

Gene.symbol	logFC	Fold Change	adj.P.Val	P.Value	Gene.symbol	Gene.title
MMP1	6.77850993	109.78	8.03E-17	1.03E-20	<i>MMP1</i>	matrix metalloproteinase 1
MMP12	5.30399168	39.51	3.04E-15	9.45E-19	<i>MMP12</i>	matrix metalloproteinase 12
SPP1	4.78450649	27.56	2.11E-14	2.12E-17	<i>SPP1</i>	secreted phosphoprotein 1
MMP10	4.65763623	25.24	1.31E-14	1.10E-17	<i>MMP10</i>	matrix metalloproteinase 10
MMP3	4.58993519	24.08	1.74E-14	1.58E-17	<i>MMP3</i>	matrix metalloproteinase 3
MAGEA6	4.29185333	19.59	2.05E-08	8.77E-10	<i>MAGEA6</i>	MAGE family member A6
CXCL8	4.25995717	19.16	4.60E-14	6.98E-17	<i>CXCL8</i>	C-X-C motif chemokine ligand 8
MAGEA6///MAGEA3	4.24611522	18.98	2.86E-08	1.29E-09	<i>MAGEA6///MAGEA3</i>	MAGE family member A6///MAGE family member A3
KRT17///JUP	4.1213016	17.40	2.72E-14	3.38E-17	<i>KRT17///JUP</i>	keratin 17///junction plakoglobin
COL1A1	4.0996896	17.14	2.57E-13	7.06E-16	<i>COL1A1</i>	collagen type I alpha 1 chain
COL11A1	3.95193991	15.48	4.15E-09	1.35E-10	<i>COL11A1</i>	collagen type XI alpha 1 chain
COL10A1	3.82367746	14.16	1.88E-11	1.93E-13	<i>COL10A1</i>	collagen type X alpha 1 chain
WDR72	3.6943889	12.95	6.11E-16	1.34E-19	<i>WDR72</i>	WD repeat domain 72
INHBA	3.66334278	12.67	4.87E-16	9.79E-20	<i>INHBA</i>	inhibin beta A subunit
CTHRC1	3.55193252	11.73	9.71E-17	1.60E-20	<i>CTHRC1</i>	collagen triple helix repeat containing 1
KRT17///JUP	3.45796275	10.99	2.29E-14	2.44E-17	<i>KRT17///JUP</i>	keratin 17///junction plakoglobin
WDR72	3.44800729	10.91	8.03E-17	9.58E-21	<i>WDR72</i>	WD repeat domain 72
CXCL5	3.38681171	10.46	1.46E-07	8.64E-09	<i>CXCL5</i>	C-X-C motif chemokine ligand 5
WISP1	3.37910679	10.40	1.67E-19	3.06E-24	<i>WISP1</i>	WNT1 inducible signaling pathway protein 1
PTHLH	3.37177529	10.35	1.36E-09	3.56E-11	<i>PTHLH</i>	parathyroid hormone like hormone
COL10A1	3.30518381	9.88	6.71E-12	5.20E-14	<i>COL10A1</i>	collagen type X alpha 1 chain
MMP9	3.29899036	9.84	2.74E-13	7.73E-16	<i>MMP9</i>	matrix metalloproteinase 9
HOXD10	3.22710763	9.36	3.97E-14	5.88E-17	<i>HOXD10</i>	homeobox D10
COL11A1	3.2188395	9.31	8.06E-09	2.98E-10	<i>COL11A1</i>	collagen type XI alpha 1 chain
CXCL1	3.20825369	9.24	9.76E-11	1.48E-12	<i>CXCL1</i>	C-X-C motif chemokine ligand 1
APOC1	3.1884033	9.12	3.82E-11	4.67E-13	<i>APOC1</i>	apolipoprotein C1
ADAM12	3.16424617	8.96	2.01E-14	1.91E-17	<i>ADAM12</i>	ADAM metalloproteinase domain 12
DUXAP10	3.1634059	8.96	2.26E-12	1.34E-14	<i>DUXAP10</i>	double homeobox A pseudogene 10
INHBA	3.15149902	8.89	2.07E-14	2.01E-17	<i>INHBA</i>	inhibin beta A subunit
CHI3L1	3.07936375	8.45	6.16E-11	8.31E-13	<i>CHI3L1</i>	chitinase 3 like 1
PTHLH	3.04230107	8.24	4.85E-09	1.64E-10	<i>PTHLH</i>	parathyroid hormone like hormone
PLA2G7	3.02062449	8.12	9.21E-14	1.77E-16	<i>PLA2G7</i>	phospholipase A2 group VII
WDR66	2.98470617	7.92	8.28E-14	1.48E-16	<i>WDR66</i>	WD repeat domain 66
ADAMTS2	2.9477472	7.72	2.22E-14	2.28E-17	<i>ADAMTS2</i>	ADAM metalloproteinase with thrombospondin type 1 motif 2
POSTN	2.93738987	7.66	1.51E-08	6.16E-10	<i>POSTN</i>	periostin
CHI3L1	2.92874622	7.61	3.31E-11	3.86E-13	<i>CHI3L1</i>	chitinase 3 like 1
CST1	2.90048735	7.47	2.43E-11	2.68E-13	<i>CST1</i>	cystatin SN

S100A7A	2.90045071	7.47	8.14E-09	3.01E-10	S100A7A	S100 calcium binding protein A7A
COL1A1	2.85564453	7.24	1.32E-12	6.42E-15	COL1A1	collagen type I alpha 1 chain
MMP13	2.84977778	7.21	8.46E-13	3.27E-15	MMP13	matrix metalloproteinase 13
SPRR2G	2.78034577	6.87	4.13E-08	2.00E-09	SPRR2G	small proline rich protein 2G
APOBEC3A_B///APOBEC3A	2.77929093	6.87	1.29E-07	7.54E-09	APOBEC3A_B///APOBEC3A	APOBEC3A and APOBEC3B deletion hybrid///apolipoprotein B mRNA editing enzyme catalytic subunit 3A
CCL18	2.77410114	6.84	3.06E-10	6.07E-12	CCL18	C-C motif chemokine ligand 18
CCL3L3///CCL3L1///CCL3	2.73903232	6.68	2.26E-14	2.36E-17	CCL3L3///CCL3L1///CCL3	C-C motif chemokine ligand 3 like 3///C-C motif chemokine ligand 3 like 1///C-C motif chemokine ligand 3
POSTN	2.70160109	6.51	7.23E-10	1.70E-11	POSTN	periostin
LOC100129518///SOD2	2.6995814	6.50	2.56E-10	4.92E-12	LOC100129518///SOD2	uncharacterized LOC100129518///superoxide dismutase 2, mitochondrial
CXCL6	2.69871115	6.49	3.11E-11	3.57E-13	CXCL6	C-X-C motif chemokine ligand 6
CXCL13	2.69538453	6.48	4.71E-06	4.86E-07	CXCL13	C-X-C motif chemokine ligand 13
ISG15	2.67141141	6.37	7.85E-13	2.95E-15	ISG15	ISG15 ubiquitin-like modifier
S100A7	2.65666168	6.31	5.36E-05	7.98E-06	S100A7	S100 calcium binding protein A7
ABCA13	2.64920345	6.27	7.27E-08	3.88E-09	ABCA13	ATP binding cassette subfamily A member 13
SLC44A5	2.62966812	6.19	2.53E-09	7.37E-11	SLC44A5	solute carrier family 44 member 5
LAMC2	2.62587716	6.17	7.85E-13	2.96E-15	LAMC2	laminin subunit gamma 2
IL36G	2.62116971	6.15	6.88E-08	3.64E-09	IL36G	interleukin 36, gamma
BCL2A1	2.60027038	6.06	2.07E-12	1.19E-14	BCL2A1	BCL2 related protein A1
COL1A2	2.57714299	5.97	1.11E-14	8.31E-18	COL1A2	collagen type I alpha 2 chain
TDO2	2.55757257	5.89	5.75E-12	4.30E-14	TDO2	tryptophan 2,3-dioxygenase
PLAU	2.54725516	5.85	6.24E-17	4.56E-21	PLAU	plasminogen activator, urokinase
ADAM12	2.50824914	5.69	6.71E-14	1.14E-16	ADAM12	ADAM metalloproteinase domain 12
LINC01296///DUXAP10	2.50407377	5.67	1.85E-11	1.90E-13	LINC01296///DUXAP10	long intergenic non-protein coding RNA 1296///double homeobox A pseudogene 10
CCL20	2.50165837	5.66	8.93E-07	7.15E-08	CCL20	C-C motif chemokine ligand 20
TNFAIP6	2.46495146	5.52	1.01E-12	4.34E-15	TNFAIP6	TNF alpha induced protein 6
CYP24A1	2.45715923	5.49	1.35E-08	5.43E-10	CYP24A1	cytochrome P450 family 24 subfamily A member 1
CCL18	2.43897622	5.42	1.31E-10	2.16E-12	CCL18	C-C motif chemokine ligand 18
TNFAIP6	2.41599508	5.34	1.58E-13	3.52E-16	TNFAIP6	TNF alpha induced protein 6
SHISA2	2.40750841	5.31	4.01E-11	4.96E-13	SHISA2	shisa family member 2
MIR8071-2///MIR8071-1///IGHV4-31///IGHM///IGHG2///IGHG1	2.40558162	5.30	6.08E-12	4.60E-14	MIR8071-2///MIR8071-1///IGHV4-31///IGHM///IGHG2///IGHG1	microRNA 8071-2///microRNA 8071-1///immunoglobulin heavy variable 4-31///immunoglobulin heavy constant mu///immunoglobulin heavy constant gamma 2 (G2m marker)///immunoglobulin

						n heavy constant gamma 1 (G1m marker)
NTS	2.36413437	5.15	1.20E-03	2.82E-04	NTS	neurotensin
HOXA10-HOXA9///MIR196B///HOXA9	2.3506187	5.10	6.94E-07	5.33E-08	HOXA10-HOXA9 readthrough///microRNA 196b///homeobox A9	HOXA10-HOXA9 readthrough///microRNA 196b///homeobox A9
HOXB7	2.34526763	5.08	1.02E-13	2.03E-16	HOXB7	homeobox B7
CXCL10	2.33815618	5.06	4.01E-08	1.93E-09	CXCL10	C-X-C motif chemokine ligand 10
ADAMDEC1	2.33563769	5.05	9.77E-09	3.72E-10	ADAMDEC1	ADAM like decysin 1
APOBEC3B	2.31385681	4.97	3.62E-09	1.15E-10	APOBEC3B	apolipoprotein B mRNA editing enzyme catalytic subunit 3B
IGK///IGKC	2.31155174	4.96	9.03E-08	4.99E-09	IGK///IGKC	immunoglobulin kappa locus///immunoglobulin kappa constant
TREM1	2.30499489	4.94	6.32E-11	8.65E-13	TREM1	triggering receptor expressed on myeloid cells 1
MAGEA12	2.29087054	4.89	4.98E-05	7.34E-06	MAGEA12	MAGE family member A12
DHRS2	2.27753185	4.85	9.27E-05	1.50E-05	DHRS2	dehydrogenase/reductase 2
ZIC2	2.27259146	4.83	2.67E-07	1.74E-08	ZIC2	Zic family member 2
SERPINE1	2.26724138	4.81	4.22E-11	5.25E-13	SERPINE1	serpin family E member 1
VCAN	2.2647579	4.81	1.52E-11	1.45E-13	VCAN	versican
MFAP2	2.24717108	4.75	8.31E-14	1.50E-16	MFAP2	microfibrillar associated protein 2
TYMP	2.21558879	4.64	3.68E-13	1.15E-15	TYMP	thymidine phosphorylase
LOXL2	2.19955256	4.59	1.31E-14	1.13E-17	LOXL2	lysyl oxidase like 2
RBP1	2.19866055	4.59	1.08E-10	1.69E-12	RBP1	retinol binding protein 1
MAGEA11	2.19799429	4.59	1.53E-05	1.89E-06	MAGEA11	MAGE family member A11
FCRL5	2.19287641	4.57	6.61E-08	3.46E-09	FCRL5	Fc receptor like 5
SFRP4	2.1879984	4.56	1.16E-06	9.73E-08	SFRP4	secreted frizzled related protein 4
SHOX2	2.1801728	4.53	6.16E-09	2.16E-10	SHOX2	short stature homeobox 2
CXCL11	2.17515339	4.52	5.32E-07	3.90E-08	CXCL11	C-X-C motif chemokine ligand 11
SIX1	2.173222	4.51	1.38E-10	2.29E-12	SIX1	SIX homeobox 1
MAGEA4	2.16993847	4.50	2.39E-05	3.13E-06	MAGEA4	MAGE family member A4
IGFBP3	2.16460293	4.48	9.92E-11	1.51E-12	IGFBP3	insulin like growth factor binding protein 3
KRT14	2.15989808	4.47	9.96E-06	1.15E-06	KRT14	keratin 14
COL5A2	2.15768379	4.46	3.32E-12	2.09E-14	COL5A2	collagen type V alpha 2 chain
IGK///IGKC	2.15286717	4.45	3.02E-07	2.02E-08	IGK///IGKC	immunoglobulin kappa locus///immunoglobulin kappa constant
COL3A1	2.15216712	4.44	1.19E-11	1.09E-13	COL3A1	collagen type III alpha 1 chain
MIR675///H19	2.14573243	4.43	9.73E-06	1.12E-06	MIR675///H19	microRNA 675///H19, imprinted maternally expressed transcript (non-protein coding)
COL5A1	2.14260276	4.42	4.72E-12	3.29E-14	COL5A1	collagen type V alpha 1 chain
LOX	2.13813776	4.40	3.87E-13	1.23E-15	LOX	lysyl oxidase
ANO1	2.13508082	4.39	3.90E-09	1.25E-10	ANO1	anoctamin 1

C5AR1	2.13019425	4.38	1.51E-13	3.34E-16	<i>C5AR1</i>	complement component 5a receptor 1
DEFB4B//DEFB4A	2.126844	4.37	4.86E-04	9.92E-05	<i>DEFB4B//DEFB4A</i>	defensin beta 4B//defensin beta 4A
IGLC1	2.12571619	4.36	2.64E-08	1.18E-09	<i>IGLC1</i>	immunoglobulin lambda constant 1
SERPINH1	2.12264854	4.35	2.12E-12	1.24E-14	<i>SERPINH1</i>	serpin family H member 1
KRTDAP	2.12212399	4.35	4.78E-04	9.74E-05	<i>KRTDAP</i>	keratinocyte differentiation associated protein
ZIC1	2.11071883	4.32	1.00E-04	1.63E-05	<i>ZIC1</i>	Zic family member 1
FSCN1	2.10698099	4.31	1.28E-12	6.17E-15	<i>FSCN1</i>	fascin actin-bundling protein 1
IGKC	2.09212931	4.26	7.01E-07	5.39E-08	<i>IGKC</i>	immunoglobulin kappa constant
MMP11	2.09126768	4.26	1.06E-11	9.27E-14	<i>MMP11</i>	matrix metalloproteinase 11
SNX10	2.08983849	4.26	3.87E-14	5.38E-17	<i>SNX10</i>	sorting nexin 10
KRT16	2.08664714	4.25	7.63E-06	8.50E-07	<i>KRT16</i>	keratin 16
CXCL8	2.08414149	4.24	9.84E-09	3.75E-10	<i>CXCL8</i>	C-X-C motif chemokine ligand 8
PLAUR	2.08378751	4.24	3.87E-14	5.45E-17	<i>PLAUR</i>	plasminogen activator, urokinase receptor
VCAN	2.08260188	4.24	6.88E-12	5.42E-14	<i>VCAN</i>	versican
IGKC	2.08051687	4.23	3.35E-06	3.27E-07	<i>IGKC</i>	immunoglobulin kappa constant
MAGEA10-MAGEA5//MAGEA5	2.05764841	4.16	1.30E-06	1.11E-07	<i>MAGEA10-MAGEA5//MAGEA5</i>	MAGEA10-MAGEA5 readthrough//MAGEA family member A5
COL5A2	2.05642392	4.16	1.74E-11	1.72E-13	<i>COL5A2</i>	collagen type V alpha 2 chain
VCAN	2.05240666	4.15	1.59E-11	1.53E-13	<i>VCAN</i>	versican
AIM2	2.0436229	4.12	4.84E-07	3.50E-08	<i>AIM2</i>	absent in melanoma 2
CXCL9	2.03485683	4.10	6.88E-08	3.64E-09	<i>CXCL9</i>	C-X-C motif chemokine ligand 9
LAMB3	2.02840574	4.08	1.39E-11	1.30E-13	<i>LAMB3</i>	laminin subunit beta 3
ADAMTS12	2.02642709	4.07	5.84E-14	9.78E-17	<i>ADAMTS12</i>	ADAM metalloproteinase with thrombospondin type 1 motif 12
IGLC1	2.02251357	4.06	1.95E-08	8.32E-10	<i>IGLC1</i>	immunoglobulin lambda constant 1
THY1	2.0197966	4.06	1.36E-12	6.74E-15	<i>THY1</i>	Thy-1 cell surface antigen
HOXA10-HOXA9//MIR196B//HOXA9	2.01269264	4.04	7.02E-07	5.40E-08	<i>HOXA10-HOXA9//MIR196B//HOXA9</i>	HOXA10-HOXA9 readthrough//microRNA 196b//homeobox A9
CXCL11	2.00736987	4.02	1.19E-05	1.41E-06	<i>CXCL11</i>	C-X-C motif chemokine ligand 11
IFI30//PIK3R2	2.00615994	4.02	4.45E-11	5.59E-13	<i>IFI30//PIK3R2</i>	IFI30, lysosomal thiol reductase//phosphoinositide-3-kinase regulatory subunit 2
ODC1	1.99961326	4.00	7.73E-12	6.23E-14	<i>ODC1</i>	ornithine decarboxylase 1
IL24	1.99818884	3.99	1.50E-08	6.11E-10	<i>IL24</i>	interleukin 24
SOX4	1.99771333	3.99	9.40E-13	3.75E-15	<i>SOX4</i>	SRY-box 4
IGK//IGKC	1.99639671	3.99	1.06E-06	8.74E-08	<i>IGK//IGKC</i>	immunoglobulin kappa locus//immunoglobulin kappa constant
THY1	1.99257334	3.98	3.65E-13	1.13E-15	<i>THY1</i>	Thy-1 cell surface antigen
COL5A1	1.99230902	3.98	1.45E-11	1.37E-13	<i>COL5A1</i>	collagen type V alpha 1 chain
CEMIP	1.98762137	3.97	1.01E-10	1.55E-12	<i>CEMIP</i>	cell migration inducing hyaluronan binding protein
GBP5	1.98673324	3.96	1.28E-07	7.47E-09	<i>GBP5</i>	guanylate binding protein 5

GNPMB	1.98506434	3.96	1.60E-11	1.55E-13	GNPMB	glycoprotein nmb
FCGR3B	1.98379129	3.96	8.28E-13	3.17E-15	FCGR3B	Fc fragment of IgG receptor IIb
FNDC1	1.98074343	3.95	9.13E-10	2.21E-11	FNDC1	fibronectin type III domain containing 1
HOXB7	1.97864226	3.94	2.01E-13	5.16E-16	HOXB7	homeobox B7
PMEPA1	1.95035515	3.86	1.81E-14	1.69E-17	PMEPA1	prostate transmembrane protein, androgen induced 1
HOXD11	1.94886393	3.86	1.50E-11	1.43E-13	HOXD11	homeobox D11
SFRP4	1.94622734	3.85	8.15E-06	9.16E-07	SFRP4	secreted frizzled related protein 4
FCER1G	1.94273767	3.84	2.74E-08	1.23E-09	FCER1G	Fc fragment of IgE receptor Ig
POU6F2-AS2	1.94201977	3.84	1.04E-08	4.02E-10	POU6F2-AS2	POU6F2 antisense RNA 2
CLDN1	1.93994613	3.84	2.29E-08	9.93E-10	CLDN1	claudin 1
MZB1	1.92583721	3.80	1.72E-07	1.06E-08	MZB1	marginal zone B and B1 cell specific protein
COL3A1	1.92259036	3.79	2.85E-12	1.75E-14	COL3A1	collagen type III alpha 1 chain
LAMP3	1.92216078	3.79	5.89E-09	2.06E-10	LAMP3	lysosomal associated membrane protein 3
THY1	1.9219152	3.79	2.02E-12	1.13E-14	THY1	Thy-1 cell surface antigen
SOCS3	1.91963751	3.78	5.27E-07	3.86E-08	SOCS3	suppressor of cytokine signaling 3
CCL4	1.90675397	3.75	3.76E-12	2.47E-14	CCL4	C-C motif chemokine ligand 4
HOXA10	1.90603219	3.75	1.83E-13	4.46E-16	HOXA10	homeobox A10
PTH1H	1.90421013	3.74	1.39E-06	1.19E-07	PTH1H	parathyroid hormone like hormone
CDH3	1.89804326	3.73	1.64E-12	8.48E-15	CDH3	cadherin 3
RSAD2	1.89572086	3.72	1.36E-08	5.44E-10	RSAD2	radical S-adenosyl methionine domain containing 2
TGFBI	1.89357754	3.72	1.28E-12	6.18E-15	TGFBI	transforming growth factor beta induced
SERPINE1	1.88330153	3.69	9.14E-11	1.38E-12	SERPINE1	serpin family E member 1
BID	1.88174729	3.69	9.58E-17	1.40E-20	BID	BH3 interacting domain death agonist
FCGR1B	1.86671566	3.65	1.06E-10	1.65E-12	FCGR1B	Fc fragment of IgG receptor Ib
COL3A1	1.86190195	3.63	1.70E-10	3.00E-12	COL3A1	collagen type III alpha 1 chain
WISP1	1.85477643	3.62	1.40E-12	6.94E-15	WISP1	WNT1 inducible signaling pathway protein 1
RGS1	1.85474254	3.62	8.42E-08	4.59E-09	RGS1	regulator of G-protein signaling 1
NRG1	1.8542435	3.62	7.51E-08	4.04E-09	NRG1	neuregulin 1
TNC	1.85412854	3.62	3.43E-10	6.92E-12	TNC	tenascin C
GBP5	1.85077424	3.61	4.30E-09	1.41E-10	GBP5	guanylate binding protein 5
SULF1	1.84735279	3.60	1.35E-09	3.51E-11	SULF1	sulfatase 1
CTSC	1.84481194	3.59	6.49E-12	4.95E-14	CTSC	cathepsin C
CT45A8///CT45A9///CT45A10///CT45A7///CT45A2///CT45A1///CT45A6///CT45A5///CT45A3	1.83893128	3.58	1.48E-03	3.59E-04	CT45A8///CT45A9///CT45A10///CT45A7///CT45A2///CT45A1///CT45A6///CT45A5///CT45A3	cancer/testis antigen family 45, member A8///cancer/testis antigen family 45, member A9///cancer/testis antigen family 45, member A10///cancer/testis antigen family 45, member A7///cancer/testis antigen family 45,

