

Table S1. Detailed information of human brains used in the study. Individually characterized brains were obtained from the the University of Florida Neuromedicine Human Brain and Tissue Bank. Experimental Group denotes the designation for this study (Fig. 7). Dx1, primary diagnosis based on neuropathology; Dx2, Dx3, Dx4, secondary diagnoses based on neuropathology; Thal phase, burden of immunostained amyloid deposits in cortical and subcortical area; CERAD score, neuritic plaque frequency; AD, Alzheimer's disease; ARTAG, Aging-related tau astroglipathy; CAA, cerebral amyloid angiopathy; CVD, cardiovascular disease; LATE-NC, limbic-predominant age-related TDP-43 encephalopathy neuropathological change; LBD, Lewy body dementia; PART, primary age-related tauopathy.

Experimental Group	Sex	APOE	Age	Dx1	Dx2	Dx3	Thal Stage	Braak Stage	CERAD Score
Control	m	3/3	90	AD low			1	II	none
Control	m	3/3	88	AD low	CVD		1	II	none
Control	f	3/3	72	PART, definite, Braak II			0	II	none
Control	m	3/3	71	PART, Braak I	CAA widespread, mild		0	I	none
Control	m	3/3	84	Atherosclerosis (moderate)	AD low		1	I	none
Control	f	3/3	76	PART, Braak I	Atherosclerosis (moderate)		0	I	none
Control	m	3/3	85	PART, definite, Braak II			0	II	none
Control	m	3/3	71	Atherosclerosis (moderate)			0	0	none
Control	m	3/3	88	Atherosclerosis (moderate)			0	0	none
Control	m	3/3	87	PART, definite, Braak I	LATE stage 1		0	I	none
Control	m	3/3	77	PART, definite, Braak I	ARTAG, subependymal		0	I	none
Control	m	3/3	72	Acute microinfarcts			0	0	none
Control	f	2/3	73	PART, definite, Braak I			0	I	none
Control	f	3/3	90	PART, definite, Braak II	subacute microinfarct corpus callosum		0	II	none
Control	f	3/3	78	PART, definite, Braak I			0	I	none
Control	m	3/3	77	PART, definite, Braak II	CAA focal, moderate		0	II	none
Control	m	2/3	51	PART, definite, Braak I	ARTAG, subependymal		0	I	none
Control	m	2/3	52	PART, definite, Braak I			0	I	none
AD	f	3/4	72	AD high	CAA widespread, severe		5	V	frequent
AD	m	3/4	84	AD high	CAA (moderate)		4	V	frequent
AD	m	3/3	83	AD high	CAA widespread, moderate		5	VI	frequent
AD	f	3/3	78	AD high	CAA widespread, moderate		5	V	frequent
AD	f	3/3	78	AD high	CAA widespread, mild to moderate	LATE-NC stage 2	4	V	frequent
AD	m	3/4	78	AD high	CAA focal, mild		5	V	frequent
AD	m	3/4	81	AD high	CAA (moderate)	LATE-NC stage 1	5	VI	frequent
AD	m	3/4	63	AD high	CAA widespread, moderate		5	VI	frequent
AD	m	3/3	66	AD high	CAA widespread, mild to moderate		5	VI	frequent
AD	m	3/4	77	AD high	CAA widespread, mild		4	V	frequent
AD	m	3/3	95	AD high	CAA focal, moderate		5	V	frequent
AD	m	3/3	83	AD high	CAA widespread, moderate		5	VI	frequent
AD	m	3/4	59	AD high	CAA widespread, moderate		5	VI	frequent
AD	m	3/3	60	AD high	CAA widespread, moderate to severe		5	VI	frequent
AD	m	4/4	70	AD high	CAA widespread, moderate		5	VI	frequent
AD	m	2/3	74	AD high	CAA widespread, moderate to severe		5	V	frequent
AD	m	4/4	75	AD high	CAA widespread, moderate		4	VI	frequent
AD	f	3/3	86	AD high	CAA focal, moderate		5	VI	frequent
AD	f	3/3	84	AD high	CAA focal, moderate	LATE-NC stage 1	5	VI	frequent
AD	f	3/3	90	AD high	CAA focal, mild	LATE-NC stage 1	5	V	frequent
AD	m	3/3	87	AD high	LATE stage 2		5	V	frequent
AD	m	3/3	73	AD high	CAA focal, mild to moderate		5	V	frequent
Mixed (AD/LBD)	f	2/4	74	AD high	CAA widespread, moderate	LBD diffuse neocortical	5	V	frequent
Mixed (AD/LBD)	m	3/4	77	AD high	CAA (moderate)	LBD (neocortical)	4	V	frequent
Mixed (AD/LBD)	f	3/4	83	AD high	LBD diffuse neocortical	CAA widespread, moderate	5	V	frequent
Mixed (AD/LBD)	m	3/3	87	AD high	LBD (neocortical)	CAA (moderate to severe)	5	VI	frequent
Mixed (AD/LBD)	m	3/4	80	AD high	LBD diffuse neocortical	CAA widespread, moderate	5	V	frequent
Mixed (AD/LBD)	f	3/4	68	LBD diffuse neocortical	AD high	CAA	5	V	frequent
Mixed (AD/LBD)	m	3/4	78	AD high	LBD diffuse neocortical	CAA focal, mild	5	VI	frequent
Mixed (AD/LBD)	m	4/4	91	AD high	CAA widespread, moderate to severe	LBD diffuse neocortical	5	VI	frequent
Mixed (AD/LBD)	f	3/4	76	AD high	LBD diffuse neocortical	LATE-NC stage 3	4	V	frequent
Mixed (AD/LBD)	m	3/3	83	AD high	CAA widespread, moderate	CAA widespread, moderate	5	VI	frequent
Mixed (AD/LBD)	m	3/3	62	AD high	LBD diffuse neocortical	CAA focal, moderate	5	VI	frequent
Mixed (AD/LBD)	f	4/4	76	AD high	CAA widespread, mild	LBD limbic-transitional	5	VI	frequent
Mixed (AD/LBD)	f	3/3	81	AD high	CAA widespread, moderate	LBD limbic-transitional	5	VI	frequent
Mixed (AD/LBD)	m	3/4	64	AD high	CAA widespread, moderate	LATE stage 2	5	VI	frequent
Mixed (AD/LBD)	f	3/3	78	AD high	CAA, widespread, moderate	LBD limbic-transitional	5	V	frequent
Mixed (AD/LBD)	f	3/3	63	AD high	LBD diffuse neocortical	LATE-NC stage 3	5	V	frequent
Mixed (AD/LBD)	f	2/3	98	AD high	LBD diffuse neocortical	LATE-NC stage 3	5	V	frequent
Mixed (AD/LBD)	f	4/4	93	AD high	CAA, widespread, moderate	LBD diffuse neocortical	5	V	frequent
Mixed (AD/LBD)	f	4/4	75	AD high	LBD diffuse neocortical	LATE stage 2	5	VI	frequent
Mixed (AD/LBD)	f	4/4	85	AD high	LBD limbic-transitional	CAA focal, moderate	5	V	frequent
Mixed (AD/LBD)	m	3/4	74	AD high	LBD diffuse neocortical		5	V	frequent

Table S2A: Selection of genes altered in E2H vs E3H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=3 mice/group.

gene_id	gene_name	Description	FPKM.E2 H_1	FPKM.E2 H_2	FPKM.E2 H_3	FPKM.E3 H_1	FPKM.E3 H_2	FPKM.E3 H_3	fc	log2 (fc)	pval	qval	Log10 (qval)	regulat ion	signifi cant
ENSMUSG000000093954	Gm16867	predicted gene	0.07	0.04	0.07	1.92	2.21	2.44	0.03	-5.26	4.76E-118	1.57E-113	-112.80	down	yes
ENSMUSG000000098975	Gm27177	predicted gene	0.06	0.12	0.07	1.35	2.02	1.59	0.05	-4.29	1.81E-58	2.99E-54	-53.52	down	yes
ENSMUSG000000118458	Gm10599	predicted pseu	0.12	0.10	0.09	2.66	2.52	2.13	0.04	-4.55	5.34E-46	5.88E-42	-41.23	down	yes
ENSMUSG000000109209	Gm45104	predicted gene	0.17	0.26	0.24	1.92	2.08	2.46	0.10	-3.28	3.63E-42	3.00E-38	-37.52	down	yes
ENSMUSG000000090338	Gm17081	predicted gene	0.07	0.07	0.06	2.40	2.39	1.58	0.03	-5.01	2.26E-40	1.49E-36	-35.83	down	yes
ENSMUSG000000096596	Gm10591	predicted gene	0.10	0.08	0.03	6.25	9.89	4.52	0.01	-6.63	3.69E-40	2.03E-36	-35.69	down	yes
ENSMUSG000000091542	Gm17167	predicted gene	0.08	0.05	0.05	1.28	1.18	0.82	0.06	-4.18	1.33E-36	6.25E-33	-32.20	down	yes
ENSMUSG000000073878	Gm13304	predicted gene	0.15	0.14	0.03	6.65	5.72	3.84	0.02	-5.66	3.59E-34	1.48E-30	-29.83	down	yes
ENSMUSG000000095675	Ccl21b	chemokine (C-C	0.14	0.10	0.01	7.91	3.65	5.15	0.02	-6.01	2.42E-33	8.88E-30	-29.05	down	yes
ENSMUSG000000073879	Gm5859	predicted pseu	0.12	0.07	0.09	1.83	1.73	1.38	0.06	-4.15	1.08E-29	3.55E-26	-25.45	down	yes
ENSMUSG000000006154	Eps8l1	EPS8-like 1 [S	0.96	0.88	0.78	0.14	0.12	0.14	6.64	2.73	1.67E-28	5.02E-25	-24.30	up	yes
ENSMUSG000000094065	Ccl21d	chemokine (C-C	0.11	0.10	0.02	2.62	3.44	3.30	0.03	-5.31	3.27E-24	8.99E-21	-20.05	down	yes
ENSMUSG000000097842	9330104G04Ri	RIKEN cDNA 933	1.37	1.56	1.63	0.33	0.24	0.23	5.74	2.52	2.38E-23	6.04E-20	-19.22	up	yes
ENSMUSG000000022066	Entpd4b	ectonucleoside	5.18	4.64	5.10	9.77	9.87	10.64	0.49	-1.02	1.11E-22	2.62E-19	-18.58	down	yes
ENSMUSG000000025453	Nnt	nicotinamide ni	4.76	4.49	5.03	2.32	1.84	2.15	2.26	1.18	5.76E-22	1.27E-18	-17.90	up	yes
ENSMUSG0000000110105	Gm45844	predicted gene	0.62	0.62	0.60	0.11	0.05	0.10	7.22	2.85	1.11E-20	2.30E-17	-16.64	up	yes
ENSMUSG000000096862	Gm13301	predicted gene	0.03	0.02	0.04	0.91	0.98	0.74	0.03	-4.91	2.40E-19	4.67E-16	-15.33	down	yes
ENSMUSG0000000116207	Nnt	nicotinamide ni	0	0	0	1.14	2.57	0.79	0.00	-13.87	1.52E-18	7.76E-15	-14.56	down	yes
ENSMUSG000000035299	Mid1	midline 1 [Sou	2.32	0.96	2.87	0.42	0.40	0.39	5.11	2.35	1.96E-18	3.41E-15	-14.47	up	yes
ENSMUSG000000109176	Zfp264	zinc finger pri	0.02	0.03	0.05	0.60	0.76	0.73	0.04	-4.48	1.18E-17	1.95E-14	-13.71	down	yes
ENSMUSG000000058626	Capn11	calpain 11 [So	0.82	1.23	0.98	0.13	0.04	0.11	11.19	3.48	8.60E-17	1.35E-13	-12.87	up	yes
ENSMUSG000000064179	Tnnt1	tropoin T1, s	6.33	4.73	4.24	1.88	1.38	1.95	2.94	1.55	4.52E-15	6.78E-12	-11.17	up	yes
ENSMUSG000000098374	Gm28043	predicted gene	1.88	1.13	1.88	3.37	4.24	4.75	0.40	-1.33	1.95E-12	2.72E-09	-8.57	down	yes
ENSMUSG000000084010	Gm13302	predicted gene	0.09	0.09	0.08	1.23	1.11	0.63	0.09	-3.46	1.98E-12	2.72E-09	-8.57	down	yes
ENSMUSG000000031762	Mt2	metallothionei	130.50	115.34	100.21	72.18	66.13	65.60	1.70	0.76	3.77E-12	4.98E-09	-8.30	up	no
ENSMUSG000000118425	Gm50470	predicted gene	0.08	0.09	0.15	1.07	1.08	0.83	0.11	-3.19	4.44E-12	5.64E-09	-8.25	down	yes
ENSMUSG000000118434	Gm13301	predicted gene	0.10	0.12	0.19	2.15	1.88	1.33	0.08	-3.67	6.82E-12	8.34E-09	-8.08	down	yes
ENSMUSG000000035429	Ptprh	protein tyrosi	0.36	0.34	0.47	0.04	0	0.04	14.79	3.89	2.91E-11	3.43E-08	-7.46	up	yes
ENSMUSG000000030413	Pglyrp1	peptidoglycan	6.08	2.37	2.14	0.77	0.89	0.81	4.28	2.10	9.67E-11	1.10E-07	-6.96	up	yes
ENSMUSG000000096256	Gm21093	predicted gene	1.14	0.68	1.17	2.46	2.80	2.93	0.36	-1.45	1.11E-10	1.22E-07	-6.91	down	yes
ENSMUSG000000093909	Gm3883	predicted gene	1.04	0.54	0.91	2.28	2.49	2.49	0.34	-1.54	1.24E-10	1.32E-07	-6.88	down	yes
ENSMUSG000000080893	Ndufa12-ps	NADH:ubiquinon	78.07	94.51	80.70	37.77	53.59	48.85	1.81	0.85	1.81E-10	1.86E-07	-6.73	up	no
ENSMUSG000000054594	Oscar	osteoclast ass	0.80	0.45	1.06	0.08	0	0.05	17.70	4.15	2.23E-10	2.23E-07	-6.65	up	yes
ENSMUSG000000090083	Rnf8	ring finger pri	2.03	1.89	1.96	1.31	1.17	1.17	1.61	0.69	4.96E-10	4.81E-07	-6.32	up	no
ENSMUSG000000095463	Entpd4	ectonucleoside	4.89	4.46	4.34	8.61	7.74	7.24	0.58	-0.79	7.25E-10	6.84E-07	-6.17	down	no
ENSMUSG000000086604	Gm15510	predicted gene	1.18	1.44	0.98	0.15	0.19	0.05	9.02	3.17	1.15E-09	1.05E-06	-5.98	up	yes
ENSMUSG000000080833	Rdh13	retinol dehydr	3.18	2.65	3.00	5.00	5.28	4.74	0.59	-0.77	1.25E-09	1.09E-06	-5.96	down	no
ENSMUSG000000031765	Mt1	metallothionei	116.71	108.43	89.72	72.25	64.05	62.35	1.59	0.66	1.26E-09	1.09E-06	-5.96	up	no
ENSMUSG000000005716	Pvalb	parvalbumin [S	71.28	75.60	55.73	38.38	44.42	41.00	1.64	0.71	1.64E-09	1.39E-06	-5.86	up	no
ENSMUSG000000053985	Zfp14	zinc finger pri	3.48	3.06	3.47	5.61	5.84	6.19	0.57	-0.82	3.36E-09	2.77E-06	-5.56	down	no
ENSMUSG000000107705	Gm45062	predicted gene	0	0.86	0	0	0	0	2878.26	11.49	5.01E-09	4.03E-06	-5.39	up	yes
ENSMUSG000000093996	Fam205a3	family with sei	0.83	0.75	0.80	1.88	2.09	1.55	0.43	-1.22	5.45E-09	4.28E-06	-5.37	down	yes
ENSMUSG000000108815	Gm49388	predicted gene	1.70	0	0	0	0	0	5680.79	12.47	8.20E-09	6.30E-06	-5.20	up	yes
ENSMUSG000000091177	Gm15494	predicted gene	0	0	0.07	1.31	1.38	1.66	0.02	-5.98	1.79E-08	1.34E-05	-4.87	down	yes
ENSMUSG000000090996	Gm20458	predicted gene	0	1.61	0	0	0	0	5360.06	12.39	2.85E-08	2.09E-05	-4.68	up	yes
ENSMUSG000000078746	Fam205a4	family with sei	0.81	0.73	0.79	1.83	2.01	1.47	0.44	-1.18	3.00E-08	2.15E-05	-4.67	down	yes
ENSMUSG000000053898	Echl	enoyl coenzyme	16.40	19.51	16.05	10.97	11.15	11.67	1.54	0.62	3.58E-08	2.51E-05	-4.60	up	no
ENSMUSG000000089865	Gm44503	predicted readi	0	0.44	0	0	0	0	1481.09	10.53	3.68E-08	2.53E-05	-4.60	up	yes
ENSMUSG000000024620	Pdgfrb	platelet deriv	2.33	2.28	2.77	4.44	4.19	4.14	0.58	-0.79	4.76E-08	3.21E-05	-4.49	down	no
ENSMUSG000000096764	Gm21985	predicted gene	0	0	0	0.11	1.08	0.33	0.00	-12.31	5.95E-08	3.93E-05	-4.41	down	yes
ENSMUSG000000057036	Gm7536	predicted gene	34.94	19.33	40.40	13.49	18.20	11.49	2.19	1.13	1.35E-07	8.75E-05	-4.06	up	yes
ENSMUSG000000116024	Gm49527	predicted gene	0.80	0.78	4.27	0.35	0.36	0.17	6.63	2.73	2.13E-07	1.35E-04	-3.87	up	yes
ENSMUSG000000094066	Fam205a2	family with sei	0.76	0.70	0.70	1.67	1.87	1.33	0.44	-1.18	2.23E-07	1.39E-04	-3.86	down	yes
ENSMUSG000000110631	Gm42047	predicted gene	0.28	0.22	0.40	0.83	0.74	0.87	0.37	-1.43	2.33E-07	1.43E-04	-3.85	down	yes
ENSMUSG000000045948	Mrps12	mitochondrial	19.11	27.00	21.04	13.20	13.92	13.62	1.65	0.72	3.28E-07	1.97E-04	-3.71	up	no
ENSMUSG000000066838	Zfp772	zinc finger pri	4.74	3.47	4.72	2.35	2.87	2.51	1.67	0.74	3.41E-07	2.10E-04	-3.70	up	no
ENSMUSG000000026193	Fnl	fibronectin 1	3.05	2.31	3.17	4.53	4.92	4.32	0.62	-0.69	3.75E-07	2.17E-04	-3.66	down	no
ENSMUSG000000114942	Gm49361	predicted gene	0	0.32	0	0	0	0	1061.17	10.05	3.81E-07	2.17E-04	-3.66	up	yes
ENSMUSG000000026678	Rgs5	regulator of G	15.14	13.05	16.15	22.52	22.49	21.27	0.67	-0.58	4.07E-07	2.28E-04	-3.64	down	no
ENSMUSG000000095348	Gm3892	predicted gene	0.28	0.19	0.24	0.85	0.81	0.62	0.31	-1.69	5.23E-07	2.88E-04	-3.54	down	yes
ENSMUSG000000095366	Gm21860	predicted gene	0.26	0.03	0.51	1.88	1.58	2.26	0.14	-2.82	5.51E-07	2.95E-04	-3.53	down	yes
ENSMUSG000000039001	Rps21	ribosomal prot	117.81	170.56	122.35	98.56	72.81	71.47	1.69	0.76	5.54E-07	2.95E-04	-3.53	up	no
ENSMUSG000000014846	Tppp3	tubulin polyme	31.04	26.56	24.12	18.27	21.14	16.75	1.46	0.54	6.26E-07	3.28E-04	-3.48	up	no
ENSMUSG000000031760	Mt3	metallothionei	115.15	169.86	114.17	93.37	73.29	73.01	1.67	0.74	7.25E-07	3.74E-04	-3.43	up	no
ENSMUSG000000102440	Pcdhga9	protocadherin	4.54	3.88	5.35	8.60	10.32	6.32	0.55	-0.87	8.91E-07	4.53E-04	-3.34	down	no
ENSMUSG000000090223	Pcp4	Purkinje cell	299.85	283.63	249.81	204.31	216.62	211.70	1.32	0.40	1.05E-06	5.26E-04	-3.28	up	no
ENSMUSG000000073616	Cops9	COP9 signaloso	27.41	35.93	26.67	20.84	19.28	17.96	1.55	0.63	1.14E-06	5.60E-04	-3.25	up	no
ENSMUSG000000079641	Rpl39	ribosomal prot	30.67	42.85	29.85	24.30	19.48	19.05	1.65	0.72	1.36E-06	6.60E-04	-3.18	up	no
ENSMUSG000000060636	Rpl35a	ribosomal prot	35.13	47.69	33.95	26.83	25.76	24.69	1.51	0.60	1.39E-06	6.63E-04	-3.18	up	no
ENSMUSG000000090733	Rps27	ribosomal prot	85.14	118.12	84.66	67.86	60.90	57.26	1.55	0.63	1.53E-06	7.21E-04	-3.14	up	no
ENSMUSG000000109205	Gm44954	predicted gene	0.47	0.02	0.25	3.00	3.30	3.65	0.07	-3.74	1.73E-06	8.04E-04	-3.09	down	yes
ENSMUSG000000020182	Ddc	dopa decarboxy	5.97	3.45	5.36	2.26	3.62	2.20	1.83	0.87	1.90E-06	8.71E-04	-3.06	up	no
ENSMUSG000000021290	Atp5mpl	ATP synthase m	40.53	55.23	40.57	31.56	28.23	29.29	1.53	0.61	2.29E-06	1.03E-03	-2.99	up	no
ENSMUSG000000057863	Rpl36	ribosomal prot	107.92	147.29	117.87	91.16	78.13	69.30	1.56	0.64					

