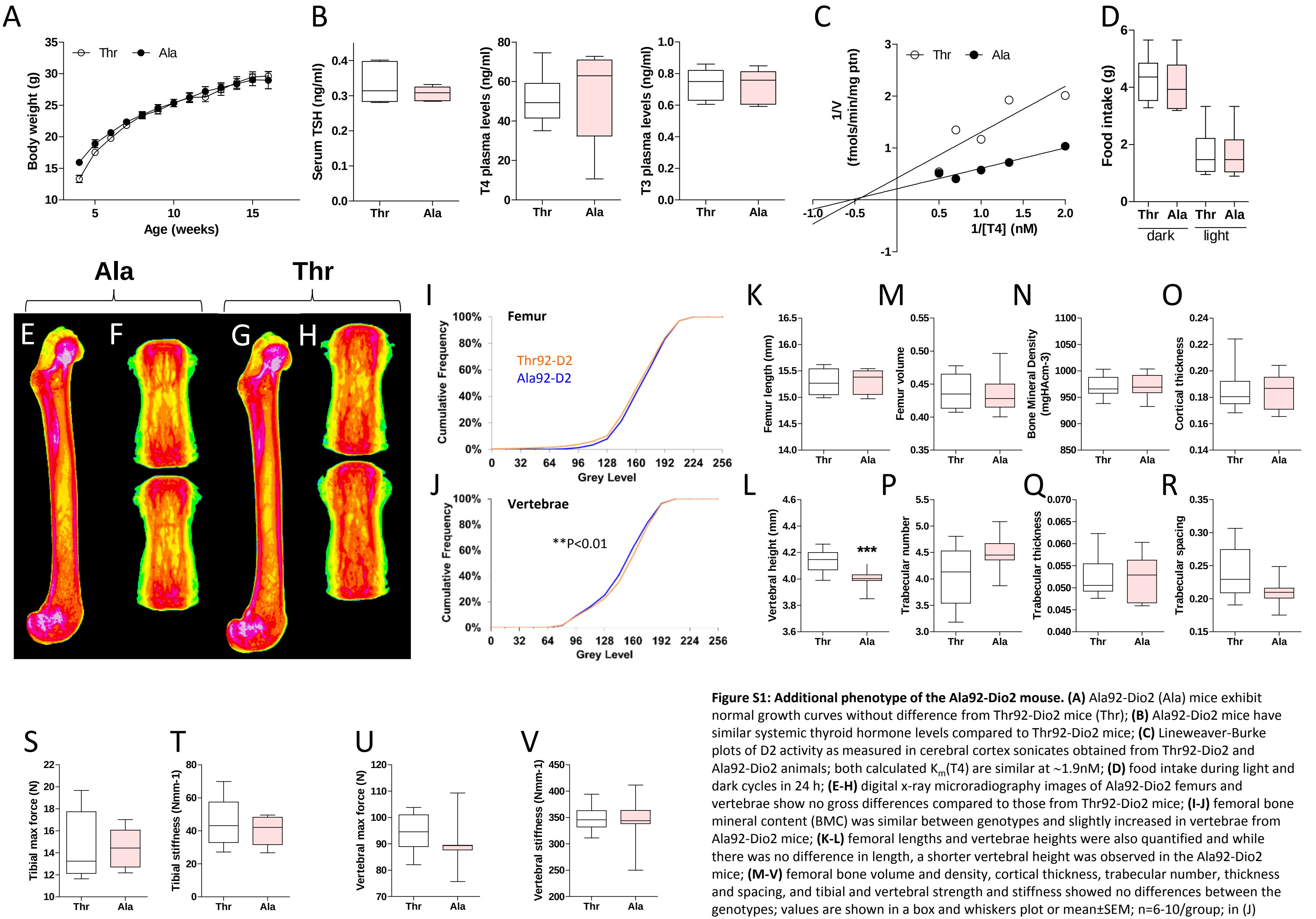

Figure S1: Additional phenotype of the Ala92-Dio2 mouse. (A) Ala92-Dio2 (Ala) mice exhibit normal growth curves without difference from Thr92-Dio2 mice (Thr); **(B)** Ala92-Dio2 mice have similar systemic thyroid hormone levels compared to Thr92-Dio2 mice; **(C)** Lineweaver-Burke plots of D2 activity as measured in cerebral cortex sonicates obtained from Thr92-Dio2 and Ala92-Dio2 animals; both calculated K_m(T4) are similar at ~1.9nM; **(D)** food intake during light and dark cycles in 24 h; **(E-H)** digital x-ray microradiography images of Ala92-Dio2 femurs and vertebrae show no gross differences compared to those from Thr92-Dio2 mice; **(I-J)** femoral bone mineral content (BMC) was similar between genotypes and slightly increased in vertebrae from Ala92-Dio2 mice; **(K-L)** femoral lengths and vertebrae heights were also quantified and while there was no difference in length, a shorter vertebral height was observed in the Ala92-Dio2 mice; **(M-V)** femoral bone volume and density, cortical thickness, trabecular number, thickness and spacing, and tibial and vertebral strength and stiffness showed no differences between the genotypes; values are shown in a box and whiskers plot or mean±SEM; n=6-10/group; in (J) Kolmogorov-Smirnov test was used; ** p≤0.01 and ***p<0.001.

Supplemental Figure 1

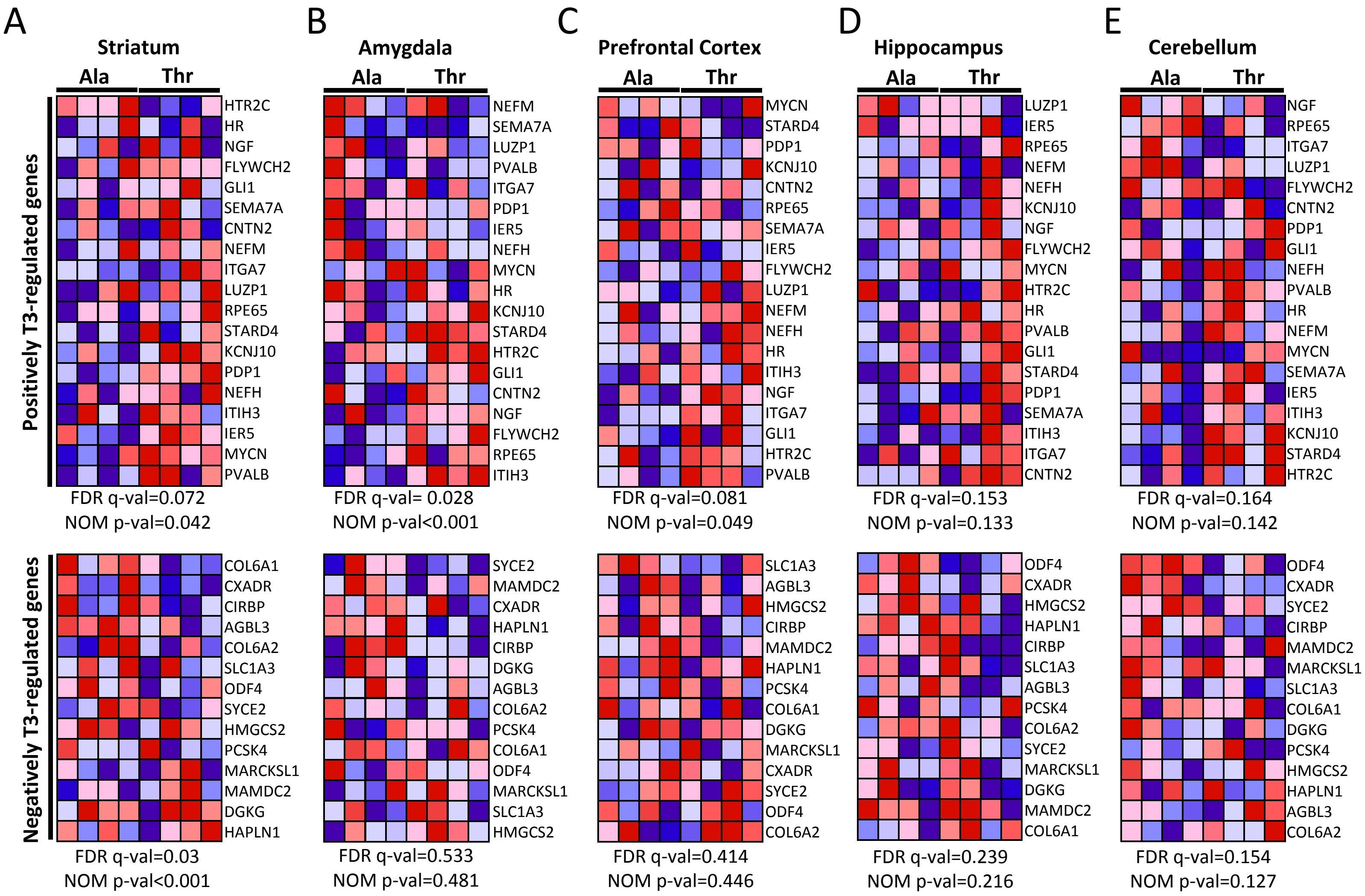

Figure S2: Expression of positively or negatively T3-regulated genes in 5 regions of the Ala92-Dio2 and Thr92-Dio2 brain. **(A)** Striatum; **(B)** Amygdala; **(C)** Prefrontal Cortex; **(D)** Hippocampus; **(E)** Cerebellum; upper heat maps feature 19 genes positively regulated by T3; lower heat maps feature 14 genes negatively regulated by T3; expression values are represented as colors (red: increased expression; blue decreased expression) with the degree of color saturation indicating level of expression; False Discovery Rate (FDR) q-value and Nominal (NOM) p-value are shown for each heat map; n=4/group.

Supplemental Figure 2

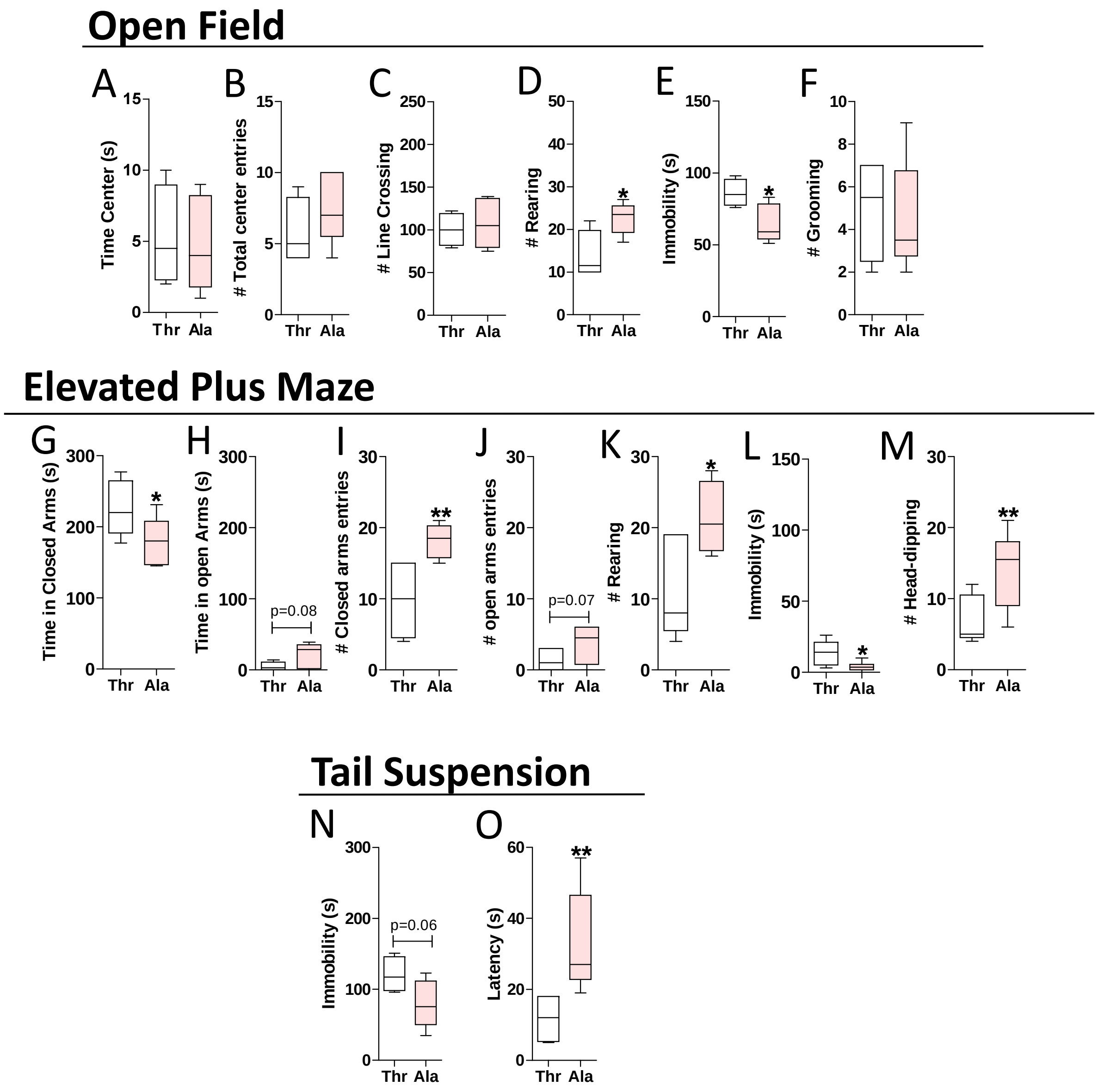

Figure S3: Additional behavioral tests in Thr92-Dio2 (Thr) and Ala92-Dio2 (Ala) mice. Open Field: **(A)** time in center; **(B)** total center entries; **(C)** total numbers of line crossing; **(D)** rearing; **(E)** immobility; **(F)** grooming. Elevated plus maze: **(G)** time spent inside closed arms or **(H)** open arms; **(I)** entries into closed arms or **(J)** open arms; **(K)** rearing; **(L)** immobility; **(M)** number of head-dips. Tail suspension test: **(N)** time of immobility; **(O)** latency to the first immobility episode; values are shown in a box and whiskers plot; n=4-6/group; Statistical analysis used was Mann-Whitney U test; * p≤0.05 and ** p≤0.01.

Supplemental Figure 3

Novel Object Recognition (Familiarization)

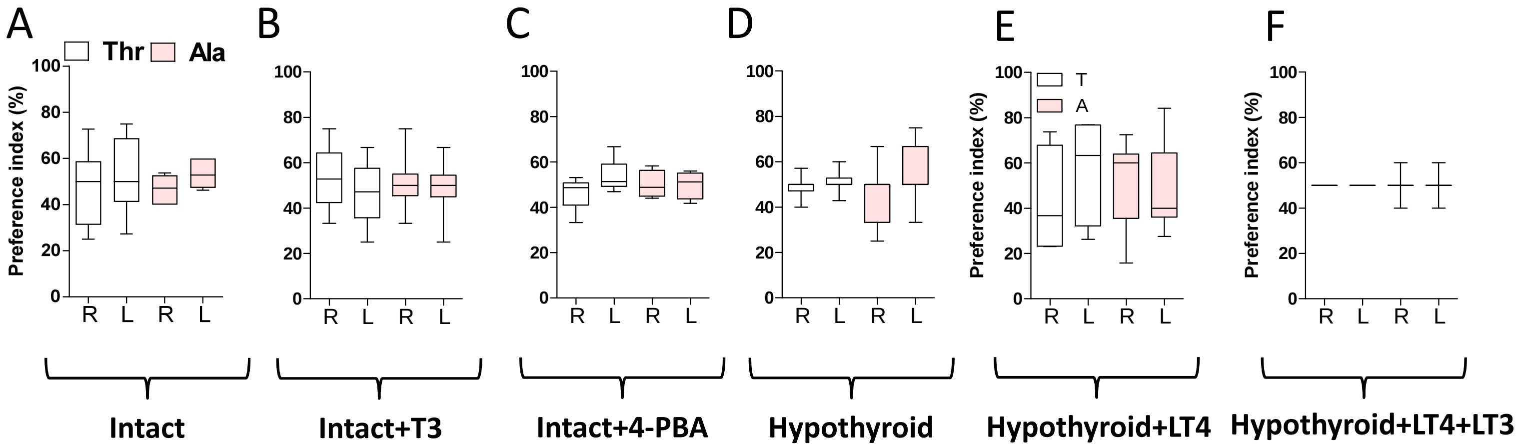

Figure S4: Familiarization session of NOR memory test displayed as preference index (%) of Thr92-Dio2 (Thr) and Ala92-Dio2 (Ala) mice. **(A)** intact animals; **(B)** intact + LT3 animals; **(C)** Intact + 4-PBA animals; **(D)** hypothyroid animals; **(E)** hypothyroid+LT4 animals; **(F)** hypothyroid+LT4+LT3 animals; in each plot, R is the right object and L is the left object; values are shown in a box and whiskers plot indicating median and quartiles; n=5-11/group; Statistical analysis used was Mann-Whitney U test.

Supplemental Figure 4

Social Interaction (Familiarization)

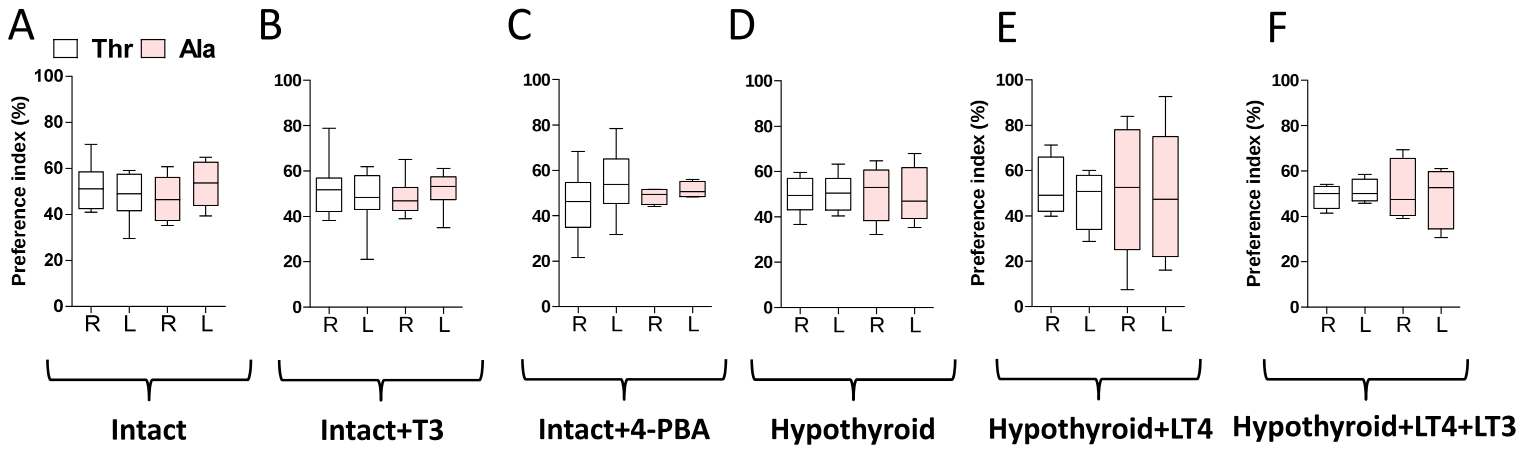

Figure S5: Familiarization session of SI memory test displayed as preference index (%) of Thr92-Dio2 (Thr) and Ala92-Dio2 (Ala) mice. **(A)** intact animals; **(B)** intact + LT3 animals; **(C)** Intact + 4-PBA animals; **(D)** hypothyroid animals; **(E)** hypothyroid+LT4 animals; **(F)** hypothyroid+LT4+LT3 animals; in each plot, R is the right subject and L is the left subject; values are shown in a box and whiskers plot indicating median and quartiles; n=5-11/group; Statistical analysis used was Mann-Whitney U test.

Supplemental Figure 5

Table S1- ER stress-related genes mRNA in Thr92-D2^{HY} and Ala92-D2^{HY} cells treated with 100uM 4-PBA during 24h.

Genes	**Thr92-D2^{HY} vs Ala92-D2^{HY} relative mRNA levels**
BIP	1.09±0.08
CHOP	1.07±0.20
sXBP1	0.99±0.08
ERGIC53	0.70±0.03**
ATF4	1.08±0.08

Results are relative to *bACTIN* mRNA levels and normalized to Thr92-D2^{HY}; **$p \leq 0.01$ vs. Thr92-D2^{HY}-4PBA cells. values are the mean ± SEM of 4-6 independent samples; gene abbreviations are as indicated in the supplemental Tables S27.

Table S2- Genes upregulated in the Amygdala of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA Amg vs. TT Amg)	ANOVA p-value (AA Amg vs. TT Amg)	FDR p-value (AA Amg vs. TT Amg)
Pcbp2	poly(rC) binding protein 2	1.09	0.040042	0.955604
Pgrmc2	progesterone receptor membrane component 2	1.09	0.024062	0.934625
Ppp4c	protein phosphatase 4, catalytic subunit	1.1	0.048309	0.955604
Adrm1	adhesion regulating molecule 1	1.1	0.049191	0.955604
Fam73a	family with sequence similarity 73, member A	1.1	0.030434	0.955027
Plppr4	phospholipid phosphatase related 4	1.11	0.041731	0.955604
Akt1s1	AKT1 substrate 1 (proline-rich); microRNA 707	1.11	0.04563	0.955604
Lrp12	low density lipoprotein-related protein 12	1.12	0.022065	0.934625
Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	1.12	0.004946	0.795858
Myo19	myosin XIX	1.12	0.02528	0.939355
Olfr1406	olfactory receptor 1406	1.13	0.043776	0.955604
Ppp2r5a	protein phosphatase 2, regulatory subunit B, alpha; protein phosphatase 2, regulatory subunit B', alpha	1.14	0.004982	0.795858
Yy1	YY1 transcription factor	1.14	0.022014	0.934625
Spcs2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	1.14	0.045703	0.955604
Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	1.14	0.035641	0.955604
Layn	layilin	1.14	0.018186	0.934625
Aak1	AP2 associated kinase 1	1.14	0.049853	0.955604
Mlxip	MLX interacting protein	1.14	0.023216	0.934625
Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	1.14	0.047044	0.955604
Mroh9	maestro heat-like repeat family member 9	1.15	0.021704	0.934625
Morc2b	microrchidia 2B	1.16	0.026019	0.944116
Ift27	intraflagellar transport 27	1.16	0.043922	0.955604
Sh3tc2	SH3 domain and tetratricopeptide repeats 2	1.16	0.037613	0.955604
Gas7	growth arrest specific 7	1.16	0.031351	0.955027

Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2; UDP glucuronosyltransferase 1 family, polypeptide A6A; UDP glucuronosyltransferase 1 family, polypeptide A6B; UDP glycosyltransferase 1 family, polypeptide A10; UDP glucuronosyltransferase 1 family, polypeptide A7C; UDP glucuronosyltransferase 1 family, polypeptide A5; UDP glucuronosyltransferase 1 family, polypeptide A9; UDP glucuronosyltransferase 1 family, polypeptide A1	1.16	0.030432	0.955027
Eif3h	eukaryotic translation initiation factor 3, subunit H	1.16	0.03426	0.955604
Mdh1	malate dehydrogenase 1, NAD (soluble)	1.16	0.02173	0.934625
Mau2	MAU2 chromatid cohesion factor homolog (C. elegans)	1.16	0.022027	0.934625
Glrb	glycine receptor, beta subunit	1.16	0.049961	0.955604
Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	1.16	0.025196	0.939355
Crnn	cornulin	1.16	0.008034	0.844445
Capza2	capping protein (actin filament) muscle Z-line, alpha 2	1.16	0.027456	0.944116
Msantd4	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils	1.16	0.023594	0.934625
Dmxl2	Dmx-like 2	1.16	0.046461	0.955604
Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	1.16	0.041437	0.955604
Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.17	0.036032	0.955604
Ddt	D-dopachrome tautomerase	1.17	0.028624	0.9504
Usp1	ubiquitin specific peptidase 1	1.17	0.002995	0.693971
Ift57	intraflagellar transport 57	1.17	0.041132	0.955604
Itfg1	integrin alpha FG-GAP repeat containing 1	1.17	0.021576	0.934625
Hspa14	heat shock protein 14	1.17	0.049523	0.955604
Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	1.17	0.018224	0.934625
Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	1.17	0.045689	0.955604
Usp7	ubiquitin specific peptidase 7	1.17	0.045661	0.955604
Tada2a	transcriptional adaptor 2A	1.17	0.019412	0.934625
Pcdhb17	protocadherin beta 17	1.18	0.002648	0.690171
Sbds	Shwachman-Bodian-Diamond	1.18	0.005722	0.801647

	syndrome homolog (human)			
Olfr1419	olfactory receptor 1419	1.18	0.033638	0.955604
Actr2	ARP2 actin-related protein 2	1.18	0.033244	0.955027
Pou2af1	POU domain, class 2, associating factor 1	1.18	0.00941	0.858114
Frrs1l	ferric-chelate reductase 1 like	1.18	0.025412	0.939355
Arf1	ADP-ribosylation factor 1	1.18	0.005616	0.801647
Gfra4	glial cell line derived neurotrophic factor family receptor alpha 4; microRNA 6973b	1.18	0.038013	0.955604
Mlx	MAX-like protein X	1.18	0.024848	0.93844
Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	1.19	0.00943	0.858114
Picalm	phosphatidylinositol binding clathrin assembly protein	1.19	0.02597	0.944116
Pdcl3	phosducin-like 3	1.19	0.032076	0.955027
Skint9	selection and upkeep of intraepithelial T cells 9	1.19	0.040837	0.955604
Zfyve9	zinc finger, FYVE domain containing 9	1.19	0.030374	0.955027
Setd2	SET domain containing 2	1.19	0.02135	0.934625
Blzf1	basic leucine zipper nuclear factor 1	1.19	0.040471	0.955604
Dhrs1	dehydrogenase/reductase (SDR family) member 1	1.19	0.049583	0.955604
Tmem239	transmembrane 239	1.19	0.038033	0.955604
Actr3	ARP3 actin-related protein 3	1.19	0.013027	0.915448
Spin2f	spindlin family, member 2F [Source:MGI Symbol;Acc:MGI:3780958]; spindlin family, member 2F	1.19	0.032213	0.955027
Ikbkb	inhibitor of kappaB kinase beta	1.19	0.016316	0.934625
Pdhx	pyruvate dehydrogenase complex, component X	1.19	0.018882	0.934625
Rab6a	RAB6A, member RAS oncogene family	1.19	0.000598	0.577367
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1.19	0.047468	0.955604
St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1.19	0.00163	0.661654
Usp54	ubiquitin specific peptidase 54	1.2	0.042528	0.955604
Rfwd3	ring finger and WD repeat domain 3	1.2	0.025356	0.939355
Cpn1	carboxypeptidase N, polypeptide 1	1.2	0.049334	0.955604
Gvin1	GTPase, very large interferon inducible 1	1.2	0.033039	0.955027
Fpgt	fucose-1-phosphate guanylyltransferase	1.2	0.043561	0.955604
Pcyox1l	prenylcysteine oxidase 1 like	1.2	0.004908	0.795519
Mesp2	mesoderm posterior 2	1.2	0.029707	0.955027
Golga2	golgi autoantigen, golgin subfamily a, 2	1.2	0.001791	0.661654
Cdc34-ps	cell division cycle 34 homolog,	1.2	0.007006	0.828491

	pseudogene (S. cerevisiae)			
Actrt1	actin-related protein T1	1.2	0.014917	0.934625
Yipf2	Yip1 domain family, member 2	1.2	0.047651	0.955604
Mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	1.2	0.024892	0.93844
Snx10	sorting nexin 10	1.2	0.035305	0.955604
Sprn	shadow of prion protein	1.2	0.028633	0.9504
Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	1.21	0.018239	0.934625
Chid1	chitinase domain containing 1	1.21	0.038805	0.955604
Brox	BRO1 domain and CAAX motif containing	1.21	0.022966	0.934625
Adprhl1	ADP-ribosylhydrolase like 1	1.21	0.047535	0.955604
Zfp316	zinc finger protein 316	1.21	0.0269	0.944116
Scmh1	sex comb on midleg homolog 1	1.22	0.037646	0.955604
Htr6	5-hydroxytryptamine (serotonin) receptor 6	1.22	0.022049	0.934625
Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1.22	0.025909	0.944116
Arx	aristaless related homeobox	1.22	0.015539	0.934625
Adat2	adenosine deaminase, tRNA-specific 2	1.22	0.002853	0.693971
Retnlb	resistin like beta	1.22	0.033134	0.955027
Ms4a4b	membrane-spanning 4-domains, subfamily A, member 4B	1.22	0.040883	0.955604
Erc2	ELKS/RAB6-interacting/CAST family member 2	1.22	0.046663	0.955604
Hspbap1	Hspb associated protein 1	1.22	0.034453	0.955604
Trim28	tripartite motif-containing 28	1.22	0.005728	0.801647
Egfl7	EGF-like domain 7; microRNA 126a	1.22	0.033274	0.955027
Olfr283	olfactory receptor 283	1.22	0.015603	0.934625
Hk1	hexokinase 1	1.22	0.020441	0.934625
Nrcam	neuronal cell adhesion molecule	1.22	0.026783	0.944116
Dlgap1	discs, large (Drosophila) homolog-associated protein 1	1.22	0.041662	0.955604
Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae); microRNA 93; microRNA 25	1.23	0.004309	0.771675
Eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta	1.23	0.014199	0.934625
Mrpl37	mitochondrial ribosomal protein L37	1.23	0.049917	0.955604
Mrpl47	mitochondrial ribosomal protein L47	1.23	0.00203	0.661654
Nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	1.23	0.008732	0.858114
Hagh	hydroxyacyl glutathione hydrolase	1.23	0.024111	0.934625
Tut1	terminal uridylyl transferase 1, U6 snRNA-specific	1.23	0.007244	0.828491
Gja4	gap junction protein, alpha 4	1.23	0.019931	0.934625

Srsx	serine-rich, secreted, X-linked [Source:MGI Symbol;Acc:MGI:3777603]; serine-rich, secreted, X-linked	1.23	0.048811	0.955604
Barx1	BarH-like homeobox 1	1.23	0.042726	0.955604
Agtpbp1	ATP/GTP binding protein 1; RIKEN cDNA A230056J06 gene	1.23	0.022878	0.934625
Cnksr2	connector enhancer of kinase suppressor of Ras 2	1.23	0.034775	0.955604
Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	1.23	0.024236	0.934625
Acot13	acyl-CoA thioesterase 13	1.23	0.003678	0.724181
Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11	1.23	0.035184	0.955604
Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	1.23	0.02727	0.944116
Cyp1a2	cytochrome P450, family 1, subfamily a, polypeptide 2	1.24	0.007797	0.835337
Eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha)	1.24	0.035857	0.955604
Lypla2	lysophospholipase 2	1.24	0.030494	0.955027
Pm20d1	peptidase M20 domain containing 1	1.24	0.04326	0.955604
Agbl1	ATP/GTP binding protein-like 1	1.24	0.029934	0.955027
Tceb1	transcription elongation factor B (SIII), polypeptide 1	1.24	0.000859	0.608562
Ddn	dendrin	1.24	0.049623	0.955604
Cant1	calcium activated nucleotidase 1	1.24	0.027216	0.944116
Tbk1	TANK-binding kinase 1	1.24	0.032111	0.955027
Uhrf1bp1	UHRF1 (ICBP90) binding protein 1	1.24	0.022617	0.934625
Iyd	iodotyrosine deiodinase	1.24	0.032506	0.955027
Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	1.24	0.014166	0.934625
Adam25	a disintegrin and metallopeptidase domain 25 (testase 2)	1.24	0.03367	0.955604
Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	1.24	0.02511	0.939355
Cemip	cell migration inducing protein, hyaluronan binding	1.24	0.041586	0.955604
Ppp5c	protein phosphatase 5, catalytic subunit	1.24	0.029758	0.955027
Coro1b	coronin, actin binding protein 1B	1.25	0.026218	0.944116
G2e3	G2/M-phase specific E3 ubiquitin ligase	1.25	0.039889	0.955604
Metrn	meteorin, glial cell differentiation regulator	1.25	0.026137	0.944116
Foxg1	forkhead box G1	1.25	0.002141	0.661654
Lonp2	lon peptidase 2, peroxisomal	1.25	0.001733	0.661654
Tbc1d14	TBC1 domain family, member 14	1.25	0.005791	0.801647
Gpatch2l	G patch domain containing 2 like	1.25	0.006495	0.801647

Nup43	nucleoporin 43	1.25	0.006498	0.801647
Nfu1	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	1.25	0.007337	0.828491
Pet117	PET117 homolog (S. cerevisiae); cysteine and glycine-rich protein 2 binding protein	1.25	0.045473	0.955604
Maml3	mastermind like 3 (Drosophila)	1.25	0.024109	0.934625
Wars	tryptophanyl-tRNA synthetase	1.25	0.031511	0.955027
Efna2	ephrin A2	1.25	0.046843	0.955604
Recql5	RecQ protein-like 5	1.25	0.044188	0.955604
Tamm41	TAM41, mitochondrial translocator assembly and maintenance protein, homolog (S. cerevisiae)	1.25	0.037893	0.955604
Ahnak2	AHNAK nucleoprotein 2	1.25	0.000987	0.626436
Stard7	START domain containing 7	1.25	0.049908	0.955604
Inpp5b	inositol polyphosphate-5-phosphatase B; microRNA 698	1.25	0.038483	0.955604
Pgs1	phosphatidylglycerophosphate synthase 1	1.25	0.020071	0.934625
Tcf4	transcription factor 4	1.25	0.047627	0.955604
Fam189a1	family with sequence similarity 189, member A1	1.25	0.039983	0.955604
Creg2	cellular repressor of E1A-stimulated genes 2	1.25	0.039376	0.955604
Rabggta	Rab geranylgeranyl transferase, a subunit	1.26	0.033195	0.955027
Zscan25	zinc finger and SCAN domain containing 25	1.26	0.035892	0.955604
Rtcb	RNA 2,3-cyclic phosphate and 5-OH ligase; RNA 2',3'-cyclic phosphate and 5'-OH ligase	1.26	0.045338	0.955604
Serpina16	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 16	1.26	0.004237	0.770544
Olfr484	olfactory receptor 484	1.26	0.023947	0.934625
Ipo5	importin 5	1.26	0.010197	0.872249
Clec11a	C-type lectin domain family 11, member a	1.26	0.040989	0.955604
Nell2	NEL-like 2	1.26	0.04646	0.955604
Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	1.27	0.041885	0.955604
Gpm6b	glycoprotein m6b	1.27	0.016288	0.934625
Ift80	intraflagellar transport 80	1.27	0.026773	0.944116
Fbxl4	F-box and leucine-rich repeat protein 4	1.27	0.002495	0.690171
Ifngr1	interferon gamma receptor 1	1.27	0.006001	0.801647
Olfr611	olfactory receptor 611	1.27	0.001804	0.661654
Cyth4	cytohesin 4	1.27	0.013763	0.925423
Gng12	guanine nucleotide binding protein (G	1.27	0.009298	0.858114

	protein), gamma 12			
Tmem150a	transmembrane protein 150A	1.27	0.009131	0.858114
Hoxb6	homeobox B6	1.27	0.032953	0.955027
Ift172	intraflagellar transport 172	1.27	0.029373	0.955027
Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3	1.27	0.02738	0.944116
Mlycd	malonyl-CoA decarboxylase	1.27	0.043658	0.955604
Dydc1	DPY30 domain containing 1	1.27	0.010414	0.872249
Rnf115	ring finger protein 115	1.27	0.001632	0.661654
Megf9	multiple EGF-like-domains 9	1.27	0.010367	0.872249
Col4a3	collagen, type IV, alpha 3	1.28	0.046076	0.955604
Dnm3os	dynamin 3, opposite strand; microRNA 214; microRNA 199a-2	1.28	0.046312	0.955604
Rwdd4a	RWD domain containing 4A	1.28	0.031289	0.955027
Myct1	myc target 1	1.28	0.007482	0.828491
Letmd1	LETM1 domain containing 1	1.28	0.021014	0.934625
Lpcat2b	lysophosphatidylcholine acyltransferase 2B	1.28	0.034571	0.955604
Enkd1	enkurin domain containing 1	1.28	0.040227	0.955604
Olfr350	olfactory receptor 350	1.28	0.043286	0.955604
Acsm4	acyl-CoA synthetase medium-chain family member 4	1.28	0.024523	0.934625
Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	1.28	0.017033	0.934625
Gpr84	G protein-coupled receptor 84	1.28	0.018437	0.934625
Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	1.28	0.022402	0.934625
Mtag2	metastasis associated gene 2	1.28	0.006032	0.801647
Rap1b	RAS related protein 1b	1.28	0.019302	0.934625
Haus1	HAUS augmin-like complex, subunit 1	1.28	0.045039	0.955604
Man1b1	mannosidase, alpha, class 1B, member 1	1.28	0.027168	0.944116
Stambpl1	STAM binding protein like 1	1.28	0.039643	0.955604
Dock1	dedicator of cytokinesis 1	1.29	0.043201	0.955604
Eno4	enolase 4	1.29	0.040301	0.955604
Atl3	atlastin GTPase 3	1.29	0.033032	0.955027
Nckap1	NCK-associated protein 1	1.29	0.001597	0.661654
Pank4	pantothenate kinase 4	1.29	0.000763	0.608562
Arl15	ADP-ribosylation factor-like 15	1.29	0.034065	0.955604
Chmp5	charged multivesicular body protein 5	1.29	0.001154	0.661654
Sval2	seminal vesicle antigen-like 2	1.29	0.043262	0.955604
Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	1.29	0.037439	0.955604
Slc26a1	solute carrier family 26 (sulfate transporter), member 1	1.29	0.042614	0.955604
Fn3krp	fructosamine 3 kinase related protein	1.29	0.046353	0.955604
Olfr955	olfactory receptor 955	1.29	0.044246	0.955604

Hsd3b4	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4; predicted gene 10681; predicted gene 4450	1.29	0.032544	0.955027
Olfr830	olfactory receptor 830	1.29	0.027858	0.945337
Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit S	1.29	0.035169	0.955604
Tspan15	tetraspanin 15	1.3	0.031601	0.955027
Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	1.3	0.015746	0.934625
Igfbp4	insulin-like growth factor binding protein 4	1.3	0.044504	0.955604
Jmjd6	jumonji domain containing 6	1.3	0.038224	0.955604
Prss54	protease, serine 54	1.3	0.037137	0.955604
Ppard	peroxisome proliferator activator receptor delta; RIKEN cDNA 1810013A23 gene	1.3	0.01894	0.934625
Olfr1322	olfactory receptor 1322	1.3	0.033388	0.955444
Ccdc149	coiled-coil domain containing 149	1.3	0.013527	0.925423
Olfr357	olfactory receptor 357	1.3	0.029054	0.955027
Foxa2	forkhead box A2	1.3	0.017342	0.934625
Olfr124	olfactory receptor 124	1.3	0.04156	0.955604
Ccdc138	coiled-coil domain containing 138	1.3	0.013197	0.921556
Pgm3	phosphoglucomutase 3	1.3	0.029812	0.955027
Olfr1095	olfactory receptor 1095	1.3	0.011947	0.894062
Zyg11a	zyg-11 family member A, cell cycle regulator	1.3	0.044736	0.955604
Fkbp15	FK506 binding protein 15	1.3	0.008141	0.844803
Hapln1	hyaluronan and proteoglycan link protein 1	1.3	0.016219	0.934625
Cacul1	CDK2 associated, cullin domain 1	1.3	0.033739	0.955604
Rbm11	RNA binding motif protein 11	1.3	0.037787	0.955604
Dhrs7	dehydrogenase/reductase (SDR family) member 7	1.31	0.038619	0.955604
S100a16	S100 calcium binding protein A16	1.31	0.031956	0.955027
Rnf181	ring finger protein 181	1.31	0.028279	0.945337
Epg5	ectopic P-granules autophagy protein 5 homolog (C. elegans)	1.31	0.014753	0.934625
Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	1.31	0.044109	0.955604
Dnajc16	DnaJ (Hsp40) homolog, subfamily C, member 16	1.31	0.019846	0.934625
Cd226	CD226 antigen	1.31	0.0076	0.832777
Rnf6	ring finger protein (C3H2C3 type) 6	1.31	0.001166	0.661654
Susd6	sushi domain containing 6	1.31	0.011663	0.892484
Ndufaf7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 7	1.31	0.024364	0.934625
Rnf2	ring finger protein 2	1.31	0.036161	0.955604
Xpo4	exportin 4	1.31	0.033194	0.955027

Ror2	receptor tyrosine kinase-like orphan receptor 2	1.31	0.009458	0.858114
Pcdhac1	protocadherin alpha subfamily C, 1; protocadherin alpha subfamily C, 2; protocadherin alpha 4; protocadherin alpha 6; protocadherin alpha 7; protocadherin alpha 5; protocadherin alpha 11; protocadherin alpha 10; protocadherin alpha 1; protocadherin alpha 9; protocadherin alpha 3; protocadherin alpha 12; protocadherin alpha 2; protocadherin alpha 8; predicted gene, 37013	1.31	0.033139	0.955027
Slitrk1	SLIT and NTRK-like family, member 1	1.31	0.004687	0.790387
Tbc1d20	TBC1 domain family, member 20	1.32	0.003473	0.720729
Tmem204	transmembrane protein 204	1.32	0.016938	0.934625
Prss2	protease, serine 2	1.32	0.048563	0.955604
Tmem88	transmembrane protein 88	1.32	0.028935	0.955027
Eif6	eukaryotic translation initiation factor 6	1.32	0.03412	0.955604
Mgme1	mitochondrial genome maintainance exonuclease 1	1.32	0.016927	0.934625
Vmn2r78	vomeronasal 2, receptor 78	1.32	0.048032	0.955604
Asph	aspartate-beta-hydroxylase	1.32	0.001909	0.661654
Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	1.32	0.046359	0.955604
Krt222	keratin 222	1.32	0.016801	0.934625
Gja6	gap junction protein, alpha 6	1.33	0.03056	0.955027
Ccdc126	coiled-coil domain containing 126	1.33	0.024407	0.934625
Bcl2l15	BCLl2-like 15	1.33	0.022682	0.934625
Lrrc4c	leucine rich repeat containing 4C	1.33	0.044954	0.955604
Olfr1000	olfactory receptor 1000	1.33	0.013357	0.923987
Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	1.33	0.038092	0.955604
Sort1	sortilin 1	1.33	0.007222	0.828491
Tbc1d22a	TBC1 domain family, member 22a	1.33	0.024889	0.93844
Acap1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	1.33	0.035535	0.955604
Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	1.33	0.001125	0.661654
Cphx3	cytoplasmic polyadenylated homeobox 3	1.33	0.01001	0.871735
Ccdc189	coiled-coil domain containing 189	1.33	0.004797	0.790387
Tmem70	transmembrane protein 70	1.33	0.021683	0.934625
Otud7a	OTU domain containing 7A	1.33	0.0067	0.807179
Psd3	pleckstrin and Sec7 domain containing 3	1.33	0.027353	0.944116
Maml1	mastermind like 1 (Drosophila)	1.34	0.002583	0.690171
Olfr237-ps1	olfactory receptor 237, pseudogene 1	1.34	0.045114	0.955604

Esrra	estrogen related receptor, alpha; microRNA 6990	1.34	0.018668	0.934625
Ppt1	palmitoyl-protein thioesterase 1	1.34	0.040717	0.955604
Plscr3	phospholipid scramblase 3	1.34	0.017514	0.934625
Ilf2	interleukin enhancer binding factor 2	1.34	0.012664	0.905716
Hunk	hormonally upregulated Neu-associated kinase	1.34	0.009239	0.858114
Abi1	abl-interactor 1	1.35	0.042733	0.955604
Cdhr4	cadherin-related family member 4	1.35	0.005715	0.801647
Olfr1391	olfactory receptor 1391	1.35	0.004735	0.790387
Fam78b	family with sequence similarity 78, member B	1.35	0.020245	0.934625
Mtpap	mitochondrial poly(A) polymerase	1.35	0.004849	0.791718
Sord	sorbitol dehydrogenase	1.35	0.002942	0.693971
Mrpl49	mitochondrial ribosomal protein L49	1.35	0.001345	0.661654
Tlr7	toll-like receptor 7	1.35	0.008822	0.858114
Vash1	vasohibin 1	1.35	0.039024	0.955604
Gtf2h2	general transcription factor II H, polypeptide 2	1.36	0.035315	0.955604
Srd5a3	steroid 5 alpha-reductase 3	1.36	0.034059	0.955604
Gpr176	G protein-coupled receptor 176	1.36	0.013609	0.925423
Krt19	keratin 19	1.36	0.016606	0.934625
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	1.36	0.039489	0.955604
Wdr24	WD repeat domain 24	1.36	0.044395	0.955604
Kcnq1	potassium voltage-gated channel, subfamily Q, member 1	1.36	0.045114	0.955604
Bcl11a	B cell CLL/lymphoma 11A (zinc finger protein)	1.36	0.011662	0.892484
Clec4g	C-type lectin domain family 4, member g	1.36	0.024229	0.934625
Olfr328	olfactory receptor 328	1.36	0.018975	0.934625
Bysl	bystin-like	1.36	0.043428	0.955604
Mtg1	mitochondrial GTPase 1 homolog (S. cerevisiae)	1.36	0.035483	0.955604
Cyp2b9	cytochrome P450, family 2, subfamily b, polypeptide 9	1.36	0.018949	0.934625
Vmn1r29	vomeronasal 1 receptor 29	1.37	0.048896	0.955604
Setmar	SET domain without mariner transposase fusion	1.37	0.027985	0.945337
Tmem120b	transmembrane protein 120B	1.37	0.043268	0.955604
Pm20d2	peptidase M20 domain containing 2	1.37	0.023456	0.934625
Cxcl11	chemokine (C-X-C motif) ligand 11	1.37	0.000534	0.56096
Farsb	phenylalanyl-tRNA synthetase, beta subunit	1.37	0.049587	0.955604
Oxr1	oxidation resistance 1	1.37	0.005722	0.801647
Gltscr1	glioma tumor suppressor candidate region gene 1	1.38	0.012802	0.905716
Impa1	inositol (myo)-1(or 4)-	1.38	0.001519	0.661654

	monophosphatase 1			
Atp2c1	ATPase, Ca++-sequestering	1.38	0.032757	0.955027
Sphk2	sphingosine kinase 2	1.38	0.037365	0.955604
Btbd6	BTB (POZ) domain containing 6	1.38	0.046721	0.955604
Dctn5	dynactin 5	1.38	0.032852	0.955027
Socs4	suppressor of cytokine signaling 4	1.38	0.043511	0.955604
Klhl28	kelch-like 28	1.38	0.045953	0.955604
Borcs5	BLOC-1 related complex subunit 5	1.38	0.026335	0.944116
Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	1.38	0.017963	0.934625
Ptdss1	phosphatidylserine synthase 1	1.38	0.01513	0.934625
Zfp133-ps	zinc finger protein 133, pseudogene; zinc finger protein pseudogene	1.39	0.02226	0.934625
Fsd2	fibronectin type III and SPRY domain containing 2	1.39	0.016985	0.934625
Fam162a	family with sequence similarity 162, member A	1.39	0.01425	0.934625
Vasn	vasorin	1.39	0.024224	0.934625
Clybl	citrate lyase beta like	1.39	0.036388	0.955604
Lrrc48	leucine rich repeat containing 48	1.39	0.015832	0.934625
Kcnk12	potassium channel, subfamily K, member 12	1.39	0.013333	0.923987
Pias3	protein inhibitor of activated STAT 3	1.39	0.049163	0.955604
Tiprl	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	1.39	0.023827	0.934625
Mtmr12	myotubularin related protein 12	1.39	0.007824	0.835337
Extl2	exostoses (multiple)-like 2	1.4	0.044623	0.955604
Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	1.4	0.022856	0.934625
Tmem81	transmembrane protein 81	1.4	0.049117	0.955604
Aldh18a1	aldehyde dehydrogenase 18 family, member A1	1.4	0.028133	0.945337
Zpbp2	zona pellucida binding protein 2	1.4	0.003292	0.709391
Krt26	keratin 26	1.4	0.012099	0.895556
Polr2d	polymerase (RNA) II (DNA directed) polypeptide D	1.4	0.01775	0.934625
Abcg8	ATP-binding cassette, sub-family G (WHITE), member 8	1.4	0.041695	0.955604
Lrrc45	leucine rich repeat containing 45	1.4	0.029529	0.955027
Coq7	demethyl-Q 7	1.4	0.001761	0.661654
Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	1.41	0.001919	0.661654
Haus6	HAUS augmin-like complex, subunit 6	1.41	0.036743	0.955604
Pomgnt1	protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase	1.41	0.026178	0.944116
Cypt8	cysteine-rich perinuclear theca 8; cysteine-rich perinuclear theca 7; cysteine-rich perinuclear theca 1	1.41	0.037227	0.955604
Pdk3	pyruvate dehydrogenase kinase,	1.41	0.011234	0.872249

	isoenzyme 3			
Csn1s2b	casein alpha s2-like B	1.41	0.040759	0.955604
Nsun2	NOL1/NOP2/Sun domain family member 2	1.41	0.003103	0.699764
Wasf1	WAS protein family, member 1	1.41	0.016547	0.934625
Olfr1447	olfactory receptor 1447	1.41	0.021255	0.934625
Edrf1	erythroid differentiation regulatory factor 1	1.41	0.026174	0.944116
Fbxw9	F-box and WD-40 domain protein 9	1.41	0.031435	0.955027
Cep126	centrosomal protein 126	1.42	0.038077	0.955604
Pou3f1	POU domain, class 3, transcription factor 1	1.42	0.039471	0.955604
Efhc2	EF-hand domain (C-terminal) containing 2	1.42	0.028087	0.945337
Dok4	docking protein 4	1.42	0.002673	0.690171
Kirrel2	kin of IRRE like 2 (Drosophila)	1.42	0.048421	0.955604
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	1.42	0.003685	0.724181
Fam81b	PREDICTED: family with sequence similarity 81, member B (Fam81b), mRNA.	1.42	0.015474	0.934625
Xcr1	chemokine (C motif) receptor 1	1.42	0.041257	0.955604
Mtl5	metallothionein-like 5, testis-specific (tesmin)	1.42	0.03459	0.955604
Tbx22	T-box 22	1.42	0.027378	0.944116
Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	1.42	0.028027	0.945337
Tyw3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	1.42	0.049233	0.955604
Zfp277	zinc finger protein 277	1.43	0.037415	0.955604
Mrgprb4	MAS-related GPR, member B4	1.43	0.000843	0.608562
Sla2	Src-like-adaptor 2	1.43	0.041156	0.955604
Pgam2	phosphoglycerate mutase 2	1.43	0.012266	0.902392
Tec	tec protein tyrosine kinase	1.43	0.038926	0.955604
Trappc1	trafficking protein particle complex 1	1.43	0.039666	0.955604
Neurod2	neurogenic differentiation 2	1.43	0.002218	0.661654
Coro2b	coronin, actin binding protein, 2B	1.44	0.02997	0.955027
Tti1	TELO2 interacting protein 1	1.44	0.028015	0.945337
Bckdk	branched chain ketoacid dehydrogenase kinase	1.44	0.005453	0.801647
Pde1a	phosphodiesterase 1A, calmodulin-dependent	1.44	0.017229	0.934625
Rps6ka4	ribosomal protein S6 kinase, polypeptide 4; microRNA 5046	1.45	0.044513	0.955604
Slco1c1	solute carrier organic anion transporter family, member 1c1	1.45	0.020942	0.934625
Slc25a35	solute carrier family 25, member 35	1.45	0.022256	0.934625
Sorl1	sortilin-related receptor, LDLR class A repeats-containing	1.45	0.024166	0.934625