						member A2///cancer/testis antigen family 45, member A1///cancer/testis antigen family 45, member A6///cancer/testis antigen family 45, member A5///cancer/testis antigen family 45, member A3
KHDC1L	1.8351326	3.57	3.23E-07	2.19E-08	<i>KHDC1L</i>	KH domain containing 1 like
STC1	1.83423043	3.57	2.69E-08	1.20E-09	<i>STC1</i>	stannocalcin 1
IGK///IGKC	1.83396185	3.57	1.11E-06	9.16E-08	<i>IGK///IGKC</i>	immunoglobulin kappa locus///immunoglobulin kappa constant
RSAD2	1.83015904	3.56	4.14E-09	1.34E-10	<i>RSAD2</i>	radical S-adenosyl methionine domain containing 2
STAT1	1.82150901	3.53	2.38E-09	6.88E-11	<i>STAT1</i>	signal transducer and activator of transcription 1
IGLJ3	1.81940638	3.53	2.45E-07	1.57E-08	<i>IGLJ3</i>	immunoglobulin lambda joining 3
MLF1	1.81922203	3.53	1.70E-10	3.01E-12	<i>MLF1</i>	myeloid leukemia factor 1
UBD///GABBR1	1.81503806	3.52	6.64E-06	7.27E-07	<i>UBD///GABBR1</i>	ubiquitin D///gamma-aminobutyric acid type B receptor subunit 1
SOX4	1.81326247	3.51	3.71E-12	2.42E-14	<i>SOX4</i>	SRY-box 4
EPHB1	1.80740058	3.50	6.92E-07	5.31E-08	<i>EPHB1</i>	EPH receptor B1
KLHL6	1.8039574	3.49	2.08E-11	2.19E-13	<i>KLHL6</i>	kelch like family member 6
IFI6	1.79263202	3.46	4.10E-09	1.32E-10	<i>IFI6</i>	interferon alpha inducible protein 6
PXDN	1.79239721	3.46	3.14E-15	1.07E-18	<i>PXDN</i>	peroxidase
LOX	1.78818441	3.45	3.40E-11	3.99E-13	<i>LOX</i>	lysyl oxidase
COL5A1	1.78375418	3.44	2.01E-10	3.69E-12	<i>COL5A1</i>	collagen type V alpha 1 chain
PPFIA1	1.78334568	3.44	1.87E-06	1.69E-07	<i>PPFIA1</i>	PTPRF interacting protein alpha 1
SPARC	1.7831938	3.44	1.36E-11	1.26E-13	<i>SPARC</i>	secreted protein acidic and cysteine rich
SCG5	1.78185237	3.44	1.03E-08	3.95E-10	<i>SCG5</i>	secretogranin V
HAS3	1.77555554	3.42	1.06E-06	8.68E-08	<i>HAS3</i>	hyaluronan synthase 3
G0S2	1.77273801	3.42	1.72E-09	4.67E-11	<i>G0S2</i>	G0/G1 switch 2
KIF14	1.7711959	3.41	2.21E-10	4.14E-12	<i>KIF14</i>	kinesin family member 14
CKAP2///IGLV@///IGLC1	1.77096868	3.41	1.68E-06	1.49E-07	<i>CKAP2///IGLV@///IGLC1</i>	cytoskeleton associated protein 2///immunoglobulin lambda variable cluster///immunoglobulin lambda constant 1
IGLJ3///IGLV1-44///CKAP2///IGLV@///IGLC1	1.77034311	3.41	2.00E-05	2.55E-06	<i>IGLJ3///IGLV1-44///CKAP2///IGLV@///IGLC1</i>	immunoglobulin lambda joining 3///immunoglobulin lambda variable 1-44///cytoskeleton associated protein 2///immunoglobulin lambda variable cluster///immunoglobulin lambda constant 1
IGHM	1.75860082	3.38	8.42E-09	3.14E-10	<i>IGHM</i>	immunoglobulin heavy constant mu
OLFML2B	1.75488833	3.38	1.20E-14	9.46E-18	<i>OLFML2B</i>	olfactomedin like 2B

SOCS1	1.75339082	3.37	1.19E-12	5.44E-15	SOCS1	suppressor of cytokine signaling 1
BMS1P20	1.75104026	3.37	2.35E-06	2.18E-07	BMS1P20	BMS1, ribosome biogenesis factor pseudogene 20
IGF2BP2	1.7507855	3.37	1.03E-08	3.96E-10	IGF2BP2	insulin like growth factor 2 mRNA binding protein 2
MFHAS1	1.75010134	3.36	9.83E-13	4.06E-15	MFHAS1	malignant fibrous histiocytoma amplified sequence 1
APOE	1.74831018	3.36	2.61E-08	1.16E-09	APOE	apolipoprotein E
WISP3	1.74530351	3.35	5.25E-07	3.84E-08	WISP3	WNT1 inducible signaling pathway protein 3
FCGR1CP///FCGR1B///FCGR1A	1.74287467	3.35	3.57E-10	7.28E-12	FCGR1CP///FCGR1B///FCGR1A	Fc fragment of IgG receptor Ic, pseudogene///Fc fragment of IgG receptor Ib///Fc fragment of IgG receptor Ia
LINC01296///DUXAP10///DUXAP8	1.74197527	3.34	3.63E-12	2.35E-14	LINC01296///DUXAP10///DUXAP8	long intergenic non-protein coding RNA 1296///double homeobox A pseudogene 10///double homeobox A pseudogene 8
FBN2	1.74065301	3.34	4.77E-06	4.93E-07	FBN2	fibrillin 2
COL4A1	1.72298944	3.30	3.14E-15	1.09E-18	COL4A1	collagen type IV alpha 1 chain
LOC101928195///LOC100996643///MTHFD1L	1.72075058	3.30	2.35E-14	2.71E-17	LOC101928195///LOC100996643///MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like pseudogene///monofunctional C1-tetrahydrofolate synthase, mitochondrial-like///methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
LRRC15	1.71991167	3.29	1.32E-09	3.41E-11	LRRC15	leucine rich repeat containing 15
COL12A1	1.71918329	3.29	9.13E-10	2.21E-11	COL12A1	collagen type XII alpha 1 chain
FAP	1.71601652	3.29	2.03E-10	3.75E-12	FAP	fibroblast activation protein alpha
LOC101928615///FNDC3B	1.71018478	3.27	6.94E-13	2.50E-15	LOC101928615///FNDC3B	uncharacterized LOC101928615///fibronectin type III domain containing 3B
PXDN	1.7100604	3.27	6.45E-15	3.54E-18	PXDN	peroxidase
CMPK2	1.70949321	3.27	2.21E-07	1.40E-08	CMPK2	cytidine/uridine monophosphate kinase 2
TMSB15B///TMSB15A	1.70708181	3.26	1.53E-07	9.18E-09	TMSB15B///TMSB15A	thymosin beta 15B///thymosin beta 15a
MUCL1	1.70482092	3.26	2.82E-06	2.68E-07	MUCL1	mucin like 1
IGSF6	1.70429762	3.26	9.57E-09	3.62E-10	IGSF6	immunoglobulin superfamily member 6
ABCA13	1.70374356	3.26	1.78E-06	1.59E-07	ABCA13	ATP binding cassette subfamily A member 13
ATAD2	1.69456976	3.24	1.22E-11	1.12E-13	ATAD2	ATPase family, AAA domain containing 2
RGS16	1.69323961	3.23	4.13E-11	5.12E-13	RGS16	regulator of G-protein signaling 16
SPP1	1.69066897	3.23	3.69E-08	1.75E-09	SPP1	secreted phosphoprotein 1
GAL	1.68553364	3.22	5.12E-06	5.37E-07	GAL	galanin and GMAP prepropeptide
CDKN3	1.68475603	3.21	1.96E-10	3.57E-12	CDKN3	cyclin dependent kinase inhibitor 3
GRP	1.68384724	3.21	1.23E-06	1.04E-07	GRP	gastrin releasing peptide
CDH11	1.67969048	3.20	1.11E-09	2.76E-11	CDH11	cadherin 11
CLC	1.67781296	3.20	2.83E-05	3.80E-06	CLC	Charcot-Leyden crystal galectin

IGLJ3	1.67697276	3.20	2.66E-08	1.18E-09	<i>IGLJ3</i>	immunoglobulin lambda joining 3
BICD1	1.6724953	3.19	2.17E-13	5.75E-16	<i>BICD1</i>	BICD cargo adaptor 1
PTGS2	1.6720161	3.19	2.04E-04	3.68E-05	<i>PTGS2</i>	prostaglandin-endoperoxide synthase 2
RNA45S5	1.66496846	3.17	4.39E-09	1.45E-10	<i>RNA45S5</i>	RNA, 45S pre-ribosomal 5
IGKC	1.66389892	3.17	2.34E-06	2.16E-07	<i>IGKC</i>	immunoglobulin kappa constant
MLIP	1.66381296	3.17	1.34E-06	1.15E-07	<i>MLIP</i>	muscular LMNA-interacting protein
CTSC	1.66193345	3.16	1.34E-12	6.59E-15	<i>CTSC</i>	cathepsin C
HMGA2	1.66154315	3.16	1.28E-08	5.09E-10	<i>HMGA2</i>	high mobility group AT-hook 2
ECT2	1.6586167	3.16	4.40E-10	9.30E-12	<i>ECT2</i>	epithelial cell transforming 2
TFRC	1.65661279	3.15	4.92E-14	7.65E-17	<i>TFRC</i>	transferrin receptor
RPL39L	1.65463488	3.15	1.28E-10	2.10E-12	<i>RPL39L</i>	ribosomal protein L39 like
IGFBP3	1.65248934	3.14	1.45E-09	3.83E-11	<i>IGFBP3</i>	insulin like growth factor binding protein 3
TIMP1	1.65180953	3.14	2.72E-09	7.99E-11	<i>TIMP1</i>	TIMP metalloproteinase inhibitor 1
HOXC10	1.64893014	3.14	4.84E-11	6.15E-13	<i>HOXC10</i>	homeobox C10
GTSE1	1.64792141	3.13	1.06E-08	4.10E-10	<i>GTSE1</i>	G2 and S-phase expressed 1
BGN	1.64752471	3.13	2.77E-10	5.43E-12	<i>BGN</i>	biglycan
TNFAIP3	1.64642229	3.13	4.65E-10	1.00E-11	<i>TNFAIP3</i>	TNF alpha induced protein 3
IFIT3	1.64388892	3.13	2.91E-08	1.32E-09	<i>IFIT3</i>	interferon induced protein with tetratricopeptide repeats 3
UBE2C	1.64324166	3.12	5.86E-13	2.04E-15	<i>UBE2C</i>	ubiquitin conjugating enzyme E2 C
COL1A2	1.63648151	3.11	4.51E-11	5.68E-13	<i>COL1A2</i>	collagen type I alpha 2 chain
IQCA1	1.63608073	3.11	4.09E-07	2.88E-08	<i>IQCA1</i>	IQ motif containing with AAA domain 1
PMEPA1	1.63495123	3.11	5.44E-12	3.93E-14	<i>PMEPA1</i>	prostate transmembrane protein, androgen induced 1
EPPK1	1.63452682	3.10	5.01E-08	2.51E-09	<i>EPPK1</i>	eipplakin 1
RDH10	1.62932617	3.09	1.04E-09	2.56E-11	<i>RDH10</i>	retinol dehydrogenase 10 (all-trans)
TFEC	1.62555148	3.09	4.27E-08	2.08E-09	<i>TFEC</i>	transcription factor EC
FCER1G	1.62176441	3.08	2.10E-09	5.95E-11	<i>FCER1G</i>	Fc fragment of IgE receptor Ig
BBOX1-AS1	1.62091449	3.08	1.45E-09	3.82E-11	<i>BBOX1-AS1</i>	BBOX1 antisense RNA 1
PDPN	1.61881388	3.07	1.58E-11	1.52E-13	<i>PDPN</i>	podoplanin
IGHV3-23///IGHV4-31///IGHM///IGHG1///IGHA1	1.61700327	3.07	5.89E-09	2.06E-10	<i>IGHV3-23///IGHV4-31///IGHM///IGHG1///IGHA1</i>	immunoglobulin heavy variable 3-23//immunoglobulin heavy variable 4-31//immunoglobulin heavy constant mu//immunoglobulin heavy constant gamma 1 (G1m marker)//immunoglobulin heavy constant alpha 1
IGLJ3	1.61696981	3.07	3.13E-08	1.44E-09	<i>IGLJ3</i>	immunoglobulin lambda joining 3
LHX2	1.61659623	3.07	3.19E-07	2.15E-08	<i>LHX2</i>	LIM homeobox 2
BMS1P20	1.61645826	3.07	2.53E-06	2.36E-07	<i>BMS1P20</i>	BMS1, ribosome biogenesis factor pseudogene 20
GZMB	1.61381791	3.06	6.27E-09	2.22E-10	<i>GZMB</i>	granzyme B

PLPP4	1.61372554	3.06	7.74E-08	4.17E-09	PLPP4	phospholipid phosphatase 4
PLAUR	1.61063832	3.05	2.01E-13	5.19E-16	PLAUR	plasminogen activator, urokinase receptor
CT45A8///CT45A9///CT45A10///CT45A7///CT45A2///CT45A1///CT45A6///CT45A5///CT45A3	1.60829146	3.05	1.08E-03	2.50E-04	CT45A8///CT45A9///CT45A10///CT45A7///CT45A2///CT45A1///CT45A6///CT45A5///CT45A3	cancer/testis antigen family 45, member A8///cancer/testis antigen family 45, member A9///cancer/testis antigen family 45, member A10///cancer/testis antigen family 45, member A7///cancer/testis antigen family 45, member A2///cancer/testis antigen family 45, member A1///cancer/testis antigen family 45, member A6///cancer/testis antigen family 45, member A5///cancer/testis antigen family 45, member A3
EPPK1	1.60807508	3.05	9.56E-08	5.33E-09	EPPK1	epiplakin 1
STC1	1.60158617	3.03	4.08E-09	1.31E-10	STC1	stanniocalcin 1
IGKV1OR2-108	1.60155942	3.03	3.29E-06	3.21E-07	IGKV1OR2-108	immunoglobulin kappa variable 1/OR2-108 (non-functional)
CTLA4	1.60140671	3.03	3.97E-09	1.28E-10	CTLA4	cytotoxic T-lymphocyte associated protein 4
FPR1	1.60132748	3.03	6.22E-11	8.47E-13	FPR1	formyl peptide receptor 1
HOXD10	1.59970204	3.03	1.56E-11	1.50E-13	HOXD10	homeobox D10
FABP6	1.5995337	3.03	2.78E-06	2.64E-07	FABP6	fatty acid binding protein 6
MYO1B	1.59824306	3.03	6.44E-11	8.86E-13	MYO1B	myosin IB
CSAG2///CSAG3	1.59674318	3.02	3.80E-05	5.36E-06	CSAG2///CSAG3	CSAG family member 2///CSAG family member 3
F2RL2	1.58993708	3.01	1.89E-10	3.42E-12	F2RL2	coagulation factor II thrombin receptor like 2
TFRC	1.58946353	3.01	2.19E-10	4.09E-12	TFRC	transferrin receptor
FOXE1	1.58944768	3.01	1.03E-06	8.44E-08	FOXE1	forkhead box E1
KIF14	1.58854275	3.01	1.29E-11	1.20E-13	KIF14	kinesin family member 14
ITGB2	1.5862627	3.00	6.58E-08	3.44E-09	ITGB2	integrin subunit beta 2
MIR6732///ZC3H12A	1.5862548	3.00	2.04E-07	1.29E-08	MIR6732///ZC3H12A	microRNA 6732///zinc finger CCCH-type containing 12A
ATAD2	1.58622594	3.00	1.89E-08	8.00E-10	ATAD2	ATPase family, AAA domain containing 2
CEBPB	1.58490169	3.00	9.99E-15	7.31E-18	CEBPB	CCAAT/enhancer binding protein beta
RGS1	1.58421247	3.00	1.46E-07	8.69E-09	RGS1	regulator of G-protein signaling 1
SESN3	1.58360234	3.00	1.08E-07	6.15E-09	SESN3	sestrin 3
CALB1	1.57949963	2.99	3.15E-04	6.07E-05	CALB1	calbindin 1
EPST11	1.57919579	2.99	5.22E-08	2.64E-09	EPST11	epithelial stromal interaction 1 (breast)
TMEM45A	1.57646913	2.98	1.70E-08	7.11E-10	TMEM45A	transmembrane protein 45A
TOP2A	1.57071207	2.97	5.88E-11	7.74E-13	TOP2A	topoisomerase (DNA) II alpha

IGLJ3///IGLV@///IGLC1	1.57041677	2.97	2.15E-05	2.77E-06	IGLJ3///IGLV@///IGLC1	immunoglobulin lambda joining 3///immunoglobulin lambda variable cluster///immunoglobulin lambda constant 1
MEST	1.57037334	2.97	4.09E-13	1.33E-15	MEST	mesoderm specific transcript
KIF26B	1.56662004	2.96	7.85E-11	1.13E-12	KIF26B	kinesin family member 26B
CDKN3	1.56326968	2.96	1.80E-12	9.78E-15	CDKN3	cyclin dependent kinase inhibitor 3
CDC25B	1.56071543	2.95	4.01E-13	1.28E-15	CDC25B	cell division cycle 25B
AKR1C1	1.56023239	2.95	1.07E-04	1.76E-05	AKR1C1	aldo-keto reductase family 1 member C1
COL1A1	1.55754545	2.94	1.08E-09	2.68E-11	COL1A1	collagen type I alpha 1 chain
PDPN	1.55753905	2.94	2.08E-11	2.22E-13	PDPN	podoplanin
CHST1	1.55728045	2.94	8.63E-10	2.07E-11	CHST1	carbohydrate sulfotransferase 1
CHST2	1.55721687	2.94	6.48E-12	4.93E-14	CHST2	carbohydrate sulfotransferase 2
GBP1	1.55616558	2.94	1.12E-07	6.38E-09	GBP1	guanylate binding protein 1
NOX4	1.55591685	2.94	1.22E-12	5.69E-15	NOX4	NADPH oxidase 4
DTL	1.55541256	2.94	9.88E-11	1.50E-12	DTL	denticleless E3 ubiquitin protein ligase homolog
IGLJ3///CKAP2///IGLV@///IGLC1	1.55457063	2.94	4.11E-05	5.88E-06	IGLJ3///CKAP2///IGLV@///IGLC1	immunoglobulin lambda joining 3///cytoskeleton associated protein 2///immunoglobulin lambda variable cluster///immunoglobulin lambda constant 1
CTSZ	1.5539342	2.94	1.19E-10	1.93E-12	CTSZ	cathepsin Z
LOC100129518///SOD2	1.55322683	2.93	2.56E-08	1.14E-09	LOC100129518///SOD2	uncharacterized LOC100129518///superoxide dismutase 2, mitochondrial
BCAT1	1.55134999	2.93	2.29E-07	1.46E-08	BCAT1	branched chain amino acid transaminase 1
IGF2BP3	1.55007604	2.93	3.57E-05	4.98E-06	IGF2BP3	insulin like growth factor 2 mRNA binding protein 3
IGK///IGKC	1.54945057	2.93	3.10E-06	2.99E-07	IGK///IGKC	immunoglobulin kappa locus///immunoglobulin kappa constant
SULF1	1.54934675	2.93	3.90E-09	1.25E-10	SULF1	sulfatase 1
ATAD2	1.54926225	2.93	3.41E-11	4.00E-13	ATAD2	ATPase family, AAA domain containing 2
MIR21///VMP1	1.54896635	2.93	1.60E-09	4.26E-11	MIR21///VMP1	microRNA 21///vacuole membrane protein 1
UHRF1	1.5485836	2.93	5.33E-13	1.83E-15	UHRF1	ubiquitin like with PHD and ring finger domains 1
SLC2A1	1.54832642	2.92	4.97E-09	1.69E-10	SLC2A1	solute carrier family 2 member 1
CDC6	1.54530203	2.92	9.92E-12	8.56E-14	CDC6	cell division cycle 6
BID	1.53986784	2.91	1.59E-13	3.57E-16	BID	BH3 interacting domain death agonist
IGHV3-23///IGHV4-31///IGHM///IGHG4///IGHG3///IGHG1///IGHD///IGHA2///IGHA1///IGH	1.53775229	2.90	1.50E-08	6.13E-10	IGHV3-23///IGHV4-31///IGHM///IGHG4///IGHG3///IGHG1///IGHD///IGHA2///IGHA1///IGH	immunoglobulin heavy variable 3-23///immunoglobulin heavy variable 4-31///immunoglobulin heavy constant mu///immunoglobulin heavy constant gamma 4 (G4m marker)///immunoglobulin heavy constant gamma 3 (G3m marker)///immunoglobulin heavy constant gamma 1 (G1m marker)///immunoglobulin

						n heavy constant delta//immunoglobulin heavy constant alpha 2 (A2m marker)//immunoglobulin heavy constant alpha 1//immunoglobulin heavy locus
PANX1	1.53660174	2.90	8.65E-12	7.20E-14	PANX1	pannexin 1
ADGRE2	1.5351723	2.90	7.64E-12	6.15E-14	ADGRE2	adhesion G protein-coupled receptor E2
IGLV1-44	1.53494116	2.90	4.62E-05	6.72E-06	IGLV1-44	immunoglobulin lambda variable 1-44
GBP1	1.53448734	2.90	5.06E-08	2.54E-09	GBP1	guanylate binding protein 1
PRSS21	1.52906414	2.89	3.92E-06	3.94E-07	PRSS21	protease, serine 21
CEP19	1.52830599	2.88	1.42E-10	2.37E-12	CEP19	centrosomal protein 19
COTL1	1.51971943	2.87	6.02E-10	1.36E-11	COTL1	coactosin like F-actin binding protein 1
TCHH	1.51783548	2.86	9.38E-05	1.51E-05	TCHH	trichohyalin
SLAMF8	1.51262699	2.85	3.48E-08	1.63E-09	SLAMF8	SLAM family member 8
CLDN1	1.51139898	2.85	2.84E-06	2.71E-07	CLDN1	claudin 1
ASPM	1.50904548	2.85	2.29E-06	2.11E-07	ASPM	abnormal spindle microtubule assembly
RSRC1	1.50738947	2.84	6.73E-12	5.28E-14	RSRC1	arginine and serine rich coiled-coil 1
ABCA12	1.50671423	2.84	1.27E-05	1.52E-06	ABCA12	ATP binding cassette subfamily A member 12
SLC2A3	1.50636924	2.84	2.84E-06	2.70E-07	SLC2A3	solute carrier family 2 member 3
GINS1	1.50600088	2.84	2.17E-13	5.78E-16	GINS1	GINS complex subunit 1
NCF2	1.50204446	2.83	3.44E-14	4.53E-17	NCF2	neutrophil cytosolic factor 2
PI15	1.50052388	2.83	2.63E-07	1.72E-08	PI15	peptidase inhibitor 15
RDH10	1.49991047	2.83	2.51E-09	7.30E-11	RDH10	retinol dehydrogenase 10 (all-trans)
PPFIA1	1.49692417	2.82	2.25E-06	2.07E-07	PPFIA1	PTPRF interacting protein alpha 1
UBE2T	1.49644167	2.82	3.20E-09	9.76E-11	UBE2T	ubiquitin conjugating enzyme E2 T
LOC101928615//FNDC3B	1.49548951	2.82	3.34E-10	6.71E-12	LOC101928615//FNDC3B	uncharacterized LOC101928615//fibronectin type III domain containing 3B
MCM2	1.49439523	2.82	3.11E-12	1.94E-14	MCM2	minichromosome maintenance complex component 2
COL4A1	1.49376139	2.82	1.06E-13	2.18E-16	COL4A1	collagen type IV alpha 1 chain
PLXNA1	1.4925317	2.81	6.20E-15	3.06E-18	PLXNA1	plexin A1
P3H4	1.48992911	2.81	7.16E-15	4.31E-18	P3H4	prolyl 3-hydroxylase family member 4 (non-enzymatic)
LCAL1	1.48971002	2.81	1.37E-06	1.18E-07	LCAL1	lung cancer associated lncRNA 1
RFC4	1.48900255	2.81	2.07E-11	2.16E-13	RFC4	replication factor C subunit 4
SOX4	1.48710369	2.80	9.32E-12	7.94E-14	SOX4	SRY-box 4
MMP2	1.48652892	2.80	1.48E-11	1.40E-13	MMP2	matrix metalloproteinase 2
MARCKSL1	1.48514039	2.80	1.44E-09	3.80E-11	MARCKSL1	MARCKS like 1
MCM10	1.48464462	2.80	6.18E-11	8.36E-13	MCM10	minichromosome maintenance 10 replication initiation factor
TLR8	1.48412543	2.80	6.71E-08	3.52E-09	TLR8	toll like receptor 8