Table S2B: Selection of genes altered in E4H vs E3H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=3 mice/group.

gene_id	gene_name	Description	FPKM.E4 H_1	FPKM.E4 H_2	FPKM.E4 H_3	FPKM.E3 H_1	FPKM.E3 H_2	FPKM.E3 H_3	fc	log2 (fc)	pval	qval	log10 (qval)	regulat ion	signifi cant
ENSMUSG000000021091	Serpina3n	serine (or cys	71.58	62.15	75.81	11.81	13.33	11.56	5.71	2.51	2.23E-214	7.41E-210	-209.13	up	yes
ENSMUSG000000096768	Gm47283	predicted gene	0.09	0.04	0.07	5.77	4.18	3.58	0.02	-6.06	1.78E-127	2.96E-123	-122.53	down	yes
ENSMUSG000000095562	Erdrl	erythroid diff	0.12	0.17	0.19	14.44	10.26	8.01	0.01	-6.12	6.13E-109	6.80E-105	-104.17	down	yes
ENSMUSG000000073643	Wdfl1	WD repeat and	2.30	2.60	2.34	6.75	8.29	8.25	0.31	-1.69	2.87E-66	2.39E-62	-61.62	down	yes
ENSMUSG000000107705	Gm45062	predicted gene	7.60	6.71	4.96	0	0	0	64232.1	15.97	8.01E-32	5.34E-28	-27.27	up	yes
ENSMUSG00000006154	Eps811	EPS8-like 1 [S	0.98	1.17	0.69	0.14	0.12	0.14	7.16	2.84	3.09E-28	1.72E-24	-23.77	up	yes
ENSMUSG000000105340	Gm42878	predicted gene	0	0	0	1.55	1.59	1.39	0.00	-13.88	5.02E-22	2.39E-18	-17.62	down	yes
ENSMUSG00000004798	Ulk2	unc-51 like ki	11.95	11.62	12.92	18.43	18.50	20.04	0.64	-0.64	1.86E-18	7.74E-15	-14.11	down	no
ENSMUSG000000076612	Ighg2c	immunoglobulin	0	0	0	3.10	2.67	2.57	0.00	-14.76	2.72E-18	1.01E-14	-14.00	down	yes
ENSMUSG00000008435	Rdh13	retinol dehydr	2.68	3.10	2.81	5.00	5.28	4.74	0.57	-0.80	2.84E-16	9.44E-13	-12.03	down	no
ENSMUSG000000054594	Oscar	osteoclast ass	0.94	1.00	0.91	0.08	0	0.05	21.79	4.45	1.19E-15	3.60E-12	-11.44	up	yes
ENSMUSG000000087467	Gm13601	predicted gene	0.05	0	0.14	3.28	3.18	4.42	0.02	-5.85	4.75E-15	1.32E-11	-10.88	down	yes
ENSMUSG000000042413	Nudt3	nudix (nucleot	57.00	56.52	58.46	45.94	45.60	46.04	1.25	0.32	2.55E-12	6.54E-09	-8.18	up	no
ENSMUSG000000035429	Ptprh	protein tyrosi	0.34	0.45	0.36	0.04	0	0.04	14.53	3.86	8.61E-12	2.05E-08	-7.69	up	yes
ENSMUSG000000076617	Ighm	immunoglobulin	8.10	9.99	8.31	14.22	16.53	14.22	0.59	-0.77	1.77E-11	3.92E-08	-7.41	down	no
ENSMUSG000000031562	Dctd	dCMP deaminase	1.11	1.06	0.94	2.28	2.54	2.11	0.45	-1.15	2.44E-11	5.08E-08	-7.29	down	yes
ENSMUSG000000106874	Gm20186	predicted gene	0	0.01	0	1.36	1.43	1.33	0.00	-8.95	4.68E-11	9.16E-08	-7.04	down	yes
ENSMUSG000000032667	Pon2	paraoxonase 2	4.97	4.30	4.26	6.44	6.98	6.70	0.67	-0.57	8.12E-11	1.50E-07	-6.82	down	no
ENSMUSG000000086604	Gm15510	predicted gene	1.10	1.33	1.27	0.15	0.19	0.05	9.27	3.21	9.25E-11	1.62E-07	-6.79	up	yes
ENSMUSG000000069049	Eif2s3y	eukaryotic tra	0.02	0	9.44	0	0	0	31543.8	14.95	1.04E-10	1.74E-07	-6.76	up	yes
ENSMUSG000000058706	0610030E20R1k	RIKEN cDNA 061	2.46	2.87	2.24	1.20	1.39	1.58	1.82	0.86	1.29E-10	2.04E-07	-6.69	up	no
ENSMUSG000000001930	Vwf	Von Willebrand	0.78	0.72	0.62	1.34	1.33	1.11	0.56	-0.84	2.01E-10	3.04E-07	-6.52	down	no
ENSMUSG000000052861	Dnah6	dynein, axoner	0.60	0.62	0.53	0.17	0.33	0.23	2.40	1.27	2.37E-10	3.43E-07	-6.46	up	yes
ENSMUSG000000050071	Bex1	brain expresse	32.21	28.37	34.19	22.91	22.05	20.52	1.45	0.53	1.70E-09	2.36E-06	-5.63	up	no
ENSMUSG000000103707	Pcdha6	protocadherin	1.27	1.02	0.65	2.70	2.35	1.99	0.42	-1.26	2.10E-09	2.79E-06	-5.55	down	yes
ENSMUSG000000089862	Umad1	UMAP1-MVP12 as	5.91	6.04	6.76	8.65	8.89	9.51	0.69	-0.53	5.61E-09	7.11E-06	-5.15	down	no
ENSMUSG000000001973	Flox5	F-box protein	1.63	2.06	1.27	0.53	0.53	0.60	2.98	1.58	5.77E-09	7.11E-06	-5.15	up	yes
ENSMUSG000000095366	Gm21860	predicted gene	0.32	0.56	0.50	1.88	1.58	2.26	0.24	-2.04	1.47E-08	1.75E-05	-4.76	down	yes
ENSMUSG000000029994	Anxa4	annexin A4 [Sc	2.01	2.00	2.01	1.12	1.21	1.25	1.68	0.75	1.67E-08	1.91E-05	-4.72	up	no
ENSMUSG000000107927	Gm44090	predicted gene	0	0.03	0.02	0.73	0.38	0.26	0.03	-4.99	1.79E-08	1.98E-05	-4.70	down	yes
ENSMUSG000000002477	Snrpd1	small nuclear	16.13	16.04	15.47	11.27	12.77	10.38	1.38	0.47	2.40E-08	2.58E-05	-4.59	up	no
ENSMUSG000000075514	Gm13375	predicted gene	6.02	6.85	6.22	11.01	11.13	11.52	0.57	-0.82	4.70E-08	4.89E-05	-4.31	down	no
ENSMUSG000000042750	Bex2	brain expresse	175.32	160.95	175.57	140.71	143.53	129.31	1.24	0.31	6.19E-08	6.19E-05	-4.21	up	no
ENSMUSG000000037860	Aim2	absent in mela	0.98	0.99	0.92	0.43	0.41	0.33	2.46	1.30	6.32E-08	6.19E-05	-4.21	up	yes
ENSMUSG000000046952	Gm5815	predicted pseu	0.98	1.48	1.48	0.38	0.16	0.19	5.40	2.43	6.63E-08	6.30E-05	-4.20	up	yes
ENSMUSG000000035781	R3hdm4	R3H domain con	26.85	27.70	27.94	36.22	34.65	34.56	0.78	-0.35	7.25E-08	6.42E-05	-4.19	down	no
ENSMUSG000000073411	H2-D1	histocompatib	17.17	16.97	17.06	22.04	24.08	21.90	0.75	-0.47	7.27E-08	6.42E-05	-4.19	down	no
ENSMUSG000000091177	Gm15494	predicted gene	0.05	0.08	0.19	1.31	1.38	1.66	0.08	-3.72	7.36E-08	6.42E-05	-4.19	down	yes
ENSMUSG000000079494	Nat8f5	N-acetyltransf	0.22	0.20	0.18	1.15	1.39	1.08	0.17	-2.60	7.52E-08	6.42E-05	-4.19	down	yes
ENSMUSG000000091228	Gm20390	predicted gene	0	0	0	0	1.19	0	0.00	-11.95	2.22E-07	1.85E-04	-3.73	down	yes
ENSMUSG000000004240	Atf4	activating tra	46.25	48.03	46.19	36.77	41.97	37.63	1.21	0.27	3.38E-07	2.74E-04	-3.56	up	no
ENSMUSG000000064345	Mt-Nd2	mitochondrial	4352.43	4282.67	4065.09	3738.38	3594.01	3509.17	1.17	0.23	4.75E-07	3.76E-04	-3.42	up	no
ENSMUSG000000030123	Plexn1	plexin D1 [Sou	7.90	8.62	8.10	11.70	10.20	11.32	0.74	-0.43	6.68E-07	5.17E-04	-3.29	down	no
ENSMUSG000000006962	Dmkn	dermokine [Sou	0.51	0.50	0.27	1.31	1.37	1.13	0.33	-1.58	9.15E-07	6.92E-04	-3.16	down	yes
ENSMUSG000000058838	Rps27a-ps2	ribosomal prot	22.37	24.08	23.02	37.58	32.38	36.74	0.65	-0.62	9.48E-07	7.01E-04	-3.15	down	no
ENSMUSG000000004104	Washc2	WASH complex s	14.42	13.95	14.14	11.32	12.07	12.44	1.19	0.25	1.09E-06	7.88E-04	-3.10	up	no
ENSMUSG000000079012	Serpina3m	serine (or cys	1.87	2.05	2.06	0.05	0.11	0	36.53	5.19	1.49E-06	1.05E-03	-2.98	up	yes
ENSMUSG000000020893	Perl	period circadi	10.27	10.11	6.92	14.36	13.65	13.02	0.67	-0.59	1.55E-06	1.07E-03	-2.97	down	no
ENSMUSG000000030126	Tmcc1	transmembrane	4.80	4.71	4.64	3.73	4.03	4.15	1.19	0.25	2.17E-06	1.47E-03	-2.83	up	no
ENSMUSG000000073418	C4b	complement cor	7.70	7.55	8.42	9.53	11.14	10.75	0.75	-0.41	2.35E-06	1.54E-03	-2.81	down	no
ENSMUSG000000031375	Bgn	biglycan [Sou	3.09	3.12	2.74	4.45	4.52	3.89	0.70	-0.52	2.35E-06	1.54E-03	-2.81	down	no
ENSMUSG0000000062995	Ical	islet cell aut	10.11	10.18	11.20	12.92	14.56	15.11	0.74	-0.44	2.50E-06	1.60E-03	-2.80	down	no
ENSMUSG000000026278	Bok	BCL2-related c	17.16	16.52	19.11	13.75	13.29	13.42	1.30	0.38	2.69E-06	1.69E-03	-2.77	up	no
ENSMUSG000000020180	Snrpd3	small nuclear	15.69	16.54	17.95	13.04	13.67	13.86	1.24	0.31	3.24E-06	2.00E-03	-2.70	up	no
ENSMUSG000000064340	mt-T11	mitochondrial	491.08	468.04	542.37	417.66	341.17	329.94	1.38	0.46	3.54E-06	2.14E-03	-2.67	up	no
ENSMUSG000000052135	Foxo6	forkhead box C	2.48	2.54	2.67	4.72	4.16	3.71	0.61	-0.71	4.24E-06	2.52E-03	-2.60	down	no
ENSMUSG000000026234	Ncl	nucleolin [Sou	26.84	26.43	29.08	21.82	23.10	24.77	1.18	0.24	4.99E-06	2.91E-03	-2.54	up	no
ENSMUSG000000090223	Pcp4	Purkinje cell	240.40	234.77	243.38	204.31	216.62	211.70	1.14	0.18	5.28E-06	3.03E-03	-2.52	up	no
ENSMUSG000000063681	Crb1	crumbs family	0.18	0.14	0.12	0.04	0.06	0.05	2.76	1.47	6.64E-06	3.75E-03	-2.43	up	yes
ENSMUSG000000029819	Npy	neuropeptide Y	61.60	64.20	52.98	47.88	40.65	44.60	1.34	0.43	7.57E-06	4.20E-03	-2.38	up	no
ENSMUSG000000079592	C1qtnf5	C1q and tumor	2.36	2.10	2.42	1.02	1.39	0.95	2.04	1.03	7.70E-06	4.20E-03	-2.38	up	yes
ENSMUSG000000064341	Mt-Nd1	mitochondrial	6903.28	6695.82	6581.76	6129.84	5745.46	5553.22	1.16	0.21	8.39E-06	4.51E-03	-2.35	up	no
ENSMUSG000000030108	Slc6a13	solute carrier	3.41	2.86	3.30	4.42	5.17	4.83	0.66	-0.59	1.04E-05	5.48E-03	-2.26	down	no
ENSMUSG000000065947	mt-Nd41	mitochondrial	2405.55	2483.45	2460.75	2141.76	1889.46	2167.16	1.19	0.25	1.19E-05	6.21E-03	-2.21	up	no
ENSMUSG000000064344	mt-Tm	mitochondrial	275.00	257.17	248.62	197.29	201.06	189.98	1.33	0.41	1.41E-05	7.21E-03	-2.14	up	no
ENSMUSG000000067736	Gm10222	predicted gene	2394.69	2497.58	2478.33	2157.49	1904.45	2170.13	1.18	0.24	1.51E-05	7.64E-03	-2.12	up	no
ENSMUSG000000103793	Pcdha6	protocadherin	6.11	7.91	6.74	9.76	8.76	11.20	0.70	-0.52	1.56E-05	7.70E-03	-2.11	down	no
ENSMUSG000000007594	Hap1n4	hyaluronan and	30.21	32.64	29.75	25.79	27.84	25.67	1.17	0.22	1.59E-05	7.70E-03	-2.11	up	no
ENSMUSG000000051359	Ncald	neurocalcin de	61.14	63.72	64.82	50.49	55.68	58.40	1.15	0.20	1.60E-05	7.70E-03	-2.11	up	no
ENSMUSG000000087412	Gm15501	predicted pseu	5.84	6.23	6.44	11.48	9.02	10.22	0.60	-0.73	1.64E-05	7.82E-03	-2.11	down	no
ENSMUSG000000044676	Zfp612	zinc finger pr	8.10	7.75	7.43	9.35	11.05	9.63	0.77	-0.37	1.70E-05	7.97E-03	-2.10	down	no
ENSMUSG000000028790	Khdrb1	KH domain cont	20.49	20.34	19.49	16.61	18.04	17.88	1.15	0.20	1.73E-05	7.98E-03	-2.10	up	no
ENSMUSG000000046056	Sbsn	suprabasin [Sc	0.90	1.16	1.00	1.84	1.87	1.66	0.57	-0.81	2.00E-05	9.13E-03	-2.04	down	no
ENSMUS															

