

## Supporting Information

**Table S1: Candidate genes involved in the etiology of FASD, catalogued in NeuroCarta**

Symbol	Gene name	Probe
Abca1	ATP-binding cassette, subfamily A (ABC1), member 1	ILMN_1650701
Abcg1	ATP-binding cassette, subfamily G (WHITE), member 1	ILMN_1354046
Actb	actin, beta	ILMN_1355039
Actb	actin, beta	ILMN_2038798
Actb	actin, beta	ILMN_2038799
Adcy8	adenylate cyclase 8 (brain)	ILMN_1350196
Akt1	v-akt murine thymoma viral oncogene homolog 1	ILMN_1353102
Alpl	alkaline phosphatase, liver/bone/kidney	ILMN_1372113
Apoe	apolipoprotein E	ILMN_1367529
Atoh1	atonal homolog 1 (Drosophila)	ILMN_1368168
Bad	BCL2-associated agonist of cell death	ILMN_1369751
Bcl2	B-cell CLL/lymphoma 2	ILMN_1366150
Bcl2l1	Bcl2-like 1	ILMN_1355163
Bcl2l1	Bcl2-like 1	ILMN_1365285
Bdnf	brain-derived neurotrophic factor	ILMN_1360447
Cacna1c	calcium channel, voltage-dependent, L type, alpha 1C subunit	ILMN_1370304
Casp3	caspase 3	ILMN_1349218
Cat	catalase	ILMN_1369530
Ccnd1	cyclin D1	ILMN_1350372
Ccnd2	cyclin D2	ILMN_1362471
Chat	choline O-acetyltransferase	ILMN_1363883
Creb1	cAMP responsive element binding protein 1	ILMN_1649829
Creb1	cAMP responsive element binding protein 1	ILMN_1376791
Cyba	cytochrome b-245, alpha polypeptide	ILMN_1366276
Dlg4	discs, large homolog 4 (Drosophila)	ILMN_1650748
Duox1	dual oxidase 1	ILMN_1367874
E2f1	E2F transcription factor 1	ILMN_1360877
Egfr	epidermal growth factor receptor	ILMN_1362571
ErbB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	ILMN_1350020
Fgfr2	fibroblast growth factor receptor 2	ILMN_1371701
Gad1	glutamate decarboxylase 1	ILMN_1351478
Gfap	glial fibrillary acidic protein	ILMN_1376423
Gpx1	glutathione peroxidase 1	ILMN_1372510
Gpx3	glutathione peroxidase 3	ILMN_1365802
Gria2	glutamate receptor, ionotropic, AMPA 2	ILMN_1356417
Gria3	glutamate receptor, ionotropic, AMPA 3	ILMN_1368538
Gria4	glutamate receptor, ionotropic, AMPA 4	ILMN_1371769
Grin1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	ILMN_1365529
Grin2b	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	ILMN_1366396
Grm5	glutamate receptor, metabotropic 5	ILMN_1361607
Gsk3b	glycogen synthase kinase 3 beta	ILMN_1349648
Gsr	glutathione reductase	ILMN_1352580
Gstm2	glutathione S-transferase mu 2	ILMN_1350896
Gstm3	glutathione S-transferase mu 3	ILMN_1374835
Hoxa1	homeo box A1	ILMN_1353666
Hoxb4	homeo box B4	ILMN_1363620
Hoxd4	homeo box D4	ILMN_1367426
Hoxd4	homeo box D4	ILMN_1353520
Igf1r	insulin-like growth factor 1 receptor	ILMN_1374575
Igf2	insulin-like growth factor 2	ILMN_1359301
Igf2r	insulin-like growth factor 2 receptor	ILMN_1349413
Insr	insulin receptor	ILMN_1360127
Irs1	insulin receptor substrate 1	ILMN_1360680

L1cam	L1 cell adhesion molecule	ILMN_1376861
Mapk1	mitogen activated protein kinase 1	ILMN_1349290
Mapt	microtubule-associated protein tau	ILMN_1354816
Ncf2	neutrophil cytosolic factor 2	ILMN_1365484
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	ILMN_1365082
Neurod1	neurogenic differentiation 1	ILMN_1363838
Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	ILMN_1365512
Notch1	notch 1	ILMN_1359640
Nox3	NADPH oxidase 3	ILMN_1376975
Noxa1	NADPH oxidase activator 1	ILMN_1365297
Noxo1	NADPH oxidase organizer 1	ILMN_1368197
Ntf3	neurotrophin 3	ILMN_1371735
Ntf4	neurotrophin 4	ILMN_1363013
Ntrk1	neurotrophic tyrosine kinase, receptor, type 1	ILMN_1370831
Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	ILMN_1366426
Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	ILMN_1362434
Plat	plasminogen activator, tissue	ILMN_1358127
Rac1	ras-related C3 botulinum toxin substrate 1	ILMN_1355225
Rara	retinoic acid receptor, alpha	ILMN_1368986
Rbp1	retinol binding protein 1, cellular	ILMN_1375320
S100b	S100 calcium binding protein B	ILMN_1373043
Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	ILMN_1357678
Serpine1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	ILMN_1376417
Serpine1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	ILMN_2040557
Sod1	superoxide dismutase 1, soluble	ILMN_1353544
Sod2	superoxide dismutase 2, mitochondrial	ILMN_1367263
Sod3	superoxide dismutase 3, extracellular	ILMN_1361581

**Table S2a: Correlation of expression profiles among all samples and among replicates in PFC microarray dataset**

	Quantiles for Pearson correlations among samples					n
	0%	25%	50%	75%	100%	
All PFC samples	0.897	0.966	0.971	0.976	1.000	96
Hybridization replicate group 1	0.957	0.971	0.979	0.982	1.000	9
Amplification replicate	0.980	0.980	0.990	1.000	1.000	2

**Table S2b: Correlation of expression profiles among all samples and among replicates in HPC microarray dataset**

	Quantiles for Pearson correlations among samples					n
	0%	25%	50%	75%	100%	
All HPC samples	0.925	0.958	0.965	0.971	1.000	96
Hybridization replicate group 1	0.964	0.970	0.974	0.984	1.000	4
Hybridization replicate group 2	0.971	0.972	0.986	0.990	1.000	4
Hybridization replicate group 3	0.957	0.963	0.980	0.989	1.000	4
Hybridization replicate group 4	0.961	0.968	0.971	0.982	1.000	4
Mean of replicates	0.963	0.968	0.978	0.986	1.000	