LOC101928615///FNDC3B	1.48328515	2.80	3.59E-13	1.10E-15	LOC101928615///FNDC3B	uncharacterized LOC101928615///fibronectin type III domain containing 3B
GTSF1	1.48292359	2.80	2.67E-04	5.02E-05	GTSF1	gametocyte specific factor 1
LAPTM4B	1.48257977	2.79	3.99E-12	2.68E-14	LAPTM4B	lysosomal protein transmembrane 4 beta
CDC20	1.48250785	2.79	8.83E-12	7.40E-14	CDC20	cell division cycle 20
BGN	1.48036813	2.79	1.77E-09	4.86E-11	BGN	biglycan
GBP1	1.47976041	2.79	1.69E-07	1.04E-08	GBP1	guanylate binding protein 1
IL1B	1.47580366	2.78	2.93E-06	2.81E-07	IL1B	interleukin 1 beta
CCR1	1.47487976	2.78	1.17E-08	4.61E-10	CCR1	C-C motif chemokine receptor 1
UCHL1	1.46999066	2.77	1.16E-05	1.38E-06	UCHL1	ubiquitin C-terminal hydrolase L1
GTSE1	1.46604285	2.76	9.05E-11	1.36E-12	GTSE1	G2 and S-phase expressed 1
LPL	1.46585083	2.76	8.75E-05	1.40E-05	LPL	lipoprotein lipase
PTGFRN	1.4656537	2.76	5.44E-12	3.95E-14	PTGFRN	prostaglandin F2 receptor inhibitor
TNFAIP3	1.46449435	2.76	4.33E-10	9.13E-12	TNFAIP3	TNF alpha induced protein 3
PIGX	1.46410483	2.76	1.12E-11	9.98E-14	PIGX	phosphatidylinositol glycan anchor biosynthesis class X
GAP43	1.46296291	2.76	2.76E-06	2.61E-07	GAP43	growth associated protein 43
MAGEA1	1.46241951	2.76	1.95E-04	3.50E-05	MAGEA1	MAGE family member A1
SHCBP1	1.46102215	2.75	1.89E-11	1.95E-13	SHCBP1	SHC binding and spindle associated 1
BCAT1	1.46022126	2.75	2.23E-07	1.42E-08	BCAT1	branched chain amino acid transaminase 1
LARP6	1.458226	2.75	6.97E-11	9.77E-13	LARP6	La ribonucleoprotein domain family member 6
BCAT1	1.45673307	2.74	1.45E-09	3.83E-11	BCAT1	branched chain amino acid transaminase 1
MSR1	1.45584439	2.74	1.57E-07	9.46E-09	MSR1	macrophage scavenger receptor 1
HEY1	1.45517934	2.74	5.60E-09	1.94E-10	HEY1	hes related family bHLH transcription factor with YRPW motif 1
MRPS12	1.45486243	2.74	3.71E-07	2.57E-08	MRPS12	mitochondrial ribosomal protein S12
IGLV1-44	1.45444056	2.74	4.40E-05	6.34E-06	IGLV1-44	immunoglobulin lambda variable 1-44
C1QB	1.4488529	2.73	3.62E-07	2.50E-08	C1QB	complement C1q B chain
FOS	1.44642699	2.73	1.33E-03	3.18E-04	FOS	Fos proto-oncogene, AP-1 transcription factor subunit
HMGB3	1.4460602	2.72	2.10E-12	1.22E-14	HMGB3	high mobility group box 3
CYBA	1.44571228	2.72	3.44E-06	3.38E-07	CYBA	cytochrome b-245 alpha chain
NELL2	1.44506875	2.72	2.00E-06	1.81E-07	NELL2	neural EGFL like 2
FCGR2A	1.4422328	2.72	5.19E-09	1.78E-10	FCGR2A	Fc fragment of IgG receptor IIa
TRIP13	1.44201671	2.72	1.47E-11	1.39E-13	TRIP13	thyroid hormone receptor interactor 13
TPX2	1.44025473	2.71	3.25E-11	3.78E-13	TPX2	TPX2, microtubule nucleation factor
PSMB9	1.43954465	2.71	1.64E-07	9.97E-09	PSMB9	proteasome subunit beta 9
UBE2S	1.43745137	2.71	1.97E-07	1.23E-08	UBE2S	ubiquitin conjugating enzyme E2 S
FAR2P3///FAR2P2	1.43582366	2.71	2.41E-05	3.17E-06	FAR2P3///FAR2P2	fatty acyl-CoA reductase 2 pseudogene 3///fatty acyl-CoA reductase 2 pseudogene 2
IL27RA	1.43394003	2.70	1.83E-07	1.13E-08	IL27RA	interleukin 27 receptor subunit alpha

ENAH	1.43314548	2.70	4.82E-09	1.62E-10	ENAH	enabled homolog (Drosophila)
CXCL3	1.42658191	2.69	1.86E-04	3.30E-05	CXCL3	C-X-C motif chemokine ligand 3
RARRES1	1.42343026	2.68	1.53E-05	1.88E-06	RARRES1	retinoic acid receptor responder 1
MYO5A	1.42313507	2.68	5.72E-12	4.27E-14	MYO5A	myosin VA
NUSAP1	1.42048986	2.68	1.25E-06	1.06E-07	NUSAP1	nucleolar and spindle associated protein 1
C4orf48	1.42025753	2.68	1.06E-13	2.16E-16	C4orf48	chromosome 4 open reading frame 48
SLC16A1	1.41668043	2.67	1.49E-08	6.10E-10	SLC16A1	solute carrier family 16 member 1
PFN2	1.4141046	2.66	9.41E-07	7.59E-08	PFN2	profilin 2
PGM2L1	1.41171253	2.66	1.19E-11	1.08E-13	PGM2L1	phosphoglucosyltransferase 2 like 1
LAPTM5	1.40919089	2.66	3.01E-10	5.97E-12	LAPTM5	lysosomal protein transmembrane 5
SNORA11E///SNORA11D///MAGED4///MAGED4B	1.40755933	2.65	1.81E-10	3.23E-12	SNORA11E///SNORA11D///MAGED4///MAGED4B	small nucleolar RNA, H/ACA box 11E///small nucleolar RNA, H/ACA box 11D///MAGE family member D4///MAGE family member D4B
NETO2	1.40733076	2.65	3.02E-09	9.16E-11	NETO2	neuropilin and tollid like 2
FXR1	1.40546721	2.65	1.54E-05	1.89E-06	FXR1	FMR1 autosomal homolog 1
SLC16A10	1.40242395	2.64	5.34E-10	1.18E-11	SLC16A10	solute carrier family 16 member 10
IL13RA2	1.40144739	2.64	3.24E-08	1.50E-09	IL13RA2	interleukin 13 receptor subunit alpha 2
APOC1	1.39913684	2.64	7.53E-09	2.74E-10	APOC1	apolipoprotein C1
SDF4	1.39897917	2.64	8.61E-08	4.72E-09	SDF4	stromal cell derived factor 4
AURKA	1.39879578	2.64	3.71E-12	2.42E-14	AURKA	aurora kinase A
IGLJ3///IGLV1-44///CKAP2///IGLV@///IGLC1	1.39710053	2.63	1.30E-05	1.57E-06	IGLJ3///IGLV1-44///CKAP2///IGLV@///IGLC1	immunoglobulin lambda joining 3///immunoglobulin lambda variable 1-44///cytoskeleton associated protein 2///immunoglobulin lambda variable cluster///immunoglobulin lambda constant 1
SNAPC1	1.39621784	2.63	6.68E-11	9.25E-13	SNAPC1	small nuclear RNA activating complex polypeptide 1
CLEC7A	1.3932633	2.63	3.03E-07	2.02E-08	CLEC7A	C-type lectin domain family 7 member A
LOXL1	1.39049069	2.62	3.56E-09	1.12E-10	LOXL1	lysyl oxidase like 1
SLC16A1	1.38706055	2.62	3.27E-07	2.22E-08	SLC16A1	solute carrier family 16 member 1
MLF1	1.384951	2.61	8.14E-08	4.41E-09	MLF1	myeloid leukemia factor 1
LUM	1.38415184	2.61	8.06E-09	2.98E-10	LUM	lumican
STEAP1B	1.38238419	2.61	1.83E-07	1.13E-08	STEAP1B	STEAP family member 1B
ATF3	1.38013616	2.60	2.54E-04	4.73E-05	ATF3	activating transcription factor 3
IGLL5	1.37865654	2.60	5.64E-06	5.99E-07	IGLL5	immunoglobulin lambda like polypeptide 5
E2F7	1.3777747	2.60	2.39E-09	6.92E-11	E2F7	E2F transcription factor 7
COL6A3	1.37690672	2.60	7.90E-11	1.14E-12	COL6A3	collagen type VI alpha 3 chain
NEK2	1.37685515	2.60	2.53E-09	7.35E-11	NEK2	NIMA related kinase 2
TMEM163	1.37413264	2.59	4.16E-05	5.96E-06	TMEM163	transmembrane protein 163
BST2	1.37397992	2.59	1.86E-05	2.35E-06	BST2	bone marrow stromal cell antigen 2

CCDC144NL-AS1	1.37135444	2.59	1.16E-04	1.92E-05	CCDC144NL-AS1	CCDC144NL antisense RNA 1
RRM2	1.3703004	2.59	2.03E-10	3.75E-12	RRM2	ribonucleotide reductase regulatory subunit M2
COL27A1	1.37025693	2.59	5.03E-09	1.72E-10	COL27A1	collagen type XXVII alpha 1 chain
NCBP2	1.36859192	2.58	1.35E-12	6.68E-15	NCBP2	nuclear cap binding protein subunit 2
NUF2	1.36782809	2.58	1.03E-08	3.98E-10	NUF2	NUF2, NDC80 kinetochore complex component
SLC38A6	1.36612635	2.58	1.11E-11	9.82E-14	SLC38A6	solute carrier family 38 member 6
LILRB2	1.36563316	2.58	1.44E-10	2.44E-12	LILRB2	leukocyte immunoglobulin like receptor B2
HAVCR2	1.36503192	2.58	4.79E-09	1.61E-10	HAVCR2	hepatitis A virus cellular receptor 2
CEP55	1.3635746	2.57	4.52E-11	5.70E-13	CEP55	centrosomal protein 55
MICB	1.36289731	2.57	1.46E-07	8.69E-09	MICB	MHC class I polypeptide-related sequence B
CYP27B1	1.36233026	2.57	6.98E-09	2.51E-10	CYP27B1	cytochrome P450 family 27 subfamily B member 1
POU2AF1	1.3619357	2.57	1.26E-04	2.11E-05	POU2AF1	POU class 2 associating factor 1
ALCAM	1.36185159	2.57	1.58E-07	9.55E-09	ALCAM	activated leukocyte cell adhesion molecule
HSPH1	1.36175355	2.57	3.05E-04	5.83E-05	HSPH1	heat shock protein family H (Hsp110) member 1
CCDC190	1.35974937	2.57	1.89E-03	4.78E-04	CCDC190	coiled-coil domain containing 190
TLR2	1.359617	2.57	1.25E-10	2.05E-12	TLR2	toll like receptor 2
IL1B	1.35876869	2.56	3.95E-06	3.97E-07	IL1B	interleukin 1 beta
OASL	1.35818525	2.56	8.08E-07	6.37E-08	OASL	2'-5'-oligoadenylate synthetase like
NEFL	1.35740172	2.56	1.65E-02	5.95E-03	NEFL	neurofilament, light polypeptide
DLGAP5	1.35565746	2.56	2.86E-09	8.51E-11	DLGAP5	DLG associated protein 5
SHOX2	1.35565424	2.56	9.97E-08	5.61E-09	SHOX2	short stature homeobox 2
HOXD10	1.3550209	2.56	1.32E-09	3.41E-11	HOXD10	homeobox D10
MNDA	1.35490545	2.56	6.95E-07	5.34E-08	MNDA	myeloid cell nuclear differentiation antigen
DCBLD1	1.35451019	2.56	3.64E-11	4.37E-13	DCBLD1	discoidin, CUB and LCCL domain containing 1
GPR158	1.35445048	2.56	1.06E-06	8.71E-08	GPR158	G protein-coupled receptor 158
LEMD1	1.35318783	2.55	2.18E-06	2.00E-07	LEMD1	LEM domain containing 1
FST	1.3531197	2.55	3.13E-05	4.28E-06	FST	follistatin
DLX2	1.35263936	2.55	9.55E-07	7.73E-08	DLX2	distal-less homeobox 2
IGLJ3///CKAP2	1.35171152	2.55	3.78E-06	3.78E-07	IGLJ3///CKAP2	immunoglobulin lambda joining 3///cytoskeleton associated protein 2
SIX4	1.35147374	2.55	2.00E-10	3.67E-12	SIX4	SIX homeobox 4
VNN1	1.35137764	2.55	8.65E-04	1.93E-04	VNN1	vanin 1
FAM26F	1.34961108	2.55	5.71E-06	6.08E-07	FAM26F	family with sequence similarity 26 member F
PLAUR	1.34956891	2.55	7.03E-11	9.90E-13	PLAUR	plasminogen activator, urokinase receptor
SNX5	1.3495607	2.55	4.24E-11	5.30E-13	SNX5	sorting nexin 5
ADAM12	1.34933715	2.55	7.54E-11	1.08E-12	ADAM12	ADAM metallopeptidase domain 12
IGF2BP3	1.34815394	2.55	1.56E-04	2.71E-05	IGF2BP3	insulin like growth factor 2 mRNA binding protein 3
FCRL5	1.34645944	2.54	3.04E-07	2.03E-08	FCRL5	Fc receptor like 5
CDH11	1.34632234	2.54	3.71E-07	2.57E-08	CDH11	cadherin 11

DUXAP10	1.34611287	2.54	1.68E-06	1.49E-07	<i>DUXAP10</i>	double homeobox A pseudogene 10
STC2	1.34536302	2.54	3.89E-14	5.55E-17	<i>STC2</i>	stanniocalcin 2
LAIR2	1.34394221	2.54	3.39E-08	1.58E-09	<i>LAIR2</i>	leukocyte associated immunoglobulin like receptor 2
IGKV1OR2-118	1.34275075	2.54	2.14E-06	1.96E-07	<i>IGKV1OR2-118</i>	immunoglobulin kappa variable 1/OR2-118 (pseudogene)
DTL	1.33870759	2.53	3.75E-09	1.19E-10	<i>DTL</i>	denticleless E3 ubiquitin protein ligase homolog
FAM26F	1.33867239	2.53	1.16E-06	9.73E-08	<i>FAM26F</i>	family with sequence similarity 26 member F
SAA2///SAA1	1.33859729	2.53	6.52E-05	9.97E-06	<i>SAA2///SAA1</i>	serum amyloid A2///serum amyloid A1
TENM2	1.33796026	2.53	4.96E-04	1.02E-04	<i>TENM2</i>	teneurin transmembrane protein 2
MAGEA2B///MAGEA2	1.33621121	2.52	1.65E-03	4.08E-04	<i>MAGEA2B///MAGEA2</i>	MAGE family member A2B///MAGE family member A2
THBS1	1.33571638	2.52	3.13E-05	4.26E-06	<i>THBS1</i>	thrombospondin 1
AURKA	1.33454251	2.52	1.62E-11	1.59E-13	<i>AURKA</i>	aurora kinase A
SLC6A14	1.33449611	2.52	5.75E-03	1.72E-03	<i>SLC6A14</i>	solute carrier family 6 member 14
AGMAT	1.33337569	2.52	6.22E-07	4.68E-08	<i>AGMAT</i>	agmatinase
SNORA11E///SNORA11D///MAGED4///MAGED4B	1.33319113	2.52	2.61E-10	5.06E-12	<i>SNORA11E///SNORA11D///MAGED4///MAGED4B</i>	small nucleolar RNA, H/ACA box 11E///small nucleolar RNA, H/ACA box 11D///MAGE family member D4///MAGE family member D4B
MND1	1.33261384	2.52	6.64E-08	3.48E-09	<i>MND1</i>	meiotic nuclear divisions 1
WISP1	1.33155382	2.52	2.66E-14	3.21E-17	<i>WISP1</i>	WNT1 inducible signaling pathway protein 1
CD14	1.33082402	2.52	2.79E-07	1.83E-08	<i>CD14</i>	CD14 molecule
LY6E	1.33017104	2.51	1.08E-08	4.19E-10	<i>LY6E</i>	lymphocyte antigen 6 complex, locus E
ASPM	1.32997475	2.51	5.51E-09	1.90E-10	<i>ASPM</i>	abnormal spindle microtubule assembly
DLX4	1.32960245	2.51	4.08E-08	1.97E-09	<i>DLX4</i>	distal-less homeobox 4
LOC440934	1.32816354	2.51	7.22E-05	1.12E-05	<i>LOC440934</i>	uncharacterized LOC440934
BUB1	1.32750945	2.51	3.72E-10	7.64E-12	<i>BUB1</i>	BUB1 mitotic checkpoint serine/threonine kinase
EPCAM	1.32710682	2.51	1.97E-04	3.53E-05	<i>EPCAM</i>	epithelial cell adhesion molecule
BAMBI	1.32613588	2.51	3.41E-06	3.35E-07	<i>BAMBI</i>	BMP and activin membrane bound inhibitor
IDO1	1.32531753	2.51	6.55E-05	1.00E-05	<i>IDO1</i>	indoleamine 2,3-dioxygenase 1
CD86	1.32517284	2.51	3.32E-07	2.26E-08	<i>CD86</i>	CD86 molecule
KYNU	1.32404595	2.50	2.40E-06	2.24E-07	<i>KYNU</i>	kynureninase
RARRES1	1.32166737	2.50	1.79E-04	3.16E-05	<i>RARRES1</i>	retinoic acid receptor responder 1
STIL	1.32143895	2.50	2.11E-11	2.25E-13	<i>STIL</i>	SCL/TAL1 interrupting locus
HIST2H2AA4///HIST2H2AA3	1.3205031	2.50	1.13E-06	9.36E-08	<i>HIST2H2AA4///HIST2H2AA3</i>	histone cluster 2, H2aa4///histone cluster 2, H2aa3
RSRC1	1.31823524	2.49	2.95E-09	8.85E-11	<i>RSRC1</i>	arginine and serine rich coiled-coil 1
DPYSL3	1.31735453	2.49	2.54E-10	4.87E-12	<i>DPYSL3</i>	dihydropyrimidinase like 3
HOMER3	1.31392879	2.49	4.04E-13	1.30E-15	<i>HOMER3</i>	homer scaffolding protein 3
FMNL2	1.31265172	2.48	5.48E-11	7.14E-13	<i>FMNL2</i>	formin like 2
CST4	1.31061176	2.48	2.46E-08	1.08E-09	<i>CST4</i>	cystatin S