Masp1	mannan-binding lectin serine peptidase 1	1.45	0.003872	0.754291
Gpd1l	glycerol-3-phosphate dehydrogenase 1-like	1.45	0.01934	0.934625
Usp3	ubiquitin specific peptidase 3	1.46	0.014879	0.934625
Ptpmt1	protein tyrosine phosphatase, mitochondrial 1	1.46	0.020785	0.934625
Tmem68	transmembrane protein 68	1.46	0.000899	0.608562
Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	1.46	0.001755	0.661654
Olfr1213	olfactory receptor 1213	1.46	0.027466	0.944116
Psmb5	proteasome (prosome, macropain) subunit, beta type 5; microRNA 686	1.46	0.006496	0.801647
Pex5l	peroxisomal biogenesis factor 5-like	1.46	0.038812	0.955604
Pbdc1	polysaccharide biosynthesis domain containing 1	1.46	0.038834	0.955604
Pgm2l1	phosphoglucomutase 2-like 1	1.46	0.003151	0.699764
Lrrc59	leucine rich repeat containing 59	1.47	0.008762	0.858114
Prrt3	proline-rich transmembrane protein 3	1.47	0.041875	0.955604
Klhl12	kelch-like 12	1.47	0.03893	0.955604
Zfp46	zinc finger protein 46	1.47	0.03694	0.955604
Zdhhc5	zinc finger, DHHC domain containing 5	1.47	0.044639	0.955604
Tpst1	protein-tyrosine sulfotransferase 1	1.48	0.02416	0.934625
Gins4	GINS complex subunit 4 (Sld5 homolog)	1.48	0.017093	0.934625
Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	1.48	0.042685	0.955604
Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	1.48	0.031877	0.955027
Fbxw2	F-box and WD-40 domain protein 2	1.48	0.022448	0.934625
Kif1bp	KIF1 binding protein	1.48	0.021112	0.934625
Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	1.49	0.048364	0.955604
Oas1f	2-5 oligoadenylate synthetase 1F; 2'-5' oligoadenylate synthetase 1F	1.49	0.004624	0.790387
Hist2h2be	histone cluster 2, H2be	1.49	0.005087	0.801155
Prpf3	PRP3 pre-mRNA processing factor 3 homolog (yeast)	1.5	0.046284	0.955604
Otulin	OTU deubiquitinase with linear linkage specificity	1.5	0.006382	0.801647
Paox	polyamine oxidase (exo-N4-amino)	1.5	0.00938	0.858114
Cd46	CD46 antigen, complement regulatory protein	1.5	0.030999	0.955027
Uggt2	UDP-glucose glycoprotein glucosyltransferase 2	1.5	0.043091	0.955604
Figf	c-fos induced growth factor	1.5	0.025874	0.944116
Hs6st3	heparan sulfate 6-O-sulfotransferase 3	1.51	0.022784	0.934625
Setdb2	SET domain, bifurcated 2; PHD finger protein 11C; PHD finger protein 11D	1.51	0.035697	0.955604

Jph1	junctophilin 1	1.51	0.017934	0.934625
Sly	Sycp3 like Y-linked	1.51	0.02661	0.944116
Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	1.51	0.007056	0.828491
Olfr1453	olfactory receptor 1453	1.52	0.003368	0.711257
Dnd1	dead end homolog 1 (zebrafish)	1.52	0.012761	0.905716
Cars	cysteinyl-tRNA synthetase	1.52	0.041808	0.955604
Btbd10	BTB (POZ) domain containing 10	1.52	0.00071	0.608562
Nfix	nuclear factor I/X	1.52	0.039562	0.955604
Cav2	caveolin 2	1.52	0.025296	0.939355
Nol8	nucleolar protein 8	1.53	0.0357	0.955604
9-Mar	membrane-associated ring finger (C3HC4) 9	1.53	0.0033	0.709391
Plscr4	phospholipid scramblase 4	1.53	0.042491	0.955604
Fem1a	feminization 1 homolog a (C. elegans)	1.54	0.011825	0.894062
Olfr1199	olfactory receptor 1199	1.54	0.04831	0.955604
Acadm	acyl-Coenzyme A dehydrogenase, medium chain	1.54	0.000904	0.608562
Olfr1487	olfactory receptor 1487	1.54	0.006253	0.801647
Polr1e	polymerase (RNA) I polypeptide E	1.54	0.037262	0.955604
Nlrp2	NLR family, pyrin domain containing 2	1.54	0.021808	0.934625
Il4ra	interleukin 4 receptor, alpha	1.54	0.022378	0.934625
Lelp1	late cornified envelope-like proline-rich 1	1.54	0.004132	0.770544
Syne1	spectrin repeat containing, nuclear envelope 1	1.55	0.03073	0.955027
Zmat5	zinc finger, matrin type 5	1.55	0.045868	0.955604
Msra	methionine sulfoxide reductase A	1.55	0.021317	0.934625
Chia1	chitinase, acidic 1	1.55	0.028175	0.945337
Fam151b	family with sequence similarity 151, member B	1.55	0.040927	0.955604
Prp2	proline rich protein 2	1.55	0.005148	0.801598
Iqcj	IQ motif containing J	1.55	0.022767	0.934625
Vimp	VCP-interacting membrane protein	1.56	0.020725	0.934625
Zfand3	zinc finger, AN1-type domain 3	1.56	0.042693	0.955604
Syce2	synaptonemal complex central element protein 2	1.56	0.04324	0.955604
Slc4a10	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	1.56	0.026626	0.944116
Zg16	zymogen granule protein 16	1.57	0.036798	0.955604
Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	1.57	0.023259	0.934625
Slc25a15	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	1.58	0.001884	0.661654
Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	1.58	0.005441	0.801647

Akr1c12	aldo-keto reductase family 1, member C12	1.58	0.000069	0.503007
Capns2	calpain, small subunit 2	1.58	0.013836	0.925423
Nanp	N-acetylneuraminic acid phosphatase	1.58	0.005386	0.801647
Tex29	testis expressed 29	1.59	0.011876	0.894062
Lrp4	low density lipoprotein receptor-related protein 4	1.59	0.007042	0.828491
Mex3b	mex3 homolog B (C. elegans)	1.59	0.013818	0.925423
Zbtb18	zinc finger and BTB domain containing 18	1.59	0.006559	0.804731
Lpar6	lysophosphatidic acid receptor 6	1.6	0.027406	0.944116
Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	1.6	0.03636	0.955604
Sgk3	serum/glucocorticoid regulated kinase 3	1.61	0.0073	0.828491
Cyp3a11	cytochrome P450, family 3, subfamily a, polypeptide 11	1.61	0.010868	0.872249
Wdr73	WD repeat domain 73	1.61	0.005244	0.801647
Dr1	down-regulator of transcription 1	1.61	0.038924	0.955604
Fam134b	family with sequence similarity 134, member B	1.62	0.01916	0.934625
Olfr1014	olfactory receptor 1014	1.62	0.019387	0.934625
Cdc25b	cell division cycle 25B	1.62	0.02822	0.945337
Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	1.62	0.008618	0.858114
Tmem178	transmembrane protein 178	1.62	0.042096	0.955604
Mmgt1	membrane magnesium transporter 1; microRNA 5116	1.63	0.048737	0.955604
Pinx1	PIN2/TERF1 interacting, telomerase inhibitor 1	1.64	0.000273	0.503007
Gsdmc4	gasdermin C4	1.64	0.044331	0.955604
Zdhhc23	zinc finger, DHHC domain containing 23	1.65	0.045468	0.955604
Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	1.65	0.020644	0.934625
Trim61	tripartite motif-containing 61; tripartite motif-containing 60	1.66	0.00208	0.661654
Mctp1	multiple C2 domains, transmembrane 1	1.67	0.03505	0.955604
Tuft1	tuftelin 1	1.67	0.022667	0.934625
Tars	threonyl-tRNA synthetase	1.67	0.017162	0.934625
Snx33	sorting nexin 33	1.68	0.01942	0.934625
Tmprss11d	transmembrane protease, serine 11d	1.69	0.017973	0.934625
B3glct	beta-3-glucosyltransferase	1.69	0.021623	0.934625
Svopl	SV2 related protein homolog (rat)-like	1.69	0.027636	0.945337
Trappc3l	trafficking protein particle complex 3 like	1.7	0.009389	0.858114
Dsg1c	desmoglein 1 gamma	1.71	0.005828	0.801647
Lce1e	late cornified envelope 1E	1.72	0.007683	0.83388
Tmem139	transmembrane protein 139	1.72	0.001896	0.661654
Vmn1r214	vomeronasal 1 receptor 214	1.73	0.030523	0.955027

Olfr693	olfactory receptor 693	1.74	0.021582	0.934625
Vmn1r36	vomeronasal 1 receptor 36	1.75	0.043994	0.955604
Cldn34-ps	claudin 34, pseudogene	1.75	0.034525	0.955604
Sowahb	sosondowah ankyrin repeat domain family member B	1.77	0.021008	0.934625
Irak2	interleukin-1 receptor-associated kinase 2	1.78	0.048242	0.955604
Krtap14	keratin associated protein 14	1.78	0.025423	0.939355
Il1rap	interleukin 1 receptor accessory protein	1.79	0.000187	0.503007
Slc37a4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	1.8	0.048923	0.955604
Cds1	CDP-diacylglycerol synthase 1	1.8	0.008025	0.844445
Olfr512	olfactory receptor 512	1.81	0.041203	0.955604
Stk32a	serine/threonine kinase 32A	1.82	0.014391	0.934625
Sult2b1	sulfotransferase family, cytosolic, 2B, member 1	1.84	0.003128	0.699764
Olfr466	olfactory receptor 466	1.86	0.049412	0.955604
Sstr4	somatostatin receptor 4	1.86	0.00265	0.690171
Adra1d	adrenergic receptor, alpha 1d	1.88	0.007446	0.828491
Tenm3	teneurin transmembrane protein 3	1.93	0.034425	0.955604
Rnf166	ring finger protein 166	1.95	0.019923	0.934625
Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5	1.96	0.022122	0.934625
Olfr170	olfactory receptor 170	1.97	0.031828	0.955027
Epha4	Eph receptor A4	1.99	0.039996	0.955604
Itpka	inositol 1,4,5-trisphosphate 3-kinase A	1.99	0.003516	0.722869
Olfr774	olfactory receptor 774	2	0.001505	0.661654
Wdhd1	WD repeat and HMG-box DNA binding protein 1	2	0.002069	0.661654
Fezf2	Fez family zinc finger 2	2	0.012798	0.905716
Cyp2c50	cytochrome P450, family 2, subfamily c, polypeptide 50	2.01	0.00037	0.503007
Cdh12	cadherin 12	2.02	0.017625	0.934625
Olfr898	olfactory receptor 898	2.03	0.008748	0.858114
Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9	2.09	0.019567	0.934625
Grp	gastrin releasing peptide; retina and anterior neural fold homeobox	2.11	0.045372	0.955604
Mpped1	metallophosphoesterase domain containing 1	2.14	0.011736	0.892484
Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	2.19	0.045637	0.955604
Colgalt2	collagen beta(1-O)galactosyltransferase 2	2.23	0.00923	0.858114
Rspo2	R-spondin 2	2.32	0.010331	0.872249

Table S3- Genes downregulated in the Amygdala of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA Amg vs. TT Amg)	ANOVA p-value (AA Amg vs. TT Amg)	FDR p-value (AA Amg vs. TT Amg)
Gpx3	glutathione peroxidase 3	-6.47	0.000963	0.626436
Gabrq	gamma-aminobutyric acid (GABA) A receptor, subunit theta	-5	0.002044	0.661654
Fezf1	Fez family zinc finger 1	-4.85	0.042001	0.955604
Barhl2	BarH-like 2 (Drosophila)	-4.57	0.000239	0.503007
Pbx3	pre B cell leukemia homeobox 3	-4.45	0.000848	0.608562
Arhgap36	Rho GTPase activating protein 36	-3.8	0.021199	0.934625
Gpr165	G protein-coupled receptor 165	-3.56	0.00998	0.871735
Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	-3.55	0.021443	0.934625
Ccdc42	coiled-coil domain containing 42	-3.45	0.019572	0.934625
Glra1	glycine receptor, alpha 1 subunit	-3.29	0.020002	0.934625
Cartpt	CART prepropeptide	-3.16	0.000283	0.503007
Tacr1	tachykinin receptor 1	-3.15	0.009893	0.868305
Mid1	midline 1	-3.11	0.015198	0.934625
Mid1	midline 1	-3.11	0.015198	0.934625
Mid1	midline 1	-3.02	0.014825	0.934625
Meis1	Meis homeobox 1	-2.92	0.02671	0.944116
Zim1	zinc finger, imprinted 1	-2.82	0.008436	0.857703
Avp	arginine vasopressin	-2.81	0.028306	0.945337
Prlr	prolactin receptor	-2.8	0.011985	0.894062
Usp29	ubiquitin specific peptidase 29	-2.62	0.008725	0.858114
Scg2	secretogranin II	-2.59	0.00505	0.800974
Tmem91	transmembrane protein 91	-2.57	0.032464	0.955027
Vwc2l	von Willebrand factor C domain-containing protein 2-like	-2.43	0.044047	0.955604
Nxph4	neurexophilin 4	-2.38	0.015803	0.934625
Magel2	melanoma antigen, family L, 2	-2.34	0.009835	0.866684
Cdh4	cadherin 4	-2.33	0.008459	0.857703
Nova1	neuro-oncological ventral antigen 1	-2.22	0.014555	0.934625
Glra3	glycine receptor, alpha 3 subunit	-2.22	0.041693	0.955604
Lhfpl3	lipoma HMGIC fusion partner-like 3	-2.18	0.013265	0.923367
Susd2	sushi domain containing 2	-2.18	0.044703	0.955604
Fndc9	fibronectin type III domain containing 9	-2.14	0.002856	0.693971
Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	-2.14	0.008112	0.844803
Baiap3	BAI1-associated protein 3	-2.09	0.001285	0.661654
Itih3	inter-alpha trypsin inhibitor, heavy chain 3	-2.08	0.010695	0.872249
Gng4	guanine nucleotide binding protein (G protein), gamma 4	-2.08	0.00214	0.661654

Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	-2.07	0.015217	0.934625
Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	-2.06	0.039885	0.955604
Calcr	calcitonin receptor	-2.04	0.004054	0.76285
Mc3r	melanocortin 3 receptor	-2.03	0.000361	0.503007
Zcchc12	zinc finger, CCHC domain containing 12	-1.99	0.009262	0.858114
Esp16	exocrine gland secreted peptide 16	-1.98	0.035577	0.955604
Klhl13	kelch-like 13	-1.97	0.015337	0.934625
Cacng5	calcium channel, voltage-dependent, gamma subunit 5	-1.96	0.004805	0.790387
Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated); microRNA 5107	-1.96	0.009662	0.861694
Sim1	single-minded homolog 1 (Drosophila)	-1.94	0.031556	0.955027
Pld2	phospholipase D2	-1.92	0.003322	0.709391
Spint1	serine protease inhibitor, Kunitz type 1	-1.91	0.003585	0.723699
Vat1	vesicle amine transport protein 1 homolog (T californica)	-1.9	0.006391	0.801647
Amotl1	angiomotin-like 1	-1.89	0.017336	0.934625
Vmn1r91	vomeronasal 1 receptor 91	-1.89	0.025779	0.944116
Tmem225	transmembrane protein 225	-1.89	0.022016	0.934625
Ahi1	Abelson helper integration site 1	-1.89	0.027374	0.944116
Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	-1.88	0.029424	0.955027
Pigr	polymeric immunoglobulin receptor	-1.87	0.041785	0.955604
Elfn1	leucine rich repeat and fibronectin type III, extracellular 1	-1.87	0.006022	0.801647
Ccdc187	coiled-coil domain containing 187	-1.86	0.009178	0.858114
Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	-1.83	0.004517	0.789838
Tpm2	tropomyosin 2, beta	-1.82	0.018177	0.934625
Sfmbt2	Scm-like with four mbt domains 2	-1.82	0.007206	0.828491
Vwa5b1	von Willebrand factor A domain containing 5B1	-1.79	0.005162	0.801598
Cfap46	cilia and flagella associated protein 46	-1.78	0.0369	0.955604
Kazn	kazrin, periplakin interacting protein	-1.77	0.023045	0.934625
Ache	acetylcholinesterase	-1.77	0.034447	0.955604
Olfr860	olfactory receptor 860	-1.77	0.036863	0.955604
Slc1a7	solute carrier family 1 (glutamate transporter), member 7	-1.77	0.01115	0.872249
Pram1	PML-RAR alpha-regulated adaptor molecule 1	-1.77	0.034638	0.955604

Cyp2j8	cytochrome P450, family 2, subfamily j, polypeptide 8	-1.76	0.011447	0.882631
Pnma5	paraneoplastic antigen family 5	-1.76	0.000336	0.503007
Peg3	paternally expressed 3	-1.76	0.010784	0.872249
Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	-1.75	0.012565	0.905716
Tsen15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	-1.75	0.032645	0.955027
Tmem130	transmembrane protein 130	-1.75	0.03258	0.955027
Ms4a3	membrane-spanning 4-domains, subfamily A, member 3	-1.74	0.049734	0.955604
Ucn3	urocortin 3	-1.74	0.002235	0.661654
Fam65c	family with sequence similarity 65, member C	-1.73	0.007245	0.828491
Olfr68	olfactory receptor 68	-1.72	0.042977	0.955604
Arl14epl	ADP-ribosylation factor-like 14 effector protein-like	-1.72	0.04912	0.955604
Chodl	chondrolectin	-1.72	0.029068	0.955027
Inpp4b	inositol polyphosphate-4-phosphatase, type II	-1.72	0.007369	0.828491
Rnd2	Rho family GTPase 2	-1.71	0.00008	0.503007
Zfp936	zinc finger protein 936	-1.71	0.013784	0.925423
Tppp3	tubulin polymerization-promoting protein family member 3	-1.71	0.041242	0.955604
Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	-1.71	0.019251	0.934625
Mroh3	maestro heat-like repeat family member 3	-1.71	0.000903	0.608562
Tdrd5	tudor domain containing 5	-1.71	0.042629	0.955604
Bcam	basal cell adhesion molecule	-1.7	0.037585	0.955604
Nhs	Nance-Horan syndrome (human)	-1.7	0.023486	0.934625
Parvb	parvin, beta	-1.7	0.001496	0.661654
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	-1.69	0.031004	0.955027
C1ql1	complement component 1, q subcomponent-like 1	-1.69	0.010977	0.872249
Skint7	selection and upkeep of intraepithelial T cells 7	-1.68	0.022149	0.934625
Cma2	chymase 2, mast cell	-1.68	0.039506	0.955604
Pcdh18	protocadherin 18	-1.68	0.005628	0.801647
Kcnk9	potassium channel, subfamily K, member 9	-1.68	0.022756	0.934625
Dner	delta/notch-like EGF repeat containing	-1.68	0.001546	0.661654
Gulp1	GULP, engulfment adaptor PTB domain containing 1	-1.67	0.004517	0.789838
Fam124a	family with sequence similarity 124, member A	-1.67	0.011399	0.881988

Hap1	huntingtin-associated protein 1	-1.67	0.04034	0.955604
Pgr15l	G protein-coupled receptor 15-like	-1.66	0.03502	0.955604
Allc	allantoicase	-1.65	0.021126	0.934625
Siah2	seven in absentia 2	-1.64	0.045714	0.955604
Hspb6	heat shock protein, alpha-crystallin-related, B6	-1.64	0.019664	0.934625
Rad1	RAD1 checkpoint DNA exonuclease	-1.64	0.008452	0.857703
Limd2	LIM domain containing 2	-1.64	0.048428	0.955604
Pid1	phosphotyrosine interaction domain containing 1	-1.64	0.016404	0.934625
Vwc2	von Willebrand factor C domain containing 2	-1.64	0.023658	0.934625
Stfa3	stefin A3	-1.63	0.009248	0.858114
Arhgap24	Rho GTPase activating protein 24	-1.63	0.018236	0.934625
Nphp3	nephronophthisis 3 (adolescent)	-1.63	0.033357	0.955444
Pipox	pipecolic acid oxidase	-1.62	0.021037	0.934625
Esp3	exocrine gland secreted peptide 3	-1.62	0.046042	0.955604
Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2	-1.62	0.001657	0.661654
Cfap70	cilia and flagella associated protein 70	-1.62	0.006939	0.828465
Sncaip	synuclein, alpha interacting protein (synphilin)	-1.61	0.032538	0.955027
Lmnb2	lamin B2	-1.61	0.000556	0.56096
Cks1b	CDC28 protein kinase 1b	-1.61	0.030297	0.955027
Mrc2	mannose receptor, C type 2	-1.61	0.038925	0.955604
Micall2	MICAL-like 2	-1.61	0.027435	0.944116
L3mbtl4	l(3)mbt-like 4 (Drosophila)	-1.61	0.022586	0.934625
Paqr6	progestin and adipoQ receptor family member VI	-1.61	0.035822	0.955604
Ubap1l	ubiquitin-associated protein 1-like	-1.6	0.009542	0.858339
Slitrk6	SLIT and NTRK-like family, member 6	-1.59	0.030942	0.955027
Papolb	poly (A) polymerase beta (testis specific)	-1.59	0.0165	0.934625
Tlr1	toll-like receptor 1	-1.58	0.000354	0.503007
Crisp4	cysteine-rich secretory protein 4	-1.58	0.040169	0.955604
Tgtp2	T cell specific GTPase 2	-1.58	0.023125	0.934625
Nrsn2	neurensin 2	-1.57	0.006496	0.801647
Cep57	centrosomal protein 57	-1.57	0.039641	0.955604
Vmn1r103	vomeronasal 1 receptor 103	-1.57	0.011975	0.894062
Fads2	fatty acid desaturase 2	-1.57	0.015907	0.934625
Fndc3b	fibronectin type III domain containing 3B	-1.56	0.000668	0.608562
Cdhr1	cadherin-related family member 1	-1.56	0.023308	0.934625
Amot	angiomotin	-1.56	0.002648	0.690171
Sorcs2	sortilin-related VPS10 domain containing receptor 2	-1.55	0.010285	0.872249
Col6a4	collagen, type VI, alpha 4	-1.55	0.018922	0.934625
Scd1	stearoyl-Coenzyme A desaturase 1	-1.55	0.022623	0.934625

Fcgr2b	Fc receptor, IgG, low affinity IIb	-1.55	0.009651	0.861694
Scamp3	secretory carrier membrane protein 3	-1.54	0.013577	0.925423
Olfr1234	olfactory receptor 1234	-1.54	0.004268	0.770544
Cfap46	cilia and flagella associated protein 46	-1.54	0.047781	0.955604
Prame	preferentially expressed antigen in melanoma	-1.54	0.010443	0.872249
Prok2	prokineticin 2	-1.54	0.049644	0.955604
Amer3	APC membrane recruitment 3	-1.54	0.014366	0.934625
Brinp2	bone morphogenic protein/retinoic acid inducible neural-specific 2	-1.54	0.039266	0.955604
Slc25a42	solute carrier family 25, member 42	-1.53	0.047077	0.955604
Evl	Ena-vasodilator stimulated phosphoprotein	-1.53	0.002365	0.690171
Pla2g2c	phospholipase A2, group IIC	-1.53	0.02002	0.934625
Irf1	interferon regulatory factor 1	-1.53	0.032034	0.955027
Col18a1	collagen, type XVIII, alpha 1	-1.53	0.047269	0.955604
Col25a1	collagen, type XXV, alpha 1	-1.53	0.033095	0.955027
Ece2	endothelin converting enzyme 2	-1.53	0.031838	0.955027
Cdnf	cerebral dopamine neurotrophic factor	-1.52	0.045804	0.955604
Stpg1	sperm tail PG rich repeat containing 1	-1.52	0.034065	0.955604
Col19a1	collagen, type XIX, alpha 1	-1.52	0.005896	0.801647
Smok3c	sperm motility kinase 3C	-1.52	0.009772	0.865989
Gdnf	glial cell line derived neurotrophic factor	-1.51	0.043704	0.955604
Tshz1	teashirt zinc finger family member 1	-1.51	0.011132	0.872249
Dgat2l6	diacylglycerol O-acyltransferase 2-like 6	-1.51	0.004168	0.770544
Hpd	4-hydroxyphenylpyruvic acid dioxygenase	-1.5	0.006658	0.807179
Caprin2	caprin family member 2	-1.5	0.017643	0.934625
Rd3l	retinal degeneration 3-like	-1.5	0.022431	0.934625
Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2	-1.5	0.016568	0.934625
Adgrg1	adhesion G protein-coupled receptor G1	-1.5	0.036435	0.955604
Cdh22	cadherin 22	-1.5	0.015997	0.934625
Adra1a	adrenergic receptor, alpha 1a	-1.5	0.028121	0.945337
Adarb2	adenosine deaminase, RNA-specific, B2	-1.5	0.023683	0.934625
Olfr845	olfactory receptor 845	-1.49	0.038276	0.955604
Mfap2	microfibrillar-associated protein 2	-1.49	0.029352	0.955027
Dclk3	doublecortin-like kinase 3	-1.48	0.031212	0.955027
Ttc16	tetratricopeptide repeat domain 16	-1.48	0.014312	0.934625
Ncapg	non-SMC condensin I complex, subunit G	-1.48	0.045968	0.955604
Syk	spleen tyrosine kinase	-1.48	0.000338	0.503007
Vat1l	vesicle amine transport protein 1 homolog-like (T. californica)	-1.47	0.011219	0.872249
Zfp442	zinc finger protein 442	-1.47	0.010355	0.872249
Stox2	storkhead box 2	-1.47	0.00597	0.801647
Ribc1	RIB43A domain with coiled-coils 1	-1.47	0.037304	0.955604
Glipr1l2	GLI pathogenesis-related 1 like 2	-1.47	0.022137	0.934625

Rhox2c	reproductive homeobox 2C	-1.47	0.040228	0.955604
Vmn1r216	vomeronasal 1 receptor 216	-1.47	0.031789	0.955027
Tectb	tectorin beta; microRNA 6715	-1.47	0.004775	0.790387
Gipc2	GIPC PDZ domain containing family, member 2	-1.46	0.039032	0.955604
Pou2f1	POU domain, class 2, transcription factor 1	-1.46	0.032228	0.955027
Zbtb12	zinc finger and BTB domain containing 12	-1.46	0.015423	0.934625
Clmp	CXADR-like membrane protein	-1.46	0.043335	0.955604
Gap43	growth associated protein 43	-1.46	0.011081	0.872249
Nrip2	nuclear receptor interacting protein 2	-1.46	0.018738	0.934625
Orai2	ORAI calcium release-activated calcium modulator 2	-1.45	0.035087	0.955604
Scn11a	sodium channel, voltage-gated, type XI, alpha	-1.45	0.017703	0.934625
Mab21l1	mab-21-like 1 (C. elegans)	-1.45	0.027309	0.944116
Casq2	calsequestrin 2	-1.44	0.046323	0.955604
Vmn1r113	vomeronasal 1 receptor 113	-1.44	0.018143	0.934625
Olfr1218	olfactory receptor 1218	-1.44	0.01809	0.934625
Elmo3	engulfment and cell motility 3	-1.44	0.005495	0.801647
Fam229b	family with sequence similarity 229, member B	-1.44	0.000331	0.503007
Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	-1.44	0.038418	0.955604
Mcpt2	mast cell protease 2	-1.44	0.037435	0.955604
Ep300	E1A binding protein p300	-1.44	0.015313	0.934625
Tsen2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	-1.43	0.033196	0.955027
Mdk	midkine	-1.43	0.039777	0.955604
Olfr164	olfactory receptor 164	-1.43	0.01313	0.919747
Arsk	arylsulfatase K	-1.43	0.009547	0.858339
Ptprc	protein tyrosine phosphatase, receptor type, C	-1.43	0.045495	0.955604
Bpifa3	BPI fold containing family A, member 3	-1.43	0.011066	0.872249
Ccdc137	coiled-coil domain containing 137	-1.43	0.029272	0.955027
Efcab12	EF-hand calcium binding domain 12	-1.43	0.025704	0.944116
Olfr1200	olfactory receptor 1200	-1.43	0.01779	0.934625
Olfr153	olfactory receptor 153	-1.43	0.038291	0.955604
Ccdc183	coiled-coil domain containing 183	-1.43	0.007965	0.844445
Efs	embryonal Fyn-associated substrate	-1.43	0.002659	0.690171
Mrap2	melanocortin 2 receptor accessory protein 2	-1.43	0.02639	0.944116
Oprm1	opioid receptor, mu 1	-1.42	0.037715	0.955604
Olfr374	olfactory receptor 374	-1.42	0.047621	0.955604
Zfp341	zinc finger protein 341	-1.42	0.024528	0.934625
Epcam	epithelial cell adhesion molecule	-1.42	0.027384	0.944116

Rsg1	REM2 and RAB-like small GTPase 1	-1.42	0.00081	0.608562
Npffr1	neuropeptide FF receptor 1	-1.42	0.016503	0.934625
Pla2g16	phospholipase A2, group XVI	-1.41	0.024733	0.937233
Zfp937	zinc finger protein 937	-1.41	0.008062	0.844445
Hip1	huntingtin interacting protein 1	-1.41	0.046334	0.955604
Rin2	Ras and Rab interactor 2	-1.41	0.03863	0.955604
Izumo1r	IZUMO1 receptor, JUNO	-1.41	0.016565	0.934625
Gstm3	glutathione S-transferase, mu 3	-1.41	0.04015	0.955604
Olfr814	olfactory receptor 814	-1.41	0.037276	0.955604
Mmp12	matrix metallopeptidase 12	-1.41	0.034378	0.955604
Aurka	aurora kinase A	-1.41	0.027252	0.944116
Sncg	synuclein, gamma	-1.41	0.044689	0.955604
H2-Aa	histocompatibility 2, class II antigen A, alpha	-1.41	0.030425	0.955027
Sfrp4	secreted frizzled-related protein 4	-1.41	0.030542	0.955027
Psd2	pleckstrin and Sec7 domain containing 2	-1.41	0.006688	0.807179
Zfp516	zinc finger protein 516	-1.4	0.022412	0.934625
Fam196b	family with sequence similarity 196, member B	-1.4	0.003395	0.711257
Krtap31-1	keratin associated protein 31-1	-1.4	0.033211	0.955027
Tcf7l1	transcription factor 7 like 1 (T cell specific, HMG box)	-1.4	0.010833	0.872249
Olfr516	olfactory receptor 516	-1.4	0.006067	0.801647
Igdcc4	immunoglobulin superfamily, DCC subclass, member 4	-1.4	0.032276	0.955027
Rybp	RING1 and YY1 binding protein	-1.4	0.04217	0.955604
Atn1	atrophin 1	-1.4	0.017392	0.934625
Itgb4	integrin beta 4	-1.39	0.019884	0.934625
Arhgap27	Rho GTPase activating protein 27	-1.39	0.011998	0.894062
Ier5l	immediate early response 5-like	-1.39	0.025274	0.939355
Iqce	IQ motif containing E	-1.39	0.004635	0.790387
Olfr1340	olfactory receptor 1340	-1.39	0.033774	0.955604
Cyp27b1	cytochrome P450, family 27, subfamily b, polypeptide 1	-1.39	0.039124	0.955604
Zfp811	zinc finger protein 811	-1.39	0.029228	0.955027
Zfp354b	zinc finger protein 354B	-1.39	0.01497	0.934625
Nap1l5	nucleosome assembly protein 1-like 5	-1.39	0.047608	0.955604
Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	-1.39	0.049962	0.955604
Nt5c1b	5-nucleotidase, cytosolic IB; 5'-nucleotidase, cytosolic IB	-1.38	0.010269	0.872249
Il21	interleukin 21	-1.38	0.003959	0.761359
Scgn	secretagogin, EF-hand calcium binding protein	-1.38	0.048697	0.955604
Dppa5a	developmental pluripotency associated 5A	-1.38	0.01784	0.934625

Gpr141	G protein-coupled receptor 141	-1.38	0.034576	0.955604
Tmem206	transmembrane protein 206	-1.38	0.01693	0.934625
Pldi	polymorphic derived intron containing	-1.38	0.002032	0.661654
Rnpc3	RNA-binding region (RNP1, RRM) containing 3	-1.38	0.002164	0.661654
Mtss1l	metastasis suppressor 1-like	-1.38	0.030275	0.955027
Pnmal2	PNMA-like 2	-1.38	0.017846	0.934625
Asic2	acid-sensing (proton-gated) ion channel 2	-1.38	0.022815	0.934625
Zfhx3	zinc finger homeobox 3	-1.37	0.036763	0.955604
Tcf7l2	transcription factor 7 like 2, T cell specific, HMG box	-1.37	0.037554	0.955604
Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	-1.37	0.043346	0.955604
Itga11	integrin alpha 11	-1.37	0.048379	0.955604
Ltb4r2	leukotriene B4 receptor 2	-1.37	0.002567	0.690171
Vax2	ventral anterior homeobox 2	-1.37	0.000031	0.503007
Rpl21	ribosomal protein L21	-1.37	0.016549	0.934625
Klf12	Kruppel-like factor 12	-1.37	0.000282	0.503007
Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.36	0.030752	0.955027
Vezf1	vascular endothelial zinc finger 1	-1.36	0.003145	0.699764
Hipk3	homeodomain interacting protein kinase 3; microRNA 1902	-1.36	0.017022	0.934625
Olfr1232	olfactory receptor 1232	-1.36	0.038101	0.955604
Slc6a5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	-1.36	0.049366	0.955604
Lcn11	lipocalin 11	-1.36	0.03879	0.955604
Aldh3b2	aldehyde dehydrogenase 3 family, member B2	-1.36	0.024314	0.934625
Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	-1.35	0.049001	0.955604
Synb	syncytin b	-1.35	0.041279	0.955604
Synb	syncytin b	-1.35	0.041279	0.955604
Frem3	Fras1 related extracellular matrix protein 3	-1.35	0.01005	0.871773
Olfr231	olfactory receptor 231	-1.35	0.00914	0.858114
Olfr1450	olfactory receptor 1450	-1.35	0.033288	0.955027
Cfi	complement component factor i	-1.35	0.032091	0.955027
Zbed4	zinc finger, BED type containing 4	-1.35	0.049185	0.955604
Spaca4	sperm acrosome associated 4	-1.35	0.008994	0.858114
Mfsd7b	major facilitator superfamily domain containing 7B	-1.35	0.019428	0.934625
Grik1	glutamate receptor, ionotropic, kainate 1	-1.35	0.047299	0.955604
Por	P450 (cytochrome) oxidoreductase	-1.34	0.027729	0.945337
Arhgap8	Rho GTPase activating protein 8	-1.34	0.001503	0.661654

Zfp873	zinc finger protein 873	-1.34	0.023318	0.934625
Cd48	CD48 antigen	-1.34	0.04339	0.955604
Nup210	nucleoporin 210	-1.34	0.016843	0.934625
Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-1.34	0.024443	0.934625
Podxl2	podocalyxin-like 2	-1.34	0.048941	0.955604
Hdac11	histone deacetylase 11	-1.34	0.047501	0.955604
Rab12	RAB12, member RAS oncogene family	-1.34	0.005433	0.801647
Sgcd	sarcoglycan, delta (dystrophin-associated glycoprotein)	-1.34	0.013959	0.930836
Ifnl3	interferon lambda 3	-1.33	0.028051	0.945337
Tmem182	transmembrane protein 182	-1.33	0.049116	0.955604
Shisa3	shisa family member 3	-1.33	0.039074	0.955604
Ttc24	tetratricopeptide repeat domain 24	-1.33	0.020407	0.934625
Dynap	dynactin associated protein	-1.33	0.032087	0.955027
Pp2d1	protein phosphatase 2C-like domain containing 1	-1.33	0.017865	0.934625
Klhl40	kelch-like 40	-1.33	0.023689	0.934625
H2-Q1	histocompatibility 2, Q region locus 1	-1.33	0.015651	0.934625
Snta1	syntrophin, acidic 1	-1.33	0.010579	0.872249
Ceacam11	carcinoembryonic antigen-related cell adhesion molecule 11	-1.33	0.047721	0.955604
Zbtb7c	zinc finger and BTB domain containing 7C	-1.33	0.045802	0.955604
Slc38a10	solute carrier family 38, member 10	-1.32	0.007439	0.828491
Gpr179	G protein-coupled receptor 179	-1.32	0.012394	0.902392
Mns1	meiosis-specific nuclear structural protein 1	-1.32	0.029676	0.955027
Olfr832	olfactory receptor 832	-1.32	0.001153	0.661654
Draxin	dorsal inhibitory axon guidance protein	-1.32	0.026374	0.944116
Zbtb7b	zinc finger and BTB domain containing 7B	-1.32	0.009341	0.858114
Ssmem1	serine-rich single-pass membrane protein 1	-1.32	0.010735	0.872249
Sfrp5	secreted frizzled-related sequence protein 5	-1.32	0.045386	0.955604
Prps1l1	phosphoribosyl pyrophosphate synthetase 1-like 1	-1.32	0.032269	0.955027
AF067061	cDNA sequence AF067061	-1.32	0.02398	0.934625
Pgpep1l	pyroglutamyl-peptidase I-like	-1.32	0.003314	0.709391
Hoxa2	homeobox A2	-1.32	0.019874	0.934625
Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	-1.32	0.045989	0.955604
Klhl15	kelch-like 15; microRNA 7673	-1.31	0.036483	0.955604
Reep4	receptor accessory protein 4	-1.31	0.024024	0.934625
Prap1	proline-rich acidic protein 1	-1.31	0.018151	0.934625

H2-L	histocompatibility 2, D region locus L; histocompatibility 2, D region locus 1	-1.31	0.005876	0.801647
Olfr811	olfactory receptor 811	-1.31	0.035491	0.955604
Vac14	Vac14 homolog (S. cerevisiae)	-1.31	0.03393	0.955604
Adck4	aarF domain containing kinase 4	-1.31	0.02655	0.944116
Ins1	insulin I	-1.31	0.018948	0.934625
Chic1	cysteine-rich hydrophobic domain 1	-1.31	0.000321	0.503007
Asgr1	asialoglycoprotein receptor 1	-1.31	0.00219	0.661654
Mtss1	metastasis suppressor 1	-1.31	0.019795	0.934625
Elfn2	leucine rich repeat and fibronectin type III, extracellular 2	-1.31	0.040763	0.955604
Faim2	Fas apoptotic inhibitory molecule 2	-1.31	0.04301	0.955604
Srf	serum response factor	-1.3	0.014575	0.934625
Klhl36	kelch-like 36	-1.3	0.024538	0.934625
Lrrk1	leucine-rich repeat kinase 1	-1.3	0.023782	0.934625
Padi4	peptidyl arginine deiminase, type IV	-1.3	0.018253	0.934625
Slamf1	signaling lymphocytic activation molecule family member 1	-1.3	0.040678	0.955604
Fsip2	fibrous sheath-interacting protein 2	-1.3	0.009092	0.858114
Zfp629	zinc finger protein 629	-1.3	0.048843	0.955604
Camkmt	calmodulin-lysine N-methyltransferase	-1.3	0.036247	0.955604
Tas2r120	taste receptor, type 2, member 120	-1.3	0.048503	0.955604
Ddc	dopa decarboxylase	-1.3	0.029429	0.955027
Mob3c	MOB kinase activator 3C	-1.3	0.032615	0.955027
Kcnip1	Kv channel-interacting protein 1	-1.3	0.031587	0.955027
Ptpn13	protein tyrosine phosphatase, non-receptor type 13	-1.29	0.022426	0.934625
Gtf3c1	general transcription factor III C 1	-1.29	0.023344	0.934625
Bmper	BMP-binding endothelial regulator	-1.29	0.03586	0.955604
Tmem30b	transmembrane protein 30B	-1.29	0.000426	0.525984
Ccdc105	coiled-coil domain containing 105	-1.29	0.024165	0.934625
Lalba	lactalbumin, alpha	-1.29	0.044712	0.955604
Fchsd2	FCH and double SH3 domains 2	-1.29	0.033451	0.955604
Chrna10	cholinergic receptor, nicotinic, alpha polypeptide 10	-1.29	0.021011	0.934625
Glra4	glycine receptor, alpha 4 subunit	-1.29	0.023115	0.934625
Dusp4	dual specificity phosphatase 4	-1.29	0.01506	0.934625
Usp10	ubiquitin specific peptidase 10	-1.29	0.033206	0.955027
Marcks	myristoylated alanine rich protein kinase C substrate	-1.29	0.022033	0.934625
Vwa3a	von Willebrand factor A domain containing 3A	-1.29	0.020979	0.934625
Dzip1l	DAZ interacting protein 1-like	-1.28	0.026802	0.944116
Olfr934	olfactory receptor 934	-1.28	0.006389	0.801647
Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	-1.28	0.021994	0.934625

Tdrd12	tudor domain containing 12	-1.28	0.010722	0.872249
Prc1	protein regulator of cytokinesis 1	-1.28	0.033907	0.955604
Olfr1380	olfactory receptor 1380	-1.28	0.035809	0.955604
Psg27	pregnancy-specific glycoprotein 27	-1.28	0.001982	0.661654
A1cf	APOBEC1 complementation factor	-1.28	0.030234	0.955027
Emc6	ER membrane protein complex subunit 6	-1.28	0.042852	0.955604
Spdya	speedy/RINGO cell cycle regulator family, member A; methyltransferase like 4, pseudogene 1	-1.28	0.028395	0.945337
Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-1.27	0.032981	0.955027
Fam90a1a	family with sequence similarity 90, member A1A	-1.27	0.013645	0.925423
Tbx19	T-box 19	-1.27	0.012807	0.905716
Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	-1.27	0.002535	0.690171
Hrct1	histidine rich carboxyl terminus 1	-1.27	0.002807	0.693971
Olfr1279	olfactory receptor 1279	-1.27	0.046318	0.955604
Lrrc56	leucine rich repeat containing 56	-1.27	0.041379	0.955604
Gon4l	gon-4-like (C.elegans)	-1.27	0.036185	0.955604
Plch1	phospholipase C, eta 1	-1.27	0.04408	0.955604
Myo3b	myosin IIIB	-1.26	0.008245	0.851525
Ptger1	prostaglandin E receptor 1 (subtype EP1)	-1.26	0.002416	0.690171
Adcy4	adenylate cyclase 4	-1.26	0.001813	0.661654
Trp53bp2	transformation related protein 53 binding protein 2	-1.26	0.040658	0.955604
Ghrhr	growth hormone releasing hormone receptor	-1.26	0.036211	0.955604
Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.26	0.032139	0.955027
Snip1	Smad nuclear interacting protein 1	-1.26	0.030109	0.955027
Krt35	keratin 35	-1.26	0.009788	0.865989
Fam179a	family with sequence similarity 179, member A	-1.26	0.041814	0.955604
Rp1l1	retinitis pigmentosa 1 homolog (human)-like 1	-1.26	0.020378	0.934625
Slc38a6	solute carrier family 38, member 6	-1.26	0.012308	0.902392
Rsph6a	radial spoke head 6 homolog A (Chlamydomonas)	-1.26	0.027414	0.944116
Ssu2	ssu-2 homolog (C. elegans)	-1.26	0.029301	0.955027
Rpl13a	ribosomal protein L13A; small nucleolar RNA, C/D box 32A; small nucleolar RNA, C/D box 33; small nucleolar RNA, C/D box 34; microRNA 5121	-1.25	0.023794	0.934625
Hist1h4j	histone cluster 1, H4j; histone cluster 1, H4m	-1.25	0.031452	0.955027

Ceacam19	carcinoembryonic antigen-related cell adhesion molecule 19	-1.25	0.007265	0.828491
C2cd4d	C2 calcium-dependent domain containing 4D	-1.25	0.021673	0.934625
Smtnl1	smoothelin-like 1	-1.25	0.026016	0.944116
Rbfa	ribosome binding factor A	-1.25	0.041975	0.955604
Olfr862	olfactory receptor 862	-1.25	0.042324	0.955604
Ankrd53	ankyrin repeat domain 53	-1.25	0.02816	0.945337
Surf6	surfeit gene 6	-1.25	0.039681	0.955604
Ipmk	inositol polyphosphate multikinase	-1.25	0.042258	0.955604
Gdf15	growth differentiation factor 15	-1.25	0.006269	0.801647
Ptx3	pentraxin related gene	-1.25	0.00646	0.801647
Fmn2	formin 2	-1.25	0.012638	0.905716
Grifin	galectin-related inter-fiber protein	-1.25	0.039695	0.955604
Dgkd	diacylglycerol kinase, delta	-1.25	0.047068	0.955604
Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-1.25	0.006725	0.807179
Plekhg4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	-1.24	0.023992	0.934625
Emp2	epithelial membrane protein 2	-1.24	0.015864	0.934625
Gnpda2	glucosamine-6-phosphate deaminase 2	-1.24	0.038601	0.955604
Gpr27	G protein-coupled receptor 27	-1.24	0.009079	0.858114
Sp8	trans-acting transcription factor 8	-1.24	0.006264	0.801647
Olfr187	olfactory receptor 187	-1.24	0.029812	0.955027
Arid3c	AT rich interactive domain 3C (BRIGHT-like)	-1.24	0.048106	0.955604
Tas2r116	taste receptor, type 2, member 116	-1.24	0.044502	0.955604
Rad54l	RAD54 like (S. cerevisiae)	-1.24	0.049218	0.955604
Nkx1-2	NK1 transcription factor related, locus 2 (Drosophila)	-1.24	0.010714	0.872249
Atp13a3	ATPase type 13A3	-1.24	0.043967	0.955604
Olfr629	olfactory receptor 629	-1.24	0.032502	0.955027
Hephl1	hephaestin-like 1	-1.24	0.040275	0.955604
Gspt2	G1 to S phase transition 2	-1.24	0.001319	0.661654
Hspa1a	heat shock protein 1A	-1.24	0.037793	0.955604
Nfx1	nuclear transcription factor, X-box binding 1	-1.23	0.047814	0.955604
Bola1	bolA-like 1 (E. coli)	-1.23	0.047973	0.955604
Ccdc70	coiled-coil domain containing 70	-1.23	0.011098	0.872249
Utf1	undifferentiated embryonic cell transcription factor 1	-1.23	0.00421	0.770544
Tbc1d9b	TBC1 domain family, member 9B	-1.23	0.045131	0.955604
Olfr513	olfactory receptor 513	-1.23	0.01471	0.934625
Actc1	actin, alpha, cardiac muscle 1	-1.23	0.049993	0.955604
Pramef12	PRAME family member 12	-1.23	0.003682	0.724181
Prdm2	PR domain containing 2, with ZNF domain	-1.23	0.029957	0.955027

Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	-1.23	0.012043	0.89438
Zfp655	zinc finger protein 655	-1.23	0.006009	0.801647
Il12b	interleukin 12b	-1.23	0.032637	0.955027
Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	-1.23	0.030714	0.955027
B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	-1.23	0.033797	0.955604
Ampd3	adenosine monophosphate deaminase 3	-1.22	0.012331	0.902392
Hoxb2	homeobox B2	-1.22	0.045505	0.955604
Fbxw24	F-box and WD-40 domain protein 24	-1.22	0.017832	0.934625
Zbtb24	zinc finger and BTB domain containing 24	-1.22	0.012914	0.910345
Erlin2	ER lipid raft associated 2	-1.22	0.004511	0.789838
Wnt5b	wingless-type MMTV integration site family, member 5B	-1.22	0.000317	0.503007
Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	-1.22	0.018493	0.934625
Fhl1	four and a half LIM domains 1	-1.22	0.041823	0.955604
Adap2	ArfGAP with dual PH domains 2	-1.21	0.046775	0.955604
Nr1h3	nuclear receptor subfamily 1, group H, member 3	-1.21	0.041134	0.955604
Wfdc16	WAP four-disulfide core domain 16	-1.21	0.018281	0.934625
Il31	interleukin 31	-1.21	0.026733	0.944116
Zmym1	zinc finger, MYM domain containing 1	-1.21	0.049047	0.955604
Crxos	cone-rod homeobox, opposite strand	-1.21	0.037794	0.955604
Rdh8	retinol dehydrogenase 8	-1.21	0.030343	0.955027
Tph1	tryptophan hydroxylase 1	-1.21	0.04754	0.955604
Ogfr	opioid growth factor receptor	-1.2	0.00594	0.801647
Lpin1	lipin 1	-1.2	0.018951	0.934625
Cckar	cholecystokinin A receptor; U7 small nuclear RNA	-1.2	0.031366	0.955027
Tex19.2	testis expressed gene 19.2	-1.2	0.049994	0.955604
Zmynd12	zinc finger, MYND domain containing 12	-1.2	0.049594	0.955604
Sprr2i	small proline-rich protein 2I	-1.2	0.021898	0.934625
Rfc5	replication factor C (activator 1) 5	-1.2	0.041423	0.955604
Slfn4	schlafen 4	-1.2	0.034692	0.955604
Ncs1	neuronal calcium sensor 1	-1.2	0.031834	0.955027
Ccdc74a	coiled-coil domain containing 74A	-1.2	0.012385	0.902392
Fbxl21	F-box and leucine-rich repeat protein 21	-1.19	0.037883	0.955604
Prss32	protease, serine 32	-1.19	0.038607	0.955604
Ces1a	carboxylesterase 1A	-1.19	0.015447	0.934625
Il21r	interleukin 21 receptor	-1.18	0.031217	0.955027
Icam1	intercellular adhesion molecule 1	-1.18	0.018789	0.934625
AA467197	expressed sequence AA467197; microRNA 147	-1.18	0.044846	0.955604
Tuba1b	tubulin, alpha 1B	-1.18	0.01263	0.905716
Plxna3	plexin A3	-1.18	0.041384	0.955604

Dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila)	-1.17	0.037788	0.955604
Wdfy1	WD repeat and FYVE domain containing 1	-1.17	0.026546	0.944116
Anks3	ankyrin repeat and sterile alpha motif domain containing 3	-1.17	0.049633	0.955604
Clec2d	C-type lectin domain family 2, member d	-1.17	0.042588	0.955604
Cd27	CD27 antigen; microRNA 8113	-1.17	0.047257	0.955604
Klhl32	kelch-like 32	-1.17	0.016188	0.934625
Map2	microtubule-associated protein 2	-1.17	0.04964	0.955604
Ccdc106	coiled-coil domain containing 106	-1.16	0.039654	0.955604
Ccl3	chemokine (C-C motif) ligand 3	-1.16	0.022157	0.934625
Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	-1.16	0.022671	0.934625
Mfsd12	major facilitator superfamily domain containing 12	-1.16	0.020336	0.934625
Tmx4	thioredoxin-related transmembrane protein 4	-1.16	0.049171	0.955604
Wbp1l	WW domain binding protein 1 like	-1.15	0.011713	0.892484
Lypd5	Ly6/Plaur domain containing 5	-1.15	0.044946	0.955604
Morn4	MORN repeat containing 4	-1.15	0.01889	0.934625
Eva1c	eva-1 homolog C (C. elegans)	-1.13	0.021712	0.934625
Olfr1395	olfactory receptor 1395	-1.13	0.04226	0.955604
Gas2	growth arrest specific 2	-1.13	0.015217	0.934625
Gng3	guanine nucleotide binding protein (G protein), gamma 3	-1.13	0.042069	0.955604
Zcchc18	zinc finger, CCHC domain containing 18	-1.13	0.047329	0.955604
Krba1	KRAB-A domain containing 1	-1.12	0.04702	0.955604
Ddhd1	DDHD domain containing 1; microRNA 5131	-1.12	0.021439	0.934625
Sdhaf2	succinate dehydrogenase complex assembly factor 2	-1.12	0.019339	0.934625
Twist2	twist basic helix-loop-helix transcription factor 2	-1.12	0.011176	0.872249
Dnal1	dynein, axonemal, light chain 1	-1.12	0.028245	0.945337
Usp21	ubiquitin specific peptidase 21	-1.11	0.026302	0.944116
Nup188	nucleoporin 188	-1.1	0.046986	0.955604
Apaf1	apoptotic peptidase activating factor 1	-1.1	0.03739	0.955604
Kcnh6	potassium voltage-gated channel, subfamily H (eag-related), member 6	-1.09	0.029996	0.955027
Pik3cg	phosphoinositide-3-kinase, catalytic, gamma polypeptide	-1.09	0.046838	0.955604
Lhx1	LIM homeobox protein 1	-1.08	0.049268	0.955604

Table S4- Genes upregulated in the Hippocampus of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA HC vs. TT HC)	ANOVA p-value (AA HC vs. TT HC)	FDR p-value (AA HC vs. TT HC)
Pdhb	pyruvate dehydrogenase (lipoamide) beta	1.04	0.037615	0.999105
Vps35	vacuolar protein sorting 35	1.07	0.044345	0.999105
Gdf7	growth differentiation factor 7	1.08	0.03222	0.999105
Barhl1	BarH-like 1 (Drosophila)	1.09	0.024698	0.999105
Cttn	cortactin	1.09	0.021089	0.999105
Nceh1	neutral cholesterol ester hydrolase 1	1.09	0.012544	0.999105
Syt1	synaptotagmin I	1.1	0.000283	0.571716
Rab7	RAB7, member RAS oncogene family	1.1	0.033074	0.999105
Tspyl2	TSPY-like 2	1.11	0.020248	0.999105
Laptm4b	lysosomal-associated protein transmembrane 4B	1.11	0.033407	0.999105
Tmem87b	transmembrane protein 87B	1.11	0.015227	0.999105
Wfdc13	WAP four-disulfide core domain 13	1.11	0.045724	0.999105
Strc	stereocilin	1.11	0.049769	0.999105
Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	1.11	0.032049	0.999105
Parg	poly (ADP-ribose) glycohydrolase	1.11	0.020965	0.999105
Krtap24-1	keratin associated protein 24-1	1.11	0.043126	0.999105
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1.12	0.026119	0.999105
Scn2a1	sodium channel, voltage-gated, type II, alpha 1	1.12	0.045635	0.999105
Fbxo28	F-box protein 28	1.12	0.008265	0.999105
Fmr1	fragile X mental retardation syndrome 1	1.12	0.040861	0.999105
Map3k7	mitogen-activated protein kinase kinase kinase 7	1.12	0.044053	0.999105
Olfr523	olfactory receptor 523	1.12	0.044314	0.999105
Hif1a	hypoxia inducible factor 1, alpha subunit	1.13	0.022851	0.999105
G3bp2	GTPase activating protein (SH3 domain) binding protein 2	1.13	0.004472	0.999105
Dnajc8	DnaJ (Hsp40) homolog, subfamily C, member 8	1.14	0.035605	0.999105