**Table S3: Sequences of primers used for RT-qPCR.**

Gene	Type	Accession	Forward primer (5'-3')	Reverse primer (5'-3')
Actb	Reference	NM_031144.2	CTGCCCTGGCTCCTAGCACCAT	CTCAGTAACAGTCCGCCTAGAAGCA
Hprt1	Reference	NM_012583.2	TGTGGCCAGTAAAGAACTAGCAGACGTT	GTGCAAATCAAAAGGGACGCAGCAACA
Pgk1	Reference	NM_053291.3	AGTCCTTCCTGGGGTGGATGCTCT	AGGGTTCCTGGTGCTGCGTCTT
Sdha	Reference	NM_130428.1	TGCCAGGGAAGATTACAAGGTGCGG	AGAGGGTGTGCTTCCTCCAGTGTC
Ubc	Reference	NM_017314.1	CACCAAGAAGGTCAAACAGGA	GCAAGAACTTTATTCAAAGTGCAA
Acsl3	Target	NM_057107.1	ACTCCCGAAACTGGTCTGGTGACTGATG	ATCCGCTCAATGTCTGCCTGGTAGTGT
Ap1s2	Target	NM_001127531.2	TGCTACTGCCTAGTCGTCGGA	GCCAACCAATGCCACTTTGCTTCAG
Atp6ap1	Target	NM_031785.1	GGGTAAAGAATGAGCGGTACACTGGGG	ACTTCTGGCTTCTTGACAGGCAATCCTT
Dusp6	Target	NM_053883.2	GTGGGATGCGACAGGTTGTGAGGA	ACACCACGAACATCATGGAGCAAGTGAA
H2afv	Target	NM_001106019.1	CTGATCGGAAAGAAGGGGCAGCAGA	CACACACAGTGAGGACAGCAGGTCA
Med28	Target	NM_001107217.1	TGCAGCACAAGAAGCCAGCCGA	GGTCTGCTTCAGAGGTGCAGGTATGTT
Ndfip1	Target	NM_001013059.1	ACTGGCTCTGGTGGGTGTTCTTGGT	AGAACTCTGGTCTGGGGAGATTTGAGA
Pex11g	Target	NM_001105902.1	AACGAGACTCAGATTCCCAGAGCGG	ATTTGAGCCCCTTTCCACCCCA
Ppp1r14a	Target	NM_130403.1	GACGAGCTGCTGGAATTGGACAGTGA	GGACGAAGTCCTCTGTGGGATTGAGG
Rnasek	Target	NM_001137561.2	TTGGGACTGTTACCCTGGCGAGAC	TCCAGGGGTTGGGCAGCAGTTT
Tcf4	Target	NM_053369.1	AGAGAAGGTGTCTCAGAGCCTCCC	GGTGGCAACTTGGACCCTTTACATC
Cnih2	Target	NM_001025132.1	GGGCCAGGCAAAGCTCTAAACAGGG	GGCCCAAATTCCTGAAACGGACA
Loc688637	Target	XM_001067706.2	AGAGGCCATGCGGAGCTTTTGTAGT	AAATCACGCTTTCTGTCCAGCATCACCC
MCG125002	Target	NM_001034154.1	TCTAGCCCAAAGGAACCCAAAGCGG	GGCTGAACGTCTTCTGGTGGAGGA
Rgs3	Target	NM_019340.1	TGGCACATGAACGGTAATAGGAGAGCC	TGGGACCAGCAAATGCCCTGAAACT

**Table S4a: Microarray expression results for common reference genes in PFC of Day 16 Saline animals.** Genes in bold were used as reference genes for RT-qPCR.

Gene Symbol	Probe_ID	Fold change			Average log2(expression)	F	P-value	Adjusted p-value
		E:C	PF:C	E:PF				
Polr2a_mapped	ILMN_1372495	0.0043	-0.0666	0.0709	7.71	0.24	0.79	0.94
Tbp	ILMN_1349379	0.0576	-0.0107	0.0683	8.04	0.29	0.75	0.93
Ubc	ILMN_1350494	0.0879	-0.0244	0.1123	13.83	0.33	0.72	0.93
<b>Pgk1</b>	<b>ILMN_1369074</b>	<b>0.0624</b>	<b>0.1493</b>	<b>-0.0869</b>	<b>12.30</b>	<b>0.52</b>	<b>0.60</b>	<b>0.89</b>
Sdha	ILMN_1357678	0.1627	-0.0170	0.1797	10.53	0.83	0.45	0.84
Hmbs	ILMN_1353365	0.0689	-0.0863	0.1552	8.13	0.96	0.40	0.82
<b>Actb</b>	<b>ILMN_1355039</b>	<b>-0.1662</b>	<b>-0.1925</b>	<b>0.0263</b>	<b>12.13</b>	<b>1.12</b>	<b>0.35</b>	<b>0.79</b>
<b>Hprt1</b>	<b>ILMN_1367708</b>	<b>0.1953</b>	<b>0.1306</b>	<b>0.0647</b>	<b>11.73</b>	<b>1.17</b>	<b>0.33</b>	<b>0.79</b>
Gusb	ILMN_1350544	0.0857	0.1865	-0.1008	7.78	1.24	0.31	0.78
H2A.1	ILMN_1372198	-0.1490	-0.0356	-0.1134	7.41	1.33	0.29	0.77
Gapdh	ILMN_1649859	0.2458	-0.0535	0.2992	13.33	1.61	0.23	0.73
Tfric	ILMN_1360908	0.2191	0.1764	0.0427	7.13	2.02	0.16	0.70
<b>Actb</b>	<b>ILMN_2038799</b>	<b>-0.2469</b>	<b>-0.1103</b>	<b>-0.1366</b>	<b>13.74</b>	<b>2.12</b>	<b>0.15</b>	<b>0.68</b>
<b>Actb</b>	<b>ILMN_2038798</b>	<b>-0.3199</b>	<b>-0.4015</b>	<b>0.0816</b>	<b>11.87</b>	<b>2.89</b>	<b>0.083</b>	<b>0.63</b>
B2m	ILMN_1368656	0.2073	-0.2072	0.4144	12.99	3.62	0.049	0.57
Ywhaz	ILMN_1373913	-0.3891	0.1622	-0.5513	13.53	4.93	0.020	0.49

**Table S4b: Microarray expression results for common reference genes in HPC of Day 16 Saline animals.** Genes in bold were used as reference genes for RT-qPCR.

Gene Symbol	Probe ID	Fold change			Average log2(expression)	F	P-value	Adjusted p-value
		E:C	E:PF	PF:C				
Sdha	ILMN_1357678	0.0006	0.0201	-0.0195	10.24	0.01	0.99	1.00
Gusb	ILMN_1350544	-0.0643	-0.0581	-0.0062	7.83	0.18	0.84	0.98
<b>Pgk1</b>	<b>ILMN_1369074</b>	<b>-0.1403</b>	<b>-0.0156</b>	<b>-0.1248</b>	<b>12.36</b>	<b>0.46</b>	<b>0.64</b>	<b>0.96</b>
Gapdh	ILMN_1649859	0.1529	-0.0998	0.2527	12.95	0.64	0.54	0.95
Tfric	ILMN_1360908	0.0033	-0.1165	0.1198	7.01	0.65	0.54	0.95
<b>Actb</b>	<b>ILMN_1355039</b>	<b>0.2317</b>	<b>-0.1115</b>	<b>0.3431</b>	<b>12.27</b>	<b>0.90</b>	<b>0.42</b>	<b>0.93</b>
<b>Actb</b>	<b>ILMN_2038798</b>	<b>0.2406</b>	<b>-0.2054</b>	<b>0.4460</b>	<b>11.87</b>	<b>1.19</b>	<b>0.33</b>	<b>0.91</b>
<b>Ubc</b>	<b>ILMN_1350494</b>	<b>0.3358</b>	<b>0.2165</b>	<b>0.1194</b>	<b>13.49</b>	<b>1.29</b>	<b>0.30</b>	<b>0.91</b>
Polr2a_mapped	ILMN_1372495	0.0352	-0.1551	0.1903	7.83	1.57	0.23	0.89
Hmbs	ILMN_1353365	-0.1870	0.0817	-0.2686	8.22	1.68	0.21	0.88
<b>Actb</b>	<b>ILMN_2038799</b>	<b>0.2694</b>	<b>-0.1511</b>	<b>0.4205</b>	<b>13.81</b>	<b>2.12</b>	<b>0.15</b>	<b>0.85</b>
Tbp	ILMN_1349379	-0.1822	0.1249	-0.3070	8.32	2.49	0.11	0.83
H2A.1	ILMN_1372198	0.0125	0.2517	-0.2391	7.83	3.00	0.07	0.78
Ywhaz	ILMN_1373913	-0.3770	-0.2804	-0.0966	13.58	3.23	0.06	0.76
Hprt1	ILMN_1367708	-0.3556	0.0844	-0.4400	11.66	3.49	0.05	0.75
B2m	ILMN_1368656	-0.0322	0.2943	-0.3265	12.96	4.31	0.03	0.72

