

Genes with the largest H3K4me3 differences between populations A and B

	score_AB	score_A'B'	exact_score_AB	exact_score_A'B'	TSS_info; CNVs	full_gene_name	function	functional_category	expression_level	CpG
Btbd9	21675	12636	23417	change retained in offspring by 60%	CNV	BTB (POZ) domain containing 9	protein-protein interaction	Cell adhesion	high	84
Slc11a2	8459	2077	10133	change lost	ENSMUST00000140535	solute carrier family 11 (proton-coupled ion transmembrane transporter dual specificity phosphatase 1	phosphatase activity	Cell cycle: apoptosis	medium	---
Dusp1	15561	-3781	18775	change lost		DNA-damage-inducible transcript 14-3-3 protein binding	phosphatase activity	Cell cycle: apoptosis, positive regulation	high	103
Ddit4	7949	-3061	11914	change lost		growth arrest and DNA-damage-inducible protein 3/p38/JNK pathway	protein binding	Cell cycle: apoptotic process; response to DNA damage	high	92
Gadd45g	9100	1381	14873	change lost		cyclin-dependent kinase inhibitor	Regulator cell cycle at G1	Cell cycle: apoptotic process; response to DNA damage	high	139
Cdkn1a	85496	3634	79188	change lost		RAD54 like 2 (S. cerevisiae)	transcription cofactor activity; helicase	Cell cycle: arrest	medium	157
Rad54l2	7260	3359	7267	change retained in offspring by 44%		microsomal glutathione S-transferase	reduction of lipid hydroperoxide	Cell cycle: proliferation; chromatin remodeling	medium	44
Mgst1	6869	329	7705	change lost		homocysteine-inducible, endoplasmic reticulum-dependent protein	cat: ER: response to unfolded protein	high	---	
Herpud1	7330	10340	21361	change retained in offspring by 52%	bidirectional promoter (Gm15890)	lipopolysaccharide binding protein	binds LPS and interacts with immune system	Immune: acute defense response	high	62
Lbp	7407	729	11007	change lost		ubiquitin-like modifier activating ubiquitination and proteasome degradation	CD97 antigen	Immune: antigen processing	high	45
Uba5	15663	3523	10588	change retained in offspring by 29%	TSS window overlapping with Acad11	serine (or cysteine) peptidase	int plasma protease inhibitor	Immune: cell adhesion; inflammatory response	high	33
Cd97	8213	-508	9516	change lost		serine (or cysteine) peptidase	int plasma protease inhibitor: Alpha	Immune: inflammation	high	---
Serpina3k	8343	-850	11470	change lost	overlaps with Serpina3m	serine (or cysteine) peptidase	int plasma protease inhibitor	Immune: inflammation	high	---
Serpina3m	8343	-850	12292	change lost	overlaps with Serpina3k	alanine-glyoxylate aminotransferase	glycine biosynthesis peroxisome	Metabolism: amino acid metabolism; ala; glycine	high	---
Agxt	9755	1822	13562	change lost		glycine N-methyltransferase	catalyzes the conversion of 5-adenosine	Metabolism: amino acid metabolism; gly; glycine	high	20
Gnmt	8855	-2316	18801	change lost		4-hydroxyphenylpyruvic acid dioxygenase	oxidoreductase activity	Metabolism: amino acid metabolism; tyro; h	high	---
Hpd	8427	2003	11709	change lost		cytochrome P450, family 4, subfamily arachidonic acid monooxygenase	Metabolism: arachidonic acid metabolism; cytochrome P450	high	---	
Cyp4a14	20790	631	40383	change lost		cytochrome P450, family 2, subfamily arachidonic acid monooxygenase	Metabolism: arachidonic acid metabolism; cytochrome P450	high	---	
Cyp2d22	8249	1238	35327	change lost		cytochrome P450, family 4, subfamily arachidonic acid monooxygenase	Metabolism: arachidonic acid metabolism; cytochrome P450	high	---	
Cyp4f14	7088	-2743	8164	change lost		glucosylase 1	metaphylglycosyl degradation	Metabolism: carbohydrate metabolism; gly	high	---
Glo1	12674	12674	62040	change retained in offspring by 27%	CNV	protein phosphatase 1, regulator of insulin signaling pathway	protein phosphatase 1, regulator of insulin signaling pathway	Metabolism: carbohydrate; glycogen me	high	24
Ppp1r3b	10086	3621	22243	change lost		protein phosphatase 1, regulator of a regulatory subunit of protein phosphatase 2	transcription factor	Metabolism: carbohydrate; glycogen me	high	37