Srpk2	serine/arginine-rich protein specific kinase 2	1.14	0.030658	0.999105
Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	1.14	0.023136	0.999105
Psma2	proteasome (prosome, macropain) subunit, alpha type 2	1.14	0.015632	0.999105
Pms1	postmeiotic segregation increased 1 (S. cerevisiae)	1.15	0.019968	0.999105
Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.15	0.045698	0.999105
Pfn2	profilin 2	1.15	0.040328	0.999105
Tuba1b	tubulin, alpha 1B	1.15	0.036746	0.999105
Aph1b	anterior pharynx defective 1b homolog (C. elegans)	1.15	0.023755	0.999105
Poglut1	protein O-glucosyltransferase 1	1.15	0.047525	0.999105
Rlim	ring finger protein, LIM domain interacting	1.15	0.038568	0.999105
Sppl2a	signal peptide peptidase like 2A	1.15	0.000825	0.796996
Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1.15	0.039247	0.999105
Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	1.15	0.040396	0.999105
Irgq	immunity-related GTPase family, Q	1.15	0.025768	0.999105
Serinc1	serine incorporator 1	1.15	0.045196	0.999105
Tmem184c	transmembrane protein 184C	1.15	0.026133	0.999105
Prh1	proline rich protein HaeIII subfamily 1	1.15	0.028253	0.999105
Zfp689	zinc finger protein 689	1.15	0.0064	0.999105
Eci2	enoyl-Coenzyme A delta isomerase 2	1.15	0.014445	0.999105
Pde2a	phosphodiesterase 2A, cGMP-stimulated	1.16	0.019992	0.999105
Omg	oligodendrocyte myelin glycoprotein	1.16	0.04361	0.999105
Dnajc21	DnaJ (Hsp40) homolog, subfamily C, member 21	1.16	0.040094	0.999105
Abca8b	ATP-binding cassette, sub-family A (ABC1), member 8b	1.16	0.011872	0.999105
Pnma5	paraneoplastic antigen family 5	1.16	0.014923	0.999105
Adk	adenosine kinase	1.16	0.010033	0.999105
Vamp7	vesicle-associated membrane protein 7	1.16	0.01524	0.999105
Ikbkb	inhibitor of kappaB kinase beta	1.16	0.007556	0.999105
Slc27a3	solute carrier family 27 (fatty acid transporter), member 3	1.16	0.032021	0.999105

Rac1	RAS-related C3 botulinum substrate 1	1.16	0.017209	0.999105
C1rb	complement component 1, r subcomponent B	1.16	0.048435	0.999105
Olfr203	olfactory receptor 203	1.16	0.046066	0.999105
E2f4	E2F transcription factor 4	1.17	0.043409	0.999105
Cbfb	core binding factor beta	1.17	0.01523	0.999105
Armc2	armadillo repeat containing 2	1.17	0.049178	0.999105
Pank1	pantothenate kinase 1	1.17	0.034753	0.999105
Zfp788	zinc finger protein 788	1.17	0.035793	0.999105
Klhl9	kelch-like 9	1.17	0.008399	0.999105
Cphx3	cytoplasmic polyadenylated homeobox 3	1.17	0.032908	0.999105
Zfp39	zinc finger protein 39	1.17	0.047342	0.999105
Pan2	PAN2 polyA specific ribonuclease subunit homolog (S. cerevisiae)	1.18	0.03069	0.999105
Btrc	beta-transducin repeat containing protein	1.18	0.026902	0.999105
Fam69a	family with sequence similarity 69, member A	1.18	0.016035	0.999105
Casr	calcium-sensing receptor	1.18	0.047062	0.999105
Reep5	receptor accessory protein 5	1.18	0.043368	0.999105
Epha1	Eph receptor A1	1.18	0.029501	0.999105
Prss37	protease, serine 37	1.18	0.048855	0.999105
Cenpw	centromere protein W	1.18	0.043167	0.999105
Fam49a	family with sequence similarity 49, member A	1.19	0.044363	0.999105
Hs3st3a1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	1.19	0.025486	0.999105
Cnep1r1	CTD nuclear envelope phosphatase 1 regulatory subunit 1	1.19	0.023041	0.999105
Tfg	Trk-fused gene	1.19	0.040591	0.999105
Tdg	thymine DNA glycosylase; thymine DNA glycosylase pseudogene	1.19	0.017885	0.999105
Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.19	0.047786	0.999105
Smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	1.19	0.008058	0.999105
Dync1i2	dynein cytoplasmic 1 intermediate chain 2	1.19	0.03881	0.999105
Scaf4	SR-related CTD-associated factor 4	1.19	0.034819	0.999105
Poc1a	POC1 centriolar protein homolog A (Chlamydomonas)	1.19	0.030738	0.999105
Tcerg1	transcription elongation regulator 1 (CA150)	1.19	0.00619	0.999105

Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1; cDNA sequence BC020402	1.19	0.039959	0.999105
Usp34	ubiquitin specific peptidase 34	1.19	0.004418	0.999105
Rabggtb	Rab geranylgeranyl transferase, b subunit; small nucleolar RNA, C/D box 45C	1.19	0.005023	0.999105
Epb41l5	erythrocyte membrane protein band 4.1 like 5	1.19	0.036635	0.999105
Olfr1229	olfactory receptor 1229	1.19	0.032186	0.999105
Zdhhc4	zinc finger, DHHC domain containing 4	1.19	0.034072	0.999105
Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)	1.19	0.002062	0.999105
Abca6	ATP-binding cassette, sub-family A (ABC1), member 6	1.19	0.030396	0.999105
Zfp493	zinc finger protein 493	1.19	0.039368	0.999105
Nkx3-1	NK-3 transcription factor, locus 1 (Drosophila)	1.19	0.032682	0.999105
Mtrf1	mitochondrial translational release factor 1	1.19	0.035017	0.999105
Sod2	superoxide dismutase 2, mitochondrial	1.19	0.014142	0.999105
Slc3a1	solute carrier family 3, member 1	1.19	0.009733	0.999105
Pcdhb1	protocadherin beta 1	1.19	0.022451	0.999105
Dcaf6	DDB1 and CUL4 associated factor 6	1.2	0.008019	0.999105
Swt1	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	1.2	0.029127	0.999105
Kif3b	kinesin family member 3B	1.2	0.02945	0.999105
Ccdc159	coiled-coil domain containing 159	1.2	0.037019	0.999105
Agps	alkylglycerone phosphate synthase	1.2	0.030459	0.999105
Serbp1	serpine1 mRNA binding protein 1	1.2	0.008183	0.999105
Myh7b	myosin, heavy chain 7B, cardiac muscle, beta	1.2	0.015997	0.999105
Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	1.2	0.021282	0.999105
Sertad3	SERTA domain containing 3	1.2	0.023319	0.999105
Ces2f	carboxylesterase 2F	1.2	0.010804	0.999105
Aph1c	anterior pharynx defective 1c homolog (C. elegans)	1.2	0.041192	0.999105
Gltpd2	glycolipid transfer protein domain containing 2	1.2	0.017979	0.999105
Ckmt2	creatine kinase, mitochondrial 2	1.2	0.014874	0.999105
Ap3m1	adaptor-related protein complex 3, mu 1 subunit	1.2	0.01096	0.999105

Gpalpp1	GPALPP motifs containing 1	1.2	0.010915	0.999105
St8sia5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	1.21	0.016624	0.999105
Gpc5	glypican 5	1.21	0.028807	0.999105
Herc3	hect domain and RLD 3	1.21	0.000133	0.422205
Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae)	1.21	0.021703	0.999105
Lztfl1	leucine zipper transcription factor-like 1	1.21	0.007973	0.999105
Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	1.21	0.029175	0.999105
Dcun1d1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	1.21	0.04869	0.999105
Abca12	ATP-binding cassette, sub-family A (ABC1), member 12	1.21	0.03636	0.999105
Patl2	protein associated with topoisomerase II homolog 2 (yeast)	1.21	0.019095	0.999105
Mapk1ip1l	mitogen-activated protein kinase 1 interacting protein 1-like	1.21	0.026275	0.999105
Tmed7	transmembrane emp24 protein transport domain containing 7	1.21	0.040011	0.999105
Plk2	polo-like kinase 2	1.22	0.040112	0.999105
Snx10	sorting nexin 10	1.22	0.028955	0.999105
Utrn	utrophin	1.22	0.020689	0.999105
Pls3	plastin 3 (T-isoform)	1.22	0.007769	0.999105
Ntn1	netrin 1	1.22	0.043562	0.999105
Ldha	lactate dehydrogenase A	1.22	0.03562	0.999105
Fam45a	family with sequence similarity 45, member A	1.22	0.048227	0.999105
Prkcb	protein kinase C, beta	1.22	0.002553	0.999105
Chchd4	coiled-coil-helix-coiled-coil-helix domain containing 4	1.22	0.037194	0.999105
Map2k5	mitogen-activated protein kinase kinase 5	1.22	0.013077	0.999105
Bcas3	breast carcinoma amplified sequence 3	1.22	0.043455	0.999105
Styx	serine/threonine/tyrosine interaction protein	1.22	0.008279	0.999105
Ugcg	UDP-glucose ceramide glucosyltransferase	1.22	0.040251	0.999105
Dld	dihydrolipoamide dehydrogenase	1.22	0.024427	0.999105
Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	1.22	0.022561	0.999105
Itm2a	integral membrane protein 2A	1.22	0.036931	0.999105
Trim45	tripartite motif-containing 45	1.22	0.044644	0.999105

Utp15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	1.22	0.045344	0.999105
Mdga2	MAM domain containing glycosylphosphatidylinositol anchor 2	1.23	0.03743	0.999105
Gnaz	guanine nucleotide binding protein, alpha z subunit	1.23	0.034091	0.999105
Dopey1	dopey family member 1	1.23	0.004989	0.999105
Gpr137c	G protein-coupled receptor 137C	1.23	0.034584	0.999105
Lclat1	lysocardiolipin acyltransferase 1	1.23	0.02578	0.999105
Rb1	retinoblastoma 1	1.23	0.014379	0.999105
Sox12	SRY (sex determining region Y)-box 12	1.23	0.042271	0.999105
Zc3h14	zinc finger CCCH type containing 14	1.23	0.041005	0.999105
Cstf2t	cleavage stimulation factor, 3 pre-RNA subunit 2, tau; cleavage stimulation factor, 3' pre-RNA subunit 2, tau	1.23	0.044348	0.999105
Rbbp6	retinoblastoma binding protein 6	1.23	0.037325	0.999105
Zbtb5	zinc finger and BTB domain containing 5	1.23	0.044097	0.999105
Wdr34	WD repeat domain 34	1.23	0.035251	0.999105
Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	1.23	0.015689	0.999105
Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	1.23	0.03347	0.999105
Hacd4	3-hydroxyacyl-CoA dehydratase 4	1.23	0.000058	0.321491
Hdlbp	high density lipoprotein (HDL) binding protein	1.23	0.005122	0.999105
Col9a1	collagen, type IX, alpha 1	1.23	0.014068	0.999105
Drd4	dopamine receptor D4	1.23	0.022227	0.999105
Tsku	tsukushi, small leucine rich proteoglycan	1.23	0.003365	0.999105
Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	1.23	0.048344	0.999105
Ccr7	chemokine (C-C motif) receptor 7	1.23	0.023775	0.999105
Csrnp3	cysteine-serine-rich nuclear protein 3	1.24	0.026231	0.999105
Galntl6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 6	1.24	0.026109	0.999105
Mkl2	MKL/myocardin-like 2	1.24	0.018085	0.999105

Smc1a	structural maintenance of chromosomes 1A	1.24	0.044315	0.999105
Nhlrc3	NHL repeat containing 3	1.24	0.041186	0.999105
Opa1	optic atrophy 1	1.24	0.002485	0.999105
Ficd	FIC domain containing	1.24	0.006235	0.999105
Dnaic2	dynein, axonemal, intermediate chain 2	1.24	0.025034	0.999105
Ubl4b	ubiquitin-like 4B	1.24	0.034813	0.999105
Cyp4a30b	cytochrome P450, family 4, subfamily a, polypeptide 30b	1.24	0.01062	0.999105
Msx1	msh homeobox 1	1.24	0.014666	0.999105
Pycard	PYD and CARD domain containing	1.24	0.012786	0.999105
Fam90a1a	family with sequence similarity 90, member A1A	1.24	0.04271	0.999105
Trpv1	transient receptor potential cation channel, subfamily V, member 1	1.24	0.025946	0.999105
Zfp944	zinc finger protein 944	1.24	0.007369	0.999105
Cdh13	cadherin 13	1.25	0.032714	0.999105
Drp2	dystrophin related protein 2	1.25	0.046182	0.999105
Ube2o	ubiquitin-conjugating enzyme E2O	1.25	0.009507	0.999105
Kpna2	karyopherin (importin) alpha 2	1.25	0.020738	0.999105
Atmin	ATM interactor	1.25	0.020919	0.999105
Ctage5	CTAGE family, member 5	1.25	0.021327	0.999105
Zbtb38	zinc finger and BTB domain containing 38; RIKEN cDNA E030011O05 gene	1.25	0.011537	0.999105
Pter	phosphotriesterase related	1.25	0.017034	0.999105
Setmar	SET domain without mariner transposase fusion	1.25	0.021731	0.999105
Mob4	MOB family member 4, phocein	1.25	0.019216	0.999105
H2-Q7	histocompatibility 2, Q region locus 7; histocompatibility 2, Q region locus 9	1.25	0.020731	0.999105
Adgrf5	adhesion G protein-coupled receptor F5	1.25	0.004811	0.999105
Lax1	lymphocyte transmembrane adaptor 1	1.25	0.042735	0.999105
Gatc	glutamyl-tRNA(Gln) amidotransferase, subunit C	1.25	0.009482	0.999105
Gspt1	G1 to S phase transition 1	1.25	0.004446	0.999105
Slc26a2	solute carrier family 26 (sulfate transporter), member 2	1.26	0.017591	0.999105
Adm	adrenomedullin	1.26	0.024222	0.999105
Acvr2b	activin receptor IIB	1.26	0.040519	0.999105

Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	1.26	0.014018	0.999105
Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoimidazole, succinocarboxamide synthetase	1.26	0.031793	0.999105
Ppat	phosphoribosyl pyrophosphate amidotransferase	1.26	0.018521	0.999105
Zfp287	zinc finger protein 287	1.26	0.010728	0.999105
Slc22a6	solute carrier family 22 (organic anion transporter), member 6	1.26	0.005735	0.999105
Prim2	DNA primase, p58 subunit	1.26	0.02415	0.999105
Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	1.26	0.019487	0.999105
Cldn7	claudin 7	1.26	0.021294	0.999105
Srsf7	serine/arginine-rich splicing factor 7	1.26	0.028495	0.999105
Socs3	suppressor of cytokine signaling 3	1.26	0.04484	0.999105
Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19	1.26	0.031972	0.999105
Entpd3	ectonucleoside triphosphate diphosphohydrolase 3	1.27	0.014958	0.999105
Kcnk3	potassium channel, subfamily K, member 3	1.27	0.042286	0.999105
Pdcd4	programmed cell death 4	1.27	0.042435	0.999105
Eya4	eyes absent 4 homolog (Drosophila)	1.27	0.04923	0.999105
Ndfip2	Nedd4 family interacting protein 2	1.27	0.031596	0.999105
Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	1.27	0.049221	0.999105
Chmp2b	charged multivesicular body protein 2B	1.27	0.040447	0.999105
Wdr48	WD repeat domain 48	1.27	0.000955	0.822518
Spopl	speckle-type POZ protein-like	1.27	0.006267	0.999105
Olfr1143	olfactory receptor 1143	1.27	0.011333	0.999105
Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	1.27	0.030443	0.999105
Nkapl	NFKB activating protein-like	1.27	0.003312	0.999105
Olfr748	olfactory receptor 748	1.27	0.036471	0.999105
Sgtb	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	1.28	0.01638	0.999105

Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	1.28	0.020832	0.999105
Ccdc127	coiled-coil domain containing 127	1.28	0.028235	0.999105
Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	1.28	0.030401	0.999105
Kirrel2	kin of IRRE like 2 (Drosophila)	1.28	0.012014	0.999105
Cpq	carboxypeptidase Q	1.28	0.000987	0.822518
Krt26	keratin 26	1.28	0.036894	0.999105
Guca2a	guanylate cyclase activator 2a (guanylin)	1.28	0.035773	0.999105
Zfp534	zinc finger protein 534	1.28	0.022931	0.999105
Cmtm2b	CKLF-like MARVEL transmembrane domain containing 2B	1.28	0.039135	0.999105
Nags	N-acetylglutamate synthase	1.28	0.032782	0.999105
Naa30	N(alpha)-acetyltransferase 30, NatC catalytic subunit	1.28	0.004622	0.999105
P2rx6	purinergic receptor P2X, ligand-gated ion channel, 6	1.28	0.040551	0.999105
Ifit1bl1	interferon induced protein with tetratricpeptide repeats 1B like 1	1.29	0.045914	0.999105
Rcor3	REST corepressor 3	1.29	0.040138	0.999105
Extl2	exostoses (multiple)-like 2	1.29	0.047946	0.999105
Zfp729a	zinc finger protein 729a	1.29	0.039887	0.999105
Wasf3	WAS protein family, member 3	1.29	0.008831	0.999105
Lpar4	lysophosphatidic acid receptor 4	1.29	0.032373	0.999105
Cmc1	COX assembly mitochondrial protein 1	1.29	0.032166	0.999105
Fes	feline sarcoma oncogene	1.29	0.018637	0.999105
Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	1.29	0.049996	0.999105
Adgrl4	adhesion G protein-coupled receptor L4	1.29	0.032925	0.999105
Klhdc7a	kelch domain containing 7A; microRNA 2139	1.29	0.012151	0.999105
Skap1	src family associated phosphoprotein 1	1.29	0.046933	0.999105
Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	1.29	0.031125	0.999105
Zkscan17	zinc finger with KRAB and SCAN domains 17	1.3	0.01367	0.999105
Arid2	AT rich interactive domain 2 (ARID, RFX-like)	1.3	0.028306	0.999105

Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	1.3	0.000258	0.571716
Tmem121	transmembrane protein 121	1.3	0.03065	0.999105
Selp	selectin, platelet	1.3	0.040678	0.999105
LOC100040786	similar to Ssty2 protein (LOC100040786), mRNA.; Y-linked testis-specific protein 1-like; spermiogenesis specific transcript on the Y 2, mRNA (cDNA clone MGC:107175 IMAGE:6774426), complete cds.; predicted gene, 21340	1.3	0.007232	0.999105
Arl5c	ADP-ribosylation factor-like 5C	1.3	0.045803	0.999105
Prss33	protease, serine 33	1.3	0.039016	0.999105
Spink6	serine peptidase inhibitor, Kazal type 6	1.3	0.025834	0.999105
Homer1	homer homolog 1 (Drosophila)	1.31	0.028388	0.999105
Wbp11	WW domain binding protein 11	1.31	0.008445	0.999105
Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	1.31	0.04175	0.999105
Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.31	0.024898	0.999105
Cntln	centlein, centrosomal protein	1.31	0.044639	0.999105
Tgm6	transglutaminase 6	1.31	0.029031	0.999105
Lmx1b	LIM homeobox transcription factor 1 beta	1.31	0.005101	0.999105
Olfr23	olfactory receptor 23	1.31	0.032181	0.999105
Olfr743	olfactory receptor 743	1.31	0.031214	0.999105
Gjd4	gap junction protein, delta 4	1.31	0.00231	0.999105
Adgrl3	adhesion G protein-coupled receptor L3	1.32	0.033023	0.999105
Mapk9	mitogen-activated protein kinase 9	1.32	0.029653	0.999105
Wdr74	WD repeat domain 74	1.32	0.0034	0.999105
Ttc38	tetratricopeptide repeat domain 38	1.32	0.043382	0.999105
Fgd3	FYVE, RhoGEF and PH domain containing 3	1.32	0.026395	0.999105
Btbd18	BTB (POZ) domain containing 18	1.32	0.023236	0.999105
Spint5	serine protease inhibitor, Kunitz type 5	1.32	0.039809	0.999105
Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	1.32	0.015563	0.999105
Vmn1r118	vomeronasal 1 receptor 118	1.32	0.046418	0.999105

Vmn1r118	vomeronasal 1 receptor 118; predicted gene 4498; predicted gene 8453	1.32	0.046418	0.999105
Zfp101	zinc finger protein 101	1.33	0.042539	0.999105
Dcaf12l2	DDB1 and CUL4 associated factor 12-like 2	1.33	0.030998	0.999105
Trim61	tripartite motif-containing 61; tripartite motif-containing 60	1.33	0.02496	0.999105
Ddx4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	1.33	0.043708	0.999105
Lyz1	lysozyme 1	1.33	0.014819	0.999105
Dus4l	dihydrouridine synthase 4-like (S. cerevisiae)	1.33	0.014382	0.999105
Fam114a1	family with sequence similarity 114, member A1	1.33	0.019359	0.999105
Clec4b2	C-type lectin domain family 4, member b2	1.33	0.021918	0.999105
Prss42	protease, serine 42	1.33	0.021464	0.999105
Akr1b7	aldo-keto reductase family 1, member B7	1.34	0.011232	0.999105
Mettl7a1	methyltransferase like 7A1	1.34	0.035429	0.999105
Zc3h15	zinc finger CCCH-type containing 15	1.34	0.033742	0.999105
Fam204a	family with sequence similarity 204, member A	1.34	0.002054	0.999105
Pqbp1	polyglutamine binding protein 1	1.34	0.005806	0.999105
Olfr1294	olfactory receptor 1294	1.34	0.016722	0.999105
Olfr1312	olfactory receptor 1312	1.34	0.049482	0.999105
Cisd2	CDGSH iron sulfur domain 2	1.34	0.013853	0.999105
Prcp	prolylcarboxypeptidase (angiotensinase C)	1.34	0.048496	0.999105
Olfr679	olfactory receptor 679	1.34	0.00649	0.999105
Thoc1	THO complex 1	1.34	0.012972	0.999105
Akap5	A kinase (PRKA) anchor protein 5	1.35	0.031813	0.999105
1-Mar	membrane-associated ring finger (C3HC4) 1	1.35	0.033089	0.999105
Rpp25	ribonuclease P/MRP 25 subunit	1.35	0.047604	0.999105
Yif1b	Yip1 interacting factor homolog B (S. cerevisiae)	1.35	0.017328	0.999105
Tram1l1	translocation associated membrane protein 1-like 1	1.35	0.002426	0.999105
Zscan26	zinc finger and SCAN domain containing 26	1.35	0.013617	0.999105
Fnip1	folliculin interacting protein 1	1.35	0.028482	0.999105
Smtnl1	smoothelin-like 1	1.35	0.040719	0.999105
Dnah8	dynein, axonemal, heavy chain 8	1.35	0.013596	0.999105
Micalcl	MICAL C-terminal like	1.35	0.036014	0.999105

Olfr871	olfactory receptor 871	1.35	0.022714	0.999105
Rfesd	Rieske (Fe-S) domain containing	1.35	0.024517	0.999105
Ccdc65	coiled-coil domain containing 65	1.36	0.023181	0.999105
Xpa	xeroderma pigmentosum, complementation group A	1.36	0.013287	0.999105
Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	1.36	0.004484	0.999105
Rgcc	regulator of cell cycle	1.36	0.030881	0.999105
Olfr1219	olfactory receptor 1219	1.36	0.02204	0.999105
Tram2	translocating chain-associating membrane protein 2	1.36	0.010373	0.999105
Ifne	interferon epsilon	1.36	0.013939	0.999105
Syne3	spectrin repeat containing, nuclear envelope family member 3	1.36	0.004478	0.999105
Slc38a9	solute carrier family 38, member 9	1.36	0.026014	0.999105
Pbdc1	polysaccharide biosynthesis domain containing 1	1.37	0.012688	0.999105
Cln6	ceroid-lipofuscinosis, neuronal 6	1.37	0.02028	0.999105
Uprt	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	1.37	0.002651	0.999105
Naip6	NLR family, apoptosis inhibitory protein 6; NLR family, apoptosis inhibitory protein 7	1.37	0.001604	0.999105
Wfdc5	WAP four-disulfide core domain 5	1.37	0.039606	0.999105
Efcab8	EF-hand calcium binding domain 8	1.37	0.00764	0.999105
Defb36	defensin beta 36	1.37	0.019034	0.999105
Pak1ip1	PAK1 interacting protein 1	1.37	0.014688	0.999105
Olfr1444	olfactory receptor 1444	1.37	0.028097	0.999105
Kctd1	potassium channel tetramerisation domain containing 1	1.38	0.012412	0.999105
Rspo1	R-spondin 1	1.38	0.011332	0.999105
Vps37c	vacuolar protein sorting 37C (yeast)	1.38	0.014238	0.999105
Zfp141	zinc finger protein 141	1.38	0.020527	0.999105
Inca1	inhibitor of CDK, cyclin A1 interacting protein 1	1.38	0.022566	0.999105
Srd5a1	steroid 5 alpha-reductase 1	1.38	0.040416	0.999105
Lrrc14	leucine rich repeat containing 14	1.38	0.049149	0.999105
Zfp383	zinc finger protein 383	1.39	0.026997	0.999105
Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	1.39	0.018475	0.999105
Nsl1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	1.39	0.005381	0.999105
Olfr3	olfactory receptor 3	1.39	0.015746	0.999105
Ubap2l	ubiquitin-associated protein 2-like	1.39	0.031572	0.999105

Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	1.39	0.029877	0.999105
Tmprss2	transmembrane protease, serine 2	1.39	0.036391	0.999105
D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	1.39	0.017262	0.999105
Nt5e	5 nucleotidase, ecto; 5' nucleotidase, ecto	1.4	0.043833	0.999105
Fam210a	family with sequence similarity 210, member A; microRNA 7219	1.4	0.047589	0.999105
Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	1.4	0.037161	0.999105
Mgp	matrix Gla protein	1.4	0.037708	0.999105
Zfp444	zinc finger protein 444	1.4	0.041602	0.999105
Zp2	zona pellucida glycoprotein 2	1.4	0.032353	0.999105
Pdlim2	PDZ and LIM domain 2	1.4	0.042693	0.999105
Tmprss6	transmembrane serine protease 6	1.4	0.033071	0.999105
Olfr1446	olfactory receptor 1446	1.4	0.045591	0.999105
Ivns1abp	influenza virus NS1A binding protein	1.41	0.046689	0.999105
Rspo3	R-spondin 3	1.41	0.037687	0.999105
Zfp963	zinc finger protein 963; zinc finger protein 866	1.41	0.000017	0.190864
Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1.41	0.013261	0.999105
Hat1	histone aminotransferase 1	1.41	0.023722	0.999105
Rrnad1	ribosomal RNA adenine dimethylase domain containing 1	1.41	0.01138	0.999105
Ino80c	INO80 complex subunit C	1.41	0.006278	0.999105
Xkr8	X Kell blood group precursor related family member 8 homolog	1.41	0.034224	0.999105
AI429214	expressed sequence AI429214	1.41	0.047753	0.999105
Rora	RAR-related orphan receptor alpha	1.42	0.02795	0.999105
Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	1.42	0.001089	0.822518
Isg20l2	interferon stimulated exonuclease gene 20-like 2	1.42	0.00453	0.999105
Fam210b	family with sequence similarity 210, member B	1.42	0.037507	0.999105
Ccdc129	coiled-coil domain containing 129	1.42	0.013371	0.999105
Hk3	hexokinase 3	1.42	0.048018	0.999105
Rxfp4	relaxin family peptide receptor 4	1.42	0.026964	0.999105
Cdh5	cadherin 5	1.42	0.000094	0.386862
Trim7	tripartite motif-containing 7	1.42	0.017883	0.999105
Zfp711	zinc finger protein 711	1.43	0.009332	0.999105

Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A	1.43	0.047848	0.999105
Tmem88	transmembrane protein 88	1.43	0.048094	0.999105
Gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	1.44	0.03238	0.999105
Tmem74	transmembrane protein 74	1.44	0.012271	0.999105
7-Mar	membrane-associated ring finger (C3HC4) 7	1.44	0.02982	0.999105
Lce3c	late cornified envelope 3C	1.44	0.007423	0.999105
Nme4	NME/NM23 nucleoside diphosphate kinase 4	1.44	0.022423	0.999105
Oxt	oxytocin	1.44	0.011688	0.999105
AI427809	expressed sequence AI427809	1.44	0.021256	0.999105
Calu	calumenin	1.44	0.029307	0.999105
Syt16	synaptotagmin XVI	1.45	0.009312	0.999105
Plpp6	phospholipid phosphatase 6	1.45	0.034059	0.999105
Fli1	Friend leukemia integration 1	1.45	0.048809	0.999105
Nes	nestin	1.45	0.03579	0.999105
Gpr174	G protein-coupled receptor 174	1.45	0.037911	0.999105
Fam83g	family with sequence similarity 83, member G	1.45	0.045909	0.999105
Vps50	VPS50 EARP/GARPII complex subunit	1.46	0.02784	0.999105
Ttll3	tubulin tyrosine ligase-like family, member 3	1.47	0.000028	0.206814
Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	1.47	0.035702	0.999105
Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.47	0.035523	0.999105
Nup107	nucleoporin 107	1.47	0.046587	0.999105
Scgb1b24	secretoglobin, family 1B, member 24	1.47	0.015911	0.999105
AU019823	expressed sequence AU019823	1.47	0.030991	0.999105
Abca9	ATP-binding cassette, sub-family A (ABC1), member 9	1.47	0.017561	0.999105
Zfp119b	zinc finger protein 119b	1.47	0.005386	0.999105
Sis	sucrase isomaltase (alpha-glucosidase)	1.48	0.011596	0.999105
Slco4a1	solute carrier organic anion transporter family, member 4a1	1.49	0.001969	0.999105
Mylip	myosin regulatory light chain interacting protein	1.49	0.0197	0.999105
Tex30	testis expressed 30	1.49	0.026537	0.999105
Olfr432	olfactory receptor 432	1.49	0.025152	0.999105

Mrgprx1	MAS-related GPR, member X1	1.49	0.039875	0.999105
Liph	lipase, member H	1.5	0.012731	0.999105
Sprr2k	small proline-rich protein 2K	1.5	0.031837	0.999105
Vmn1r126	vomeronasal 1 receptor 126	1.5	0.027015	0.999105
Ssbp2	single-stranded DNA binding protein 2	1.51	0.004727	0.999105
Vmn2r96	vomeronasal 2, receptor 96	1.51	0.035719	0.999105
C87977	expressed sequence C87977	1.51	0.006375	0.999105
Nkd1	naked cuticle 1 homolog (Drosophila)	1.51	0.001308	0.907752
Samt2	spermatogenesis associated multipass transmembrane protein 2; RIKEN cDNA 4930524N10 gene	1.51	0.035744	0.999105
Car7	carbonic anhydrase 7	1.52	0.035774	0.999105
Cdh10	cadherin 10	1.52	0.030229	0.999105
Zfp677	zinc finger protein 677	1.52	0.034887	0.999105
Zmat4	zinc finger, matrin type 4	1.53	0.035802	0.999105
Pcdhb3	protocadherin beta 3	1.53	0.018946	0.999105
Lpar6	lysophosphatidic acid receptor 6	1.53	0.039467	0.999105
Crhbp	corticotropin releasing hormone binding protein	1.54	0.01549	0.999105
Glt8d2	glycosyltransferase 8 domain containing 2	1.54	0.024972	0.999105
Pcdhb7	protocadherin beta 7	1.54	0.003498	0.999105
Impad1	inositol monophosphatase domain containing 1	1.54	0.020294	0.999105
Nox1	NADPH oxidase 1	1.54	0.012199	0.999105
Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	1.55	0.042079	0.999105
Rpap1	RNA polymerase II associated protein 1	1.56	0.020633	0.999105
Pidd1	p53 induced death domain protein 1	1.56	0.007941	0.999105
Cpne8	copine VIII	1.57	0.017209	0.999105
Supt16	suppressor of Ty 16	1.57	0.028373	0.999105
Tex12	testis expressed gene 12	1.57	0.02441	0.999105
Vwa5a	von Willebrand factor A domain containing 5A	1.58	0.027123	0.999105
Uaca	uveal autoantigen with coiled-coil domains and ankyrin repeats	1.58	0.033118	0.999105
Zfp459	zinc finger protein 459	1.58	0.010298	0.999105
Erg	avian erythroblastosis virus E-26 (v-ets) oncogene related	1.58	0.027642	0.999105
Zfp90	zinc finger protein 90	1.59	0.029067	0.999105
Bgn	biglycan	1.59	0.00034	0.629305
Mal2	mal, T cell differentiation protein 2	1.6	0.036319	0.999105

Ceacam10	carcinoembryonic antigen-related cell adhesion molecule 10	1.6	0.001771	0.999105
Olfr1297	olfactory receptor 1297	1.6	0.031664	0.999105
Gsap	gamma-secretase activating protein	1.62	0.041655	0.999105
Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	1.63	0.034576	0.999105
Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	1.63	0.000689	0.742883
Cd34	CD34 antigen	1.64	0.023765	0.999105
Armc6	armadillo repeat containing 6	1.64	0.042372	0.999105
Mfsd3	major facilitator superfamily domain containing 3	1.64	0.013979	0.999105
Vmn1r223	vomeronasal 1 receptor 223	1.64	0.04829	0.999105
Hcrtr2	hypocretin (orexin) receptor 2	1.65	0.005704	0.999105
Cstl1	cystatin-like 1	1.65	0.03324	0.999105
Rpia	ribose 5-phosphate isomerase A	1.66	0.002296	0.999105
Tmem211	transmembrane protein 211	1.66	0.011708	0.999105
Ccdc88c	coiled-coil domain containing 88C	1.67	0.045019	0.999105
Pcdhb2	protocadherin beta 2	1.69	0.002361	0.999105
Lrp2bp	Lrp2 binding protein	1.7	0.045288	0.999105
Lamp5	lysosomal-associated membrane protein family, member 5	1.71	0.037308	0.999105
Msrb3	methionine sulfoxide reductase B3	1.73	0.036282	0.999105
Serpinb1b	serine (or cysteine) peptidase inhibitor, clade B, member 1b	1.74	0.024245	0.999105
Vmn1r101	vomeronasal 1 receptor 101	1.74	0.008089	0.999105
Arl14epl	ADP-ribosylation factor-like 14 effector protein-like	1.74	0.039052	0.999105
Fbn2	fibrillin 2	1.74	0.026562	0.999105
Plau	plasminogen activator, urokinase	1.75	0.017072	0.999105
Pramef6	PRAME family member 6	1.75	0.030639	0.999105
Zkscan4	zinc finger with KRAB and SCAN domains 4	1.79	0.017689	0.999105
Manea	mannosidase, endo-alpha	1.83	0.005605	0.999105
Pth2r	parathyroid hormone 2 receptor	1.84	0.01912	0.999105
Egr2	early growth response 2	1.87	0.047209	0.999105
Odam	odontogenic, ameloblast asssociated	1.88	0.008739	0.999105
Mlip	muscular LMNA-interacting protein	1.97	0.002434	0.999105
Tas2r105	taste receptor, type 2, member 105	1.97	0.047217	0.999105
Gnb4	guanine nucleotide binding protein (G protein), beta 4	1.99	0.005437	0.999105
Khdrbs2	KH domain containing, RNA binding, signal transduction associated 2	2.08	0.032877	0.999105

Chsy3	chondroitin sulfate synthase 3	2.3	0.04444	0.999105
Fmod	fibromodulin	2.44	0.045175	0.999105
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	2.54	0.035903	0.999105

Table S5- Genes downregulated in the Hippocampus of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	**Description**	**Fold Change (linear) (AA HC vs. TT HC)**	**ANOVA p-value (AA HC vs. TT HC)**	**FDR p-value (AA HC vs. TT HC)**
Zic1	zinc finger protein of the cerebellum 1	-7.81	0.027729	0.999105
Calb2	calbindin 2	-3.38	0.002918	0.999105
Mid1	midline 1	-2.72	0.029202	0.999105
Mid1	midline 1	-2.72	0.029202	0.999105
Zic3	zinc finger protein of the cerebellum 3	-2.43	0.015394	0.999105
Mid1	midline 1	-2.41	0.009703	0.999105
Rnf17	ring finger protein 17	-2.34	0.003132	0.999105
H2-Ke6	H2-K region expressed gene 6	-2.18	0.018676	0.999105
Vangl1	vang-like 1 (van gogh, Drosophila)	-2.16	0.01166	0.999105
Vmn2r71	vomeronasal 2, receptor 71	-2.15	0.037342	0.999105
Zic5	zinc finger protein of the cerebellum 5	-2.11	0.015156	0.999105
Mup-ps19	major urinary protein, pseudogene 19; major urinary protein 20	-2.03	0.027245	0.999105
Mroh1	maestro heat-like repeat family member 1; microRNA 6954	-2.01	0.043927	0.999105
Cpne9	copine family member IX	-2	0.031405	0.999105
Slc9c1	solute carrier family 9, subfamily C (Na+-transporting carboxylic acid decarboxylase), member 1	-1.98	0.003128	0.999105
Olfr1204	olfactory receptor 1204	-1.96	0.0418	0.999105
Fabp7	fatty acid binding protein 7, brain	-1.95	0.002318	0.999105
Fam78a	family with sequence similarity 78, member A	-1.9	0.04978	0.999105
Cyp2a12	cytochrome P450, family 2, subfamily a, polypeptide 12	-1.83	0.047101	0.999105
Ehd1	EH-domain containing 1	-1.82	0.037447	0.999105

Olfr1220	olfactory receptor 1220	-1.82	0.011884	0.999105
Prkcd	protein kinase C, delta	-1.8	0.045911	0.999105
Eomes	eomesodermin homolog (Xenopus laevis)	-1.8	0.000953	0.822518
Trmt1	tRNA methyltransferase 1	-1.76	0.002633	0.999105
Stard6	StAR-related lipid transfer (START) domain containing 6	-1.74	0.004528	0.999105
Olfr1496	olfactory receptor 1496	-1.74	0.015523	0.999105
Elmsan1	ELM2 and Myb/SANT-like domain containing 1	-1.73	0.027274	0.999105
Il1rl1	interleukin 1 receptor-like 1	-1.73	0.034868	0.999105
Ube2t	ubiquitin-conjugating enzyme E2T (putative)	-1.71	0.029326	0.999105
Mmel1	membrane metallo-endopeptidase-like 1	-1.7	0.014589	0.999105
Smpd2	sphingomyelin phosphodiesterase 2, neutral	-1.7	0.018614	0.999105
Hist1h3f	histone cluster 1, H3f	-1.7	0.037879	0.999105
Olfr611	olfactory receptor 611	-1.69	0.044445	0.999105
Srp14	signal recognition particle 14	-1.69	0.000651	0.742883
Gdf11	growth differentiation factor 11	-1.68	0.017512	0.999105
Pop5	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)	-1.68	0.018646	0.999105
Ifnb1	interferon beta 1, fibroblast	-1.68	0.03055	0.999105
Olfr1225	olfactory receptor 1225	-1.66	0.001283	0.907752
Tspan1	tetraspanin 1	-1.66	0.029584	0.999105
Dmrtc1b	DMRT-like family C1b	-1.66	0.033086	0.999105
Taf4a	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.65	0.022702	0.999105
Olfr75-ps1	olfactory receptor 75, pseudogene 1	-1.65	0.018504	0.999105
Olfr836	olfactory receptor 836	-1.65	0.035781	0.999105

Nsun2	NOL1/NOP2/Sun domain family member 2	-1.64	0.03373	0.999105
Ppip5k1	diphosphoinositol pentakisphosphate kinase 1	-1.63	0.044381	0.999105
Klrg2	killer cell lectin-like receptor subfamily G, member 2	-1.62	0.009135	0.999105
Nudt16l1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	-1.61	0.007372	0.999105
Tradd	TNFRSF1A-associated via death domain	-1.61	0.035493	0.999105
Gpr149	G protein-coupled receptor 149	-1.6	0.026551	0.999105
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	-1.6	0.026303	0.999105
Zfp936	zinc finger protein 936	-1.59	0.024284	0.999105
Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	-1.59	0.011334	0.999105
Vmn1r157	vomeronasal 1 receptor 157	-1.59	0.044659	0.999105
Olfr1034	olfactory receptor 1034	-1.59	0.008704	0.999105
Adck4	aarF domain containing kinase 4	-1.58	0.038314	0.999105
Serpina1c	serine (or cysteine) peptidase inhibitor, clade A, member 1C	-1.58	0.001003	0.822518
Prl3d3	prolactin family 3, subfamily d, member 3	-1.58	0.006853	0.999105
Ptger2	prostaglandin E receptor 2 (subtype EP2)	-1.57	0.020218	0.999105
Esp31	exocrine gland secreted peptide 31	-1.57	0.022794	0.999105
Sall2	sal-like 2 (Drosophila)	-1.56	0.029249	0.999105
Kank3	KN motif and ankyrin repeat domains 3	-1.55	0.020767	0.999105
Olfr628	olfactory receptor 628	-1.55	0.027603	0.999105
Dbn1	drebrin 1	-1.54	0.018663	0.999105

Baat	bile acid-Coenzyme A: amino acid N-acyltransferase	-1.54	0.005833	0.999105
Olfr1206	olfactory receptor 1206	-1.54	0.02383	0.999105
Tmub1	transmembrane and ubiquitin-like domain containing 1	-1.54	0.042108	0.999105
Olfr930	olfactory receptor 930	-1.54	0.027061	0.999105
Lrrc18	leucine rich repeat containing 18	-1.54	0.021484	0.999105
Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	-1.53	0.029263	0.999105
Mybl2	myeloblastosis oncogene-like 2	-1.53	0.008357	0.999105
Olfr1271	olfactory receptor 1271	-1.53	0.049732	0.999105
Rhox13	reproductive homeobox 13	-1.53	0.037246	0.999105
Olfr1316	olfactory receptor 1316	-1.52	0.029984	0.999105
Spin2d	spindlin family, member 2D	-1.52	0.006816	0.999105
Rpl11	ribosomal protein L11	-1.52	0.034553	0.999105
Osbpl7	oxysterol binding protein-like 7	-1.51	0.031434	0.999105
Tmem14c	transmembrane protein 14C	-1.51	0.000694	0.742883
C4bp	complement component 4 binding protein	-1.51	0.048732	0.999105
Rasl2-9	RAS-like, family 2, locus 9	-1.51	0.047846	0.999105
Elp6	elongator acetyltransferase complex subunit 6	-1.51	0.017272	0.999105
Adarb1	adenosine deaminase, RNA-specific, B1	-1.5	0.00877	0.999105
Rab3ip	RAB3A interacting protein	-1.5	0.03695	0.999105
Rangrf	RAN guanine nucleotide release factor	-1.5	0.032943	0.999105
Commd9	COMM domain containing 9	-1.5	0.007656	0.999105
Popdc2	popeye domain containing 2	-1.5	0.007976	0.999105

Sema3g	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	-1.49	0.00471	0.999105
Il23r	interleukin 23 receptor	-1.49	0.021998	0.999105
Olfr478	olfactory receptor 478	-1.49	0.020413	0.999105
Clmn	calmin	-1.48	0.015641	0.999105
Gpnmb	glycoprotein (transmembrane) nmb	-1.48	0.003577	0.999105
Ak2	adenylate kinase 2	-1.48	0.000008	0.180798
Olfr1094	olfactory receptor 1094	-1.48	0.021136	0.999105
Dpm3	dolichyl-phosphate mannosyltransferase polypeptide 3	-1.48	0.020912	0.999105
Olfr266	olfactory receptor 266	-1.48	0.041102	0.999105
Cib4	calcium and integrin binding family member 4	-1.48	0.044819	0.999105
Zfp865	zinc finger protein 865	-1.48	0.046921	0.999105
Padi2	peptidyl arginine deiminase, type II	-1.47	0.010193	0.999105
Plcd4	phospholipase C, delta 4	-1.47	0.01515	0.999105
Tbx6	T-box 6	-1.47	0.014637	0.999105
Olfr1049	olfactory receptor 1049	-1.47	0.038941	0.999105
Spint3	serine peptidase inhibitor, Kunitz type, 3	-1.47	0.00326	0.999105
Olfr18	olfactory receptor 18	-1.47	0.046789	0.999105
Sytl3	synaptotagmin-like 3	-1.47	0.014868	0.999105
S100b	S100 protein, beta polypeptide, neural	-1.46	0.037669	0.999105
Slc27a5	solute carrier family 27 (fatty acid transporter), member 5	-1.46	0.04753	0.999105
Cdc25a	cell division cycle 25A	-1.45	0.017739	0.999105
Top1mt	DNA topoisomerase 1, mitochondrial	-1.45	0.022521	0.999105
Tiam1	T cell lymphoma invasion and metastasis 1	-1.45	0.002166	0.999105
Trh	thyrotropin releasing hormone	-1.45	0.047079	0.999105
Acly	ATP citrate lyase	-1.45	0.019457	0.999105
Cotl1	coactosin-like 1 (Dictyostelium)	-1.45	0.043356	0.999105

Tex19.2	testis expressed gene 19.2	-1.45	0.018411	0.999105
Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1	-1.44	0.033989	0.999105
Gusb	glucuronidase, beta	-1.44	0.002055	0.999105
Rnh1	ribonuclease/angiogenin inhibitor 1	-1.44	0.036584	0.999105
Ifrd2	interferon-related developmental regulator 2	-1.44	0.02285	0.999105
Tmem189	transmembrane protein 189	-1.44	0.032032	0.999105
Slc25a28	solute carrier family 25, member 28	-1.44	0.007612	0.999105
Tmem210	transmembrane protein 210	-1.44	0.015434	0.999105
Olfr1226	olfactory receptor 1226	-1.44	0.029545	0.999105
Ssxb8	synovial sarcoma, X member B, breakpoint 8	-1.44	0.019221	0.999105
Fam181b	family with sequence similarity 181, member B	-1.43	0.010218	0.999105
Adam8	a disintegrin and metallopeptidase domain 8	-1.43	0.040189	0.999105
Defa1	defensin, alpha 1	-1.43	0.037433	0.999105
Ccdc134	coiled-coil domain containing 134	-1.42	0.021618	0.999105
Olfr484	olfactory receptor 484	-1.42	0.007116	0.999105
Uchl1	ubiquitin carboxy-terminal hydrolase L1	-1.41	0.009087	0.999105
Slc10a4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	-1.41	0.047131	0.999105
Isl1	ISL1 transcription factor, LIM/homeodomain	-1.41	0.033311	0.999105
Arsj	arylsulfatase J	-1.41	0.00917	0.999105
Enox2	ecto-NOX disulfide-thiol exchanger 2	-1.41	0.037927	0.999105
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13; YjeF N-terminal domain containing 3	-1.41	0.047618	0.999105

B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	-1.41	0.03067	0.999105
Wbp1	WW domain binding protein 1	-1.41	0.015431	0.999105
Vmn2r111	vomeronasal 2, receptor 111	-1.41	0.024077	0.999105
Klhl29	kelch-like 29	-1.4	0.005774	0.999105
Prr13	proline rich 13	-1.4	0.040889	0.999105
Rai2	retinoic acid induced 2	-1.4	0.008146	0.999105
Lynx1	Ly6/neurotoxin 1	-1.4	0.004431	0.999105
Ppp1r35	protein phosphatase 1, regulatory subunit 35	-1.4	0.012405	0.999105
Asb1	ankyrin repeat and SOCS box-containing 1	-1.4	0.015065	0.999105
Olfr640	olfactory receptor 640	-1.4	0.017308	0.999105
Nfya	nuclear transcription factor-Y alpha	-1.4	0.00444	0.999105
Olfr600	olfactory receptor 600	-1.4	0.016358	0.999105
Mroh8	maestro heat-like repeat family member 8	-1.4	0.045166	0.999105
Khdc3	KH domain containing 3, subcortical maternal complex member	-1.4	0.021582	0.999105
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	-1.4	0.009963	0.999105
Grm1	glutamate receptor, metabotropic 1	-1.39	0.021151	0.999105
Cxxc5	CXXC finger 5	-1.39	0.001111	0.822518
Trnp1	TMF1-regulated nuclear protein 1	-1.39	0.008358	0.999105
Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	-1.39	0.019031	0.999105
Anxa6	annexin A6	-1.39	0.025571	0.999105
Phgdh	3-phosphoglycerate dehydrogenase	-1.39	0.030175	0.999105
Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	-1.39	0.015072	0.999105
Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	-1.39	0.038581	0.999105

Umps	uridine monophosphate synthetase	-1.39	0.018822	0.999105
Fam227b	family with sequence similarity 227, member B	-1.39	0.029318	0.999105
Olfr726	olfactory receptor 726	-1.39	0.044336	0.999105
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-1.39	0.013133	0.999105
Dynll1	dynein light chain LC8-type 1	-1.38	0.020507	0.999105
Rltpr	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing	-1.38	0.006222	0.999105
Plcb2	phospholipase C, beta 2	-1.38	0.033401	0.999105
Dcaf5	DDB1 and CUL4 associated factor 5	-1.38	0.000272	0.571716
Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	-1.38	0.028097	0.999105
Il1f10	interleukin 1 family, member 10	-1.38	0.031547	0.999105
Cutal	cutA divalent cation tolerance homolog-like	-1.38	0.009368	0.999105
Slc45a4	solute carrier family 45, member 4	-1.38	0.0413	0.999105
Zfp13	zinc finger protein 13	-1.38	0.01029	0.999105
Mc2r	melanocortin 2 receptor	-1.38	0.025294	0.999105
Plcb3	phospholipase C, beta 3	-1.37	0.002552	0.999105
Plch2	phospholipase C, eta 2	-1.37	0.031744	0.999105
Atp6v1f	ATPase, H+ transporting, lysosomal V1 subunit F	-1.37	0.005199	0.999105
Adamts9	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9	-1.37	0.00675	0.999105
Psg18	pregnancy specific glycoprotein 18	-1.37	0.017006	0.999105
Zfp521	zinc finger protein 521	-1.36	0.043108	0.999105
Cfp	complement factor properdin	-1.36	0.042483	0.999105

Sart3	squamous cell carcinoma antigen recognized by T cells 3	-1.36	0.04872	0.999105
Fam53a	family with sequence similarity 53, member A	-1.36	0.013054	0.999105
Hdac6	histone deacetylase 6	-1.36	0.044195	0.999105
Olfr689	olfactory receptor 689	-1.36	0.006817	0.999105
Chmp4c	charged multivesicular body protein 4C	-1.36	0.017506	0.999105
Ube2d2b	ubiquitin-conjugating enzyme E2D 2B	-1.36	0.041604	0.999105
Cd19	CD19 antigen	-1.36	0.007646	0.999105
Elf4	E74-like factor 4 (ets domain transcription factor)	-1.36	0.015012	0.999105
Sp110	Sp110 nuclear body protein	-1.36	0.026624	0.999105
Hint1	histidine triad nucleotide binding protein 1	-1.36	0.000408	0.697304
Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	-1.36	0.008837	0.999105
Metrn	meteorin, glial cell differentiation regulator	-1.35	0.033504	0.999105
Mical3	microtubule associated monooxygenase, calponin and LIM domain containing 3	-1.35	0.001835	0.999105
Shf	Src homology 2 domain containing F	-1.35	0.042749	0.999105
Rpl10	ribosomal protein L10; small nucleolar RNA, H/ACA box 70	-1.35	0.015881	0.999105
Nos1	nitric oxide synthase 1, neuronal	-1.35	0.024222	0.999105
Pgs1	phosphatidylglycerophosphate synthase 1	-1.35	0.00071	0.742883
Spata33	spermatogenesis associated 33	-1.35	0.01991	0.999105
Anapc13	anaphase promoting complex subunit 13	-1.35	0.016405	0.999105
Agtr1a	angiotensin II receptor, type 1a	-1.35	0.005296	0.999105
Tfec	transcription factor EC	-1.35	0.02863	0.999105