ENSMUSG00000029634	Rnf6	ring finger pr	15.80	16.23	15.68	12.45	13.15	14.69	1.18	0.24	1.35E-04	4.67E-02	-1.33 up	no
ENSMUSG00000036644	Tbcd9b	TBC1 domain fa	27.13	26.82	29.47	32.91	33.85	33.21	0.83	-0.26	1.36E-04	4.67E-02	-1.33 down	no
ENSMUSG00000001774	Chordc1	cysteine and h	9.90	10.40	9.98	8.35	9.24	8.85	1.15	0.20	1.41E-04	4.81E-02	-1.32 up	no
ENSMUSG00000042831	Alkbh6	alkB homolog 6	5.17	5.54	6.09	7.65	7.76	7.20	0.74	-0.43	1.44E-04	4.85E-02	-1.31 down	no

Table S2C: Selection of genes robustly altered in E4H vs E2H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=3 mice/group.

gene_id	gene_name	Description	FPKM. E4H_1	FPKM.E 4H_2	FPKM. E4H_3	FPKM.E 2H_1	FPKM.E H_2	FPKM.E 2H_3	fc	log2 (fc)	pval	qval	log10 (qval)	regula tion	signif icant
ENSMUSG00000093954	Gm16867	predicted gene,	2.53	2.22	2.10	0.07	0.04	0.07	39.97	5.32	9.91E-130	3.29E-125	-124.48	up	yes
ENSMUSG00000096768	Gm47283	predicted gene,	0.09	0.04	0.07	7.73	3.26	5.04	0.01	-6.30	2.01E-97	3.33E-93	-92.48	down	yes
ENSMUSG00000095562	Erdrl1	erythroid diffe	0.12	0.17	0.19	17.85	7.97	11.38	0.01	-6.30	7.07E-96	7.81E-92	-91.11	down	yes
ENSMUSG00000021091	Serpina3n	serine (or cyst	71.58	62.15	75.81	14.64	13.27	12.50	5.19	2.37	2.60E-95	2.15E-91	-90.67	up	yes
ENSMUSG00000098975	Gm27177	predicted gene	2.16	1.95	1.33	0.06	0.12	0.07	21.40	4.42	5.04E-58	3.34E-54	-53.48	up	yes
ENSMUSG000000109209	Gm45104	predicted gene	2.39	2.20	2.43	0.17	0.26	0.24	10.57	3.40	6.36E-53	3.51E-49	-48.45	up	yes
ENSMUSG00000073643	Wdfy1	WD repeat and F	2.30	2.60	2.34	7.96	6.64	7.02	0.33	-1.58	2.27E-47	1.07E-43	-42.97	down	yes
ENSMUSG000000118458	Gm10599	predicted pseud	2.91	3.87	1.98	0.12	0.10	0.09	27.98	4.81	1.09E-44	4.51E-41	-40.35	up	yes
ENSMUSG00000090338	Gm17081	predicted gene	2.53	3.36	1.71	0.07	0.07	0.06	38.38	5.26	1.30E-43	4.80E-40	-39.32	up	yes
ENSMUSG00000091542	Gm17167	predicted gene	1.18	1.79	0.87	0.08	0.05	0.05	21.21	4.41	3.86E-37	1.28E-33	-32.89	up	yes
ENSMUSG00000095675	Ccl21b	chemokine (C-C	4.18	4.66	5.32	0.14	0.10	0.01	54.75	5.77	2.84E-36	8.57E-33	-32.07	up	yes
ENSMUSG00000073878	Gm13304	predicted gene	4.45	4.42	4.45	0.15	0.14	0.03	41.49	5.37	1.10E-33	3.03E-30	-29.52	up	yes
ENSMUSG00000073879	Gm5859	predicted pseud	1.82	2.64	1.51	0.12	0.07	0.09	21.45	4.42	2.10E-33	5.36E-30	-29.27	up	yes
ENSMUSG00000096596	Gm10591	predicted gene	4.18	3.85	3.96	0.10	0.08	0.03	57.66	5.85	2.30E-33	5.44E-30	-29.26	up	yes
ENSMUSG00000094065	Ccl21d	chemokine (C-C	3.75	2.80	3.40	0.11	0.10	0.02	42.29	5.40	1.42E-26	3.13E-23	-22.50	up	yes
ENSMUSG00000097842	9330104G04Ri	RIKEN cDNA 9330	0.22	0.31	0.30	1.37	1.56	1.11	0.18	-2.46	5.88E-24	1.22E-20	-19.92	down	yes
ENSMUSG00000079012	Serpina3m	serine (or cyst	1.87	2.05	2.06	0.03	0	0	175.63	7.46	6.24E-24	1.22E-20	-19.92	up	yes
ENSMUSG00000035299	Midl1	midline 1 [Sou	0.33	0.32	0.21	2.32	0.96	2.87	0.14	-2.82	3.26E-21	6.01E-18	-17.22	down	yes
ENSMUSG00000096862	Gm13301	predicted gene	1.01	1.33	0.67	0.03	0.02	0.04	34.56	5.11	7.12E-21	1.24E-17	-16.91	up	yes
ENSMUSG000000110105	Gm45844	predicted gene	0.10	0.12	0.05	0.62	0.62	0.60	0.15	-2.74	3.89E-19	6.45E-16	-15.19	down	yes
ENSMUSG00000052861	Dnah6	dynein, axonema	0.60	0.62	0.53	0.18	0.09	0.11	4.64	2.21	5.03E-19	7.93E-16	-15.10	up	yes
ENSMUSG00000076612	Ighg2c	immunoglobulin	0	0	0	2.32	4.23	2.57	0.00	-14.89	1.40E-18	2.11E-15	-14.68	down	yes
ENSMUSG00000022066	Entpd4b	ectonucleoside	8.97	8.60	9.27	5.18	4.64	5.10	1.80	0.85	2.08E-18	3.00E-15	-14.52	up	no
ENSMUSG00000078897	Gm4724	predicted gene	0.60	0.70	0.65	2.28	1.98	2.06	0.31	-1.69	6.34E-17	8.76E-14	-13.06	down	yes
ENSMUSG00000087467	Gm13601	predicted gene	0.05	0	0.14	3.71	4.40	3.63	0.02	-5.96	2.02E-16	2.68E-13	-12.57	down	yes
ENSMUSG00000084010	Gm13302	predicted gene	1.11	1.49	0.79	0.09	0.09	0.08	12.60	3.66	6.93E-16	8.83E-13	-12.05	up	yes
ENSMUSG000000118434	Gm13301	predicted gene	2.01	2.44	1.66	0.10	0.12	0.19	14.54	3.86	3.69E-15	4.54E-12	-11.34	up	yes
ENSMUSG00000093909	Gm3883	predicted gene	2.93	3.31	2.55	1.04	0.54	0.91	3.54	1.82	6.87E-15	8.13E-12	-11.09	up	yes
ENSMUSG000000118425	Gm50470	predicted gene	1.20	1.44	0.85	0.08	0.09	0.15	10.70	3.42	9.22E-15	1.05E-11	-10.98	up	yes
ENSMUSG00000096256	Gm21093	predicted gene	3.60	3.45	2.71	1.14	0.68	1.17	3.26	1.71	1.35E-14	1.49E-11	-10.83	up	yes
ENSMUSG00000053985	Zfp14	zinc finger pro	6.31	6.39	6.33	3.48	3.06	3.47	1.90	0.93	1.82E-14	1.94E-11	-10.71	up	no
ENSMUSG00000095463	Entpd4	ectonucleoside	8.03	7.66	7.99	4.89	4.46	4.34	1.73	0.79	2.36E-14	2.45E-11	-10.61	up	no
ENSMUSG00000058626	Capn11	calpain 11 [Sou	0.05	0.08	0.18	0.82	1.23	0.98	0.10	-3.29	9.79E-14	9.84E-11	-10.01	down	yes
ENSMUSG00000094066	Fam205a2	family with seq	1.86	2.14	1.64	0.76	0.70	0.70	2.61	1.39	3.50E-12	3.41E-09	-8.47	up	yes
ENSMUSG00000030413	Pglyrpl	peptidoglycan r	0.71	0.69	0.71	6.08	2.37	2.14	0.20	-2.32	1.10E-11	1.04E-08	-7.98	down	yes
ENSMUSG00000093996	Fam205a3	family with seq	1.93	2.10	1.66	0.83	0.75	0.80	2.39	1.26	2.42E-11	2.23E-08	-7.65	up	yes
ENSMUSG00000031562	Dctd	dCMP deaminase	1.11	1.06	0.94	2.51	2.35	2.02	0.45	-1.14	7.45E-11	6.68E-08	-7.18	down	yes
ENSMUSG00000078746	Fam205a4	family with seq	1.87	2.02	1.60	0.81	0.73	0.79	2.35	1.23	1.10E-10	9.60E-08	-7.02	up	yes
ENSMUSG00000095348	Gm3892	predicted gene	0.98	1.30	0.72	0.28	0.19	0.24	4.23	2.08	1.17E-10	9.98E-08	-7.00	up	yes
ENSMUSG00000032667	Pon2	paraoxonase 2 [	4.97	4.30	4.26	7.07	7.92	7.13	0.61	-0.71	1.21E-10	1.01E-07	-7.00	down	no
ENSMUSG000000116207	Nnt	nicotinamide nu	3.53	0.35	3.17	0	0	0	23504.15	14.52	2.18E-10	1.76E-07	-6.75	up	yes
ENSMUSG00000079494	Nat8f5	N-acetyltransfe	0.22	0.20	0.18	1.16	1.39	1.65	0.14	-2.81	2.92E-10	2.31E-07	-6.64	down	yes
ENSMUSG00000021171	Eysy2	extended synapt	5.71	5.35	5.52	3.66	3.11	3.69	1.58	0.66	4.17E-10	3.21E-07	-6.49	up	no
ENSMUSG000000108815	Gm49388	predicted gene	0	0	0	1.70	0	0	0.00	-12.47	5.42E-10	4.08E-07	-6.39	down	yes
ENSMUSG00000068457	Uty	ubiquitously tr	0	0	1.14	0	0	0	3787.61	11.89	1.13E-09	8.36E-07	-6.08	up	yes
ENSMUSG000000106874	Gm20186	predicted gene	0	0.01	0	1.28	0.48	0.94	0.00	-8.33	5.08E-09	3.66E-06	-5.44	down	yes
ENSMUSG00000089945	Pakap	paralemin A ki	2.38	1.80	1.23	0.87	0.39	0.57	2.96	1.56	8.70E-09	6.14E-06	-5.21	up	yes
ENSMUSG00000090996	Gm20458	predicted gene	0	0	0	0	1.61	0	0.00	-12.39	9.26E-09	6.39E-06	-5.19	down	yes
ENSMUSG00000046952	Gm5815	predicted pseud	0.98	1.48	1.48	0.19	0.07	0.29	7.19	2.85	1.04E-08	7.02E-06	-5.15	up	yes
ENSMUSG00000089865	Gm44503	predicted readt	0	0	0	0	0.44	0	0.00	-10.53	1.19E-08	7.90E-06	-5.10	down	yes
ENSMUSG00000058838	Rps27a-ps2	ribosomal prote	22.37	24.08	23.02	34.46	48.08	43.46	0.55	-0.86	1.48E-08	9.59E-06	-5.02	down	no
ENSMUSG00000091228	Gm20390	predicted gene	0	0	0	1.67	0	0	0.00	-12.44	1.91E-08	1.22E-05	-4.91	down	yes
ENSMUSG00000021647	Cartpt	CART prepropte	4.96	4.52	6.05	9.10	8.61	11.30	0.54	-0.90	3.90E-08	2.44E-05	-4.61	down	no
ENSMUSG000000114942	Gm49361	predicted gene	0	0	0	0	0.32	0	0.00	-10.05	4.06E-08	2.50E-05	-4.60	down	yes
ENSMUSG00000095258	Gm10593	predicted gene	0.71	0.87	0.51	0.22	0.17	0.17	3.72	1.90	4.17E-08	2.52E-05	-4.60	up	yes
ENSMUSG00000048108	Tmem72	transmembrane p	0.69	0.51	0.36	0.24	0.19	0.19	2.54	1.35	4.41E-08	2.61E-05	-4.58	up	yes
ENSMUSG000000108348	Gm42372	predicted gene	16.06	16.04	15.60	22.01	19.91	21.16	0.76	-0.40	5.27E-08	3.07E-05	-4.51	down	no
ENSMUSG00000085105	Gm12758	predicted gene	0.71	0.55	0.33	1.39	1.17	1.50	0.39	-1.35	5.67E-08	3.24E-05	-4.49	down	yes
ENSMUSG00000045948	Mrps12	mitochondrial r	11.85	13.31	12.80	19.11	27.00	21.04	0.57	-0.82	8.78E-08	4.93E-05	-4.31	down	no
ENSMUSG000000109176	Zfp264	zinc finger pro	0.74	0.44	0.12	0.02	0.03	0.05	13.91	3.80	1.87E-07	1.03E-04	-3.99	up	yes
ENSMUSG00000056553	Ptprn2	protein tyrosin	26.22	29.82	25.98	18.56	13.48	19.32	1.60	0.68	1.97E-07	1.07E-04	-3.97	up	no
ENSMUSG00000063681	Crb1	crumbs family m	0.18	0.14	0.12	0.03	0.04	0.05	3.79	1.92	2.64E-07	1.41E-04	-3.85	up	yes
ENSMUSG00000094293	Gm3893	predicted gene	1.43	2.46	1.01	0.22	0.34	0.27	5.85	2.55	4.13E-07	2.17E-04	-3.66	up	yes
ENSMUSG000000107927	Gm44090	predicted gene	0	0.03	0.02	0.40	0.32	0.31	0.04	-4.56	4.39E-07	2.28E-04	-3.64	down	yes
ENSMUSG00000004798	Ulk2	unc-51 like kin	11.95	11.62	12.92	17.17	14.64	18.01	0.73	-0.45	5.48E-07	2.79E-04	-3.55	down	no
ENSMUSG00000074358	Ccdc61	coiled-coil dom	1.02	0.95	1.09	1.98	2.49	1.83	0.49	-1.04	5.77E-07	2.90E-04	-3.54	down	yes
ENSMUSG00000019478	Rab4a	RAB4A, member R	17.85	18.89	19.04	25.28	27.80	25.50	0.71	-0.49	7.58E-07	3.75E-04	-3.43	down	no
ENSMUSG00000098374	Gm28043	predicted gene	4.26	2.73	3.01	1.88	1.13	1.88	2.04	1.03	9.62E-07	4.69E-04	-3.33	up	yes
ENSMUSG00000089862	Umad1	UMAP1-MVP12 ass	5.91	6.04	6.76	8.57	8.96	8.65	0.71	-0.48	1.24E-06	5.97E-04	-3.22	down	no
ENSMUSG00000090083	Rnf8	ring finger pro	1.20	1.32	1.48	2.03	1.89	1.96	0.68	-0.56	1.34E-06	6.33E-04	-3.20	down	no
ENSMUSG000000118603	BX666061	protein FAM205A	0.62	0.75	0.54	0.16	0.14	0.17	3.97	1.99	1.41E-06	6.57E-04	-3.18	up	yes
ENSMUSG000000019773	Fbxo5	F-box protein 5	1.63	2.06	1.27	0.46	0.60	0.69	2.84	1.50	1.51E-06	6.93E-04	-3.16	up	yes
ENSMUSG00000053898	Echl	enoyl coenzyme	11.10	11.09	12.53	16.40	19.51	16.05	0.67	-0.58	1.75E-06	7.85E-04	-3.11	down	no
ENSMUSG000000103770	Pcdha9	protocadherin a	1.08	0.85	1.33	0.53	0.36	0.19	3.02	1.60	1.75E-06	7.85E-04	-3.11	up	yes
ENSMUSG00000079641	Rpl39	ribosomal prote	20.75	20.36											

ENSMUSG00000046056	Sbsn	suprabasin [Sou	0.90	1.16	1.00	1.99	1.48	2.08	0.55	-0.86	6.57E-06	2.48E-03	-2.61	down	no
ENSMUSG00000078721	Fam205a1	family with seq	0.92	0.98	0.72	0.42	0.38	0.36	2.25	1.17	7.08E-06	2.64E-03	-2.58	up	yes
ENSMUSG00000082414	Gm13303	predicted gene	1.25	1.22	0.96	0.42	0.22	0.36	3.45	1.79	7.19E-06	2.65E-03	-2.58	up	yes
ENSMUSG00000042831	Alkbh6	alkB homolog 6	5.17	5.54	6.09	7.98	9.23	7.69	0.67	-0.57	8.05E-06	2.93E-03	-2.53	down	no
ENSMUSG00000024208	Uqcc2	ubiquinol-cytoc	29.87	27.80	30.72	39.93	58.10	41.88	0.63	-0.66	9.49E-06	3.42E-03	-2.47	down	no
ENSMUSG00000018659	Pnp	pyridoxine 5'-p	17.02	15.14	17.11	21.35	21.35	21.70	0.77	-0.39	1.09E-05	3.90E-03	-2.41	down	no
ENSMUSG00000029993	Nful	NFul iron-sulfu	5.46	5.42	6.07	7.60	8.43	7.49	0.72	-0.47	1.17E-05	4.10E-03	-2.39	down	no
ENSMUSG00000020396	Nefh	neurofilament, I	23.33	21.24	25.73	43.16	28.55	31.77	0.68	-0.56	1.18E-05	4.10E-03	-2.39	down	no
ENSMUSG00000001911	Nfix	nuclear factor	14.17	15.20	13.05	10.26	9.60	10.82	1.38	0.47	1.21E-05	4.17E-03	-2.38	up	no
ENSMUSG00000099041	Gm28035	predicted gene,	2.84	1.75	1.60	1.13	0.67	1.01	2.20	1.13	1.23E-05	4.20E-03	-2.38	up	yes
ENSMUSG00000061983	Rps12	ribosomal prote	27.81	25.33	30.20	40.56	43.81	34.37	0.70	-0.51	1.28E-05	4.32E-03	-2.36	down	no
ENSMUSG00000029994	Anxa4	annexin A4 [Sou	2.01	2.00	2.01	1.01	1.30	1.13	1.75	0.80	1.29E-05	4.32E-03	-2.36	up	no