Ppp1r3c	7241	-302	10993	change lost		neuronal PAS domain protein 2	transcription factor	Metabolism: cellular lipid metabolic proc	NA	103
Npas2	11082	4979	7545	change retained in offspring by 71%		insulin induced gene 2	essential for the feedback inhibition of insulin	Metabolism: cholesterol biosynthetic pro	high	---
Insig2	12967	5281	29234	change retained in offspring by 32%		flavin containing monooxygenase	monooxygenase activity	Metabolism: drug metabolism - cytochr	high	---
Fmo5	7076	1817	20756	change lost		acyl-Coenzyme A dehydrogenase	oxidoreductase activity	Metabolism: fatty acid beta-oxidation	low	45
Acad11	15897	3917	9229	change lost	TSS window overlapping with Uba5	carboxylesterase 3A (Ces3a)	hydrolysis or transesterification	Metabolism: fatty acyl and cholesterol es	NA	---
Es31	8841	757	8841	change lost		5,10-methylenetetrahydrofolate conversion of 5,10-methylenetetrahydrofolate	glucose 6-phosphatase, catalytic	Metabolism: folic acid metabolic process	medium	73
Mthfr	7809	-937	10872	change lost	bidirectional promoter (Cln6)	glucose 6-phosphatase, catalytic	hydrolysis of D-glucose 6-phosphate	Metabolism: glucose homeostasis	high	---
G6pc	8259	459	17344	change lost		solute carrier organic anion transmembrane acid/salt transporter	Metabolism: lipid and lipoprotein	high	---	
Slco1a1	12403	-1523	19640	change lost		ethanolamine kinase 2	kinase activity	Metabolism: lipid metabolism; glycerophospholipid metabolism	medium	71
Atn2k2	15574	-1006	22322	change lost		perilipin 5 - Ldgp5	LSDP5 is stimulated by ligand and acts as a lipid droplet	Metabolism: lipid storage	high	---
Pln5	211	15580	23096	change lost	bidirectional promoter (3110009E18Rik)	diazepam binding inhibitor	acyl-CoA-binding protein: acyl-CoA oxidase	Metabolism: lipid; PPAR signaling	high	35
Dbi	8908	-154	17086	change lost		nuclear receptor subfamily 0, group 1, class 1, member 1	transcription factor	Metabolism: regulation of insulin secretion	medium	---
Nr0b2	9801	2911	14919	change lost		cytochrome P450, family 2, subfamily monooxygenase	activity	Metabolism: triglyceride metabolic proc	high	---
Cyp2e1	7091	2748	7242	change retained in offspring by 44%	ENSMUST00000153886	solute carrier family 25 (mitochondrial calcium transmembrane transporter)	Mitochondrion: calcium transporter	high	---	
Slc25a25	7542	-2343	8746	change lost		thyroid cancer-1	May decrease apoptosis (By siml)	ND	high	---
1810011010Rik	7591	-2136	8789	change lost	CNV (genomic vicinity to Plekhf1 and Pop4)	hypothetical protein LOC72244	ND	ND	high	36
1600014C10Rik	18311	67904	27459	change retained in offspring > 100%		paroxysmal nonkinetogenic dyskinesia	hydroxyacylglutathione hydrolase	ND	high	38
Pnk1	16550	-1640	22013	change lost		Down syndrome critical region	glucocorticoid receptor	transcription factor	high	99
Dscr3	7460	-450	8258	change lost		region of SNORA24	ND	NA	high	76
AC124005.1	7047	-642	6996	change lost	chr3:123,210,238-123,212,243	AN1, ubiquitin-like, homolog of XerC	Zinc finger protein	ND	medium	---
Anub1	6859	5068	9484	change retained in offspring by 94%	Zfand4	transmembrane inner ear	membrane protein	Sensory perception: sound	medium	57
Tnfr1	7425	-1137	11019	change lost	bidirectional promoter (Als2cl)	transmembrane inner ear	membrane protein	Transcription: positive regulation	NA	---
AL592283.1	7233	-35	7233	change lost	bidirectional promoter (Nfia)	zinc finger protein 36, C3H type-1	zinc ion binding protein	Transcription/translation: mRNA stability	high	23, 42
Zfp361	7941	-601	8619	change lost		serine/arginine repetitive matrix	RNA binding	Transcription/translation: RNA splicing	high	23
Srrm4	11793	2035	11793	change lost	ENSMUST00000139425	processing of precursor 4, ribonuclease subunit of the small nucleolar ribonuclease P	ND	Transcription: RNA transport; ribosome biogenesis	high	25
Pop4	12490	10837	12490	change retained in offspring by 89%	CNV (genomic vicinity to Plekhf1 and 1600014C10Rik)	secreted phosphoprotein 2	ND	Bone remodeling	high	---
Spp2	-6732	-2869	-10209	change lost		folliculin interacting protein 2	regulation of protein phosphorylation	Cell cycle: apoptosis, DNA damage response	high	---