**Table S5a: Genes showing common change in expression in PFC of E and PF compared to C animals under steady state conditions.**

Bold =  $p < 0.05$ . na = probe had no specific alignment to current RefSeq RNA database

Gene Symbol	Gene Name	Average Expression	F	p-value	q-value	Fold change		
						Ethanol/Control	Ethanol/Pair-fed	Pair-fed/Control
Rpusd1	RNA pseudouridylate synthase domain containing 1	9.4	11.9	5.7E-04	0.23	<b>0.68</b>	0.93	<b>0.73</b>
Nme2	NME/NM23 nucleoside diphosphate kinase 2	11.5	10.7	9.7E-04	0.25	<b>0.70</b>	0.89	<b>0.79</b>
Klhl24	kelch-like 24 (Drosophila)	9.6	10.7	9.4E-04	0.25	<b>0.69</b>	0.91	<b>0.75</b>
Ndrp2	N-myc downstream regulated gene 2	13.5	11.2	7.6E-04	0.23	<b>0.71</b>	0.95	<b>0.75</b>
ILMN_1370609	na	7.1	12.3	4.8E-04	0.23	<b>0.60</b>	1.10	<b>0.55</b>
Rasl10a	RAS-like, family 10, member A	8.5	13.3	3.2E-04	0.23	<b>0.74</b>	1.14	<b>0.64</b>
ILMN_1359879	na	9.2	10.9	8.6E-04	0.24	<b>0.76</b>	1.17	<b>0.65</b>
Grik5	glutamate receptor, ionotropic, kainate 5	9.4	12.6	4.3E-04	0.23	<b>1.33</b>	0.84	<b>1.58</b>
RGD1309651	similar to 1190005I06Rik protein	7.7	14.0	2.4E-04	0.22	<b>1.31</b>	0.88	<b>1.49</b>
ILMN_1368369	na	7.6	11.1	7.8E-04	0.23	<b>1.38</b>	0.92	<b>1.50</b>
Satb1	SATB homeobox 1	10.2	12.2	5.0E-04	0.23	<b>1.42</b>	0.91	<b>1.55</b>
Tmem178b	transmembrane protein 178B	9.5	15.5	1.4E-04	0.16	<b>1.37</b>	0.87	<b>1.56</b>
ILMN_1356747	na	14.1	10.7	9.7E-04	0.25	<b>1.41</b>	0.97	<b>1.45</b>
ILMN_1351805	na	12.1	12.0	5.4E-04	0.23	<b>1.45</b>	0.95	<b>1.53</b>
Mapkapk2	mitogen-activated protein kinase-activated protein kinase 2	8.4	11.9	5.7E-04	0.23	<b>1.33</b>	0.97	<b>1.38</b>
Igfbp7	insulin-like growth factor binding protein 7	11.9	11.2	7.6E-04	0.23	<b>1.43</b>	0.99	<b>1.45</b>
Nrxn3	neurexin 3	10.7	16.5	9.8E-05	0.13	<b>1.46</b>	0.86	<b>1.69</b>
Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	11.8	11.4	7.0E-04	0.23	<b>1.38</b>	1.01	<b>1.37</b>
ILMN_1352779	na	7.1	11.7	6.0E-04	0.23	<b>1.35</b>	1.00	<b>1.36</b>
Gpkow	G patch domain and KOW motifs	7.1	10.9	8.8E-04	0.24	<b>1.37</b>	1.04	<b>1.32</b>
LOC685828	hypothetical protein LOC685828	7.6	12.6	4.3E-04	0.23	<b>1.47</b>	0.99	<b>1.49</b>
Gabbr2	gamma-aminobutyric acid (GABA) A receptor, rho 2	7.1	12.5	4.3E-04	0.23	<b>1.37</b>	1.01	<b>1.36</b>
Chn1	chimerin (chimaerin) 1	13.3	11.6	6.5E-04	0.23	<b>1.51</b>	1.08	<b>1.40</b>
RGD1565784	RGD1565784	9.4	11.8	5.9E-04	0.23	<b>1.37</b>	1.05	<b>1.30</b>
ILMN_1366825	na	9.9	13.1	3.4E-04	0.23	<b>1.42</b>	1.01	<b>1.41</b>
Rpl27-l1	ribosomal protein L27-like 1	9.9	11.5	6.8E-04	0.23	<b>1.40</b>	1.16	<b>1.21</b>
ILMN_1366004	na	8.2	11.8	5.8E-04	0.23	<b>1.42</b>	1.11	<b>1.28</b>
ILMN_1359502	na	8.5	13.0	3.7E-04	0.23	<b>1.53</b>	1.06	<b>1.44</b>
ILMN_1366169	na	9.3	16.6	9.3E-05	0.13	<b>1.55</b>	0.98	<b>1.58</b>
ILMN_1367588	na	9.4	13.2	3.3E-04	0.23	<b>1.61</b>	1.18	<b>1.37</b>
ILMN_1359650	na	8.2	14.1	2.3E-04	0.22	<b>1.48</b>	1.10	<b>1.34</b>
RGD1309730	similar to RIKEN cDNA B230118H07	9.2	16.7	9.2E-05	0.13	<b>1.57</b>	1.02	<b>1.53</b>
Sep15	selenoprotein 15	11.3	18.0	5.9E-05	0.12	<b>1.55</b>	1.00	<b>1.55</b>
Hint3	histidine triad nucleotide binding protein 3	9.0	16.2	1.1E-04	0.14	<b>1.52</b>	1.07	<b>1.43</b>
ILMN_1352441	na	13.1	15.0	1.7E-04	0.18	<b>1.74</b>	1.19	<b>1.46</b>
ILMN_1366381	na	10.5	16.5	9.9E-05	0.13	<b>1.55</b>	1.07	<b>1.45</b>
Psma7	proteasome (prosome, macropain) subunit, alpha type 7	11.8	25.5	6.9E-06	0.06	<b>1.68</b>	0.86	<b>1.97</b>
ILMN_1368258	na	10.5	19.8	3.4E-05	0.10	<b>1.76</b>	1.05	<b>1.68</b>
LOC301193	similar to Discs large homolog 5	10.5	21.4	2.1E-05	0.07	<b>1.74</b>	1.04	<b>1.67</b>

**Table S5b: Genes showing common change in expression in HPC of E and PF compared to C animals under steady-state conditions.**

Bold =  $p < 0.05$ . na = probe had no specific alignment to current RefSeq RNA database

Gene Symbol	Gene Name	Average Expression	F	p-value	q-value	Fold change		
						Ethanol/ Control	Ethanol/ Pair-fed	Pair-fed/ Control
LOC100360417	RUN and SH3 domain containing 1-like	10.4	12.8	2.9E-04	0.21	<b>1.65</b>	1.10	<b>1.50</b>
Atp5a1	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	13.1	13.5	2.2E-04	0.20	<b>1.35</b>	0.91	<b>1.48</b>
Acsl1	acyl-CoA synthetase long-chain family member 1	9.5	13.0	2.7E-04	0.21	<b>1.34</b>	0.91	<b>1.47</b>
Sqle	squalene epoxidase	10.0	14.1	1.7E-04	0.17	<b>1.44</b>	1.01	<b>1.42</b>

**Table S6a: Genes differentially expressed in PFC among all 3 prenatal treatment groups under steady-state conditions.**

(p < 0.05 for each contrast).