Chil3	chitinase-like 3	-1.35	0.037874	0.999105
Ly6g5c	lymphocyte antigen 6 complex, locus G5C	-1.35	0.006143	0.999105
B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	-1.35	0.030412	0.999105
Col3a1	collagen, type III, alpha 1	-1.35	0.04495	0.999105
Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	-1.35	0.027937	0.999105
Wdr59	WD repeat domain 59	-1.35	0.032703	0.999105
Glb1l3	galactosidase, beta 1 like 3	-1.35	0.039906	0.999105
Mageb5	melanoma antigen, family B, 5	-1.35	0.011667	0.999105
Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	-1.34	0.001533	0.999105
Hpdl	4-hydroxyphenylpyruvate dioxygenase-like	-1.34	0.030182	0.999105
Apex1	apurinic/apyrimidinic endonuclease 1	-1.34	0.009569	0.999105
Rps6kc1	ribosomal protein S6 kinase polypeptide 1	-1.34	0.021296	0.999105
Slc35b1	solute carrier family 35, member B1	-1.34	0.040809	0.999105
Ifi44l	interferon-induced protein 44 like	-1.34	0.006731	0.999105
Arid5a	AT rich interactive domain 5A (MRF1-like)	-1.34	0.031296	0.999105
Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	-1.34	0.009868	0.999105
Apoa4	apolipoprotein A-IV	-1.34	0.033574	0.999105
Vmn2r89	vomeronasal 2, receptor 89	-1.34	0.04859	0.999105
St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-1.33	0.03927	0.999105
Sesn1	sestrin 1	-1.33	0.034165	0.999105
Psrc1	proline/serine-rich coiled-coil 1	-1.33	0.049446	0.999105
Gyg	glycogenin	-1.33	0.025639	0.999105

Mmp14	matrix metallopeptidase 14 (membrane-inserted)	-1.33	0.035436	0.999105
Snx29	sorting nexin 29	-1.33	0.002685	0.999105
Trim28	tripartite motif-containing 28	-1.33	0.009541	0.999105
Srebf1	sterol regulatory element binding transcription factor 1; microRNA 6922	-1.33	0.016206	0.999105
Bola1	bolA-like 1 (E. coli)	-1.33	0.046972	0.999105
Polr2j	polymerase (RNA) II (DNA directed) polypeptide J	-1.33	0.028094	0.999105
Krt23	keratin 23	-1.33	0.016354	0.999105
Nt5c3b	5-nucleotidase, cytosolic IIIB; 5'-nucleotidase, cytosolic IIIB	-1.33	0.027941	0.999105
Phpt1	phosphohistidine phosphatase 1	-1.32	0.012116	0.999105
Fnip2	folliculin interacting protein 2	-1.32	0.039282	0.999105
Gstm5	glutathione S-transferase, mu 5	-1.32	0.040536	0.999105
Lrrc75b	leucine rich repeat containing 75B	-1.32	0.03602	0.999105
Ubac2	ubiquitin associated domain containing 2	-1.32	0.026835	0.999105
Tceb2	transcription elongation factor B (SIII), polypeptide 2	-1.32	0.0121	0.999105
Fan1	FANCD2/FANCI-associated nuclease 1	-1.32	0.018977	0.999105
Rpl35	ribosomal protein L35	-1.32	0.049361	0.999105
Nsun2	NOL1/NOP2/Sun domain family member 2	-1.32	0.036983	0.999105
Mib2	mindbomb homolog 2 (Drosophila)	-1.32	0.003114	0.999105
Col6a1	collagen, type VI, alpha 1	-1.31	0.047899	0.999105
Psen1	presenilin 1	-1.31	0.038673	0.999105

B4galt2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	-1.31	0.024613	0.999105
Grcc10	gene rich cluster, C10 gene	-1.31	0.013169	0.999105
Hsdl1	hydroxysteroid dehydrogenase like 1	-1.31	0.047796	0.999105
Qars	glutaminyl-tRNA synthetase	-1.31	0.043092	0.999105
Chtf8	CTF8, chromosome transmission fidelity factor 8	-1.31	0.015666	0.999105
Dstyk	dual serine/threonine and tyrosine protein kinase	-1.31	0.047134	0.999105
Fam173a	family with sequence similarity 173, member A	-1.31	0.016807	0.999105
Serpina10	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	-1.31	0.039342	0.999105
Col5a2	collagen, type V, alpha 2	-1.31	0.024873	0.999105
Olfr1120	olfactory receptor 1120	-1.31	0.028852	0.999105
Mbd3	methyl-CpG binding domain protein 3	-1.31	0.040474	0.999105
Fem1c	fem-1 homolog c (C.elegans)	-1.3	0.041436	0.999105
Pcp4	Purkinje cell protein 4	-1.3	0.045298	0.999105
Arpc4	actin related protein 2/3 complex, subunit 4	-1.3	0.000253	0.571716
Msrb1	methionine sulfoxide reductase B1	-1.3	0.014733	0.999105
Ubl5	ubiquitin-like 5	-1.3	0.043452	0.999105
Pla2g1b	phospholipase A2, group IB, pancreas	-1.3	0.03895	0.999105
Gcsh	glycine cleavage system protein H (aminomethyl carrier)	-1.3	0.033118	0.999105
Sgca	sarcoglycan, alpha (dystrophin-associated glycoprotein)	-1.3	0.048972	0.999105
Olfr1417	olfactory receptor 1417	-1.3	0.017258	0.999105
Wdr6	WD repeat domain 6	-1.29	0.03325	0.999105

Gabrd	gamma-aminobutyric acid (GABA) A receptor, subunit delta	-1.29	0.049588	0.999105
Alg14	asparagine-linked glycosylation 14	-1.29	0.010294	0.999105
Nacc2	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	-1.29	0.020588	0.999105
Kctd20	potassium channel tetramerisation domain containing 20	-1.29	0.02344	0.999105
Olfr1282	olfactory receptor 1282	-1.29	0.03296	0.999105
Yap1	yes-associated protein 1	-1.29	0.016744	0.999105
Rhox4g	reproductive homeobox 4G	-1.29	0.031711	0.999105
Mrpl22	mitochondrial ribosomal protein L22	-1.29	0.035338	0.999105
Gfra3	glial cell line derived neurotrophic factor family receptor alpha 3	-1.29	0.0499	0.999105
Slc43a2	solute carrier family 43, member 2	-1.28	0.01057	0.999105
Mtfr1l	mitochondrial fission regulator 1-like	-1.28	0.018629	0.999105
Wdr81	WD repeat domain 81	-1.28	0.031794	0.999105
Il21	interleukin 21	-1.28	0.023306	0.999105
B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	-1.28	0.023409	0.999105
Pex14	peroxisomal biogenesis factor 14	-1.28	0.04224	0.999105
Ccdc8	coiled-coil domain containing 8	-1.28	0.049383	0.999105
Trpm1	transient receptor potential cation channel, subfamily M, member 1	-1.28	0.015781	0.999105
Ube2s	ubiquitin-conjugating enzyme E2S	-1.28	0.049145	0.999105
Fbxw14	F-box and WD-40 domain protein 14	-1.28	0.013648	0.999105
Rpl26	ribosomal protein L26; ribosomal protein L26 pseudogene	-1.28	0.044601	0.999105

Ptrh2	peptidyl-tRNA hydrolase 2	-1.28	0.037458	0.999105
Nek8	NIMA (never in mitosis gene a)-related expressed kinase 8	-1.28	0.014694	0.999105
Asic4	acid-sensing (proton-gated) ion channel family member 4	-1.27	0.012227	0.999105
Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.27	0.04496	0.999105
Cacng4	calcium channel, voltage-dependent, gamma subunit 4	-1.27	0.006057	0.999105
Comt	catechol-O-methyltransferase	-1.27	0.012364	0.999105
Calcr	calcitonin receptor	-1.27	0.033752	0.999105
Rpl24	ribosomal protein L24; zinc finger and BTB domain containing 11	-1.27	0.01876	0.999105
Uqcc2	ubiquinol-cytochrome c reductase complex assembly factor 2	-1.27	0.027197	0.999105
Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	-1.27	0.049062	0.999105
Tkt	transketolase; microRNA 3076	-1.27	0.023302	0.999105
Ech1	enoyl coenzyme A hydratase 1, peroxisomal	-1.27	0.031085	0.999105
Ormdl2	ORM1-like 2 (S. cerevisiae)	-1.27	0.046647	0.999105
Asna1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	-1.27	0.037063	0.999105
Brat1	BRCA1-associated ATM activator 1	-1.27	0.045355	0.999105
Kmo	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-1.27	0.004889	0.999105
Gpx4	glutathione peroxidase 4	-1.27	0.040082	0.999105

Cnpy2	canopy 2 homolog (zebrafish)	-1.27	0.0029	0.999105
Galr2	galanin receptor 2	-1.27	0.030944	0.999105
Sv2c	synaptic vesicle glycoprotein 2c	-1.26	0.005038	0.999105
Mief1	mitochondrial elongation factor 1	-1.26	0.019836	0.999105
Klhl21	kelch-like 21	-1.26	0.034172	0.999105
Ctse	cathepsin E	-1.26	0.046155	0.999105
Atraid	all-trans retinoic acid induced differentiation factor	-1.26	0.010879	0.999105
Csn3	casein kappa	-1.26	0.031233	0.999105
Rab19	RAB19, member RAS oncogene family	-1.26	0.019687	0.999105
Olfr64	olfactory receptor 64	-1.26	0.035331	0.999105
Eif4a3	eukaryotic translation initiation factor 4A3	-1.26	0.034938	0.999105
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-1.25	0.026736	0.999105
Pgp	phosphoglycolate phosphatase	-1.25	0.005432	0.999105
Rps14	ribosomal protein S14	-1.25	0.004885	0.999105
Clstn3	calsyntenin 3	-1.25	0.025854	0.999105
Pabpn1	poly(A) binding protein, nuclear 1	-1.25	0.031989	0.999105
Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	-1.25	0.015186	0.999105
Ftl1	ferritin light polypeptide 1	-1.25	0.008888	0.999105
Rpl7l1	ribosomal protein L7-like 1	-1.25	0.023966	0.999105
Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	-1.25	0.037774	0.999105
Mgat5	mannoside acetylglucosaminyltransferase 5	-1.25	0.037065	0.999105
Tmed1	transmembrane emp24 domain containing 1	-1.25	0.035046	0.999105
Gja10	gap junction protein, alpha 10	-1.25	0.01572	0.999105
Olfr608	olfactory receptor 608	-1.25	0.006522	0.999105
Mrpl34	mitochondrial ribosomal protein L34	-1.25	0.049217	0.999105

Snx20	sorting nexin 20	-1.25	0.006352	0.999105
T	brachyury; t-complex	-1.25	0.037875	0.999105
Nol3	nucleolar protein 3 (apoptosis repressor with CARD domain)	-1.24	0.035496	0.999105
Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	-1.24	0.02191	0.999105
Col4a2	collagen, type IV, alpha 2	-1.24	0.027315	0.999105
Rpl19	ribosomal protein L19	-1.24	0.033987	0.999105
Sez6l2	seizure related 6 homolog like 2	-1.24	0.034816	0.999105
Maml3	mastermind like 3 (Drosophila)	-1.24	0.040031	0.999105
Dll3	delta-like 3 (Drosophila)	-1.24	0.039295	0.999105
Pyhin1	pyrin and HIN domain family, member 1	-1.24	0.011336	0.999105
Rrp15	ribosomal RNA processing 15 homolog (S. cerevisiae)	-1.24	0.038645	0.999105
Atoh1	atonal homolog 1 (Drosophila)	-1.24	0.012485	0.999105
Ercc6l	excision repair cross-complementing rodent repair deficiency complementation group 6 like	-1.24	0.036003	0.999105
Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)	-1.24	0.044939	0.999105
Psmb11	proteasome (prosome, macropain) subunit, beta type, 11	-1.24	0.046892	0.999105
Snx31	sorting nexin 31	-1.24	0.03604	0.999105
H2-Eb1	histocompatibility 2, class II antigen E beta	-1.24	0.039152	0.999105
Rnf32	ring finger protein 32	-1.23	0.021348	0.999105
Dynlrb1	dynein light chain roadblock-type 1	-1.23	0.00664	0.999105
Nt5c	5,3-nucleotidase, cytosolic; 5',3'-nucleotidase, cytosolic	-1.23	0.014686	0.999105

Keap1	kelch-like ECH-associated protein 1	-1.23	0.044251	0.999105
Lrrc51	leucine rich repeat containing 51	-1.23	0.032741	0.999105
Kcnk16	potassium channel, subfamily K, member 16	-1.23	0.010381	0.999105
Pabpc1l	poly(A) binding protein, cytoplasmic 1-like	-1.23	0.042983	0.999105
Prl3d2	prolactin family 3, subfamily d, member 1	-1.23	0.025225	0.999105
Mllt4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4	-1.23	0.040639	0.999105
Macrod1	MACRO domain containing 1	-1.23	0.048748	0.999105
Wwc1	WW, C2 and coiled-coil domain containing 1	-1.22	0.010074	0.999105
Fasn	fatty acid synthase	-1.22	0.048684	0.999105
Rfxank	regulatory factor X-associated ankyrin-containing protein	-1.22	0.038511	0.999105
Msn	moesin	-1.22	0.024212	0.999105
Enho	energy homeostasis associated	-1.22	0.025892	0.999105
Dusp23	dual specificity phosphatase 23	-1.22	0.038872	0.999105
Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	-1.22	0.048361	0.999105
Lsm10	U7 snRNP-specific Sm-like protein LSM10	-1.22	0.020141	0.999105
Scnm1	sodium channel modifier 1	-1.22	0.048528	0.999105
Pole	polymerase (DNA directed), epsilon	-1.22	0.016203	0.999105
Olfr410	olfactory receptor 410	-1.22	0.002646	0.999105
Olfr1510	olfactory receptor 1510	-1.22	0.046172	0.999105
Gemin6	gem (nuclear organelle) associated protein 6	-1.22	0.018707	0.999105
Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type	-1.21	0.011871	0.999105

Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	-1.21	0.014204	0.999105
Rbck1	RanBP-type and C3HC4-type zinc finger containing 1	-1.21	0.038465	0.999105
Lats2	large tumor suppressor 2	-1.21	0.022986	0.999105
Selo	selenoprotein O	-1.21	0.043438	0.999105
Adgrg1	adhesion G protein-coupled receptor G1	-1.21	0.011821	0.999105
Bola2	bolA-like 2 (E. coli)	-1.21	0.005512	0.999105
Rps3	ribosomal protein S3; small nucleolar RNA, C/D box 14B	-1.21	0.019283	0.999105
Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-1.21	0.024807	0.999105
Ssr4	signal sequence receptor, delta	-1.21	0.004599	0.999105
Lgals1	lectin, galactose binding, soluble 1	-1.21	0.035456	0.999105
Supt4b	predicted gene 3258	-1.21	0.004599	0.999105
Rpl7	ribosomal protein L7	-1.21	0.006107	0.999105
Slc30a9	solute carrier family 30 (zinc transporter), member 9	-1.21	0.044851	0.999105
Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	-1.21	0.040961	0.999105
Pou3f4	POU domain, class 3, transcription factor 4	-1.2	0.034453	0.999105
Gipc1	GIPC PDZ domain containing family, member 1	-1.2	0.049874	0.999105
Id3	inhibitor of DNA binding 3	-1.2	0.036861	0.999105
Rnf135	ring finger protein 135	-1.2	0.04246	0.999105
Zfp324	zinc finger protein 324	-1.2	0.022309	0.999105
Tlx2	T cell leukemia, homeobox 2	-1.2	0.01176	0.999105
Ccdc66	coiled-coil domain containing 66	-1.2	0.044608	0.999105

Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	-1.19	0.036325	0.999105
Zfp827	zinc finger protein 827	-1.19	0.048296	0.999105
Dctn3	dynactin 3	-1.19	0.038569	0.999105
Pdcl	phosducin-like	-1.19	0.043348	0.999105
Psmb1	proteasome (prosome, macropain) subunit, beta type 1	-1.19	0.008951	0.999105
Fam193a	family with sequence similarity 193, member A	-1.19	0.021689	0.999105
Uba52	ubiquitin A-52 residue ribosomal protein fusion product 1	-1.19	0.011115	0.999105
Bcan	brevican	-1.19	0.012471	0.999105
Bdkrb1	bradykinin receptor, beta 1	-1.19	0.044482	0.999105
Edf1	endothelial differentiation-related factor 1	-1.19	0.026626	0.999105
Kprp	keratinocyte expressed, proline-rich	-1.19	0.038516	0.999105
Dmap1	DNA methyltransferase 1-associated protein 1	-1.19	0.046901	0.999105
Clasrp	CLK4-associating serine/arginine rich protein	-1.19	0.000511	0.742883
Pdilt	protein disulfide isomerase-like, testis expressed	-1.19	0.0005	0.742883
Spata31d1b	spermatogenesis associated 31 subfamily D, member 1B	-1.19	0.034189	0.999105
Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-1.19	0.030475	0.999105
H2-Pb	histocompatibility 2, P region beta locus [Source:MGI Symbol;Acc:MGI:95926]; histocompatibility 2, P region beta locus	-1.19	0.027312	0.999105

Ldoc1l	leucine zipper, down-regulated in cancer 1-like	-1.18	0.00767	0.999105
Med12l	mediator complex subunit 12-like	-1.18	0.040452	0.999105
Dnase1l2	deoxyribonuclease 1-like 2	-1.18	0.008219	0.999105
Por	P450 (cytochrome) oxidoreductase	-1.18	0.041024	0.999105
Preb	prolactin regulatory element binding	-1.18	0.048219	0.999105
Usf2	upstream transcription factor 2	-1.18	0.010842	0.999105
Ascc1	activating signal cointegrator 1 complex subunit 1	-1.18	0.012868	0.999105
Cts7	cathepsin 7	-1.18	0.01259	0.999105
Defb10	defensin beta 10	-1.18	0.032966	0.999105
Sap30bp	SAP30 binding protein	-1.18	0.046233	0.999105
Col11a2	collagen, type XI, alpha 2	-1.18	0.041306	0.999105
Sbpl	spermine binding protein-like	-1.18	0.031123	0.999105
Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	-1.18	0.011623	0.999105
Inpp5j	inositol polyphosphate 5-phosphatase J	-1.17	0.020917	0.999105
Klc1	kinesin light chain 1	-1.17	0.014628	0.999105
Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	-1.17	0.011594	0.999105
Ppp1r18	protein phosphatase 1, regulatory subunit 18	-1.17	0.019046	0.999105
Dedd	death effector domain-containing	-1.17	0.046459	0.999105
Mrpl11	mitochondrial ribosomal protein L11	-1.17	0.03784	0.999105
Olfr1087	olfactory receptor 1087	-1.17	0.01496	0.999105
Smcp	sperm mitochondria-associated cysteine-rich protein	-1.17	0.038375	0.999105
Trim14	tripartite motif-containing 14	-1.17	0.047211	0.999105
Steap4	STEAP family member 4	-1.17	0.028881	0.999105
Olfr649	olfactory receptor 649	-1.17	0.025849	0.999105

Olfr493	olfactory receptor 493	-1.17	0.042464	0.999105
Foxl2	forkhead box L2	-1.17	0.005964	0.999105
Enthd2	ENTH domain containing 2	-1.17	0.012104	0.999105
Mgat4c	MGAT4 family, member C	-1.16	0.007482	0.999105
Abat	4-aminobutyrate aminotransferase	-1.16	0.021157	0.999105
Cep112	centrosomal protein 112	-1.16	0.026837	0.999105
Stmn3	stathmin-like 3	-1.16	0.023486	0.999105
Clta	clathrin, light polypeptide (Lca)	-1.16	0.029573	0.999105
Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	-1.16	0.046226	0.999105
Ccdc174	coiled-coil domain containing 174	-1.16	0.001046	0.822518
Ahcy	S-adenosylhomocysteine hydrolase; predicted gene 4737	-1.16	0.04692	0.999105
Neurog3	neurogenin 3	-1.16	0.000723	0.742883
Pigs	phosphatidylinositol glycan anchor biosynthesis, class S	-1.16	0.013443	0.999105
Eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha)	-1.16	0.029881	0.999105
G0s2	G0/G1 switch gene 2	-1.16	0.01018	0.999105
Apon	apolipoprotein N	-1.16	0.008854	0.999105
Lrr1	leucine rich repeat protein 1	-1.16	0.048699	0.999105
Rrp36	ribosomal RNA processing 36 homolog (S. cerevisiae)	-1.16	0.012556	0.999105
Pomgnt1	protein O-linked mannose beta 1,2-N-acetylglucosaminyltransferase	-1.15	0.047564	0.999105
Pirb	paired Ig-like receptor B	-1.15	0.024406	0.999105
Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	-1.15	0.018958	0.999105
Shmt1	serine hydroxymethyltransferase 1 (soluble)	-1.15	0.047906	0.999105

Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	-1.14	0.030831	0.999105
Prdx1	peroxiredoxin 1	-1.14	0.047414	0.999105
Cluap1	clusterin associated protein 1	-1.14	0.025793	0.999105
Fbxl15	F-box and leucine-rich repeat protein 15	-1.14	0.026432	0.999105
Fads2	fatty acid desaturase 2	-1.13	0.014065	0.999105
Cd151	CD151 antigen	-1.13	0.025857	0.999105
Prkcsh	protein kinase C substrate 80K-H	-1.13	0.037276	0.999105
Slc2a10	solute carrier family 2 (facilitated glucose transporter), member 10	-1.13	0.040575	0.999105
Srgap2	SLIT-ROBO Rho GTPase activating protein 2	-1.12	0.016074	0.999105
Msl1	male-specific lethal 1 homolog (Drosophila)	-1.12	0.043098	0.999105
Ngdn	neuroguidin, EIF4E binding protein	-1.12	0.031938	0.999105
Tpi1	triosephosphate isomerase 1	-1.12	0.019162	0.999105
Fuz	fuzzy homolog (Drosophila)	-1.12	0.038145	0.999105
Pabpn1l	poly(A)binding protein nuclear 1-like	-1.12	0.037309	0.999105
Ly6c1	lymphocyte antigen 6 complex, locus C1	-1.11	0.031933	0.999105
Fam96a	family with sequence similarity 96, member A	-1.11	0.042875	0.999105
Rfpl4	ret finger protein-like 4	-1.11	0.045927	0.999105
Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.1	0.041995	0.999105
Rnf167	ring finger protein 167	-1.1	0.038683	0.999105
Rps4x	ribosomal protein S4, X-linked	-1.1	0.035636	0.999105
Fn3krp	fructosamine 3 kinase related protein	-1.1	0.033097	0.999105
Dr1	down-regulator of transcription 1	-1.1	0.008808	0.999105
Aes	amino-terminal enhancer of split	-1.1	0.011934	0.999105

Vps28	vacuolar protein sorting 28 (yeast)	-1.1	0.034823	0.999105
Lbhd1	LBH domain containing 1; RIKEN cDNA 1810009A15 gene	-1.1	0.037918	0.999105
Lpin2	lipin 2	-1.09	0.011178	0.999105
Fam216a	family with sequence similarity 216, member A	-1.09	0.006716	0.999105
Ehmt2	euchromatic histone lysine N-methyltransferase 2	-1.08	0.04379	0.999105
Clec3a	C-type lectin domain family 3, member a	-1.08	0.04023	0.999105
Uox	urate oxidase	-1.06	0.030491	0.999105

Table S6- Genes upregulated in the Cerebellum of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA CB vs. TT CB)	ANOVA p-value (AA CB vs. TT CB)	FDR p-value (AA CB vs. TT CB)
ATP8	ATP synthase F0 subunit 8; ATP synthase F0 subunit 6; cytochrome c oxidase subunit III	1.01	0.036993	0.999382
COX2	cytochrome c oxidase subunit II	1.06	0.046433	0.999382
Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	1.07	0.028331	0.999382
Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	1.07	0.043826	0.999382
Mbd2	methyl-CpG binding domain protein 2	1.07	0.023721	0.999382
Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	1.08	0.026022	0.999382
Ptov1	prostate tumor over expressed gene 1	1.08	0.036119	0.999382
Adk	adenosine kinase	1.08	0.03424	0.999382
Setd3	SET domain containing 3	1.09	0.011953	0.999382
Ncoa4	nuclear receptor coactivator 4	1.09	0.025418	0.999382
Slc12a5	solute carrier family 12, member 5	1.1	0.019766	0.999382
Prdx2	peroxiredoxin 2	1.1	0.016058	0.999382
Lsm12	LSM12 homolog (S. cerevisiae)	1.1	0.012718	0.999382
Tmem180	transmembrane protein 180	1.1	0.016785	0.999382
Tgfbrap1	transforming growth factor, beta receptor associated protein 1	1.11	0.021036	0.999382
Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3; heterogeneous nuclear ribonucleoprotein A3 pseudogene	1.11	0.043443	0.999382
Rbbp6	retinoblastoma binding protein 6	1.11	0.04118	0.999382
Vps26b	vacuolar protein sorting 26 homolog B (yeast)	1.11	0.049934	0.999382
Bbs4	Bardet-Biedl syndrome 4 (human)	1.11	0.048099	0.999382
Mthfsl	5, 10-methenyltetrahydrofolate synthetase-like	1.11	0.048423	0.999382
Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1.11	0.033505	0.999382
Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8	1.12	0.03973	0.999382
Tspyl1	testis-specific protein, Y-encoded-like 1	1.12	0.038787	0.999382
Hoxc4	homeobox C4	1.12	0.043752	0.999382

Nkx2-5	NK2 homeobox 5	1.12	0.032231	0.999382
Txnl4a	thioredoxin-like 4A	1.12	0.044543	0.999382
Ssna1	Sjogrens syndrome nuclear autoantigen 1; Sjogren's syndrome nuclear autoantigen 1	1.13	0.043389	0.999382
Cpa5	carboxypeptidase A5	1.13	0.04113	0.999382
Rpusd4	RNA pseudouridylate synthase domain containing 4	1.13	0.019977	0.999382
Puf60	poly-U binding splicing factor 60	1.13	0.046587	0.999382
Tuba1b	tubulin, alpha 1B	1.13	0.004062	0.97863
Csnk1a1	casein kinase 1, alpha 1	1.13	0.012851	0.999382
Fer1l5	fer-1-like 5 (C. elegans)	1.14	0.045112	0.999382
Fmn1	formin 1	1.14	0.03715	0.999382
Ptpra	protein tyrosine phosphatase, receptor type, A	1.14	0.00531	0.999382
Rab33b	RAB33B, member RAS oncogene family	1.14	0.029261	0.999382
Ptp4a2	protein tyrosine phosphatase 4a2	1.14	0.048922	0.999382
Rad52	RAD52 homolog (S. cerevisiae)	1.14	0.028263	0.999382
Smim19	small integral membrane protein 19	1.14	0.037295	0.999382
Gas7	growth arrest specific 7	1.14	0.009604	0.999382
Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	1.15	0.028099	0.999382
Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	1.15	0.034676	0.999382
Lmna	lamin A	1.15	0.027924	0.999382
Stambp	STAM binding protein	1.15	0.006841	0.999382
Prmt1	protein arginine N-methyltransferase 1	1.15	0.010298	0.999382
Rnf141	ring finger protein 141	1.15	0.009648	0.999382
Rps23	ribosomal protein S23	1.15	0.044558	0.999382
Tcstv3	2-cell-stage, variable group, member 3	1.15	0.047962	0.999382
St13	suppression of tumorigenicity 13	1.15	0.035189	0.999382
Anks1	ankyrin repeat and SAM domain containing 1	1.15	0.047105	0.999382
Camk2d	calcium/calmodulin-dependent protein kinase II, delta	1.16	0.020175	0.999382
Cdc42	cell division cycle 42	1.16	0.017486	0.999382
Atraid	all-trans retinoic acid induced differentiation factor	1.16	0.037707	0.999382
Bean1	brain expressed, associated with Nedd4, 1	1.16	0.032431	0.999382

Vwa5a	von Willebrand factor A domain containing 5A	1.16	0.042856	0.999382
Morf4l2	mortality factor 4 like 2	1.16	0.015329	0.999382
Wdpcp	WD repeat containing planar cell polarity effector	1.16	0.034305	0.999382
Dtnbp1	dystrobrevin binding protein 1	1.16	0.04849	0.999382
Srp9	signal recognition particle 9	1.17	0.04302	0.999382
Crmp1	collapsin response mediator protein 1	1.17	0.046504	0.999382
Sval2	seminal vesicle antigen-like 2	1.17	0.020646	0.999382
Rab7	RAB7, member RAS oncogene family	1.17	0.037878	0.999382
Carkd	carbohydrate kinase domain containing	1.17	0.045263	0.999382
Fnta	farnesyltransferase, CAAX box, alpha	1.17	0.045772	0.999382
Cxx1a	CAAX box 1A	1.17	0.042034	0.999382
Mrps27	mitochondrial ribosomal protein S27	1.17	0.045078	0.999382
Lrrc16a	leucine rich repeat containing 16A	1.17	0.033583	0.999382
Pfn3	profilin 3	1.17	0.030717	0.999382
Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	1.17	0.015093	0.999382
Pabpn1	poly(A) binding protein, nuclear 1	1.17	0.019005	0.999382
Tap2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	1.17	0.027918	0.999382
Clic5	chloride intracellular channel 5	1.17	0.021223	0.999382
Myl12b	myosin, light chain 12B, regulatory	1.17	0.023666	0.999382
Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	1.18	0.045885	0.999382
Oaz3	ornithine decarboxylase antizyme 3	1.18	0.033435	0.999382
Por	P450 (cytochrome) oxidoreductase	1.18	0.007966	0.999382
Arpc1b	actin related protein 2/3 complex, subunit 1B	1.18	0.034877	0.999382
Fgfr1op2	FGFR1 oncogene partner 2	1.18	0.001844	0.834811
Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	1.18	0.043317	0.999382
Comp	cartilage oligomeric matrix protein	1.18	0.044604	0.999382
Frg1	FSHD region gene 1	1.18	0.020361	0.999382
Cwc15	CWC15 homolog (S. cerevisiae)	1.18	0.024584	0.999382
Tma7	translational machinery associated 7 homolog (S. cerevisiae)	1.18	0.001665	0.834085
Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	1.18	0.006272	0.999382
Pnmt	phenylethanolamine-N-methyltransferase	1.18	0.033311	0.999382
Zmym5	zinc finger, MYM-type 5	1.18	0.049627	0.999382
Hacl1	2-hydroxyacyl-CoA lyase 1	1.18	0.020891	0.999382
Fem1a	feminization 1 homolog a (C. elegans)	1.18	0.046651	0.999382

Ltbp1	latent transforming growth factor beta binding protein 1	1.18	0.020798	0.999382
Slc26a2	solute carrier family 26 (sulfate transporter), member 2	1.18	0.000369	0.834085
Aqp12	aquaporin 12	1.19	0.005189	0.999382
Kctd18	potassium channel tetramerisation domain containing 18	1.19	0.01043	0.999382
Kdsr	3-ketodihydrosphingosine reductase	1.19	0.027009	0.999382
Epc2	enhancer of polycomb homolog 2 (Drosophila)	1.19	0.013409	0.999382
Dync1i2	dynein cytoplasmic 1 intermediate chain 2	1.19	0.024847	0.999382
Rab14	RAB14, member RAS oncogene family	1.19	0.037577	0.999382
15-Sep	selenoprotein	1.19	0.018224	0.999382
Ccl19	chemokine (C-C motif) ligand 19	1.19	0.024304	0.999382
Get4	golgi to ER traffic protein 4 homolog (S. cerevisiae)	1.19	0.037627	0.999382
Tas2r143	taste receptor, type 2, member 143	1.19	0.014058	0.999382
Smco3	single-pass membrane protein with coiled-coil domains 3	1.19	0.012172	0.999382
Ergic2	ERGIC and golgi 2	1.19	0.000549	0.834085
Rassf7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	1.19	0.027715	0.999382
Rbmx2	RNA binding motif protein, X-linked 2	1.19	0.027072	0.999382
Tmem255a	transmembrane protein 255A	1.19	0.006445	0.999382
Atg5	autophagy related 5	1.19	0.015422	0.999382
Lyz1	lysozyme 1	1.19	0.014731	0.999382
Gphn	gephyrin	1.19	0.01143	0.999382
Ajuba	ajuba LIM protein	1.19	0.024841	0.999382
Rbx1	ring-box 1	1.19	0.04275	0.999382
Scd1	stearoyl-Coenzyme A desaturase 1	1.19	0.023173	0.999382
Gstm2	glutathione S-transferase, mu 2	1.2	0.014787	0.999382
Atp6v0e2	ATPase, H+ transporting, lysosomal V0 subunit E2	1.2	0.009158	0.999382
Fkbp4	FK506 binding protein 4	1.2	0.00891	0.999382
Nphs1	nephrosis 1, nephrin	1.2	0.001491	0.834085
Zfp719	zinc finger protein 719	1.2	0.022663	0.999382
Olfr547	olfactory receptor 547	1.2	0.016851	0.999382
E2f8	E2F transcription factor 8	1.2	0.048892	0.999382
Olfr609	olfactory receptor 609	1.2	0.012231	0.999382
Rras2	related RAS viral (r-ras) oncogene homolog 2	1.2	0.029506	0.999382
Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	1.2	0.02213	0.999382
Lrrc2	leucine rich repeat containing 2	1.2	0.044027	0.999382

Reps1	RalBP1 associated Eps domain containing protein	1.2	0.04539	0.999382
Igfbp4	insulin-like growth factor binding protein 4	1.2	0.04065	0.999382
Flii	flightless I homolog (Drosophila)	1.2	0.03549	0.999382
Ppp2r5c	protein phosphatase 2, regulatory subunit B, gamma; protein phosphatase 2, regulatory subunit B', gamma	1.2	0.016798	0.999382
Rgr	retinal G protein coupled receptor	1.2	0.040458	0.999382
Zhx1	zinc fingers and homeoboxes 1	1.2	0.013672	0.999382
Fkbpl	FK506 binding protein-like	1.2	0.037946	0.999382
Ik	IK cytokine	1.2	0.012002	0.999382
Swi5	SWI5 recombination repair homolog (yeast)	1.21	0.048935	0.999382
Rpl34	ribosomal protein L34; ribosomal protein L34, pseudogene 1	1.21	0.026107	0.999382
Schip1	schwannomin interacting protein 1; predicted gene, 21949	1.21	0.032606	0.999382
Rpa2	replication protein A2	1.21	0.005262	0.999382
Ppcs	phosphopantothenoylcysteine synthetase	1.21	0.02214	0.999382
Msantd4	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils	1.21	0.019968	0.999382
Ptges3l	prostaglandin E synthase 3 (cytosolic)-like; alanyl-tRNA synthetase domain containing 1	1.21	0.043977	0.999382
Spink13	serine peptidase inhibitor, Kazal type 13	1.21	0.036783	0.999382
Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	1.22	0.028708	0.999382
Ptprt	protein tyrosine phosphatase, receptor type, T	1.22	0.024526	0.999382
Gabbr2	gamma-aminobutyric acid (GABA) B receptor, 2	1.22	0.01454	0.999382
St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1.22	0.002195	0.886072
Vmn2r55	vomeronasal 2, receptor 55	1.22	0.048664	0.999382
Olfr589	olfactory receptor 589	1.22	0.046915	0.999382
Rab21	RAB21, member RAS oncogene family	1.22	0.017553	0.999382
Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	1.22	0.016186	0.999382
Hist1h2ad	histone cluster 1, H2ad; histone cluster 1, H3b; histone cluster 1, H3d	1.22	0.025364	0.999382
Mapk1	mitogen-activated protein kinase 1	1.22	0.015395	0.999382
Ankrd44	ankyrin repeat domain 44	1.23	0.016832	0.999382

Arpc5l	actin related protein 2/3 complex, subunit 5-like	1.23	0.004554	0.97863
Acp2	acid phosphatase 2, lysosomal	1.23	0.02039	0.999382
Nsun6	NOL1/NOP2/Sun domain family member 6	1.23	0.044664	0.999382
Phgdh	3-phosphoglycerate dehydrogenase	1.23	0.047409	0.999382
Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	1.23	0.003659	0.97863
Mtg1	mitochondrial GTPase 1 homolog (S. cerevisiae)	1.23	0.046205	0.999382
Hexa	hexosaminidase A	1.23	0.0211	0.999382
Vmn1r216	vomeronasal 1 receptor 216	1.23	0.029514	0.999382
Prl3d1	prolactin family 3, subfamily d, member 1	1.23	0.001064	0.834085
Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	1.23	0.046898	0.999382
Ndc80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	1.23	0.004652	0.97863
Cfb	complement factor B	1.23	0.00623	0.999382
Rgs7	regulator of G protein signaling 7	1.24	0.048665	0.999382
Cypt12	cysteine-rich perinuclear theca 12	1.24	0.022937	0.999382
Tmem54	transmembrane protein 54	1.24	0.01967	0.999382
Pex26	peroxisomal biogenesis factor 26	1.24	0.035612	0.999382
Pik3c2g	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide	1.24	0.021	0.999382
Vmn1r158	vomeronasal 1 receptor 158	1.24	0.046108	0.999382
Usp35	ubiquitin specific peptidase 35	1.24	0.048824	0.999382
Use1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	1.24	0.032301	0.999382
Sumo2	small ubiquitin-like modifier 2; microRNA 684-1	1.24	0.049007	0.999382
Pcnp	PEST proteolytic signal containing nuclear protein	1.24	0.044463	0.999382
Ppic	peptidylprolyl isomerase C	1.24	0.021353	0.999382
Ccdc190	coiled-coil domain containing 190	1.25	0.02282	0.999382
Uxs1	UDP-glucuronate decarboxylase 1	1.25	0.009769	0.999382
Setx	senataxin	1.25	0.00911	0.999382
Wfdc5	WAP four-disulfide core domain 5	1.25	0.007979	0.999382
Myoz2	myozenin 2	1.25	0.002667	0.925416
Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	1.25	0.020796	0.999382
Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	1.25	0.011297	0.999382
Ap4m1	adaptor-related protein complex AP-4, mu 1	1.25	0.02834	0.999382

Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	1.25	0.002466	0.913123
Higd1a	HIG1 domain family, member 1A	1.25	0.004099	0.97863
Wbp5	WW domain binding protein 5	1.25	0.046195	0.999382
Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	1.25	0.012671	0.999382
Pgk2	phosphoglycerate kinase 2	1.25	0.03776	0.999382
Ndfip1	Nedd4 family interacting protein 1	1.25	0.037823	0.999382
Ctsw	cathepsin W	1.25	0.029743	0.999382
Nkx1-1	NK1 transcription factor related, locus 1 (Drosophila)	1.25	0.012666	0.999382
Alg5	asparagine-linked glycosylation 5 (dolichyl-phosphate beta-glucosyltransferase)	1.26	0.004521	0.97863
Toporsl	topoisomerase I binding, arginine/serine-rich like	1.26	0.010748	0.999382
Lpcat2b	lysophosphatidylcholine acyltransferase 2B	1.26	0.034334	0.999382
Tpcn1	two pore channel 1	1.26	0.043981	0.999382
Tgfb1i1	transforming growth factor beta 1 induced transcript 1	1.26	0.00565	0.999382
Dll3	delta-like 3 (Drosophila)	1.26	0.028192	0.999382
Gapdhs	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	1.26	0.01022	0.999382
Fgl1	fibrinogen-like protein 1	1.26	0.036519	0.999382
Zdhhc15	zinc finger, DHHC domain containing 15	1.26	0.008915	0.999382
Fbxo7	F-box protein 7	1.26	0.005729	0.999382
Zc3h10	zinc finger CCCH type containing 10	1.26	0.020836	0.999382
Mctp1	multiple C2 domains, transmembrane 1	1.26	0.046995	0.999382
Rpl8	ribosomal protein L8	1.26	0.040599	0.999382
Neu1	neuraminidase 1	1.26	0.016002	0.999382
Cplx4	complexin 4	1.26	0.001324	0.834085
Stat1	signal transducer and activator of transcription 1	1.27	0.030106	0.999382
Col6a3	collagen, type VI, alpha 3	1.27	0.020339	0.999382
Gpr37l1	G protein-coupled receptor 37-like 1	1.27	0.001728	0.834085
Eppin	epididymal peptidase inhibitor	1.27	0.047704	0.999382
Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	1.27	0.0454	0.999382
Rac1	RAS-related C3 botulinum substrate 1	1.27	0.022232	0.999382
Olfr594	olfactory receptor 594	1.27	0.043114	0.999382
Ilk	integrin linked kinase	1.27	0.001086	0.834085
Defb33	defensin beta 33	1.27	0.027783	0.999382

Slc25a43	solute carrier family 25, member 43	1.27	0.022268	0.999382
Rhox7b	reproductive homeobox 7B	1.27	0.045931	0.999382
Olfr1353	olfactory receptor 1353	1.27	0.047901	0.999382
Grap	GRB2-related adaptor protein	1.27	0.043807	0.999382
Canx	calnexin	1.27	0.000005	0.114912
Olfr1364	olfactory receptor 1364	1.27	0.006001	0.999382
Ctsl	cathepsin L	1.27	0.045982	0.999382
Pcdhb21	protocadherin beta 21; protocadherin beta 22	1.27	0.024068	0.999382
Tmem163	transmembrane protein 163	1.28	0.039432	0.999382
Zfp697	zinc finger protein 697	1.28	0.011252	0.999382
Noa1	nitric oxide associated 1	1.28	0.019132	0.999382
Epo	erythropoietin	1.28	0.000029	0.317906
Olfr552	olfactory receptor 552	1.28	0.026674	0.999382
Vmn1r129	vomeronasal 1 receptor 129	1.28	0.044648	0.999382
Defa21	defensin, alpha, 21	1.28	0.031024	0.999382
Enkd1	enkurin domain containing 1	1.28	0.043157	0.999382
Chrdl1	chordin-like 1	1.28	0.044885	0.999382
Snrpd3	small nuclear ribonucleoprotein D3	1.28	0.036178	0.999382
Naca	nascent polypeptide-associated complex alpha polypeptide	1.28	0.031369	0.999382
Myl6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	1.28	0.004115	0.97863
Gm2a	GM2 ganglioside activator protein	1.28	0.03459	0.999382
Trpv3	transient receptor potential cation channel, subfamily V, member 3	1.28	0.043027	0.999382
Eml1	echinoderm microtubule associated protein like 1	1.28	0.020137	0.999382
Mplkip	M-phase specific PLK1 intereacting protein	1.28	0.023599	0.999382
Mcat	malonyl CoA:ACP acyltransferase (mitochondrial)	1.28	0.035936	0.999382
Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	1.28	0.049805	0.999382
Muc20	mucin 20	1.28	0.020651	0.999382
Trim36	tripartite motif-containing 36	1.28	0.010559	0.999382
Insrr	insulin receptor-related receptor	1.29	0.013136	0.999382
Urod	uroporphyrinogen decarboxylase	1.29	0.047629	0.999382
Rpl6	ribosomal protein L6	1.29	0.037945	0.999382
Nutf2	nuclear transport factor 2; nuclear transport factor 2, pseudogene 1	1.29	0.007886	0.999382
Acta1	actin, alpha 1, skeletal muscle	1.29	0.036305	0.999382
Tmppe	transmembrane protein with metallophosphoesterase domain; galactosidase, beta 1	1.29	0.008461	0.999382
Sf3b6	splicing factor 3B, subunit 6	1.29	0.03359	0.999382

Eapp	E2F-associated phosphoprotein	1.29	0.000841	0.834085
Rps24	ribosomal protein S24	1.29	0.049652	0.999382
Atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	1.29	0.036258	0.999382
Med30	mediator complex subunit 30	1.29	0.029921	0.999382
Scarf2	scavenger receptor class F, member 2	1.29	0.011296	0.999382
Ubald1	UBA-like domain containing 1	1.29	0.025333	0.999382
Onecut2	one cut domain, family member 2	1.29	0.035256	0.999382
Rpl17	ribosomal protein L17	1.29	0.021572	0.999382
Cd28	CD28 antigen	1.3	0.036628	0.999382
Obp2b	odorant binding protein 2B	1.3	0.034384	0.999382
Olfr1123	olfactory receptor 1123	1.3	0.02877	0.999382
Oasl2	2-5 oligoadenylate synthetase-like 2; 2'-5' oligoadenylate synthetase-like 2	1.3	0.028464	0.999382
Wdr95	WD40 repeat domain 95	1.3	0.005949	0.999382
Cpz	carboxypeptidase Z	1.3	0.047575	0.999382
Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1	1.3	0.012174	0.999382
Vmn1r48	vomeronasal 1 receptor 48	1.3	0.023338	0.999382
Klk4	kallikrein related-peptidase 4 (prostase, enamel matrix, prostate)	1.3	0.03189	0.999382
Olfr312	olfactory receptor 312	1.3	0.015889	0.999382
Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-like 1	1.3	0.008264	0.999382
Rps27a	ribosomal protein S27A	1.3	0.040559	0.999382
Rpl10l	ribosomal protein L10-like	1.3	0.033708	0.999382
Gphb5	glycoprotein hormone beta 5	1.3	0.046293	0.999382
Faf2	Fas associated factor family member 2	1.3	0.019881	0.999382
Ypel5	yippee-like 5 (Drosophila)	1.3	0.001373	0.834085
Nme3	NME/NM23 nucleoside diphosphate kinase 3	1.3	0.002069	0.864268
Stx5a	syntaxin 5A; microRNA 6992	1.3	0.046896	0.999382
Cnnm1	cyclin M1	1.3	0.041784	0.999382
Chtop	chromatin target of PRMT1	1.31	0.029938	0.999382
Fam222a	family with sequence similarity 222, member A	1.31	0.010073	0.999382
Pbp2	phosphatidylethanolamine binding protein 2	1.31	0.033497	0.999382
Bhlhe41	basic helix-loop-helix family, member e41	1.31	0.02166	0.999382
Cml5	camello-like 5	1.31	0.044244	0.999382
Kat8	K(lysine) acetyltransferase 8	1.31	0.030275	0.999382
Hook2	hook homolog 2 (Drosophila)	1.31	0.032951	0.999382
Crispld2	cysteine-rich secretory protein LCCL domain containing 2	1.31	0.018085	0.999382

Psmb10	proteasome (prosome, macropain) subunit, beta type 10	1.31	0.009854	0.999382
Wdr61	WD repeat domain 61	1.31	0.021699	0.999382
Atg14	autophagy related 14	1.31	0.023485	0.999382
Fbln1	fibulin 1	1.31	0.010578	0.999382
Rab12	RAB12, member RAS oncogene family	1.31	0.000163	0.794959
Spata3	spermatogenesis associated 3	1.32	0.033696	0.999382
Sned1	sushi, nidogen and EGF-like domains 1; microRNA 6901	1.32	0.049109	0.999382
Ppp1r26	protein phosphatase 1, regulatory subunit 26	1.32	0.045378	0.999382
Asphd1	aspartate beta-hydroxylase domain containing 1	1.32	0.035867	0.999382
Cirbp	cold inducible RNA binding protein	1.32	0.029016	0.999382
Olfr59	olfactory receptor 59	1.32	0.016372	0.999382
Fyb	FYN binding protein	1.32	0.002738	0.935243
Treml4	triggering receptor expressed on myeloid cells-like 4	1.32	0.033185	0.999382
Zfp119a	zinc finger protein 119a	1.32	0.046263	0.999382
Bpifb1	BPI fold containing family B, member 1	1.33	0.034987	0.999382
Kif2c	kinesin family member 2C	1.33	0.035385	0.999382
Rps17	ribosomal protein S17	1.33	0.011571	0.999382
F11	coagulation factor XI	1.33	0.041624	0.999382
Cc2d1a	coiled-coil and C2 domain containing 1A	1.33	0.042226	0.999382
Pnldc1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	1.33	0.020647	0.999382
Pax6	paired box 6	1.34	0.00908	0.999382
Polr3gl	polymerase (RNA) III (DNA directed) polypeptide G like	1.34	0.032899	0.999382
Corin	corin	1.34	0.045043	0.999382
Olfr460	olfactory receptor 460	1.34	0.046593	0.999382
Dguok	deoxyguanosine kinase	1.34	0.01616	0.999382
Ip6k2	inositol hexaphosphate kinase 2	1.34	0.037539	0.999382
Wif1	Wnt inhibitory factor 1	1.34	0.007058	0.999382
Neurog1	neurogenin 1	1.34	0.00188	0.834811
Plppr5	phospholipid phosphatase related 5	1.35	0.033317	0.999382
Srp72	signal recognition particle 72	1.35	0.034057	0.999382
Arhgap33	Rho GTPase activating protein 33	1.35	0.038623	0.999382
Qtrt1	queuine tRNA-ribosyltransferase 1	1.35	0.040735	0.999382
Ccdc166	coiled-coil domain containing 166	1.35	0.044987	0.999382
Nifk	nucleolar protein interacting with the FHA domain of MKI67	1.36	0.026697	0.999382
Col5a1	collagen, type V, alpha 1	1.36	0.037295	0.999382

Asb6	ankyrin repeat and SOCS box-containing 6	1.36	0.035706	0.999382
Ago4	argonaute RISC catalytic subunit 4	1.36	0.029431	0.999382
Pole	polymerase (DNA directed), epsilon	1.36	0.012104	0.999382
Tet1	tet methylcytosine dioxygenase 1	1.36	0.03225	0.999382
Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	1.36	0.02263	0.999382
Pdia5	protein disulfide isomerase associated 5	1.36	0.0188	0.999382
Abhd10	abhydrolase domain containing 10	1.36	0.00131	0.834085
Vmn2r91	vomeronasal 2, receptor 91	1.36	0.017877	0.999382
Ppp1r2-ps3	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 3	1.36	0.006904	0.999382
Speer4c	spermatogenesis associated glutamate (E)-rich protein 4C	1.37	0.026996	0.999382
Tbrg1	transforming growth factor beta regulated gene 1	1.37	0.009007	0.999382
Hspa2	heat shock protein 2	1.37	0.028296	0.999382
E2f3	E2F transcription factor 3	1.37	0.048449	0.999382
Arhgap24	Rho GTPase activating protein 24	1.38	0.032906	0.999382
Fbxw25	F-box and WD-40 domain protein 25	1.38	0.02362	0.999382
Polrmt	polymerase (RNA) mitochondrial (DNA directed)	1.38	0.004365	0.97863
Wnt3	wingless-type MMTV integration site family, member 3	1.38	0.018395	0.999382
Gabra1	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 1	1.38	0.019907	0.999382
Cd99	CD99 antigen	1.38	0.013332	0.999382
Olfr1032	olfactory receptor 1032	1.39	0.034612	0.999382
Shf	Src homology 2 domain containing F	1.39	0.029173	0.999382
Usp18	ubiquitin specific peptidase 18	1.39	0.005531	0.999382
Adgrg5	adhesion G protein-coupled receptor G5	1.39	0.040892	0.999382
Srpk3	serine/arginine-rich protein specific kinase 3	1.39	0.033335	0.999382
Tuba1a	tubulin, alpha 1A	1.39	0.036206	0.999382
Lonp1	lon peptidase 1, mitochondrial	1.39	0.046125	0.999382
Apcdd1	adenomatosis polyposis coli down-regulated 1	1.39	0.030933	0.999382
Tmem167b	transmembrane protein 167B	1.4	0.010972	0.999382
Kdm5a	lysine (K)-specific demethylase 5A	1.4	0.035676	0.999382
Zfp110	zinc finger protein 110	1.4	0.037505	0.999382