Table S2D: Selection of genes robustly altered in PS/E2H vs PS/E3H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=4 mice/group. PE2H, PS19 mice homozygous for APOE2; PE3H, PS19 mice homozygous for APOE3.

gene_id	gene_name	Description	FPKM. PE2H_1	FPKM. PE2H_2	FPKM. PE2H_3	FPKM. PE2H_4	FPKM. PE3H_1	FPKM. PE3H_2	FPKM. PE3H_3	FPKM. PE3H_4	fc	log2 (fc)	pval	qval	log10 (qval)	regula tion	signif icant
ENSMUSG00000109209	Gm45104	predicted gene	0.14	0.04	0.08	0.09	1.92	2.52	2.62	1.66	0.04	-4.61	1.00E-63	3.37E-59	-58.47	down	yes
ENSMUSG00000098975	Gm27177	predicted gene	0.05	0.07	0.08	0.05	1.92	0.88	0.75	1.83	0.05	-4.43	5.06E-40	8.52E-36	-35.07	down	yes
ENSMUSG00000096596	Gm10591	predicted gene	0.12	0.06	0.09	0.08	3.54	1.99	5.03	6.67	0.02	-5.61	1.74E-31	1.96E-27	-26.71	down	yes
ENSMUSG00000073878	Gm13304	predicted gene	0.19	0.15	0.13	0.11	3.69	2.10	5.68	5.87	0.03	-4.90	1.14E-30	9.58E-27	-26.02	down	yes
ENSMUSG00000090338	Gm17081	predicted gene	0.06	0.09	0.09	0.06	0.95	0.94	1.74	1.34	0.06	-4.10	3.46E-29	2.33E-25	-24.63	down	yes
ENSMUSG00000093954	Gm16867	predicted gene	0.02	0.06	0.09	0.05	2.44	1.21	1.34	1.95	0.03	-4.97	4.09E-27	2.29E-23	-22.64	down	yes
ENSMUSG00000095675	Ccl21b	chemokine (C-C)	0.11	0.15	0.06	0.11	3.04	1.53	6.16	6.29	0.02	-5.33	2.07E-26	9.97E-23	-22.00	down	yes
ENSMUSG00000118458	Gm10599	predicted pseu	0.09	0.12	0.11	0.09	0.85	0.87	1.90	1.50	0.08	-3.60	1.37E-22	5.76E-19	-18.24	down	yes
ENSMUSG00000094065	Ccl21d	chemokine (C-C)	0.10	0.13	0.11	0.06	1.64	1.45	3.89	4.22	0.04	-4.80	2.15E-21	8.06E-18	-17.09	down	yes
ENSMUSG00000073879	Gm5859	predicted pseu	0.09	0.12	0.13	0.08	0.70	0.76	1.38	1.31	0.10	-3.33	2.23E-19	7.52E-16	-15.12	down	yes
ENSMUSG00000006154	Eps811	EP88-like 1 [S	0.82	0.53	0.71	0.96	0.18	0.16	0.14	0.22	4.27	2.09	8.39E-17	2.57E-13	-12.59	up	yes
ENSMUSG000000091542	Gm17167	predicted gene	0.10	0.09	0.10	0.04	0.41	0.48	1.03	0.81	0.12	-3.05	1.01E-16	2.85E-13	-12.55	down	yes
ENSMUSG000000025453	Nnt	nicotinamide n	4.55	3.91	4.80	4.53	1.32	1.07	2.45	1.62	2.75	1.46	5.19E-15	1.34E-11	-10.87	up	yes
ENSMUSG000000095562	Erd1	erythroid diff	10.90	7.65	7.90	11.85	4.23	3.34	3.00	3.84	2.66	1.41	1.68E-14	4.04E-11	-10.39	up	yes
ENSMUSG00000107705	Gm45062	predicted gene	0	0	0	0	0	0	0	5.76	0.00	-13.81	2.10E-14	4.71E-11	-10.33	down	yes
ENSMUSG000000054594	Oscar	osteoclast ass	0.57	0.52	0.62	0.85	0.06	0.03	0.05	0.07	11.95	3.58	4.20E-14	8.85E-11	-10.05	up	yes
ENSMUSG000000053985	Zfp14	zinc finger pr	2.79	2.63	2.68	2.74	4.28	5.29	6.22	4.66	0.53	-0.92	1.28E-12	2.54E-09	-8.60	down	no
ENSMUSG00000096862	Gm13301	predicted gene	0.05	0.04	0.05	0.03	0.52	0.27	0.53	0.61	0.09	-3.51	3.62E-12	6.78E-09	-8.17	down	yes
ENSMUSG00000096768	Gm47283	predicted gene	5.23	4.64	3.21	5.14	1.52	2.49	1.35	1.78	2.55	1.35	4.08E-12	7.24E-09	-8.14	up	yes
ENSMUSG00000068457	Uty	ubiquitously t	0.01	0.88	0	0	0	0	0	0	2207.08	11.11	4.44E-12	7.37E-09	-8.13	up	yes
ENSMUSG00000101015	Gm45844	predicted gene	0.48	0.43	0.50	0.47	0.05	0.06	0.18	0.08	5.21	2.38	4.60E-12	7.37E-09	-8.13	up	yes
ENSMUSG00000086604	Gm15510	predicted gene	1.23	1.25	0.50	1.75	0.15	0.13	0.12	0.11	9.40	3.23	1.17E-11	1.79E-08	-7.75	up	yes
ENSMUSG00000089865	Gm44503	predicted read	0	0	0	0	0	0	0	0.72	0.00	-10.81	2.23E-11	3.27E-08	-7.49	down	yes
ENSMUSG00000109176	Zfp264	zinc finger pr	0.05	0.02	0	0.02	0.37	0.41	0.55	0.27	0.06	-4.16	3.56E-11	4.49E-08	-7.30	down	yes
ENSMUSG00000109061	Gm49320	predicted gene	0	0	0	0	0.65	0	0	0	0.00	-10.67	8.19E-11	1.10E-07	-6.96	down	yes
ENSMUSG00000099876	Gm29650	predicted gene	0	3.61	0	0	0	0	0	0	9028.21	13.14	1.76E-10	2.28E-07	-6.64	up	yes
ENSMUSG00000076508	Igkv17-127	immunoglobulin	0	0	0	0	0	0	3.78	0	0.00	-13.21	2.43E-10	3.03E-07	-6.52	down	yes
ENSMUSG00000030413	Pglyrpl	peptidoglycan	2.49	2.78	2.34	5.70	0.63	0.93	1.18	1.06	3.51	1.81	4.83E-10	5.81E-07	-6.24	up	yes
ENSMUSG00000095753	Igkv4-53	immunoglobulin	0	0	0	0	0	2.45	0	0	0.00	-12.58	6.73E-10	7.81E-07	-6.11	down	yes
ENSMUSG00000090996	Gm20458	predicted gene	0	0	0	0.70	0	0	0	0	1746.25	10.77	1.83E-09	2.03E-06	-5.69	up	yes
ENSMUSG00000071470	Ccnbl1p1	cyclin B1 inte	0	0.51	0	0	0	0	0	0	1271.39	10.31	1.87E-09	2.03E-06	-5.69	up	yes
ENSMUSG00000030037	Mrp153	mitochondrial	9.20	8.13	11.10	8.06	5.36	3.84	4.16	3.42	2.17	1.12	2.89E-09	3.04E-06	-5.52	up	yes
ENSMUSG00000072676	Tmem254a	transmembrane	1.76	2.48	1.74	1.97	4.05	4.85	3.59	3.71	0.49	-1.03	4.19E-09	4.27E-06	-5.37	down	yes
ENSMUSG00000053964	Lgals4	lectin, galact	0.78	0.83	0.85	1.24	0.22	0.33	0.26	0.34	3.18	1.67	1.03E-08	1.02E-05	-4.99	up	yes
ENSMUSG00000074358	Ccdc61	coiled-coil dc	2.29	1.89	2.01	1.99	1.10	0.71	1.18	0.95	2.07	1.05	3.46E-08	3.33E-05	-4.48	up	yes
ENSMUSG00000035299	Mid1	midline 1 [Sou	1.39	0.78	1.14	1.53	0.67	0.36	0.34	0.41	2.72	1.45	4.56E-08	4.27E-05	-4.37	up	yes
ENSMUSG000000084010	Gm13302	predicted gene	0.11	0.06	0.11	0.04	0.35	0.39	0.75	0.64	0.15	-2.74	7.42E-08	6.76E-05	-4.17	down	yes
ENSMUSG00000064179	Tnnt1	troponin T1, a	4.88	6.78	3.13	3.93	1.84	2.25	2.46	2.13	2.16	1.11	1.35E-07	1.20E-04	-3.92	up	yes
ENSMUSG000000039629	Strip2	striatin inter	5.19	4.90	5.12	4.29	6.32	8.80	7.18	7.39	0.66	-0.61	1.40E-07	1.21E-04	-3.92	down	no
ENSMUSG00000109205	Gm44954	predicted gene	0.29	0.53	0.78	0.45	3.27	4.63	2.65	3.01	0.15	-2.72	1.63E-07	1.37E-04	-3.86	down	yes
ENSMUSG00000074361	C5ar2	complement com	0.15	0.20	0.30	0.21	0.05	0.03	0.03	0.01	7.00	2.81	2.31E-07	1.90E-04	-3.72	up	yes
ENSMUSG00000093909	Gm3883	predicted gene	0.91	0.79	1.16	0.70	1.61	1.58	2.24	1.97	0.48	-1.06	2.57E-07	2.06E-04	-3.69	down	yes
ENSMUSG00000095463	Entpd4	ectonucleoside	4.12	4.57	3.83	2.77	7.48	6.19	5.76	7.76	0.56	-0.83	3.65E-07	2.86E-04	-3.54	down	no
ENSMUSG000000045948	Mrp512	mitochondrial	21.25	24.31	17.12	18.51	14.34	11.94	11.86	10.87	1.66	0.73	4.00E-07	3.06E-04	-3.51	up	no
ENSMUSG00000058626	Capn11	calpain 11 [Sc	0.13	0.06	0.10	0.06	0.08	1.17	0.46	1.61	0.11	-3.25	4.59E-07	3.44E-04	-3.46	down	yes
ENSMUSG00000096256	Gm21093	predicted gene	1.04	0.89	1.21	1.02	1.82	1.64	2.07	2.26	0.54	-0.90	4.83E-07	3.54E-04	-3.45	down	no
ENSMUSG00000118425	Gm50470	predicted gene	0.16	0.11	0.15	0.14	0.38	0.46	0.88	0.72	0.22	-2.17	5.22E-07	3.74E-04	-3.43	down	yes
ENSMUSG00000035429	Ptprh	protein tyrosi	0.31	0.30	0.29	0.39	0	0.06	0.07	0.04	7.39	2.88	5.37E-07	3.77E-04	-3.42	up	yes
ENSMUSG00000035692	Isg15	ISG15 ubiquiti	10.13	10.17	7.63	8.89	2.77	3.55	3.66	6.50	2.23	1.16	1.42E-06	9.73E-04	-3.01	up	yes
ENSMUSG000000040569	Slc26a7	solute carrier	0.49	0.47	0.81	0.35	0.83	1.45	1.20	1.56	0.42	-1.25	1.93E-06	1.30E-03	-2.89	down	yes
ENSMUSG00000053898	Echl	enoyl coenzyme	18.75	20.25	15.72	18.24	10.94	13.03	11.64	14.48	1.46	0.54	2.57E-06	1.70E-03	-2.77	up	no
ENSMUSG00000070469	Adamts13	ADAMTS-like 3	0.29	0.20	0.38	0.18	0.42	0.71	0.62	0.90	0.39	-1.34	2.95E-06	1.91E-03	-2.72	down	yes
ENSMUSG00000108366	Gm5586	predicted gene	9.86	0.34	0.36	10.58	0.15	0.15	0.17	0.11	36.49	5.19	3.80E-06	2.42E-03	-2.62	up	yes
ENSMUSG00000089998	Phtflos	putative homec	2.72	2.08	0.66	1.19	0.65	0.35	0.72	0.52	2.97	1.57	5.29E-06	3.30E-03	-2.48	up	yes
ENSMUSG00000118434	Gm13301	predicted gene	0.17	0.13	0.34	0.26	0.99	0.63	1.40	1.26	0.21	-2.26	6.09E-06	3.73E-03	-2.43	down	yes
ENSMUSG000000044042	Fmn1	formin 1 [Sou	0.73	0.62	0.88	0.89	1.22	1.16	1.24	1.16	0.65	-0.62	6.88E-06	4.14E-03	-2.38	down	no
ENSMUSG00000033061	Resp18	regulated endo	89.72	87.99	88.71	95.57	59.37	79.64	73.60	64.15	1.31	0.39	7.19E-06	4.25E-03	-2.37	up	no
ENSMUSG00000030306	Tmtc1	transmembrane	7.38	6.87	8.09	6.95	9.38	9.87	10.32	8.91	0.76	-0.39	8.49E-06	4.93E-03	-2.31	down	no
ENSMUSG00000095348	Gm3892	predicted gene	0.28	0.15	0.28	0.15	0.47	0.51	0.70	0.67	0.37	-1.44	1.01E-05	5.74E-03	-2.24	down	yes
ENSMUSG00000096257	Ccer2	coiled-coil gl	1.96	2.48	2.13	2.03	4.15	3.25	5.05	3.80	0.53	-0.92	1.17E-05	6.56E-03	-2.18	down	no
ENSMUSG00000008435	Rdh13	retinol dehydr	3.00	3.07	2.54	2.83	4.17	3.76	4.62	3.94	0.69	-0.53	1.24E-05	6.82E-03	-2.17	down	no
ENSMUSG00000029561	Oas12	2'-5' oligoad	3.70	2.32	2.60	4.05	0.95	1.67	1.95	2.09	1.00	0.93	1.28E-05	6.91E-03	-2.16	up	no
ENSMUSG00000073647	Gm10557	predicted gene	2.89	3.08	3.96	1.91	5.76	8.09	5.97	5.50	0.47	-1.10	1.29E-05	6.91E-03	-2.16	down	yes
ENSMUSG00000005575	Ube2m	ubiquitin-conj	48.12	57.90	42.84	50.10	38.40	33.83	34.38	37.25	1.38	0.47	1.41E-05	7.41E-03	-2.13	up	no
ENSMUSG00000034218	Atm	ataxia telangi	0.49	0.36	0.69	0.48	0.74	0.96	0.99	0.89	0.56	-0.83	1.60E-05	8.31E-03	-2.08	down	no
ENSMUSG00000064215	Ifi27	interferon, al	36.74	35.03	30.49	31.19	20.71	23.90	26.29	27.30	1.36	0.44	1.70E-05	8.69E-03	-2.06	up	no
ENSMUSG00000038775	Vill1	villin-like [S	1.00	1.03	1.28	1.41	0.72	0.61	0.48	0.74	1.85	0.88	1.73E-05	8.72E-03	-2.06	up	no
ENSMUSG00000031626	Sorbs2	sorbin and SH3	2														

Table S2E: Selection of genes altered in P5/E4H vs P5/E3H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=4 mice/group. PE4H, P519 mice homozygous for APOE4; PE3H, P519 mice homozygous for APOE3.