Gene Symbol	Gene Name	Average Expression	F	p-value	q-value	Fold change		
						Ethanol/Control	Ethanol/Pairfed	Pairfed/Control
Baiap2	BAI1-associated protein 2	10.8	10.6	9.8E-04	0.25	0.69	0.83	0.83
Lxn	latexin	8.3	15.8	1.2E-04	0.15	0.77	1.42	0.54
Tuba1a	tubulin, alpha 1A	14.1	25.2	7.5E-06	0.06	0.77	1.38	0.56
Tom1	target of myb1 homolog (chicken)	8.2	10.7	9.3E-04	0.25	0.83	1.17	0.71
Sumf1	sulfatase modifying factor 1	8.3	12.8	3.8E-04	0.23	1.17	1.45	0.81
Acat1	acetyl-CoA acetyltransferase 1	8.3	12.5	4.3E-04	0.23	1.20	0.80	1.49
Dynlrb1	dynein light chain roadblock-type 1	12.2	11.4	6.8E-04	0.23	1.21	0.79	1.54
Rnd2	Rho family GTPase 2	11.0	11.0	8.1E-04	0.23	1.22	0.85	1.43
Epn1	Epsin 1	8.7	22.7	1.4E-05	0.06	1.24	0.75	1.66
LOC100361558	histone H3.3B-like	11.4	11.8	5.9E-04	0.23	1.24	0.79	1.56
Acly	ATP citrate lyase	10.0	11.4	7.1E-04	0.23	1.25	0.78	1.60
Peo1	progressive external ophthalmoplegia 1	8.7	13.9	2.6E-04	0.22	1.26	0.80	1.58
Hbb-b1	hemoglobin, beta adult major chain	10.8	24.7	8.6E-06	0.06	1.28	1.73	0.74
Anxa4	annexin A4	9.8	13.7	2.7E-04	0.22	1.29	0.84	1.54
Ckb	creatine kinase, brain	12.8	16.5	9.8E-05	0.13	1.34	0.72	1.86
Scd	stearoyl-Coenzyme A desaturase 1	13.2	12.6	4.1E-04	0.23	1.36	0.78	1.75
LOC501223	similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large protein P-dlg)	11.2	13.9	2.5E-04	0.22	1.55	1.21	1.27
Rps27l3	ribosomal protein S27-like 3	7.4	18.5	5.0E-05	0.11	1.65	1.21	1.37
LOC363320	similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large protein P-dlg)	9.4	22.6	1.5E-05	0.06	1.90	1.26	1.50

**Table S6b: Genes differentially expressed in HPC among all 3 prenatal treatment groups under steady-state conditions.**

(p < 0.05 for each contrast).

Gene Symbol	Gene Name	Average Expression	F	p-value	q-value	Fold change		
						Ethanol/Control	Ethanol/Pairfed	Pairfed/Control
Phlpp1	PH domain and leucine rich repeat protein phosphatase 1	10.2	12.7	3.1E-04	0.21	0.78	0.63	1.24
RGD1565117	similar to 40S ribosomal protein S26	9.6	22.4	9.5E-06	0.04	1.24	1.61	0.77
Trpv4	transient receptor potential cation channel, subfamily V, member 4	7.4	27.0	2.6E-06	0.02	1.26	1.84	0.69
Agap1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	10.1	12.7	3.0E-04	0.21	1.30	0.81	1.59
Mgp	matrix Gla protein	9.0	12.9	2.8E-04	0.21	1.42	1.97	0.72
Col8a1	collagen, type VIII, alpha 1	7.9	17.2	5.2E-05	0.12	1.46	2.47	0.59
Igf2	insulin-like growth factor 2	11.8	13.4	2.3E-04	0.20	1.63	2.80	0.58

E<PF<C

C<PF<E

PF<E<C

C<E<PF

E<C<PF

**Table S7a: Genes differentially expressed in PFC of Pair-fed vs both E and C animals under steady-state conditions.**Bold =  $p < 0.05$ . na = probe had no specific alignment to current RefSeq RNA database.

Gene Symbol	Gene name	Average Expression	F	p-value	q-value	Fold change		
						Pair-fed/ Control	Ethanol/ Pair-fed	Ethanol/ Control
ILMN_1358743	na	8.0	11.5	6.8E-04	0.23	<b>0.81</b>	<b>1.44</b>	1.17
Lrp1	low density lipoprotein receptor-related protein 1	8.8	12.4	4.6E-04	0.23	<b>1.38</b>	<b>0.69</b>	0.95
ILMN_1361625	na	9.8	11.4	6.9E-04	0.23	<b>1.58</b>	<b>0.72</b>	1.13
Ak2	adenylate kinase 2	9.9	13.4	3.1E-04	0.23	<b>1.69</b>	<b>0.67</b>	1.13
ILMN_1359487	na	10.6	11.0	8.3E-04	0.24	<b>1.53</b>	<b>0.76</b>	1.16
Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	10.8	11.7	6.2E-04	0.23	<b>1.47</b>	<b>0.72</b>	1.06
Park7	parkinson protein 7	12.2	12.5	4.4E-04	0.23	<b>0.70</b>	<b>1.38</b>	0.97

**Table S7b: Genes differentially expressed in HPC of Pair-fed vs both E and C animals under steady-state conditions.**Bold =  $p < 0.05$ . na = probe had no specific alignment to current RefSeq RNA database.

Gene Symbol	Gene Name	Average Expression	F	p-value	q-value	Fold change		
						Pair-fed/ Control	Ethanol/ Pair-fed	Ethanol/ Control
ILMN_1351851	na	8.9	12.4	3.5E-04	0.24	<b>0.77</b>	<b>1.49</b>	1.15
Sostdc1	sclerostin domain containing 1	8.7	26.4	3.1E-06	0.02	<b>0.28</b>	<b>4.40</b>	1.23
Nt5dc2	5'-nucleotidase domain containing 2	7.8	14.6	1.4E-04	0.15	<b>0.68</b>	<b>1.70</b>	1.16
Retsat	retinol saturase (all trans retinol 13,14 reductase)	8.4	15.8	8.7E-05	0.14	<b>1.68</b>	<b>0.49</b>	0.82
ILMN_1356875	na	10.0	22.2	1.0E-05	0.04	<b>0.46</b>	<b>2.68</b>	1.22
Aqp1	aquaporin 1	7.6	15.9	8.6E-05	0.14	<b>0.63</b>	<b>1.75</b>	1.10
Igf2bp2	insulin-like growth factor binding protein 2	10.0	14.7	1.4E-04	0.15	<b>0.47</b>	<b>3.45</b>	1.62
Lxn	latexin	8.3	15.4	1.0E-04	0.14	<b>0.57</b>	<b>1.69</b>	0.96
Ttr	transthyretin	11.7	19.3	2.5E-05	0.08	<b>0.20</b>	<b>9.87</b>	1.96
Slco1a5	solute carrier organic anion transporter family, member 1a5	8.2	15.4	1.0E-04	0.14	<b>0.43</b>	<b>2.57</b>	1.11
Glb1l	galactosidase, beta 1-like	7.4	18.6	3.2E-05	0.09	<b>0.68</b>	<b>1.47</b>	1.00
Epn3	epsin 3	7.5	12.8	2.9E-04	0.21	<b>0.76</b>	<b>1.46</b>	1.11
F5	coagulation factor V (proaccelerin, labile factor)	8.6	17.8	4.3E-05	0.11	<b>0.33</b>	<b>4.27</b>	1.39
Cox8b	cytochrome c oxidase, subunit VIIIb	7.4	13.5	2.1E-04	0.20	<b>0.71</b>	<b>1.48</b>	1.06
Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	12.7	27.2	2.5E-06	0.02	<b>0.47</b>	<b>2.45</b>	1.16