Trpc2	transient receptor potential cation channel, subfamily C, member 2; Xrcc1 N-terminal domain containing 1; Xndc1-transient receptor potential cation channel, subfamily C, member 2 readthrough	1.4	0.029283	0.999382
Birc3	baculoviral IAP repeat-containing 3	1.4	0.001372	0.834085
Cntd1	cyclin N-terminal domain containing 1	1.4	0.024098	0.999382
Crhbp	corticotropin releasing hormone binding protein	1.4	0.013399	0.999382
Tppp2	tubulin polymerization-promoting protein family member 2	1.4	0.006204	0.999382
Traf1	TNF receptor-associated factor 1	1.41	0.015986	0.999382
Lrfn1	leucine rich repeat and fibronectin type III domain containing 1; microRNA 466f-2	1.42	0.010323	0.999382
Glra4	glycine receptor, alpha 4 subunit	1.42	0.014885	0.999382
Ccl9	chemokine (C-C motif) ligand 9	1.42	0.021765	0.999382
Ube2d2a	ubiquitin-conjugating enzyme E2D 2A	1.42	0.00437	0.97863
Cenpl	centromere protein L	1.43	0.036306	0.999382
Dsn1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	1.43	0.024792	0.999382
Zfp428	zinc finger protein 428	1.43	0.04659	0.999382
Setd2	SET domain containing 2	1.43	0.001823	0.834811
Zfp729b	zinc finger protein 729b	1.43	0.017906	0.999382
Asic4	acid-sensing (proton-gated) ion channel family member 4	1.44	0.044968	0.999382
Slfn9	schlafen 9	1.44	0.028101	0.999382
Mapk8	mitogen-activated protein kinase 8	1.44	0.003816	0.97863
Cyb5r1	cytochrome b5 reductase 1	1.45	0.033609	0.999382
Hdgfrp3	hepatoma-derived growth factor, related protein 3	1.45	0.027951	0.999382
Mas1	MAS1 oncogene	1.45	0.036835	0.999382
Rpl23	ribosomal protein L23	1.46	0.043314	0.999382
Gskip	GSK3B interacting protein	1.46	0.004961	0.999382
Gdf10	growth differentiation factor 10	1.46	0.001713	0.834085
Rnase6	ribonuclease, RNase A family, 6	1.46	0.00489	0.999382
Cdhr1	cadherin-related family member 1	1.46	0.01547	0.999382
Grik1	glutamate receptor, ionotropic, kainate 1	1.46	0.013432	0.999382
Chac1	ChaC, cation transport regulator 1	1.47	0.048231	0.999382
Vmn1r113	vomeronasal 1 receptor 113	1.47	0.029248	0.999382
Ccnb3	cyclin B3	1.47	0.030969	0.999382
Spata6	spermatogenesis associated 6	1.48	0.006369	0.999382
Fam96b	family with sequence similarity 96, member B	1.48	0.033137	0.999382

Prl2c3	prolactin family 2, subfamily c, member 3; prolactin family 2, subfamily c, member 4	1.48	0.047119	0.999382
Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	1.49	0.019587	0.999382
Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	1.49	0.022953	0.999382
Vmn1r6	vomeronasal 1 receptor 6	1.49	0.034801	0.999382
Olfr585	olfactory receptor 585	1.49	0.016178	0.999382
Olfr147	olfactory receptor 147	1.49	0.016891	0.999382
Olfr906	olfactory receptor 906	1.49	0.011483	0.999382
Itih4	inter alpha-trypsin inhibitor, heavy chain 4	1.49	0.014641	0.999382
Snrnp200	small nuclear ribonucleoprotein 200 (U5)	1.5	0.015373	0.999382
Tmod4	tropomodulin 4	1.5	0.031684	0.999382
Tmed3	transmembrane emp24 domain containing 3	1.5	0.047342	0.999382
Krtap13	keratin associated protein 13	1.5	0.041875	0.999382
Olfr133	olfactory receptor 133	1.5	0.038258	0.999382
Npepl1	aminopeptidase-like 1	1.51	0.007633	0.999382
Tas2r108	taste receptor, type 2, member 108	1.51	0.041762	0.999382
Il34	interleukin 34	1.51	0.03297	0.999382
Tubb2b	tubulin, beta 2B class IIB	1.51	0.00952	0.999382
Myl12a	myosin, light chain 12A, regulatory, non-sarcomeric	1.51	0.003175	0.973966
Sult6b1	sulfotransferase family, cytosolic, 6B, member 1	1.51	0.007837	0.999382
Rtkn	rhotekin	1.52	0.006081	0.999382
Usp27x	ubiquitin specific peptidase 27, X chromosome	1.52	0.02978	0.999382
Vmn1r232	vomeronasal 1 receptor 232	1.53	0.045278	0.999382
Zfp473	zinc finger protein 473	1.54	0.043398	0.999382
Defb38	defensin beta 38	1.54	0.009039	0.999382
Isoc2b	isochorismatase domain containing 2b	1.55	0.011251	0.999382
Col6a4	collagen, type VI, alpha 4	1.55	0.007787	0.999382
Pde8b	phosphodiesterase 8B	1.55	0.033853	0.999382
Dnajb7	DnaJ (Hsp40) homolog, subfamily B, member 7	1.56	0.043538	0.999382
Wdr90	WD repeat domain 90	1.56	0.02434	0.999382
Cd46	CD46 antigen, complement regulatory protein	1.57	0.031625	0.999382
Uckl1	uridine-cytidine kinase 1-like 1	1.57	0.016875	0.999382
Ephb2	Eph receptor B2	1.57	0.0312	0.999382
Med9	mediator complex subunit 9	1.57	0.010002	0.999382
Klf6	Kruppel-like factor 6	1.57	0.009046	0.999382

Espl1	extra spindle pole bodies 1, separase	1.57	0.01389	0.999382
Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.59	0.021786	0.999382
Stmn4	stathmin-like 4	1.6	0.012269	0.999382
Isg20l2	interferon stimulated exonuclease gene 20-like 2	1.61	0.001275	0.834085
Scn7a	sodium channel, voltage-gated, type VII, alpha	1.62	0.032804	0.999382
Reep6	receptor accessory protein 6	1.63	0.018284	0.999382
Flna	filamin, alpha	1.64	0.023752	0.999382
Gpr161	G protein-coupled receptor 161	1.66	0.006326	0.999382
Synj2	synaptojanin 2	1.66	0.022753	0.999382
Nudt17	nudix (nucleoside diphosphate linked moiety X)-type motif 17	1.67	0.003922	0.97863
Hist1h2bm	histone cluster 1, H2bm	1.7	0.039899	0.999382
Zfp457	zinc finger protein 457	1.7	0.047567	0.999382
Phf7	PHD finger protein 7	1.72	0.02251	0.999382
Ttc5	tetratricopeptide repeat domain 5	1.78	0.010135	0.999382
Vmn2r99	vomeronasal 2, receptor 99	1.84	0.043939	0.999382
Gpr26	G protein-coupled receptor 26	1.9	0.036138	0.999382
Ulk4	unc-51-like kinase 4	1.91	0.01595	0.999382
Qpct	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	1.97	0.005801	0.999382
Cck	cholecystokinin	1.98	0.021953	0.999382
Cd59a	CD59a antigen	2.41	0.009247	0.999382

Table S7- Genes downregulated in the Cerebellum of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA CB vs. TT CB)	ANOVA p-value (AA CB vs. TT CB)	FDR p-value (AA CB vs. TT CB)
Glra1	glycine receptor, alpha 1 subunit	-2.84	0.032811	0.999382
Mid1	midline 1	-2.43	0.031002	0.999382
Mid1	midline 1	-2.43	0.031002	0.999382
Mrgpra2a	MAS-related GPR, member A2A	-2.16	0.002549	0.913123
Svs6	seminal vesicle secretory protein 6	-2.14	0.022288	0.999382
Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	-2.05	0.028302	0.999382
Olfr1167	olfactory receptor 1167	-1.97	0.015587	0.999382
Anxa11	annexin A11	-1.84	0.012511	0.999382
Murc	muscle-related coiled-coil protein	-1.79	0.00966	0.999382
Gimap4	GTPase, IMAP family member 4	-1.75	0.038181	0.999382
Esyt1	extended synaptotagmin-like protein 1	-1.75	0.048554	0.999382
Itga10	integrin, alpha 10	-1.71	0.001351	0.834085
Prss12	protease, serine 12 neurotrypsin (motopsin)	-1.69	0.003829	0.97863
Pofut1	protein O-fucosyltransferase 1	-1.67	0.023611	0.999382
N4bp2	NEDD4 binding protein 2	-1.67	0.001223	0.834085
Ell3	elongation factor RNA polymerase II-like 3	-1.66	0.004557	0.97863
Vmn2r5	vomeronasal 2, receptor 5	-1.66	0.009451	0.999382
Vmn1r10	vomeronasal 1 receptor 10	-1.66	0.002418	0.913123
Cyp2j7	cytochrome P450, family 2, subfamily j, polypeptide 7	-1.65	0.00104	0.834085
Klk1b24	kallikrein 1-related peptidase b24	-1.65	0.027924	0.999382
Mcpt9	mast cell protease 9	-1.63	0.021876	0.999382
Olfr57	olfactory receptor 57	-1.62	0.017853	0.999382
Gdpd4	glycerophosphodiester phosphodiesterase domain containing 4	-1.61	0.034069	0.999382
Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	-1.61	0.006801	0.999382
Layn	layilin	-1.6	0.000741	0.834085
Lcn6	lipocalin 6	-1.58	0.036478	0.999382
Adam24	a disintegrin and metallopeptidase domain 24 (testase 1)	-1.58	0.048259	0.999382
Olfr1155	olfactory receptor 1155	-1.56	0.018145	0.999382
Dusp16	dual specificity phosphatase 16	-1.56	0.000565	0.834085
Npy6r	neuropeptide Y receptor Y6	-1.56	0.00749	0.999382
Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	-1.56	0.002327	0.913123
Olfr1136	olfactory receptor 1136	-1.55	0.017751	0.999382
Neb	nebulin	-1.54	0.025373	0.999382
Ccna1	cyclin A1	-1.54	0.040411	0.999382

Defb7	defensin beta 7	-1.54	0.019895	0.999382
Hephl1	hephaestin-like 1	-1.54	0.027726	0.999382
Ankfn1	ankyrin-repeat and fibronectin type III domain containing 1	-1.54	0.000788	0.834085
Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	-1.54	0.045206	0.999382
Olfr1384	olfactory receptor 1384	-1.53	0.020247	0.999382
Apob	apolipoprotein B	-1.53	0.004814	0.999064
Kctd6	potassium channel tetramerisation domain containing 6	-1.53	0.019343	0.999382
Acvrl1	activin A receptor, type II-like 1	-1.53	0.034016	0.999382
Parp10	poly (ADP-ribose) polymerase family, member 10	-1.53	0.028563	0.999382
Vmn1r233	vomeronasal 1 receptor 233	-1.53	0.013453	0.999382
Mdfic	MyoD family inhibitor domain containing	-1.52	0.01036	0.999382
Sytl5	synaptotagmin-like 5	-1.52	0.015458	0.999382
Tc2n	tandem C2 domains, nuclear	-1.52	0.018846	0.999382
Slc45a4	solute carrier family 45, member 4	-1.52	0.00661	0.999382
Ccdc93	coiled-coil domain containing 93	-1.51	0.002005	0.856408
Olfr1077-ps1	olfactory receptor 1077, pseudogene 1	-1.5	0.042409	0.999382
Olfr1082	olfactory receptor 1082	-1.5	0.025517	0.999382
Olfr1170	olfactory receptor 1170	-1.5	0.025289	0.999382
Ryr3	ryanodine receptor 3	-1.5	0.00303	0.965219
Lce1i	late cornified envelope 1I	-1.5	0.017951	0.999382
Olfr65	olfactory receptor 65	-1.5	0.016442	0.999382
Olfr937	olfactory receptor 937	-1.5	0.029574	0.999382
Nab1	Ngfi-A binding protein 1	-1.49	0.019716	0.999382
Olfr1016	olfactory receptor 1016	-1.49	0.003696	0.97863
Sh3tc1	SH3 domain and tetratricopeptide repeats 1	-1.49	0.020571	0.999382
Kif9	kinesin family member 9	-1.49	0.026382	0.999382
Irx2	Iroquois related homeobox 2 (Drosophila)	-1.49	0.043783	0.999382
Cts7	cathepsin 7	-1.49	0.039867	0.999382
Cd82	CD82 antigen	-1.47	0.043748	0.999382
Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	-1.47	0.006099	0.999382
Gpnmb	glycoprotein (transmembrane) nmb	-1.47	0.017432	0.999382
Nefl	neurofilament, light polypeptide	-1.47	0.048272	0.999382
Fkbp5	FK506 binding protein 5	-1.47	0.046038	0.999382
Prcp	prolylcarboxypeptidase (angiotensinase C)	-1.45	0.002805	0.942904
Tcl1b5	T cell leukemia/lymphoma 1B, 5	-1.45	0.011855	0.999382
Dppa5a	developmental pluripotency associated 5A	-1.44	0.019526	0.999382
Pyroxd2	pyridine nucleotide-disulphide oxidoreductase domain 2	-1.44	0.026456	0.999382
Ccdc108	coiled-coil domain containing 108	-1.43	0.017262	0.999382
Tm4sf4	transmembrane 4 superfamily member 4	-1.43	0.010518	0.999382

Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	-1.43	0.010078	0.999382
Cmtm2b	CKLF-like MARVEL transmembrane domain containing 2B	-1.43	0.00749	0.999382
Vmn1r220	vomeronasal 1 receptor 220	-1.43	0.003298	0.973966
Pla2g1b	phospholipase A2, group IB, pancreas	-1.42	0.006439	0.999382
Vmn1r9	vomeronasal 1 receptor 9	-1.42	0.021176	0.999382
Crx	cone-rod homeobox	-1.42	0.000717	0.834085
Slc5a4a	solute carrier family 5, member 4a	-1.42	0.027683	0.999382
Lect2	leukocyte cell-derived chemotaxin 2	-1.42	0.017531	0.999382
Olfr221	olfactory receptor 221	-1.42	0.030817	0.999382
C1ra	complement component 1, r subcomponent A	-1.41	0.009268	0.999382
Sbk3	SH3 domain binding kinase family, member 3	-1.41	0.036009	0.999382
Klf1	Kruppel-like factor 1 (erythroid)	-1.41	0.046004	0.999382
Fam149a	family with sequence similarity 149, member A	-1.41	0.012673	0.999382
Ar	androgen receptor	-1.41	0.001568	0.834085
Fam132b	family with sequence similarity 132, member B	-1.4	0.038747	0.999382
Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	-1.4	0.007132	0.999382
Cypt2	cysteine-rich perinuclear theca 2	-1.4	0.010123	0.999382
Nup43	nucleoporin 43	-1.4	0.000882	0.834085
Wfdc17	WAP four-disulfide core domain 17	-1.4	0.043282	0.999382
Olfr398	olfactory receptor 398	-1.4	0.007148	0.999382
St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	-1.4	0.001306	0.834085
Csrnp2	cysteine-serine-rich nuclear protein 2	-1.4	0.001555	0.834085
Nrg2	neuregulin 2	-1.4	0.00932	0.999382
Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	-1.39	0.02076	0.999382
Entpd8	ectonucleoside triphosphate diphosphohydrolase 8	-1.39	0.007745	0.999382
Usp13	ubiquitin specific peptidase 13 (isopeptidase T-3)	-1.39	0.006402	0.999382
Nipa1	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	-1.39	0.005178	0.999382
Myct1	myc target 1	-1.39	0.041204	0.999382
Ccdc138	coiled-coil domain containing 138	-1.39	0.040686	0.999382
Arsg	arylsulfatase G	-1.39	0.034829	0.999382
Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	-1.39	0.026635	0.999382
Krtap27-1	keratin associated protein 27-1	-1.39	0.047129	0.999382

Prnd	prion protein dublet; prion protein; prion protein gene complex	-1.38	0.031395	0.999382
8030411F24Rik	RIKEN cDNA 8030411F24 gene	-1.38	0.019785	0.999382
Tspyl3	TSPY-like 3	-1.38	0.010282	0.999382
Fhl3	four and a half LIM domains 3	-1.38	0.031898	0.999382
Wtip	WT1-interacting protein	-1.38	0.012352	0.999382
Olfr901	olfactory receptor 901	-1.38	0.016051	0.999382
Bcl2l10	Bcl2-like 10	-1.38	0.032637	0.999382
Olfr773	olfactory receptor 773	-1.38	0.015594	0.999382
Vmn2r124	vomeronasal 2, receptor 124	-1.38	0.02815	0.999382
Olfr137	olfactory receptor 137	-1.38	0.047559	0.999382
Rhot2	ras homolog gene family, member T2	-1.38	0.013854	0.999382
Fam53c	family with sequence similarity 53, member C	-1.38	0.000414	0.834085
Hoxd3	homeobox D3; homeobox D4	-1.37	0.038542	0.999382
Ttc39b	tetratricopeptide repeat domain 39B	-1.37	0.026725	0.999382
Gimap8	GTPase, IMAP family member 8	-1.37	0.028619	0.999382
Cfap46	cilia and flagella associated protein 46	-1.37	0.036076	0.999382
Ano1	anoctamin 1, calcium activated chloride channel	-1.37	0.036567	0.999382
Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	-1.37	0.01936	0.999382
Pnpo	pyridoxine 5-phosphate oxidase; pyridoxine 5'-phosphate oxidase	-1.37	0.010054	0.999382
Tpo	thyroid peroxidase	-1.37	0.026818	0.999382
Vmn2r117	vomeronasal 2, receptor 117	-1.37	0.046783	0.999382
Rnf208	ring finger protein 208	-1.36	0.015518	0.999382
Wisp2	WNT1 inducible signaling pathway protein 2	-1.36	0.046945	0.999382
Tti1	TELO2 interacting protein 1	-1.36	0.034081	0.999382
Adra2c	adrenergic receptor, alpha 2c	-1.36	0.023102	0.999382
Adam39	a disintegrin and metallopeptidase domain 39	-1.36	0.021999	0.999382
Fuk	fucokinase	-1.36	0.023333	0.999382
Sowahd	sosondowah ankyrin repeat domain family member D	-1.36	0.028468	0.999382
Lrig3	leucine-rich repeats and immunoglobulin-like domains 3	-1.36	0.002541	0.913123
Rdh1	retinol dehydrogenase 1 (all trans); retinol dehydrogenase 9	-1.36	0.022474	0.999382
Olfr815	olfactory receptor 815	-1.36	0.002845	0.942904
Olfr1388	olfactory receptor 1388	-1.36	0.012735	0.999382
Stard3	START domain containing 3	-1.36	0.028782	0.999382
Vrk1	vaccinia related kinase 1	-1.36	0.035791	0.999382
Fgd4	FYVE, RhoGEF and PH domain containing 4	-1.36	0.004588	0.97863
Vmn1r236	vomeronasal 1 receptor 236	-1.36	0.000901	0.834085
Syt12	synaptotagmin XII	-1.36	0.010694	0.999382

Aven	apoptosis, caspase activation inhibitor	-1.35	0.032169	0.999382
Prkci	protein kinase C, iota	-1.35	0.003577	0.97863
Mest	mesoderm specific transcript	-1.35	0.025784	0.999382
Hrc	histidine rich calcium binding protein	-1.35	0.026794	0.999382
Olfr531	olfactory receptor 531	-1.35	0.0391	0.999382
Rnaseh2a	ribonuclease H2, large subunit	-1.35	0.000324	0.834085
Kcng4	potassium voltage-gated channel, subfamily G, member 4	-1.35	0.041354	0.999382
Ngp	neutrophilic granule protein	-1.35	0.016543	0.999382
Nphp3	nephronophthisis 3 (adolescent)	-1.35	0.034688	0.999382
Lace1	lactation elevated 1	-1.35	0.022083	0.999382
C1qtnf2	C1q and tumor necrosis factor related protein 2	-1.35	0.017753	0.999382
Amdhd2	amidohydrolase domain containing 2	-1.35	0.038396	0.999382
Il17a	interleukin 17A	-1.34	0.004366	0.97863
Usp40	ubiquitin specific peptidase 40	-1.34	0.008963	0.999382
Il20	interleukin 20	-1.34	0.019727	0.999382
Ccdc30	coiled-coil domain containing 30	-1.34	0.027683	0.999382
Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C	-1.34	0.033844	0.999382
Trap1a	tumor rejection antigen P1A	-1.34	0.016765	0.999382
Slc39a3	solute carrier family 39 (zinc transporter), member 3	-1.34	0.037671	0.999382
Ccdc57	coiled-coil domain containing 57	-1.34	0.031998	0.999382
Zbtb1	zinc finger and BTB domain containing 1	-1.34	0.044663	0.999382
Sec16b	SEC16 homolog B (S. cerevisiae)	-1.33	0.01137	0.999382
Zfp442	zinc finger protein 442	-1.33	0.019516	0.999382
Rbp7	retinol binding protein 7, cellular	-1.33	0.009014	0.999382
Pxn	paxillin	-1.33	0.02652	0.999382
Zfp568	zinc finger protein 568	-1.33	0.010204	0.999382
Alpk3	alpha-kinase 3	-1.33	0.016395	0.999382
Olfr632	olfactory receptor 632	-1.33	0.001418	0.834085
Olfr701	olfactory receptor 701	-1.33	0.008018	0.999382
Nr2f6	nuclear receptor subfamily 2, group F, member 6	-1.33	0.049431	0.999382
Olfr963	olfactory receptor 963	-1.33	0.000615	0.834085
Oog1	oogenesin 1; predicted gene 2042	-1.33	0.030637	0.999382
Adssl1	adenylosuccinate synthetase like 1	-1.33	0.011134	0.999382
Dio2	deiodinase, iodothyronine, type II	-1.33	0.001357	0.834085
Wdr60	WD repeat domain 60	-1.33	0.017184	0.999382
Casp7	caspase 7	-1.33	0.045572	0.999382
Prlhr	prolactin releasing hormone receptor	-1.33	0.003004	0.965219
Nvl	nuclear VCP-like	-1.32	0.043581	0.999382
Olfr1084	olfactory receptor 1084	-1.32	0.034839	0.999382
Olfr1239	olfactory receptor 1239	-1.32	0.025405	0.999382
Usp45	ubiquitin specific petidase 45	-1.32	0.016134	0.999382

Mkrn2os	makorin, ring finger protein 2, opposite strand	-1.32	0.028943	0.999382
Psg26	pregnancy-specific glycoprotein 26	-1.32	0.037446	0.999382
Gcdh	glutaryl-Coenzyme A dehydrogenase	-1.32	0.00805	0.999382
Otx2	orthodenticle homolog 2	-1.32	0.04531	0.999382
Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	-1.31	0.034896	0.999382
Olfr1206	olfactory receptor 1206	-1.31	0.035549	0.999382
Olfr1109	olfactory receptor 1109	-1.31	0.029099	0.999382
Olfr71	olfactory receptor 71	-1.31	0.014886	0.999382
Vmn1r160	vomeronasal 1 receptor 160	-1.31	0.009746	0.999382
Ltbp4	latent transforming growth factor beta binding protein 4	-1.31	0.021447	0.999382
Cks1brt	CDC28 protein kinase 1b, retrogene	-1.31	0.017275	0.999382
Taar8a	trace amine-associated receptor 8A	-1.31	0.002623	0.924525
Nuak1	NUAK family, SNF1-like kinase, 1	-1.31	0.001578	0.834085
Slfn8	schlafen 8	-1.31	0.036818	0.999382
Strn	striatin, calmodulin binding protein	-1.31	0.009531	0.999382
Sdhaf2	succinate dehydrogenase complex assembly factor 2	-1.31	0.034143	0.999382
Rragc	Ras-related GTP binding C	-1.3	0.013623	0.999382
Jun	jun proto-oncogene	-1.3	0.017782	0.999382
Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	-1.3	0.002102	0.864268
Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	-1.3	0.004204	0.97863
Cry1	cryptochrome 1 (photolyase-like)	-1.3	0.036762	0.999382
Zfp2	zinc finger protein 2	-1.3	0.046275	0.999382
Msi2	musashi RNA-binding protein 2	-1.3	0.007798	0.999382
Pyy	peptide YY	-1.3	0.017765	0.999382
Map3k9	mitogen-activated protein kinase kinase kinase 9	-1.3	0.001532	0.834085
Aldh5a1	aldhehyde dehydrogenase family 5, subfamily A1	-1.3	0.017796	0.999382
Prkcd	protein kinase C, delta	-1.3	0.04091	0.999382
Hspa13	heat shock protein 70 family, member 13	-1.3	0.000893	0.834085
Olfr127	olfactory receptor 127	-1.3	0.016454	0.999382
Adrb2	adrenergic receptor, beta 2	-1.3	0.039393	0.999382
Pnliprp1	pancreatic lipase related protein 1	-1.3	0.027498	0.999382
Sh2d1b1	SH2 domain containing 1B1	-1.29	0.025734	0.999382
Dedd	death effector domain-containing	-1.29	0.022558	0.999382
Tnp1	transition protein 1	-1.29	0.036688	0.999382
Mapkbp1	mitogen-activated protein kinase binding protein 1	-1.29	0.031157	0.999382
Rnf224	ring finger protein 224	-1.29	0.022362	0.999382
Ano3	anoctamin 3	-1.29	0.034372	0.999382

Cyp4a29	cytochrome P450, family 4, subfamily a, polypeptide 29	-1.29	0.034288	0.999382
Bud31	BUD31 homolog (yeast)	-1.29	0.034072	0.999382
Man2b1	mannosidase 2, alpha B1	-1.29	0.02555	0.999382
Rhox5	reproductive homeobox 5	-1.29	0.048961	0.999382
Vnn3	vanin 3	-1.29	0.018153	0.999382
Ccno	cyclin O	-1.29	0.025894	0.999382
Ranbp9	RAN binding protein 9	-1.29	0.037455	0.999382
Ang3	angiogenin, ribonuclease A family, member 3; angiogenin, ribonuclease A family, member 5	-1.29	0.009903	0.999382
Ccdc122	coiled-coil domain containing 122	-1.29	0.036748	0.999382
Rnase13	ribonuclease, RNase A family, 13 (non-active)	-1.29	0.030809	0.999382
Slc52a3	solute carrier protein family 52, member 3	-1.28	0.008284	0.999382
Defb28	defensin beta 28	-1.28	0.047159	0.999382
Olfr1195	olfactory receptor 1195	-1.28	0.018257	0.999382
Cog6	component of oligomeric golgi complex 6	-1.28	0.01417	0.999382
Sfn	stratifin	-1.28	0.023771	0.999382
Tmem214	transmembrane protein 214	-1.28	0.030725	0.999382
Mesp2	mesoderm posterior 2	-1.28	0.038004	0.999382
Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)	-1.28	0.044181	0.999382
Zmat5	zinc finger, matrin type 5	-1.28	0.049194	0.999382
Mmgt2	membrane magnesium transporter 2	-1.28	0.032077	0.999382
Mier3	mesoderm induction early response 1, family member 3	-1.28	0.021942	0.999382
Slc22a23	solute carrier family 22, member 23	-1.28	0.046988	0.999382
Fbp2	fructose bisphosphatase 2	-1.28	0.040101	0.999382
Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	-1.28	0.014296	0.999382
Tagap1	T cell activation GTPase activating protein 1	-1.28	0.039495	0.999382
Slamf6	SLAM family member 6	-1.27	0.03295	0.999382
Hoxd1	homeobox D1	-1.27	0.023285	0.999382
Rnf24	ring finger protein 24	-1.27	0.00343	0.973966
Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-1.27	0.042812	0.999382
Cela2a	chymotrypsin-like elastase family, member 2A	-1.27	0.029383	0.999382
Acad12	acyl-Coenzyme A dehydrogenase family, member 12	-1.27	0.041429	0.999382
Strn4	striatin, calmodulin binding protein 4	-1.27	0.021853	0.999382
Klk1	kallikrein 1	-1.27	0.004628	0.97863
Zfp276	zinc finger protein (C2H2 type) 276	-1.27	0.008885	0.999382
Tubd1	tubulin, delta 1	-1.27	0.036462	0.999382
Mrpl16	mitochondrial ribosomal protein L16	-1.27	0.009118	0.999382

Lenep	lens epithelial protein; RFad1, flavin adenine dinucleotide synthetase, homolog (yeast)	-1.26	0.013636	0.999382
Nom1	nucleolar protein with MIF4G domain 1	-1.26	0.048964	0.999382
Ccdc60	coiled-coil domain containing 60	-1.26	0.004414	0.97863
Fam71f1	family with sequence similarity 71, member F1	-1.26	0.013401	0.999382
Tpra1	transmembrane protein, adipocyte asscociated 1	-1.26	0.047541	0.999382
Myo7a	myosin VIIA	-1.26	0.009574	0.999382
Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-1.26	0.008568	0.999382
Npy5r	neuropeptide Y receptor Y5	-1.26	0.016078	0.999382
Usp3	ubiquitin specific peptidase 3	-1.26	0.01629	0.999382
Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	-1.26	0.044277	0.999382
Yy2	Yy2 transcription factor; membrane-bound transcription factor peptidase, site 2	-1.26	0.001002	0.834085
Gabrp	gamma-aminobutyric acid (GABA) A receptor, pi	-1.26	0.035253	0.999382
Nqo2	NAD(P)H dehydrogenase, quinone 2	-1.26	0.024361	0.999382
Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	-1.26	0.013111	0.999382
Krtap16-3	keratin associated protein 16-3	-1.26	0.042091	0.999382
Hlcs	holocarboxylase synthetase (biotin-[propriony-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)	-1.26	0.022983	0.999382
Vav1	vav 1 oncogene	-1.26	0.042746	0.999382
H2-K1	histocompatibility 2, K1, K region	-1.26	0.011047	0.999382
Noc3l	nucleolar complex associated 3 homolog (S. cerevisiae)	-1.26	0.038744	0.999382
Sh2d1b2	SH2 domain containing 1B2	-1.25	0.040008	0.999382
Olfr1118	olfactory receptor 1118	-1.25	0.048651	0.999382
Lcn12	lipocalin 12	-1.25	0.027423	0.999382
Actrt2	actin-related protein T2	-1.25	0.043292	0.999382
Csn1s2a	casein alpha s2-like A	-1.25	0.02018	0.999382
Tbl2	transducin (beta)-like 2	-1.25	0.035342	0.999382
Ccl26	chemokine (C-C motif) ligand 26	-1.25	0.008751	0.999382
Vmn1r120	vomeronasal 1 receptor 120	-1.25	0.017167	0.999382
Olfr67	olfactory receptor 67	-1.25	0.010153	0.999382
Slc18a1	solute carrier family 18 (vesicular monoamine), member 1	-1.25	0.016371	0.999382
Hemk1	HemK methyltransferase family member 1	-1.25	0.03928	0.999382
Ptchd1	patched domain containing 1	-1.25	0.044279	0.999382
Zfp946	zinc finger protein 946	-1.25	0.00431	0.97863
Zfp804a	zinc finger protein 804A	-1.24	0.030547	0.999382
Rabl6	RAB, member RAS oncogene family-like 6	-1.24	0.029594	0.999382

Pde7a	phosphodiesterase 7A	-1.24	0.042076	0.999382
Actr3b	ARP3 actin-related protein 3B	-1.24	0.04937	0.999382
Tctn2	tectonic family member 2	-1.24	0.004393	0.97863
Tmem233	transmembrane protein 233	-1.24	0.027821	0.999382
Sh2d6	SH2 domain containing 6	-1.24	0.012651	0.999382
Arhgap25	Rho GTPase activating protein 25	-1.24	0.032078	0.999382
Olfr483	olfactory receptor 483	-1.24	0.040136	0.999382
Spag11b	sperm associated antigen 11B	-1.24	0.049113	0.999382
Polb	polymerase (DNA directed), beta	-1.24	0.046595	0.999382
Impg1	interphotoreceptor matrix proteoglycan 1	-1.24	0.040978	0.999382
Ptprk	protein tyrosine phosphatase, receptor type, K	-1.24	0.010798	0.999382
Ssh2	slingshot homolog 2 (Drosophila)	-1.24	0.015066	0.999382
Hoxc6	homeobox C6	-1.24	0.003308	0.973966
Chd1	chromodomain helicase DNA binding protein 1	-1.24	0.049422	0.999382
Rorb	RAR-related orphan receptor beta	-1.24	0.028472	0.999382
Cytip	cytohesin 1 interacting protein	-1.23	0.032549	0.999382
Slc30a7	solute carrier family 30 (zinc transporter), member 7	-1.23	0.040657	0.999382
Ept1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	-1.23	0.035073	0.999382
Cpa4	carboxypeptidase A4	-1.23	0.045562	0.999382
Iqgap1	IQ motif containing GTPase activating protein 1	-1.23	0.037357	0.999382
Ciapin1	cytokine induced apoptosis inhibitor 1	-1.23	0.01962	0.999382
Kars	lysyl-tRNA synthetase	-1.23	0.008314	0.999382
Olfr24	olfactory receptor 24	-1.23	0.037363	0.999382
Tmsb15a	thymosin beta 15a	-1.23	0.039086	0.999382
Dram1	DNA-damage regulated autophagy modulator 1	-1.23	0.006764	0.999382
Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	-1.23	0.029116	0.999382
Atp13a4	ATPase type 13A4	-1.23	0.021112	0.999382
Rcan2	regulator of calcineurin 2	-1.23	0.018608	0.999382
Teddm1b	transmembrane epididymal protein 1B	-1.22	0.007626	0.999382
Aph1a	anterior pharynx defective 1a homolog (C. elegans)	-1.22	0.015357	0.999382
Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	-1.22	0.013762	0.999382
Phf14	PHD finger protein 14	-1.22	0.006528	0.999382
Ninj2	ninjurin 2	-1.22	0.033224	0.999382
Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	-1.22	0.048381	0.999382
Fiz1	Flt3 interacting zinc finger protein 1	-1.22	0.04375	0.999382
Cpt1c	carnitine palmitoyltransferase 1c	-1.22	0.020694	0.999382

Obox2	oocyte specific homeobox 2	-1.22	0.038665	0.999382
Ces1d	carboxylesterase 1D	-1.22	0.023325	0.999382
Olfr151	olfactory receptor 151	-1.22	0.015779	0.999382
Sik2	salt inducible kinase 2	-1.22	0.010134	0.999382
Herc4	hect domain and RLD 4	-1.22	0.012903	0.999382
Ccdc28a	coiled-coil domain containing 28A	-1.22	0.039236	0.999382
Armc7	armadillo repeat containing 7	-1.22	0.042341	0.999382
Syce3	synaptonemal complex central element protein 3	-1.22	0.022962	0.999382
Wdr24	WD repeat domain 24	-1.22	0.000653	0.834085
Cd14	CD14 antigen	-1.22	0.037904	0.999382
Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.22	0.013119	0.999382
Thnsl1	threonine synthase-like 1 (bacterial)	-1.21	0.000346	0.834085
Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	-1.21	0.044484	0.999382
Mavs	mitochondrial antiviral signaling protein	-1.21	0.027322	0.999382
Zfp932	zinc finger protein 932	-1.21	0.011423	0.999382
Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	-1.21	0.033079	0.999382
Tspan33	tetraspanin 33	-1.21	0.039637	0.999382
Wee2	WEE1 homolog 2 (S. pombe)	-1.21	0.035948	0.999382
Zfp638	zinc finger protein 638	-1.21	0.041766	0.999382
Mtmr14	myotubularin related protein 14	-1.21	0.030807	0.999382
Arpc4	actin related protein 2/3 complex, subunit 4	-1.21	0.015535	0.999382
Zfp109	zinc finger protein 109	-1.21	0.002402	0.913123
Slco3a1	solute carrier organic anion transporter family, member 3a1	-1.21	0.022122	0.999382
Mmp21	matrix metallopeptidase 21	-1.21	0.034139	0.999382
Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	-1.21	0.040678	0.999382
Ptcd2	pentatricopeptide repeat domain 2	-1.21	0.046667	0.999382
E4f1	E4F transcription factor 1	-1.21	0.007995	0.999382
Cdc25c	cell division cycle 25C	-1.21	0.001277	0.834085
Fam126b	family with sequence similarity 126, member B	-1.2	0.01615	0.999382
Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A; microRNA 7011	-1.2	0.040821	0.999382
Snx30	sorting nexin family member 30	-1.2	0.036039	0.999382
Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	-1.2	0.040416	0.999382
Cfap57	cilia and flagella associated protein 57	-1.2	0.041298	0.999382
Klf3	Kruppel-like factor 3 (basic)	-1.2	0.037389	0.999382

Slc8b1	solute carrier family 8 (sodium/lithium/calcium exchanger), member B1	-1.2	0.034924	0.999382
Zfp771	zinc finger protein 771	-1.2	0.006084	0.999382
Ubxn8	UBX domain protein 8	-1.2	0.029138	0.999382
Sidt2	SID1 transmembrane family, member 2	-1.2	0.017623	0.999382
Zfp449	zinc finger protein 449	-1.2	0.030208	0.999382
Ankrd36	ankyrin repeat domain 36	-1.2	0.047961	0.999382
Acly	ATP citrate lyase	-1.2	0.047216	0.999382
Pcdhb18	protocadherin beta 18	-1.2	0.030174	0.999382
Pm20d1	peptidase M20 domain containing 1	-1.19	0.01186	0.999382
Edem3	ER degradation enhancer, mannosidase alpha-like 3	-1.19	0.003369	0.973966
Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	-1.19	0.013678	0.999382
Cdca8	cell division cycle associated 8	-1.19	0.026365	0.999382
Nudc	nuclear distribution gene C homolog (Aspergillus)	-1.19	0.044253	0.999382
Sgsm1	small G protein signaling modulator 1	-1.19	0.007608	0.999382
Cabp1	calcium binding protein 1	-1.19	0.027152	0.999382
Vamp8	vesicle-associated membrane protein 8	-1.19	0.049516	0.999382
Nrip3	nuclear receptor interacting protein 3	-1.19	0.023122	0.999382
Olfr905	olfactory receptor 905	-1.19	0.011161	0.999382
Mrpl55	mitochondrial ribosomal protein L55	-1.19	0.001661	0.834085
Zkscan3	zinc finger with KRAB and SCAN domains 3	-1.19	0.029962	0.999382
Ltb4r2	leukotriene B4 receptor 2	-1.19	0.044996	0.999382
Cnih1	cornichon homolog 1 (Drosophila)	-1.19	0.01659	0.999382
Glis2	GLIS family zinc finger 2	-1.19	0.044609	0.999382
Sdf2l1	stromal cell-derived factor 2-like 1	-1.19	0.011917	0.999382
Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	-1.19	0.008199	0.999382
Cyp2c69	cytochrome P450, family 2, subfamily c, polypeptide 69	-1.19	0.049611	0.999382
Pign	phosphatidylinositol glycan anchor biosynthesis, class N	-1.18	0.042513	0.999382
Sohlh1	spermatogenesis and oogenesis specific basic helix-loop-helix 1	-1.18	0.017	0.999382
Ugt8a	UDP galactosyltransferase 8A	-1.18	0.021486	0.999382
Vmn1r179	vomeronasal 1 receptor 179	-1.18	0.006035	0.999382
Capns1	calpain, small subunit 1	-1.18	0.025655	0.999382
Col4a1	collagen, type IV, alpha 1	-1.18	0.018713	0.999382
Olfr287	olfactory receptor 287	-1.18	0.020662	0.999382
Cd320	CD320 antigen	-1.18	0.003803	0.97863
Amy1	amylase 1, salivary	-1.17	0.028922	0.999382
Cpsf3l	cleavage and polyadenylation specific factor 3-like	-1.17	0.043805	0.999382

Olfr1337	olfactory receptor 1337	-1.17	0.001785	0.834811
Vmn1r88	vomeronasal 1 receptor, 88	-1.17	0.009012	0.999382
Cracr2b	calcium release activated channel regulator 2B	-1.17	0.007229	0.999382
Rab20	RAB20, member RAS oncogene family	-1.17	0.008762	0.999382
Lztfl1	leucine zipper transcription factor-like 1	-1.17	0.048809	0.999382
Rtn4ip1	reticulon 4 interacting protein 1	-1.17	0.020885	0.999382
Efna2	ephrin A2	-1.17	0.048618	0.999382
Hils1	histone H1-like protein in spermatids 1	-1.17	0.032248	0.999382
Lrrc26	leucine rich repeat containing 26	-1.16	0.016655	0.999382
Slc35f6	solute carrier family 35, member F6; microRNA 5625	-1.16	0.004443	0.97863
Gal3st4	galactose-3-O-sulfotransferase 4	-1.16	0.033625	0.999382
Mpv17l2	MPV17 mitochondrial membrane protein-like 2	-1.16	0.047278	0.999382
Fig4	FIG4 homolog (S. cerevisiae)	-1.16	0.046062	0.999382
Sall2	sal-like 2 (Drosophila)	-1.16	0.012073	0.999382
Nos1ap	nitric oxide synthase 1 (neuronal) adaptor protein	-1.15	0.047064	0.999382
Gpatch4	G patch domain containing 4	-1.15	0.020827	0.999382
Ufsp1	UFM1-specific peptidase 1	-1.15	0.009798	0.999382
Casd1	CAS1 domain containing 1	-1.15	0.041019	0.999382
Cln3	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	-1.15	0.033153	0.999382
Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	-1.15	0.000096	0.710567
Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	-1.15	0.017598	0.999382
Irf1	interferon regulatory factor 1	-1.15	0.017224	0.999382
Olfr288	olfactory receptor 288	-1.15	0.020902	0.999382
Qk	quaking	-1.15	0.048548	0.999382
Ammecr1l	AMME chromosomal region gene 1-like	-1.15	0.028363	0.999382
Pggt1b	protein geranylgeranyltransferase type I, beta subunit	-1.15	0.00929	0.999382
Rbm45	RNA binding motif protein 45	-1.14	0.002498	0.913123
Unc5c	unc-5 homolog C (C. elegans)	-1.14	0.026368	0.999382
Tas2r117	taste receptor, type 2, member 117	-1.14	0.006141	0.999382
Tmem25	transmembrane protein 25	-1.14	0.02549	0.999382
Maged2	melanoma antigen, family D, 2	-1.14	0.042975	0.999382
Tifab	TRAF-interacting protein with forkhead-associated domain, family member B	-1.14	0.014329	0.999382
Atad1	ATPase family, AAA domain containing 1	-1.14	0.031971	0.999382
Setd7	SET domain containing (lysine methyltransferase) 7	-1.13	0.045328	0.999382
Lmtk2	lemur tyrosine kinase 2	-1.13	0.026747	0.999382

Crebl2	cAMP responsive element binding protein-like 2	-1.13	0.049203	0.999382
Olfr493	olfactory receptor 493	-1.13	0.014465	0.999382
Herpud2	HERPUD family member 2	-1.13	0.028611	0.999382
Snrnp48	small nuclear ribonucleoprotein 48 (U11/U12)	-1.13	0.044927	0.999382
Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	-1.12	0.046437	0.999382
Spint5	serine protease inhibitor, Kunitz type 5	-1.12	0.043364	0.999382
Bglap2	bone gamma-carboxyglutamate protein 2	-1.12	0.036483	0.999382
Map3k6	mitogen-activated protein kinase kinase kinase 6	-1.12	0.000724	0.834085
Letm2	leucine zipper-EF-hand containing transmembrane protein 2	-1.12	0.048478	0.999382
Cnot7	CCR4-NOT transcription complex, subunit 7	-1.12	0.024491	0.999382
Il1rapl1	interleukin 1 receptor accessory protein-like 1	-1.12	0.033572	0.999382
Ppil6	peptidylprolyl isomerase (cyclophilin)-like 6	-1.12	0.047549	0.999382
Klhl11	kelch-like 11	-1.12	0.031527	0.999382
Rin3	Ras and Rab interactor 3	-1.12	0.023024	0.999382
Fam135b	family with sequence similarity 135, member B	-1.12	0.015562	0.999382
Zfyve27	zinc finger, FYVE domain containing 27	-1.12	0.038613	0.999382
Wt1	Wilms tumor 1 homolog	-1.11	0.037337	0.999382
Tmem160	transmembrane protein 160	-1.11	0.030671	0.999382
March_6	membrane-associated ring finger (C3HC4) 6	-1.11	0.016886	0.999382
Stxbp3	syntaxin binding protein 3	-1.1	0.049926	0.999382
Gtf2ird1	general transcription factor II I repeat domain-containing 1	-1.1	0.017004	0.999382
Olfr881	olfactory receptor 881	-1.1	0.024902	0.999382
Mocs3	molybdenum cofactor synthesis 3	-1.09	0.015159	0.999382
Stau1	staufen (RNA binding protein) homolog 1 (Drosophila)	-1.09	0.043662	0.999382
Tex10	testis expressed gene 10	-1.09	0.042794	0.999382
Ulk2	unc-51 like kinase 2	-1.09	0.047283	0.999382
Serinc5	serine incorporator 5	-1.09	0.02269	0.999382
Zc3h7a	zinc finger CCCH type containing 7 A	-1.09	0.032093	0.999382
Acss2	acyl-CoA synthetase short-chain family member 2	-1.08	0.036992	0.999382
Qk	quaking	-1.08	0.04436	0.999382
Baz2b	bromodomain adjacent to zinc finger domain, 2B	-1.07	0.035883	0.999382
Arl3	ADP-ribosylation factor-like 3	-1.06	0.046431	0.999382

Table S8- Genes upregulated in the Striatum of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA Str vs. TT Str)	ANOVA p-value (AA Str vs. TT Str)	FDR p-value (AA Str vs. TT Str)
Rbbp5	retinoblastoma binding protein 5	1.07	0.032942	0.999844
Fam175b	family with sequence similarity 175, member B	1.09	0.043189	0.999844
Fev	FEV (ETS oncogene family)	1.1	0.03287	0.999844
Tmod1	tropomodulin 1	1.1	0.006985	0.999844
Defa-rs10	defensin, alpha, related sequence 10	1.11	0.026761	0.999844
Ube2d2b	ubiquitin-conjugating enzyme E2D 2B	1.12	0.020075	0.999844
Olfr458	olfactory receptor 458	1.12	0.045915	0.999844
Aipl1	aryl hydrocarbon receptor-interacting protein-like 1	1.12	0.034178	0.999844
Adad1	adenosine deaminase domain containing 1 (testis specific)	1.13	0.015202	0.999844
F7	coagulation factor VII	1.13	0.018205	0.999844
Stambp	STAM binding protein	1.14	0.017066	0.999844
Zmynd8	zinc finger, MYND-type containing 8	1.14	0.03782	0.999844
Clec4f	C-type lectin domain family 4, member f	1.14	0.030637	0.999844
Fktn	fukutin	1.15	0.0409	0.999844
Myl6b	myosin, light polypeptide 6B	1.15	0.0167	0.999844
Vit	vitrin	1.16	0.033024	0.999844
Cldn34b3	claudin 34B3	1.16	0.032574	0.999844
Tmem71	transmembrane protein 71	1.16	0.035344	0.999844
Aptx	aprataxin	1.17	0.00026	0.995461
Ints7	integrator complex subunit 7	1.17	0.028237	0.999844
Kif22	kinesin family member 22	1.17	0.026221	0.999844
Mtfmt	mitochondrial methionyl-tRNA formyltransferase	1.17	0.036422	0.999844
Mbd6	methyl-CpG binding domain protein 6	1.18	0.039123	0.999844
Mapk14	mitogen-activated protein kinase 14	1.18	0.021668	0.999844
Dnah9	dynein, axonemal, heavy chain 9	1.19	0.027428	0.999844
Zfp661	zinc finger protein 661	1.19	0.040294	0.999844
Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	1.19	0.001341	0.999844
Epha6	Eph receptor A6	1.19	0.043851	0.999844
Cluap1	clusterin associated protein 1	1.19	0.047028	0.999844
Ablim3	actin binding LIM protein family, member 3	1.2	0.032827	0.999844
Sncaip	synuclein, alpha interacting protein (synphilin)	1.2	0.04428	0.999844
Mfsd7b	major facilitator superfamily domain containing 7B	1.2	0.029065	0.999844

Olfr348	olfactory receptor 348	1.2	0.033051	0.999844
Gjb5	gap junction protein, beta 5	1.2	0.011567	0.999844
Pigv	phosphatidylinositol glycan anchor biosynthesis, class V	1.2	0.031609	0.999844
Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae); microRNA 93; microRNA 25	1.2	0.027527	0.999844
Zfp212	Zinc finger protein 212	1.2	0.040473	0.999844
Hspbap1	Hspb associated protein 1	1.2	0.027092	0.999844
H1foo	H1 histone family, member O, oocyte-specific	1.21	0.016012	0.999844
Tbc1d16	TBC1 domain family, member 16	1.21	0.006411	0.999844
Ercc4	excision repair cross-complementing rodent repair deficiency, complementation group 4	1.21	0.043145	0.999844
Il18bp	interleukin 18 binding protein	1.21	0.049729	0.999844
Olfr800	olfactory receptor 800	1.21	0.022408	0.999844
Ccl7	chemokine (C-C motif) ligand 7	1.21	0.016285	0.999844
Gbp2b	guanylate binding protein 2b; guanylate binding protein 5	1.22	0.036322	0.999844
Thbd	thrombomodulin	1.22	0.012012	0.999844
Fbxl2	F-box and leucine-rich repeat protein 2	1.22	0.00288	0.999844
Zfp647	zinc finger protein 647	1.22	0.040251	0.999844
Pla2g15	phospholipase A2, group XV	1.23	0.002875	0.999844
Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	1.23	0.027159	0.999844
Lipt1	lipoyltransferase 1	1.23	0.001655	0.999844
Wwtr1	WW domain containing transcription regulator 1	1.23	0.005874	0.999844
Angptl8	angiopoietin-like 8	1.23	0.02325	0.999844
Ankrd49	ankyrin repeat domain 49	1.23	0.046555	0.999844
Dcxr	dicarbonyl L-xylulose reductase	1.23	0.007193	0.999844
Olfr1461	olfactory receptor 1461	1.23	0.030318	0.999844
Adrb1	adrenergic receptor, beta 1	1.23	0.016222	0.999844
Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	1.24	0.018374	0.999844
Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	1.24	0.00427	0.999844
Drd3	dopamine receptor D3	1.24	0.025696	0.999844
Thnsl1	threonine synthase-like 1 (bacterial)	1.24	0.015789	0.999844
Scnn1g	sodium channel, nonvoltage-gated 1 gamma	1.24	0.004225	0.999844
Egfl8	EGF-like domain 8	1.24	0.04041	0.999844
Myo9b	myosin IXb	1.25	0.015329	0.999844
Olfr1020	olfactory receptor 1020	1.25	0.045867	0.999844
Nelfcd	negative elongation factor complex member C/D, Th1l	1.25	0.02368	0.999844
Spata21	spermatogenesis associated 21	1.25	0.033601	0.999844
Zfp157	zinc finger protein 157	1.25	0.028641	0.999844

Podxl2	podocalyxin-like 2	1.25	0.024145	0.999844
Mrgprb8	MAS-related GPR, member B8	1.25	0.002513	0.999844
Chrdl2	chordin-like 2	1.25	0.014194	0.999844
Olfr145	olfactory receptor 145	1.25	0.044243	0.999844
Zfp810	zinc finger protein 810	1.25	0.016917	0.999844
Tgfb3	transforming growth factor, beta 3	1.25	0.026887	0.999844
Usp14	ubiquitin specific peptidase 14	1.25	0.00441	0.999844
Rufy2	RUN and FYVE domain-containing 2	1.26	0.044706	0.999844
Cldn6	claudin 6	1.26	0.042767	0.999844
Tmed1	transmembrane emp24 domain containing 1	1.26	0.015144	0.999844
Rnf148	ring finger protein 148	1.26	0.037788	0.999844
Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	1.26	0.045404	0.999844
Zfp511	zinc finger protein 511	1.26	0.046504	0.999844
Olfr895	olfactory receptor 895	1.26	0.007782	0.999844
Cebpe	CCAAT/enhancer binding protein (C/EBP), epsilon	1.26	0.030074	0.999844
Anxa6	annexin A6	1.27	0.044121	0.999844
Fam189a2	family with sequence similarity 189, member A2	1.27	0.046635	0.999844
Adar	adenosine deaminase, RNA-specific	1.27	0.038041	0.999844
Vmn2r65	vomeronasal 2, receptor 65	1.27	0.027842	0.999844
Mvb12a	multivesicular body subunit 12A	1.27	0.048752	0.999844
Inpp4b	inositol polyphosphate-4-phosphatase, type II	1.27	0.019141	0.999844
Cysltr1	cysteinyl leukotriene receptor 1	1.27	0.020751	0.999844
Gba2	glucosidase beta 2	1.28	0.042969	0.999844
Serpinb12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	1.28	0.03929	0.999844
Rab3gap2	RAB3 GTPase activating protein subunit 2	1.28	0.042567	0.999844
Sema4c	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	1.28	0.047549	0.999844
Cfap61	cilia and flagella associated protein 61	1.28	0.037963	0.999844
Snapc4	small nuclear RNA activating complex, polypeptide 4	1.28	0.000165	0.995461
Igsf10	immunoglobulin superfamily, member 10	1.28	0.019709	0.999844
Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	1.28	0.03764	0.999844
Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	1.29	0.047619	0.999844
Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	1.29	0.036853	0.999844
Xrra1	X-ray radiation resistance associated 1	1.29	0.039053	0.999844
Olfr533	olfactory receptor 533	1.29	0.030266	0.999844
Hbq1a	hemoglobin, theta 1A	1.29	0.019139	0.999844