gene_id	gene_name	Description	FPKM. PE4H_1	FPKM. PE4H_2	FPKM. PE4H_3	FPKM. PE4H_4	FPKM. PE3H_1	FPKM. PE3H_2	FPKM. PE3H_3	FPKM. PE3H_4	fc	log2 (fc)	pval	qval	log10 (qval)	regula tion	signif icant	
ENSMUSG00000086604	Gm15510	predicted gene	1.31	1.41	0.88	1.41	0.15	0.13	0.12	0.11	9.93	3.31	1.28E-16	4.33E-12	-11.36	up	yes	
ENSMUSG00000054594	Oscar	osteoclast ass	0.68	0.52	0.53	0.68	0.06	0.03	0.05	0.07	11.24	3.49	6.51E-14	7.84E-10	-9.11	up	yes	
ENSMUSG00000006154	Eps811	EPS8-like 1 [S	0.45	0.81	0.66	0.91	0.18	0.16	0.14	0.22	4.00	2.00	6.99E-14	7.84E-10	-9.11	up	yes	
ENSMUSG00000031562	Dctd	dCMP deaminase	0.90	0.79	0.86	0.90	1.58	2.05	1.77	1.91	0.47	-1.08	9.35E-13	7.87E-09	-8.10	down	yes	
ENSMUSG00000089865	Gm44503	predicted read	0	0	0	0	0	0	0	0.72	0.00	-10.81	2.26E-11	1.52E-07	-6.82	down	yes	
ENSMUSG000000021342	Pr1	prolactin [Sou	0	1.59	0	0	0	0	0	0	3979.5	11.96	1.95E-10	1.09E-06	-5.96	up	yes	
ENSMUSG00000076508	Igkv17-127	immunoglobulin	0	0	0	0	0	0	3.78	0	0.00	-13.21	2.43E-10	1.17E-06	-5.93	down	yes	
ENSMUSG000000078519	2310026L22Rik	RIKEN cDNA 231	0	0	0	0	0	2.42	0	0	0.00	-12.56	5.51E-10	2.32E-06	-5.63	down	yes	
ENSMUSG00000095753	Igkv4-53	immunoglobulin	0	0	0	0	2.45	0	0	0	0.00	-12.58	6.70E-10	2.51E-06	-5.60	down	yes	
ENSMUSG00000095007	Igkv12-41	immunoglobulin	0	3.48	0	0	0	0	0	0	8709.1	13.09	1.05E-09	3.52E-06	-5.45	up	yes	
ENSMUSG00000092232	Gm20521	predicted gene	0	2.22	0	0	0	0	0	0	5553.9	12.44	2.00E-09	6.11E-06	-5.21	up	yes	
ENSMUSG000000087467	Gm13601	predicted gene	0	0	0	0.31	2.11	2.38	1.88	1.99	0.04	-4.75	2.53E-08	7.11E-05	-4.15	down	yes	
ENSMUSG00000069045	Ddx3y	DEAD (Asp-Glu-	10.64	0.04	0.06	11.96	0.02	0.02	0.02	0.01	334.97	8.39	3.01E-08	7.80E-05	-4.11	up	yes	
ENSMUSG000000110899	Gm48840	predicted gene	0.02	0.02	0.35	0.10	0	0	0	0	1258.5	10.30	7.83E-08	1.87E-04	-3.73	up	yes	
ENSMUSG000000001119	Col6a1	collagen, type	5.05	5.21	3.86	6.02	6.49	8.54	9.44	8.51	0.61	-0.71	8.34E-08	1.87E-04	-3.73	down	no	
ENSMUSG000000091177	Gm15494	predicted gene	0	0.21	0.06	0.14	0.86	1.18	1.92	1.24	0.08	-3.64	1.22E-07	2.56E-04	-3.59	down	yes	
ENSMUSG000000074280	Gm6166	predicted gene	1.28	29.43	22.90	28.61	1.18	1.07	0.61	1.29	19.80	4.31	1.93E-07	3.82E-04	-3.42	up	yes	
ENSMUSG000000004798	Ulk2	unc-51 like k1	15.01	13.16	11.21	12.31	16.91	17.27	18.87	18.77	0.72	-0.47	3.80E-07	7.11E-04	-3.15	down	no	
ENSMUSG000000062132	Arhgap33os	Rho GTPase act	0.17	0.27	0.11	0.16	0	0.02	0	0	40.90	5.35	5.06E-07	8.97E-04	-3.05	up	yes	
ENSMUSG0000000027375	Mal	myelin and lym	105.1	104.3	101.2	110.44	83.77	84.12	93.85	83.29	1.22	0.29	7.30E-07	1.23E-03	-2.91	up	no	
ENSMUSG000000064179	Tnnt1	troponin T1, s	5.29	3.60	3.79	3.11	1.84	2.25	2.46	2.13	1.82	0.86	1.21E-06	1.94E-03	-2.71	up	no	
ENSMUSG00000068457	Uty	ubiquitously t	1.24	0.00	0.01	1.22	0	0	0	0	6203.3	12.60	2.80E-06	4.28E-03	-2.37	up	yes	
ENSMUSG00000008435	Rdh13	retinol dehydr	3.05	3.18	2.42	2.80	4.17	3.76	4.62	3.94	0.69	-0.53	3.30E-06	4.83E-03	-2.32	down	no	
ENSMUSG000000058740	Kcnt1	potassium chan	7.92	6.97	7.29	7.90	8.88	9.94	10.45	8.83	0.79	-0.34	3.81E-06	5.22E-03	-2.28	down	no	
ENSMUSG000000030123	Plexnd1	plexin D1 [Sou	5.94	4.89	5.98	4.73	8.10	8.12	6.89	8.01	0.69	-0.53	3.88E-06	5.22E-03	-2.28	down	no	
ENSMUSG000000035429	Ptptrh	protein tyrosi	0.24	0.30	0.27	0.38	0	0.06	0.07	0.04	6.80	2.76	4.09E-06	5.30E-03	-2.28	up	yes	
ENSMUSG000000081406	Rps6-ps4	ribosomal prot	35.19	37.65	34.82	37.59	25.14	28.87	26.80	29.73	1.31	0.39	5.29E-06	6.60E-03	-2.18	up	no	
ENSMUSG000000046056	Sbsn	suprabasin [So	1.21	0.72	0.90	1.13	1.40	2.83	2.03	1.70	0.50	-1.01	7.18E-06	8.63E-03	-2.06	down	yes	
ENSMUSG000000069049	Eif2a3y	eukaryotic tra	8.41	0.04	0.01	8.60	0.01	0	0.01	0	774.18	9.60	8.28E-06	9.62E-03	-2.02	up	yes	
ENSMUSG000000022565	Plec	plectin [Sourc	4.36	3.56	3.72	3.65	5.10	4.88	4.92	4.99	0.77	-0.38	9.55E-06	1.04E-02	-1.98	down	no	
ENSMUSG000000043773	1700048020Rik	RIKEN cDNA 170	1.91	3.09	2.73	2.63	4.74	3.67	4.78	4.98	0.58	-0.80	9.57E-06	1.04E-02	-1.98	down	no	
ENSMUSG000000072676	Tmem254a	transmembrane	1.84	1.64	2.92	2.59	4.05	4.85	3.59	3.71	0.56	-0.85	1.24E-05	1.31E-02	-1.88	down	no	
ENSMUSG000000108282	Gm44317	predicted gene	0	0	0	0	0.02	0.06	0.08	0.04	0.00	-8.92	1.36E-05	1.39E-02	-1.86	down	yes	
ENSMUSG000000057021	Vmn2r-ps159	vomeronasal 2,	0	0.15	0.09	0.16	0	0	0	0	990.18	9.95	1.40E-05	1.39E-02	-1.86	up	yes	
ENSMUSG000000072680	Tmem254c	transmembrane	5.17	3.91	4.91	6.88	9.39	7.45	7.86	10.51	0.59	-0.75	1.55E-05	1.49E-02	-1.83	down	no	
ENSMUSG000000053141	Ptptrh	protein tyrosi	7.42	6.45	6.65	7.08	8.62	8.56	9.48	7.93	0.80	-0.33	3.16E-05	1.51E-02	-1.82	down	no	
ENSMUSG000000032517	Mobp	myelin-associa	192.2	211.8	192.8	165.38	141.83	155.60	151.91	142.76	1.29	0.36	2.57E-05	2.34E-02	-1.63	up	no	
ENSMUSG000000020102	Slc16a2	solute carrier	0.39	0.41	0.39	0.41	2.41	2.30	0.46	1.59	0.24	-2.08	2.74E-05	2.43E-02	-1.61	down	yes	
ENSMUSG000000010690	Gm4327	predicted gene	2.77	1.88	0	0	2.84	0.09	0	0.11	0	37.35	5.22	3.07E-05	2.65E-02	-1.58	up	yes
ENSMUSG000000032128	Robo3	roundabout gui	0.51	0.38	0.67	0.53	0.98	0.93	1.10	0.73	0.56	-0.84	3.87E-05	3.26E-02	-1.49	down	no	
ENSMUSG000000052353	Cemip	cell migration	0.93	0.69	0.72	0.60	1.21	0.98	1.21	1.15	0.65	-0.63	4.02E-05	3.30E-02	-1.48	down	no	
ENSMUSG000000067916	Zfp991	zinc finger pr	1.44	0.83	0.82	0.96	1.45	1.92	2.14	1.89	0.55	-0.87	4.52E-05	3.63E-02	-1.44	down	no	
ENSMUSG000000019577	Pdk4	pyruvate dehyd	5.03	5.00	6.17	5.73	3.50	3.01	4.66	3.78	1.47	0.55	4.68E-05	3.66E-02	-1.44	up	no	
ENSMUSG000000044783	Hjxrp	Holliday junct	5.01	4.11	4.29	5.45	7.09	8.72	5.31	6.71	0.68	-0.56	5.55E-05	4.25E-02	-1.37	down	no	
ENSMUSG000000026463	Atp2b4	ATPase, Ca++ t	11.44	10.29	9.71	10.08	14.60	12.82	13.39	12.35	0.78	-0.36	6.01E-05	4.50E-02	-1.35	down	no	
ENSMUSG0000000087263	Gm15726	predicted gene	0.04	0.03	0.05	0	0.76	0.52	0.42	0.55	0.05	-4.24	6.78E-05	4.97E-02	-1.30	down	yes	
ENSMUSG000000105096	Gbp10	guanylate-bind	0.37	0.26	0.30	0.18	0.04	0.05	0.07	0.14	3.67	1.88	7.25E-05	5.20E-02	-1.28	up	no	
ENSMUSG000000029695	Aass	aminoadipate-s	1.96	1.78	2.21	1.83	1.22	1.37	1.43	1.37	1.44	0.53	7.76E-05	5.42E-02	-1.27	up	no	
ENSMUSG000000056673	Kdm5d	lysine (K)-spe	1.42	0.00	0	1.44	0.00	0.00	0	0.00	407.50	8.67	7.88E-05	5.42E-02	-1.27	up	no	
ENSMUSG000000107478	Gm45234	predicted gene	0	0	0	0	0.02	0.10	0.01	0.05	0.00	-8.78	8.61E-05	5.78E-02	-1.24	down	no	
ENSMUSG000000085813	Gm15870	predicted gene	0	0	0	0	0.34	0.19	0.41	0.09	0.00	-11.31	8.75E-05	5.78E-02	-1.24	down	no	
ENSMUSG000000045482	Ttrap	transformation	3.07	2.54	2.90	2.55	3.36	3.53	3.75	3.39	0.79	-0.34	9.15E-05	5.92E-02	-1.23	down	no	
ENSMUSG000000102742	Pcdhgal	protocadherin	6.70	7.53	8.16	6.57	9.82	9.76	9.02	10.21	0.75	-0.42	9.76E-05	6.20E-02	-1.21	down	no	
ENSMUSG000000084350	Znf41-ps	ZNF41, pseudog	1.12	0.80	0.46	0.89	1.44	1.38	2.35	1.59	0.48	-1.05	1.17E-04	7.30E-02	-1.14	down	no	
ENSMUSG000000090222	Ifi203-ps	interferon act	0	0	0	0	0.02	0.07	0.07	0.07	0.00	-9.23	1.28E-04	7.84E-02	-1.11	down	no	
ENSMUSG000000010631	Gm42047	predicted gene	0.23	0.23	0.20	0.71	0.65	1.56	2.17	1.25	0.24	-2.03	1.36E-04	8.13E-02	-1.09	down	no	
ENSMUSG000000068740	Celsr2	cadherin, EGF	9.10	7.11	7.99	7.32	10.68	10.97	9.49	9.84	0.77	-0.38	1.43E-04	8.32E-02	-1.08	down	no	
ENSMUSG000000073643	Wdlyf1	WD repeat and	2.53	4.70	5.28	2.45	7.18	8.85	9.54	8.30	0.44	-1.18	1.43E-04	8.32E-02	-1.08	down	no	
ENSMUSG000000018707	Dync1h1	dynein cytopla	24.41	17.68	19.75	18.42	25.65	26.83	26.14	25.21	0.77	-0.37	1.52E-04	8.66E-02	-1.06	down	no	
ENSMUSG000000010386	Gm42031	predicted gene	0.09	0.04	0.22	0.06	0.07	0.85	0.70	0.93	0.16	-2.64	1.58E-04	8.85E-02	-1.05	down	no	
ENSMUSG000000041936	Agrn	agrin [Source:	9.49	7.30	8.02	7.50	10.36	10.78	10.36	9.81	0.78	-0.35	1.64E-04	8.93E-02	-1.05	down	no	
ENSMUSG000000074065	Gm10617	predicted gene	0	0	0	0	0.15	0.11	0.09	0.13	0.00	-10.22	1.64E-04	8.93E-02	-1.05	down	no	
ENSMUSG000000066553	Gm6969	predicted pseu	56.61	63.96	1.74	1.55	1.37	1.87	1.39	1.70	19.57	4.29	1.72E-04	9.08E-02	-1.04	up	no	
ENSMUSG000000021223	Papln	papilin, prot	0.11	0.14	0.13	0.17	0.23	0.27	0.42	0.29	0.45	-1.14	1.73E-04	9.08E-02	-1.04	down	no	
ENSMUSG000000041453	Rpl21	ribosomal prot	12.84	14.47	15.09	11.16	8.44	7.69	11.39	10.24	1.42	0.50	1.75E-04	9.08E-02	-1.04	up	no	
ENSMUSG0000000103144	Pcdhgal	protocadherin	0.66	0.71	0.48	0.54	2.11	0.77	1.40	0.83	0.47	-1.09	1.89E-04	9.54E-02	-1.02	down	no	
ENSMUSG000000014496	Gm47601	predicted gene	0	0	0	0	0.07	0.04	0.16	0.02	0.00	-9.50	1.90E-04	9.54E-02	-1.02	down	no	
ENSMUSG0000000107927	Gm44090	predicted gene	0	0														

Table S2F: Selection of genes altered in P5/E4H vs P5/E2H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=4 mice/group. PE4H, PS19 mice homozygous for APOE4; PE2H, PS19 mice homozygous for APOE2.