CKS1B	1.309031	2.48	1.15E-11	1.04E-13	<i>CKS1B</i>	CDC28 protein kinase regulatory subunit 1B
KIF4A	1.30900253	2.48	5.67E-11	7.41E-13	<i>KIF4A</i>	kinesin family member 4A
ETS1	1.30872713	2.48	1.63E-07	9.91E-09	<i>ETS1</i>	ETS proto-oncogene 1, transcription factor
NETO2	1.30649235	2.47	8.59E-09	3.21E-10	<i>NETO2</i>	neuropilin and tolloid like 2
SRGN	1.30517761	2.47	1.15E-06	9.59E-08	<i>SRGN</i>	serglycin
EGR3	1.30421166	2.47	9.90E-05	1.61E-05	<i>EGR3</i>	early growth response 3
MMP19	1.30370659	2.47	1.12E-12	4.87E-15	<i>MMP19</i>	matrix metalloproteinase 19
CENPN	1.30368576	2.47	9.54E-08	5.32E-09	<i>CENPN</i>	centromere protein N
POPDC3	1.30338743	2.47	4.67E-04	9.48E-05	<i>POPDC3</i>	popeye domain containing 3
TYROBP	1.30224753	2.47	1.45E-07	8.61E-09	<i>TYROBP</i>	TYRO protein tyrosine kinase binding protein
ALOX12B	1.30042414	2.46	1.23E-03	2.90E-04	<i>ALOX12B</i>	arachidonate 12-lipoxygenase, 12R type
SLC35F6//CENPA	1.30040179	2.46	2.94E-10	5.80E-12	<i>SLC35F6//CENPA</i>	solute carrier family 35 member F6//centromere protein A
IL1RAP	1.30001027	2.46	1.58E-08	6.54E-10	<i>IL1RAP</i>	interleukin 1 receptor accessory protein
LY96	1.29116858	2.45	8.56E-10	2.05E-11	<i>LY96</i>	lymphocyte antigen 96
MELTF	1.28916408	2.44	7.87E-10	1.87E-11	<i>MELTF</i>	melanotransferrin
NEK6	1.28886637	2.44	8.06E-11	1.17E-12	<i>NEK6</i>	NIMA related kinase 6
MIR21//VMP1	1.28815977	2.44	1.37E-08	5.52E-10	<i>MIR21//VMP1</i>	microRNA 21//vacuole membrane protein 1
LRP12	1.28805881	2.44	1.45E-09	3.82E-11	<i>LRP12</i>	LDL receptor related protein 12
RUVBL1	1.28649486	2.44	6.06E-11	8.08E-13	<i>RUVBL1</i>	RuvB like AAA ATPase 1
MRGBP	1.28588334	2.44	2.62E-14	3.09E-17	<i>MRGBP</i>	MRG/MORF4L binding protein
KRT75	1.28498442	2.44	2.28E-06	2.10E-07	<i>KRT75</i>	keratin 75
NCK1-AS1	1.28496019	2.44	8.83E-11	1.32E-12	<i>NCK1-AS1</i>	NCK1 antisense RNA 1 (head to head)
EXT1	1.28491829	2.44	9.41E-13	3.77E-15	<i>EXT1</i>	exostosin glycosyltransferase 1
MIR7112//BOP1	1.28461816	2.44	2.61E-10	5.05E-12	<i>MIR7112//BOP1</i>	microRNA 7112//block of proliferation 1
GLIPR1	1.2842962	2.44	7.00E-08	3.72E-09	<i>GLIPR1</i>	GLI pathogenesis related 1
CD84	1.28403266	2.44	3.61E-05	5.04E-06	<i>CD84</i>	CD84 molecule
CD300LF	1.28388435	2.43	3.04E-08	1.39E-09	<i>CD300LF</i>	CD300 molecule like family member f
RAB31	1.28350576	2.43	3.82E-08	1.82E-09	<i>RAB31</i>	RAB31, member RAS oncogene family
FST	1.28273787	2.43	2.43E-07	1.56E-08	<i>FST</i>	follistatin
DFNA5	1.28250727	2.43	4.70E-07	3.39E-08	<i>DFNA5</i>	DFNA5, deafness associated tumor suppressor
DLX1	1.28112959	2.43	2.63E-06	2.47E-07	<i>DLX1</i>	distal-less homeobox 1
NMRAL1P1	1.27915153	2.43	1.57E-03	3.86E-04	<i>NMRAL1P1</i>	NmrA like redox sensor 1 pseudogene 1
MIR4454//ESRG	1.27795851	2.42	2.81E-03	7.52E-04	<i>MIR4454//ESRG</i>	microRNA 4454//embryonic stem cell related (non-protein coding)
SLC1A4	1.27551797	2.42	4.00E-09	1.29E-10	<i>SLC1A4</i>	solute carrier family 1 member 4
FOXM1	1.27469288	2.42	3.22E-11	3.72E-13	<i>FOXM1</i>	forkhead box M1
CENPW	1.27460983	2.42	1.25E-07	7.26E-09	<i>CENPW</i>	centromere protein W
EPPK1	1.27391903	2.42	1.59E-06	1.40E-07	<i>EPPK1</i>	epiplakin 1

CHEK1	1.27328326	2.42	1.79E-10	3.19E-12	CHEK1	checkpoint kinase 1
KIF2C	1.2732609	2.42	2.50E-12	1.51E-14	KIF2C	kinesin family member 2C
PRR11	1.27151763	2.41	6.99E-11	9.80E-13	PRR11	proline rich 11
VCAN	1.27109014	2.41	6.68E-07	5.09E-08	VCAN	versican
IRF6	1.26838781	2.41	3.78E-09	1.21E-10	IRF6	interferon regulatory factor 6
SLCO1B3	1.26779049	2.41	3.43E-03	9.43E-04	SLCO1B3	solute carrier organic anion transporter family member 1B3
IL11	1.26778855	2.41	3.44E-09	1.07E-10	IL11	interleukin 11
EGFL6	1.26676911	2.41	2.22E-09	6.36E-11	EGFL6	EGF like domain multiple 6
CYP27C1	1.26587378	2.40	2.44E-06	2.27E-07	CYP27C1	cytochrome P450 family 27 subfamily C member 1
COL4A2	1.2646975	2.40	4.99E-12	3.55E-14	COL4A2	collagen type IV alpha 2 chain
LOC101928615//FNDC3B	1.26373827	2.40	5.79E-09	2.01E-10	LOC101928615//FNDC3B	uncharacterized LOC101928615//fibronectin type III domain containing 3B
TNS4	1.26208552	2.40	1.15E-07	6.57E-09	TNS4	tensin 4
XAF1	1.26181731	2.40	1.26E-05	1.51E-06	XAF1	XIAP associated factor 1
MIR1182//FAM89A	1.26168076	2.40	2.12E-11	2.27E-13	MIR1182//FAM89A	microRNA 1182//family with sequence similarity 89 member A
LINC00491	1.25983142	2.39	6.72E-12	5.26E-14	LINC00491	long intergenic non-protein coding RNA 491
FPR3	1.25980603	2.39	2.39E-08	1.05E-09	FPR3	formyl peptide receptor 3
COL8A1	1.25816986	2.39	2.61E-06	2.46E-07	COL8A1	collagen type VIII alpha 1 chain
JPH1	1.25680888	2.39	1.60E-07	9.67E-09	JPH1	junctophilin 1
FZD2	1.25665523	2.39	8.96E-12	7.55E-14	FZD2	frizzled class receptor 2
CCNE2	1.25542266	2.39	1.86E-08	7.85E-10	CCNE2	cyclin E2
MTFR2	1.25389776	2.38	1.80E-12	9.65E-15	MTFR2	mitochondrial fission regulator 2
LOC101928173	1.25219418	2.38	3.76E-11	4.54E-13	LOC101928173	uncharacterized LOC101928173
CYBB	1.25207237	2.38	3.47E-09	1.08E-10	CYBB	cytochrome b-245 beta chain
THBS1	1.25044629	2.38	9.78E-08	5.48E-09	THBS1	thrombospondin 1
IGKC	1.24867815	2.38	7.56E-08	4.06E-09	IGKC	immunoglobulin kappa constant
APOE	1.24825465	2.38	8.19E-08	4.45E-09	APOE	apolipoprotein E
BIRC5	1.24765904	2.37	8.70E-11	1.29E-12	BIRC5	baculoviral IAP repeat containing 5
SOAT1	1.2474379	2.37	2.21E-07	1.40E-08	SOAT1	sterol O-acyltransferase 1
WDHD1	1.24711509	2.37	7.52E-12	6.04E-14	WDHD1	WD repeat and HMG-box DNA binding protein 1
IFI35	1.24685368	2.37	2.28E-09	6.55E-11	IFI35	interferon induced protein 35
IFI44	1.24624173	2.37	5.87E-06	6.29E-07	IFI44	interferon induced protein 44
GRB10	1.24578181	2.37	3.77E-11	4.56E-13	GRB10	growth factor receptor bound protein 10
IBSP	1.24449147	2.37	7.94E-09	2.93E-10	IBSP	integrin binding sialoprotein
CENPN	1.2442186	2.37	7.22E-10	1.69E-11	CENPN	centromere protein N
LRRC8D	1.2430847	2.37	5.15E-14	8.25E-17	LRRC8D	leucine rich repeat containing 8 family member D
WDHD1	1.24259478	2.37	6.11E-11	8.20E-13	WDHD1	WD repeat and HMG-box DNA binding protein 1
LOC105379362	1.24106894	2.36	2.93E-06	2.80E-07	LOC105379362	uncharacterized LOC105379362

DNAH17	1.24067642	2.36	8.91E-06	1.01E-06	<i>DNAH17</i>	dynein axonemal heavy chain 17
EIF5A2	1.23917039	2.36	5.19E-10	1.13E-11	<i>EIF5A2</i>	eukaryotic translation initiation factor 5A2
APOL1	1.23798888	2.36	2.32E-06	2.14E-07	<i>APOL1</i>	apolipoprotein L1
CXCL2	1.23786152	2.36	3.74E-03	1.04E-03	<i>CXCL2</i>	C-X-C motif chemokine ligand 2
THBS2	1.23675911	2.36	4.39E-07	3.13E-08	<i>THBS2</i>	thrombospondin 2
SLC20A1	1.23620358	2.36	6.79E-06	7.45E-07	<i>SLC20A1</i>	solute carrier family 20 member 1
MYO1B	1.23578361	2.36	7.11E-11	1.01E-12	<i>MYO1B</i>	myosin IB
TREM2	1.23544553	2.35	2.75E-10	5.39E-12	<i>TREM2</i>	triggering receptor expressed on myeloid cells 2
ORC6	1.23450436	2.35	6.43E-12	4.88E-14	<i>ORC6</i>	origin recognition complex subunit 6
ZFAS1	1.23339841	2.35	9.16E-12	7.79E-14	<i>ZFAS1</i>	ZNF1 antisense RNA 1
CENPF	1.23212307	2.35	1.50E-10	2.55E-12	<i>CENPF</i>	centromere protein F
PNKD	1.22861467	2.34	6.87E-08	3.63E-09	<i>PNKD</i>	paroxysmal nonkinesigenic dyskinesia
ESCO2	1.22815649	2.34	2.29E-08	9.93E-10	<i>ESCO2</i>	establishment of sister chromatid cohesion N-acetyltransferase 2
BASP1	1.22791246	2.34	5.96E-10	1.34E-11	<i>BASP1</i>	brain abundant membrane attached signal protein 1
CTSK	1.22782643	2.34	2.71E-08	1.21E-09	<i>CTSK</i>	cathepsin K
SLC16A1	1.22726501	2.34	1.23E-07	7.11E-09	<i>SLC16A1</i>	solute carrier family 16 member 1
RAI14	1.226234	2.34	2.95E-12	1.82E-14	<i>RAI14</i>	retinoic acid induced 14
H1FX	1.22621447	2.34	3.73E-08	1.78E-09	<i>H1FX</i>	H1 histone family member X
SLC25A32	1.22573448	2.34	7.09E-13	2.58E-15	<i>SLC25A32</i>	solute carrier family 25 member 32
LINC00673///LINC00511	1.22417022	2.34	2.02E-09	5.69E-11	<i>LINC00673///LINC00511</i>	long intergenic non-protein coding RNA 673///long intergenic non-protein coding RNA 511
COL7A1	1.22403926	2.34	1.90E-07	1.18E-08	<i>COL7A1</i>	collagen type VII alpha 1 chain
THEMIS2	1.22372033	2.34	4.33E-09	1.42E-10	<i>THEMIS2</i>	thymocyte selection associated family member 2
LPL	1.22279301	2.33	6.68E-05	1.03E-05	<i>LPL</i>	lipoprotein lipase
ASXL1	1.22273131	2.33	1.19E-12	5.43E-15	<i>ASXL1</i>	additional sex combs like 1, transcriptional regulator
TRA2B	1.22258445	2.33	1.19E-10	1.92E-12	<i>TRA2B</i>	transformer 2 beta homolog (Drosophila)
LIPG	1.21900898	2.33	1.94E-07	1.21E-08	<i>LIPG</i>	lipase G, endothelial type
TMEM132A	1.216565	2.32	2.00E-10	3.66E-12	<i>TMEM132A</i>	transmembrane protein 132A
CKAP2///IGLC1	1.21506137	2.32	1.35E-04	2.29E-05	<i>CKAP2///IGLC1</i>	cytoskeleton associated protein 2///immunoglobulin lambda constant 1
TAPBP	1.21358581	2.32	1.64E-07	1.00E-08	<i>TAPBP</i>	TAP binding protein (tapasin)
CALB1	1.21357629	2.32	7.91E-04	1.74E-04	<i>CALB1</i>	calbindin 1
SPC25	1.21227749	2.32	1.16E-08	4.56E-10	<i>SPC25</i>	SPC25, NDC80 kinetochore complex component
CLEC7A	1.21026876	2.31	2.71E-09	7.97E-11	<i>CLEC7A</i>	C-type lectin domain family 7 member A
ASPN	1.2101166	2.31	9.51E-07	7.69E-08	<i>ASPN</i>	asporin

FAM72A///FAM72D///FAM72B///FAM72C	1.20929146	2.31	2.94E-09	8.83E-11	FAM72A///FAM72D///FAM72B///FAM72C	family with sequence similarity 72 member A///family with sequence similarity 72 member D///family with sequence similarity 72 member B///family with sequence similarity 72 member C
PPFIA1	1.20896824	2.31	3.03E-06	2.92E-07	PPFIA1	PTPRF interacting protein alpha 1
ANKRD36BP2	1.20893036	2.31	4.34E-04	8.72E-05	ANKRD36BP2	ankyrin repeat domain 36B pseudogene 2
KIF20A	1.20839851	2.31	7.33E-10	1.72E-11	KIF20A	kinesin family member 20A
MELTF	1.20760959	2.31	1.06E-08	4.10E-10	MELTF	melanotransferrin
MZB1	1.20690039	2.31	1.65E-06	1.46E-07	MZB1	marginal zone B and B1 cell specific protein
XCL2///XCL1	1.2068187	2.31	5.99E-11	7.96E-13	XCL2///XCL1	X-C motif chemokine ligand 2///X-C motif chemokine ligand 1
PLEKHG4B	1.20631264	2.31	3.53E-07	2.42E-08	PLEKHG4B	pleckstrin homology and RhoGEF domain containing G4B
MIR6741///PYCR2	1.20560025	2.31	8.74E-08	4.80E-09	MIR6741///PYCR2	microRNA 6741///pyrroline-5-carboxylate reductase family member 2
TNC	1.204723	2.30	1.25E-05	1.49E-06	TNC	tenascin C
ANP32E	1.20331694	2.30	5.19E-10	1.14E-11	ANP32E	acidic nuclear phosphoprotein 32 family member E
B2M	1.20270824	2.30	7.08E-07	5.46E-08	B2M	beta-2-microglobulin
FCRL5	1.20056114	2.30	2.54E-06	2.38E-07	FCRL5	Fc receptor like 5
CD38	1.20047665	2.30	1.21E-09	3.09E-11	CD38	CD38 molecule
SELL	1.19987983	2.30	2.85E-05	3.83E-06	SELL	selectin L
SLC1A4	1.19966384	2.30	3.01E-09	9.09E-11	SLC1A4	solute carrier family 1 member 4
HCK	1.19966373	2.30	1.16E-10	1.84E-12	HCK	HCK proto-oncogene, Src family tyrosine kinase
ANOS1	1.19905231	2.30	5.06E-07	3.68E-08	ANOS1	anosmin 1
IGHV4-31///IGHM///IGHG3///IGHG2///IGHG1///IGHD///IGHA2///IGHA1///IGH	1.19895552	2.30	6.34E-06	6.88E-07	IGHV4-31///IGHM///IGHG3///IGHG2///IGHG1///IGHD///IGHA2///IGHA1///IGH	immunoglobulin heavy variable 4-31///immunoglobulin heavy constant mu///immunoglobulin heavy constant gamma 3 (G3m marker)//immunoglobulin heavy constant gamma 2 (G2m marker)//immunoglobulin heavy constant gamma 1 (G1m marker)//immunoglobulin heavy constant delta//immunoglobulin heavy constant alpha 2 (A2m marker)//immunoglobulin heavy constant alpha 1//immunoglobulin heavy locus
LRP12	1.19820157	2.29	3.08E-06	2.97E-07	LRP12	LDL receptor related protein 12
CHST11	1.1974612	2.29	6.48E-10	1.49E-11	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11
CECR2	1.19717297	2.29	2.80E-05	3.74E-06	CECR2	CECR2, histone acetyllysine reader
PIGX	1.19657529	2.29	1.39E-09	3.66E-11	PIGX	phosphatidylinositol glycan anchor biosynthesis class X

RTP4	1.19652264	2.29	8.48E-06	9.59E-07	RTP4	receptor transporter protein 4
CENPM	1.19642415	2.29	2.05E-12	1.17E-14	CENPM	centromere protein M
OSM	1.1962542	2.29	1.63E-08	6.76E-10	OSM	oncostatin M
C6orf62	1.19520792	2.29	5.16E-10	1.12E-11	C6orf62	chromosome 6 open reading frame 62
PPFIA1	1.19431463	2.29	1.16E-06	9.71E-08	PPFIA1	PTPRF interacting protein alpha 1
CCL8	1.19333531	2.29	6.32E-04	1.34E-04	CCL8	C-C motif chemokine ligand 8
TK1	1.19206505	2.28	1.97E-12	1.10E-14	TK1	thymidine kinase 1
BRMS1L	1.19182942	2.28	1.69E-07	1.04E-08	BRMS1L	breast cancer metastasis-suppressor 1-like
MMP7	1.19181681	2.28	1.71E-03	4.26E-04	MMP7	matrix metalloproteinase 7
TEAD4	1.19178325	2.28	1.77E-11	1.77E-13	TEAD4	TEA domain transcription factor 4
CCR1	1.1905813	2.28	5.49E-08	2.80E-09	CCR1	C-C motif chemokine receptor 1
GNLY	1.18851879	2.28	5.48E-06	5.80E-07	GNLY	granulysin
IFI44L	1.18816847	2.28	1.01E-03	2.32E-04	IFI44L	interferon induced protein 44 like
CHST11	1.18710237	2.28	1.39E-09	3.66E-11	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11
BMP7	1.18605202	2.28	2.82E-04	5.34E-05	BMP7	bone morphogenetic protein 7
NCEH1	1.18588064	2.28	3.35E-06	3.28E-07	NCEH1	neutral cholesterol ester hydrolase 1
PMEPA1	1.18538341	2.27	1.09E-08	4.24E-10	PMEPA1	prostate transmembrane protein, androgen induced 1
LAPTM4B	1.18514327	2.27	5.13E-11	6.60E-13	LAPTM4B	lysosomal protein transmembrane 4 beta
LSG1	1.18335325	2.27	3.78E-10	7.79E-12	LSG1	large 60S subunit nuclear export GTPase 1
ESM1	1.18233085	2.27	2.82E-08	1.27E-09	ESM1	endothelial cell specific molecule 1
IGHD	1.18227407	2.27	1.63E-06	1.44E-07	IGHD	immunoglobulin heavy constant delta
SPAG5	1.18154812	2.27	3.99E-12	2.66E-14	SPAG5	sperm associated antigen 5
SLC1A4	1.18127318	2.27	1.99E-09	5.58E-11	SLC1A4	solute carrier family 1 member 4
PLXNC1	1.181141	2.27	1.26E-07	7.28E-09	PLXNC1	plexin C1
GOLIM4	1.18011067	2.27	1.21E-03	2.84E-04	GOLIM4	golgi integral membrane protein 4
ATP6V1C1	1.17980406	2.27	1.09E-11	9.60E-14	ATP6V1C1	ATPase H+ transporting V1 subunit C1
CDC6	1.17854531	2.26	5.09E-11	6.53E-13	CDC6	cell division cycle 6
RAD51AP1	1.17809547	2.26	2.95E-09	8.87E-11	RAD51AP1	RAD51 associated protein 1
XCL1	1.17785639	2.26	5.88E-12	4.41E-14	XCL1	X-C motif chemokine ligand 1
CCDC88A	1.17744569	2.26	4.77E-04	9.71E-05	CCDC88A	coiled-coil domain containing 88A
GNLY	1.17730346	2.26	1.84E-06	1.65E-07	GNLY	granulysin
FMNL2	1.17724252	2.26	1.73E-06	1.54E-07	FMNL2	formin like 2
MFHAS1	1.17700626	2.26	1.89E-11	1.94E-13	MFHAS1	malignant fibrous histiocytoma amplified sequence 1
MTHFD2	1.17659458	2.26	3.55E-12	2.29E-14	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methylenetetrahydrofolate cyclohydrolase
HSP90AA1	1.17504487	2.26	1.62E-03	3.98E-04	HSP90AA1	heat shock protein 90 alpha family class A member 1
COTL1	1.17369816	2.26	3.56E-09	1.12E-10	COTL1	coactosin like F-actin binding protein 1

APOE	1.17324897	2.26	1.75E-05	2.20E-06	APOE	apolipoprotein E
NMB	1.1725349	2.25	5.02E-07	3.64E-08	NMB	neuromedin B
PGF	1.17211392	2.25	1.53E-08	6.28E-10	PGF	placental growth factor
MIR155///MIR155HG	1.17207103	2.25	4.81E-05	7.04E-06	MIR155///MIR155HG	microRNA 155///MIR155 host gene
KIF18B	1.16925359	2.25	1.27E-11	1.17E-13	KIF18B	kinesin family member 18B
STK17B	1.16896268	2.25	3.63E-09	1.15E-10	STK17B	serine/threonine kinase 17b
HEY1	1.16768442	2.25	7.93E-07	6.23E-08	HEY1	hes related family bHLH transcription factor with YRPW motif 1
SLC39A14	1.16752149	2.25	2.93E-07	1.95E-08	SLC39A14	solute carrier family 39 member 14
CTSL	1.1672545	2.25	7.33E-10	1.72E-11	CTSL	cathepsin L
SIK1	1.16625326	2.24	1.94E-05	2.46E-06	SIK1	salt inducible kinase 1
TAP1	1.16600813	2.24	3.74E-08	1.78E-09	TAP1	transporter 1, ATP binding cassette subfamily B member
HELLS	1.16578634	2.24	4.23E-09	1.38E-10	HELLS	helicase, lymphoid-specific
ENPEP	1.16557734	2.24	9.15E-08	5.08E-09	ENPEP	glutamyl aminopeptidase
FAM26F	1.16504887	2.24	2.46E-05	3.24E-06	FAM26F	family with sequence similarity 26 member F
PLD3	1.16375255	2.24	5.30E-08	2.69E-09	PLD3	phospholipase D family member 3
KNL1	1.16359018	2.24	4.54E-09	1.51E-10	KNL1	kinetochore scaffold 1
LOC101928100	1.16341901	2.24	7.77E-06	8.70E-07	LOC101928100	uncharacterized LOC101928100
IGK///IGKC	1.16338728	2.24	6.95E-05	1.07E-05	IGK///IGKC	immunoglobulin kappa locus///immunoglobulin kappa constant
LOC102724714	1.16285481	2.24	1.86E-03	4.70E-04	LOC102724714	uncharacterized LOC102724714
IFI27	1.1622728	2.24	6.57E-04	1.40E-04	IFI27	interferon alpha inducible protein 27
LOC100129518///SOD2	1.16204897	2.24	4.11E-08	1.99E-09	LOC100129518///SOD2	uncharacterized LOC100129518///superoxide dismutase 2, mitochondrial
TP63	1.16156077	2.24	8.01E-05	1.26E-05	TP63	tumor protein p63
U2SURP	1.16154444	2.24	1.50E-10	2.56E-12	U2SURP	U2 snRNP associated SURP domain containing
DUSP2	1.16069285	2.24	8.57E-08	4.69E-09	DUSP2	dual specificity phosphatase 2
CTTN	1.16005434	2.23	7.49E-05	1.17E-05	CTTN	cortactin
IGHV4-31///IGHM///IGHG4///IGHG3///IGHG1///IGHD///IGHA2///IGHA1///IGH	1.15854687	2.23	3.74E-08	1.78E-09	IGHV4-31///IGHM///IGHG4///IGHG3///IGHG1///IGHD///IGHA2///IGHA1///IGH	immunoglobulin heavy variable 4-31///immunoglobulin heavy constant mu///immunoglobulin heavy constant gamma 4 (G4m marker)//immunoglobulin heavy constant gamma 3 (G3m marker)//immunoglobulin heavy constant gamma 1 (G1m marker)//immunoglobulin heavy constant delta//immunoglobulin heavy constant alpha 2 (A2m marker)//immunoglobulin heavy constant alpha 1//immunoglobulin heavy locus
DOK3	1.15766046	2.23	2.21E-07	1.40E-08	DOK3	docking protein 3