Lpar3	lysophosphatidic acid receptor 3	1.3	0.039761	0.999844
Armc9	armadillo repeat containing 9	1.3	0.017536	0.999844
Acy1	aminoacylase 1	1.3	0.045437	0.999844
Gon4l	gon-4-like (C.elegans)	1.3	0.015212	0.999844
Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	1.3	0.02984	0.999844
Olfr291	olfactory receptor 291	1.3	0.042471	0.999844
Msantd4	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils	1.3	0.028524	0.999844
Baiap2l2	BAI1-associated protein 2-like 2	1.3	0.025657	0.999844
Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	1.3	0.047202	0.999844
Tnfaip8	tumor necrosis factor, alpha-induced protein 8	1.3	0.020319	0.999844
Wbscr22	Williams Beuren syndrome chromosome region 22	1.31	0.023443	0.999844
Nr2c2	nuclear receptor subfamily 2, group C, member 2	1.31	0.038283	0.999844
Rad52	RAD52 homolog (S. cerevisiae)	1.31	0.03826	0.999844
Mlkl	mixed lineage kinase domain-like	1.31	0.008612	0.999844
Ankrd54	ankyrin repeat domain 54	1.31	0.025359	0.999844
Nr3c1	nuclear receptor subfamily 3, group C, member 1	1.31	0.031124	0.999844
Tmem114	transmembrane protein 114	1.32	0.025121	0.999844
Hhat	hedgehog acyltransferase	1.32	0.009689	0.999844
Prrx2	paired related homeobox 2	1.32	0.036238	0.999844
Olfr1246	olfactory receptor 1246	1.32	0.02804	0.999844
Ripply2	ripply2 homolog (zebrafish)	1.32	0.014869	0.999844
Wbp2	WW domain binding protein 2	1.32	0.038847	0.999844
Olfr729	olfactory receptor 729	1.33	0.034198	0.999844
Fig4	FIG4 homolog (S. cerevisiae)	1.33	0.014664	0.999844
Sdpr	serum deprivation response	1.33	0.030934	0.999844
Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	1.33	0.024511	0.999844
Vmn1r130	vomeronasal 1 receptor 130; vomeronasal 1 receptor 178; vomeronasal 1 receptor 165; vomeronasal 1 receptor 155	1.33	0.029767	0.999844
Ddi1	DDI1, DNA-damage inducible 1, homolog 1 (S. cerevisiae)	1.33	0.045611	0.999844
Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	1.33	0.045403	0.999844
Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	1.33	0.014128	0.999844
Abhd12b	abhydrolase domain containing 12B	1.33	0.044482	0.999844
Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	1.34	0.026765	0.999844

Adprh	ADP-ribosylarginine hydrolase	1.34	0.012514	0.999844
Dennd1b	DENN/MADD domain containing 1B	1.34	0.049821	0.999844
Map2k5	mitogen-activated protein kinase kinase 5	1.34	0.007473	0.999844
Sharpin	SHANK-associated RH domain interacting protein	1.34	0.03007	0.999844
Cacna1e	calcium channel, voltage-dependent, R type, alpha 1E subunit	1.34	0.01669	0.999844
Mctp1	multiple C2 domains, transmembrane 1	1.34	0.017675	0.999844
Fabp12	fatty acid binding protein 12	1.34	0.044167	0.999844
Muc5b	mucin 5, subtype B, tracheobronchial	1.34	0.038286	0.999844
Adam26b	a disintegrin and metallopeptidase domain 26B	1.34	0.03425	0.999844
Nxpe4	neurexophilin and PC-esterase domain family, member 4	1.34	0.034511	0.999844
Iqch	IQ motif containing H	1.34	0.036991	0.999844
Tmed3	transmembrane emp24 domain containing 3	1.34	0.02607	0.999844
Cdc6	cell division cycle 6	1.34	0.019379	0.999844
Incenp	inner centromere protein	1.34	0.038931	0.999844
Gpr85	G protein-coupled receptor 85	1.35	0.038157	0.999844
Ssbp4	single stranded DNA binding protein 4	1.35	0.024181	0.999844
Blvrb	biliverdin reductase B (flavin reductase (NADPH))	1.35	0.032846	0.999844
Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	1.35	0.023106	0.999844
Ccdc144b	coiled-coil domain containing 144B	1.35	0.023824	0.999844
Zfp560	zinc finger protein 560	1.35	0.033891	0.999844
Usp44	ubiquitin specific peptidase 44	1.35	0.04271	0.999844
Grap	GRB2-related adaptor protein	1.35	0.00498	0.999844
Il17rd	interleukin 17 receptor D	1.35	0.002657	0.999844
Chmp3	charged multivesicular body protein 3	1.36	0.023421	0.999844
Ptgfr	prostaglandin F receptor	1.36	0.007606	0.999844
Rnf6	ring finger protein (C3H2C3 type) 6	1.36	0.035533	0.999844
Acsm2	acyl-CoA synthetase medium-chain family member 2	1.36	0.024718	0.999844
Xdh	xanthine dehydrogenase	1.36	0.013941	0.999844
Olfr419	olfactory receptor 419	1.37	0.010657	0.999844
Gapvd1	GTPase activating protein and VPS9 domains 1	1.37	0.040172	0.999844
Olfr1209	olfactory receptor 1209	1.37	0.02601	0.999844
Fam65a	family with sequence similarity 65, member A; microRNA 1966	1.37	0.031999	0.999844
Rbpms	RNA binding protein gene with multiple splicing	1.37	0.016494	0.999844
Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)	1.38	0.01811	0.999844
Pla2g2c	phospholipase A2, group IIC	1.38	0.005594	0.999844

Ccdc157	coiled-coil domain containing 157	1.38	0.03439	0.999844
Bbof1	basal body orientation factor 1	1.38	0.045819	0.999844
Ap5s1	adaptor-related protein 5 complex, sigma 1 subunit	1.39	0.007963	0.999844
Ulk3	unc-51-like kinase 3	1.39	0.035714	0.999844
Usp2	ubiquitin specific peptidase 2	1.39	0.041774	0.999844
Lpl	lipoprotein lipase	1.39	0.04946	0.999844
Ankrd42	ankyrin repeat domain 42	1.39	0.030757	0.999844
Rnf167	ring finger protein 167	1.4	0.012878	0.999844
Ackr2	atypical chemokine receptor 2	1.4	0.023652	0.999844
Hs6st2	heparan sulfate 6-O-sulfotransferase 2	1.4	0.049115	0.999844
Ifi30	interferon gamma inducible protein 30	1.4	0.022826	0.999844
Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	1.41	0.013026	0.999844
Dio1	deiodinase, iodothyronine, type I	1.41	0.018843	0.999844
Slc2a9	solute carrier family 2 (facilitated glucose transporter), member 9	1.41	0.041919	0.999844
Cdyl	chromodomain protein, Y chromosome-like	1.41	0.047131	0.999844
Rhod	ras homolog gene family, member D	1.41	0.012877	0.999844
Sirt7	sirtuin 7; microRNA 6936	1.42	0.027932	0.999844
Sgcz	sarcoglycan zeta	1.42	0.029771	0.999844
Spg11	spastic paraplegia 11	1.42	0.037346	0.999844
Hspa4l	heat shock protein 4 like	1.42	0.029248	0.999844
Tas2r137	taste receptor, type 2, member 137	1.42	0.022299	0.999844
Zkscan17	zinc finger with KRAB and SCAN domains 17	1.42	0.028708	0.999844
Stap2	signal transducing adaptor family member 2	1.42	0.004035	0.999844
Prrg4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	1.43	0.037175	0.999844
Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1.43	0.007491	0.999844
Iqca	IQ motif containing with AAA domain	1.43	0.031967	0.999844
Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	1.44	0.041058	0.999844
Tmem72	transmembrane protein 72	1.44	0.040926	0.999844
Zfp563	zinc finger protein 563	1.44	0.045379	0.999844
Vmn1r233	vomeronasal 1 receptor 233	1.44	0.013946	0.999844
Calca	calcitonin/calcitonin-related polypeptide, alpha	1.45	0.002224	0.999844
Vash2	vasohibin 2	1.45	0.015374	0.999844
Rfc3	replication factor C (activator 1) 3	1.45	0.020421	0.999844
Hamp2	hepcidin antimicrobial peptide 2	1.45	0.00359	0.999844
Ccdc189	coiled-coil domain containing 189	1.45	0.04488	0.999844
Cercam	cerebral endothelial cell adhesion molecule	1.46	0.001042	0.999844
Phactr3	phosphatase and actin regulator 3	1.46	0.032581	0.999844

Ttc30a2	tetratricopeptide repeat domain 30A2; tetratricopeptide repeat domain 30A1	1.46	0.0135	0.999844
Ascl3	achaete-scute complex homolog 3 (Drosophila)	1.46	0.015729	0.999844
Ndp	Norrie disease (pseudoglioma) (human)	1.46	0.038693	0.999844
Taar7a	trace amine-associated receptor 7A	1.46	0.044872	0.999844
Bok	BCL2-related ovarian killer	1.47	0.024975	0.999844
Uck2	uridine-cytidine kinase 2	1.47	0.048201	0.999844
Ano6	anoctamin 6	1.47	0.048806	0.999844
Cyp2c55	cytochrome P450, family 2, subfamily c, polypeptide 55	1.47	0.01781	0.999844
Hspb1	heat shock protein 1	1.48	0.01017	0.999844
Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	1.48	0.030294	0.999844
L3mbtl1	l(3)mbt-like (Drosophila)	1.48	0.024605	0.999844
Olfr1039	olfactory receptor 1039	1.48	0.030311	0.999844
Enho	energy homeostasis associated	1.48	0.013119	0.999844
Eqtn	equatorin, sperm acrosome associated	1.48	0.040191	0.999844
Il13ra2	interleukin 13 receptor, alpha 2	1.48	0.012296	0.999844
Mmp14	matrix metallopeptidase 14 (membrane-inserted)	1.48	0.019233	0.999844
Olfr127	olfactory receptor 127	1.49	0.001149	0.999844
Asb11	ankyrin repeat and SOCS box-containing 11	1.49	0.013224	0.999844
Olfr60	olfactory receptor 60	1.49	0.034789	0.999844
Chaf1b	chromatin assembly factor 1, subunit B (p60)	1.49	0.033647	0.999844
Dnah11	dynein, axonemal, heavy chain 11	1.5	0.00608	0.999844
Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	1.5	0.013788	0.999844
Gphb5	glycoprotein hormone beta 5	1.5	0.045231	0.999844
Cyp2j13	cytochrome P450, family 2, subfamily j, polypeptide 13	1.5	0.047814	0.999844
Zc2hc1c	zinc finger, C2HC-type containing 1C	1.5	0.043842	0.999844
Zbtb3	zinc finger and BTB domain containing 3	1.5	0.04011	0.999844
Sgms2	sphingomyelin synthase 2	1.51	0.024533	0.999844
Dpp7	dipeptidylpeptidase 7	1.51	0.025643	0.999844
Mak	male germ cell-associated kinase	1.52	0.047341	0.999844
Kif27	kinesin family member 27; microRNA 6369	1.52	0.049078	0.999844
Olfr651	olfactory receptor 651	1.52	0.010045	0.999844
Pgap3	post-GPI attachment to proteins 3	1.53	0.006769	0.999844
F13b	coagulation factor XIII, beta subunit	1.53	0.039231	0.999844
Gml	glycosylphosphatidylinositol anchored molecule like	1.53	0.041023	0.999844
Hic2	hypermethylated in cancer 2	1.53	0.046653	0.999844
Mcmdc2	minichromosome maintenance domain containing 2	1.54	0.018975	0.999844
Metap1	methionyl aminopeptidase 1	1.54	0.032645	0.999844

Cramp1l	Crm, cramped-like (Drosophila)	1.54	0.048907	0.999844
Adgrf2	adhesion G protein-coupled receptor F2	1.54	0.000385	0.995461
Gemin2	gem (nuclear organelle) associated protein 2	1.55	0.04113	0.999844
Il9	interleukin 9	1.55	0.035714	0.999844
Brwd3	bromodomain and WD repeat domain containing 3	1.56	0.032265	0.999844
Asic3	acid-sensing (proton-gated) ion channel 3	1.56	0.034888	0.999844
Zfp941	zinc finger protein 941	1.56	0.00641	0.999844
Ngly1	N-glycanase 1	1.56	0.034583	0.999844
Tsku	tsukushi, small leucine rich proteoglycan	1.57	0.031072	0.999844
Glb1l2	galactosidase, beta 1-like 2	1.57	0.027659	0.999844
Aff2	AF4/FMR2 family, member 2	1.57	0.036643	0.999844
Adck5	aarF domain containing kinase 5	1.57	0.032281	0.999844
Neurl1b	neuralized E3 ubiquitin protein ligase 1B	1.57	0.038875	0.999844
Efcab1	EF hand calcium binding domain 1	1.58	0.012681	0.999844
Tm4sf1	transmembrane 4 superfamily member 1	1.58	0.038307	0.999844
Oxgr1	oxoglutarate (alpha-ketoglutarate) receptor 1	1.58	0.002067	0.999844
Lrriq1	leucine-rich repeats and IQ motif containing 1	1.58	0.023476	0.999844
Thap2	THAP domain containing, apoptosis associated protein 2	1.59	0.00043	0.995461
Prl2b1	prolactin family 2, subfamily b, member 1	1.59	0.010374	0.999844
Slc29a4	solute carrier family 29 (nucleoside transporters), member 4	1.6	0.038602	0.999844
Mapkbp1	mitogen-activated protein kinase binding protein 1	1.6	0.038926	0.999844
Ccdc60	coiled-coil domain containing 60	1.6	0.033908	0.999844
Pnmal1	PNMA-like 1	1.6	0.038931	0.999844
Abhd14b	abhydrolase domain containing 14b	1.61	0.032313	0.999844
Scrib	scribbled homolog (Drosophila)	1.62	0.025306	0.999844
Mettl1	methyltransferase like 1	1.62	0.002538	0.999844
Scnn1a	sodium channel, nonvoltage-gated 1 alpha	1.62	0.01814	0.999844
Mettl8	methyltransferase like 8	1.62	0.01465	0.999844
Ephb2	Eph receptor B2	1.62	0.04295	0.999844
Cdk20	cyclin-dependent kinase 20	1.64	0.013639	0.999844
Ido1	indoleamine 2,3-dioxygenase 1	1.66	0.035729	0.999844
Prmt6	protein arginine N-methyltransferase 6	1.66	0.034744	0.999844
Trim68	tripartite motif-containing 68	1.67	0.046315	0.999844
Vgll3	vestigial like 3 (Drosophila)	1.67	0.048696	0.999844
Zfp831	zinc finger protein 831	1.68	0.002258	0.999844
Ulk4	unc-51-like kinase 4	1.68	0.04547	0.999844
Muc3a	mucin 3A, cell surface associated [Source:MGI Symbol;Acc:MGI:3588263]; RIKEN cDNA A630081J09 gene	1.69	0.027882	0.999844
Capsl	calcyphosine-like	1.7	0.024805	0.999844

Rab11fip1	RAB11 family interacting protein 1 (class I)	1.71	0.009326	0.999844
Cxcl13	chemokine (C-X-C motif) ligand 13	1.72	0.017979	0.999844
Bzrap1	benzodiazepine receptor associated protein 1	1.76	0.00037	0.995461
Tceanc2	transcription elongation factor A (SII) N-terminal and central domain containing 2	1.77	0.041668	0.999844
Nek10	NIMA (never in mitosis gene a)- related kinase 10	1.78	0.002918	0.999844
Pcdhb8	protocadherin beta 8	1.78	0.046011	0.999844
Dlx2	distal-less homeobox 2	1.79	0.013249	0.999844
Cfap69	cilia and flagella associated protein 69	1.81	0.020964	0.999844
Stra6	stimulated by retinoic acid gene 6	1.83	0.025498	0.999844
Ppp1r32	protein phosphatase 1, regulatory subunit 32	1.83	0.02278	0.999844
Clic6	chloride intracellular channel 6	1.83	0.027654	0.999844
Agbl2	ATP/GTP binding protein-like 2	1.84	0.033127	0.999844
Igfbp2	insulin-like growth factor binding protein 2	1.84	0.043121	0.999844
Tfrc	transferrin receptor	1.86	0.027247	0.999844
Phactr2	phosphatase and actin regulator 2	1.87	0.01784	0.999844
Sostdc1	sclerostin domain containing 1	1.91	0.044514	0.999844
Dnah12	dynein, axonemal, heavy chain 12	1.91	0.003507	0.999844
Fam221b	family with sequence similarity 221, member B	1.93	0.005176	0.999844
H2-DMb1	histocompatibility 2, class II, locus Mb1	1.95	0.00192	0.999844
Fam216b	family with sequence similarity 216, member B	1.96	0.039715	0.999844
Pltp	phospholipid transfer protein	1.98	0.022416	0.999844
Aqp1	aquaporin 1	1.98	0.032662	0.999844
Pnma3	paraneoplastic antigen MA3	2.02	0.030735	0.999844
Slc24a5	solute carrier family 24, member 5	2.1	0.006324	0.999844
Prelp	proline arginine-rich end leucine-rich repeat	2.2	0.020632	0.999844
Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	2.28	0.01243	0.999844
Igf2	insulin-like growth factor 2	2.31	0.049152	0.999844
Slc14a2	solute carrier family 14 (urea transporter), member 2	2.34	0.001727	0.999844
Drc7	dynein regulatory complex subunit 7	2.39	0.003817	0.999844
Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	2.76	0.009565	0.999844
Folr1	folate receptor 1 (adult)	3.75	0.034497	0.999844
Kl	klotho	4.06	0.017733	0.999844
Kcnj13	potassium inwardly-rectifying channel, subfamily J, member 13	4.86	0.013447	0.999844
Cd59a	CD59a antigen	4.87	0.0051	0.999844
Lbp	lipopolysaccharide binding protein	5.75	0.004043	0.999844

Table S9- Genes downregulated in the Striatum of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA Str vs. TT Str)	ANOVA p-value (AA Str vs. TT Str)	FDR p-value (AA Str vs. TT Str)
Mup2	major urinary protein 2; major urinary protein 1	-44.05	0.00089	0.999844
Mup1	major urinary protein 1	-40.95	0.000549	0.999844
Mup7	major urinary protein 7; major urinary protein 1	-33.43	0.001898	0.999844
Mup2	major urinary protein 2; major urinary protein 10; major urinary protein 11; major urinary protein 1	-32.66	0.001305	0.999844
Mup12	major urinary protein 12	-32.18	0.001691	0.999844
Mup13	major urinary protein 13; major urinary protein 18; major urinary protein 16; major urinary protein 14; major urinary protein 17; major urinary protein 2; major urinary protein 15	-31.45	0.00141	0.999844
Mup19	major urinary protein 19	-24.18	0.001914	0.999844
Mup8	major urinary protein 8; major urinary protein 9; major urinary protein 2; major urinary protein 1	-16.82	0.002334	0.999844
Alb	albumin	-16.22	0.007903	0.999844
Mup3	major urinary protein 3	-3.4	0.02485	0.999844
Mid1	midline 1	-3.33	0.004704	0.999844
Mid1	midline 1	-3.33	0.004704	0.999844
Serpina1c	serine (or cysteine) peptidase inhibitor, clade A, member 1C	-2.99	0.039767	0.999844
Mid1	midline 1	-2.63	0.010961	0.999844
Fga	fibrinogen alpha chain	-2.51	0.014157	0.999844
Mup21	major urinary protein 21	-2.46	0.020502	0.999844
Hp	haptoglobin	-2.39	0.047759	0.999844
Btnl5-ps	butyrophilin-like 5, pseudogene	-2.36	0.02005	0.999844
Fgb	fibrinogen beta chain	-2.29	0.027021	0.999844
Olfr806	olfactory receptor 806	-2.28	0.012985	0.999844
Mrc1	mannose receptor, C type 1	-2.23	0.023339	0.999844
Olfr171	olfactory receptor 171	-2.21	0.017277	0.999844
Nts	neurotensin	-2.11	0.042359	0.999844
Ces1c	carboxylesterase 1C	-2.08	0.029178	0.999844
Serpina1b	serine (or cysteine) preptidase inhibitor, clade A, member 1B	-2.05	0.04973	0.999844

Serpina3m	serine (or cysteine) peptidase inhibitor, clade A, member 3M; serine (or cysteine) peptidase inhibitor, clade A, member 3K	-2.04	0.005807	0.999844
Sel1l2	sel-1 suppressor of lin-12-like 2 (C. elegans)	-2.02	0.036348	0.999844
Vmn1r7	vomeronasal 1 receptor 7	-2.01	0.000117	0.995461
Olfr878	olfactory receptor 878	-2	0.00184	0.999844
Vmn1r112	vomeronasal 1 receptor 112	-1.98	0.045961	0.999844
Mis18bp1	MIS18 binding protein 1	-1.93	0.017065	0.999844
Akr1d1	aldo-keto reductase family 1, member D1	-1.91	0.033895	0.999844
Sly	Sycp3 like Y-linked	-1.89	0.02236	0.999844
Ly6g5c	lymphocyte antigen 6 complex, locus G5C	-1.89	0.024857	0.999844
Tcl1b4	T cell leukemia/lymphoma 1B, 4	-1.88	0.00496	0.999844
Olfr120	olfactory receptor 120	-1.88	0.040882	0.999844
Adam5	a disintegrin and metallopeptidase domain 5	-1.87	0.030141	0.999844
Il10	interleukin 10	-1.86	0.036288	0.999844
Cpa3	carboxypeptidase A3, mast cell	-1.86	0.016961	0.999844
Chil4	chitinase-like 4	-1.86	0.030993	0.999844
Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	-1.85	0.006571	0.999844
Zc3h8	zinc finger CCCH type containing 8	-1.84	0.016866	0.999844
Vmn2r84	vomeronasal 2, receptor 84	-1.82	0.039485	0.999844
Cyp2b19	cytochrome P450, family 2, subfamily b, polypeptide 19	-1.82	0.033285	0.999844
Tinag	tubulointerstitial nephritis antigen	-1.81	0.03657	0.999844
Vmn1r29	vomeronasal 1 receptor 29	-1.78	0.048289	0.999844
Tmed11	transmembrane emp24 protein transport domain containing	-1.77	0.031571	0.999844
Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 6	-1.76	0.016156	0.999844
Daw1	dynein assembly factor with WDR repeat domains 1	-1.72	0.014625	0.999844
Olfr1262	olfactory receptor 1262	-1.69	0.00101	0.999844
Ly6g6c	lymphocyte antigen 6 complex, locus G6C	-1.69	0.003301	0.999844
Insrr	insulin receptor-related receptor	-1.67	0.041692	0.999844
Olfr898	olfactory receptor 898	-1.66	0.00376	0.999844
Vsig2	V-set and immunoglobulin domain containing 2	-1.66	0.049789	0.999844
Myl1	myosin, light polypeptide 1	-1.65	0.021762	0.999844

Glyat	glycine-N-acyltransferase	-1.64	0.034816	0.999844
Olfr923	olfactory receptor 923	-1.63	0.034449	0.999844
Cr2	complement receptor 2	-1.61	0.012564	0.999844
Fam114a2	family with sequence similarity 114, member A2	-1.61	0.048775	0.999844
Neu4	sialidase 4	-1.6	0.044102	0.999844
Hsd3b2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	-1.6	0.020407	0.999844
Apoh	apolipoprotein H	-1.6	0.043417	0.999844
Vmn2r9	vomeronasal 2, receptor 9	-1.59	0.031071	0.999844
Olfr1098	olfactory receptor 1098	-1.58	0.026665	0.999844
Nmur2	neuromedin U receptor 2	-1.58	0.033744	0.999844
Prkcd	protein kinase C, delta	-1.58	0.048932	0.999844
Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	-1.57	0.000194	0.995461
Ikbke	inhibitor of kappaB kinase epsilon	-1.57	0.001018	0.999844
Olfr285	olfactory receptor 285; olfactory receptor 257	-1.57	0.04608	0.999844
Vmn1r127	vomeronasal 1 receptor 127	-1.56	0.031196	0.999844
Olfr1340	olfactory receptor 1340	-1.55	0.008616	0.999844
Gk2	glycerol kinase 2	-1.55	0.038899	0.999844
Rtl1	retrotransposon-like 1; microRNA 3071	-1.55	0.007906	0.999844
Nmu	neuromedin U	-1.54	0.018835	0.999844
Klhl42	kelch-like 42	-1.54	0.00029	0.995461
Btf3	basic transcription factor 3	-1.54	0.030494	0.999844
Itfg2	integrin alpha FG-GAP repeat containing 2	-1.53	0.01927	0.999844
Unc45b	unc-45 homolog B (C. elegans)	-1.53	0.046683	0.999844
Ahrr	aryl-hydrocarbon receptor repressor	-1.53	0.021427	0.999844
Zfp345	zinc finger protein 345	-1.52	0.004599	0.999844
Tmem27	transmembrane protein 27	-1.52	0.010603	0.999844
Ly6i	lymphocyte antigen 6 complex, locus I	-1.52	0.029745	0.999844
Wfdc21	WAP four-disulfide core domain 21	-1.51	0.033418	0.999844
Kdm6b	KDM1 lysine (K)-specific demethylase 6B	-1.51	0.001927	0.999844
Atp13a3	ATPase type 13A3	-1.51	0.03165	0.999844
Esp38	exocrine gland secreted peptide 38	-1.51	0.010932	0.999844
Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	-1.51	0.018675	0.999844
Rgs6	regulator of G-protein signaling 6	-1.5	0.009225	0.999844
Dnajc21	DnaJ (Hsp40) homolog, subfamily C, member 21	-1.5	0.043173	0.999844

Serpinc1	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	-1.5	0.028999	0.999844
Olfr353	olfactory receptor 353	-1.5	0.043372	0.999844
4930572O03Rik	spermatogenesis associated glutamate (E)-rich protein pseudogene	-1.5	0.040058	0.999844
Hyal6	hyaluronoglucosaminidase 6	-1.5	0.011252	0.999844
Klkb1	kallikrein B, plasma 1; cytochrome P450, family 4, subfamily v, polypeptide 3	-1.5	0.017699	0.999844
Nt5c1b	5-nucleotidase, cytosolic IB; 5'-nucleotidase, cytosolic IB	-1.5	0.032456	0.999844
Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	-1.49	0.015801	0.999844
Olfr715	olfactory receptor 715	-1.49	0.016066	0.999844
Neu2	neuraminidase 2	-1.49	0.035905	0.999844
S100a8	S100 calcium binding protein A8 (calgranulin A)	-1.49	0.01161	0.999844
Speer4f2	spermatogenesis associated glutamate (E)-rich protein 4f2 [Source:MGI Symbol;Acc:MGI:3781672]; Novel spermatogenesis associated glutamate (E)-rich protein; predicted gene 3495	-1.49	0.036568	0.999844
Cyp2e1	cytochrome P450, family 2, subfamily e, polypeptide 1	-1.49	0.03093	0.999844
Slc22a28	solute carrier family 22, member 28	-1.49	0.019906	0.999844
Wdr27	WD repeat domain 27	-1.48	0.024631	0.999844
Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	-1.47	0.020115	0.999844
Col23a1	collagen, type XXIII, alpha 1	-1.47	0.017083	0.999844
Olfr1219	olfactory receptor 1219	-1.47	0.030281	0.999844
Olfr1154	olfactory receptor 1154	-1.47	0.043125	0.999844
Mgst1	microsomal glutathione S-transferase 1	-1.47	0.013165	0.999844
Rassf8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	-1.47	0.011076	0.999844
Scgb1b20	secretoglobin, family 1B, member 20	-1.47	0.018828	0.999844
Mettl18	methyltransferase like 18	-1.46	0.040925	0.999844
Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	-1.46	0.047552	0.999844
Stra6l	STRA6-like	-1.46	0.037435	0.999844

Abcg3	ATP-binding cassette, sub-family G (WHITE), member 3	-1.46	0.023527	0.999844
Mtap7d3	MAP7 domain containing 3	-1.46	0.027878	0.999844
Phka1	phosphorylase kinase alpha 1	-1.46	0.046998	0.999844
Fbxw17	F-box and WD-40 domain protein 17	-1.46	0.047933	0.999844
Rap2b	RAP2B, member of RAS oncogene family	-1.45	0.036998	0.999844
P2ry14	purinergic receptor P2Y, G-protein coupled, 14; RIKEN cDNA F630111L10 gene	-1.44	0.008622	0.999844
Vmn2r59	vomeronasal 2, receptor 59	-1.44	0.02476	0.999844
Mettl7b	methyltransferase like 7B	-1.44	0.010373	0.999844
Irf1	interferon regulatory factor 1	-1.43	0.042995	0.999844
Scnn1b	sodium channel, nonvoltage-gated 1 beta	-1.43	0.023004	0.999844
Crb3	crumbs family member 3	-1.43	0.038927	0.999844
Aox2	aldehyde oxidase 2	-1.43	0.043224	0.999844
Olfr243	olfactory receptor 243	-1.43	0.002234	0.999844
Acsm1	acyl-CoA synthetase medium-chain family member 1	-1.43	0.028452	0.999844
Olfr66	olfactory receptor 66	-1.43	0.015927	0.999844
Pycrl	pyrroline-5-carboxylate reductase-like	-1.42	0.037597	0.999844
Ivl	involucrin	-1.42	0.013185	0.999844
Samt1	spermatogenesis associated multipass transmembrane protein 1; predicted gene 15140	-1.42	0.038931	0.999844
Spdl1	spindle apparatus coiled-coil protein 1	-1.42	0.010784	0.999844
Cacng1	calcium channel, voltage-dependent, gamma subunit 1	-1.42	0.031974	0.999844
Lect1	leukocyte cell derived chemotaxin 1	-1.42	0.01042	0.999844
Ifna6	interferon alpha 6; interferon alpha B	-1.41	0.038886	0.999844
Tmem125	transmembrane protein 125	-1.41	0.016088	0.999844
Pcdh9	protocadherin 9	-1.41	0.02507	0.999844
Sptlc3	serine palmitoyltransferase, long chain base subunit 3	-1.4	0.034091	0.999844
Corin	corin	-1.4	0.025666	0.999844
Mcm2	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	-1.4	0.007643	0.999844
Olfr531	olfactory receptor 531	-1.4	0.04464	0.999844
Mettl22	methyltransferase like 22	-1.4	0.025221	0.999844
Thrsp	thyroid hormone responsive	-1.39	0.014537	0.999844
Slc23a3	solute carrier family 23 (nucleobase transporters), member 3	-1.39	0.049282	0.999844
Vmn2r5	vomeronasal 2, receptor 5	-1.39	0.028146	0.999844

Defb50	defensin beta 50	-1.39	0.014063	0.999844
Kcnh8	potassium voltage-gated channel, subfamily H (eag-related), member 8	-1.39	0.034233	0.999844
Trim36	tripartite motif-containing 36	-1.39	0.031759	0.999844
Ccne1	cyclin E1	-1.38	0.026643	0.999844
Dexi	dexamethasone-induced transcript	-1.38	0.007421	0.999844
Bloc1s6	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin	-1.38	0.043804	0.999844
Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	-1.38	0.028173	0.999844
Ruvbl2	RuvB-like protein 2	-1.38	0.028123	0.999844
Cks1brt	CDC28 protein kinase 1b, retrogene	-1.38	0.045983	0.999844
Ighmbp2	immunoglobulin mu binding protein 2	-1.38	0.014758	0.999844
Tuba8	tubulin, alpha 8	-1.37	0.019143	0.999844
Vmn1r157	vomeronasal 1 receptor 157	-1.37	0.017741	0.999844
Kdf1	keratinocyte differentiation factor 1	-1.37	0.013442	0.999844
Olfr2	olfactory receptor 2	-1.37	0.036594	0.999844
Acvr2b	activin receptor IIB	-1.37	0.039473	0.999844
Pyurf	Pigy upstream reading frame	-1.36	0.018625	0.999844
Glp2r	glucagon-like peptide 2 receptor	-1.36	0.041276	0.999844
Ceacam13	carcinoembryonic antigen-related cell adhesion molecule 13	-1.36	0.033784	0.999844
Pus1	pseudouridine synthase 1	-1.36	0.036895	0.999844
Itpripl2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	-1.36	0.007371	0.999844
Osm	oncostatin M	-1.36	0.027682	0.999844
Itga2	integrin alpha 2	-1.36	0.028441	0.999844
Smim3	small integral membrane protein 3	-1.36	0.01961	0.999844
Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	-1.35	0.037627	0.999844
Efcab8	EF-hand calcium binding domain 8	-1.35	0.009387	0.999844
Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.35	0.037417	0.999844
Abhd1	abhydrolase domain containing 1	-1.35	0.024943	0.999844
Hand2	heart and neural crest derivatives expressed transcript 2	-1.35	0.028214	0.999844
Mybbp1a	MYB binding protein (P160) 1a	-1.35	0.017299	0.999844
Slc22a27	solute carrier family 22, member 27	-1.35	0.011636	0.999844
Qser1	glutamine and serine rich 1	-1.34	0.00633	0.999844
Olfr477	olfactory receptor 477	-1.34	0.008934	0.999844

Obox8	oocyte specific homeobox 8 [Source:MGI Symbol;Acc:MGI:3645855]; PREDICTED: predicted gene 5585 (Gm5585), mRNA.	-1.34	0.023151	0.999844
Cyp2c67	cytochrome P450, family 2, subfamily c, polypeptide 67	-1.34	0.003203	0.999844
Shisa3	shisa family member 3	-1.33	0.002222	0.999844
Cfl2	cofilin 2, muscle	-1.33	0.004671	0.999844
H3f3a	H3 histone, family 3A	-1.33	0.010917	0.999844
Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	-1.33	0.021037	0.999844
Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	-1.33	0.040508	0.999844
Vpreb1	pre-B lymphocyte gene 1	-1.33	0.03425	0.999844
Gif	gastric intrinsic factor	-1.33	0.020989	0.999844
Glipr1	GLI pathogenesis-related 1 (glioma)	-1.32	0.031554	0.999844
Comp	cartilage oligomeric matrix protein	-1.32	0.003803	0.999844
Csprs	component of Sp100-rs	-1.32	0.035138	0.999844
Olfr1084	olfactory receptor 1084	-1.32	0.010107	0.999844
Ptgfrn	prostaglandin F2 receptor negative regulator	-1.32	0.031622	0.999844
Trmo	tRNA methyltransferase O	-1.32	0.044247	0.999844
Zfp513	zinc finger protein 513	-1.31	0.034166	0.999844
Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-1.31	0.021216	0.999844
Chit1	chitinase 1 (chitotriosidase)	-1.31	0.016582	0.999844
Lrat	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)	-1.31	0.000448	0.995461
Ifna5	interferon alpha 5	-1.31	0.002671	0.999844
Hrc	histidine rich calcium binding protein	-1.31	0.03435	0.999844
Olfr370	olfactory receptor 370	-1.31	0.011846	0.999844
Cdt1	chromatin licensing and DNA replication factor 1	-1.31	0.044095	0.999844
Hmg20b	high mobility group 20B	-1.31	0.031518	0.999844
Slc47a1	solute carrier family 47, member 1	-1.31	0.025704	0.999844
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	-1.3	0.010836	0.999844
Cyp24a1	cytochrome P450, family 24, subfamily a, polypeptide 1	-1.3	0.025407	0.999844
Dnaaf2	dynein, axonemal assembly factor 2	-1.3	0.004649	0.999844
Scd1	stearoyl-Coenzyme A desaturase 1	-1.3	0.048153	0.999844

Olfr316	olfactory receptor 316	-1.29	0.007793	0.999844
Ptges	prostaglandin E synthase	-1.29	0.031228	0.999844
Olfm5	olfactomedin 5	-1.29	0.014143	0.999844
Olfr146	olfactory receptor 146	-1.29	0.04396	0.999844
Iqcf4	IQ motif containing F4	-1.29	0.03582	0.999844
Scn10a	sodium channel, voltage-gated, type X, alpha	-1.29	0.018212	0.999844
Olfr384	olfactory receptor 384	-1.29	0.019689	0.999844
Cdca2	cell division cycle associated 2	-1.29	0.038864	0.999844
Btnl4	butyrophilin-like 4	-1.29	0.021929	0.999844
Olfr94	olfactory receptor 94	-1.29	0.004863	0.999844
Grhl3	grainyhead-like 3 (Drosophila)	-1.28	0.049572	0.999844
Tubal3	tubulin, alpha-like 3	-1.28	0.027154	0.999844
Mrpl15	mitochondrial ribosomal protein L15	-1.28	0.034866	0.999844
B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	-1.28	0.03214	0.999844
Pzp	pregnancy zone protein	-1.28	0.046005	0.999844
Pth1r	parathyroid hormone 1 receptor	-1.28	0.018372	0.999844
Pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101	-1.28	0.016022	0.999844
Gabra6	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 6	-1.28	0.017024	0.999844
Tmem132c	transmembrane protein 132C	-1.27	0.029298	0.999844
Med24	mediator complex subunit 24	-1.27	0.004136	0.999844
Nifk	nucleolar protein interacting with the FHA domain of MKI67	-1.27	0.036439	0.999844
Mrgprb1	MAS-related GPR, member B1	-1.27	0.005595	0.999844
Pdgfrl	platelet-derived growth factor receptor-like	-1.27	0.042603	0.999844
Col12a1	collagen, type XII, alpha 1	-1.27	0.016195	0.999844
Gsg1l2	GSG1-like 2	-1.27	0.025398	0.999844
Olfr329-ps	olfactory receptor 329, pseudogene; olfactory receptor 330	-1.27	0.022588	0.999844
Olfr1361	olfactory receptor 1361	-1.27	0.006414	0.999844
Ubxn7	UBX domain protein 7	-1.26	0.016859	0.999844
Zc3h18	zinc finger CCCH-type containing 18	-1.26	0.044256	0.999844
Pds5a	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	-1.26	0.003786	0.999844
Gbp11	guanylate binding protein 11	-1.26	0.03175	0.999844
Mmp10	matrix metallopeptidase 10	-1.26	0.049015	0.999844
9030619P08Rik	lymphocyte antigen 6 complex pseudogene	-1.26	0.006798	0.999844
Cbs	cystathionine beta-synthase	-1.26	0.047488	0.999844
Tmem200c	transmembrane protein 200C	-1.25	0.041433	0.999844
Olfr1380	olfactory receptor 1380	-1.25	0.049677	0.999844

Trip12	thyroid hormone receptor interactor 12	-1.25	0.039536	0.999844
Gmpr2	guanosine monophosphate reductase 2	-1.25	0.02418	0.999844
Vwa5b1	von Willebrand factor A domain containing 5B1	-1.24	0.036081	0.999844
Myo18b	myosin XVIIIb	-1.24	0.007034	0.999844
Tirap	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	-1.24	0.002399	0.999844
Lcn3	lipocalin 3	-1.23	0.032477	0.999844
Rnaseh1	ribonuclease H1	-1.23	0.021158	0.999844
Tacc1	transforming, acidic coiled-coil containing protein 1; microRNA 8108	-1.23	0.030874	0.999844
Agps	alkylglycerone phosphate synthase	-1.23	0.031824	0.999844
Col15a1	collagen, type XV, alpha 1	-1.23	0.036757	0.999844
Kmt2c	lysine (K)-specific methyltransferase 2C	-1.23	0.017278	0.999844
Mvp	major vault protein	-1.23	0.005897	0.999844
Bcl2l10	Bcl2-like 10	-1.23	0.037026	0.999844
Rdh19	retinol dehydrogenase 19	-1.23	0.024039	0.999844
Rsad1	radical S-adenosyl methionine domain containing 1	-1.23	0.019983	0.999844
Tpsg1	tryptase gamma 1	-1.23	0.017517	0.999844
Sv2a	synaptic vesicle glycoprotein 2 a	-1.22	0.02826	0.999844
Esp4	exocrine gland secreted peptide 4	-1.22	0.005611	0.999844
Mcidas	multiciliate differentiation and DNA synthesis associated cell cycle protein	-1.22	0.029102	0.999844
Ccnk	cyclin K	-1.22	0.030427	0.999844
Galnt5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5	-1.22	0.005501	0.999844
Olfr1214	olfactory receptor 1214	-1.22	0.02006	0.999844
Olfr628	olfactory receptor 628	-1.22	0.022869	0.999844
Mia	melanoma inhibitory activity	-1.22	0.047553	0.999844
Nanos3	nanos homolog 3 (Drosophila)	-1.22	0.004742	0.999844
Cnot1	CCR4-NOT transcription complex, subunit 1	-1.22	0.035583	0.999844
Uba7	ubiquitin-like modifier activating enzyme 7	-1.22	0.029582	0.999844
Olfr803	olfactory receptor 803	-1.22	0.021059	0.999844
Mbtd1	mbt domain containing 1	-1.22	0.039053	0.999844
Abt1	activator of basal transcription 1	-1.22	0.000097	0.995461
Sftpd	surfactant associated protein D	-1.22	0.033396	0.999844
Igll1	immunoglobulin lambda-like polypeptide 1	-1.22	0.031025	0.999844

Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	-1.21	0.013915	0.999844
Zfp410	zinc finger protein 410	-1.21	0.034046	0.999844
Pdcd2l	programmed cell death 2-like	-1.21	0.017428	0.999844
C2cd4d	C2 calcium-dependent domain containing 4D	-1.21	0.028997	0.999844
Tmem217	transmembrane protein 217	-1.21	0.047044	0.999844
Wasf3	WAS protein family, member 3	-1.21	0.034793	0.999844
Dlg4	discs, large homolog 4 (Drosophila)	-1.21	0.012915	0.999844
Bend6	BEN domain containing 6	-1.2	0.041109	0.999844
Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	-1.2	0.001831	0.999844
Rln3	relaxin 3	-1.2	0.049674	0.999844
Rrbp1	ribosome binding protein 1	-1.2	0.041086	0.999844
Sfi1	Sfi1 homolog, spindle assembly associated (yeast)	-1.2	0.01512	0.999844
Loxl2	lysyl oxidase-like 2; microRNA 6950	-1.2	0.012842	0.999844
Brd2	bromodomain containing 2	-1.2	0.045962	0.999844
Fzd1	frizzled homolog 1 (Drosophila)	-1.19	0.01673	0.999844
Rimbp2	RIMS binding protein 2	-1.19	0.002894	0.999844
Ghdc	GH3 domain containing	-1.19	0.048687	0.999844
Zgpat	zinc finger, CCCH-type with G patch domain; Lck interacting transmembrane adaptor 1	-1.19	0.02361	0.999844
Muc1	mucin 1, transmembrane	-1.19	0.025378	0.999844
Mos	Moloney sarcoma oncogene	-1.19	0.03036	0.999844
Kmt2e	lysine (K)-specific methyltransferase 2E	-1.19	0.004746	0.999844
Cct8l1	chaperonin containing TCP1, subunit 8 (theta)-like 1	-1.19	0.032073	0.999844
Apoc3	apolipoprotein C-III	-1.19	0.048538	0.999844
Sprr2a2	small proline-rich protein 2A2; small proline-rich protein 2A1	-1.18	0.011388	0.999844
Olfr381	olfactory receptor 381	-1.18	0.003998	0.999844
Trh	thyrotropin releasing hormone	-1.17	0.04254	0.999844
Trim44	tripartite motif-containing 44	-1.17	0.005159	0.999844
Cadm4	cell adhesion molecule 4	-1.17	0.016654	0.999844
Slco2a1	solute carrier organic anion transporter family, member 2a1	-1.17	0.016368	0.999844
Fbxl14	F-box and leucine-rich repeat protein 14	-1.17	0.042307	0.999844
Socs5	suppressor of cytokine signaling 5	-1.17	0.032504	0.999844
Pofut1	protein O-fucosyltransferase 1	-1.17	0.027735	0.999844
Rnf19b	ring finger protein 19B	-1.17	0.024144	0.999844
H2bfm	H2B histone family, member M	-1.17	0.038469	0.999844

Pou4f3	POU domain, class 4, transcription factor 3	-1.17	0.03481	0.999844
Trp53rkb	transformation related protein 53 regulating kinase B	-1.16	0.011879	0.999844
Fcna	ficolin A	-1.16	0.043509	0.999844
Trp53rka	transformation related protein 53 regulating kinase A	-1.16	0.025612	0.999844
Banp	BTG3 associated nuclear protein	-1.16	0.00506	0.999844
Bpifc	BPI fold containing family C	-1.15	0.045575	0.999844
Adamts14	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 14	-1.15	0.045821	0.999844
Nova1	neuro-oncological ventral antigen 1	-1.15	0.039407	0.999844
Dennd1c	DENN/MADD domain containing 1C	-1.15	0.032432	0.999844
Hist1h4j	histone cluster 1, H4j; histone cluster 1, H4m	-1.14	0.013843	0.999844
Olfr1331	olfactory receptor 1331	-1.13	0.047844	0.999844
Rragc	Ras-related GTP binding C	-1.13	0.02586	0.999844
Olfr138	olfactory receptor 138	-1.13	0.035203	0.999844
Arntl	aryl hydrocarbon receptor nuclear translocator-like	-1.12	0.049096	0.999844
Klhl25	kelch-like 25	-1.12	0.046702	0.999844
Sync	syncoilin	-1.1	0.041845	0.999844
Mkln1	muskelin 1, intracellular mediator containing kelch motifs	-1.1	0.000683	0.999844
Gzmn	granzyme N	-1.09	0.039973	0.999844
Atp9b	ATPase, class II, type 9B	-1.09	0.001135	0.999844
Clasp2	CLIP associating protein 2	-1.07	0.027809	0.999844
Wif1	Wnt inhibitory factor 1	-1.07	0.046737	0.999844

Table S10- Genes upregulated in the Prefrontal cortex of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	Description	Fold Change (linear) (AA Pre Frontal Cx vs. TT Pre Frontal Cx)	ANOVA p-value (AA Pre Frontal Cx vs. TT Pre Frontal Cx)	FDR p-value (AA Pre Frontal Cx vs. TT Pre Frontal Cx)
Qrich2	glutamine rich 2	1.05	0.036258	0.999919
Ints4	integrator complex subunit 4	1.09	0.043187	0.999919
Gopc	golgi associated PDZ and coiled-coil motif containing	1.1	0.032092	0.999919
Slc35e1	solute carrier family 35, member E1	1.11	0.033845	0.999919
Akap11	A kinase (PRKA) anchor protein 11	1.11	0.03221	0.999919
Eif4enif1	eukaryotic translation initiation factor 4E nuclear import factor 1	1.11	0.025956	0.999919
Cnrip1	cannabinoid receptor interacting protein 1	1.12	0.035063	0.999919
Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4	1.12	0.032078	0.999919
Phldb3	pleckstrin homology-like domain, family B, member 3	1.12	0.035106	0.999919
Olfr685	olfactory receptor 685	1.12	0.028307	0.999919
Azi2	5-azacytidine induced gene 2	1.12	0.011012	0.999919
Klhl12	kelch-like 12	1.13	0.018121	0.999919
Fam124b	family with sequence similarity 124, member B	1.13	0.006116	0.999919
Rnaseh1	ribonuclease H1	1.13	0.000815	0.999919
Olfr157	olfactory receptor 157	1.14	0.028393	0.999919
Neil1	nei endonuclease VIII-like 1 (E. coli)	1.14	0.028976	0.999919
Slc20a2	solute carrier family 20, member 2	1.15	0.035117	0.999919
Rnf208	ring finger protein 208	1.15	0.017508	0.999919
Pomt2	protein-O-mannosyltransferase 2	1.15	0.008739	0.999919
Wnt10b	wingless-type MMTV integration site family, member 10B	1.15	0.019262	0.999919
Usp2	ubiquitin specific peptidase 2	1.15	0.046235	0.999919
Fate1	fetal and adult testis expressed 1	1.15	0.005162	0.999919
Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	1.15	0.014863	0.999919
Gab1	growth factor receptor bound protein 2-associated protein 1	1.16	0.026638	0.999919
Rpa2	replication protein A2	1.16	0.035817	0.999919
Brox	BRO1 domain and CAAX motif containing	1.16	0.00008	0.590269

Tmem54	transmembrane protein 54	1.16	0.028738	0.999919
Bcam	basal cell adhesion molecule	1.16	0.031029	0.999919
Nol6	nucleolar protein family 6 (RNA-associated)	1.16	0.044882	0.999919
Lrrc39	leucine rich repeat containing 39	1.16	0.00697	0.999919
Abca14	ATP-binding cassette, sub-family A (ABC1), member 14	1.16	0.019026	0.999919
Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	1.16	0.046221	0.999919
Zc3h10	zinc finger CCCH type containing 10	1.16	0.049761	0.999919
Kif19a	kinesin family member 19A	1.16	0.017745	0.999919
Ccdc85b	coiled-coil domain containing 85B	1.17	0.000357	0.999919
Eya3	eyes absent 3 homolog (Drosophila)	1.17	0.033559	0.999919
Zscan20	zinc finger and SCAN domains 20	1.17	0.028338	0.999919
Tgfa	transforming growth factor alpha	1.17	0.002415	0.999919
Oraov1	oral cancer overexpressed 1	1.17	0.040289	0.999919
Frs2	fibroblast growth factor receptor substrate 2	1.17	0.03536	0.999919
Ccng1	cyclin G1	1.17	0.038428	0.999919
Vmn2r104	vomeronasal 2, receptor 104	1.17	0.030448	0.999919
Tmem120b	transmembrane protein 120B	1.18	0.036101	0.999919
Pkd1	polycystic kidney disease 1 homolog	1.18	0.038089	0.999919
Hectd3	HECT domain containing 3	1.18	0.026231	0.999919
Cyp26a1	cytochrome P450, family 26, subfamily a, polypeptide 1	1.18	0.028574	0.999919
Zrsr2	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	1.18	0.016564	0.999919
Man1a2	mannosidase, alpha, class 1A, member 2	1.18	0.020524	0.999919
Susd4	sushi domain containing 4	1.18	0.040942	0.999919
Stfa2l1	stefin A2 like 1	1.19	0.03119	0.999919
Tph1	tryptophan hydroxylase 1	1.19	0.007698	0.999919
Trank1	tetratricopeptide repeat and ankyrin repeat containing 1	1.19	0.021434	0.999919
Speer1	spermatogenesis associated glutamate (E)-rich protein 1	1.19	0.026647	0.999919
Ccdc97	coiled-coil domain containing 97	1.19	0.026595	0.999919
Ppm1h	protein phosphatase 1H (PP2C domain containing); microRNA 8104	1.19	0.045071	0.999919
Myrfl	myelin regulatory factor-like	1.19	0.025901	0.999919
Bicd2	bicaudal D homolog 2 (Drosophila)	1.19	0.014056	0.999919

Apex1	apurinic/apyrimidinic endonuclease 1	1.2	0.020134	0.999919
Rasgrp1	RAS guanyl releasing protein 1	1.2	0.039882	0.999919
F5	coagulation factor V	1.2	0.03169	0.999919
Klk1b3	kallikrein 1-related peptidase b3	1.2	0.044929	0.999919
Vasp	vasodilator-stimulated phosphoprotein	1.2	0.040735	0.999919
Nfkbib	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta	1.2	0.044882	0.999919
Tmem126a	transmembrane protein 126A	1.2	0.038492	0.999919
Arhgap9	Rho GTPase activating protein 9	1.2	0.034365	0.999919
Nme4	NME/NM23 nucleoside diphosphate kinase 4	1.2	0.04467	0.999919
Cdc23	CDC23 cell division cycle 23	1.2	0.018389	0.999919
Sfxn2	sideroflexin 2	1.2	0.025069	0.999919
Phykpl	5-phosphohydroxy-L-lysine phospholyase	1.21	0.036005	0.999919
Trim28	tripartite motif-containing 28	1.21	0.047326	0.999919
Cldnd2	claudin domain containing 2	1.21	0.027002	0.999919
Olfr954	olfactory receptor 954	1.21	0.035149	0.999919
Olfr1373	olfactory receptor 1373	1.21	0.024844	0.999919
Parn	poly(A)-specific ribonuclease (deadenylation nuclease)	1.21	0.022562	0.999919
Tmem30c	transmembrane protein 30C	1.21	0.018886	0.999919
Pcnxl3	pecanex-like 3 (Drosophila)	1.21	0.04869	0.999919
Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	1.22	0.030842	0.999919
Tmem55b	transmembrane protein 55b	1.22	0.03223	0.999919
Ctsm	cathepsin M	1.22	0.018122	0.999919
Mob1b	MOB kinase activator 1B	1.22	0.041421	0.999919
Slc26a1	solute carrier family 26 (sulfate transporter), member 1	1.22	0.029186	0.999919
Klk1b27	kallikrein 1-related peptidase b27	1.22	0.023588	0.999919
Cmc1	COX assembly mitochondrial protein 1	1.22	0.041437	0.999919
Gfm2	G elongation factor, mitochondrial 2	1.22	0.037157	0.999919
Cyp2d26	cytochrome P450, family 2, subfamily d, polypeptide 26	1.22	0.010153	0.999919
Hnrnph2	heterogeneous nuclear ribonucleoprotein H2	1.23	0.048228	0.999919
Stx12	syntaxin 12	1.23	0.010606	0.999919
Vmn2r55	vomeronasal 2, receptor 55	1.23	0.043331	0.999919