gene_id	gene_name	Description	FPKM. PE4H_1	FPKM. PE4H_2	FPKM. PE4H_3	FPKM. PE4H_4	FPKM. PE2H_1	FPKM. PE2H_2	FPKM. PE2H_3	FPKM. PE2H_4	fc	log2 (fc)	pval	qval	log10 (qval)	regula tion	signif icant	
ENSMUSG00000095675	Ccl21b	chemokine (C-C	6.34	6.73	5.38	4.95	0.11	0.15	0.06	0.11	55.12	5.78	3.58E-57	1.19E-52	-51.92	up	yes	
ENSMUSG00000109209	Gm45104	predicted gene	2.00	1.30	1.76	1.89	0.14	0.04	0.08	0.09	19.49	4.28	2.44E-53	4.06E-49	-48.39	up	yes	
ENSMUSG00000073878	Gm13304	predicted gene	6.37	4.94	5.22	3.51	0.19	0.15	0.13	0.11	34.47	5.11	1.36E-44	1.51E-40	-39.82	up	yes	
ENSMUSG00000098975	Gm27177	predicted gene	0.81	0.85	1.74	2.06	0.05	0.07	0.08	0.05	21.81	4.45	3.64E-44	3.03E-40	-39.52	up	yes	
ENSMUSG00000096596	Gm10591	predicted gene	5.53	5.22	4.48	3.09	0.12	0.06	0.09	0.08	51.87	5.70	1.34E-42	8.94E-39	-38.05	up	yes	
ENSMUSG00000094065	Ccl21d	chemokine (C-C	4.97	3.95	4.25	3.12	0.10	0.13	0.11	0.06	40.57	5.34	2.05E-41	1.13E-37	-36.95	up	yes	
ENSMUSG00000110105	Gm45844	predicted gene	0.04	0.07	0.06	0.07	0.48	0.43	0.50	0.47	0.13	-2.96	1.28E-28	6.07E-25	-24.22	down	yes	
ENSMUSG00000097842	9330104G04Rik	RIKEN cDNA 9330	0.23	0.17	0.35	0.34	1.39	1.52	1.60	1.36	0.18	-2.44	7.80E-25	3.24E-21	-20.49	down	yes	
ENSMUSG00000035299	Mid1	midline 1 [Sour	0.35	0.27	0.26	0.31	1.39	0.78	1.14	1.53	0.25	-2.01	6.71E-20	2.48E-16	-15.61	down	yes	
ENSMUSG00000090338	Gm17081	predicted gene	1.42	0.77	1.13	0.48	0.06	0.09	0.09	0.06	13.18	3.72	9.10E-18	3.03E-14	-13.52	up	yes	
ENSMUSG00000053985	Zfp14	zinc finger pro	5.72	5.15	4.46	5.50	2.79	2.63	2.68	2.74	1.92	0.94	2.99E-16	9.03E-13	-12.04	up	no	
ENSMUSG00000118458	Gm10599	predicted pseud	1.79	0.83	1.07	0.52	0.09	0.12	0.11	0.09	9.94	3.31	3.25E-15	8.35E-12	-11.08	up	yes	
ENSMUSG00000093954	Gm16867	predicted gene	1.04	0.54	2.17	2.37	0.02	0.06	0.09	0.05	27.66	4.79	3.26E-15	8.35E-12	-11.08	up	yes	
ENSMUSG00000107705	Gm45062	predicted gene	0	0	6.24	0	0	0	0	0	15591.60	13.93	3.41E-13	8.09E-10	-9.09	up	yes	
ENSMUSG00000066107	Gm12666	predicted gene	1.44	1.10	0.70	0.92	0	0	0	0	10373.24	13.34	1.18E-12	2.61E-09	-8.58	up	yes	
ENSMUSG00000044783	Hjupr	Holliday juncti	5.01	4.11	4.29	5.45	7.75	6.77	8.43	7.53	0.62	-0.69	3.32E-12	6.90E-09	-8.16	down	no	
ENSMUSG00000073879	Gm5859	predicted pseud	1.12	0.70	0.82	0.41	0.09	0.12	0.13	0.08	7.41	2.89	3.53E-12	6.91E-09	-8.16	up	yes	
ENSMUSG00000091542	Gm17167	predicted gene	0.81	0.49	0.52	0.28	0.10	0.09	0.10	0.04	6.42	2.68	5.18E-12	9.57E-09	-8.02	up	yes	
ENSMUSG00000094006	Igkv4-59	immunoglobulin	2.87	17.19	0	0	0	0	0	0	50170.09	15.61	8.81E-12	1.54E-08	-7.81	up	yes	
ENSMUSG00000029994	Anxa4	annexin A4 [Sou	5.08	3.57	2.47	3.90	1.48	1.53	1.82	1.43	2.40	1.26	1.04E-11	1.73E-08	-7.76	up	yes	
ENSMUSG00000074358	Ccdc61	coiled-coil dom	0.93	0.95	0.79	1.05	2.29	1.89	2.01	1.99	0.45	-1.14	1.12E-11	1.77E-08	-7.75	down	yes	
ENSMUSG00000096862	Gm13301	predicted gene	0.66	0.45	0.53	0.24	0.05	0.04	0.05	0.03	11.10	3.47	5.07E-11	1.67E-08	-7.12	up	yes	
ENSMUSG00000030413	Pglyrpl	peptidoglycan r	1.16	0.74	0.91	0.55	2.49	2.78	2.34	5.70	0.25	-1.99	9.20E-11	1.33E-07	-6.88	down	yes	
ENSMUSG00000092232	Gm20521	predicted gene	0	2.22	0	0	0	0	0	0	5553.92	12.44	1.36E-10	1.88E-07	-6.73	up	yes	
ENSMUSG00000031562	Dctd1	dCMP deaminase	0.90	0.79	0.86	0.90	1.89	1.78	2.18	1.44	0.47	-1.08	2.12E-10	2.83E-07	-6.55	down	yes	
ENSMUSG00000096764	Gm12985	predicted gene	0	0	0	0	0	0	0	0.79	0	0.00	-10.95	2.22E-10	2.83E-07	-6.55	down	yes
ENSMUSG00000021342	Pr1	prolactin [Sour	0	1.59	0	0	0	0	0	0	3979.54	11.96	2.30E-10	2.83E-07	-6.55	up	yes	
ENSMUSG00000090996	Gm20458	predicted gene	0	0	0	0	0	0	0	0	0.70	0.00	-10.77	5.01E-10	5.95E-07	-6.23	down	yes
ENSMUSG00000095007	Igkv12-41	immunoglobulin	0	3.48	0	0	0	0	0	0	8709.14	13.09	1.20E-09	1.37E-06	-5.86	up	yes	
ENSMUSG00000001240	Ramp2	receptor (calci	2.84	3.46	3.49	4.36	6.12	6.69	5.98	9.50	0.50	-1.00	1.35E-09	1.49E-06	-5.83	down	yes	
ENSMUSG00000095351	Igkv3-2	immunoglobulin	3.02	0	0	0	0	0	0	0	7559.13	12.88	1.50E-09	1.58E-06	-5.80	up	yes	
ENSMUSG00000053964	Lgals4	lectin, galacto	0.22	0.32	0.21	0.13	0.78	0.83	0.85	1.24	0.24	-2.07	1.52E-09	1.58E-06	-5.80	down	yes	
ENSMUSG00000092511	Gm20547	predicted gene	0.85	0	0	0	0	0	0	0	2127.73	11.06	1.65E-09	1.67E-06	-5.78	up	yes	
ENSMUSG00000109176	Zfp264	zinc finger pro	0.27	0.42	0.65	0.22	0.05	0.02	0	0.02	17.38	4.12	1.72E-09	1.68E-06	-5.77	up	yes	
ENSMUSG00000087067	Gm11532	predicted gene	0	0	0.18	0	0	0	0	0	453.68	8.83	2.19E-09	2.08E-06	-5.68	up	yes	
ENSMUSG00000052861	Dnah6	dynein, axonema	0.44	0.36	0.45	0.44	0.16	0.09	0.23	0.15	2.70	1.43	1.51E-08	1.39E-05	-4.86	up	yes	
ENSMUSG00000066838	Zfp772	zinc finger pro	2.26	2.16	2.46	1.73	3.64	3.62	4.09	3.62	0.58	-0.80	4.84E-08	4.35E-05	-4.36	down	no	
ENSMUSG00000030123	Plxnd1	plexin D1 [Sour	5.94	4.89	5.98	4.73	8.43	8.33	8.40	7.22	0.67	-0.59	5.38E-08	4.71E-05	-4.33	down	no	
ENSMUSG00000046688	Tifa	TRAF-interactin	5.52	4.62	4.65	4.93	3.45	2.99	3.24	2.67	1.60	0.68	1.02E-07	8.69E-05	-4.06	up	no	
ENSMUSG00000038642	Ctss	cathepsin S [S	235.60	172.70	201.19	224.71	146.02	141.30	155.61	131.80	1.45	0.54	1.34E-07	1.11E-04	-3.95	up	no	
ENSMUSG00000107927	Gm44090	predicted gene	0	0.02	0.03	0	0.31	0.43	0.18	0.27	0.04	-4.63	2.00E-07	1.63E-04	-3.79	down	yes	
ENSMUSG00000095562	Erd1r1	erythroid diffe	1.09	1.14	0.13	1.70	10.90	7.65	7.90	11.85	0.11	-3.24	3.41E-07	2.70E-04	-3.57	down	yes	
ENSMUSG00000035722	Abca7	ATP-binding cas	1.78	1.72	1.75	1.59	2.82	2.47	2.31	2.53	0.67	-0.57	5.11E-07	3.95E-04	-3.40	down	no	
ENSMUSG00000030577	Cd22	CD22 antigen [S	2.45	1.22	1.30	1.25	0.77	0.39	0.75	0.56	2.53	1.34	5.24E-07	3.96E-04	-3.40	up	yes	
ENSMUSG00000098900	Gm18190	predicted gene	0	0	0	0	0.28	0.14	0.19	0.15	0.00	-10.88	5.61E-07	4.14E-04	-3.38	down	yes	
ENSMUSG00000074280	Gm166	predicted gene	1.28	29.43	22.90	28.61	0.90	1.80	1.11	0.79	17.85	4.16	7.00E-07	5.06E-04	-3.30	up	yes	
ENSMUSG00000095463	Entpd4	ectonucleoside	5.80	5.49	6.95	7.77	4.12	4.57	3.83	2.77	1.70	0.77	7.69E-07	5.44E-04	-3.26	up	no	
ENSMUSG000000021091	Serpina3n	serine (or cyst	248.90	182.80	185.58	121.22	51.49	45.44	85.65	81.03	2.80	1.49	8.07E-07	5.59E-04	-3.25	up	yes	
ENSMUSG000000007440	Pcdhall	protocadherin a	0.49	0.60	1.28	0.51	1.14	2.25	2.03	2.31	0.37	-1.42	1.12E-06	7.61E-04	-3.12	down	yes	
ENSMUSG000000023367	Tmem176a	transmembrane p	9.45	8.58	8.35	7.79	5.47	6.19	6.48	4.97	1.48	0.56	1.44E-06	9.56E-04	-3.02	up	no	
ENSMUSG00000001119	Col6a1	collagen, type	5.05	5.21	3.86	6.02	7.52	7.02	7.24	8.51	0.66	-0.59	1.60E-06	1.04E-03	-2.98	down	no	
ENSMUSG000000110631	Gm42047	predicted gene	0.23	0.23	0.20	0.71	1.12	0.94	1.14	0.81	0.34	-1.54	1.73E-06	1.11E-03	-2.96	down	yes	
ENSMUSG000000026204	Ptprn	protein tyrosin	75.15	68.54	76.33	71.17	92.71	101.30	87.75	108.89	0.75	-0.42	1.89E-06	1.18E-03	-2.93	down	no	
ENSMUSG000000062132	Arhgap33os	Rho GTPase acti	0.17	0.27	0.11	0.16	0	0.02	0	0.02	19.09	4.25	2.03E-06	1.24E-03	-2.91	up	yes	
ENSMUSG000000045948	Mrp31	mitochondrial r	13.20	11.90	13.45	14.63	21.25	24.31	17.12	18.51	0.65	-0.61	2.05E-06	1.24E-03	-2.91	down	no	
ENSMUSG000000084010	Gm13302	predicted gene	0.73	0.40	0.52	0.26	0.11	0.06	0.11	0.04	6.01	2.59	2.18E-06	1.27E-03	-2.89	up	yes	
ENSMUSG000000046056	Sbsn	suprabasin [Sou	1.21	0.72	0.90	1.13	1.92	2.54	1.64	1.62	0.51	-0.97	2.18E-06	1.27E-03	-2.89	down	no	
ENSMUSG000000040552	C3ar1	complement comp	3.72	2.51	2.76	3.14	1.93	1.61	2.14	1.50	1.69	0.76	3.03E-06	1.74E-03	-2.76	up	no	
ENSMUSG000000074361	C5ar2	complement comp	0.04	0.02	0.04	0	0.15	0.20	0.30	0.21	0.11	-3.13	4.18E-06	2.35E-03	-2.63	down	yes	
ENSMUSG000000031246	Sh3bgr1	SH3-binding dom	26.85	27.33	25.00	27.37	19.63	21.21	22.01	19.85	1.29	0.37	4.44E-06	2.46E-03	-2.61	up	no	
ENSMUSG000000027858	Tspan2	tetraspanin 2 [	39.10	31.50	27.03	34.19	22.41	21.15	26.38	18.30	1.49	0.58	4.66E-06	2.54E-03	-2.59	up	no	
ENSMUSG00000096768	Gm47283	predicted gene	0.66	0.46	0.05	0.85	5.23	4.64	3.21	5.14	0.11	-3.18	5.19E-06	2.78E-03	-2.56	down	yes	
ENSMUSG00000031503	Col4a2	collagen, type	2.72	2.74	3.47	2.57	4.23	3.65	4.75	6.16	0.61	-0.71	5.73E-06	3.03E-03	-2.52	down	no	
ENSMUSG00000069184	Zfp72	zinc finger pro	1.99	1.89	1.56	1.86	1.18	1.14	1.13	1.16	1.58	0.66	6.20E-06	3.22E-03	-2.49	up	no	
ENSMUSG00000092375	A730060N03Rik	RIKEN cDNA A730	0.38	0.15	0.40	0.16	0.70	0.80	1.19	0.90	0.30	-1.74	6.30E-06	3.22E-03	-2.49	down	yes	
ENSMUSG00000118425	Gm50470	predicted gene	0.83	0.49	0.57	0.34	0.16	0.11	0.15	0.14	4.11	2.04	6.53E-06	3.29E-03	-2.48	up	yes	
ENSMUSG000000022899	Sic15a2	solute carrier	5.59	4.07	5.33	4.93	3.57	3.18	3.56	3.49	1.44	0.53	6.78E-06	3.36E-03	-2.47	up	no	

Table S2G: Selection of genes altered in P5/E4H vs E4H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=3-4 mice/group. PE4H, PS19 mice homozygous for APOE4.

gene_id	gene_name	Description	FPKM. PE4H_1	FPKM. PE4H_2	FPKM. PE4H_3	FPKM. PE4H_4	FPKM. E4H_1	FPKM. E4H_2	FPKM. E4H_3	fc	log2 (fc)	pval	qval	log10 (qval)	regulat ion	signifi cant
ENSMUSG00000020932	Gfap	glial fibrillary	545.98	404.34	385.09	394.91	51.50	51.45	51.25	8.42	3.07	1.66E-182	5.56E-178	-177.25	up	yes
ENSMUSG00000036887	Clqa	complement compon	203.76	159.52	159.22	166.67	32.88	35.00	33.12	5.12	2.36	4.92E-142	8.24E-138	-137.08	up	yes
ENSMUSG00000038642	Ctss	cathepsin S [Sourc	235.60	172.70	201.19	224.71	51.04	49.94	56.47	3.97	1.99	1.57E-95	1.57E-91	-90.76	up	yes
ENSMUSG00000068129	Cst7	cystatin F (leuko	22.41	10.73	9.29	11.62	0.16	0.27	0.18	66.74	6.06	3.57E-72	2.99E-68	-67.52	up	yes
ENSMUSG00000036905	Clqb	complement compon	180.35	119.35	128.74	156.31	37.34	38.76	36.27	3.90	1.96	1.61E-64	1.08E-60	-59.97	up	yes
ENSMUSG00000046805	Mpeg1	macrophage expres	46.93	31.96	31.03	31.02	7.25	7.43	8.29	4.60	2.20	2.72E-62	1.52E-58	-57.82	up	yes
ENSMUSG00000022037	Clu	clusterin [Source	440.33	444.20	452.07	458.09	235.74	213.62	235.05	1.97	0.98	2.71E-59	1.30E-55	-54.89	up	no
ENSMUSG00000024610	Cd74	CD74 antigen (inv	28.89	28.58	38.64	18.90	3.83	3.65	3.12	8.14	3.02	1.79E-57	7.47E-54	-53.13	up	yes
ENSMUSG00000023992	Trem2	triggering recept	10.36	8.14	7.17	9.57	2.47	2.26	2.11	3.87	1.95	3.64E-57	1.35E-53	-52.87	up	yes
ENSMUSG00000036896	Clqc	complement compon	88.76	56.92	56.96	69.56	16.98	17.11	17.39	3.97	1.99	1.53E-54	5.14E-51	-50.29	up	yes
ENSMUSG00000030579	Tyrobp	TYRO protein tyro	72.12	63.93	51.96	54.02	16.67	14.82	16.32	3.80	1.92	5.98E-53	1.82E-49	-48.74	up	yes
ENSMUSG000000018927	Ccl6	chemokine (C-C mo	6.57	6.23	5.61	5.55	0.91	0.65	1.05	6.90	2.79	2.02E-52	5.63E-49	-48.25	up	yes
ENSMUSG00000073411	H2-D1	histocompatibility	60.40	42.41	47.19	58.58	17.17	16.97	17.06	3.06	1.61	1.04E-51	2.68E-48	-47.57	up	yes
ENSMUSG00000040552	C3arl	complement compon	3.72	2.51	2.76	3.14	0.56	0.54	0.58	5.41	2.43	6.41E-51	1.53E-47	-46.81	up	yes
ENSMUSG00000038147	Cd84	CD84 antigen [Sou	3.38	2.29	2.29	2.49	0.37	0.48	0.47	5.91	2.56	6.38E-50	1.42E-46	-45.85	up	yes
ENSMUSG00000021665	Hexb	hexosaminidase B	170.48	134.18	128.19	173.64	55.15	57.06	57.78	2.68	1.42	3.73E-48	7.79E-45	-44.11	up	yes
ENSMUSG00000033685	Ucp2	uncoupling protei	8.29	7.84	7.37	7.77	3.37	2.87	2.65	2.64	1.40	5.12E-47	1.01E-43	-43.00	up	yes
ENSMUSG00000059498	Fcgr3	Fc receptor, IgG,	24.18	19.72	29.30	23.99	6.86	7.33	6.74	3.48	1.80	2.47E-44	4.59E-41	-40.34	up	yes
ENSMUSG00000073421	H2-Ab1	histocompatibility	3.93	4.05	4.37	2.91	0.58	0.59	0.57	6.56	2.71	3.55E-44	6.25E-41	-40.20	up	yes
ENSMUSG00000026556	Fcgr2b	Fc receptor, IgG,	4.24	2.93	3.40	3.27	0.73	0.90	0.66	4.53	2.18	7.10E-44	1.19E-40	-39.93	up	yes
ENSMUSG00000079293	Clec7a	C-type lectin dom	12.01	8.65	7.53	7.31	0.35	0.26	0.12	36.11	5.17	1.05E-43	1.67E-40	-39.78	up	yes
ENSMUSG00000006519	Cyba	cytochrome b-245,	15.72	14.34	14.44	14.17	3.43	3.46	4.58	3.84	1.94	2.59E-43	3.93E-40	-39.41	up	yes
ENSMUSG00000026701	Prdx6	peroxiredoxin 6 [	90.40	77.74	70.80	83.53	39.50	37.62	38.21	2.10	1.07	4.48E-43	6.52E-40	-39.19	up	yes
ENSMUSG000000007891	Ctad	cathepsin D [Sour	713.67	477.17	441.43	534.96	171.20	160.32	172.41	3.23	1.69	6.78E-43	9.46E-40	-39.02	up	yes
ENSMUSG000000006682	Cd52	CD52 antigen [Sou	8.64	6.77	5.62	6.31	1.12	0.86	0.84	7.28	2.86	9.97E-43	1.33E-39	-38.87	up	yes
ENSMUSG00000016256	Ctaz	cathepsin Z [Sour	102.32	74.47	66.52	80.50	27.33	27.14	26.67	2.99	1.58	1.38E-41	1.77E-38	-37.75	up	yes
ENSMUSG00000028581	Lapmt5	lysosomal-associa	23.18	19.26	18.46	20.35	7.92	8.41	9.17	2.39	1.26	1.46E-41	1.81E-38	-37.74	up	yes
ENSMUSG00000017009	Sdc4	syndecan 4 [Sour	46.29	39.26	44.21	42.60	20.11	15.94	18.24	2.38	1.25	2.26E-41	2.71E-38	-37.57	up	yes
ENSMUSG00000018774	Cd68	CD68 antigen [Sou	44.87	34.69	23.91	33.08	7.96	7.10	7.97	4.45	2.15	6.21E-41	7.17E-38	-37.14	up	yes
ENSMUSG00000058715	Fcer1g	Fc receptor, IgE,	28.08	21.74	20.26	21.66	6.84	5.35	5.48	3.89	1.96	9.45E-41	1.05E-37	-36.98	up	yes
ENSMUSG00000027995	Tlr2	toll-like recepto	4.44	2.76	2.74	3.85	0.47	0.54	0.59	6.43	2.69	1.68E-39	1.81E-36	-35.74	up	yes
ENSMUSG00000030560	Ctsc	cathepsin C [Sour	4.68	4.15	3.79	3.71	1.47	1.29	1.43	2.92	1.55	2.59E-38	2.71E-35	-34.57	up	yes
ENSMUSG00000015852	Fcrls	Fc receptor-like	27.13	18.71	21.48	27.54	8.19	8.25	7.78	2.94	1.55	2.14E-37	2.17E-34	-33.66	up	yes
ENSMUSG00000030789	Itgax	integrin alpha X	7.53	3.67	3.96	4.09	0.21	0.11	0.10	34.11	5.09	2.89E-37	2.84E-34	-33.55	up	yes
ENSMUSG00000021423	Ly86	lymphocyte antigen	9.29	6.73	5.72	8.34	1.44	1.81	2.09	4.22	2.08	1.10E-35	1.05E-32	-31.98	up	yes
ENSMUSG00000021242	Npc2	NPC intracellular	23.75	21.12	19.56	22.52	11.64	10.30	11.15	1.97	0.98	3.19E-35	2.97E-32	-31.53	up	no
ENSMUSG00000022548	Apod	apolipoprotein D	249.64	248.73	215.72	189.21	87.89	65.15	87.15	2.82	1.50	4.69E-35	4.25E-32	-31.37	up	yes
ENSMUSG00000015950	Ncf1	neutrophil cytosol	5.47	4.66	4.45	5.18	1.77	1.80	1.44	2.95	1.56	7.33E-35	6.46E-32	-31.19	up	yes
ENSMUSG00000019970	Sgk1	serum/glucocortic	45.63	36.66	32.55	42.40	16.55	12.88	11.51	2.88	1.53	1.67E-34	1.43E-31	-30.84	up	yes
ENSMUSG000000097415	AU020206	expressed sequenc	5.33	4.60	4.35	5.48	1.01	1.52	1.44	3.73	1.90	1.16E-33	9.73E-31	-30.01	up	yes
ENSMUSG00000004707	Ly9	lymphocyte antigen	3.38	2.10	2.45	1.83	0.36	0.23	0.31	8.07	3.01	1.44E-33	1.18E-30	-29.93	up	yes
ENSMUSG000000059336	Slc14a1	solute carrier fa	9.30	7.95	6.28	9.08	2.60	2.19	2.87	3.20	1.68	1.56E-33	1.24E-30	-29.91	up	yes
ENSMUSG00000021998	Lcp1	lymphocyte cytosol	3.09	2.50	2.50	2.96	1.12	1.12	1.19	2.42	1.27	3.47E-33	2.70E-30	-29.57	up	yes
ENSMUSG00000004730	Adgre1	adhesion G protei	8.89	5.50	6.64	7.27	1.94	2.06	2.18	3.43	1.78	9.82E-33	7.47E-30	-29.13	up	yes
ENSMUSG00000004266	Ptpn6	protein tyrosine p	5.47	4.23	4.03	4.51	1.40	1.39	1.45	3.23	1.69	5.27E-32	3.92E-29	-28.41	up	yes
ENSMUSG00000020120	Plek	pleckstrin [Sour	13.70	9.43	10.24	12.12	3.67	3.92	4.58	2.80	1.49	5.49E-32	3.99E-29	-28.40	up	yes
ENSMUSG00000036594	H2-Aa	histocompatibility	4.17	3.89	5.22	2.98	0.44	0.47	0.85	6.90	2.79	5.61E-32	4.00E-29	-28.40	up	yes
ENSMUSG00000015355	Cd48	CD48 antigen [Sou	3.91	4.79	3.61	3.80	0.60	0.52	0.70	6.62	2.73	6.87E-32	4.79E-29	-28.32	up	yes
ENSMUSG00000060802	B2m	beta-2 microglobu	244.98	202.27	215.59	297.08	107.23	102.84	94.64	2.36	1.24	1.70E-31	1.16E-28	-27.94	up	yes
ENSMUSG00000000290	Itgb2	integrin beta 2 [	10.69	6.87	6.30	6.80	1.95	2.02	1.85	3.95	1.98	3.67E-31	2.46E-28	-27.61	up	yes
ENSMUSG00000079037	Prnp	prion protein [So	654.04	578.21	706.09	780.93	324.89	326.99	353.81	2.03	1.02	4.25E-31	2.79E-28	-27.55	up	yes
ENSMUSG00000026480	Ncf2	neutrophil cytosol	1.42	1.33	1.47	1.21	0.43	0.42	0.46	3.12	1.64	7.13E-31	4.59E-28	-27.34	up	yes
ENSMUSG00000029810	Tmem176b	transmembrane pro	25.67	26.01	23.53	22.11	12.20	11.18	10.86	2.13	1.09	8.91E-31	5.63E-28	-27.25	up	yes
ENSMUSG00000025351	Cd63	CD63 antigen [Sou	42.15	37.11	27.57	36.63	13.46	12.77	15.35	2.59	1.37	9.49E-31	5.88E-28	-27.23	up	yes
ENSMUSG00000032359	Ctsh	cathepsin H [Sour	8.28	6.51	4.88	6.81	1.92	1.81	2.19	3.36	1.75	1.41E-30	8.58E-28	-27.07	up	yes
ENSMUSG00000030342	Cd9	CD9 antigen [Sour	60.52	47.49	36.34	57.11	17.99	15.80	18.48	2.89	1.53	5.42E-30	3.24E-27	-26.49	up	yes
ENSMUSG00000015340	Cybb	cytochrome b-245,	1.39	1.05	1.06	0.55	0.08	0.10	0.07	12.41	3.63	5.54E-30	3.25E-27	-26.49	up	yes
ENSMUSG00000023367	Tmem176a	transmembrane pro	9.45	8.58	8.35	7.79	3.64	2.96	3.80	2.47	1.30	5.50E-29	3.17E-26	-25.50	up	yes
ENSMUSG00000024300	Myof1	myosin IF [Source	2.66	1.96	1.68	1.98	0.41	0.40	0.56	4.57	2.19	6.95E-29	3.94E-26	-25.40	up	yes
ENSMUSG00000015947	Fcgr1	Fc receptor, IgG,	4.46	3.40	4.00	3.81	1.19	1.06	1.29	3.31	1.73	7.73E-29	4.31E-26	-25.37	up	yes
ENSMUSG00000041559	Pmod	fibromodulin [Sou	12.33	11.16	10.37	12.54	5.96	5.11	4.83	2.19	1.13	9.95E-29	5.46E-26	-25.26	up	yes
ENSMUSG00000029622	Arpc1b	actin related pro	6.73	5.64	4.80	5.66	2.25	2.31	2.40	2.46	1.30	1.71E-28	9.21E-26	-25.04	up	yes
ENSMUSG00000034957	Cebpa	CCAAT/enhancer b	7.73	6.49	6.76	8.01	3.24	2.71	3.02	2.42	1.28	7.01E-28	3.72E-25	-24.43	up	yes
ENSMUSG00000028859	Csf3r	colony stimulatin	4.85	3.41	4.28	4.27	1.31	1.54	1.27	3.07	1.62	1.01E-27	5.30E-25	-24.28	up	yes
ENSMUSG00000040747	Cd53	CD53 antigen [Sou	10.02	8.35	8.19	9.49	3.56	2.85	3.64	2.69	1.43	3.36E-27	1.73E-24	-23.76	up	yes
ENSMUSG00000024621	Csf1r	colony stimulatin	34.41	28.88	31.19	29.80	17.48	15.62	17.58	1.84	0.88	6.51E-27	3.30E-24	-23.48	up	no
ENSMUSG00000027848	Olfrml3	olfactomedin-like	8.01	6.27	6.26	7.80	3.33	3.39	3.28	2.13	1.09	1.94E-26	9.68E-24	-23.01	up	yes
ENSMUSG00000022817	Itgb5	integrin beta 5 [	30.13	24.87	27.07	24.62	13.45	11.36	13.69	2.08	1.06	2.81E-26	1.39E-23	-22.86	up	yes
ENSMUSG00000015090	Ptgsd	prostaglandin D2	605.29	704.97	647.09											