**Table S8: Accessions and probe sequences for differentially expressed genes**

Gene Symbol	Probe ID	Current Accession	Probe Sequence
Acat1	ILMN_1373473	NM_017075.1	GGCATGGCTCAGCCGTTAAGAGCACTTGTGCTACCTGTGTGGTGCATGG
Acly	ILMN_1366910	NM_016987.2	TGTCAAGGGGAGGAGGGTTGGGGCCATTGTACCCTTAGCCATCGTCACAC
Acs1	ILMN_1363750	NM_012820.1	GAAGCCACTGTTGTTGGCTGTGTGACAGTGTGTGTATCTTGAAGCACAAC
Acs13	ILMN_1368504	NM_057107.1	CCCACTGAAAATTCTGTTTGAGCCCTGACCCATGGACTCCCGAAACTGGTC
Agap1	ILMN_1357547	NM_001108230.1	GGCCTCAGCCACTCCCGATCCACAAAGTCTGAATCACCCAGGTTTCTGTC
Ak2	ILMN_1359709	NM_001033967.2	GCCTGGCACTGGAAAGCCTTGGGTTCCGGTCTCTACAGTGAAGGGTTAGG
Anxa11	ILMN_1376793	NM_001011918.1	GTTTCTGGAGAGAATGGTAGGTGAGCGGGCCACCCGTCTTGCCTAGGAC
Anxa4	ILMN_1349705	NM_024155.3	GAGTGGACTCGGCCAAGGTTGTCTGGTAATGAGATGCTCTGGGTGTGGC
Ap1s2	ILMN_1372527	NM_001127531.2	GCAGACTTGACAGCAGCTCCCTATCCTTTTCATGCTACTGCCTAGTCGTCG
Aqp1	ILMN_1358325	NM_012778.1	CCCTAGCAGGCACTATACTCACTTCACAGGTCAGGACACTGAGGACCCAT
Arl4a	ILMN_1351318	NM_019186.1	TGAAGAGTGTCTACAGCCTGGTTTGCTGTCTGCCCTCACGGATGCTATT
Asah3l_predicted	ILMN_1364753	XM_001053269.1	GCTTGCCATAGCCCCACCATTTCAGGCTCTCTATTACACAGGAGTCA
Atp5a1	ILMN_1359244	NM_023093.1	CCCATGGCTATTGAAGAACAGGTGGCTGTCTATGCAGGCGTCCGGGG
Atp6ap1	ILMN_1359644	NM_031785.1	GGCGGGTGGGGGTTAAGAATGAGCGGTACACTGGGGTTTATTTCTGTGAC
Baiap2	ILMN_1365343	NM_057196.1	AGTTCCTGCCTTCTCTCAGGGTCTGGATGACTACGGGGCACGGTCTGTGA
Bhlhe40	ILMN_1374180	NM_053328.1	GCTAAGGTGGTGAGGTAGCCAACACTGGCATGTCTCGGTAGTGGTTTGGG
Caap1	ILMN_1349802	NM_001034154.1	GTGCTGATGGAGGACGCCTCTTGTGGATGTGAGTTTCCTAGTTAAACT
Chn1	ILMN_1376930	NM_032083.1	CTTCCTCTCTCAGACATAGTGCTTTGTCTTCAGCAGAAGCGAGACGTGT
Cib1	ILMN_1370750	NM_031145.1	CTCTCCGAGTTCCAGCACGTCATCTCTCGCTCACCAGACTTTGCCAGCTC
Ckb	ILMN_1370888	NM_012529.2	AAGTGAAGCCGTGGCCCTAGCCACCACCAGGCTGCCGCTTCTAACTTAT
Cnih2	ILMN_1372279	NM_001025132.1	TGGAAGGGGTAGGACTTCCGGTCTTGCCGTTTCAGGGGAATTTGGGCCC
Col8a1	ILMN_1362033	NM_001107100.1	CGGAGACCGGGTGTTCTCCAAATGCCTTCAGAACAGGCTGCTGGACTCT
Cops4	ILMN_1368937	NM_001004275.1	AAGCAGTGCAGCCTTGAAGCAGTAGCTCCCGTGCCGCTGGGTCTATGTT
Cox8b	ILMN_1374366	NM_012786.1	GGCCAAGGAAAGAGTGCGACCCCGAGAATCATGCCAAGGCTTCCCCTAT
Crtac1	ILMN_2040211	XM_574670.2	ATGGCAAGATGCTGAGCCGAAGTGTGGCCAACAGGGAGATGAACGCGTG
Csda	ILMN_1355756	XM_001069862.1	ACTAACAAGTGCAAAGGGAAGGAGCCCGCACTGTCCATCAAGCTGCGTCC
Ctgf	ILMN_1364113	NM_022266.2	CCACGAGGAAGTGTGTTGCTGCTTCTTGACTATGACTGGTTTGGGAGGCA
Ddit4	ILMN_1357747	NM_080906.1	GGGGGGATCGGAGCTTCACTACTGACCTGTTGAGGCAGCTATCTTACAG
Dusp6	ILMN_1362834	NM_053883.2	ATGCTCGCCATTCAACGGGTGGGATGCGACAGGTTGTGAGGAAGGGAAA
Dynlrb1	ILMN_1372238	NM_131910.3	CCACCAAGGAGTGCCTCTGATGATCCGGTCACTCCCAGAAGAGCTCAGT
Eef1a2l1	ILMN_2039949	NM_033539.1	GAGGCAGACAGTTGCTGTGGGTGTCATCAAAGCCGTGGACAAGAAGGCTG
Enpp2	ILMN_1376810	NM_057104.2	AGCGAGATTTAACTTTCTGGGCTGGGCAGTGTAGTCTTAGCAACTGGTG
Epn1	ILMN_1351904	NM_057136.1	TACACCGCCAGGAGCCAAGGCTTCAACCCATTCTTCCAAGTGGAGCTC
Epn3	ILMN_1365679	NM_001024791.1	CAAGCTAGGGACTGACTGCATCTTGGGATCGAGGACTACGCCCGCCTAAT
F5	ILMN_1371753	XM_222831.4	CAAGAAGGTAACGGCCATCGTAACTCAGGGTTGCAAGTCTGTGCTCTG
Flna	ILMN_1368821	NM_001134599.1	CCTGCGCTGTGTTACCTGCCTTTGGGCTTCACTTGGGCAGAGGGAGTT
Gabrr2	ILMN_1366995	NM_017292.1	GGTGGATACATGGACCTAATGACCACACTTCTACACCAGGCCAAGCAGC
Ghrhr	ILMN_1368059	NM_012850.1	GCTCTGAAGGGGAGCTCTTGTGACAGCCATTATTTGCACTTCCGGTGCA
Glb1l	ILMN_1364521	NM_001127529.2	GGACAATGCGGGGTCCACAACAGACCCTATACGTGCCAAGACCTCTGCTG
Gpd1	ILMN_1353571	NM_022215.2	ATGAAGGTCAGAGCCATTGGGAAAGGTGAAGTGGGGGAGCCCTGTCATCG
Gpkow	ILMN_1357200	NM_001109381.1	CTGGCAAGGGCATCGGCAATACATTCACTCAGGTAGTGAAGCCCCGAGTC
Grik5	ILMN_1376501	NM_031508.2	CCAGGCGGACAGGACGCCGCGATTTTGCCTTCACTTCTGGTGAAGTCCA
H2afv	ILMN_1356468	NM_001106019.1	TCCTCACTGTGTGTGACTGGGCAGAGGGTACCAGTCGGTGTGTGGGAAAG
Hba-a2	ILMN_1356639	NM_013096.1	CCCTCCCTTGACCTATACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGA
Hbb	ILMN_1353696	NM_033234.1	TGATGATGTTGGTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTT
Hbb-b1	ILMN_1361935	NM_198776.1	GGGGAAAGGTGAACCCTGTTGAAATTGGCGCTGAGTCCCTTGCCAGTCTG
Hint3	ILMN_1350504	XM_341742.3	CAGCCTGAAGGTTGCTGGCTCACATGTAACACTACCACTGGGGAGCCTTA
Igf2	ILMN_1359301	NM_031511.2	CCCATGTCATCCAGCAGTGGCCCCGGGTATTTGCCCAACTCAGTCTTTT
Igfbp2	ILMN_1360048	NM_013122.2	ATAGAGAGGGTGGTGGCACTGGGGATACTGGGTACAGGCTTGGGAATGGG
Igfbp7	ILMN_1368086	NM_001013048.1	CGCGTCCAATCCCAAGGACAGGCTTCAGCGTCGGCCAAAATTACAGTGG
ILMN_1351665	ILMN_1351665	na	CTCAGCCCCGTAAGTATGATGTGGCTTGTGACTGGGTTGTGACTGTGTCGTG
ILMN_1351805	ILMN_1351805	na	CTGCAGGGTCTGTGATCAGCAAGGTAGTGTGAGTGTGGGCTCCATGCTAG
ILMN_1351851	ILMN_1351851	na	CATGCTCTGTGTGGGATGGCTCGTGTGCAGCGTAAATCTATCTCGTGTGG