ZNF281	1.15704354	2.23	1.68E-09	4.55E-11	ZNF281	zinc finger protein 281
HIST2H2AAA4///HIST2H2AA3	1.15675629	2.23	2.98E-07	1.98E-08	HIST2H2AAA4///HIST2H2AA3	histone cluster 2, H2aa4///histone cluster 2, H2aa3
MSANTD3-TMEFF1///TMEFF1	1.15650848	2.23	1.41E-08	5.70E-10	MSANTD3-TMEFF1///TMEFF1	MSANTD3-TMEFF1 readthrough///transmembrane protein with EGF like and two follistatin like domains 1
EPST11	1.15583568	2.23	3.19E-06	3.10E-07	EPST11	epithelial stromal interaction 1 (breast)
AURKB	1.15554612	2.23	1.61E-10	2.81E-12	AURKB	aurora kinase B
KLHL6	1.1537422	2.22	3.91E-05	5.55E-06	KLHL6	kelch like family member 6
FSCN1	1.15346498	2.22	2.27E-11	2.46E-13	FSCN1	fascin actin-bundling protein 1
ARPC1B	1.15345153	2.22	2.35E-10	4.45E-12	ARPC1B	actin related protein 2/3 complex subunit 1B
MET	1.15331268	2.22	1.44E-10	2.43E-12	MET	MET proto-oncogene, receptor tyrosine kinase
JAK3	1.15294831	2.22	5.18E-07	3.79E-08	JAK3	Janus kinase 3
TOP2A	1.15275948	2.22	3.88E-09	1.24E-10	TOP2A	topoisomerase (DNA) II alpha
ACTL6A	1.15209945	2.22	4.47E-08	2.20E-09	ACTL6A	actin like 6A
HSPD1	1.1517117	2.22	5.91E-03	1.78E-03	HSPD1	heat shock protein family D (Hsp60) member 1
SLC25A37	1.1513687	2.22	1.00E-06	8.17E-08	SLC25A37	solute carrier family 25 member 37
CDCA5	1.15087073	2.22	3.52E-13	1.07E-15	CDCA5	cell division cycle associated 5
MLLT11	1.14957468	2.22	6.81E-07	5.21E-08	MLLT11	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 11
ERF	1.14946362	2.22	2.61E-09	7.65E-11	ERF	ETS2 repressor factor
IL21R	1.14850233	2.22	1.51E-07	9.03E-09	IL21R	interleukin 21 receptor
CDK1	1.14710346	2.21	2.89E-08	1.31E-09	CDK1	cyclin dependent kinase 1
FAM19A5	1.14600319	2.21	4.91E-06	5.11E-07	FAM19A5	family with sequence similarity 19 member A5, C-C motif chemokine like
STAT1	1.14437797	2.21	1.64E-07	9.94E-09	STAT1	signal transducer and activator of transcription 1
ALCAM	1.1442052	2.21	3.51E-07	2.41E-08	ALCAM	activated leukocyte cell adhesion molecule
KMO	1.14312124	2.21	4.27E-10	8.94E-12	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
LAPTM5	1.14168409	2.21	2.91E-06	2.78E-07	LAPTM5	lysosomal protein transmembrane 5
PSMB8	1.14148416	2.21	1.56E-06	1.36E-07	PSMB8	proteasome subunit beta 8
C16orf95	1.14066132	2.20	4.53E-06	4.65E-07	C16orf95	chromosome 16 open reading frame 95
KLHL7	1.1398582	2.20	1.43E-10	2.41E-12	KLHL7	kelch like family member 7
GPX7	1.13803524	2.20	1.15E-10	1.82E-12	GPX7	glutathione peroxidase 7
FAM60A	1.13793644	2.20	4.56E-06	4.68E-07	FAM60A	family with sequence similarity 60 member A
CDCA3	1.13773404	2.20	3.49E-10	7.09E-12	CDCA3	cell division cycle associated 3
MAGEA9B///MAGEA9	1.13766576	2.20	1.42E-04	2.41E-05	MAGEA9B///MAGEA9	MAGE family member A9B///MAGE family member A9
DCBLD1	1.13678772	2.20	4.65E-10	1.00E-11	DCBLD1	discoidin, CUB and LCCL domain containing 1
UCP2	1.13660078	2.20	3.56E-05	4.98E-06	UCP2	uncoupling protein 2
DHFR	1.13555108	2.20	3.79E-08	1.81E-09	DHFR	dihydrofolate reductase

STAT1	1.13405511	2.19	6.06E-07	4.53E-08	STAT1	signal transducer and activator of transcription 1
POLR3K	1.13394698	2.19	2.54E-08	1.12E-09	POLR3K	RNA polymerase III subunit K
GCLM	1.13316132	2.19	8.18E-05	1.29E-05	GCLM	glutamate-cysteine ligase modifier subunit
ZC3H12D	1.13291532	2.19	4.15E-04	8.31E-05	ZC3H12D	zinc finger CCCH-type containing 12D
ARMC8	1.13269915	2.19	1.83E-07	1.13E-08	ARMC8	armadillo repeat containing 8
CHST11	1.13188785	2.19	5.61E-10	1.25E-11	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11
FAM46C	1.13089602	2.19	1.95E-04	3.49E-05	FAM46C	family with sequence similarity 46 member C
GNPMB	1.12845264	2.19	1.53E-11	1.47E-13	GNPMB	glycoprotein nmb
HSPH1	1.12843953	2.19	3.33E-05	4.60E-06	HSPH1	heat shock protein family H (Hsp110) member 1
COL4A2	1.12766298	2.19	5.12E-08	2.58E-09	COL4A2	collagen type IV alpha 2 chain
UBXN7	1.12663992	2.18	1.03E-08	3.97E-10	UBXN7	UBX domain protein 7
MME	1.12560551	2.18	2.41E-08	1.05E-09	MME	membrane metallo-endopeptidase
KIF23	1.1242023	2.18	3.74E-08	1.78E-09	KIF23	kinesin family member 23
CCNA2	1.12378906	2.18	8.28E-09	3.08E-10	CCNA2	cyclin A2
GMPS	1.12370077	2.18	1.79E-11	1.80E-13	GMPS	guanine monophosphate synthase
COL12A1	1.12349126	2.18	8.95E-07	7.17E-08	COL12A1	collagen type XII alpha 1 chain
COL1A2	1.12308546	2.18	3.80E-05	5.37E-06	COL1A2	collagen type I alpha 2 chain
MIR6787///SLC16A3	1.12280981	2.18	3.42E-08	1.60E-09	MIR6787///SLC16A3	microRNA 6787///solute carrier family 16 member 3
DDHD1	1.12144454	2.18	1.62E-11	1.58E-13	DDHD1	DDHD domain containing 1
MIR1908///FADS1	1.12136201	2.18	9.78E-11	1.49E-12	MIR1908///FADS1	microRNA 1908///fatty acid desaturase 1
KIAA0226L	1.12120028	2.18	9.97E-05	1.62E-05	KIAA0226L	KIAA0226 like
MIR24-2///MIR23A///LOC284454	1.12096981	2.17	7.93E-07	6.23E-08	MIR24-2///MIR23A///LOC284454	microRNA 24-2///microRNA 23a///uncharacterized LOC284454
SAMSN1	1.12089832	2.17	3.88E-05	5.50E-06	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
CCL2	1.11991132	2.17	2.25E-03	5.84E-04	CCL2	C-C motif chemokine ligand 2
KIF18A	1.1192998	2.17	8.46E-09	3.15E-10	KIF18A	kinesin family member 18A
SGO2	1.11917411	2.17	9.13E-10	2.21E-11	SGO2	shugoshin 2
LAPTM4B	1.11771704	2.17	6.69E-09	2.38E-10	LAPTM4B	lysosomal protein transmembrane 4 beta
XAF1	1.11768227	2.17	1.06E-06	8.68E-08	XAF1	XIAP associated factor 1
TGIF2	1.11627208	2.17	4.52E-12	3.13E-14	TGIF2	TGFB induced factor homeobox 2
GINS2	1.11623276	2.17	9.77E-09	3.71E-10	GINS2	GINS complex subunit 2
MCM4	1.11612202	2.17	6.96E-10	1.61E-11	MCM4	minichromosome maintenance complex component 4
LOC374443	1.11586673	2.17	2.53E-11	2.82E-13	LOC374443	C-type lectin domain family 2 member D pseudogene
ORAOV1	1.11577915	2.17	9.53E-04	2.16E-04	ORAOV1	oral cancer overexpressed 1
ITGAX	1.11568291	2.17	1.93E-11	1.99E-13	ITGAX	integrin subunit alpha X
FST	1.11546913	2.17	1.03E-06	8.47E-08	FST	folistatin

OSMR	1.11545117	2.17	2.34E-07	1.49E-08	OSMR	oncostatin M receptor
SH3PXD2B	1.11528461	2.17	1.04E-11	9.11E-14	SH3PXD2B	SH3 and PX domains 2B
PITX2	1.11519368	2.17	1.80E-04	3.19E-05	PITX2	paired like homeodomain 2
ANPEP	1.11496604	2.17	2.03E-06	1.84E-07	ANPEP	alanyl aminopeptidase, membrane
PLAG1	1.11336978	2.16	3.67E-07	2.54E-08	PLAG1	PLAG1 zinc finger
IGLC1	1.11222605	2.16	1.15E-07	6.57E-09	IGLC1	immunoglobulin lambda constant 1
PHC3	1.11187948	2.16	3.38E-09	1.04E-10	PHC3	polyhomeotic homolog 3
IL32	1.11140248	2.16	7.67E-06	8.56E-07	IL32	interleukin 32
SEL1L3	1.10912573	2.16	2.86E-06	2.73E-07	SEL1L3	SEL1L family member 3
THBS1	1.10898412	2.16	3.44E-05	4.77E-06	THBS1	thrombospondin 1
LYN	1.10865128	2.16	7.05E-07	5.43E-08	LYN	LYN proto-oncogene, Src family tyrosine kinase
GALNT2	1.10816266	2.16	3.99E-10	8.27E-12	GALNT2	polypeptide N-acetylgalactosaminyltransferase 2
FOSL1	1.10811255	2.16	1.07E-04	1.76E-05	FOSL1	FOS like 1, AP-1 transcription factor subunit
FAM92A1	1.10727735	2.15	3.38E-09	1.05E-10	FAM92A1	family with sequence similarity 92 member A1
SELE	1.10659656	2.15	4.00E-02	1.69E-02	SELE	selectin E
MMD	1.1065478	2.15	1.11E-10	1.74E-12	MMD	monocyte to macrophage differentiation associated
ADA	1.10628608	2.15	4.10E-09	1.33E-10	ADA	adenosine deaminase
CPXM1	1.1054089	2.15	1.05E-09	2.59E-11	CPXM1	carboxypeptidase X, M14 family member 1
GREM1	1.10516273	2.15	1.69E-05	2.11E-06	GREM1	gremlin 1, DAN family BMP antagonist
DUSP6	1.10502189	2.15	1.48E-07	8.81E-09	DUSP6	dual specificity phosphatase 6
CD86	1.10445622	2.15	3.54E-09	1.11E-10	CD86	CD86 molecule
TROAP	1.10327314	2.15	1.13E-09	2.83E-11	TROAP	trophinin associated protein
MIR490///LOC349160	1.10296962	2.15	3.70E-06	3.68E-07	MIR490///LOC349160	microRNA 490///uncharacterized LOC349160
RUNX2	1.10288857	2.15	3.28E-06	3.19E-07	RUNX2	runt related transcription factor 2
LPCAT1	1.10226003	2.15	5.90E-11	7.77E-13	LPCAT1	lysophosphatidylcholine acyltransferase 1
FLT1	1.10224534	2.15	3.74E-07	2.60E-08	FLT1	fms related tyrosine kinase 1
PCOLCE	1.10185753	2.15	2.25E-07	1.43E-08	PCOLCE	procollagen C-endopeptidase enhancer
SP110	1.1016143	2.15	4.80E-05	7.03E-06	SP110	SP110 nuclear body protein
IFIT1	1.10045502	2.14	5.24E-04	1.08E-04	IFIT1	interferon induced protein with tetratricopeptide repeats 1
FKBP11	1.10017013	2.14	1.06E-06	8.73E-08	FKBP11	FK506 binding protein 11
WARS	1.09800287	2.14	2.36E-08	1.03E-09	WARS	tryptophanyl-tRNA synthetase
CLIC4	1.09642333	2.14	4.45E-09	1.47E-10	CLIC4	chloride intracellular channel 4
MCM7	1.09591029	2.14	2.25E-09	6.46E-11	MCM7	minichromosome maintenance complex component 7
PSMB2	1.09496533	2.14	4.90E-12	3.45E-14	PSMB2	proteasome subunit beta 2
FAM49A	1.09481939	2.14	2.01E-12	1.13E-14	FAM49A	family with sequence similarity 49 member A
EXO1	1.09477373	2.14	7.49E-09	2.72E-10	EXO1	exonuclease 1

GCLM	1.09465852	2.14	2.46E-04	4.55E-05	GCLM	glutamate-cysteine ligase modifier subunit
IGHV4-31//IGHM//IGHG3//IGHG1//IGHD//IGHA1	1.09361592	2.13	7.43E-08	3.99E-09	IGHV4-31//IGHM//IGHG3//IGHG1//IGHD//IGHA1	immunoglobulin heavy variable 4-31//immunoglobulin heavy constant mu//immunoglobulin heavy constant gamma 3 (G3m marker)//immunoglobulin heavy constant gamma 1 (G1m marker)//immunoglobulin heavy constant delta//immunoglobulin heavy constant alpha 1
LAPTM4B	1.09161801	2.13	1.38E-10	2.31E-12	LAPTM4B	lysosomal protein transmembrane 4 beta
LAGE3	1.09159763	2.13	6.08E-10	1.38E-11	LAGE3	L antigen family member 3
RAB31	1.09094302	2.13	3.79E-11	4.62E-13	RAB31	RAB31, member RAS oncogene family
INHBA	1.09093726	2.13	5.01E-07	3.63E-08	INHBA	inhibin beta A subunit
C4B_2//C4B//C4A	1.09071651	2.13	6.31E-06	6.83E-07	C4B_2//C4B//C4A	complement component 4B (Chido blood group), copy 2//complement component 4B (Chido blood group)//complement component 4A (Rodgers blood group)
SAA2-SAA4//SAA2//SAA1	1.09043312	2.13	4.66E-06	4.80E-07	SAA2-SAA4//SAA2//SAA1	SAA2-SAA4 readthrough//serum amyloid A2//serum amyloid A1
CXCL16	1.0904155	2.13	1.11E-10	1.76E-12	CXCL16	C-X-C motif chemokine ligand 16
ITGB2	1.09022853	2.13	8.55E-06	9.67E-07	ITGB2	integrin subunit beta 2
CYBB	1.08986704	2.13	4.72E-06	4.88E-07	CYBB	cytochrome b-245 beta chain
MCM5	1.089585	2.13	6.71E-11	9.32E-13	MCM5	minichromosome maintenance complex component 5
MCM4	1.08886012	2.13	3.39E-08	1.58E-09	MCM4	minichromosome maintenance complex component 4
EGR1	1.08868634	2.13	2.31E-03	6.02E-04	EGR1	early growth response 1
LOC101928916//NNMT	1.08860386	2.13	1.96E-06	1.77E-07	LOC101928916//NNMT	uncharacterized LOC101928916//nicotinamide N-methyltransferase
ABCC5	1.08807713	2.13	1.68E-05	2.09E-06	ABCC5	ATP binding cassette subfamily C member 5
ZNF114	1.08757509	2.13	2.63E-07	1.72E-08	ZNF114	zinc finger protein 114
DNAH14	1.08702638	2.12	6.63E-06	7.24E-07	DNAH14	dynein axonemal heavy chain 14
POLQ	1.08690808	2.12	3.35E-12	2.13E-14	POLQ	DNA polymerase theta
CENPI	1.08624908	2.12	1.18E-08	4.63E-10	CENPI	centromere protein I
PAG1	1.08622126	2.12	1.61E-10	2.82E-12	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1
IGHV3-23//IGHV4-31//IGHM//IGHG3//IGHG1//IGHA2//IGHA1	1.08616486	2.12	3.80E-05	5.36E-06	IGHV3-23//IGHV4-31//IGHM//IGHG3//IGHG1//IGHA2//IGHA1	immunoglobulin heavy variable 3-23//immunoglobulin heavy variable 4-31//immunoglobulin heavy constant mu//immunoglobulin heavy constant gamma 3 (G3m marker)//immunoglobulin heavy constant gamma 1 (G1m)

						marker)//immunoglobulin heavy constant alpha 2 (A2m marker)//immunoglobulin heavy constant alpha 1
ITGB4	1.08595254	2.12	2.45E-08	1.08E-09	ITGB4	integrin subunit beta 4
MYO10	1.08575335	2.12	7.55E-06	8.40E-07	MYO10	myosin X
AGO2	1.08528824	2.12	3.70E-09	1.17E-10	AGO2	argonaute 2, RISC catalytic component
GLRX	1.08505308	2.12	7.33E-07	5.68E-08	GLRX	glutaredoxin
LOC102725526//IGHV4-31//IGHM//IGHG3//IGHG2//IGHG1//IGHA2//IGHA1//IGH	1.08350193	2.12	1.82E-06	1.63E-07	LOC102725526//IGHV4-31//IGHM//IGHG3//IGHG2//IGHA2//IGHA1//IGH	uncharacterized LOC102725526//immunoglobulin heavy variable 4-31//immunoglobulin heavy constant mu//immunoglobulin heavy constant gamma 3 (G3m marker)//immunoglobulin heavy constant gamma 2 (G2m marker)//immunoglobulin heavy constant gamma 1 (G1m marker)//immunoglobulin heavy constant alpha 2 (A2m marker)//immunoglobulin heavy constant alpha 1//immunoglobulin heavy locus
APMAP	1.08267458	2.12	1.25E-15	3.21E-19	APMAP	adipocyte plasma membrane associated protein
KCNS3	1.08193255	2.12	1.03E-06	8.48E-08	KCNS3	potassium voltage-gated channel modifier subfamily S member 3
ZNF281	1.08139803	2.12	1.67E-11	1.65E-13	ZNF281	zinc finger protein 281
KMO	1.08101788	2.12	3.00E-09	9.05E-11	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
TGFB1	1.08039116	2.11	3.37E-08	1.57E-09	TGFB1	transforming growth factor beta 1
IFI44	1.0801444	2.11	4.23E-05	6.07E-06	IFI44	interferon induced protein 44
KCNMB2-AS1	1.07931354	2.11	2.81E-05	3.76E-06	KCNMB2-AS1	KCNMB2 antisense RNA 1
ICAM1	1.07862047	2.11	2.68E-07	1.75E-08	ICAM1	intercellular adhesion molecule 1
LOC101928615//FNDC3B	1.07791483	2.11	6.97E-11	9.75E-13	LOC101928615//FNDC3B	uncharacterized LOC101928615//fibronectin type III domain containing 3B
FUS	1.07643645	2.11	6.11E-08	3.16E-09	FUS	FUS RNA binding protein
LOC101929272	1.0748338	2.11	5.09E-06	5.32E-07	LOC101929272	uncharacterized LOC101929272
STK17A	1.07303891	2.10	6.24E-09	2.20E-10	STK17A	serine/threonine kinase 17a
IL6	1.07218399	2.10	7.25E-03	2.26E-03	IL6	interleukin 6
PLOD1	1.07209099	2.10	1.84E-11	1.88E-13	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1
LRP8	1.07123127	2.10	1.37E-07	8.07E-09	LRP8	LDL receptor related protein 8
USB1	1.07061519	2.10	2.10E-13	5.53E-16	USB1	U6 snRNA biogenesis phosphodiesterase 1
ATP13A3	1.07036077	2.10	5.89E-09	2.06E-10	ATP13A3	ATPase 13A3
FANCI	1.07006258	2.10	5.90E-09	2.06E-10	FANCI	Fanconi anemia complementation group I
LY6K	1.07006101	2.10	4.76E-04	9.69E-05	LY6K	lymphocyte antigen 6 complex, locus K