Table S2H: Selection of genes altered in PS/E3H vs E3H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=3-4 mice/group. PE3H, PS19 mice homozygous for APOE3.

gene_id	gene_name	Description	FPKM. PE3H_1	FPKM. PE3H_2	FPKM. PE3H_3	FPKM. PE3H_4	FPKM. E3H_1	FPKM. E3H_2	FPKM. E3H_3	fc	log2 (fc)	pval	qval	log10 (qval)	regulat ion	signifi cant
ENSMUSG00000030789	Itgax	integrin alpha	2.88	4.65	4.35	3.28	0.22	0.25	0.15	18.05	4.17	5.41E-98	1.82E-93	-92.74	up	yes
ENSMUSG00000068129	Cst7	cystatin F (leu	7.60	11.75	15.76	12.52	0.42	0.27	0.50	30.28	4.92	5.65E-76	9.53E-72	-71.02	up	yes
ENSMUSG00000079293	Clec7a	C-type lectin d	3.81	8.09	7.15	8.06	0.36	0.40	0.29	19.31	4.27	2.16E-75	2.43E-71	-70.61	up	yes
ENSMUSG00000015852	Fcrls	Fc receptor-lik	20.55	25.53	28.35	25.25	8.37	9.58	9.79	2.69	1.43	1.29E-46	1.08E-42	-41.96	up	yes
ENSMUSG00000030124	Lag3	lymphocyte-acti	12.46	13.50	11.75	11.63	4.32	3.50	3.28	3.33	1.74	1.64E-41	1.11E-37	-36.96	up	yes
ENSMUSG00000036887	Clqa	complement comp	86.57	148.90	140.49	155.87	41.90	39.09	39.93	3.30	1.72	4.56E-34	2.57E-30	-29.59	up	yes
ENSMUSG000000024610	Cd74	CD74 antigen (i	12.01	17.51	18.23	22.87	4.05	4.28	4.87	4.01	2.00	3.18E-33	1.53E-29	-28.82	up	yes
ENSMUSG00000036905	Clqb	complement comp	87.01	105.74	130.46	142.18	42.00	40.18	36.48	2.94	1.56	5.81E-33	2.45E-29	-28.61	up	yes
ENSMUSG00000020932	Gfap	glial fibrillar	206.22	390.94	365.89	418.36	54.27	57.79	53.91	6.24	2.64	1.48E-32	5.53E-29	-28.26	up	yes
ENSMUSG00000036896	Clqc	complement comp	39.79	50.22	57.24	70.04	20.29	17.59	18.23	2.90	1.54	8.83E-28	2.98E-24	-23.53	up	yes
ENSMUSG00000007891	Ctsd	cathepsin D [So	317.84	509.94	501.51	556.62	175.08	188.03	180.72	2.60	1.38	1.99E-27	6.10E-24	-23.21	up	yes
ENSMUSG00000031762	Mt2	metallothionein	165.58	160.63	210.82	271.67	72.18	66.13	65.60	2.97	1.57	3.55E-27	9.99E-24	-23.00	up	yes
ENSMUSG00000023992	Trem2	triggering rece	5.69	8.09	7.72	8.45	3.03	2.25	2.79	2.78	1.48	1.23E-25	3.19E-22	-21.50	up	yes
ENSMUSG00000030579	Tyrobp	TYRO protein ty	35.11	66.70	57.32	67.84	16.35	17.19	17.92	3.31	1.73	5.54E-25	1.33E-21	-20.87	up	yes
ENSMUSG00000038642	Ctsa	cathepsin S [So	101.97	167.65	171.67	193.91	54.75	57.72	60.68	2.75	1.46	1.15E-24	2.58E-21	-20.59	up	yes
ENSMUSG00000030342	Cd9	CD9 antigen [So	29.92	44.04	43.93	49.48	16.73	18.14	16.89	2.43	1.28	1.50E-24	3.17E-21	-20.50	up	yes
ENSMUSG00000018774	Cd68	CD68 antigen [S	16.48	31.90	31.25	36.60	8.02	8.58	7.71	3.59	1.84	1.37E-23	2.72E-20	-19.56	up	yes
ENSMUSG00000005142	Man2b1	mannosidase 2, .	9.78	10.28	11.46	10.78	6.40	6.75	6.18	1.64	0.71	3.49E-23	6.54E-20	-19.19	up	no
ENSMUSG00000018927	Ccl6	chemokine (C-C	4.54	6.73	6.67	9.58	1.54	0.77	1.38	5.60	2.49	5.70E-23	1.01E-19	-18.99	up	yes
ENSMUSG00000031765	Mt1	metallothionein	122.83	132.11	160.34	182.96	72.25	64.05	62.35	2.26	1.18	7.25E-23	1.22E-19	-18.91	up	yes
ENSMUSG000000020674	Pxdn	peroxidase [So	2.84	3.61	3.54	2.91	6.38	6.34	5.91	0.52	-0.95	1.24E-21	2.00E-18	-17.70	down	no
ENSMUSG00000016256	Ctsz	cathepsin Z [So	46.62	77.14	67.34	81.13	27.08	29.51	27.87	2.42	1.27	4.71E-21	7.23E-18	-17.14	up	yes
ENSMUSG000000021423	Ly86	lymphocyte anti	3.87	5.32	6.20	6.91	1.92	1.71	2.02	2.96	1.56	9.57E-21	1.40E-17	-16.85	up	yes
ENSMUSG000000021342	Pr1	prolactin [Sour	0	0	0	0	2.98	2.03	1.34	0.00	-14.37	1.37E-20	1.93E-17	-16.71	down	yes
ENSMUSG00000030577	Cd22	CD22 antigen [S	0.44	1.21	1.03	0.94	0.05	0.13	0.10	9.48	3.24	1.55E-20	2.09E-17	-16.68	up	yes
ENSMUSG00000017009	Sdc4	syndecan 4 [Sou	30.90	33.54	42.36	41.70	16.99	20.75	18.50	1.98	0.99	3.12E-20	4.04E-17	-16.39	up	no
ENSMUSG000000027848	Olfrml3	olfactomedin-li	5.78	6.79	6.27	6.87	3.42	3.81	3.78	1.75	0.81	1.03E-19	1.29E-16	-15.89	up	yes
ENSMUSG000000112148	Lilrb4a	leukocyte immun	0.46	1.99	1.34	1.75	0.12	0.16	0.17	9.45	3.24	1.25E-19	1.50E-16	-15.82	up	yes
ENSMUSG00000033685	Ucp2	uncoupling prot	5.63	6.50	7.48	7.59	3.54	3.49	2.83	2.07	1.05	1.98E-19	2.30E-16	-15.64	up	yes
ENSMUSG000000021665	Hexb	hexosaminidase	91.63	127.50	138.90	139.87	61.66	61.52	64.66	1.99	0.99	2.95E-19	3.32E-16	-15.48	up	no
ENSMUSG00000026656	Fcgr2b	Fc receptor, Ig	1.58	3.41	3.24	4.12	0.78	0.81	0.71	4.02	2.01	4.37E-19	4.76E-16	-15.32	up	yes
ENSMUSG000000022817	Itgb5	integrin beta 5	19.50	27.26	25.13	25.21	13.62	14.12	12.88	1.79	0.84	2.63E-18	2.73E-15	-14.56	up	no
ENSMUSG00000015340	Cybb	cytochrome b-24	0.41	1.27	1.25	1.58	0.15	0.15	0.14	7.58	2.92	2.67E-18	2.73E-15	-14.56	up	yes
ENSMUSG00000030701	Plekhhb1	pleckstrin homo	126.98	147.90	145.66	149.97	89.59	102.75	91.91	1.51	0.59	8.34E-18	8.27E-15	-14.08	up	no
ENSMUSG000000079037	Prnp	prion protein [	662.54	561.58	570.67	608.60	351.93	358.11	381.50	1.65	0.72	2.31E-17	2.23E-14	-13.65	up	no
ENSMUSG00000059498	Fcgr3	Fc receptor, Ig	12.89	17.60	22.02	23.24	7.35	8.35	7.05	2.50	1.32	4.07E-17	3.81E-14	-13.42	up	yes
ENSMUSG00000036833	Pnp1a7	patatin-like ph	2.83	3.41	3.46	3.75	1.75	1.73	1.87	1.89	0.92	6.09E-17	5.55E-14	-13.26	up	no
ENSMUSG00000064267	Hvcln1	hydrogen voltag	1.41	2.27	2.57	3.21	0.59	0.39	0.64	4.39	2.13	7.15E-17	6.35E-14	-13.20	up	yes
ENSMUSG00000036594	H2-Aa	histocompatibil	1.47	3.01	2.82	3.64	0.76	0.62	0.67	4.02	2.01	8.51E-17	7.37E-14	-13.13	up	yes
ENSMUSG00000040055	Gjb6	gap junction pr	24.96	28.85	36.61	32.77	15.85	18.08	16.86	1.82	0.86	1.14E-16	9.65E-14	-13.02	up	no
ENSMUSG000000028874	Fgr	FGR proto-oncog	0.29	0.75	0.56	0.86	0.05	0.05	0.06	11.10	3.47	2.34E-16	1.92E-13	-12.72	up	yes
ENSMUSG000000020120	Plek	pleckstrin [Sou	6.75	9.66	10.26	12.01	4.42	4.00	4.37	2.27	1.18	3.95E-16	3.10E-13	-12.51	up	yes
ENSMUSG000000021702	Thbs4	thrombospondin	4.46	5.28	7.45	4.67	2.02	2.53	1.87	2.55	1.35	3.95E-16	3.10E-13	-12.51	up	yes
ENSMUSG000000044811	Cd300c2	CD300C molecule	4.61	8.32	9.36	8.50	2.19	2.13	2.65	3.32	1.73	5.47E-16	4.19E-13	-12.38	up	yes
ENSMUSG000000071637	Cebpd	CCAAT/enhancer	1.84	1.70	1.92	2.64	0.65	0.77	0.58	3.04	1.60	7.44E-16	5.58E-13	-12.25	up	yes
ENSMUSG000000059336	Slc14al	solute carrier	4.81	7.73	7.07	7.59	2.99	3.05	3.30	2.18	1.13	1.10E-15	8.09E-13	-12.09	up	yes
ENSMUSG00000058715	Fcgr1g	Fc receptor, Ig	12.01	21.73	17.36	21.05	6.89	6.97	6.67	2.63	1.40	1.27E-15	9.10E-13	-12.04	up	yes
ENSMUSG00000079419	Ms4a6c	membrane-spanni	0.76	1.10	2.11	2.24	0.15	0.14	0.23	9.07	3.18	2.07E-15	1.45E-12	-11.84	up	yes
ENSMUSG00000039013	Siglecf	sialic acid bin	0.72	1.20	0.83	0.76	0.13	0.14	0.18	5.90	2.56	2.80E-15	1.92E-12	-11.72	up	yes
ENSMUSG000000055541	Lair1	leukocyte-assoc	1.84	2.46	2.75	2.59	1.17	1.14	1.17	2.08	1.05	2.84E-15	1.92E-12	-11.72	up	yes
ENSMUSG000000041559	Fmod	fibromodulin [S	11.59	12.72	13.23	14.18	8.15	7.01	6.35	1.80	0.85	7.03E-15	4.60E-12	-11.34	up	no
ENSMUSG000000040552	C3ar1	complement comp	1.38	2.63	3.31	3.17	0.81	0.73	0.69	3.54	1.82	7.08E-15	4.60E-12	-11.34	up	yes
ENSMUSG000000040167	Mbp	myelin basic pr	338.77	386.47	380.50	365.42	250.74	288.66	256.33	1.39	0.47	9.33E-15	5.94E-12	-11.23	up	yes
ENSMUSG000000095562	Erdrl	erythroid diffe	4.23	3.34	3.00	3.84	14.44	10.26	8.01	0.33	-1.60	1.98E-14	1.23E-11	-10.91	down	yes
ENSMUSG000000040709	Ly9	lymphocyte anti	0.82	1.99	1.90	2.59	0.39	0.35	0.35	5.01	2.33	2.27E-14	1.39E-11	-10.86	up	yes
ENSMUSG00000072893	4933439C1010R	RIKEN cDNA 4933	1.25	1.40	1.24	1.25	2.71	2.79	2.30	0.49	-1.02	2.50E-14	1.51E-11	-10.82	down	yes
ENSMUSG000000024621	Csflr	colony stimulat	23.31	29.46	30.45	33.43	17.25	17.46	17.83	1.67	0.74	2.70E-14	1.60E-11	-10.80	up	no
ENSMUSG000000022037	Clu	clusterin [Sour	299.98	396.41	381.66	409.46	226.04	247.57	232.85	1.58	0.66	3.01E-14	1.75E-11	-10.76	up	yes
ENSMUSG000000002090	Itgb2	integrin beta 2	3.88	7.93	7.77	9.15	2.58	2.63	2.12	2.94	1.56	4.10E-14	2.35E-11	-10.63	up	yes
ENSMUSG000000104415	Gm37069	predicted gene,	1.33	1.34	1.53	1.22	0.51	0.35	0.53	2.93	1.55	5.44E-14	3.02E-11	-10.52	up	yes
ENSMUSG000000044668	Tent5c	terminal nucleo	1.19	1.80	1.92	2.29	0.57	0.78	0.53	2.89	1.53	5.46E-14	3.02E-11	-10.52	up	yes
ENSMUSG000000040426	Ptpn6	protein tyrosin	2.45	4.35	3.85	4.62	1.42	1.38	1.40	2.73	1.45	6.88E-14	3.74E-11	-10.43	up	yes
ENSMUSG000000029723	Tsc22d4	TSC22 domain fa	9.86	9.90	10.27	12.03	6.54	6.87	5.92	1.63	0.71	7.18E-14	3.85E-11	-10.42	up	yes
ENSMUSG000000044827	Tlr1	toll-like recep	0.54	1.04	0.77	0.79	0.14	0.13	0.19	5.21	2.38	1.15E-13	6.08E-11	-10.22	up	no
ENSMUSG000000027447	Cst3	cystatin C [Sou	707.51	738.18	701.10	897.14	488.31	481.70	445.47	1.61	0.69	1.50E-13	7.79E-11	-10.11	up	no
ENSMUSG000000023067	Cdkn1a	cyclin-dependen	5.34	10.08	11.06	10.08	3.66	3.71	3.94	2.42	1.28	1.76E-13	8.99E-11	-10.05	up	yes
ENSMUSG000000015947	Fcgr1r	Fc receptor, Ig	2.28	2.75	3.27	3.27	1.29	1.11	1.05	2.51	1.33	2.02E-13	1.02E-10	-9.99	up	yes
ENSMUSG000000047330	Adgrel	adhesion G prot	3.75	7.03	5.96	7.45	2.25	2.04	2.65	2.61	1.39	2.15E-13	1.07E-10	-9.97	up	yes
ENSMUSG000000031610	Scrg1	scrapie respons	22.87	24.01	24.02	25.25										