ILMN_1351971	ILMN_1351971	na	AATTTCTACTCAGTGTGGATGGCTTTTCTTAATACCCCCACGCCAAC
ILMN_1352441	ILMN_1352441	na	GTAAGTGTCTACTATGTCTCCAAGGCAAGCCACAGGCTATAAGCCA
ILMN_1352779	ILMN_1352779	na	TCAACTGACCACTGGCCTTAGCTCTGGGATGCTGGGTGGAAGCTGGGGCT
ILMN_1354124	ILMN_1354124	na	CTCGGTTTCGGAGAGCCCTGAATTTCTCAACCTTGGTCTCGGTGGGCAGC
ILMN_1356747	ILMN_1356747	na	TAGATCGCTTGCCTAGAAAGCACAAGGCCCTGGGTTCTGTCCCCAGCTCG
ILMN_1356875	ILMN_1356875	na	CCTCCTCTCCACAGGCCCAAGATGTAACCCACCACTGCCTTTTGTCTTC
ILMN_1358743	ILMN_1358743	na	TTTGGATACACCCTGTTTCTCTCCGGTCCCAGGCACTGCGGGAGCTGCA
ILMN_1359487	ILMN_1359487	na	TGGCCTCTACTGCACTCTCCACCAGAGAAGCACAGATCCAGGGGCACT
ILMN_1359502	ILMN_1359502	na	TGGAGGAAGTCAGAGAAGTGTGATGCACATCAATCAAGAGCTGCTGGTC
ILMN_1359650	ILMN_1359650	na	ATGGATAGCATAAATCTAGGTGTCAGATCACTGAGTACTGGTGGTCAGGC
ILMN_1359879	ILMN_1359879	na	CAGTCAAGGAGAACACGCTCATCCTGCTGGGGCACTCACTGACAAATGGT
ILMN_1361625	ILMN_1361625	na	AAAGCAACCCTAAGAGAACACAAATGCCAGCCCAGGTTACTGTATCCTGC
ILMN_1364624	ILMN_1364624	na	TGGCAAGTCCCACACTGTGCCCAAGAAGCTACTGATGTTGGCTGGTATAG
ILMN_1366004	ILMN_1366004	na	CCTACAACCTCCTCAGCATCCAGAGCCAGCCAAAGGATCAGTGGCGGACC
ILMN_1366169	ILMN_1366169	na	GGTATAACATTGAATACGGCTACAGCAACAGGGTGGTGGATCTCACGTCC
ILMN_1366381	ILMN_1366381	na	GGCCGTGAGACCATTATGTTTATTAAACGTTGTGGCTTTCTGGAAGGAGGG
ILMN_1366825	ILMN_1366825	na	GTCAGGAGCAAAAGACAAGGGCTGAGAGAGGGAGCAGAGTCCATGAGCAC
ILMN_1367588	ILMN_1367588	na	GTACTTGTCTGAGTGGTCAACCAGAAGAGTTTCATGGAGATTAGTTTAC
ILMN_1368258	ILMN_1368258	na	GATGCACATCAATCAAGAGCTGCTGGTATCCAGAAAGACCGTGCATGTG
ILMN_1368369	ILMN_1368369	na	TTAGGGGCTCCCTGGTTAGAGGGTTGTAAGGTACAGGGTGTCTGTTAGCC
ILMN_1370609	ILMN_1370609	na	GGTGAACCTCAGGTTGCTCTCCTGGACTGCCGTGAAGATAGCGTGACTTC
ILMN_1372588	ILMN_1372588	na	AAAGGCTCTGTGAAGAGGCCGGAATGAACATCTGTGACCCCACTGCCACG
ILMN_1372701	ILMN_1372701	na	TCTCTAGGAGCCTTGCTGTCCAAGTCTATCAGCAGACTGTGTTCTCTGC
ILMN_1374168	ILMN_1374168	na	CTACTTGGCAGATACAACTGACCAATGGATGATGTGAGGGAGTCTACAC
Klhl24	ILMN_1651132	NM_181473.2	ATCACAGGAGTGGCTGCGATGCCAGACCAGTGTCTACCATGGCTGTGT
Lcn2	ILMN_1363606	NM_130741.1	TGAACAGACGGTGAGCGTGGCTGACTGGGATGTGCAGTGGCCTGATGGTT
Lgi3_predicted	ILMN_1367471	XM_224337.4	GGCAAGAATCCTGGGAGAGCCTGTATGGGTGCCAGGAACGTGTTGGTAGC
LOC100360417	ILMN_1354182	XM_003749319.1	TACTGGATGGAAGCCTGGACACCCCTGGTGGGTAAAGCCTGTGCCAATGGT
LOC100361558	ILMN_1649986	XM_002728043.2	GATTTCGAAGCTCCCTTTTCACTGTCTGGAGCGAGAAATTGCTCAGGACC
LOC287167	ILMN_1376663	NM_001013853.1	GCGCAGAGACCATAGGGAGGTTGTTTATTGTCTTCCCCTCCTCCAAGACC
LOC301193	ILMN_1364278	LOC301193	GGATTGAATAGGCTGTACTTTCACCTCAGCTCTCTCCAACAAGTGTGCAC
LOC360975	ILMN_1354780	XM_573650.1	GGCAGGTGAGAAGCAGATCAATGGATAAGGGCAAGGTGTCCCAGGAGCC
LOC363181	ILMN_1359502	XM_001061883.1	TGGAGGAAGTCAGAGAAGTGTGATGCACATCAATCAAGAGCTGCTGGTC
LOC363306	ILMN_1352300	XM_343647.2	CACCAATGCCCCCAGGAAAGGCTTTGGTTAAAGAAGGGAGGTAAGTATG
LOC363320	ILMN_1363630	XM_001075455.3	GGCCTTACTTTTACCCCACTCTCTCCAGCAAGTGTGCACTTTTAGAGGG
LOC363320	ILMN_1352441	XM_343660.3	GTAAGTGTCTACTATGTCTCCAAGGCAAGCCACAGGCTATAAGCCA
LOC363433	ILMN_1364278	XM_343755.3	GGATTGAATAGGCTGTACTTTCACCTCAGCTCTCTCCAACAAGTGTGCAC
LOC498989	ILMN_1363791	XM_574280.1	CCAGGTCTGCTGCCAGGCTCCAAGGGTGGGTCTCTGAGGGGCTAGAAAAT
LOC499079	ILMN_1650602	XM_574363.1	GGCAGGACCCCAAGAGCAAACTTGAAGCTTGAACCAAGAGGAGGAGTA
LOC500488	ILMN_1359785	XM_580072.1	ACAGGTGGCATGTACCTGGCTGAGGTAACATTAGTCACTTGTCTGGGGG
LOC501089	ILMN_1363630	XM_576504.1	GGCCTTACTTTTACCCCACTCTCTCCAGCAAGTGTGCACTTTTAGAGGG
LOC501223	ILMN_1350559	XM_001071000.3	ACCACCAGTAACTGCTTTTCTACTATGTCTCCAAGGCAAGCCACAGGCTA
LOC501300	ILMN_1352504	XM_576713.1	CTGAGCCCTCTGACAATGACTTACTCTGGGAGAGAAACATCATCCCCTGG
LOC685828	ILMN_1352300	XM_003754483.1	CACCAATGCCCCCAGGAAAGGCTTTGGTTAAAGAAGGGAGGTAAGTATG
LOC688637	ILMN_1363581	XM_001067706.1	GGACGGCGGGTCAATAGAGGCCATGCGGAGCTTTTGTAGTATGATCGGGG
LOC689577	ILMN_1371567	XM_001071243.1	CAGCGTCATCCTCATCCACACCCAGGTGAAACTGTTGGCCTCACCAGCAC
Lrg1	ILMN_1353943	NM_001009717.1	CAGAGCTGGGGACCTTGTGAGGATGGCAACTGGGGTGCAGCCAAGGGTA
Lrp1	ILMN_1357522	NM_001130490.1	TTAGTTGAGGGAAGTACCCCAAGCCCACTCTCCACTTTTAGGGGCACG
Lxn	ILMN_1362583	NM_031655.1	GCACAACAGCCGCTCCCAAAGGAAGCACCAGCAGAGTAAACAAGACCCC
Mapkapk2	ILMN_1376451	NM_178102.2	AGGATTGAGGAGGAGCAGGTGGGGAAGAGTCTTTGTGCCATGGTCCCCCA
Mcf2d	ILMN_1369244	NM_139253.1	GGAAGAGCAGTAGTAGCTGAAAGAGAAACAGCCATAGGTCTGACTTTGCG
Med28	ILMN_1355511	NM_001107217.1	GACATGCCTCAGGGCTCCTTGGCCTACCTTGAAGCAGGCATCTGCCAACAT
MGC125002	ILMN_1349802	NM_001034154.1	GTGCTGATGGAGGACGCCTCTTTGTGGATGTGAGTTTCTAGTTAAACT
MGC72973	ILMN_1361935	NM_198776.1	GGGGAAAGGTGAACCCTGTTGAAATTGGCGCTGAGTCCCTTGCCAGTCTG
Mgp	ILMN_1351917	NM_012862.1	CTACTTCAGGCAGCGCCGAGGAGCCAAATAAGAGCGCAAGGAAACAGTCG
Mrpl37	ILMN_1369643	NM_001004235.1	CTTGATGGTGTGTGTGAACCAGGAACCTTCTGGGGCCTGATGCCTCTG