Flnp2	-7303	1091	-11451	change lost	bidirectional promoter (ENSMUST00000091023)	yippee-like 3 (Drosophila)	protein with grp	Cell cycle: apoptosis	high	56
Ypel3	-8869	798	-8869	change lost		tumor necrosis factor, alpha-inducible	angiogenesis	Cell cycle: cell differentiation	high	44
Tnfrap2	-7082	-2524	-8797	change lost		Holliday junction recognition protein	CENP-A chromatin assembly factor	Cell cycle: centromeric core chromatin assembly	high	49
Hjurp	-19558	-19389	-16068	change retained in offspring by 106%	CNV	insulin-like growth factor binding growth factor binding protein	serine (or cysteine) peptidase	int alpha-globulin protein with corticosteroid	high	32, 20
Igf2bp2	-13736	4531	-13736	change lost		deiodinase, iodothyronine, type I	oxidoreductase activity	Hormonal regulation: glucocorticoid transport	high	---
Serpina6	-7667	-2807	-10349	change lost		B-cell leukemia/lymphoma 3	transcriptional co-activator	Immune: antimicrobial humoral response	high	43
Dcl1	-17776	-5716	-38703	change lost	ENSMUST00000139680	histocompatibility 2, D region	MHC class I receptor activity	Immune: defense response	NA	115
Bcl3	-11260	-5732	-11260	change retained in offspring by 89%		B-cell leukemia/lymphoma 6	zinc finger transcription factor	Immune: negative regulation of type 2 immune response	high	---
H2-L	-10206	-4056	-10206	change retained in offspring by 27%	ENSMUST00000135352	ATP-binding cassette, sub-family A	ATP-binding cassette (ABC) transporter	Inflammation: may be regulated by tumor necrosis factor	high	62
Abcf1	-7227	1384	-7269	change lost		protein phosphatase 1, regulatory (inhibitor) subunit 3G	Metabolism: carbohydrate; glycogen me	high	102	
Ppp1r3g	-7192	-810	-7454	change lost		acetyl-Coenzyme A carboxylase	carboxylation of acetyl-CoA to malonyl-CoA	Metabolism: fatty acid biosynthesis (rate limiting)	low	---
Acab3	-7556	1831	-8788	change lost	ENSMUST00000102582 (upstream gene TSS)	ring finger protein 186	Zn finger protein	ND	medium	---
Rnf186	-7134	-1253	-7934	change lost		Purkinje cell protein 4-like 1	ND	ND	high	25
Pcp4l1	-10262	-307	-11819	change lost		kelch domain containing 7A	membrane protein	ND	low	21
Klhd7a	-12305	-6294	-14652	change retained in offspring by 92%		RIKEN cDNA E030030106 gene; A	ND	ND	low	221
E030030106Rik	-13383	-1189	-12537	change lost		hypothetical protein LOC73747	ND	ND	high	---
1110034624Rik	-15218	5745	-15218	change lost	ENSMUST00000141460 (AL935270.6)	transforming growth factor, beta	serine/threonine kinase receptor	Signal transduction: ser/thr kinase recept	high	83
AC132460.2	-20303	-4013	-20303	change lost	chr17:28,144,377-28,146,377	Ral GEF with PH domain and SH3 domain	guanine nucleotide exchange factor	Signal transduction: small GTPase mediated	high	112
Tgfb2	-7836	137	-8388	change lost		frizzled homolog 8 (Drosophila)	Wnt-activated receptor activity	Signal transduction: Wnt signaling pathway	medium	218
Ralgap2	-8671	-283	-9200	change lost		AT rich interactive domain 1A (SV)	helicase and ATPase activities	Transcription regulation: chromatin organization	medium	30
Fzd8	-8502	1636	-25536	change lost	ENSMUST00000008024	D site albumin promoter binding	transcription factor	Transcription: positive regulation, circadi	high	26, 19, 49
Arid1a	-7328	-1483	-8179	change lost		ribosomal RNA, small subunit	ribosome	Transcription/translation: ribosome	NA	360, 81
Ddp	-10264	-632	-16956	change lost		CWC22 spliceosome-associated protein	homolog (S. cerevisiae)	Transcription/translation: RNA/DNA bind	high	39
SSU_rRNA_5	-10501	12740	-42155	change lost	near mir-715, highly marked region	elacA homolog 1 (E. coli)	endoribonuclease activity	Transcription/translation: tRNA process	low	65
Cwc22	-1662660	-520398	-1570329	change retained in offspring by 32%	CNV	ribonuclease P 21 subunit (human)	ribonuclease P activity	Transcription/translation: tRNA process	high	26
Elac1	-8361	142	-8361	change lost						
Rpp21	-15232	-1553	-15250	change lost						

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