DEPDC1	1.06987759	2.10	1.27E-07	7.35E-09	<i>DEPDC1</i>	DEP domain containing 1
NDE1	1.06917054	2.10	4.11E-10	8.55E-12	<i>NDE1</i>	nudE neurodevelopment protein 1
LGALS3BP	1.06868583	2.10	8.98E-05	1.44E-05	<i>LGALS3BP</i>	galectin 3 binding protein
NREP	1.06820202	2.10	2.97E-08	1.35E-09	<i>NREP</i>	neuronal regeneration related protein
LYN	1.06743516	2.10	4.25E-06	4.32E-07	<i>LYN</i>	LYN proto-oncogene, Src family tyrosine kinase
HSP90AB1	1.06714312	2.10	6.53E-03	2.00E-03	<i>HSP90AB1</i>	heat shock protein 90 alpha family class B member 1
CDK1	1.06667033	2.09	2.90E-07	1.92E-08	<i>CDK1</i>	cyclin dependent kinase 1
NOCT	1.06592577	2.09	3.15E-08	1.45E-09	<i>NOCT</i>	nocturnin
E2F3	1.06575859	2.09	5.04E-14	7.92E-17	<i>E2F3</i>	E2F transcription factor 3
C4orf46	1.06495267	2.09	1.69E-09	4.58E-11	<i>C4orf46</i>	chromosome 4 open reading frame 46
TMEM200A	1.0645249	2.09	1.06E-05	1.24E-06	<i>TMEM200A</i>	transmembrane protein 200A
NRIP3	1.06444033	2.09	1.42E-10	2.39E-12	<i>NRIP3</i>	nuclear receptor interacting protein 3
ANGPT2	1.06441468	2.09	1.89E-09	5.27E-11	<i>ANGPT2</i>	angiopoietin 2
RNASEH2A	1.06391795	2.09	1.43E-10	2.41E-12	<i>RNASEH2A</i>	ribonuclease H2 subunit A
ARMC8	1.0635772	2.09	1.49E-06	1.29E-07	<i>ARMC8</i>	armadillo repeat containing 8
FYB	1.06225211	2.09	3.16E-05	4.32E-06	<i>FYB</i>	FYN binding protein
ZNF469	1.06109571	2.09	8.87E-10	2.14E-11	<i>ZNF469</i>	zinc finger protein 469
PDIA4	1.06077474	2.09	1.22E-09	3.13E-11	<i>PDIA4</i>	protein disulfide isomerase family A member 4
P3H1	1.06049263	2.09	4.88E-14	7.50E-17	<i>P3H1</i>	prolyl 3-hydroxylase 1
SERPINA1	1.06026032	2.09	7.49E-03	2.34E-03	<i>SERPINA1</i>	serpin family A member 1
COMMD2	1.05971782	2.08	6.13E-11	8.25E-13	<i>COMMD2</i>	COMM domain containing 2
CYTIP	1.05931606	2.08	5.38E-05	8.02E-06	<i>CYTIP</i>	cytohesin 1 interacting protein
LOC440173	1.05861087	2.08	4.51E-07	3.23E-08	<i>LOC440173</i>	uncharacterized LOC440173
PRAME	1.05826613	2.08	6.59E-07	5.00E-08	<i>PRAME</i>	preferentially expressed antigen in melanoma
YEATS2	1.05806493	2.08	1.83E-11	1.86E-13	<i>YEATS2</i>	YEATS domain containing 2
POPDC2///COX17	1.05799414	2.08	3.53E-11	4.21E-13	<i>POPDC2///COX17</i>	popeye domain containing 2///COX17, cytochrome c oxidase copper chaperone
TP63	1.05762776	2.08	1.73E-05	2.17E-06	<i>TP63</i>	tumor protein p63
CTSB	1.05657862	2.08	1.44E-11	1.35E-13	<i>CTSB</i>	cathepsin B
ACP1	1.05570599	2.08	1.00E-10	1.53E-12	<i>ACP1</i>	acid phosphatase 1, soluble
SULF1	1.05517314	2.08	4.04E-08	1.95E-09	<i>SULF1</i>	sulfatase 1
TYMP	1.05504437	2.08	3.11E-08	1.42E-09	<i>TYMP</i>	thymidine phosphorylase
LSG1	1.05363029	2.08	2.37E-12	1.42E-14	<i>LSG1</i>	large 60S subunit nuclear export GTPase 1
EMILIN2	1.05351196	2.08	2.50E-11	2.78E-13	<i>EMILIN2</i>	elastin microfibril interfacer 2
RNFT2	1.05312716	2.08	6.14E-07	4.61E-08	<i>RNFT2</i>	ring finger protein, transmembrane 2
FUS	1.05256564	2.07	1.80E-08	7.58E-10	<i>FUS</i>	FUS RNA binding protein
GALNT2	1.05232843	2.07	2.78E-11	3.13E-13	<i>GALNT2</i>	polypeptide N-acetylgalactosaminyltransferase 2
SERPINA1	1.05222105	2.07	4.36E-03	1.25E-03	<i>SERPINA1</i>	serpin family A member 1

MIR1204///PVT1	1.05141128	2.07	6.18E-06	6.67E-07	MIR1204///PVT1	microRNA 1204///Pvt1 oncogene (non-protein coding)
PARP9	1.05063565	2.07	3.51E-08	1.65E-09	PARP9	poly(ADP-ribose) polymerase family member 9
DUSP6	1.05018841	2.07	7.22E-07	5.59E-08	DUSP6	dual specificity phosphatase 6
PDE7A	1.04907942	2.07	2.87E-10	5.65E-12	PDE7A	phosphodiesterase 7A
FCN1	1.04785991	2.07	6.63E-07	5.04E-08	FCN1	ficolin 1
TTK	1.04714356	2.07	2.22E-07	1.40E-08	TTK	TTK protein kinase
WIPF1	1.04633353	2.07	2.92E-09	8.75E-11	WIPF1	WAS/WASL interacting protein family member 1
CD300A	1.04570043	2.06	1.15E-08	4.48E-10	CD300A	CD300a molecule
MSI2	1.0453695	2.06	5.98E-10	1.35E-11	MSI2	musashi RNA binding protein 2
SOST	1.04475277	2.06	6.78E-04	1.46E-04	SOST	sclerostin
SLAMF7	1.0446986	2.06	3.16E-05	4.33E-06	SLAMF7	SLAM family member 7
ELAVL2	1.04452266	2.06	9.25E-04	2.09E-04	ELAVL2	ELAV like neuron-specific RNA binding protein 2
HSPA13	1.04448448	2.06	2.39E-08	1.04E-09	HSPA13	heat shock protein family A (Hsp70) member 13
SDK1	1.04426869	2.06	1.49E-10	2.53E-12	SDK1	sidekick cell adhesion molecule 1
RARRES1	1.04410566	2.06	1.43E-04	2.44E-05	RARRES1	retinoic acid receptor responder 1
SDF2L1	1.04364483	2.06	1.14E-09	2.86E-11	SDF2L1	stromal cell derived factor 2 like 1
ACVR1C	1.04334951	2.06	3.02E-07	2.02E-08	ACVR1C	activin A receptor type 1C
DLX6	1.0429838	2.06	4.76E-05	6.96E-06	DLX6	distal-less homeobox 6
PPP1R14C	1.04229509	2.06	1.11E-05	1.31E-06	PPP1R14C	protein phosphatase 1 regulatory inhibitor subunit 14C
DEPDC1	1.04202814	2.06	3.49E-08	1.64E-09	DEPDC1	DEP domain containing 1
CBX3	1.04186451	2.06	5.18E-08	2.62E-09	CBX3	chromobox 3
CDK1	1.04106239	2.06	3.31E-09	1.02E-10	CDK1	cyclin dependent kinase 1
EIF5A	1.04084174	2.06	9.44E-04	2.14E-04	EIF5A	eukaryotic translation initiation factor 5A
PXYLP1	1.04044068	2.06	1.97E-07	1.23E-08	PXYLP1	2-phosphoxylose phosphatase 1
CALML5	1.04028485	2.06	2.42E-04	4.47E-05	CALML5	calmodulin like 5
KRT10	1.03987086	2.06	1.66E-07	1.01E-08	KRT10	keratin 10
PIK3AP1	1.03878546	2.05	8.65E-07	6.89E-08	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
SLC7A7	1.03841076	2.05	3.23E-08	1.49E-09	SLC7A7	solute carrier family 7 member 7
PARP12	1.03805446	2.05	1.84E-09	5.08E-11	PARP12	poly(ADP-ribose) polymerase family member 12
TPR	1.03794175	2.05	1.53E-02	5.43E-03	TPR	translocated promoter region, nuclear basket protein
MINPP1	1.03756128	2.05	4.95E-10	1.08E-11	MINPP1	multiple inositol-polyphosphate phosphatase 1
OLR1	1.03739012	2.05	3.34E-06	3.26E-07	OLR1	oxidized low density lipoprotein receptor 1
ANLN	1.03730741	2.05	2.71E-06	2.57E-07	ANLN	anillin actin binding protein
PTP4A3	1.03728509	2.05	4.00E-12	2.70E-14	PTP4A3	protein tyrosine phosphatase type IVA, member 3
CENPF	1.03695877	2.05	6.85E-09	2.46E-10	CENPF	centromere protein F
CLEC4E	1.03665358	2.05	6.84E-08	3.60E-09	CLEC4E	C-type lectin domain family 4 member E

DDX39A	1.0365342	2.05	4.97E-11	6.35E-13	<i>DDX39A</i>	DEAD-box helicase 39A
MIAT	1.03552291	2.05	5.90E-07	4.40E-08	<i>MIAT</i>	myocardial infarction associated transcript (non-protein coding)
IKBIP	1.03505917	2.05	2.10E-09	5.97E-11	<i>IKBIP</i>	IKKKB interacting protein
TP63	1.03477238	2.05	1.06E-06	8.73E-08	<i>TP63</i>	tumor protein p63
ENAH	1.03467202	2.05	2.53E-10	4.84E-12	<i>ENAH</i>	enabled homolog (Drosophila)
C3orf52	1.03368882	2.05	1.89E-05	2.40E-06	<i>C3orf52</i>	chromosome 3 open reading frame 52
VOPP1	1.0330292	2.05	3.56E-11	4.25E-13	<i>VOPP1</i>	vesicular, overexpressed in cancer, prosurvival protein 1
PGM2L1	1.03302663	2.05	7.60E-09	2.77E-10	<i>PGM2L1</i>	phosphoglucosyltransferase 2 like 1
KRT23	1.03280492	2.05	4.39E-03	1.26E-03	<i>KRT23</i>	keratin 23
HIST1H2BD	1.03264402	2.05	1.07E-05	1.25E-06	<i>HIST1H2BD</i>	histone cluster 1, H2bd
SERPINE1	1.03260818	2.05	2.97E-08	1.35E-09	<i>SERPINE1</i>	serpin family E member 1
FXR1	1.03187374	2.04	5.12E-09	1.75E-10	<i>FXR1</i>	FMR1 autosomal homolog 1
GFM1	1.03100843	2.04	1.99E-10	3.64E-12	<i>GFM1</i>	G elongation factor mitochondrial 1
NEB	1.03095138	2.04	2.15E-06	1.97E-07	<i>NEB</i>	nebulin
SLC38A5	1.03088331	2.04	8.62E-07	6.85E-08	<i>SLC38A5</i>	solute carrier family 38 member 5
LIMK1	1.03081742	2.04	3.87E-14	5.31E-17	<i>LIMK1</i>	LIM domain kinase 1
PABPC1L	1.03076356	2.04	6.00E-12	4.51E-14	<i>PABPC1L</i>	poly(A) binding protein cytoplasmic 1 like
MRPL47	1.03067235	2.04	1.97E-10	3.60E-12	<i>MRPL47</i>	mitochondrial ribosomal protein L47
RUNX3	1.03032675	2.04	8.86E-06	1.01E-06	<i>RUNX3</i>	runt related transcription factor 3
CTSC	1.02986178	2.04	3.08E-09	9.37E-11	<i>CTSC</i>	cathepsin C
KRT8	1.02936095	2.04	3.15E-03	8.54E-04	<i>KRT8</i>	keratin 8
TAF1A	1.02926556	2.04	8.77E-08	4.83E-09	<i>TAF1A</i>	TATA-box binding protein associated factor, RNA polymerase I subunit A
UBE2L6	1.02849488	2.04	4.30E-08	2.09E-09	<i>UBE2L6</i>	ubiquitin conjugating enzyme E2 L6
TMEM184B	1.0283902	2.04	1.78E-13	4.13E-16	<i>TMEM184B</i>	transmembrane protein 184B
BID	1.02797865	2.04	2.15E-12	1.26E-14	<i>BID</i>	BH3 interacting domain death agonist
KLHDC7B	1.02619607	2.04	1.06E-06	8.77E-08	<i>KLHDC7B</i>	kelch domain containing 7B
JUN	1.02611008	2.04	7.33E-04	1.59E-04	<i>JUN</i>	Jun proto-oncogene, AP-1 transcription factor subunit
INHBB	1.02511302	2.04	6.72E-07	5.13E-08	<i>INHBB</i>	inhibin beta B subunit
FAM111B	1.02508392	2.04	7.56E-06	8.41E-07	<i>FAM111B</i>	family with sequence similarity 111 member B
CMSS1	1.02482556	2.03	3.52E-08	1.67E-09	<i>CMSS1</i>	cms1 ribosomal small subunit homolog (yeast)
MCM4	1.02481819	2.03	5.79E-10	1.30E-11	<i>MCM4</i>	minichromosome maintenance complex component 4
GUSBP11	1.02466633	2.03	3.37E-07	2.29E-08	<i>GUSBP11</i>	glucuronidase, beta pseudogene 11
CCDC71L	1.02463185	2.03	9.74E-09	3.70E-10	<i>CCDC71L</i>	coiled-coil domain containing 71-like
SMYD3	1.02436572	2.03	3.98E-09	1.28E-10	<i>SMYD3</i>	SET and MYND domain containing 3
NAV1	1.02408959	2.03	1.81E-09	4.98E-11	<i>NAV1</i>	neuron navigator 1
MYO10	1.02397375	2.03	1.03E-05	1.20E-06	<i>MYO10</i>	myosin X
NKAIN2	1.02350669	2.03	2.14E-04	3.88E-05	<i>NKAIN2</i>	Na ⁺ /K ⁺ transporting ATPase interacting 2

PCDH17	1.02347583	2.03	2.06E-06	1.88E-07	<i>PCDH17</i>	protocadherin 17
PLTP	1.02334324	2.03	3.70E-05	5.20E-06	<i>PLTP</i>	phospholipid transfer protein
DTX3L	1.02305505	2.03	5.63E-11	7.34E-13	<i>DTX3L</i>	deltex E3 ubiquitin ligase 3L
HMGB3P1	1.02282745	2.03	5.22E-11	6.73E-13	<i>HMGB3P1</i>	high mobility group box 3 pseudogene 1
PLAU	1.02237735	2.03	3.16E-08	1.45E-09	<i>PLAU</i>	plasminogen activator, urokinase
SNAI2	1.02211009	2.03	4.39E-08	2.15E-09	<i>SNAI2</i>	snail family transcriptional repressor 2
PNPT1	1.02173104	2.03	2.01E-13	5.16E-16	<i>PNPT1</i>	polyribonucleotide nucleotidyltransferase 1
PLEK	1.02023018	2.03	1.52E-07	9.13E-09	<i>PLEK</i>	pleckstrin
GNS	1.02011575	2.03	9.12E-10	2.21E-11	<i>GNS</i>	glucosamine (N-acetyl)-6-sulfatase
CHPF2	1.01962692	2.03	2.57E-13	7.03E-16	<i>CHPF2</i>	chondroitin polymerizing factor 2
TOPBP1	1.01880327	2.03	3.32E-11	3.88E-13	<i>TOPBP1</i>	topoisomerase (DNA) II binding protein 1
SGK1	1.01854453	2.03	6.49E-08	3.39E-09	<i>SGK1</i>	serum/glucocorticoid regulated kinase 1
AQP9	1.01725785	2.02	4.29E-08	2.09E-09	<i>AQP9</i>	aquaporin 9
PARP14	1.01671703	2.02	4.42E-10	9.36E-12	<i>PARP14</i>	poly(ADP-ribose) polymerase family member 14
IGLV1-44	1.0147938	2.02	2.40E-04	4.42E-05	<i>IGLV1-44</i>	immunoglobulin lambda variable 1-44
CALU	1.0141167	2.02	1.07E-10	1.67E-12	<i>CALU</i>	calumenin
TMEM185B	1.01404606	2.02	3.60E-10	7.36E-12	<i>TMEM185B</i>	transmembrane protein 185B
CD163	1.01375903	2.02	1.91E-05	2.42E-06	<i>CD163</i>	CD163 molecule
MKI67	1.01234698	2.02	4.12E-08	2.00E-09	<i>MKI67</i>	marker of proliferation Ki-67
GTSE1	1.01226432	2.02	4.87E-09	1.65E-10	<i>GTSE1</i>	G2 and S-phase expressed 1
IGLC1	1.01189664	2.02	1.52E-07	9.09E-09	<i>IGLC1</i>	immunoglobulin lambda constant 1
SLAMF7	1.01164698	2.02	4.25E-05	6.10E-06	<i>SLAMF7</i>	SLAM family member 7
PTH2R	1.0113087	2.02	1.71E-03	4.25E-04	<i>PTH2R</i>	parathyroid hormone 2 receptor
BLM	1.01097224	2.02	3.60E-10	7.35E-12	<i>BLM</i>	Bloom syndrome RecQ like helicase
IQCG	1.01027654	2.01	3.22E-05	4.43E-06	<i>IQCG</i>	IQ motif containing G
DSCC1	1.00948008	2.01	1.96E-08	8.35E-10	<i>DSCC1</i>	DNA replication and sister chromatid cohesion 1
IGK///IGKC	1.00798563	2.01	7.22E-07	5.59E-08	<i>IGK///IGKC</i>	immunoglobulin kappa locus///immunoglobulin kappa constant
NOLC1	1.00777048	2.01	1.91E-10	3.46E-12	<i>NOLC1</i>	nucleolar and coiled-body phosphoprotein 1
GALNS	1.00757822	2.01	1.54E-11	1.47E-13	<i>GALNS</i>	galactosamine (N-acetyl)-6-sulfatase
IRF1	1.00754579	2.01	1.25E-05	1.50E-06	<i>IRF1</i>	interferon regulatory factor 1
ACKR3	1.00709553	2.01	4.19E-05	6.00E-06	<i>ACKR3</i>	atypical chemokine receptor 3
ASPRV1	1.00669019	2.01	5.40E-04	1.12E-04	<i>ASPRV1</i>	aspartic peptidase, retroviral-like 1
EML4	1.0064864	2.01	1.65E-09	4.44E-11	<i>EML4</i>	echinoderm microtubule associated protein like 4
PAX5	1.00581061	2.01	1.69E-02	6.11E-03	<i>PAX5</i>	paired box 5
MELK	1.00520319	2.01	6.05E-11	8.06E-13	<i>MELK</i>	maternal embryonic leucine zipper kinase
RANBP1	1.00494462	2.01	1.42E-07	8.42E-09	<i>RANBP1</i>	RAN binding protein 1
CORO1A	1.00483667	2.01	2.11E-04	3.82E-05	<i>CORO1A</i>	coronin 1A
PAK2	1.00441312	2.01	1.77E-08	7.40E-10	<i>PAK2</i>	p21 (RAC1) activated kinase 2

GPR183	1.00410193	2.01	1.33E-04	2.24E-05	<i>GPR183</i>	G protein-coupled receptor 183
PDE4B	1.00354032	2.00	3.71E-06	3.69E-07	<i>PDE4B</i>	phosphodiesterase 4B
LGALS1	1.00314833	2.00	1.35E-05	1.63E-06	<i>LGALS1</i>	galectin 1
IL7R	1.00303967	2.00	2.38E-04	4.39E-05	<i>IL7R</i>	interleukin 7 receptor
B3GALT6	1.00303931	2.00	2.89E-11	3.29E-13	<i>B3GALT6</i>	beta-1,3-galactosyltransferase 6
MCM10	1.00289497	2.00	1.54E-09	4.10E-11	<i>MCM10</i>	minichromosome maintenance 10 replication initiation factor
FOSB	1.00224025	2.00	1.74E-02	6.32E-03	<i>FOSB</i>	FosB proto-oncogene, AP-1 transcription factor subunit
CECR1	1.00052869	2.00	1.57E-05	1.94E-06	<i>CECR1</i>	cat eye syndrome chromosome region, candidate 1
BCL2L11	1.00046096	2.00	1.89E-08	7.97E-10	<i>BCL2L11</i>	BCL2 like 11
CD53	0.99977406	2.00	5.03E-06	5.24E-07	<i>CD53</i>	CD53 molecule
C16orf74	0.99974448	2.00	2.99E-09	9.03E-11	<i>C16orf74</i>	chromosome 16 open reading frame 74
LRP8	0.99974076	2.00	6.64E-08	3.48E-09	<i>LRP8</i>	LDL receptor related protein 8
PNO1	0.99882435	2.00	4.63E-08	2.29E-09	<i>PNO1</i>	partner of NOB1 homolog
PLAC1	0.99851226	2.00	1.96E-05	2.49E-06	<i>PLAC1</i>	placenta specific 1
ENY2	0.99838503	2.00	1.09E-11	9.63E-14	<i>ENY2</i>	ENY2, transcription and export complex 2 subunit
FTL	0.99827885	2.00	1.94E-04	3.48E-05	<i>FTL</i>	ferritin light chain
DHX36	0.99800785	2.00	2.45E-08	1.08E-09	<i>DHX36</i>	DEAH-box helicase 36
SLC25A37	0.99799466	2.00	7.18E-07	5.55E-08	<i>SLC25A37</i>	solute carrier family 25 member 37
DERL1	0.99767793	2.00	8.80E-14	1.66E-16	<i>DERL1</i>	derlin 1
KLHL42	0.99647676	2.00	2.81E-09	8.34E-11	<i>KLHL42</i>	kelch like family member 42
FADD	0.99571313	1.99	1.03E-05	1.19E-06	<i>FADD</i>	Fas associated via death domain
IL20	0.99543372	1.99	1.50E-04	2.57E-05	<i>IL20</i>	interleukin 20
SLC20A1	0.99538042	1.99	4.86E-08	2.42E-09	<i>SLC20A1</i>	solute carrier family 20 member 1
CENPE	0.99512671	1.99	1.10E-07	6.28E-09	<i>CENPE</i>	centromere protein E
PRPS1	0.99476136	1.99	2.35E-09	6.79E-11	<i>PRPS1</i>	phosphoribosyl pyrophosphate synthetase 1
PGBD5	0.99423756	1.99	1.28E-04	2.14E-05	<i>PGBD5</i>	piggyBac transposable element derived 5
TRIO	0.99375525	1.99	1.06E-10	1.64E-12	<i>TRIO</i>	trio Rho guanine nucleotide exchange factor
CKS2	0.99335872	1.99	1.49E-09	3.95E-11	<i>CKS2</i>	CDC28 protein kinase regulatory subunit 2
GALNT18	0.99270972	1.99	4.20E-09	1.37E-10	<i>GALNT18</i>	polypeptide N-acetylgalactosaminyltransferase 18
WNT2	0.99178864	1.99	4.61E-09	1.54E-10	<i>WNT2</i>	Wnt family member 2
ADGRV1	0.99171295	1.99	2.65E-05	3.52E-06	<i>ADGRV1</i>	adhesion G protein-coupled receptor V1
CCL26	0.99141153	1.99	2.94E-05	3.98E-06	<i>CCL26</i>	C-C motif chemokine ligand 26
MSANTD3	0.98994955	1.99	2.87E-10	5.64E-12	<i>MSANTD3</i>	Myb/SANT DNA binding domain containing 3
HMMR	0.98981783	1.99	2.04E-07	1.28E-08	<i>HMMR</i>	hyaluronan mediated motility receptor
RRM2	0.98932117	1.99	5.51E-09	1.90E-10	<i>RRM2</i>	ribonucleotide reductase regulatory subunit M2
FOXP4-AS1	0.98928238	1.99	6.75E-04	1.45E-04	<i>FOXP4-AS1</i>	FOXP4 antisense RNA 1