Myh11	ILMN_1371040	XM_573030.2	CATTACCCACCTCTCACCAGGAGTCAACCACAGCCCTGCACAAAGGATG
Ndfip1	ILMN_1650482	NM_001013059.1	CTCAGCTGCGGGAAGGTATGGGGCCATCTCAGGATTTGGTCTTTCTCTAA
Ndn	ILMN_1358752	NM_001008558.1	GGGACTGATGGTCCGTATCGACAAAGAAGGCCCTGGAGAGTTAGCAGGAC
Ndrp2	ILMN_1356551	NM_133583.1	GGGACTGGGGGAAAGAACTTAGGTCCGACTGCTTGGGGTTTGGCATCAGG
Nfkb1a	ILMN_1356628	XM_343065.3	GTTGAACCGCCATAGACTGTAGCTGACCCAGTGTGCCCTCTCACGTAAG
Nme2	ILMN_1370390	NM_031833.2	CAAGCGATTGAGCAGAAAGGGGTTCCGCCTGGTGGCCATGAAGTTCCTTC
Npc2	ILMN_1352122	NM_173118.1	GGCTGGCCGGGAGTATTACCTCTTCTGTATCTAAGTGCCTCCTGAGTCCC
Npepl1_predicted	ILMN_1373909	XM_001055241.1	GCCAGGGTACGTGTGGTGAAGTGGCTGTTAGGGACCCATTCTGTGAAGCAG
Nrxn3	ILMN_1370048	NM_053817.2	ACGATGGTGTATCTCTGTGAATGGTGAGCCATGGTGAAGGTCATAGCC
Nt5dc2	ILMN_1356169	NM_001009271.1	GCCCTGTTCAACGCTCAGTTTGGGAGCATCTTCCGCACCTTCCACAACCC
Park7	ILMN_1370124	NM_057143.1	GTCCACAGCCAGTGAACCTCAGGAACCTAACGTGTGAAGTAGCCCGCTGC
Peo1	ILMN_1357847	NM_001107599.1	CAACAAGAGTTCCTTACCTTCTCCATCCACCTAAGAGCAAAGCCCGAC
Per1	ILMN_1353839	XM_340822.2	GACTGTCCGTCTGGTTAAGGCTGCTGACAAGCTGCTGAAGTGGTCTCTCC
Pex11g	ILMN_1360592	NM_001105902.1	AGACTCAGATTCAGAGCGGGAACCACTGGCGGGGGGAGCATCCATAAT
Phlpp1	ILMN_1362245	NM_021657.1	ACCTCGCCCATGTGCAGTGTGGGCCATTGCTTAGTGTGCTTCTGTGCAG
Ppp1r14a	ILMN_1374409	NM_130403.1	GCAGGGAGGCGAGACATGCCAGATGAGGTCAACATCGACGAGCTGTGGAA
Ppp1r1b	ILMN_2040370	NM_138521.1	CATTCTGGATGTCGTCCCTTATTGTCCTGTTCTGCTGGGTGCCTGCAAG
Psma7	ILMN_1376320	NM_001008217.1	GTCAGGTGGCAAAACATTGAACCTGCTGTCATGAGGCGGGATCAGCCCC
Rap1ga1	ILMN_1372167	XM_233609.4	GCCGTGAGCCAAGTCTTGTGTGTATCTGTTCACTCTTAGGAGCCACGCC
Rasd1	ILMN_1369914	XM_340809.3	TGTGGGGCCAGGACTAACAGGGCATTATCTCGTCTGTGATTGGTGTGCC
Rasl10a	ILMN_1350810	NM_001108862.1	TGCAGCCCGACAGTTTCGATTATGTGAAAGCCCTGAGGCAACGCATAGC
Retsat	ILMN_1356474	NM_145084.1	ACTGTTCCACAGCTGGAAGGCAAGGTGGAGAGTGTGACTGGAGGATCCC
RGD1309651	ILMN_1350558	XM_001078912.1	CTCTCTGAGCAGCTGGATGGGGACAGCCAAATGGGCCCTGGACTAAGACA
RGD1309730	ILMN_1354640	NM_001106491.2	CTGAGGGGAAGCCAACGCCCGCTGTGGGAAGAACTCAGACGCAAACTGAA
RGD1311122	ILMN_1355336	NM_001037792.1	GTGGCAGTTTATCTGTGGGTGGCAGTTTTCTGTAGTCTTGACGGTGACG
RGD1359349	ILMN_1369723	NM_001007738.1	GGGACCATGTTCAAGAAAACAGCGGCCTGAAGGAAGGCGAAGAACCCTGC
RGD1359529	ILMN_1366485	NM_001014193.1	ACTGCACTTTACTGAGGGGTTCTGTGTCAGCATCAGCTCACCTGCCTGAG
RGD1562162_predicted	ILMN_1649986	XR_008163.1	GATTGCAAGCTCCCTTTTCACTGTCTGGAGCGAGAAATTGCTCAGGACC
RGD1564290	ILMN_1362582	XM_574121.3	AAGGTTGACATTGCTGGTAAGCAGCTGGAAGGTGGCCGTACTTTGTCTG
RGD1565117	ILMN_1360197	XM_235217.1	GTCACCAGGAATCCATCTCGTGAGGACCGAACACCCCCACCACGATTGAG