Card9	caspase recruitment domain family, member 9	1.23	0.007548	0.999919
Map2k5	mitogen-activated protein kinase kinase 5	1.23	0.023238	0.999919
Tlcd2	TLC domain containing 2	1.23	0.042706	0.999919
Pde6a	phosphodiesterase 6A, cGMP-specific, rod, alpha	1.23	0.031397	0.999919
Gbas	glioblastoma amplified sequence	1.24	0.011574	0.999919
Zfp518a	zinc finger protein 518A; microRNA 8092	1.24	0.041092	0.999919
Pdgfrl	platelet-derived growth factor receptor-like	1.24	0.035098	0.999919
Inf2	inverted formin, FH2 and WH2 domain containing	1.24	0.035395	0.999919
Lhx2	LIM homeobox protein 2	1.24	0.026707	0.999919
Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.24	0.042927	0.999919
Vmn2r8	vomeronasal 2, receptor 8	1.24	0.010722	0.999919
Bnc1	basonuclin 1	1.24	0.029486	0.999919
Itpripl2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	1.24	0.017257	0.999919
Cyp2c40	cytochrome P450, family 2, subfamily c, polypeptide 40	1.24	0.003765	0.999919
Mpo	myeloperoxidase	1.25	0.009087	0.999919
Celf4	CUGBP, Elav-like family member 4	1.25	0.043548	0.999919
Zzz3	zinc finger, ZZ domain containing 3	1.25	0.013591	0.999919
Lamb1	laminin B1	1.26	0.03796	0.999919
Zfp335	zinc finger protein 335	1.26	0.000482	0.999919
Ano10	anoctamin 10	1.26	0.046089	0.999919
Grm5	glutamate receptor, metabotropic 5	1.26	0.006572	0.999919
Prpf18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	1.26	0.037141	0.999919
Enpep	glutamyl aminopeptidase	1.26	0.015115	0.999919
Golga7	golgi autoantigen, golgin subfamily a, 7	1.26	0.039474	0.999919
Zfp810	zinc finger protein 810	1.26	0.049622	0.999919
Brf1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	1.26	0.047963	0.999919
Krt73	keratin 73	1.26	0.02117	0.999919
Heatr5b	HEAT repeat containing 5B	1.26	0.039809	0.999919
Tmco6	transmembrane and coiled-coil domains 6	1.26	0.017258	0.999919

Cfap44	cilia and flagella associated protein 44	1.27	0.015362	0.999919
Tusc2	tumor suppressor candidate 2	1.27	0.009143	0.999919
Rab14	RAB14, member RAS oncogene family	1.27	0.040837	0.999919
Rad52	RAD52 homolog (S. cerevisiae)	1.27	0.039885	0.999919
Cts8	cathepsin 8	1.27	0.003361	0.999919
Mgrn1	mahogunin, ring finger 1	1.27	0.019745	0.999919
Sgms1	sphingomyelin synthase 1	1.28	0.045031	0.999919
Pdc	phosducin	1.28	0.041241	0.999919
Tmed11	transmembrane emp24 protein transport domain containing	1.28	0.039152	0.999919
Ceacam19	carcinoembryonic antigen-related cell adhesion molecule 19	1.28	0.037189	0.999919
Gpr20	G protein-coupled receptor 20	1.28	0.034401	0.999919
Olfr127	olfactory receptor 127	1.28	0.048254	0.999919
Cenpf	centromere protein F	1.29	0.019963	0.999919
Cdnf	cerebral dopamine neurotrophic factor	1.29	0.030356	0.999919
Nup210l	nucleoporin 210-like	1.29	0.031837	0.999919
Clec2g	C-type lectin domain family 2, member g	1.29	0.037615	0.999919
Tmie	transmembrane inner ear	1.29	0.020862	0.999919
Slc7a15	solute carrier family 7 (cationic amino acid transporter, y+ system), member 15	1.29	0.017933	0.999919
Hnrnpa0	heterogeneous nuclear ribonucleoprotein A0	1.29	0.049928	0.999919
Oit1	oncoprotein induced transcript 1	1.29	0.022266	0.999919
Olfr94	olfactory receptor 94	1.29	0.036559	0.999919
C2	complement component 2 (within H-2S)	1.29	0.034	0.999919
Cox10	cytochrome c oxidase assembly protein 10	1.3	0.009849	0.999919
E2f3	E2F transcription factor 3	1.3	0.032545	0.999919
Actrt3	actin related protein T3	1.3	0.028702	0.999919
Dmp1	dentin matrix protein 1	1.3	0.005155	0.999919
Zar1	zygote arrest 1	1.3	0.041494	0.999919
Ubqlnl	ubiquilin-like	1.3	0.010854	0.999919
Nbas	neuroblastoma amplified sequence	1.3	0.001823	0.999919
Zfp957	zinc finger protein 957	1.3	0.01576	0.999919
Kank1	KN motif and ankyrin repeat domains 1	1.3	0.045724	0.999919
Mab21l2	mab-21-like 2 (C. elegans)	1.31	0.041286	0.999919
Nphp3	nephronophthisis 3 (adolescent)	1.31	0.043919	0.999919

Bend4	BEN domain containing 4	1.31	0.031731	0.999919
Gpr155	G protein-coupled receptor 155	1.31	0.032781	0.999919
Apom	apolipoprotein M	1.31	0.010698	0.999919
Usp24	ubiquitin specific peptidase 24	1.32	0.034964	0.999919
Malsu1	mitochondrial assembly of ribosomal large subunit 1	1.32	0.012366	0.999919
Tgfbr2	transforming growth factor, beta receptor II	1.32	0.028272	0.999919
Cypt9	cysteine-rich perinuclear theca 9; cysteine-rich perinuclear theca 10; cysteine-rich perinuclear theca 4	1.32	0.036417	0.999919
Mrgpra2a	MAS-related GPR, member A2A	1.32	0.029146	0.999919
Haus7	HAUS augmin-like complex, subunit 7	1.32	0.035775	0.999919
Amhr2	anti-Mullerian hormone type 2 receptor	1.32	0.032217	0.999919
Rcor3	REST corepressor 3	1.33	0.014869	0.999919
Slx4ip	SLX4 interacting protein	1.33	0.036707	0.999919
Acta1	actin, alpha 1, skeletal muscle	1.33	0.021467	0.999919
Tnip2	TNFAIP3 interacting protein 2	1.33	0.032846	0.999919
Mogat1	monoacylglycerol O-acyltransferase 1	1.33	0.048471	0.999919
Rab3ip	RAB3A interacting protein	1.33	0.035702	0.999919
Acot12	acyl-CoA thioesterase 12	1.33	0.00877	0.999919
Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	1.33	0.009266	0.999919
Palm3	paralemmin 3	1.34	0.000806	0.999919
Adar	adenosine deaminase, RNA-specific	1.34	0.039349	0.999919
Il20ra	interleukin 20 receptor, alpha	1.34	0.039246	0.999919
Ptpn11	protein tyrosine phosphatase, non-receptor type 11	1.34	0.001282	0.999919
Mnt	max binding protein	1.34	0.038516	0.999919
Btbd17	BTB (POZ) domain containing 17	1.34	0.048346	0.999919
Tex19.2	testis expressed gene 19.2	1.34	0.022195	0.999919
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage); microRNA 7676-1; microRNA 7676-2	1.34	0.011011	0.999919
Ahsp	alpha hemoglobin stabilizing protein	1.34	0.011702	0.999919
Ptchd2	patched domain containing 2	1.35	0.021881	0.999919
St6gal2	beta galactoside alpha 2,6 sialyltransferase 2	1.35	0.049003	0.999919

Nfxl1	nuclear transcription factor, X-box binding-like 1	1.35	0.00218	0.999919
Muc3	mucin 3, intestinal	1.35	0.002787	0.999919
Rpain	RPA interacting protein	1.35	0.015844	0.999919
Mfsd2b	major facilitator superfamily domain containing 2B	1.35	0.035591	0.999919
Colq	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase	1.35	0.002323	0.999919
Fam199x	family with sequence similarity 199, X-linked	1.36	0.007672	0.999919
Oaz2	ornithine decarboxylase antizyme 2	1.36	0.017047	0.999919
Necab1	N-terminal EF-hand calcium binding protein 1	1.36	0.027609	0.999919
Olfr365	olfactory receptor 365	1.36	0.030454	0.999919
Btbd8	BTB (POZ) domain containing 8	1.36	0.043027	0.999919
Vmn1r179	vomeronasal 1 receptor 179	1.36	0.02723	0.999919
Dpf3	D4, zinc and double PHD fingers, family 3	1.37	0.035433	0.999919
Lrrc47	leucine rich repeat containing 47	1.37	0.031388	0.999919
Sympk	symplekin	1.37	0.013335	0.999919
Ifnl3	interferon lambda 3	1.37	0.01624	0.999919
Tbc1d22a	TBC1 domain family, member 22a	1.37	0.049862	0.999919
Kif20a	kinesin family member 20A	1.37	0.018008	0.999919
Gstt2	glutathione S-transferase, theta 2	1.38	0.032897	0.999919
Mapk14	mitogen-activated protein kinase 14	1.38	0.01803	0.999919
Pign	phosphatidylinositol glycan anchor biosynthesis, class N	1.38	0.047697	0.999919
Olfr338	olfactory receptor 338	1.38	0.045082	0.999919
Wipf1	WAS/WASL interacting protein family, member 1	1.38	0.048832	0.999919
She	src homology 2 domain-containing transforming protein E	1.38	0.022075	0.999919
Spats1	spermatogenesis associated, serine-rich 1	1.38	0.047041	0.999919
Grwd1	glutamate-rich WD repeat containing 1	1.39	0.037593	0.999919
Gpr61	G protein-coupled receptor 61	1.39	0.026972	0.999919
Chtop	chromatin target of PRMT1	1.39	0.021859	0.999919
Olfr62	olfactory receptor 62	1.39	0.026167	0.999919
Cml3	camello-like 3	1.39	0.037477	0.999919
Dgke	diacylglycerol kinase, epsilon	1.39	0.04233	0.999919
Ccdc54	coiled-coil domain containing 54	1.39	0.032633	0.999919
Emb	embigin	1.4	0.026508	0.999919

Trip11	thyroid hormone receptor interactor 11	1.4	0.031554	0.999919
Atr	ataxia telangiectasia and Rad3 related	1.4	0.021491	0.999919
Dhrs3	dehydrogenase/reductase (SDR family) member 3	1.4	0.046851	0.999919
Polr3e	polymerase (RNA) III (DNA directed) polypeptide E	1.4	0.039648	0.999919
Als2cl	ALS2 C-terminal like	1.4	0.012195	0.999919
Slc22a23	solute carrier family 22, member 23	1.4	0.043388	0.999919
Ubr2	ubiquitin protein ligase E3 component n-recognin 2	1.4	0.042483	0.999919
Dmrtb1	DMRT-like family B with proline-rich C-terminal, 1	1.41	0.029237	0.999919
Speer4b	spermatogenesis associated glutamate (E)-rich protein 4B	1.41	0.04072	0.999919
Olfr613	olfactory receptor 613	1.41	0.039928	0.999919
Atm	ataxia telangiectasia mutated	1.41	0.010182	0.999919
Batf	basic leucine zipper transcription factor, ATF-like	1.41	0.008218	0.999919
F2r	coagulation factor II (thrombin) receptor	1.41	0.02229	0.999919
Zfp7	zinc finger protein 7	1.41	0.045228	0.999919
Vti1a	vesicle transport through interaction with t-SNAREs 1A	1.41	0.030904	0.999919
Tfap2a	transcription factor AP-2, alpha	1.42	0.019274	0.999919
Cog5	component of oligomeric golgi complex 5	1.42	0.032708	0.999919
Dcdc2c	doublecortin domain containing 2C	1.42	0.045174	0.999919
Bmp3	bone morphogenetic protein 3	1.42	0.001506	0.999919
Flg2	filaggrin family member 2	1.42	0.000809	0.999919
Tceanc2	transcription elongation factor A (SII) N-terminal and central domain containing 2	1.42	0.025349	0.999919
Ppcdc	phosphopantothenoylcysteine decarboxylase	1.42	0.015994	0.999919
Lrrc17	leucine rich repeat containing 17	1.43	0.021949	0.999919
Zfp853	zinc finger protein 853 [Source:MGI Symbol;Acc:MGI:2685638]; zinc finger protein 853	1.43	0.003699	0.999919
Polr1a	polymerase (RNA) I polypeptide A	1.43	0.029169	0.999919
Otop3	otopetrin 3	1.43	0.020851	0.999919
Olfr1260	olfactory receptor 1260	1.44	0.00622	0.999919

Olfr1196	olfactory receptor 1196	1.44	0.04424	0.999919
Atg4a	autophagy related 4A, cysteine peptidase; autophagy related 4A, pseudogene	1.44	0.044373	0.999919
Mutyh	mutY homolog (E. coli)	1.44	0.021462	0.999919
Cnbd1	cyclic nucleotide binding domain containing 1	1.44	0.037592	0.999919
Usp17ld	ubiquitin specific peptidase 17-like D	1.44	0.034287	0.999919
Trappc10	trafficking protein particle complex 10	1.44	0.035959	0.999919
Ska1	spindle and kinetochore associated complex subunit 1	1.44	0.018759	0.999919
Henmt1	HEN1 methyltransferase homolog 1 (Arabidopsis)	1.45	0.005281	0.999919
Saxo2	stablizer of axonemal microtubules 2	1.45	0.004535	0.999919
Olfr584	olfactory receptor 584	1.45	0.034696	0.999919
Atl3	atlastin GTPase 3	1.46	0.041697	0.999919
Olfr891	olfactory receptor 891	1.46	0.032817	0.999919
Egln3	EGL nine homolog 3 (C. elegans), mRNA (cDNA clone MGC:36685 IMAGE:5371854), complete cds.	1.46	0.04986	0.999919
Ifnk	interferon kappa	1.46	0.002459	0.999919
Nsun4	NOL1/NOP2/Sun domain family, member 4	1.47	0.001837	0.999919
Megf11	multiple EGF-like-domains 11	1.48	0.002394	0.999919
Olfr552	olfactory receptor 552	1.48	0.01532	0.999919
Olfr1178	olfactory receptor 1178	1.49	0.014406	0.999919
Stfa3	stefin A3	1.5	0.003004	0.999919
Robo4	roundabout homolog 4 (Drosophila)	1.5	0.027851	0.999919
Olfr924	olfactory receptor 924	1.5	0.037599	0.999919
Zfp354a	zinc finger protein 354A	1.5	0.003202	0.999919
Zswim8	zinc finger SWIM-type containing 8	1.5	0.030568	0.999919
Apol7c	apolipoprotein L 7c	1.5	0.015245	0.999919
Shc4	SHC (Src homology 2 domain containing) family, member 4	1.51	0.007148	0.999919
Cyp4f13	cytochrome P450, family 4, subfamily f, polypeptide 13	1.51	0.021976	0.999919
Zbed4	zinc finger, BED type containing 4	1.51	0.016818	0.999919
Slc6a18	solute carrier family 6 (neurotransmitter transporter), member 18	1.51	0.013217	0.999919
Wdr13	WD repeat domain 13	1.51	0.02321	0.999919

Dppa5a	developmental pluripotency associated 5A	1.51	0.009488	0.999919
Arl13b	ADP-ribosylation factor-like 13B	1.51	0.029164	0.999919
Otud7b	OTU domain containing 7B	1.52	0.033416	0.999919
Plek	pleckstrin	1.52	0.021745	0.999919
Nlrc5	NLR family, CARD domain containing 5; microRNA 7072	1.52	0.009437	0.999919
Prl3d3	prolactin family 3, subfamily d, member 3	1.52	0.020333	0.999919
Clcn7	chloride channel, voltage-sensitive 7	1.52	0.045277	0.999919
Npr3	natriuretic peptide receptor 3	1.53	0.015922	0.999919
Farsa	phenylalanyl-tRNA synthetase, alpha subunit	1.53	0.017912	0.999919
Olfr1158	olfactory receptor 1158	1.55	0.008622	0.999919
Tmem45b	transmembrane protein 45b	1.55	0.046443	0.999919
Nlrp10	NLR family, pyrin domain containing 10	1.56	0.016677	0.999919
Efr3a	EFR3 homolog A (S. cerevisiae)	1.56	0.027807	0.999919
Vax2	ventral anterior homeobox 2	1.57	0.024665	0.999919
Serpinb9c	serine (or cysteine) peptidase inhibitor, clade B, member 9c	1.58	0.013355	0.999919
Zscan29	zinc finger SCAN domains 29	1.62	0.023974	0.999919
Olfr877	olfactory receptor 877	1.63	0.001616	0.999919
Ttc41	tetratricopeptide repeat domain 41	1.65	0.01689	0.999919
Car1	carbonic anhydrase 1	1.68	0.009815	0.999919
Vmn2r24	vomeronasal 2, receptor 24	1.69	0.014839	0.999919
Olfr904	olfactory receptor 904	1.76	0.047777	0.999919
Pnma3	paraneoplastic antigen MA3	1.87	0.031335	0.999919
Pqlc3	PQ loop repeat containing	1.88	0.035519	0.999919
Slc47a1	solute carrier family 47, member 1	1.93	0.027549	0.999919
Ttll3	tubulin tyrosine ligase-like family, member 3	1.94	0.019458	0.999919
Cd59a	CD59a antigen	3.06	0.01836	0.999919
Ttr	transthyretin	6.64	0.026115	0.999919

Table S11- Genes downregulated in the Prefrontal cortex of Ala92-Dio2 mice. (p<0.05)

Gene Symbol	**Description**	**Fold Change (linear) (AA Pre Frontal Cx vs. TT Pre Frontal Cx)**	**ANOVA p-value (AA Pre Frontal Cx vs. TT Pre Frontal Cx)**	**FDR p-value (AA Pre Frontal Cx vs. TT Pre Frontal Cx)**
Mid1	midline 1	-2.65	0.0292	0.999919
Mid1	midline 1	-2.65	0.0292	0.999919
Vmn1r122	vomeronasal 1 receptor 122	-2.62	0.049469	0.999919
Mid1	midline 1	-2.53	0.033521	0.999919
Erdr1	erythroid differentiation regulator 1	-2.32	0.043881	0.999919
Mrgprx2	MAS-related GPR, member X2	-2.1	0.011241	0.999919
Olfr77	olfactory receptor 77	-2.03	0.020094	0.999919
Olfr883	olfactory receptor 883	-1.97	0.019883	0.999919
Olfr243	olfactory receptor 243	-1.95	0.020899	0.999919
Klhl14	kelch-like 14	-1.94	0.037885	0.999919
Olfr147	olfactory receptor 147	-1.93	0.004876	0.999919
Olfr1285	olfactory receptor 1285	-1.92	0.048921	0.999919
Ccl3	chemokine (C-C motif) ligand 3	-1.89	0.023916	0.999919
Rgsl1	regulator of G-protein signaling like 1	-1.79	0.040271	0.999919
Tex11	testis expressed gene 11	-1.79	0.042696	0.999919
Vmn1r112	vomeronasal 1 receptor 112	-1.78	0.000053	0.586974
Samd3	sterile alpha motif domain containing 3	-1.7	0.025044	0.999919
Vmn1r222	vomeronasal 1 receptor 222	-1.7	0.048312	0.999919
Cd244	CD244 natural killer cell receptor 2B4	-1.63	0.011282	0.999919
Tas2r107	taste receptor, type 2, member 107	-1.63	0.002443	0.999919
Klhl21	kelch-like 21	-1.62	0.005642	0.999919
Obp1a	odorant binding protein IA	-1.62	0.025264	0.999919
Fam109b	family with sequence similarity 109, member B	-1.61	0.032222	0.999919
Pnliprp1	pancreatic lipase related protein 1	-1.6	0.022578	0.999919
Oas1f	2-5 oligoadenylate synthetase 1F; 2'-5' oligoadenylate synthetase 1F	-1.6	0.002379	0.999919
Ltf	lactotransferrin	-1.59	0.00335	0.999919
Gpr55	G protein-coupled receptor 55	-1.58	0.002944	0.999919
Crb2	crumbs family member 2	-1.58	0.033538	0.999919
Vmn1r87	vomeronasal 1 receptor 87	-1.58	0.007387	0.999919
Agmo	alkylglycerol monooxygenase	-1.58	0.003834	0.999919
Samd14	sterile alpha motif domain containing 14	-1.57	0.01391	0.999919
Qtrt1	queuine tRNA-ribosyltransferase 1	-1.57	0.038344	0.999919
Zfp125	zinc finger protein 125 [Source:MGI Symbol;Acc:MGI:1336211]	-1.57	0.003845	0.999919

Adgrg2	adhesion G protein-coupled receptor G2	-1.57	0.020471	0.999919
Pdpn	podoplanin	-1.56	0.00184	0.999919
Rnase2b	ribonuclease, RNase A family, 2B (liver, eosinophil-derived neurotoxin)	-1.56	0.044088	0.999919
Hps6	Hermansky-Pudlak syndrome 6	-1.55	0.023239	0.999919
Msh4	mutS homolog 4 (E. coli)	-1.55	0.030502	0.999919
Tdpoz4	TD and POZ domain containing 4	-1.55	0.001513	0.999919
Pth	parathyroid hormone	-1.55	0.048317	0.999919
Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	-1.54	0.03484	0.999919
Pgpep1l	pyroglutamyl-peptidase I-like	-1.54	0.009006	0.999919
Olfr911-ps1	olfactory receptor 911, pseudogene 1	-1.54	0.010198	0.999919
Olfr180	olfactory receptor 180	-1.54	0.012659	0.999919
Zfp869	zinc finger protein 869	-1.53	0.026618	0.999919
Vmn1r11	vomeronasal 1 receptor 11	-1.53	0.004033	0.999919
Sfrp2	secreted frizzled-related protein 2	-1.52	0.018472	0.999919
Mex3d	mex3 homolog D (C. elegans)	-1.52	0.023413	0.999919
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13; YjeF N-terminal domain containing 3	-1.51	0.009251	0.999919
Nhej1	nonhomologous end-joining factor 1	-1.51	0.000036	0.586974
Hmgb2	high mobility group box 2	-1.5	0.029268	0.999919
Tha1	threonine aldolase 1	-1.5	0.029927	0.999919
Gtf2h3	general transcription factor IIH, polypeptide 3	-1.5	0.034726	0.999919
Kcna5	potassium voltage-gated channel, shaker-related subfamily, member 5	-1.5	0.001856	0.999919
Olfr316	olfactory receptor 316	-1.5	0.044826	0.999919
Cdk3-ps	cyclin-dependent kinase 3, pseudogene	-1.5	0.01112	0.999919
Olfr837	olfactory receptor 837	-1.49	0.003481	0.999919
Oxtr	oxytocin receptor	-1.49	0.014787	0.999919
Usp18	ubiquitin specific peptidase 18	-1.49	0.015111	0.999919
Lsm7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.49	0.046512	0.999919
Ccbl2	cysteine conjugate-beta lyase 2	-1.48	0.004513	0.999919
Actl7a	actin-like 7a	-1.48	0.039757	0.999919
Orc1	origin recognition complex, subunit 1	-1.48	0.008631	0.999919
Cblc	Casitas B-lineage lymphoma c	-1.48	0.012031	0.999919
Olfr943	olfactory receptor 943	-1.48	0.016581	0.999919
Bcl2a1d	B cell leukemia/lymphoma 2 related protein A1d	-1.48	0.034982	0.999919
Olfr807	olfactory receptor 807	-1.48	0.039181	0.999919
Sh3rf2	SH3 domain containing ring finger 2	-1.48	0.009105	0.999919

Ppp2r3d	protein phosphatase 2 (formerly 2A), regulatory subunit B, delta; protein phosphatase 2 (formerly 2A), regulatory subunit B'', delta	-1.47	0.041497	0.999919
Nphs2	nephrosis 2, podocin	-1.47	0.003716	0.999919
Acbd7	acyl-Coenzyme A binding domain containing 7	-1.47	0.030712	0.999919
Mpp4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	-1.46	0.040094	0.999919
Fam227b	family with sequence similarity 227, member B	-1.46	0.045022	0.999919
Gzmf	granzyme F	-1.46	0.000389	0.999919
Wnt9b	wingless-type MMTV integration site family, member 9B	-1.46	0.031133	0.999919
Dgcr6	DiGeorge syndrome critical region gene 6	-1.46	0.019353	0.999919
Lcn5	lipocalin 5	-1.45	0.011412	0.999919
Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	-1.45	0.002808	0.999919
Depdc7	DEP domain containing 7	-1.45	0.02768	0.999919
Syce1	synaptonemal complex central element protein 1	-1.45	0.00756	0.999919
Mmp2	matrix metallopeptidase 2	-1.45	0.025379	0.999919
Tmed6	transmembrane emp24 protein transport domain containing 6	-1.45	0.009284	0.999919
Rsph14	radial spoke head homolog 14 (Chlamydomonas)	-1.45	0.011001	0.999919
Olfr773	olfactory receptor 773	-1.45	0.045817	0.999919
Tmsb15a	thymosin beta 15a	-1.44	0.011804	0.999919
Olfr314	olfactory receptor 314	-1.44	0.039362	0.999919
Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	-1.43	0.031916	0.999919
Olfr1386	olfactory receptor 1386	-1.43	0.005032	0.999919
Pgk2	phosphoglycerate kinase 2	-1.43	0.047303	0.999919
Klrb1f	killer cell lectin-like receptor subfamily B member 1F	-1.43	0.024027	0.999919
Bcl2l14	BCL2-like 14 (apoptosis facilitator)	-1.43	0.034484	0.999919
Olfr118	olfactory receptor 118	-1.43	0.04957	0.999919
Gimap4	GTPase, IMAP family member 4	-1.42	0.037748	0.999919
Crip3	cysteine-rich protein 3	-1.42	0.029165	0.999919
Srf	serum response factor	-1.42	0.019696	0.999919
Mfsd7c	major facilitator superfamily domain containing 7C	-1.41	0.003359	0.999919
Stk31	serine threonine kinase 31	-1.41	0.016883	0.999919
Fabp1	fatty acid binding protein 1, liver	-1.41	0.035511	0.999919
Pld6	phospholipase D family, member 6	-1.41	0.013794	0.999919

Olfr1179	olfactory receptor 1179	-1.4	0.040924	0.999919
Tbxa2r	thromboxane A2 receptor	-1.4	0.022473	0.999919
Pkdrej	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly homolog, sea urchin)	-1.4	0.023044	0.999919
Olfr135	olfactory receptor 135	-1.4	0.000932	0.999919
Mlana	melan-A	-1.4	0.03072	0.999919
Pcdh11x	protocadherin 11 X-linked	-1.39	0.043316	0.999919
Vps37b	vacuolar protein sorting 37B (yeast)	-1.39	0.032364	0.999919
Nup210	nucleoporin 210	-1.39	0.035934	0.999919
Esr1	estrogen receptor 1 (alpha)	-1.39	0.039817	0.999919
Ltv1	LTV1 homolog (S. cerevisiae)	-1.39	0.010767	0.999919
Tgm5	transglutaminase 5	-1.38	0.008372	0.999919
Akr1cl	aldo-keto reductase family 1, member C-like	-1.38	0.033942	0.999919
Fgd5	FYVE, RhoGEF and PH domain containing 5	-1.38	0.021196	0.999919
Vmn2r22	vomeronasal 2, receptor 22	-1.38	0.004995	0.999919
Olfr9	olfactory receptor 9	-1.38	0.046248	0.999919
Olfr394	olfactory receptor 394	-1.38	0.006027	0.999919
Xlr5b	X-linked lymphocyte-regulated 5B	-1.37	0.006775	0.999919
Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	-1.36	0.033475	0.999919
Ccdc153	coiled-coil domain containing 153	-1.36	0.040656	0.999919
Olfr272	olfactory receptor 272	-1.36	0.022428	0.999919
Nlrp4c	NLR family, pyrin domain containing 4C	-1.36	0.0094	0.999919
Tmigd1	transmembrane and immunoglobulin domain containing 1	-1.36	0.015208	0.999919
Ppp1r18	protein phosphatase 1, regulatory subunit 18	-1.36	0.004394	0.999919
Dnah6	dynein, axonemal, heavy chain 6	-1.35	0.046051	0.999919
Car9	carbonic anhydrase 9	-1.35	0.001255	0.999919
Med29	mediator complex subunit 29	-1.35	0.002234	0.999919
Gucy2e	guanylate cyclase 2e	-1.35	0.001504	0.999919
Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10	-1.35	0.022183	0.999919
Fancl	Fanconi anemia, complementation group L	-1.35	0.025776	0.999919
Fhit	fragile histidine triad gene	-1.35	0.024509	0.999919
Olfr16	olfactory receptor 16	-1.35	0.036608	0.999919
Olfr1023	olfactory receptor 1023	-1.35	0.002866	0.999919
Tfpi	tissue factor pathway inhibitor	-1.35	0.010841	0.999919
Olfr1164	olfactory receptor 1164	-1.35	0.010076	0.999919
Gnat2	guanine nucleotide binding protein, alpha transducing 2	-1.35	0.047338	0.999919
Papolb	poly (A) polymerase beta (testis specific)	-1.35	0.014935	0.999919
Gdnf	glial cell line derived neurotrophic factor	-1.35	0.010525	0.999919

Sgpp2	sphingosine-1-phosphate phosphotase 2	-1.34	0.024056	0.999919
Prlr	prolactin receptor	-1.34	0.017139	0.999919
Cenpc1	centromere protein C1	-1.34	0.040097	0.999919
Olfr1412	olfactory receptor 1412	-1.34	0.046753	0.999919
Vmn2r41	vomeronasal 2, receptor 41	-1.34	0.043263	0.999919
Tmem221	transmembrane protein 221	-1.34	0.032175	0.999919
Srebf1	sterol regulatory element binding transcription factor 1; microRNA 6922	-1.34	0.007319	0.999919
Nox3	NADPH oxidase 3	-1.34	0.03113	0.999919
Ceacam5	carcinoembryonic antigen-related cell adhesion molecule 5	-1.33	0.04802	0.999919
Pigg	phosphatidylinositol glycan anchor biosynthesis, class G	-1.33	0.014012	0.999919
Cox7b2	cytochrome c oxidase subunit VIIb2	-1.33	0.017515	0.999919
Sec1	secretory blood group 1	-1.33	0.00159	0.999919
Sfta2	surfactant associated 2	-1.33	0.015405	0.999919
H2-M9	histocompatibility 2, M region locus 9	-1.33	0.032414	0.999919
Klc4	kinesin light chain 4	-1.33	0.042578	0.999919
Zfp467	zinc finger protein 467	-1.32	0.030146	0.999919
Hoxc5	homeobox C5	-1.32	0.004021	0.999919
Crabp1	cellular retinoic acid binding protein I	-1.32	0.032255	0.999919
Dusp23	dual specificity phosphatase 23	-1.32	0.010532	0.999919
Hsd3b4	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4 (Hsd3b4), transcript variant 1, mRNA.; predicted gene 10681 (Gm10681), mRNA.; hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4 (Hsd3b4), transcript variant 2, mRNA.; predicted gene 10681 [Source:MGI Symbol;Acc:MGI:3711284]; hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4, mRNA (cDNA clone MGC:18496 IMAGE:4221849), complete cds.; hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4, mRNA (cDNA clone MGC:164033 IMAGE:40130679), complete cds.; predicted gene 10681	-1.32	0.010476	0.999919
Olfr643	olfactory receptor 643; olfactory receptor 639	-1.32	0.017997	0.999919
Miox	myo-inositol oxygenase	-1.32	0.004579	0.999919
Vmn2r96	vomeronasal 2, receptor 96	-1.32	0.047353	0.999919
Sfxn3	sideroflexin 3	-1.31	0.026332	0.999919
Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	-1.31	0.011712	0.999919

Bbs12	Bardet-Biedl syndrome 12 (human)	-1.31	0.025385	0.999919
Tyr	tyrosinase	-1.31	0.017354	0.999919
Dmrtc1c1	DMRT-like family C1c1; DMRT-like family C1c2	-1.31	0.012153	0.999919
Mbl2	mannose-binding lectin (protein C) 2	-1.31	0.028349	0.999919
Spin4	spindlin family, member 4	-1.3	0.020319	0.999919
Vmn2r46	vomeronasal 2, receptor 46	-1.3	0.021181	0.999919
Lpin3	lipin 3	-1.3	0.028804	0.999919
Olfr1101	olfactory receptor 1101	-1.3	0.032772	0.999919
Lama5	laminin, alpha 5	-1.3	0.02579	0.999919
Prok1	prokineticin 1	-1.3	0.041259	0.999919
Acsm1	acyl-CoA synthetase medium-chain family member 1	-1.3	0.002076	0.999919
Mrpl4	mitochondrial ribosomal protein L4	-1.3	0.008819	0.999919
Rln1	relaxin 1	-1.3	0.01501	0.999919
Plekhg4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	-1.29	0.037182	0.999919
Ppp2r1b	protein phosphatase 2, regulatory subunit A, beta	-1.29	0.03875	0.999919
Vmn1r36	vomeronasal 1 receptor 36	-1.29	0.009924	0.999919
Fank1	fibronectin type 3 and ankyrin repeat domains 1	-1.29	0.018312	0.999919
Slc26a3	solute carrier family 26, member 3	-1.29	0.035681	0.999919
Sowahd	sosondowah ankyrin repeat domain family member D	-1.28	0.001397	0.999919
Fundc2	FUN14 domain containing 2	-1.28	0.047684	0.999919
Arl4d	ADP-ribosylation factor-like 4D	-1.28	0.023032	0.999919
H1fx	H1 histone family, member X	-1.28	0.04732	0.999919
Hmcn1	hemicentin 1	-1.28	0.041559	0.999919
Olfr703	olfactory receptor 703	-1.28	0.038946	0.999919
Cldn34c4	claudin 34C4	-1.28	0.043782	0.999919
Olfr1082	olfactory receptor 1082	-1.27	0.018393	0.999919
Ccdc125	coiled-coil domain containing 125	-1.27	0.01372	0.999919
Defb9	defensin beta 9	-1.27	0.034485	0.999919
Reg2	regenerating islet-derived 2	-1.27	0.048125	0.999919
Ccdc169	coiled-coil domain containing 169	-1.27	0.044732	0.999919
Myct1	myc target 1	-1.27	0.027003	0.999919
Taar7d	trace amine-associated receptor 7D	-1.27	0.012009	0.999919
Ddit3	DNA-damage inducible transcript 3	-1.27	0.010927	0.999919
Smtnl2	smoothelin-like 2	-1.27	0.048071	0.999919
Glrx5	glutaredoxin 5 homolog (S. cerevisiae)	-1.27	0.049693	0.999919
Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	-1.26	0.009098	0.999919
Mtpap	mitochondrial poly(A) polymerase	-1.26	0.027655	0.999919

Adam39	a disintegrin and metallopeptidase domain 39	-1.26	0.044889	0.999919
Zfp503	zinc finger protein 503	-1.26	0.008074	0.999919
Dusp28	dual specificity phosphatase 28	-1.26	0.048775	0.999919
Lmod1	leiomodin 1 (smooth muscle)	-1.26	0.03012	0.999919
Commd7	COMM domain containing 7	-1.26	0.018271	0.999919
Btk	Bruton agammaglobulinemia tyrosine kinase	-1.26	0.028026	0.999919
Olfr765	olfactory receptor 765	-1.26	0.020341	0.999919
Il9r	interleukin 9 receptor	-1.26	0.029707	0.999919
Efcab5	EF-hand calcium binding domain 5	-1.26	0.031802	0.999919
Mtl5	metallothionein-like 5, testis-specific (tesmin)	-1.26	0.042098	0.999919
Kif22	kinesin family member 22	-1.25	0.000245	0.999919
Ecsit	ECSIT homolog (Drosophila)	-1.25	0.01082	0.999919
Ppef2	protein phosphatase, EF hand calcium-binding domain 2	-1.25	0.03846	0.999919
Prss43	protease, serine 43	-1.25	0.003964	0.999919
Dux	double homeobox	-1.25	0.024476	0.999919
Sar1b	SAR1 gene homolog B (S. cerevisiae)	-1.25	0.01126	0.999919
Prr15l	proline rich 15-like	-1.25	0.01871	0.999919
Cryba1	crystallin, beta A1	-1.25	0.000416	0.999919
Akr1c13	aldo-keto reductase family 1, member C13	-1.25	0.046663	0.999919
Icosl	icos ligand	-1.24	0.039936	0.999919
Il20	interleukin 20	-1.24	0.046712	0.999919
Slc45a3	solute carrier family 45, member 3	-1.24	0.018713	0.999919
Olfr57	olfactory receptor 57	-1.24	0.010833	0.999919
Sox17	SRY (sex determining region Y)-box 17	-1.24	0.01633	0.999919
Ttc22	tetratricopeptide repeat domain 22	-1.24	0.020938	0.999919
Fam212a	family with sequence similarity 212, member A	-1.24	0.015299	0.999919
Olfr1353	olfactory receptor 1353	-1.24	0.016796	0.999919
Olfr1356	olfactory receptor 1356	-1.24	0.030153	0.999919
Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	-1.23	0.010518	0.999919
Jakmip3	janus kinase and microtubule interacting protein 3	-1.23	0.026602	0.999919
Ankrd36	ankyrin repeat domain 36	-1.23	0.031168	0.999919
Dse	dermatan sulfate epimerase	-1.23	0.014223	0.999919
Tns1	tensin 1	-1.23	0.036378	0.999919
Slc19a3	solute carrier family 19, member 3	-1.23	0.035847	0.999919
Slfnl1	schlafen like 1	-1.23	0.026115	0.999919
Vmn2r48	vomeronasal 2, receptor 48	-1.23	0.031187	0.999919
Olfr176	olfactory receptor 176; olfactory receptor 177	-1.23	0.045764	0.999919
Tmem217	transmembrane protein 217	-1.23	0.008666	0.999919

Creb5	cAMP responsive element binding protein 5; RIKEN cDNA 9430076C15 gene	-1.22	0.033695	0.999919
C5ar1	complement component 5a receptor 1	-1.22	0.022478	0.999919
Myh3	myosin, heavy polypeptide 3, skeletal muscle, embryonic	-1.22	0.027027	0.999919
Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-1.21	0.043908	0.999919
Iqca	IQ motif containing with AAA domain	-1.21	0.022362	0.999919
Cst9	cystatin 9	-1.21	0.048612	0.999919
Olfr1341	olfactory receptor 1341	-1.21	0.038295	0.999919
Ccl19	chemokine (C-C motif) ligand 19	-1.21	0.020858	0.999919
Ccrl2	chemokine (C-C motif) receptor-like 2	-1.21	0.036214	0.999919
Ifi47	interferon gamma inducible protein 47; olfactory receptor 56	-1.21	0.049162	0.999919
Lrrn4cl	LRRN4 C-terminal like	-1.21	0.035503	0.999919
Nbea	neurobeachin	-1.2	0.016247	0.999919
Tspan31	tetraspanin 31	-1.2	0.043648	0.999919
Mgarp	mitochondria localized glutamic acid rich protein	-1.2	0.016404	0.999919
Gigyf1	GRB10 interacting GYF protein 1	-1.2	0.013841	0.999919
Prodh2	proline dehydrogenase (oxidase) 2	-1.2	0.043982	0.999919
Myl7	myosin, light polypeptide 7, regulatory	-1.2	0.016401	0.999919
Olfr1458	olfactory receptor 1458	-1.2	0.000983	0.999919
Rab43	RAB43, member RAS oncogene family	-1.19	0.023442	0.999919
Gorab	golgin, RAB6-interacting	-1.19	0.035394	0.999919
Trim54	tripartite motif-containing 54	-1.19	0.019554	0.999919
Dynlrb1	dynein light chain roadblock-type 1	-1.19	0.00321	0.999919
Phb2	prohibitin 2	-1.19	0.033338	0.999919
Plcg1	phospholipase C, gamma 1	-1.19	0.00291	0.999919
Iqcd	IQ motif containing D	-1.19	0.018679	0.999919
Olfr862	olfactory receptor 862	-1.19	0.028998	0.999919
Ntsr2	neurotensin receptor 2	-1.19	0.03885	0.999919
Nlrc3	NLR family, CARD domain containing 3	-1.19	0.024032	0.999919
Umodl1	uromodulin-like 1	-1.19	0.01235	0.999919
Pgc	progastricsin (pepsinogen C)	-1.19	0.049751	0.999919
Slc25a45	solute carrier family 25, member 45	-1.19	0.047083	0.999919
Trex1	three prime repair exonuclease 1; ATR interacting protein	-1.18	0.006324	0.999919
Flnc	filamin C, gamma	-1.18	0.047084	0.999919
Efcab8	EF-hand calcium binding domain 8	-1.18	0.031362	0.999919
Zfp772	zinc finger protein 772	-1.18	0.039834	0.999919
Krt4	keratin 4	-1.18	0.0217	0.999919
Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	-1.17	0.030008	0.999919

Hao2	hydroxyacid oxidase 2	-1.17	0.041552	0.999919
Slc7a9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	-1.17	0.038962	0.999919
Phox2a	paired-like homeobox 2a	-1.17	0.022342	0.999919
Ssty2	spermiogenesis specific transcript on the Y 2	-1.17	0.037048	0.999919
Atp8b3	ATPase, class I, type 8B, member 3	-1.17	0.019509	0.999919
Peo1	progressive external ophthalmoplegia 1 (human)	-1.17	0.016199	0.999919
Zfyve9	zinc finger, FYVE domain containing 9	-1.16	0.006727	0.999919
Arid4b	AT rich interactive domain 4B (RBP1-like)	-1.16	0.018962	0.999919
Eef1a1	eukaryotic translation elongation factor 1 alpha 1	-1.16	0.022582	0.999919
Kir3dl1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	-1.16	0.048069	0.999919
Tsga8	testis specific gene A8	-1.16	0.01473	0.999919
Spz1	spermatogenic leucine zipper 1	-1.16	0.027363	0.999919
Zfp758	zinc finger protein 758	-1.16	0.034907	0.999919
Sncg	synuclein, gamma	-1.15	0.025144	0.999919
Myo15b	myosin XVB	-1.15	0.013371	0.999919
Rbbp9	retinoblastoma binding protein 9	-1.15	0.024872	0.999919
St7	suppression of tumorigenicity 7	-1.15	0.035355	0.999919
Krt34	keratin 34	-1.15	0.001007	0.999919
Rnaseh2a	ribonuclease H2, large subunit	-1.14	0.017703	0.999919
Drd4	dopamine receptor D4	-1.14	0.038018	0.999919
Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2	-1.14	0.029107	0.999919
Actbl2	actin, beta-like 2	-1.13	0.00283	0.999919
Chst12	carbohydrate sulfotransferase 12	-1.13	0.021573	0.999919
Plac9b	placenta specific 9b	-1.13	0.01864	0.999919
Pard3b	par-3 family cell polarity regulator beta	-1.12	0.029105	0.999919
Cnga1	cyclic nucleotide gated channel alpha 1	-1.12	0.036728	0.999919
Exoc1	exocyst complex component 1	-1.1	0.041464	0.999919
Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1	-1.1	0.047262	0.999919
Sec62	SEC62 homolog (S. cerevisiae)	-1.09	0.004318	0.999919
Kif2b	kinesin family member 2B	-1.09	0.039659	0.999919
Ap1m2	adaptor protein complex AP-1, mu 2 subunit	-1.09	0.045156	0.999919

Table S12- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in amygdala. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Ala mice (Amygdala)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_2_IRON_2_SULFUR_CLUSTER_BINDING	21	0.5956	1.8438	0.0001	0.417798
GO_REGULATION_OF_SPINDLE_ORGANIZATION	19	0.523	1.8291	0.0001	0.259903
GO_RIBOSOME_BINDING	43	0.4778	1.747	0.0001	0.638125
GO_PROTEASOME_COMPLEX	75	0.3605	1.7375	0.0001	0.56275
GO_U2_SNRNP	17	0.5258	1.7311	0.0001	0.504011
GO_VESICLE_COATING	72	0.4785	1.7218	0.0001	0.49115
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	26	0.5996	1.7002	0.0001	0.49272
GO_VESICLE_TARGETING	75	0.4542	1.6941	0.0001	0.428952
GO_CLATHRIN_ADAPTOR_COMPLEX	27	0.4473	1.6771	0.0001	0.484221
GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS	81	0.3793	1.6715	0.0001	0.475923
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	34	0.4526	1.6696	0.0001	0.453664
GO_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	28	0.5132	1.6669	0.0001	0.44665
GO_NEGATIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	15	0.5536	1.6621	0.0001	0.437825
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	17	0.5069	1.6595	0.0001	0.420588
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	72	0.3752	1.657	0.0001	0.408492
GO_GOLGI_TO_ENDOSOME_TRANSPORT	16	0.515	1.6545	0.0001	0.398645
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	26	0.519	1.6515	0.0001	0.395867
GO_SNRNA_METABOLIC_PROCESS	74	0.4056	1.6512	0.0001	0.378508
GO_SIGNAL_SEQUENCE_BINDING	36	0.4625	1.6481	0.0001	0.378934
GO_PROTEIN_N_TERMINUS_BINDING	100	0.3248	1.6135	0.0001	0.503611
GO_GOLGI_STACK	113	0.4005	1.6076	0.0001	0.517795
GO_SINGLE_ORGANISM_MEMBRANE_BUDDING	71	0.4252	1.6069	0.0001	0.503229
GO_NEGATIVE_REGULATION_OF_DNA_REPLICATION	53	0.4289	1.6045	0.0001	0.493259
GO_POSITIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	116	0.3314	1.6028	0.0001	0.469894
GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX	18	0.5115	1.6023	0.0001	0.456322
GO_GOLGI_CISTERNA	83	0.4017	1.5989	0.0001	0.460914
GO_RIBONUCLEOPROTEIN_COMPLEX_BINDING	90	0.4124	1.5975	0.0001	0.453378
GO_RESPONSE_TO_MANGANESE_ION	17	0.5849	1.5879	0.0001	0.458725

GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	30	0.5398	1.5867	0.0001	0.442218
GO_POSITIVE_REGULATION_OF_DNA_REPAIR	34	0.461	1.5712	0.0001	0.476845
GO_HISTONE_MRNA_METABOLIC_PROCESS	28	0.5093	1.5608	0.0001	0.496273
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	87	0.3441	1.5584	0.0001	0.500629
GO_VESICLE_DOCKING	52	0.4346	1.5577	0.0001	0.49412
GO_MRNA_CLEAVAGE_FACTOR_COMPLEX	17	0.5197	1.5481	0.0001	0.517586
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	102	0.3149	1.5477	0.0001	0.510625
GO_CLATHRIN_COAT	45	0.342	1.5381	0.0001	0.533793
GO_NEGATIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	26	0.4969	1.5364	0.0001	0.53622
GO_NAD_BINDING	53	0.4095	1.5355	0.0001	0.531756
GO_RESPONSE_TO_SALT	16	0.5411	1.5355	0.0001	0.522421
GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	189	0.2997	1.5333	0.0001	0.524679
GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	19	0.5072	1.5321	0.0001	0.522885
GO_POSITIVE_REGULATION_OF_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	24	0.5234	1.5278	0.0001	0.530312
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	21	0.4685	1.5234	0.0001	0.537596
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	48	0.3923	1.5204	0.0001	0.535727
GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	77	0.3447	1.5145	0.0001	0.539793
GO_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	267	0.2934	1.514	0.0001	0.535291
GO_CELLULAR_RESPONSE_TO_VITAMIN	26	0.458	1.4937	0.0001	0.588231
GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING	18	0.5492	1.4927	0.0001	0.577932
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	28	0.502	1.4873	0.0001	0.59201
GO_POSITIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	255	0.2958	1.4866	0.0001	0.581244
GO_MEMBRANE_DOCKING	63	0.39	1.4811	0.0001	0.58794
GO_PHOSPHATE_ION_TRANSPORT	18	0.4735	1.4758	0.0001	0.579455
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	163	0.3177	1.4747	0.0001	0.577862
GO_NEGATIVE_REGULATION_OF_HISTONE_ACETYLATION	15	0.4141	1.4639	0.0001	0.608734
GO_TELOMERE_CAPPING	15	0.5149	1.4597	0.0001	0.596819
GO_CYTOPLASMIC_MRNA_PROCESSING_BODY	59	0.2934	1.4556	0.0001	0.597779
GO_UBIQUITIN_LIKE_PROTEIN_BINDING	113	0.2831	1.4509	0.0001	0.596518

GO_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	34	0.4043	1.4507	0.0001	0.592201
GO_SINGLE_STRANDED_DNA_BINDING	75	0.3079	1.4499	0.0001	0.586431
GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	380	0.2742	1.4316	0.0001	0.609399
GO_MACROAUTOPHAGY	242	0.3012	1.4302	0.0001	0.605898
GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	189	0.2902	1.4298	0.0001	0.603337
GO_REGULATION_OF_RNA_STABILITY	134	0.2668	1.4276	0.0001	0.604496
GO_LIPOPROTEIN_METABOLIC_PROCESS	111	0.2915	1.4254	0.0001	0.610814
GO_K63_LINKED_POLYUBIQUITIN_BINDING	16	0.4295	1.413	0.0001	0.617385
GO_RECOMBINATIONAL_REPAIR	68	0.363	1.3975	0.0001	0.643519
GO_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	269	0.2747	1.3794	0.0001	0.647621
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	20	0.4254	1.3564	0.0001	0.664034
GO_RESPONSE_TO_IRON_ION	35	0.4079	1.3545	0.0001	0.667409
GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	183	0.2726	1.3384	0.0001	0.695869
GO_NEURON_DEATH	45	0.3052	1.3004	0.0001	0.734823
GO_AUTOPHAGY	343	0.2437	1.2762	0.0001	0.74166
GO_FC_RECEPTOR_SIGNALING_PATHWAY	181	0.2034	1.2668	0.0001	0.75463
GO_NADP_BINDING	40	0.3356	1.2624	0.0001	0.758898
GO_DNA_RECOMBINATION	188	0.2909	1.245	0.0001	0.755322
GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	421	0.2222	1.1697	0.0001	0.815954

Table S13- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in amygdala. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Thr mice (Amygdala)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_RESPIRATORY_GASEOUS_EXCHANGE	46	-0.46311	-1.82442	0.0001	0.54823
GO_BETA_CATENIN_TCF_COMPLEX_ASSEMBLY	29	-0.44371	-1.80358	0.0001	0.49428
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	26	-0.69051	-1.78054	0.0001	0.44927
GO_REGULATION_OF_RESPIRATORY_SYSTEM_PROCESS	15	-0.5949	-1.77756	0.0001	0.35429
GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	38	-0.57471	-1.71792	0.0001	0.57195
GO_CHRONIC_INFLAMMATORY_RESPONSE	15	-0.65652	-1.69726	0.0001	0.65335
GO_MULTI_ORGANISM_BEHAVIOR	70	-0.44019	-1.67432	0.0001	0.80225
GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	34	-0.56175	-1.66033	0.0001	0.85589
GO_PROTEIN_BINDING_INVOLVED_IN_CELL_ADHESION	16	-0.71357	-1.65895	0.0001	0.77971
GO_MYOSIN_FILAMENT	22	-0.60874	-1.6199	0.0001	1
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RENIN_ANGIOTENSIN	22	-0.57434	-1.61582	0.0001	1
GO_PHAGOCYTOSIS_ENGULFMENT	15	-0.57164	-1.59811	0.0001	1
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	28	-0.51271	-1.59522	0.0001	1
GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	64	-0.47135	-1.59295	0.0001	1
GO_RESPONSE_TO_STIMULUS_INVOLVED_IN_REGULATION_OF_MUSCLE_ADAPTATION	15	-0.60144	-1.59032	0.0001	1
GO_ACYLGLYCEROL_HOMEOSTASIS	25	-0.56965	-1.58681	0.0001	0.96301
GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	101	-0.36721	-1.56862	0.0001	1
GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	36	-0.45642	-1.56826	0.0001	1
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	51	-0.45927	-1.56114	0.0001	1
GO_SERTOLI_CELL_DIFFERENTIATION	18	-0.50333	-1.55623	0.0001	1
GO_POSITIVE_REGULATION_OF_VASODILATION	31	-0.52652	-1.5498	0.0001	1
GO_NARROW_PORE_CHANNEL_ACTIVITY	16	-0.53539	-1.54891	0.0001	1

GO_POSITIVE_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	19	-0.63296	-1.54703	0.0001	1
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HORMONE	34	-0.52584	-1.54432	0.0001	1
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	50	-0.48506	-1.54214	0.0001	1
GO_REGULATION_OF_CORTICOSTEROID_HORMONE_SECRETION	15	-0.68808	-1.53902	0.0001	1
GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHANNEL_ACTIVITY	25	-0.42082	-1.53531	0.0001	0.97259
GO_NEUROPEPTIDE_RECEPTOR_ACTIVITY	40	-0.57159	-1.53304	0.0001	0.94161
GO_ATRIAL_SEPTUM_DEVELOPMENT	18	-0.56796	-1.52999	0.0001	0.91764
GO_STABILIZATION_OF_MEMBRANE_POTENTIAL	15	-0.55681	-1.52574	0.0001	0.90705
GO_SERTOLI_CELL_DEVELOPMENT	15	-0.5492	-1.51716	0.0001	0.96011
GO_CARDIAC_ATRIUM_DEVELOPMENT	30	-0.48888	-1.51332	0.0001	0.91015
GO_POSITIVE_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	24	-0.573	-1.51223	0.0001	0.90282
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	28	-0.52655	-1.51104	0.0001	0.89263
GO_REGULATION_OF_ENDOCRINE_PROCESS	46	-0.49804	-1.51056	0.0001	0.87868
GO_NEPHRON_TUBULE_FORMATION	18	-0.60778	-1.50823	0.0001	0.88222
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	17	-0.60703	-1.50802	0.0001	0.86654
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	78	-0.41426	-1.50669	0.0001	0.86153
GO_NEGATIVE_REGULATION_OF_AXON_GUIDANCE	27	-0.52863	-1.5048	0.0001	0.86075
GO_FEEDING_BEHAVIOR	86	-0.47803	-1.49831	0.0001	0.8709
GO_REGULATION_OF_BLOOD_PRESSURE	158	-0.37162	-1.49788	0.0001	0.85891
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	61	-0.39984	-1.48785	0.0001	0.85654
GO_NITRIC_OXIDE_SYNTHASE_BINDING	19	-0.49447	-1.48619	0.0001	0.81976
GO_RESPONSE_TO_HEAT	80	-0.37511	-1.48267	0.0001	0.81188
GO_AMPA_GLUTAMATE_RECEPTOR_COMPLEX	27	-0.45041	-1.47318	0.0001	0.8111
GO_OSTEOBLAST_DEVELOPMENT	18	-0.50507	-1.47306	0.0001	0.80146
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIATED_BY_A_CHEMICAL_SIGNAL	44	-0.46405	-1.47025	0.0001	0.80328

GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	65	-0.39713	-1.46851	0.0001	0.80698
GO_REGULATION_OF_STEROID_HORMONE_SECRETION	20	-0.57736	-1.4648	0.0001	0.8101
GO_TRANSMITTER_GATED_CHANNEL_ACTIVITY	26	-0.49171	-1.46194	0.0001	0.81223
GO_CELL_FATE_DETERMINATION	43	-0.46967	-1.46023	0.0001	0.8145
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	76	-0.38995	-1.45179	0.0001	0.85489
GO_REGULATION_OF_VASODILATION	46	-0.44594	-1.44908	0.0001	0.85355
GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	23	-0.50736	-1.44334	0.0001	0.86138
GO_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY	16	-0.48951	-1.44296	0.0001	0.85463
GO_PHOTORECEPTOR_CELL_DEVELOPMENT	38	-0.43549	-1.44022	0.0001	0.85491
GO_REGULATION_OF_ACTIVATED_T_CELL_PROLIFERATION	34	-0.46315	-1.44012	0.0001	0.84692
GO_POSITIVE_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION	19	-0.45106	-1.43996	0.0001	0.83936
GO_CELL_FATE_COMMITMENT	223	-0.3621	-1.43848	0.0001	0.83153
GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	18	-0.46271	-1.42369	0.0001	0.8686
GO_POSITIVE_REGULATION_OF_ERBB_SIGNALING_PATHWAY	33	-0.4735	-1.42364	0.0001	0.86131
GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	70	-0.4252	-1.42315	0.0001	0.85779
GO_RESPONSE_TO_ZINC_ION	45	-0.36784	-1.4228	0.0001	0.84505
GO_REGULATION_OF_LIPASE_ACTIVITY	80	-0.39836	-1.41867	0.0001	0.84374
GO_MIDBODY	124	-0.30645	-1.41867	0.0001	0.83667
GO_REGULATION_OF_EPIDERMAL_CELL_DIFFERENTIATION	42	-0.37482	-1.41481	0.0001	0.82718
GO_EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	51	-0.43366	-1.41395	0.0001	0.82655
GO_REGULATION_OF_EXTENT_OF_CELL_GROWTH	96	-0.36798	-1.41148	0.0001	0.81784
GO_KIDNEY_MORPHOGENESIS	81	-0.40524	-1.40215	0.0001	0.84098
GO_PROTEIN_DNA_COMPLEX	105	-0.31311	-1.40123	0.0001	0.82291
GO_NEURAL_CREST_CELL_MIGRATION	51	-0.4501	-1.39205	0.0001	0.79782
GO_MESONEPHROS_DEVELOPMENT	89	-0.42794	-1.38859	0.0001	0.78325
GO_SH3_DOMAIN_BINDING	112	-0.26524	-1.38328	0.0001	0.78277
GO_CELL_CYCLE_ARREST	137	-0.27911	-1.3737	0.0001	0.79861
GO_SCAFFOLD_PROTEIN_BINDING	43	-0.35137	-1.36759	0.0001	0.79727
GO_RESPONSE_TO_ALKALOID	132	-0.34141	-1.36751	0.0001	0.79334
GO_MUSCLE_CONTRACTION	229	-0.3322	-1.36248	0.0001	0.80586

GO_REGULATION_OF_RECEPTOR_ACTIVITY	113	-0.29833	-1.35564	0.0001	0.80325
GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	49	-0.41585	-1.35203	0.0001	0.81397
GO_DNA_PACKAGING_COMPLEX	40	-0.33831	-1.34783	0.0001	0.78749
GO_REGULATION_OF_B_CELL_DIFFERENTIATION	22	-0.45428	-1.34687	0.0001	0.78534
GO_DIGESTIVE_SYSTEM_DEVELOPMENT	144	-0.34157	-1.34315	0.0001	0.78866
GO_PROTEIN_SECRETION	103	-0.30299	-1.3402	0.0001	0.79512
GO_CLATHRIN_COATED_VESICLE_MEMBRANE	67	-0.28278	-1.33656	0.0001	0.79675
GO_MUSCLE_SYSTEM_PROCESS	276	-0.322	-1.33537	0.0001	0.79679
GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	194	-0.34554	-1.32992	0.0001	0.79832
GO_REGULATION_OF_VASOCONSTRICTION	65	-0.37408	-1.31382	0.0001	0.81856
GO_POSITIVE_REGULATION_OF_SECRETION	343	-0.2889	-1.30661	0.0001	0.82845
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_LINEAR_AMIDES	79	-0.27023	-1.30628	0.0001	0.82719
GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	45	-0.35467	-1.28998	0.0001	0.81424
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	144	-0.34086	-1.27574	0.0001	0.82383
GO_CIRCULATORY_SYSTEM_PROCESS	346	-0.2949	-1.26212	0.0001	0.84458
GO_HEART_PROCESS	84	-0.29859	-1.24703	0.0001	0.85588

Table S14- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in cerebellum. Listed gene sets were significant at a nominal p-value <1% or FDR < 25% .