THEMIS2	0.98926266	1.99	4.53E-08	2.23E-09	THEMIS2	thymocyte selection associated family member 2
S100A6	0.98926187	1.99	1.83E-07	1.14E-08	S100A6	S100 calcium binding protein A6
IGSF9	0.98904459	1.98	6.73E-06	7.36E-07	IGSF9	immunoglobulin superfamily member 9
MCM7	0.98860419	1.98	1.15E-10	1.83E-12	MCM7	minichromosome maintenance complex component 7
AGRN	0.98802326	1.98	1.19E-12	5.41E-15	AGRN	agrin
ETV7	0.98799963	1.98	7.96E-07	6.26E-08	ETV7	ETS variant 7
WHSC1	0.98788684	1.98	3.97E-10	8.23E-12	WHSC1	Wolf-Hirschhorn syndrome candidate 1
GLS	0.98769186	1.98	1.33E-07	7.78E-09	GLS	glutaminase
GPC1	0.98764067	1.98	2.55E-06	2.39E-07	GPC1	glypican 1
SLC6A8	0.98746815	1.98	2.40E-05	3.14E-06	SLC6A8	solute carrier family 6 member 8
PFDN2	0.98731733	1.98	7.99E-12	6.53E-14	PFDN2	prefoldin subunit 2
ABCC5	0.9873042	1.98	6.04E-05	9.16E-06	ABCC5	ATP binding cassette subfamily C member 5
MIR146A	0.98694685	1.98	5.56E-05	8.31E-06	MIR146A	microRNA 146a
FLJ32255	0.98691275	1.98	6.78E-06	7.43E-07	FLJ32255	uncharacterized LOC643977
SIRPA	0.98630733	1.98	1.61E-11	1.56E-13	SIRPA	signal regulatory protein alpha
ZGRF1	0.98629447	1.98	2.45E-08	1.08E-09	ZGRF1	zinc finger GRF-type containing 1
NUP62CL	0.9860718	1.98	7.23E-05	1.12E-05	NUP62CL	nucleoporin 62 C-terminal like
ADAP2	0.98510519	1.98	1.60E-10	2.77E-12	ADAP2	ArfGAP with dual PH domains 2
MLEC	0.98415779	1.98	4.62E-08	2.28E-09	MLEC	malectin
MX2	0.98410566	1.98	4.49E-06	4.59E-07	MX2	MX dynamin like GTPase 2
MCM8	0.98326915	1.98	1.89E-10	3.41E-12	MCM8	minichromosome maintenance 8 homologous recombination repair factor
BUB1B	0.98321378	1.98	3.57E-09	1.12E-10	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B
NID2	0.98265661	1.98	1.29E-06	1.10E-07	NID2	nidogen 2
FAM46C	0.98264522	1.98	1.20E-06	1.01E-07	FAM46C	family with sequence similarity 46 member C
CXCR4	0.98247725	1.98	4.10E-03	1.16E-03	CXCR4	C-X-C motif chemokine receptor 4
CYAT1///IGLV1-44///IGLC1	0.98239368	1.98	4.13E-07	2.91E-08	CYAT1///IGLV1-44///IGLC1	immunoglobulin lambda light chain-like///immunoglobulin lambda variable 1-44///immunoglobulin lambda constant 1
PTK7	0.98205846	1.98	3.13E-09	9.52E-11	PTK7	protein tyrosine kinase 7 (inactive)
PSME4	0.98175894	1.97	2.88E-05	3.88E-06	PSME4	proteasome activator subunit 4
CHEK1	0.9815301	1.97	4.96E-09	1.69E-10	CHEK1	checkpoint kinase 1
PHLDB2	0.98126189	1.97	2.03E-04	3.67E-05	PHLDB2	pleckstrin homology like domain family B member 2
CST2	0.98120349	1.97	9.20E-08	5.11E-09	CST2	cystatin SA
SLC12A8	0.98093861	1.97	9.87E-08	5.55E-09	SLC12A8	solute carrier family 12 member 8
HSP90B1	0.9805005	1.97	9.22E-06	1.05E-06	HSP90B1	heat shock protein 90 beta family member 1
PLAT	0.9803214	1.97	4.99E-04	1.02E-04	PLAT	plasminogen activator, tissue type

IMPAD1	0.98015503	1.97	1.12E-11	1.00E-13	IMPAD1	inositol monophosphatase domain containing 1
GLA	0.98012711	1.97	1.68E-12	8.84E-15	GLA	galactosidase alpha
FBXO11	0.98005332	1.97	2.39E-08	1.05E-09	FBXO11	F-box protein 11
MIR675///H19	0.97989876	1.97	2.42E-03	6.34E-04	MIR675///H19	microRNA 675///H19, imprinted maternally expressed transcript (non-protein coding)
SLC39A6	0.97963013	1.97	3.39E-08	1.58E-09	SLC39A6	solute carrier family 39 member 6
AIF1	0.97937625	1.97	2.69E-06	2.54E-07	AIF1	allograft inflammatory factor 1
ALPK2	0.97923499	1.97	1.35E-08	5.39E-10	ALPK2	alpha kinase 2
COL27A1	0.97919438	1.97	1.38E-07	8.12E-09	COL27A1	collagen type XXVII alpha 1 chain
SLC7A5	0.97900828	1.97	1.96E-04	3.51E-05	SLC7A5	solute carrier family 7 member 5
KISS1R	0.9781776	1.97	4.40E-05	6.36E-06	KISS1R	KISS1 receptor
CD163	0.97782592	1.97	3.95E-05	5.61E-06	CD163	CD163 molecule
CAD	0.97777075	1.97	1.11E-09	2.77E-11	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
SLC6A10PB///SLC6A10P///SLC6A8	0.977605	1.97	9.68E-06	1.12E-06	SLC6A10PB///SLC6A10P///SLC6A8	solute carrier family 6 member 8 pseudogene///solute carrier family 6 member 10, pseudogene///solute carrier family 6 member 8
CXCL14	0.97736644	1.97	1.96E-03	4.98E-04	CXCL14	C-X-C motif chemokine ligand 14
RGS16	0.97684747	1.97	1.80E-09	4.96E-11	RGS16	regulator of G-protein signaling 16
FUS	0.97668908	1.97	1.14E-08	4.45E-10	FUS	FUS RNA binding protein
CTSD	0.97584664	1.97	9.10E-06	1.04E-06	CTSD	cathepsin D
OSMR	0.97540924	1.97	4.50E-10	9.59E-12	OSMR	oncostatin M receptor
CDCA2	0.97521896	1.97	1.73E-08	7.22E-10	CDCA2	cell division cycle associated 2
AKR1B1	0.97511307	1.97	1.49E-12	7.54E-15	AKR1B1	aldo-keto reductase family 1 member B
OAS3	0.97458015	1.97	1.23E-06	1.04E-07	OAS3	2'-5'-oligoadenylate synthetase 3
XPR1	0.97440651	1.96	1.71E-12	9.02E-15	XPR1	xenotropic and polytropic retrovirus receptor 1
HOXC6	0.97430017	1.96	2.58E-05	3.41E-06	HOXC6	homeobox C6
IFI16	0.97327335	1.96	2.31E-05	3.02E-06	IFI16	interferon gamma inducible protein 16
CHTF18	0.97160396	1.96	1.84E-11	1.87E-13	CHTF18	chromosome transmission fidelity factor 18
COL13A1	0.97126623	1.96	3.37E-08	1.56E-09	COL13A1	collagen type XIII alpha 1 chain
BCL11B	0.97107515	1.96	4.38E-10	9.23E-12	BCL11B	B-cell CLL/lymphoma 11B
TNFAIP2	0.97107297	1.96	6.54E-05	1.00E-05	TNFAIP2	TNF alpha induced protein 2
RAB3B	0.97061656	1.96	8.64E-04	1.93E-04	RAB3B	RAB3B, member RAS oncogene family
KLHL7	0.96960492	1.96	4.85E-07	3.50E-08	KLHL7	kelch like family member 7
ATP6V1C1	0.96945422	1.96	5.65E-10	1.26E-11	ATP6V1C1	ATPase H+ transporting V1 subunit C1
RDH10	0.96941694	1.96	1.34E-05	1.62E-06	RDH10	retinol dehydrogenase 10 (all-trans)
RBL1	0.96871291	1.96	6.39E-10	1.46E-11	RBL1	RB transcriptional corepressor like 1
TCIRG1	0.96838565	1.96	9.95E-09	3.80E-10	TCIRG1	T-cell immune regulator 1, ATPase H+ transporting V0 subunit a3

MIR7110///PDIA5	0.96793638	1.96	4.69E-08	2.32E-09	MIR7110///PDIA5	microRNA 7110///protein disulfide isomerase family A member 5
GPR84	0.96768145	1.96	2.47E-08	1.09E-09	GPR84	G protein-coupled receptor 84
ATP13A3	0.96739693	1.96	2.43E-11	2.68E-13	ATP13A3	ATPase 13A3
FBXO45	0.96733861	1.96	1.67E-06	1.48E-07	FBXO45	F-box protein 45
CTSS	0.96729512	1.96	2.86E-04	5.42E-05	CTSS	cathepsin 5
HTR2C	0.96728735	1.96	9.60E-05	1.55E-05	HTR2C	5-hydroxytryptamine receptor 2C
UBE2G1	-0.98579117	0.50	1.64E-09	4.42E-11	UBE2G1	ubiquitin conjugating enzyme E2 G1
FHL5	-0.98591533	0.50	9.06E-06	1.03E-06	FHL5	four and a half LIM domains 5
C14orf28	-0.98630855	0.50	2.46E-08	1.08E-09	C14orf28	chromosome 14 open reading frame 28
GAS2	-0.98634927	0.50	9.51E-10	2.32E-11	GAS2	growth arrest specific 2
PLD1	-0.98638379	0.50	4.65E-06	4.78E-07	PLD1	phospholipase D1
DENND4C	-0.9866709	0.50	8.80E-11	1.31E-12	DENND4C	DENN domain containing 4C
MAPT	-0.98688196	0.50	5.24E-10	1.15E-11	MAPT	microtubule associated protein tau
GATSL3	-0.98778565	0.50	6.29E-06	6.81E-07	GATSL3	GATS protein like 3
LINC00417	-0.98801826	0.50	5.10E-07	3.71E-08	LINC00417	long intergenic non-protein coding RNA 417
CAMK2N1	-0.98817242	0.50	3.17E-05	4.34E-06	CAMK2N1	calcium/calmodulin dependent protein kinase II inhibitor 1
ARNTL2	-0.98831347	0.50	2.89E-05	3.89E-06	ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2
NBEA	-0.98938959	0.50	4.67E-06	4.82E-07	NBEA	neurobeachin
SLK	-0.99064456	0.50	1.32E-10	2.19E-12	SLK	STE20 like kinase
SMAP1	-0.99310986	0.50	2.61E-10	5.05E-12	SMAP1	small ArfGAP 1
ZEB2	-0.99346433	0.50	1.29E-06	1.10E-07	ZEB2	zinc finger E-box binding homeobox 2
LOC101927507	-0.99456516	0.50	1.20E-09	3.05E-11	LOC101927507	uncharacterized LOC101927507
DIO2	-0.99511697	0.50	6.65E-04	1.43E-04	DIO2	deiodinase, iodothyronine, type II
C15orf62	-0.99515249	0.50	7.00E-10	1.63E-11	C15orf62	chromosome 15 open reading frame 62
NCAM1	-0.99515808	0.50	9.76E-08	5.47E-09	NCAM1	neural cell adhesion molecule 1
AGA	-0.99533998	0.50	3.72E-08	1.77E-09	AGA	aspartylglucosaminidase
VAV3	-0.99685885	0.50	2.48E-05	3.26E-06	VAV3	vav guanine nucleotide exchange factor 3
PLCXD3	-0.99692745	0.50	6.27E-10	1.43E-11	PLCXD3	phosphatidylinositol specific phospholipase C X domain containing 3
NTRK3	-0.99703664	0.50	2.23E-09	6.41E-11	NTRK3	neurotrophic receptor tyrosine kinase 3
TNS1	-0.99750713	0.50	1.50E-07	8.97E-09	TNS1	tensin 1
SORCS1	-0.99778592	0.50	2.33E-09	6.73E-11	SORCS1	sortilin related VPS10 domain containing receptor 1
LIPH	-0.99791633	0.50	1.13E-09	2.84E-11	LIPH	lipase H
PGR	-0.99874526	0.50	1.51E-10	2.59E-12	PGR	progesterone receptor
ZFPM2	-0.99891686	0.50	2.07E-04	3.74E-05	ZFPM2	zinc finger protein, FOG family member 2
SNX24	-1.00000742	0.50	8.16E-11	1.19E-12	SNX24	sorting nexin 24
RBM47	-1.0002166	0.50	1.54E-10	2.67E-12	RBM47	RNA binding motif protein 47
MIR4680///PDCD4	-1.00031566	0.50	1.79E-11	1.80E-13	MIR4680///PDCD4	microRNA 4680///programmed cell

						death 4 (neoplastic transformation inhibitor)
TTY14	-1.00066448	0.50	2.58E-03	6.82E-04	TTY14	testis-specific transcript, Y-linked 14 (non-protein coding)
TRIP10	-1.00134325	0.50	1.05E-09	2.60E-11	TRIP10	thyroid hormone receptor interactor 10
GKN1	-1.00225693	0.50	1.31E-01	7.00E-02	GKN1	gastrokine 1
LOC101927490	-1.00309423	0.50	4.23E-09	1.38E-10	LOC101927490	uncharacterized LOC101927490
OSBPL10	-1.0034927	0.50	2.24E-11	2.42E-13	OSBPL10	oxysterol binding protein like 10
HILPDA	-1.004124	0.50	2.77E-03	7.37E-04	HILPDA	hypoxia inducible lipid droplet associated
FRY	-1.00416457	0.50	1.54E-04	2.66E-05	FRY	FRY microtubule binding protein
PHYHD1	-1.00446934	0.50	1.60E-12	8.20E-15	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1
FIGN	-1.00506413	0.50	2.00E-05	2.55E-06	FIGN	fidgetin, microtubule severing factor
DAPP1	-1.00516998	0.50	1.20E-08	4.71E-10	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides 1
RBM24	-1.00543642	0.50	4.21E-06	4.28E-07	RBM24	RNA binding motif protein 24
SSTR1	-1.00544095	0.50	6.92E-05	1.07E-05	SSTR1	somatostatin receptor 1
C8orf88	-1.00595879	0.50	5.90E-08	3.04E-09	C8orf88	chromosome 8 open reading frame 88
NPEPPS	-1.00605713	0.50	1.28E-10	2.11E-12	NPEPPS	aminopeptidase puromycin sensitive
DCLK1	-1.00630735	0.50	2.05E-05	2.63E-06	DCLK1	doublecortin like kinase 1
KRCC1	-1.00645571	0.50	1.10E-09	2.72E-11	KRCC1	lysine rich coiled-coil 1
PPP1R3B	-1.00696212	0.50	1.40E-08	5.64E-10	PPP1R3B	protein phosphatase 1 regulatory subunit 3B
NFIA	-1.00703108	0.50	9.15E-04	2.06E-04	NFIA	nuclear factor I A
LOC101927057///OMG	-1.00716992	0.50	1.65E-08	6.86E-10	LOC101927057///OMG	uncharacterized LOC101927057///oligodendrocyte myelin glycoprotein
LOC102724093///GOLGA6L4///GOLGA6L9///GOLGA6L5P	-1.00737441	0.50	1.65E-09	4.46E-11	LOC102724093///GOLGA6L4///GOLGA6L9///GOLGA6L5P	golgin subfamily A member 6-like protein 4///golgin A6 family-like 4///golgin A6 family-like 9///golgin A6 family-like 5, pseudogene
MMEL1	-1.00783102	0.50	3.44E-11	4.05E-13	MMEL1	membrane metallo-endopeptidase-like 1
TMX2-CTNND1///CTNND1	-1.00803067	0.50	6.71E-12	5.24E-14	TMX2-CTNND1///CTNND1	TMX2-CTNND1 readthrough (NMD candidate)///catenin delta 1
CCNG1	-1.00804997	0.50	3.47E-08	1.63E-09	CCNG1	cyclin G1
MAP3K9	-1.00829878	0.50	6.79E-07	5.19E-08	MAP3K9	mitogen-activated protein kinase kinase kinase 9
ZNF426	-1.00888206	0.50	3.94E-11	4.83E-13	ZNF426	zinc finger protein 426
RPL15	-1.00928918	0.50	2.11E-09	6.01E-11	RPL15	ribosomal protein L15
PPM1L	-1.00971732	0.50	3.44E-05	4.78E-06	PPM1L	protein phosphatase, Mg2+/Mn2+ dependent 1L
ALDH9A1	-1.00986399	0.50	2.05E-12	1.16E-14	ALDH9A1	aldehyde dehydrogenase 9 family member A1
CUL4B	-1.01273507	0.50	3.70E-07	2.56E-08	CUL4B	cullin 4B
BDH2	-1.01304246	0.50	8.83E-08	4.87E-09	BDH2	3-hydroxybutyrate dehydrogenase, type 2
ITCH	-1.01327881	0.50	1.73E-06	1.54E-07	ITCH	itchy E3 ubiquitin protein ligase
C12orf29	-1.01413107	0.50	3.44E-11	4.06E-13	C12orf29	chromosome 12 open reading frame 29

EREG	-1.01439158	0.50	1.09E-02	3.61E-03	<i>EREG</i>	epiregulin
PHACTR2	-1.01455542	0.49	4.44E-08	2.18E-09	<i>PHACTR2</i>	phosphatase and actin regulator 2
EEF1A1	-1.01497288	0.49	8.75E-09	3.28E-10	<i>EEF1A1</i>	eukaryotic translation elongation factor 1 alpha 1
LOC202025	-1.01503117	0.49	4.32E-08	2.11E-09	<i>LOC202025</i>	uncharacterized LOC202025
RERG	-1.01604467	0.49	2.30E-05	3.00E-06	<i>RERG</i>	RAS like estrogen regulated growth inhibitor
DOCK9	-1.01636593	0.49	9.66E-08	5.40E-09	<i>DOCK9</i>	dedicator of cytokinesis 9
LGR4	-1.01679719	0.49	6.51E-08	3.41E-09	<i>LGR4</i>	leucine rich repeat containing G protein-coupled receptor 4
CD24	-1.01719869	0.49	2.84E-09	8.46E-11	<i>CD24</i>	CD24 molecule
FAR1	-1.01748371	0.49	4.26E-09	1.40E-10	<i>FAR1</i>	fatty acyl-CoA reductase 1
ZFAND5	-1.01772838	0.49	6.05E-07	4.53E-08	<i>ZFAND5</i>	zinc finger AN1-type containing 5
SERPINB6	-1.01795654	0.49	2.18E-13	5.85E-16	<i>SERPINB6</i>	serpin family B member 6
PRDM16	-1.01924489	0.49	4.53E-05	6.57E-06	<i>PRDM16</i>	PR/SET domain 16
ACACB	-1.01935146	0.49	7.56E-08	4.06E-09	<i>ACACB</i>	acetyl-CoA carboxylase beta
PLBD1	-1.01987312	0.49	1.09E-06	9.05E-08	<i>PLBD1</i>	phospholipase B domain containing 1
ACOX1	-1.0201792	0.49	1.42E-10	2.39E-12	<i>ACOX1</i>	acyl-CoA oxidase 1
RYR2	-1.02025659	0.49	2.06E-06	1.87E-07	<i>RYR2</i>	ryanodine receptor 2
FAM63A	-1.02077215	0.49	1.31E-14	1.10E-17	<i>FAM63A</i>	family with sequence similarity 63 member A
TMEM184A	-1.02083094	0.49	4.94E-08	2.46E-09	<i>TMEM184A</i>	transmembrane protein 184A
ZSCAN18	-1.02110756	0.49	2.92E-07	1.94E-08	<i>ZSCAN18</i>	zinc finger and SCAN domain containing 18
SLC12A6	-1.02205632	0.49	1.17E-06	9.81E-08	<i>SLC12A6</i>	solute carrier family 12 member 6
FGD4	-1.02252642	0.49	6.76E-09	2.41E-10	<i>FGD4</i>	FYVE, RhoGEF and PH domain containing 4
BCL2L15	-1.02255608	0.49	7.56E-07	5.89E-08	<i>BCL2L15</i>	BCL2 like 15
PRIMA1	-1.02278857	0.49	5.08E-06	5.31E-07	<i>PRIMA1</i>	proline rich membrane anchor 1
ITPR2	-1.02284994	0.49	5.72E-12	4.26E-14	<i>ITPR2</i>	inositol 1,4,5-trisphosphate receptor type 2
NME5	-1.02300683	0.49	1.39E-08	5.59E-10	<i>NME5</i>	NME/NM23 family member 5
PDE1A	-1.02362893	0.49	2.89E-08	1.31E-09	<i>PDE1A</i>	phosphodiesterase 1A
RBPMS	-1.02427901	0.49	1.31E-12	6.38E-15	<i>RBPMS</i>	RNA binding protein with multiple splicing
GKAP1	-1.02452081	0.49	1.69E-09	4.58E-11	<i>GKAP1</i>	G kinase anchoring protein 1
FAM129B	-1.02453669	0.49	2.73E-08	1.22E-09	<i>FAM129B</i>	family with sequence similarity 129 member B
ATP6V1D	-1.02508394	0.49	2.57E-10	4.96E-12	<i>ATP6V1D</i>	ATPase H+ transporting V1 subunit D
ZNF204P	-1.02509182	0.49	7.64E-08	4.11E-09	<i>ZNF204P</i>	zinc finger protein 204, pseudogene
ZNF300P1	-1.02549331	0.49	1.39E-05	1.69E-06	<i>ZNF300P1</i>	zinc finger protein 300 pseudogene 1
ARHGAP27	-1.02633895	0.49	1.19E-12	5.27E-15	<i>ARHGAP27</i>	Rho GTPase activating protein 27
MAGI3	-1.02686795	0.49	8.73E-12	7.30E-14	<i>MAGI3</i>	membrane associated guanylate kinase, WW and PDZ domain containing 3
MYLK	-1.02741549	0.49	2.51E-07	1.62E-08	<i>MYLK</i>	myosin light chain kinase
PHACTR2	-1.02768285	0.49	2.82E-09	8.38E-11	<i>PHACTR2</i>	phosphatase and actin regulator 2