RGD1565715_predicted	ILMN_1362392	XM_341434.3	GTTGATGATGTCTTGTGGGCAAGAGGAGAGAAGAGGCTTGAAGACGGGC
RGD1565784	ILMN_1354616	NM_001109028.1	GCGCATGTCTTCGTTGCTTAAAGGACTTGGATGGCGCTCTTGTGCTGAC
Rgs3	ILMN_1370455	NM_019340.1	GGCAGCTGGGCCTTCTAGACTGACATGACCTTGAGAGGGGATGCTGCAGAA
Rnasek	ILMN_1373564	NM_001137561.2	AGTCCATCTGTTCCACTCATCTGGTGTCTTTGGGACTGTTACCCTGGCG
Rnd2	ILMN_1356527	NM_001010953.1	GGGTAGGCATCGGAGGCATGAACCTGGATAGGGCAGGTAGGTGTTGCGAA
Rpl27-l1	ILMN_1651060	XM_001068279.2	TTTGCTGGGTGCCGGCTGCTTGTGCTGCGAAATGGGCAAGCTTATGAAACC
Rpl7	ILMN_1370118	NM_001100534.1	TCCGGCTGGAACCATGGAGGCTGTACCAGAGAAGAAAAAGAGGTTGCCG
Rps8	ILMN_1362384	NM_031706.1	TCTTCCAGCCAGCGCCGAGCGATGGGCATCTCTCGGGACAACCTGGCACA
Rpusd1	ILMN_1358460	NM_001105774.1	TGTACCACCTGCCTGGCTTCCACATAGCCATAGAGTATCAGCGTCAGCC
S100a8	ILMN_1350690	NM_053822.1	GTTCTTGCGTTGGTGATAAGGGTGGGCGTGGCAGCTCATAAAGACAGCC
Satb1	ILMN_1376648	NM_001012129.1	ACTGCTTGGCGGCCCCAGGTGAAGCGTCAAGGATTGTTGGGTAGAATTG
Scd	ILMN_1359586	NM_031841.1	CGTGAATCATGGGACAGACTCAAACCGTAGCACTGGGCATGTCGCTAAC
Sep15	ILMN_1355675	NM_133297.2	GAAAGTAAGTGACAGAAAACGCAAAACAGCACGCCCCGCCAGAGCCTG
Sgk1	ILMN_1349269	NM_019232.3	GGGTTTTTATGGACCAATGCCCCAGTTGTGAGTCAGAGCCGTTGGTGTTC
Slc38a5	ILMN_1349808	NM_138854.1	AGTCACTTCTCTGAGTCCCTTCTGCCTGGGACATGGAGGTGGCTGGTCTC
Slco1a5	ILMN_1363789	NM_030838.1	GGAGAGGTGTGCTTTCTACCAAGCCTGACAAGGTGGGTTTGATCTCTGGG
Snai3_predicted	ILMN_1358708	XM_001079335.1	CCTTCTCCGAATGTCTCTTGGTGAGGCACGAGGATGCCGGCTGCTGT
Sostdc1	ILMN_1352748	NM_153737.1	ATCCCCCTCGTGTTGACCTCTCTTGGAGTGGAATGCCAGCAATGCAAGGC
Sqle	ILMN_1364854	NM_017136.2	GTCAGAGCCATGGGCTACAAAACCTCGGGCTCTTTTCACTAGTGGTGCTA
Sumf1	ILMN_1360059	NM_001108639.1	GAAGGAAAGCGCTGGAGGAGCTGCCATGAGGGAAATGGACATGTGGCCAG
Tcf4	ILMN_1369541	NM_053369.1	GGGAGACACAGCGAATCACATGGGTGAGTGTGAAAGGGTCCAAGTTGCC
Timp3	ILMN_1348821	NM_012886.2	GACCACCTCACACTGTCCAGCGCAAGGGCTCAATTACCGCTACCACCT
Tmem178b	ILMN_1369758	NM_001195277.1	CTGTGCACCTGTGTGGCTGGGATCAACTTTGAGCTATCACGTTACCCACG
Tmod1	ILMN_1373707	NM_013044.2	CTGCAGGGACAGCCAGCTCCACTCAGCTTCTCCTTGAACACAACCTGCAG

Tom1	ILMN_1351051	NM_001008365.1	GGAGCCTGAAGAGGGCTTTAGTGGCTTATTAGGAAGGGCAATGGTGGCCC
Trpv4	ILMN_1360233	NM_023970.1	CCCGGGCTAGGGTGGGTCTTCTGTACTTTGTAGAGATCGGGGCTGTTGGT
Ttr	ILMN_1363307	NM_012681.2	TGTCGTCAGTAACCCCCAGAACTGAGGGACCCAGCCACGAGGACCAAGA
Tuba1a	ILMN_1354206	NM_022298.1	TAAGTGTGAATGATTTGTCAGAGACCCGAGCCGTCCACTTCACTGATGGG
Upp1	ILMN_1370862	NM_001030025.1	ACCATGTGCAGTGCCTGTGGCCTGAAAGCGGCTGTGGTGTGTGTCACTCT
Vwf	ILMN_1352807	XM_001066203.3	TGCAGATGTTCTCCCCGTAATTGTGGCAAGTGAGGCCTGTGCAGCCACGG
Ywha9	ILMN_1365334	NM_013053.1	GGTGATATCCATATTTCTGCATTGTGGTACACTTGTCTAGGGTGCCTGGC