Name of the Gene ontology (GO) gene sets enriched in Ala mice (Cerebellum)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_U2_SNRNP	17	0.63	1.98	0.0001	0.047
GO_MULTI_ORGANISM_ORGANELLE_ORGANIZATION	22	0.46	1.88	0.0001	0.2083
GO_U2_TYPE_SPLICEOSOMAL_COMPLEX	27	0.58	1.88	0.0001	0.1426
GO_MULTIVESICULAR_BODY_ORGANIZATION	29	0.46	1.86	0.0001	0.1378
GO_CAJAL_BODY	46	0.48	1.84	0.0001	0.1457
GO_PRESPLICEOSOME	20	0.54	1.83	0.0001	0.1386
GO_DRUG_METABOLIC_PROCESS	19	0.63	1.82	0.0001	0.142
GO_ESCRT_COMPLEX	23	0.47	1.82	0.0001	0.1348
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	23	0.59	1.81	0.0001	0.1278
GO_PROTEIN_TARGETING_TO_MEMBRANE	148	0.52	1.79	0.0465	0.126
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	53	0.69	1.78	0.0455	0.1266
GO_PROTEIN_REFOLDING	19	0.58	1.78	0.0001	0.117
GO_MANNOSE_BINDING	15	0.62	1.78	0.0001	0.1106
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	111	0.58	1.78	0.0457	0.111
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	97	0.63	1.78	0.0465	0.1059
GO_MITOCHONDRIAL_GENOME_MAINTENANCE	19	0.59	1.78	0.0001	0.101
GO_TRANSLATIONAL_INITIATION	134	0.58	1.78	0.0706	0.0957
GO_CYTOSOLIC_RIBOSOME	99	0.63	1.77	0.0468	0.0955
GO_CATALYTIC_STEP_2_SPLICEOSOME	81	0.42	1.76	0.0302	0.1046
GO_COPI_COATED_VESICLE	20	0.57	1.75	0.0001	0.1203
GO_RNA_CATABOLIC_PROCESS	207	0.42	1.75	0.0001	0.1222
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	116	0.56	1.74	0.0468	0.1235
GO_INTERSTRAND_CROSS_LINK_REPAIR	36	0.55	1.72	0.0001	0.1543
GO_NOTCH_BINDING	16	0.57	1.72	0.0001	0.1483
GO_SPLICEOSOMAL_COMPLEX_ASSEMBLY	49	0.38	1.71	0.0001	0.162
GO_ACTIN_NUCLEATION	20	0.5	1.71	0.0001	0.1588
GO_SPLICEOSOMAL_COMPLEX	155	0.36	1.71	0.0001	0.1558

GO_BETA_CATENIN_DESTRUCTION_COMPLEX_DISASSEMBLY	21	0.56	1.7	0.0001	0.1564
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	38	0.65	1.7	0.0472	0.1526
GO_THYROID_HORMONE_RECEPTOR_BINDING	29	0.48	1.7	0.0001	0.1485
GO_MULTI_ORGANISM_METABOLIC_PROCESS	127	0.5	1.68	0.0692	0.1825
GO_FILAMENTOUS_ACTIN	19	0.63	1.68	0.0248	0.1772
GO_H4_HISTONE_ACETYLTRANSFERASE_COMPLEX	17	0.49	1.68	0.0239	0.182
GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR	31	0.44	1.68	0.0001	0.1815
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	16	0.64	1.68	0.0339	0.18
GO_COATED_MEMBRANE	78	0.32	1.67	0.0001	0.1901
GO_RIBOSOMAL_SUBUNIT	146	0.53	1.67	0.0704	0.1909
GO_POSITIVE_REGULATION_OF_MRNA_PROCESSING	30	0.4	1.66	0.0001	0.1987
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY	28	0.5	1.66	0.0341	0.1985
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	405	0.36	1.65	0.0001	0.2022
GO_SMALL_RIBOSOMAL_SUBUNIT	61	0.57	1.65	0.071	0.2041
GO_SINGLE_STRANDED_DNA_BINDING	75	0.36	1.64	0.0001	0.2221
GO_U5_SNRNP	15	0.57	1.63	0.0001	0.2292
GO_U1_SNRNP	16	0.58	1.63	0.0001	0.2257
GO_SMALL_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	57	0.39	1.63	0.0001	0.2234
GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	29	0.41	1.63	0.0001	0.2342
GO_LARGE_RIBOSOMAL_SUBUNIT	85	0.52	1.63	0.0696	0.2331
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	28	0.44	1.62	0.0001	0.2414
GO_RRNA_METABOLIC_PROCESS	239	0.41	1.62	0.0468	0.2473
GO_RIBOSOME_BIOGENESIS	287	0.38	1.61	0.0001	0.2539
GO_COMPLEMENT_BINDING	16	0.61	1.6	0.0001	0.2876
GO_PROTEIN_K63_LINKED_UBIQUITINATION	33	0.38	1.6	0.0001	0.2914
GO_MLL1_2_COMPLEX	25	0.41	1.58	0.0001	0.3268
GO_BASAL_LAMINA	20	0.49	1.58	0.0001	0.3227
GO_SYNAPSE_ASSEMBLY	55	0.38	1.57	0.0001	0.3373
GO_N_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	23	0.46	1.56	0.0001	0.3565

GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	17	0.46	1.56	0.0001	0.3543
GO_NUCLEOID	37	0.38	1.55	0.0001	0.3914
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE	26	0.38	1.55	0.0001	0.3871
GO_EMBRYONIC_FORELIMB_MORPHOGENESIS	32	0.54	1.54	0.0001	0.4177
GO_ACETYLTRANSFERASE_COMPLEX	82	0.35	1.53	0.0001	0.4164
GO_POSTREPLICATION_REPAIR	49	0.35	1.53	0.0001	0.4015
GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	48	0.37	1.53	0.0001	0.4137
GO_NUCLEAR_REPLICATION_FORK	37	0.41	1.53	0.0001	0.3987
GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	23	0.45	1.53	0.0001	0.3992
GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS	82	0.33	1.52	0.0001	0.3965
GO_NEGATIVE_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	31	0.39	1.52	0.0001	0.3919
GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE	35	0.45	1.52	0.0001	0.4102
GO_DNA_GEOMETRIC_CHANGE	75	0.38	1.51	0.0001	0.4326
GO_CELL_SUBSTRATE_JUNCTION	384	0.32	1.5	0.0001	0.4338
GO_ACTIN_FILAMENT	67	0.39	1.49	0.0001	0.4627
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	45	0.41	1.49	0.0001	0.4604
GO_REGULATION_OF_PROTEIN_ACTIVATION_CASCADE	29	0.46	1.49	0.0001	0.4581
GO_CADHERIN_BINDING	28	0.49	1.48	0.0001	0.4528
GO_ANCHORING_JUNCTION	473	0.3	1.47	0.0001	0.4824
GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY	16	0.53	1.45	0.0001	0.5138
GO_HISTONE_METHYLTRANSFERASE_COMPLEX	63	0.31	1.45	0.0001	0.5266
GO_NONRIBOSOMAL_PEPTIDE_BIOSYNTHETIC_PROCESS	15	0.48	1.44	0.0001	0.5319
GO_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	262	0.25	1.43	0.0001	0.5403
GO_REGULATION_OF_TELOMERASE_ACTIVITY	40	0.35	1.41	0.0001	0.5693
GO_REPLISOME	27	0.48	1.4	0.0001	0.5747
GO_REGULATION_OF_TELOMERE_MAINTENANCE	62	0.32	1.4	0.0001	0.5692
GO_PROTEIN_AUTOUBIQUITINATION	47	0.35	1.39	0.0001	0.572
GO_DNA_REPAIR	421	0.27	1.39	0.0001	0.5706

GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	50	0.34	1.38	0.0001	0.5905
GO_ERYTHROCYTE_DEVELOPMENT	22	0.43	1.37	0.0001	0.6066
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	155	0.29	1.36	0.0001	0.6055
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	69	0.43	1.36	0.0001	0.6061
GO_TELOMERE_ORGANIZATION	77	0.36	1.35	0.0001	0.6133
GO_REGULATION_OF_PROTEIN_POLYMERIZATION	163	0.24	1.34	0.0001	0.6149
GO_PROTEIN_ACYLATION	138	0.25	1.33	0.0001	0.6451
GO_OSTEOBLAST_DIFFERENTIATION	125	0.29	1.33	0.0001	0.6418
GO_WNT_SIGNALING_PATHWAY	336	0.24	1.32	0.0001	0.6338
GO_EPIDERMAL_GROWTH_FACTOR_RECEPTOR_BINDING	30	0.42	1.32	0.0001	0.6375
GO_POSITIVE_REGULATION_OF_AXONOGENESIS	66	0.28	1.32	0.0001	0.6408
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	131	0.32	1.31	0.0001	0.6484
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_NITROGENOUS_GROUPS	21	0.35	1.31	0.0001	0.6479
GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	39	0.36	1.31	0.0001	0.646
GO_ACTIN_CYTOSKELETON_REORGANIZATION	54	0.32	1.3	0.0001	0.6478
GO_TRANSCRIPTION_COREPRESSOR_ACTIVITY	201	0.24	1.3	0.0001	0.648
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	197	0.28	1.26	0.0001	0.7109
GO_NUCLEAR_CHROMOSOME	435	0.23	1.22	0.0001	0.7705

Table S15- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in cerebellum. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Thr mice (Cerebellum)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_LYMPH_NODE_DEVELOPMENT	17	-0.66	-1.795	0.0001	1
GO_SYNCYTIUM_FORMATION	21	-0.51	-1.709	0.0001	1
GO_MYOBLAST_FUSION	17	-0.54	-1.701	0.0001	1
GO_GLYCOPROTEIN_COMPLEX	21	-0.63	-1.659	0.0001	1
GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	39	-0.46	-1.644	0.0001	1
GO_NEUTROPHIL_MEDIATED_IMMUNITY	17	-0.56	-1.631	0.0001	1
GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	21	-0.65	-1.628	0.0001	1
GO_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	20	-0.57	-1.627	0.0001	1
GO_GRANULOCYTE_ACTIVATION	18	-0.69	-1.618	0.0001	1
GO_PROTEIN_HYDROXYLATION	15	-0.57	-1.615	0.0001	1
GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	39	-0.54	-1.587	0.0001	1
GO_ENDOSOME_LUMEN	22	-0.47	-1.565	0.0001	1
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	36	-0.49	-1.562	0.0001	1
GO_POSITIVE_REGULATION_OF_JUN_KINASE_ACTIVITY	60	-0.46	-1.53	0.0001	1
GO_LIPOPOLYSACCHARIDE_BINDING	19	-0.59	-1.502	0.0001	1
GO_LYMPHOCYTE_COSTIMULATION	61	-0.45	-1.49	0.0001	1
GO_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	73	-0.35	-1.468	0.0001	1
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	135	-0.4	-1.464	0.0001	1
GO_PROTEIN_SERINE_THREONINE_TYROSINE_KINASE_ACTIVITY	38	-0.38	-1.451	0.0001	1

GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	51	-0.44	-1.447	0.0001	1
GO_REGULATION_OF_JUN_KINASE_ACTIVITY	75	-0.41	-1.436	0.0001	1
GO_REGULATION_OF_GLUCOSE_IMPORT	56	-0.37	-1.427	0.0001	1
GO_CELL_CELL_JUNCTION_ASSEMBLY	73	-0.33	-1.416	0.0001	1
GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	90	-0.32	-1.415	0.0001	1
GO_FILOPODIUM_MEMBRANE	18	-0.46	-1.406	0.0001	1
GO_RESPONSE_TO_ACTIVITY	65	-0.37	-1.398	0.0001	1
GO_BICELLULAR_TIGHT_JUNCTION_ASSEMBLY	31	-0.42	-1.379	0.0001	1
GO_RESPONSE_TO_STEROL	23	-0.37	-1.377	0.0001	1
GO_AMINO_SUGAR_METABOLIC_PROCESS	37	-0.38	-1.35	0.0001	1
GO_PLATELET_ALPHA_GRANULE_LUMEN	53	-0.38	-1.348	0.0001	1
GO_APICAL_JUNCTION_ASSEMBLY	39	-0.36	-1.335	0.0001	1
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	256	-0.33	-1.332	0.0001	1
GO_LIPID_LOCALIZATION	235	-0.32	-1.321	0.0001	1
GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	25	-0.4	-1.319	0.0001	1
GO_ACTIVATION_OF_MAPK_ACTIVITY	131	-0.31	-1.291	0.0001	1
GO_REGULATION_OF_KIDNEY_DEVELOPMENT	55	-0.36	-1.284	0.0001	1
GO_DETECTION_OF_STIMULUS	419	-0.33	-1.276	0.0001	1
GO_HEXOSE_METABOLIC_PROCESS	147	-0.28	-1.262	0.0001	1
GO_REGULATION_OF_CELL_ACTIVATION	416	-0.27	-1.2	0.0001	1

Table S16- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in hippocampus. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Ala mice (hippocampus)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_AP_TYPE_MEMBRANE_COAT_ADAPTOR_COMPLEX	36	0.48	1.781	1E-04	1
GO_INTRACELLULAR_LIPID_TRANSPORT	20	0.548	1.777	1E-04	0.6691
GO_MRNA_TRANSCRIPTION	21	0.383	1.747	1E-04	0.7079
GO_MRNA_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	15	0.489	1.717	1E-04	0.8021
GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING	18	0.661	1.656	1E-04	1
GO_MYOSIN_BINDING	58	0.419	1.609	1E-04	1
GO_COMPLEMENT_BINDING	16	0.685	1.586	1E-04	1
GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	37	0.475	1.582	1E-04	1
GO_VESICLE_DOCKING	52	0.429	1.556	1E-04	1
GO_CILIARY_TIP	42	0.439	1.554	1E-04	1
GO_RESPONSE_TO_AMINE	48	0.473	1.552	1E-04	1
GO_RIBONUCLEOPROTEIN_GRANULE	132	0.324	1.549	1E-04	1
GO_VESICLE_DOCKING_INVOLVED_IN_EXOCYTOSIS	34	0.391	1.539	1E-04	1
GO_HEXOSE_CATABOLIC_PROCESS	44	0.384	1.531	1E-04	1
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	26	0.549	1.523	1E-04	1
GO_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	17	0.517	1.519	1E-04	1
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	71	0.417	1.506	1E-04	1
GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	25	0.542	1.499	1E-04	1
GO_RESPONSE_TO_X_RAY	30	0.472	1.499	1E-04	1
GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	28	0.472	1.498	1E-04	1
GO_GANGLIOSIDE_METABOLIC_PROCESS	23	0.392	1.49	1E-04	1
GO_REGULATION_OF_SYNAPTIC_VESICLE_EXOCYTOSIS	19	0.533	1.488	1E-04	1

GO_TRNA_METHYLTRANSFERASE_ACTIVITY	16	0.481	1.485	1E-04	1
GO_MEMBRANE_DOCKING	63	0.389	1.482	1E-04	1
GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	48	0.386	1.48	1E-04	1
GO_CRANIAL_NERVE_MORPHOGENESIS	22	0.497	1.476	1E-04	1
GO_RESPONSE_TO_ANTIBIOTIC	43	0.427	1.475	1E-04	1
GO_PEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	20	0.495	1.474	1E-04	1
GO_DNA_REPAIR_COMPLEX	37	0.433	1.466	1E-04	1
GO_MONOSACCHARIDE_CATABOLIC_PROCESS	53	0.362	1.456	1E-04	1
GO_ORGAN_FORMATION	34	0.382	1.446	1E-04	1
GO_REGULATION_OF_PROTEIN_ACTIVATION_CASCADE	29	0.467	1.445	1E-04	1
GO_APOPTOTIC_CELL_CLEARANCE	24	0.437	1.435	1E-04	1
GO_ATRIOVENTRICULAR_VALVE_MORPHOGENESIS	16	0.442	1.427	1E-04	1
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	31	0.4	1.421	1E-04	1
GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	60	0.343	1.421	1E-04	1
GO_RESPONSE_TO_INTERLEUKIN_1	98	0.361	1.402	1E-04	1
GO_REGULATION_OF_NON_CANONICAL_WNT_SIGNALING_PATHWAY	19	0.51	1.39	1E-04	1
GO_VESICLE_ORGANIZATION	263	0.272	1.344	1E-04	1
GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	80	0.32	1.333	1E-04	1
GO_DORSAL_VENTRAL_PATTERN_FORMATION	89	0.337	1.331	1E-04	1
GO_SPLEEN_DEVELOPMENT	38	0.368	1.325	1E-04	1
GO_HEART_VALVE_DEVELOPMENT	32	0.379	1.322	1E-04	1
GO_VASCULATURE_DEVELOPMENT	452	0.289	1.318	1E-04	1
GO_CELL_AGING	62	0.331	1.311	1E-04	1
GO_MYELOID_LEUKOCYTE_MIGRATION	80	0.345	1.308	1E-04	1
GO_MEMBRANE_FUSION	137	0.261	1.218	1E-04	1
GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	306	0.224	1.195	1E-04	1

Table S17- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in hippocampus. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Thr mice (hippocampus)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_PROTEIN_DEACETYLASE_ACTIVITY	42	-0.44	-1.77	1E-04	1
GO_LONG_TERM_MEMORY	28	-0.53	-1.74	1E-04	1
GO_REGULATION_OF_GLUCOSE_IMPORT_IN_RESPONSE_TO_INSULIN_STIMULUS	16	-0.64	-1.7	1E-04	1
GO_DEACETYLASE_ACTIVITY	53	-0.38	-1.7	1E-04	1
GO_PRE_AUTOPHAGOSOMAL_STRUCTURE_MEMBRANE	15	-0.55	-1.69	1E-04	0.987
GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	18	-0.53	-1.68	1E-04	0.924
GO_NUCLEAR_TRANSCRIPTIONAL_REPRESSOR_COMPLEX	21	-0.45	-1.68	1E-04	0.83
GO_DNA_DIRECTED_RNA_POLYMERASE_II_CORE_COMPLEX	15	-0.56	-1.66	1E-04	0.763
GO_POSITIVE_REGULATION_OF_DNA_BINDING	41	-0.43	-1.58	1E-04	1
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN	19	-0.56	-1.57	1E-04	1
GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING	72	-0.38	-1.55	1E-04	1
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_CYCLIC_AMIDINES	26	-0.52	-1.55	1E-04	1
GO_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER	23	-0.44	-1.55	1E-04	1
GO_NAD_DEPENDENT_PROTEIN_DEACETYLASE_ACTIVITY	17	-0.54	-1.54	1E-04	0.968
GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	16	-0.71	-1.54	1E-04	0.913
GO_REGULATION_OF_PROTEIN_ACETYLATION	61	-0.4	-1.53	1E-04	0.871

GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	76	-0.44	-1.52	1E-04	0.919
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	46	-0.5	-1.52	1E-04	0.89
GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	31	-0.47	-1.51	1E-04	0.893
GO_CONDENSED_NUCLEAR_CHROMOSOME_CENTROMERIC_REGION	16	-0.68	-1.51	1E-04	0.877
GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	50	-0.47	-1.51	1E-04	0.858
GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR	37	-0.42	-1.5	1E-04	0.869
GO_RESPONSE_TO_PAIN	29	-0.51	-1.49	1E-04	0.913
GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	40	-0.36	-1.46	1E-04	0.93
GO_WIDE_PORE_CHANNEL_ACTIVITY	23	-0.48	-1.46	1E-04	0.924
GO_REGULATION_OF_DNA_BINDING	89	-0.35	-1.46	1E-04	0.915
GO_AROMATIC_AMINO_ACID_FAMILY_METABOLIC_PROCESS	26	-0.55	-1.43	1E-04	0.949
GO_GAP_JUNCTION_CHANNEL_ACTIVITY	16	-0.62	-1.42	1E-04	0.956
GO_REGULATION_OF_CATENIN_IMPORT_INTO_NUCLEUS	27	-0.42	-1.41	1E-04	0.951
GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	32	-0.41	-1.41	1E-04	0.931
GO_NEGATIVE_REGULATION_OF_CELLULAR_CATABOLIC_PROCESS	148	-0.3	-1.4	1E-04	0.943
GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	19	-0.36	-1.39	1E-04	0.95
GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	125	-0.33	-1.38	1E-04	1
GO_WNT_SIGNALING_PATHWAY_CALCIUM_MODULATING_PATHWAY	35	-0.41	-1.38	1E-04	1

GO_EMBRYONIC_DIGESTIVE_TRACT_DEVELOPMENT	32	-0.42	-1.37	1E-04	1
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	31	-0.36	-1.37	1E-04	1
GO_POSITIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	117	-0.33	-1.35	1E-04	1
GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	90	-0.38	-1.32	1E-04	1
GO_POSITIVE_REGULATION_OF_PROTEIN_IMPORT	101	-0.34	-1.32	1E-04	1
GO_STRUCTURE_SPECIFIC_DNA_BINDING	116	-0.26	-1.32	1E-04	1
GO_POSITIVE_REGULATION_OF_BINDING	125	-0.27	-1.3	1E-04	1
GO_COFACTOR_BINDING	248	-0.25	-1.29	1E-04	1
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	234	-0.24	-1.27	1E-04	1
GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	36	-0.38	-1.26	1E-04	1
GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	108	-0.28	-1.22	1E-04	1

Table S18- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in pre-frontal cortex. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Ala mice (pre-frontal cortex)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT_MEMBRANE	57	0.4554	1.844	0.0001	0.398
GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT	96	0.4408	1.768	0.0001	0.435
GO_PROTEIN_N_LINKED_GLYCOSYLATION	69	0.4144	1.738	0.0001	0.453
GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	23	0.4867	1.725	0.0001	0.448
GO_RESPONSE_TO_WATER	18	0.4663	1.706	0.0001	0.499
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	34	0.4909	1.698	0.0001	0.486
GO_CELLULAR_RESPONSE_TO_GAMMA_RADIATION	19	0.4945	1.696	0.0001	0.458
GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	24	0.4676	1.695	0.0001	0.42
GO_MYELIN_ASSEMBLY	15	0.5798	1.66	0.0001	0.623
GO_NEUTROPHIL_MEDIATED_IMMUNITY	17	0.5115	1.628	0.0001	0.719
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	27	0.4592	1.615	0.0001	0.794
GO_INTRACELLULAR_LIPID_TRANSPORT	20	0.4322	1.564	0.0001	1
GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	37	0.3939	1.552	0.0001	1
GO_NADP_BINDING	40	0.4329	1.545	0.0001	1
GO_RETINA_LAYER_FORMATION	22	0.4855	1.545	0.0001	1
GO_ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY	45	0.4351	1.542	0.0001	1
GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	60	0.3543	1.53	0.0001	1
GO_CALMODULIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	27	0.4487	1.524	0.0001	1
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	22	0.5761	1.521	0.0001	1
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	37	0.3978	1.517	0.0001	1

GO_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	92	0.3118	1.508	0.0001	0.963
GO_BILE_ACID_BIOSYNTHETIC_PROCESS	19	0.5096	1.455	0.0001	1
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	42	0.3636	1.455	0.0001	1
GO_ER_TO_GOLGI_TRANSPORT_VESICLE	52	0.3016	1.453	0.0001	1
GO_N_GLYCAN_PROCESSING	19	0.4395	1.446	0.0001	1
GO_MONOSACCHARIDE_TRANSPORT	53	0.4291	1.429	0.0001	1
GO_POSTTRANSCRIPTIONAL_GENE_SILENCING	36	0.3817	1.411	0.0001	1
GO_SARCOPLASMIC_RETICULUM_MEMBRANE	36	0.3971	1.405	0.0001	1
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	70	0.3427	1.405	0.0001	1
GO_GOLGI_TO_VACUOLE_TRANSPORT	24	0.4359	1.402	0.0001	1
GO_BASE_EXCISION_REPAIR	39	0.3646	1.401	0.0001	1
GO_MYOTUBE_CELL_DEVELOPMENT	23	0.4133	1.384	0.0001	1
GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	228	0.2331	1.361	0.0001	1
GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	59	0.3424	1.339	0.0001	1

Table S19- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in pre-frontal cortex. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Thr mice (pre-frontal cortex)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	29	-0.58	-1.935	0.0001	0.08791
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	20	-0.6	-1.745	0.0001	1
GO_PROTEIN_IMPORT_INTO_NUCLEUS_TRANSLOCATION	28	-0.48	-1.718	0.0001	1
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	36	-0.43	-1.708	0.0001	1
GO_POSITIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	33	-0.55	-1.688	0.0001	1
GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	17	-0.52	-1.663	0.0001	1
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	22	-0.6	-1.643	0.0001	1
GO_POSITIVE_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	15	-0.56	-1.643	0.0001	1
GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	32	-0.53	-1.636	0.0001	1
GO_ENDOCYTIC_VESICLE_MEMBRANE	129	-0.34	-1.625	0.0001	1
GO_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM	26	-0.49	-1.618	0.0001	1
GO_NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	32	-0.48	-1.612	0.0001	1
GO_SEX_DETERMINATION	22	-0.66	-1.611	0.0001	1
GO_HAIR_CELL_DIFFERENTIATION	35	-0.44	-1.607	0.0001	1
GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	25	-0.46	-1.591	0.0001	1
GO_ISOPRENOID_BINDING	27	-0.6	-1.581	0.0001	1
GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	18	-0.56	-1.575	0.0001	1
GO_ALCOHOL_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	21	-0.55	-1.562	0.0001	1

GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	35	-0.4	-1.545	0.0001	1
GO_COFACTOR_TRANSPORT	25	-0.46	-1.535	0.0001	1
GO_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	28	-0.41	-1.529	0.0001	1
GO_MATURE_B_CELL_DIFFERENTIATION	17	-0.53	-1.518	0.0001	1
GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	32	-0.45	-1.511	0.0001	1
GO_BLOOD_COAGULATION_FIBRIN_CLOT_FORMATION	23	-0.57	-1.508	0.0001	1
GO_EPHRIN_RECEPTOR_BINDING	24	-0.4	-1.506	0.0001	1
GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	29	-0.47	-1.506	0.0001	1
GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	64	-0.41	-1.497	0.0001	1
GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	25	-0.5	-1.486	0.0001	1
GO_CARDIAC_CELL_DEVELOPMENT	49	-0.39	-1.484	0.0001	1
GO_I_BAND	117	-0.37	-1.484	0.0001	1
GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	74	-0.39	-1.484	0.0001	1
GO_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	114	-0.34	-1.477	0.0001	1
GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	28	-0.5	-1.476	0.0001	1
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	64	-0.37	-1.474	0.0001	1
GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	21	-0.44	-1.471	0.0001	1
GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	54	-0.44	-1.466	0.0001	1
GO_REGULATION_OF_MAST_CELL_ACTIVATION	37	-0.47	-1.465	0.0001	1
GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	18	-0.48	-1.463	0.0001	1
GO_REGULATION_OF_VIRAL_TRANSCRIPTION	57	-0.38	-1.463	0.0001	1
GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	177	-0.3	-1.456	0.0001	1
GO_CONTRACTILE_FIBER	203	-0.35	-1.455	0.0001	1
GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	225	-0.36	-1.455	0.0001	1

GO_PARASYMPATHETIC_NERVOUS_SYSTEM_DEVELOPMENT	17	-0.5	-1.453	0.0001	1
GO_LIPID_PARTICLE	58	-0.3	-1.452	0.0001	1
GO_REGULATION_OF_APPETITE	21	-0.53	-1.444	0.0001	1
GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	75	-0.36	-1.437	0.0001	1
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_STIMULUS	22	-0.46	-1.435	0.0001	1
GO_LEUKOTRIENE_METABOLIC_PROCESS	23	-0.52	-1.426	0.0001	1
GO_CARDIOCYTE_DIFFERENTIATION	95	-0.37	-1.42	0.0001	1
GO_FERTILIZATION	127	-0.36	-1.416	0.0001	1
GO_SINGLE_FERTILIZATION	95	-0.37	-1.414	0.0001	1
GO_RESPONSE_TO_STARVATION	143	-0.28	-1.413	0.0001	1
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	27	-0.37	-1.409	0.0001	1
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	32	-0.43	-1.408	0.0001	1
GO_PROTEOGLYCAN_BINDING	26	-0.41	-1.391	0.0001	1
GO_RESPONSE_TO_PROSTAGLANDIN_E	25	-0.41	-1.39	0.0001	1
GO_PEPTIDASE_REGULATOR_ACTIVITY	177	-0.36	-1.386	0.0001	1
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	27	-0.42	-1.386	0.0001	1
GO_CARDIAC_CHAMBER_MORPHOGENESIS	103	-0.35	-1.385	0.0001	1
GO_REGULATION_OF_HEART_RATE	83	-0.32	-1.38	0.0001	1
GO_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS	19	-0.44	-1.378	0.0001	1
GO_MULTICELLULAR_ORGANISM_AGING	29	-0.47	-1.368	0.0001	1
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	31	-0.44	-1.353	0.0001	1
GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	163	-0.3	-1.344	0.0001	1
GO_RESPONSE_TO_PROSTAGLANDIN	31	-0.41	-1.341	0.0001	1
GO_TRABECULA_FORMATION	23	-0.44	-1.341	0.0001	1
GO_CELLULAR_RESPONSE_TO_FATTY_ACID	49	-0.35	-1.333	0.0001	1
GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	92	-0.35	-1.323	0.0001	1
GO_HORMONE_METABOLIC_PROCESS	139	-0.37	-1.315	0.0001	1
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	366	-0.28	-1.303	0.0001	1

GO_CARDIAC_CHAMBER_DEVELOPMENT	141	-0.3	-1.297	0.0001	1
GO_TUMOR_NECROSIS_FACTOR_RECEPTOR_SUPERFAMILY_BINDING	44	-0.32	-1.269	0.0001	1
GO_PROTEIN_HETEROOLIGOMERIZATION	83	-0.28	-1.267	0.0001	1
GO_OVULATION_CYCLE	108	-0.28	-1.238	0.0001	1
GO_ACTIVATION_OF_IMMUNE_RESPONSE	354	-0.24	-1.232	0.0001	1
GO_NEGATIVE_REGULATION_OF_SECRETION	185	-0.28	-1.22	0.0001	1

Table S20- Gene set enrichment analysis by gene ontology of microarray data obtained from Ala92-Dio2 mice and Thr92-Dio2 mice in striatum. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Ala mice (striatum)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_PHOSPHATIDIC_ACID_METABOLIC_PROCESS	30	0.495	1.74	0.0001	1
GO_PHOSPHATIDYLGLYCEROL_ACYL_CHAIN_REMODELING	16	0.685	1.72	0.0001	1
GO_NEUROPILIN_BINDING	15	0.553	1.664	0.0001	1
GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	18	0.522	1.653	0.0001	1
GO_CENTRIOLE_ASSEMBLY	19	0.484	1.637	0.0001	1
GO_RRNA_METHYLATION	17	0.521	1.605	0.0001	1
GO_DNA_STRAND_ELONGATION	30	0.514	1.587	0.0001	1
GO_CHROMOSOME_SEPARATION	18	0.571	1.586	0.0001	1
GO_CILIARY_PLASM	72	0.39	1.57	0.0001	1
GO_G2_DNA_DAMAGE_CHECKPOINT	33	0.435	1.568	0.0001	1
GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	17	0.671	1.568	0.0001	1
GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	39	0.574	1.563	0.0001	1
GO_VITAMIN_TRANSPORTER_ACTIVITY	20	0.552	1.556	0.0001	1
GO_OUTFLOW_TRACT_MORPHOGENESIS	56	0.398	1.556	0.0001	1
GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT_MEMBRANE	57	0.417	1.554	0.0001	1
GO_APICAL_JUNCTION_COMPLEX	124	0.347	1.553	0.0001	1
GO_RESPONSE_TO_X_RAY	30	0.461	1.545	0.0001	1
GO_TELOMERE_ORGANIZATION	77	0.45	1.539	0.0001	1
GO_PHOSPHATIDYLGLYCEROL_METABOLIC_PROCESS	30	0.466	1.538	0.0001	1
GO_NEGATIVE_REGULATION_OF_CELL_AGING	17	0.439	1.531	0.0001	1
GO_4_IRON_4_SULFUR_CLUSTER_BINDING	38	0.463	1.53	0.0001	1
GO_PHOSPHATIDYLSERINE_ACYL_CHAIN_REMODELING	16	0.648	1.518	0.0001	1
GO_ACYLGLYCEROL_O_ACYLTRANSFERASE_ACTIVITY	25	0.455	1.518	0.0001	1
GO_RESPONSE_TO_NITRIC_OXIDE	21	0.523	1.513	0.0001	1

GO_3_5_EXONUCLEASE_ACTIVITY	44	0.471	1.511	0.0001	1
GO_SULFUR_COMPOUND_TRANSPORT	30	0.513	1.507	0.0001	1
GO_PEPTIDE_CATABOLIC_PROCESS	20	0.536	1.504	0.0001	1
GO_PROTEIN_SELF_ASSOCIATION	41	0.506	1.503	0.0001	1
GO_CELL_AGING	62	0.382	1.501	0.0001	1
GO_EMBRYONIC_CRANIAL_SKELETON_MORPHOGENESIS	46	0.379	1.497	0.0001	1
GO_NEGATIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	26	0.514	1.496	0.0001	1
GO_COPPER_ION_TRANSPORT	18	0.649	1.493	0.0001	1
GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	332	0.378	1.485	0.0001	1
GO_CELLULAR_RESPONSE_TO_REACTIVE_NITROGEN_SPECIES	19	0.532	1.481	0.0001	1
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	39	0.482	1.48	0.0001	1
GO_CORTICAL_CYTOSKELETON_ORGANIZATION	35	0.399	1.479	0.0001	1
GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	216	0.432	1.475	0.0001	1
GO_PHOSPHATIDYLCHOLINE_ACYL_CHAIN_REMODELING	25	0.556	1.472	0.0001	1
GO_SPECIFICATION_OF_SYMMETRY	108	0.346	1.468	0.0001	1
GO_POSITIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	15	0.555	1.464	0.0001	1
GO_PHOSPHATIDYLINOSITOL_ACYL_CHAIN_REMODELING	16	0.679	1.46	0.0001	1
GO_STRAND_DISPLACEMENT	26	0.501	1.44	0.0001	1
GO_CELLULAR_RESPONSE_TO_NITRIC_OXIDE	15	0.512	1.438	0.0001	1
GO_SULFUR_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	25	0.502	1.431	0.0001	1
GO_ER_TO_GOLGI_TRANSPORT_VESICLE_MEMBRANE	36	0.394	1.431	0.0001	1
GO_NEGATIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	15	0.463	1.431	0.0001	1
GO_METHYLATED_HISTONE_BINDING	45	0.337	1.429	0.0001	1
GO_SYMPORTER_ACTIVITY	140	0.413	1.42	0.0001	1
GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	28	0.496	1.419	0.0001	1
GO_PHOSPHATIDYLETHANOLAMINE_ACYL_CHAIN_REMODELING	22	0.591	1.419	0.0001	1
GO_CARDIAC_CELL_DEVELOPMENT	49	0.428	1.412	0.0001	1

GO_MITOTIC_DNA_INTEGRITY_CHECKPOINT	96	0.31	1.409	0.0001	1
GO_METALLOPEPTIDASE_ACTIVITY	174	0.331	1.406	0.0001	1
GO_SARCOLEMMA	124	0.323	1.4	0.0001	1
GO_DEOXYRIBONUCLEASE_ACTIVITY	61	0.369	1.398	0.0001	1
GO_METALLOENDOPEPTIDASE_ACTIVITY	106	0.347	1.393	0.0001	1
GO_RESPONSE_TO_IONIZING_RADIATION	135	0.268	1.387	0.0001	1
GO_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	268	0.402	1.378	0.0001	1
GO_INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	117	0.401	1.378	0.0001	1
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_POLYMERIZATION	62	0.31	1.377	0.0001	1
GO_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	92	0.288	1.374	0.0001	1
GO_ER_TO_GOLGI_TRANSPORT_VESICLE	52	0.378	1.368	0.0001	1
GO_REGULATION_OF_CELLULAR_PH	70	0.362	1.367	0.0001	1
GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	49	0.435	1.365	0.0001	1
GO_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	48	0.338	1.357	0.0001	1
GO_APOPTOTIC_CELL_CLEARANCE	24	0.418	1.354	0.0001	1
GO_NODE_OF_RANVIER	15	0.494	1.347	0.0001	1
GO_CELLULAR_RESPONSE_TO_ALKALOID	32	0.384	1.344	0.0001	1
GO_AXIS_ELONGATION	27	0.439	1.34	0.0001	1
GO_CILIARY_PART	272	0.261	1.331	0.0001	1
GO_ION_GATED_CHANNEL_ACTIVITY	40	0.358	1.326	0.0001	1
GO_DETECTION_OF_BIOTIC_STIMULUS	20	0.492	1.321	0.0001	1
GO_VITAMIN_METABOLIC_PROCESS	104	0.294	1.321	0.0001	1
GO_CILIUM	413	0.253	1.319	0.0001	1
GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	162	0.432	1.313	0.0001	1
GO_CELLULAR_DEFENSE_RESPONSE	46	0.504	1.307	0.0001	1
GO_CARDIAC_SEPTUM_DEVELOPMENT	83	0.31	1.303	0.0001	1
GO_ACTIN_CYTOSKELETON	423	0.25	1.289	0.0001	1
GO_ANION_TRANSMEMBRANE_TRANSPORT	232	0.377	1.274	0.0001	1
GO_HEART_DEVELOPMENT	449	0.244	1.258	0.0001	1

GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	200	0.225	1.227	0.0001	1
GO_MACROMOLECULE_METHYLATION	180	0.252	1.2	0.0001	1
GO_POSITIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	197	0.269	1.198	0.0001	1

Table S21- Gene set enrichment analysis by gene ontology of microarray data obtained Ala92-Dio2 mice and Thr92-Dio2 mice in striatum. Listed gene sets were significant at a nominal p-value <1%.

Name of the Gene ontology (GO) gene sets enriched in Thr mice (striatum)	Size of gene sets	ES	NES	NOM p-val	FDR q-val
GO_LUNG_CELL_DIFFERENTIATION	25	-0.53	-1.7	1E-04	1
GO_NEGATIVE_REGULATION_OF_CIRCADIAN_RHYTHM	15	-0.58	-1.6	1E-04	1
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	34	-0.53	-1.6	1E-04	1
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	32	-0.42	-1.6	1E-04	1
GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	15	-0.56	-1.6	1E-04	1
GO_LIPASE_INHIBITOR_ACTIVITY	15	-0.65	-1.5	1E-04	1
GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	27	-0.53	-1.5	1E-04	1
GO_HEAT_SHOCK_PROTEIN_BINDING	84	-0.36	-1.5	1E-04	1
GO_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_DNA_BINDING	64	-0.4	-1.4	1E-04	1
GO_CIS_TRANS_ISOMERASE_ACTIVITY	39	-0.41	-1.4	1E-04	1
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_4	23	-0.48	-1.4	1E-04	1
GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	88	-0.3	-1.4	1E-04	1
GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	73	-0.29	-1.4	1E-04	1
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS	64	-0.31	-1.4	1E-04	1

GO_CORE_PROMOTER_BINDING	146	-0.28	-1.4	1E-04	1
GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	101	-0.28	-1.3	1E-04	1
GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	23	-0.39	-1.3	1E-04	1

Table S22 - Custom gene set enrichment analysis of positively regulated T3 responsive genes obtained from the microarray performed in the Striatum of Ala92-Dio2 vs Thr92-Dio2 mice.

Gene Symbol	**Gene title**
Htr2c	5-hydroxytryptamine (serotonin) receptor 2C
Hr	hairless homolog (mouse)
Ngf	nerve growth factor
Flywch2	FLYWCH family member 2
Gli1	glioma-associated oncogene homolog 1 (zinc finger protein)
Sema7a	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
Cntn2	contactin 2 (axonal)
Nefm	neurofilament, medium polypeptide
Itga7	integrin, alpha 7
Luzp1	leucine zipper protein 1
Rpe65	retinal pigment epithelium-specific protein 65kDa
Stard4	START domain containing 4, sterol regulated
Kcnj10	potassium inwardly-rectifying channel, subfamily J, member 10
Pdp1	pyruvate dehyrogenase phosphatase catalytic subunit 1
Nefh	neurofilament, heavy polypeptide 200kDa
Itih3	inter-alpha (globulin) inhibitor H3
Ier5	immediate early response 5
Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
Pvalb	parvalbumin

Table S23 - Custom gene set enrichment analysis of negatively regulated T3 responsive genes obtained from the microarray performed in the Striatum of Ala92-Dio2 vs Thr92-Dio2 mice.

Gene Symbol	Gene title
Col6a1	collagen, type VI, alpha 1
Cxadr	coxsackie virus and adenovirus receptor
Cirbp	cold inducible RNA binding protein
Agbl3	ATP/GTP binding protein-like 3
Col6a2	collagen, type VI, alpha 2
Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3
Odf4	outer dense fiber of sperm tails 4
Syce2	synaptonemal complex central element protein 2
Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
Pcsk4	proprotein convertase subtilisin/kexin type 4
Marcksl1	MARCKS-like 1
Mamdc2	MAM domain containing 2
Dgkg	diacylglycerol kinase, gamma 90kDa
Hapln1	hyaluronan and proteoglycan link protein 1

Table S24 - T3-responsive gene expression from striatum in Thr92-Dio2 and Ala92-Dio2 mice.

Genes	Thr92-Dio2 vs Ala92-Dio2 relative mRNA levels
Ier5	0.69±0.05***
Odf4	1.22±0.07*

Results are relative to *CycloB* mRNA levels and normalized to Thr92-Dio2 baseline animals; Values are the mean ± SEM of 9-10 independent samples; gene abbreviations are as indicated in the Table S27; $^*p \leq 0.05$ and $^{***}p \leq 0.001$ vs. Thr92-Dio2 baseline animals.

Table S25 - ER stress-related gene expression from the brain areas in Thr92-Dio2 and Ala92-Dio2 mice treated with 4-PBA.

Genes	**Cortex**	**Amygdala**
Bip	0.94±0.02	1.05±0.08
Chop	1.08±0.03	1.02±0.06
sXbp1	0.97±0.06	0.96±0.22
Ergic53	0.89±0.08	0.89±0.08
Pdi	0.88±0.05	1.01±0.08

Results are relative to *CycloB* mRNA levels and normalized to Thr92-Dio2 animals; Values are the mean ± SEM of 5-6 independent samples; gene abbreviations are as indicated in the Table S27.

Table S26 - Metabolic parameters in Thr92-Dio2 and Ala92-Dio2 mice.

Parameter	Reference	Hypothyroid+LT4	
		Thr92-Dio2	**Ala92-Dio2**
Distance	Fold	1.0±0.09	0.87±0.08
Sleep Time	%	36±8.3	53±5.8
VO2 - dark	Fold	1.0±0.08	0.89±0.02
VO2 - light	Fold	0.91±0.08	0.80±0.02

Except for sleep time, results are fold change in Ala92-Dio2 relative to Thr92-Dio2 animals for each specific group; for distance travelled 1.0 = 1332 and 1367 ft/48h respectively for Hypothyroid+LT4; for VO2 1.0 = 101 and 132 L/Kg•24h respectively for Hypothyroid+LT4; all groups were repeated twice with similar results; entries are the mean±SEM of 5-6 animals.

Table S27 – Oligonucleotide Primers

Mouse Gene		Sequence
Heat Shock Protein Family A (Hsp70) Member 5	*Bip* Forward	ACTTGGGGACCACCTATTCCT
	Bip Reverse	ATCGCCAATCAGACGCTCC
DNA-damage inducible transcript 3	*Chop* Forward	CTGGAAGCCTGGTATGAGGAT
	Chop Reverse	CAGGGTCAAGAGTAGTGAAGGT
Spliced X-box binding protein 1	*sXbp1* Forward	TTACGAGAGAAAACTCATGGGC
	sXbp1 Reverse	GGGTCCAACTTGTCCAGAATGC
Endoplasmic reticulum-golgi intermediate compartment 1	*Ergic53* Forward	TGCTGTCTTTCAGCCAATTCA
	Ergic53 Reverse	AGCTGTATTTGTACTCGAAACGG
Protein disulfide isomerase	*Pdi* Forward	GCCGCAAAACTGAAGGCAG
	Pdi Reverse	GGTAGCCACGGACACCATAC
Immediate early response 5	*Ier5* Forward	TCACCGCATCGTCAGCATC
	Ier5 Reverse	GGTCACTCAGGTAGACTTGGC
Outer dense fiber of sperm tails 4	*Odf4* Forward	ATGGAACCTGACTTGAATGAGGA
	Odf4 Reverse	CATTGAAAGGGCAATAGGGAGTT
Human Gene		**Sequence**
Heat Shock Protein Family A (Hsp70) Member 5	*BIP* Forward	TGTTCAACCAATTATCAGCAAACTC
	BIP Reverse	TTCTGCTGTATCCTCTTCACCAGT
DNA-damage inducible transcript 3	*CHOP* Forward	AGAACCAGGAAACGGAAACAGA
	CHOP Reverse	TCTCCTTCATGCGCTGCTTT
Spliced X-box binding protein 1	*sXBP1* Forward	CTGAGTCCGAATCAGGTGCAG
	sXBP1 Reverse	ATCCATGGGGAGATGTTCTGG
Total X-box binding protein 1	*tXBP1*Forward	TGGCCGGGTCTGCTGAGTCCG
	tXBP1 Reverse	ATCCATGGGGAGATGTTCTGG
Activating transcription factor 4	*ATF4* Forward	GTTCTCCAGCGACAAGGCTA
	ATF4 Reverse	ATCCTGCTTGCTGTTGTTGG