ENSMUSG000000026285	Pdcd1	programmed cell	0.57	0.85	0.88	0.69	0.14	0.06	0.10	7.56	2.92	1.17E-11	4.17E-09	-8.38 up	yes
ENSMUSG000000022488	Nckap1l	NCK associated ;	3.19	4.43	4.86	4.91	1.99	2.32	2.52	1.91	0.93	1.21E-11	4.24E-09	-8.37 up	no
ENSMUSG000000081229	Lamr1-ps1	laminin recepto	1.59	0.92	0.76	1.19	0	0	0	#####	13.44	1.29E-11	4.48E-09	-8.35 up	yes
ENSMUSG000000035805	Mlc1	megalencephalic	67.73	87.48	89.19	94.20	51.69	54.14	58.25	1.55	0.63	1.44E-11	4.97E-09	-8.30 up	no
ENSMUSG00000000982	Ccl3	chemokine (C-C ;	1.86	4.18	3.08	3.42	0.47	0.34	0.79	5.84	2.55	1.58E-11	5.40E-09	-8.27 up	yes

Table S2f: Selection of genes altered in P5/E2H vs E2H mice. FPKM values of genes in individual mice (indicated in underscored numeral), along with fold change (fc) value, p value adjusted for false discovery rate of 0.05 (q value, qval) are presented. N=3-4 mice/group. PE2H, P519 mice homozygous for APOE2.

gene_id	gene_name	Description	FPKM. PE2H_1	FPKM. PE2H_2	FPKM. PE2H_3	FPKM. PE2H_4	FPKM. E2H_1	FPKM. E2H_2	FPKM. E2H_3	fc	log2 (fc)	pval	qval	log10 (qval)	regulat ion	signifi cant
ENSMUSG000000033880	Lgals3bp	lectin, galactc	32.25	23.66	31.52	32.74	7.32	7.37	8.60	3.87	1.95	4.87E-45	1.61E-40	-39.79	up	yes
ENSMUSG000000020932	Gfap	glial fibrillar	252.75	261.69	365.94	273.41	42.93	67.11	61.24	5.05	2.34	1.10E-42	1.82E-38	-37.74	up	yes
ENSMUSG000000030789	Itgax	integrin alpha	1.96	3.15	4.25	1.76	0.15	0.23	0.20	14.30	3.84	6.24E-39	6.87E-35	-34.16	up	yes
ENSMUSG000000073418	C4b	complement comp	39.70	30.52	49.85	32.65	9.95	7.89	10.05	4.11	2.04	8.60E-39	7.10E-35	-34.15	up	yes
ENSMUSG000000021091	Serpina3n	serine (or cyst	51.49	45.44	85.65	81.03	14.64	13.27	12.50	4.89	2.29	3.22E-32	2.13E-28	-27.67	up	yes
ENSMUSG000000036887	C1qa	complement comp	125.64	136.57	133.80	123.41	45.62	53.76	41.80	2.76	1.46	4.39E-30	2.41E-26	-25.62	up	yes
ENSMUSG000000034708	Grn	granulin [Sourc	29.10	30.87	34.83	31.64	13.64	14.24	15.23	2.20	1.14	8.59E-27	4.05E-23	-22.39	up	yes
ENSMUSG000000029561	Oas12	2'-5' oligoaden	3.70	2.32	2.60	4.05	0.64	0.52	0.81	4.84	2.28	3.16E-25	1.30E-21	-20.88	up	yes
ENSMUSG000000035692	Isg15	ISG15 ubiquitin	10.13	10.17	7.63	8.89	2.20	2.11	1.95	4.41	2.14	1.42E-23	5.22E-20	-19.28	up	yes
ENSMUSG000000061232	H2-K1	histocompatibil	24.84	24.49	25.95	21.13	9.36	10.54	11.78	2.28	1.19	4.13E-21	1.36E-17	-16.87	up	yes
ENSMUSG000000073411	H2-D1	histocompatibil	50.16	50.31	53.53	50.11	16.75	23.67	21.27	2.48	1.31	5.43E-21	1.63E-17	-16.79	up	yes
ENSMUSG000000030124	Lag3	lymphocyte-acti	13.34	18.75	12.50	11.25	2.47	4.44	3.28	4.11	2.04	9.85E-20	2.71E-16	-15.57	up	yes
ENSMUSG000000036905	C1qb	complement comp	113.91	127.81	121.42	106.91	49.08	56.85	42.49	2.38	1.25	1.39E-19	3.54E-16	-15.45	up	yes
ENSMUSG000000079037	Prnp	prion protein [	690.35	734.63	669.32	707.99	345.76	385.49	364.74	1.92	0.94	6.87E-19	1.62E-15	-14.79	up	no
ENSMUSG000000058626	Capn11	calpain 11 [Sou	0.13	0.06	0.10	0.06	0.82	1.23	0.98	0.09	-3.53	7.90E-19	1.74E-15	-14.76	down	yes
ENSMUSG000000036896	C1qc	complement comp	52.66	52.71	59.19	44.44	19.99	25.24	20.46	2.39	1.25	1.49E-18	3.07E-15	-14.51	up	yes
ENSMUSG000000074896	Ifit3	interferon-indu	20.83	18.22	18.94	14.20	5.50	7.11	7.15	2.74	1.45	4.34E-18	8.42E-15	-14.07	up	yes
ENSMUSG000000040264	Gbp2b	guanylate bindi	1.04	1.21	2.01	0.66	0	0	12308.52	13.59	2.86E-17	5.25E-14	-13.28	up	yes	
ENSMUSG000000028037	Ifi44	interferon-indu	1.09	0.60	0.86	1.03	0.07	0.19	0.12	7.02	2.81	3.25E-17	5.65E-14	-13.25	up	yes
Gm28043		predicted gene,	5.40	4.54	4.33	4.03	1.88	1.13	1.88	2.80	1.49	3.57E-17	5.89E-14	-13.23	up	yes
ENSMUSG000000038642	Ctss	cathepsin S [Sc	146.02	141.30	155.61	131.80	63.36	77.99	59.36	2.15	1.10	3.37E-16	5.31E-13	-12.28	up	yes
ENSMUSG000000024610	CD74	CD74 antigen (i	9.73	16.74	15.61	11.12	2.27	4.46	3.41	3.93	1.98	5.41E-16	8.13E-13	-12.09	up	yes
ENSMUSG000000030107	Usp18	ubiquitin speci	2.52	1.58	2.33	1.77	0.43	0.58	0.49	4.10	2.04	8.84E-16	1.27E-12	-11.90	up	yes
ENSMUSG000000035929	H2-Q4	histocompatibil	3.68	3.70	4.25	3.55	0.94	1.43	1.41	3.01	1.59	1.13E-15	1.56E-12	-11.81	up	yes
ENSMUSG000000028341	Nr4a3	nuclear receptc	2.24	2.38	2.21	2.76	4.66	4.64	5.72	0.48	-1.06	5.62E-15	7.42E-12	-11.13	down	yes
ENSMUSG000000007891	Ctsd	cathepsin D [Sc	381.31	442.15	531.74	359.94	185.13	216.04	179.13	2.22	1.15	6.01E-15	7.64E-12	-11.12	up	yes
ENSMUSG000000015950	Ncf1	neutrophil cytc	4.12	4.27	4.48	3.62	1.95	1.93	1.86	2.16	1.11	8.19E-15	1.00E-11	-11.00	up	yes
ENSMUSG000000040552	C3ar1	complement comp	1.93	1.61	2.14	1.50	0.71	0.59	0.55	2.92	1.55	1.96E-14	2.31E-11	-10.64	up	yes
ENSMUSG000000046718	Bst2	bone marrow str	11.97	10.45	9.21	15.75	3.26	3.13	4.55	3.25	1.70	4.51E-14	5.13E-11	-10.29	up	yes
ENSMUSG000000073489	Ifi204	interferon acti	1.01	0.56	0.90	1.00	0.16	0.20	0.12	5.53	2.47	2.84E-13	3.12E-10	-9.51	up	yes
ENSMUSG000000079293	Clec7a	C-type lectin c	5.14	4.14	10.20	1.87	0.31	0.28	0.28	18.36	4.20	3.15E-13	3.36E-10	-9.47	up	yes
ENSMUSG000000039146	Ifi441	interferon-indu	0.85	1.04	1.12	0.79	0	0	0.07	42.18	5.40	3.45E-13	3.57E-10	-9.45	up	yes
ENSMUSG000000038147	CD84	CD84 antigen [S	1.69	1.23	2.20	1.34	0.57	0.54	0.54	2.95	1.56	4.70E-13	4.71E-10	-9.33	up	yes
ENSMUSG000000018927	Ccl6	chemokine (C-C	4.85	2.99	6.10	2.89	0.83	1.07	1.18	4.11	2.04	5.13E-13	4.98E-10	-9.30	up	yes
ENSMUSG0000000110631	Gm42047	predicted gene,	1.12	0.94	1.14	0.81	0.28	0.22	0.40	3.33	1.74	8.25E-13	7.79E-10	-9.11	up	yes
ENSMUSG000000081229	Lamr1-ps1	laminin receptc	1.20	1.30	1.11	1.41	0	0	0	12539.39	13.61	2.61E-12	2.39E-09	-8.62	up	yes
ENSMUSG000000042613	Pbxip1	pre B cell leuk	17.06	16.65	19.25	17.75	9.94	10.47	11.15	1.68	0.75	2.69E-12	2.40E-09	-8.62	up	no
ENSMUSG000000025492	Ifitm3	interferon indu	31.56	30.35	27.14	36.61	15.45	15.53	14.72	2.06	1.04	4.25E-12	3.69E-09	-8.43	up	yes
ENSMUSG000000068129	Cst7	cystatin F (leu	7.90	10.09	18.97	8.18	0.23	1.04	0.60	18.14	4.18	8.96E-12	7.59E-09	-8.12	up	yes
ENSMUSG000000028268	Gbp3	guanylate bindi	3.25	2.67	3.63	1.92	0.79	0.74	1.19	3.16	1.66	9.68E-12	8.00E-09	-8.10	up	yes
ENSMUSG000000024529	Lox	lysyl oxidase [	0.49	0.39	0.65	0.42	0.09	0.06	0.12	5.47	2.45	1.11E-11	8.97E-09	-8.05	up	yes
ENSMUSG000000051439	CD14	CD14 antigen [S	3.43	3.09	4.75	4.30	1.67	1.02	1.06	3.12	1.64	1.20E-11	9.44E-09	-8.02	up	yes
ENSMUSG000000004707	Ly9	lymphocyte anti	1.45	0.91	2.44	0.97	0.27	0.34	0.21	5.27	2.40	1.38E-11	1.06E-08	-7.97	up	yes
ENSMUSG000000056739	Capg	capping protein	2.87	2.74	3.51	2.53	1.18	1.26	1.19	2.41	1.27	1.51E-11	1.14E-08	-7.94	up	yes
ENSMUSG000000034459	Ifit1	interferon-indu	4.22	2.24	4.00	2.48	0.71	0.92	1.18	3.45	1.79	2.31E-11	1.68E-08	-7.77	up	yes
ENSMUSG0000000108815	Gm49388	predicted gene,	0	0	0	0	1.70	0	0	0.00	-12.47	2.38E-11	1.68E-08	-7.77	down	yes
ENSMUSG0000000029622	Arpc1b	actin related f	4.66	4.23	5.28	4.32	2.76	2.30	2.42	1.85	0.89	2.39E-11	1.68E-08	-7.77	up	no
ENSMUSG000000094685	Gm5900	predicted pseud	5.84	2.53	6.10	3.86	0.70	0.59	0.45	7.90	2.98	4.35E-11	2.99E-08	-7.52	up	yes
ENSMUSG0000000107705	Gm45062	predicted gene,	0	0	0	0	0	0.86	0	0.00	-11.49	5.82E-11	3.92E-08	-7.41	down	yes
ENSMUSG000000093938	Evi2b	ecotropic viral	1.15	0.58	0.11	0.61	0	0	0	6119.77	12.58	6.43E-11	4.24E-08	-7.37	up	yes
ENSMUSG000000030577	CD22	CD22 antigen [S	0.77	0.39	0.75	0.56	0.04	0.14	0.10	6.53	2.71	8.51E-11	5.51E-08	-7.26	up	yes
ENSMUSG000000032359	Ctsh	cathepsin H [Sc	5.32	5.48	5.84	4.36	2.56	2.94	2.57	1.95	0.96	1.21E-10	7.66E-08	-7.12	up	no
ENSMUSG000000033355	Rtp4	receptor transp	3.22	2.41	2.96	3.60	1.33	1.07	1.21	2.53	1.34	1.30E-10	8.11E-08	-7.09	up	yes
ENSMUSG000000033777	Tlr13	toll-like recep	1.09	1.22	1.35	1.58	0.52	0.51	0.38	2.79	1.48	1.41E-10	8.63E-08	-7.06	up	yes
ENSMUSG000000026728	Vim	vimentin [Sourc	15.63	15.90	32.01	18.54	7.85	8.19	8.67	2.49	1.32	1.63E-10	9.76E-08	-7.01	up	yes
ENSMUSG000000024737	Slc15a3	solute carrier	1.31	0.98	1.40	0.71	0.29	0.40	0.27	3.44	1.78	1.84E-10	1.09E-07	-6.96	up	yes
ENSMUSG000000036103	Colec12	collectin sub-f	1.95	2.01	2.15	2.40	0.81	0.95	1.24	2.13	1.09	2.92E-10	1.69E-07	-6.77	up	yes
ENSMUSG000000005142	Man2b1	mannosidase 2,	10.11	12.01	10.69	8.74	5.34	5.94	6.07	1.80	0.84	3.14E-10	1.79E-07	-6.75	up	no
ENSMUSG000000026104	Stat1	signal transduc	6.69	4.95	6.97	5.86	3.52	3.09	3.43	1.83	0.87	3.57E-10	2.00E-07	-6.70	up	yes
ENSMUSG000000068457	Uty	ubiquitously tr	0.01	0.88	0	0	0	0	0	2207.08	11.11	3.65E-10	2.01E-07	-6.70	up	yes
ENSMUSG000000027015	Cybrd1	cytochrome b re	0.85	0.73	1.06	1.00	0.34	0.33	0.36	2.64	1.40	3.92E-10	2.12E-07	-6.67	up	yes
ENSMUSG000000036594	H2-Aa	histocompatibil	1.37	2.37	3.04	1.57	0.54	0.70	0.67	3.28	1.71	4.40E-10	2.34E-07	-6.63	up	yes
ENSMUSG000000022218	Tgm1	transglutaminas	0.27	0.52	1.66	0.11	0.02	0.03	0.03	25.59	4.68	5.22E-10	2.73E-07	-6.56	up	yes
ENSMUSG000000097415	AU020206	expressed seque	3.82	3.23	4.07	2.50	1.36	1.30	1.68	2.35	1.23	5.77E-10	2.98E-07	-6.53	up	yes
ENSMUSG000000089865	Gm44503	predicted readt	0	0	0	0	0	0.44	0	0.00	-10.53	6.13E-10	3.11E-07	-6.51	down	yes
ENSMUSG000000033685	Ucp2	uncoupling prot	6.10	6.80	7.22	10.17	3.59	3.84	3.05	2.17	1.12	6.62E-10	3.31E-07	-6.48	up	yes
ENSMUSG000000020681	Ace	angiotensin I c	7.76	7.34	7.81	8.55	4.91	4.70	4.98	1.62	0.69	6.98E-10	3.44E-07	-6.46	up	no
ENSMUSG000000026556	Fcgr2b	Fc receptor, Ig	2.21	1.20	3.49	2.67	0.80	0.77	0.69	3.19	1.67	7.47E-10	3.63E-07	-6.44	up	yes
ENSMUSG000000037321	Tap1	transporter 1,	1.64	1.25	1.84	1.39	0.56	0.64	0.75	2.35	1.24	7.67E-10	3.67E-07	-6.44	up	yes
ENSMUSG000000022436	Sh3bp1	SH3-domain bind	3.69	3.48	2.96	5.42	1.59	1.45	1.61	2.						

ENSMUSG000000024079	Eif2ak2	eukaryotic tran	1.51	1.27	1.98	1.37	0.74	0.58	0.75	2.22	1.15	1.64E-08	5.63E-06	-5.25 up	yes
ENSMUSG000000052911	Lamb2	laminin, beta 2	5.67	5.78	6.55	4.44	2.97	3.15	3.35	1.78	0.83	1.81E-08	6.15E-06	-5.21 up	no
ENSMUSG000000046879	Irgm1	immunity-relate	3.18	2.47	3.29	2.95	1.25	1.53	1.79	1.95	0.96	2.02E-08	6.81E-06	-5.17 up	no
ENSMUSG000000000386	Mx1	MX dynamin-like	0.49	0.26	0.36	0.50	0.08	0.02	0.09	6.20	2.63	2.25E-08	7.50E-06	-5.13 up	yes