AIM1L	-1.02794641	0.49	4.56E-05	6.62E-06	AIM1L	absent in melanoma 1-like
TPM1	-1.02833252	0.49	2.25E-07	1.43E-08	TPM1	tropomyosin 1 (alpha)
GCHFR	-1.02835553	0.49	6.48E-06	7.06E-07	GCHFR	GTP cyclohydrolase I feedback regulator
KIAA0232	-1.02923353	0.49	5.35E-12	3.85E-14	KIAA0232	KIAA0232
RNASE7	-1.02927749	0.49	6.48E-05	9.90E-06	RNASE7	ribonuclease A family member 7
FGD4	-1.03031431	0.49	3.38E-09	1.04E-10	FGD4	FYVE, RhoGEF and PH domain containing 4
SCNN1G	-1.03038719	0.49	2.34E-05	3.06E-06	SCNN1G	sodium channel epithelial 1 gamma subunit
C3orf70	-1.0311581	0.49	1.49E-06	1.29E-07	C3orf70	chromosome 3 open reading frame 70
WISP2	-1.03125697	0.49	6.26E-06	6.77E-07	WISP2	WNT1 inducible signaling pathway protein 2
GAB1	-1.03140515	0.49	1.89E-08	7.98E-10	GAB1	GRB2 associated binding protein 1
PBX1	-1.0321062	0.49	4.61E-09	1.54E-10	PBX1	PBX homeobox 1
IGSF10	-1.03233786	0.49	1.37E-05	1.66E-06	IGSF10	immunoglobulin superfamily member 10
SNX16	-1.03272357	0.49	4.44E-08	2.17E-09	SNX16	sorting nexin 16
MPZL2	-1.03332958	0.49	1.87E-07	1.16E-08	MPZL2	myelin protein zero like 2
SH3GL3	-1.03354234	0.49	4.18E-06	4.25E-07	SH3GL3	SH3 domain containing GRB2 like 3, endophilin A3
SUCLG2	-1.03453971	0.49	3.30E-12	2.07E-14	SUCLG2	succinate-CoA ligase GDP-forming beta subunit
PIGN	-1.03512017	0.49	2.23E-09	6.38E-11	PIGN	phosphatidylinositol glycan anchor biosynthesis class N
NUCB2	-1.03581233	0.49	1.16E-11	1.05E-13	NUCB2	nucleobindin 2
SH3BGR	-1.03583666	0.49	5.94E-08	3.06E-09	SH3BGR	SH3 domain binding glutamate rich protein
MYL9	-1.03616335	0.49	3.02E-06	2.91E-07	MYL9	myosin light chain 9
PPP1R12B	-1.0386254	0.49	6.11E-08	3.16E-09	PPP1R12B	protein phosphatase 1 regulatory subunit 12B
CSGALNACT1	-1.03872019	0.49	6.94E-07	5.33E-08	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1
TRIM16	-1.03968433	0.49	1.02E-06	8.32E-08	TRIM16	tripartite motif containing 16
ZNF57	-1.03968818	0.49	2.56E-09	7.46E-11	ZNF57	zinc finger protein 57
SUCLG2	-1.04000299	0.49	1.06E-13	2.19E-16	SUCLG2	succinate-CoA ligase GDP-forming beta subunit
MRVI1	-1.04010149	0.49	5.13E-07	3.74E-08	MRVI1	murine retrovirus integration site 1 homolog
SUCLG2	-1.04051236	0.49	3.97E-14	5.81E-17	SUCLG2	succinate-CoA ligase GDP-forming beta subunit
ABCA6	-1.04052692	0.49	9.09E-08	5.03E-09	ABCA6	ATP binding cassette subfamily A member 6
NHLH2	-1.04153079	0.49	4.04E-05	5.76E-06	NHLH2	nescent helix-loop-helix 2
OCLN	-1.04329092	0.49	2.04E-11	2.12E-13	OCLN	occludin
MGST2	-1.04364922	0.49	1.20E-12	5.55E-15	MGST2	microsomal glutathione S-transferase 2
KRT24	-1.04669857	0.48	1.29E-01	6.86E-02	KRT24	keratin 24
RAP1A	-1.04690723	0.48	9.15E-09	3.45E-10	RAP1A	RAP1A, member of RAS oncogene family
ACOX2	-1.04761901	0.48	2.55E-10	4.90E-12	ACOX2	acyl-CoA oxidase 2
ITIHS	-1.04765211	0.48	2.03E-09	5.71E-11	ITIHS	inter-alpha-trypsin inhibitor heavy chain family member 5
AFDN-AS1	-1.04829505	0.48	2.18E-10	4.08E-12	AFDN-AS1	AFDN antisense RNA 1 (head to head)
SH3RF2	-1.04836326	0.48	5.62E-06	5.97E-07	SH3RF2	SH3 domain containing ring finger 2

LOC100505555///ZNF846	-1.04860861	0.48	5.41E-11	7.03E-13	LOC100505555///ZNF846	uncharacterized LOC100505555///zinc finger protein 846
CAPN5	-1.04887414	0.48	2.14E-11	2.30E-13	CAPN5	calpain 5
MECOM	-1.04897951	0.48	2.35E-06	2.18E-07	MECOM	MDS1 and EVI1 complex locus
FCHO2	-1.04918828	0.48	2.27E-10	4.28E-12	FCHO2	FCH domain only 2
TMEM80	-1.04966505	0.48	6.40E-08	3.34E-09	TMEM80	transmembrane protein 80
ASB5	-1.05019939	0.48	5.76E-06	6.14E-07	ASB5	ankyrin repeat and SOCS box containing 5
LIPF	-1.05128114	0.48	1.58E-01	8.83E-02	LIPF	lipase F, gastric type
NTN4	-1.05149517	0.48	3.58E-06	3.53E-07	NTN4	netrin 4
GAB1	-1.05288927	0.48	3.13E-07	2.11E-08	GAB1	GRB2 associated binding protein 1
PMM1	-1.05504647	0.48	6.55E-11	9.03E-13	PMM1	phosphomannomutase 1
TJP1	-1.0551726	0.48	1.88E-10	3.39E-12	TJP1	tight junction protein 1
BICDL2	-1.05593656	0.48	6.10E-10	1.38E-11	BICDL2	BICD family like cargo adaptor 2
SLITRK3	-1.05781267	0.48	2.62E-08	1.17E-09	SLITRK3	SLIT and NTRK like family member 3
TIAM1	-1.05782449	0.48	5.14E-06	5.39E-07	TIAM1	T-cell lymphoma invasion and metastasis 1
ZDHHC21	-1.05784644	0.48	1.70E-08	7.10E-10	ZDHHC21	zinc finger DHHC-type containing 21
EPB41L4A	-1.05788358	0.48	2.15E-11	2.31E-13	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A
BBIP1	-1.05795351	0.48	1.35E-13	2.92E-16	BBIP1	BBSome interacting protein 1
MAL2	-1.05856402	0.48	2.35E-07	1.50E-08	MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene)
SAP18	-1.06088057	0.48	2.15E-12	1.26E-14	SAP18	Sin3A associated protein 18
CPE	-1.06132578	0.48	6.07E-08	3.14E-09	CPE	carboxypeptidase E
RSPO2	-1.06138842	0.48	2.38E-09	6.88E-11	RSPO2	R-spondin 2
SLC24A3	-1.06149503	0.48	3.58E-07	2.46E-08	SLC24A3	solute carrier family 24 member 3
FAXDC2	-1.06200792	0.48	3.30E-11	3.83E-13	FAXDC2	fatty acid hydroxylase domain containing 2
FYCO1	-1.06264667	0.48	2.29E-14	2.52E-17	FYCO1	FYVE and coiled-coil domain containing 1
ECHDC2	-1.064144	0.48	1.45E-10	2.45E-12	ECHDC2	enoyl-CoA hydratase domain containing 2
MAML3	-1.06514906	0.48	5.91E-10	1.33E-11	MAML3	mastermind like transcriptional coactivator 3
LDB3	-1.06548491	0.48	6.74E-09	2.40E-10	LDB3	LIM domain binding 3
KANK2	-1.06643146	0.48	1.66E-07	1.02E-08	KANK2	KN motif and ankyrin repeat domains 2
KRCC1	-1.06673611	0.48	1.62E-08	6.70E-10	KRCC1	lysine rich coiled-coil 1
MUC20	-1.0689061	0.48	1.39E-03	3.34E-04	MUC20	mucin 20, cell surface associated
ZBTB7C	-1.0694321	0.48	1.49E-06	1.29E-07	ZBTB7C	zinc finger and BTB domain containing 7C
MFAP4	-1.06946104	0.48	7.71E-07	6.02E-08	MFAP4	microfibrillar associated protein 4
STXBP5	-1.06986947	0.48	2.25E-10	4.24E-12	STXBP5	syntaxin binding protein 5
ID4	-1.07058054	0.48	3.59E-06	3.55E-07	ID4	inhibitor of DNA binding 4, HLH protein
PRSS3P2	-1.07076042	0.48	1.54E-08	6.34E-10	PRSS3P2	protease, serine 3 pseudogene 2
ITGA1	-1.07129974	0.48	1.63E-06	1.44E-07	ITGA1	integrin subunit alpha 1
HS3ST6	-1.07145275	0.48	1.74E-04	3.07E-05	HS3ST6	heparan sulfate-glucosamine 3-sulfotransferase 6

HCG11	-1.07180073	0.48	2.65E-07	1.73E-08	HCG11	HLA complex group 11 (non-protein coding)
S100A14	-1.07189108	0.48	3.17E-07	2.13E-08	S100A14	S100 calcium binding protein A14
PITPNM3	-1.07278761	0.48	1.26E-07	7.30E-09	PITPNM3	PITPNM family member 3
PTN	-1.07309877	0.48	5.18E-05	7.66E-06	PTN	pleiotrophin
KATNBL1	-1.07338816	0.48	6.23E-08	3.24E-09	KATNBL1	katanin regulatory subunit B1 like 1
RALGPS1	-1.07342868	0.48	4.89E-11	6.22E-13	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1
UGT1A3///UGT1A1///UGT1A4///UGT1A9///UGT1A5///UGT1A6///UGT1A7///UGT1A8///UGT1A10	-1.07464802	0.47	2.14E-03	5.50E-04	UGT1A3///UGT1A1///UGT1A4///UGT1A9///UGT1A5///UGT1A6///UGT1A7///UGT1A8///UGT1A10	UDP glucuronosyltransferase family 1 member A3///UDP glucuronosyltransferase family 1 member A1///UDP glucuronosyltransferase family 1 member A4///UDP glucuronosyltransferase family 1 member A9///UDP glucuronosyltransferase family 1 member A5///UDP glucuronosyltransferase family 1 member A6///UDP glucuronosyltransferase family 1 member A7///UDP glucuronosyltransferase family 1 member A8///UDP glucuronosyltransferase family 1 member A10
SERPINB4	-1.07585392	0.47	1.64E-02	5.89E-03	SERPINB4	serpin family B member 4
MEOX2	-1.0758795	0.47	7.63E-06	8.51E-07	MEOX2	mesenchyme homeobox 2
FBXL16	-1.07610806	0.47	1.14E-06	9.51E-08	FBXL16	F-box and leucine rich repeat protein 16
PLLP	-1.07617795	0.47	3.20E-08	1.47E-09	PLLP	plasmolipin
ESPL1	-1.07637306	0.47	1.33E-06	1.14E-07	ESPL1	extra spindle pole bodies like 1, separase
CNKSR3	-1.07790624	0.47	1.06E-07	5.99E-09	CNKSR3	CNKSR family member 3
SMAD9	-1.07849694	0.47	7.98E-06	8.96E-07	SMAD9	SMAD family member 9
PDE1A	-1.07894617	0.47	3.65E-08	1.73E-09	PDE1A	phosphodiesterase 1A
RNF125	-1.07933062	0.47	9.13E-07	7.33E-08	RNF125	ring finger protein 125
SLC26A2	-1.07992442	0.47	2.62E-05	3.48E-06	SLC26A2	solute carrier family 26 member 2
GNAQ	-1.08041	0.47	7.93E-11	1.15E-12	GNAQ	G protein subunit alpha q
AFDN	-1.08067038	0.47	6.73E-11	9.35E-13	AFDN	afadin, adherens junction formation factor
UGT1A1///UGT1A4///UGT1A9///UGT1A6///UGT1A8///UGT1A10	-1.08144506	0.47	2.23E-03	5.78E-04	UGT1A1///UGT1A4///UGT1A9///UGT1A6///UGT1A8///UGT1A10	UDP glucuronosyltransferase family 1 member A1///UDP glucuronosyltransferase family 1 member A4///UDP glucuronosyltransferase family 1 member A9///UDP glucuronosyltransferase family 1 member A6///UDP glucuronosyltransferase family 1 member A8///UDP glucuronosyltransferase

						family 1 member A10
DTNA	-1.08224927	0.47	8.79E-06	9.99E-07	DTNA	dystrobrevin alpha
TNFRSF11A	-1.08231179	0.47	5.12E-06	5.36E-07	TNFRSF11A	TNF receptor superfamily member 11a
MYH11	-1.08313347	0.47	5.27E-09	1.81E-10	MYH11	myosin heavy chain 11
SAMD9	-1.08424653	0.47	5.37E-08	2.73E-09	SAMD9	sterile alpha motif domain containing 9
EHF	-1.08842296	0.47	8.05E-09	2.97E-10	EHF	ETS homologous factor
CNTN4	-1.08882675	0.47	3.57E-06	3.52E-07	CNTN4	contactin 4
LRRFIP2	-1.08947631	0.47	9.28E-11	1.40E-12	LRRFIP2	LRR binding FLII interacting protein 2
C1orf21	-1.08972516	0.47	9.90E-13	4.17E-15	C1orf21	chromosome 1 open reading frame 21
BMS1P20	-1.09010937	0.47	1.82E-11	1.85E-13	BMS1P20	BMS1, ribosome biogenesis factor pseudogene 20
SUN1	-1.09019133	0.47	3.10E-06	3.00E-07	SUN1	Sad1 and UNC84 domain containing 1
TCF21	-1.09069134	0.47	4.72E-07	3.40E-08	TCF21	transcription factor 21
OCLN	-1.09229419	0.47	8.70E-11	1.29E-12	OCLN	occludin
SLC7A2	-1.09320231	0.47	2.32E-06	2.15E-07	SLC7A2	solute carrier family 7 member 2
TMEM79	-1.09322912	0.47	2.51E-05	3.31E-06	TMEM79	transmembrane protein 79
ITM2A	-1.0935741	0.47	1.23E-09	3.15E-11	ITM2A	integral membrane protein 2A
CEP126	-1.09398789	0.47	3.72E-06	3.70E-07	CEP126	centrosomal protein 126
ENTPD5	-1.09459255	0.47	1.83E-09	5.06E-11	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5
DNALI1	-1.0951959	0.47	3.27E-09	1.00E-10	DNALI1	dynein axonemal light intermediate chain 1
PHACTR4	-1.09521504	0.47	2.03E-10	3.75E-12	PHACTR4	phosphatase and actin regulator 4
CNTNAP3B///CNTNAP3	-1.09584753	0.47	2.10E-09	5.95E-11	CNTNAP3B///CNTNAP3	contactin associated protein-like 3B///contactin associated protein-like 3
MYOT	-1.09631599	0.47	4.84E-09	1.63E-10	MYOT	myotilin
FXYP1	-1.09662644	0.47	6.70E-13	2.37E-15	FXYP1	FXYP domain containing ion transport regulator 1
EVPL	-1.0967265	0.47	2.83E-06	2.70E-07	EVPL	envoplakin
MUC20	-1.09694114	0.47	2.39E-05	3.14E-06	MUC20	mucin 20, cell surface associated
ITCH	-1.09722535	0.47	5.76E-07	4.28E-08	ITCH	itchy E3 ubiquitin protein ligase
HIGD1A	-1.09725486	0.47	9.32E-14	1.81E-16	HIGD1A	HIG1 hypoxia inducible domain family member 1A
MIR4680///PDCD4	-1.09931011	0.47	5.15E-14	8.29E-17	MIR4680///PDCD4	microRNA 4680///programmed cell death 4 (neoplastic transformation inhibitor)
PHACTR4	-1.0993559	0.47	4.22E-12	2.87E-14	PHACTR4	phosphatase and actin regulator 4
RASGEF1B	-1.09983178	0.47	7.00E-08	3.72E-09	RASGEF1B	RasGEF domain family member 1B
PKIB	-1.1000308	0.47	9.69E-06	1.12E-06	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta
MUC1	-1.10087405	0.47	1.30E-07	7.61E-09	MUC1	mucin 1, cell surface associated
RASAL1	-1.10115475	0.47	2.04E-13	5.29E-16	RASAL1	RAS protein activator like 1
MIR4680///PDCD4	-1.10225199	0.47	1.01E-12	4.27E-15	MIR4680///PDCD4	microRNA 4680///programmed cell

						death 4 (neoplastic transformation inhibitor)
GRAMD1C	-1.10278823	0.47	2.54E-06	2.38E-07	GRAMD1C	GRAM domain containing 1C
DIO2	-1.1029986	0.47	4.18E-04	8.37E-05	DIO2	deiodinase, iodothyronine, type II
KIAA0232	-1.10347915	0.47	2.87E-11	3.26E-13	KIAA0232	KIAA0232
C12orf29	-1.10367678	0.47	7.09E-09	2.56E-10	C12orf29	chromosome 12 open reading frame 29
LOC101930404//SNORD116-28//SNORD115-26//SNORD115-13//SNORD115-7//SNORD116-22//SNORD116-4//PWARSN//SNORD107//IPW	-1.10399884	0.47	2.80E-07	1.84E-08	LOC101930404//SNORD116-28//SNORD115-26//SNORD115-13//SNORD115-7//SNORD116-22//SNORD116-4//PWARSN//SNORD107//IPW	uncharacterized LOC101930404//small nucleolar RNA, C/D box 116-28//small nucleolar RNA, C/D box 115-26//small nucleolar RNA, C/D box 115-13//small nucleolar RNA, C/D box 115-7//small nucleolar RNA, C/D box 116-22//small nucleolar RNA, C/D box 116-4//Prader Willi/Angelman region RNA, SNRPN neighbor//small nucleolar RNA, C/D box 107//imprinted in Prader-Willi syndrome (non-protein coding)
PRELP	-1.10406081	0.47	3.24E-08	1.50E-09	PRELP	proline and arginine rich end leucine rich repeat protein
SERPINB13	-1.10507541	0.46	2.28E-06	2.10E-07	SERPINB13	serpin family B member 13
KCNK3	-1.10605688	0.46	3.30E-08	1.53E-09	KCNK3	potassium two pore domain channel subfamily K member 3
REEP1	-1.10796581	0.46	2.07E-06	1.89E-07	REEP1	receptor accessory protein 1
ROR1	-1.10853828	0.46	1.62E-11	1.58E-13	ROR1	receptor tyrosine kinase like orphan receptor 1
NEGR1	-1.10879861	0.46	6.94E-11	9.69E-13	NEGR1	neuronal growth regulator 1
ZDHHC20	-1.10942061	0.46	3.47E-07	2.38E-08	ZDHHC20	zinc finger DHHC-type containing 20
RNF141	-1.11202021	0.46	2.36E-08	1.03E-09	RNF141	ring finger protein 141
ANGPTL1	-1.11262185	0.46	3.01E-09	9.11E-11	ANGPTL1	angiotensinogen like 1
PDZRN3	-1.11271252	0.46	7.62E-10	1.80E-11	PDZRN3	PDZ domain containing ring finger 3
LYPD3	-1.11303449	0.46	4.90E-05	7.19E-06	LYPD3	LY6/PLAUR domain containing 3
CAPN6	-1.113156	0.46	3.74E-05	5.26E-06	CAPN6	calpain 6
ARG1	-1.11399126	0.46	6.12E-04	1.30E-04	ARG1	arginase 1
FAM221A	-1.11421958	0.46	1.86E-10	3.36E-12	FAM221A	family with sequence similarity 221 member A
PARD6B	-1.11437235	0.46	1.29E-10	2.13E-12	PARD6B	par-6 family cell polarity regulator beta
GP2	-1.11446792	0.46	2.58E-03	6.80E-04	GP2	glycoprotein 2
SLC16A7	-1.11457157	0.46	8.12E-08	4.40E-09	SLC16A7	solute carrier family 16 member 7
ADGRD1	-1.11464588	0.46	2.12E-05	2.73E-06	ADGRD1	adhesion G protein-coupled receptor D1
ZNF667-AS1	-1.11601936	0.46	9.06E-07	7.27E-08	ZNF667-AS1	ZNF667 antisense RNA 1 (head to head)
UBXN10-AS1	-1.11637713	0.46	1.53E-08	6.29E-10	UBXN10-AS1	UBXN10 antisense RNA 1
LCN2	-1.11778969	0.46	1.49E-03	3.63E-04	LCN2	lipocalin 2
ABHD5	-1.11821513	0.46	1.86E-10	3.35E-12	ABHD5	abhydrolase domain containing 5
LMO3	-1.11862976	0.46	6.35E-07	4.79E-08	LMO3	LIM domain only 3
C1QTNF7	-1.11866109	0.46	4.32E-12	2.96E-14	C1QTNF7	C1q and tumor necrosis factor related protein 7

AIF1L	-1.1200696	0.46	1.05E-10	1.62E-12	AIF1L	allograft inflammatory factor 1 like
TMPRSS2	-1.12111288	0.46	1.27E-06	1.08E-07	TMPRSS2	transmembrane protease, serine 2
CHAC1	-1.12113498	0.46	2.54E-10	4.87E-12	CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1
LINC00551	-1.12134212	0.46	1.04E-10	1.61E-12	LINC00551	long intergenic non-protein coding RNA 551
FAM149A	-1.12302741	0.46	5.35E-11	6.94E-13	FAM149A	family with sequence similarity 149 member A
LOC101929340	-1.12335522	0.46	2.29E-14	2.56E-17	LOC101929340	uncharacterized LOC101929340
COL28A1	-1.12377564	0.46	2.43E-08	1.07E-09	COL28A1	collagen type XXVIII alpha 1 chain
ACOX1	-1.12398874	0.46	1.78E-10	3.17E-12	ACOX1	acyl-CoA oxidase 1
MAOA	-1.12419549	0.46	5.84E-07	4.34E-08	MAOA	monoamine oxidase A
MYO5B	-1.12424685	0.46	1.10E-07	6.25E-09	MYO5B	myosin VB
CDKL5	-1.12429261	0.46	1.18E-09	2.99E-11	CDKL5	cyclin dependent kinase like 5
CAPNS2	-1.12536768	0.46	7.09E-04	1.53E-04	CAPNS2	calpain small subunit 2
PLN	-1.12742517	0.46	3.42E-05	4.74E-06	PLN	phospholamban
RBM47	-1.12890071	0.46	4.09E-07	2.88E-08	RBM47	RNA binding motif protein 47
LIPH	-1.12945434	0.46	1.78E-07	1.10E-08	LIPH	lipase H
ANXA1	-1.13074747	0.46	1.30E-03	3.09E-04	ANXA1	annexin A1
COBLL1	-1.13249341	0.46	8.06E-09	2.98E-10	COBLL1	cordon-bleu WH2 repeat protein like 1
CRYL1	-1.13294866	0.46	1.20E-14	9.36E-18	CRYL1	crystallin lambda 1
HPSE	-1.13335695	0.46	4.27E-05	6.14E-06	HPSE	heparanase
NDNF	-1.13374081	0.46	1.12E-09	2.80E-11	NDNF	neuron derived neurotrophic factor
GPR27	-1.13433283	0.46	7.41E-05	1.16E-05	GPR27	G protein-coupled receptor 27
CRABP2	-1.1345383	0.46	4.57E-05	6.64E-06	CRABP2	cellular retinoic acid binding protein 2
BOC	-1.13476722	0.46	5.83E-06	6.23E-07	BOC	BOC cell adhesion associated, oncogene regulated
EXPH5	-1.13501612	0.46	3.74E-05	5.26E-06	EXPH5	exophilin 5
CYBRD1	-1.13522496	0.46	2.84E-08	1.28E-09	CYBRD1	cytochrome b reductase 1
NOSTRIN	-1.13528495	0.46	1.62E-07	9.86E-09	NOSTRIN	nitric oxide synthase trafficking
DAAM2	-1.13636449	0.45	3.56E-10	7.23E-12	DAAM2	dishevelled associated activator of morphogenesis 2
CCBE1	-1.13661462	0.45	2.86E-10	5.62E-12	CCBE1	collagen and calcium binding EGF domains 1
PLEKHA7	-1.13662424	0.45	6.93E-09	2.49E-10	PLEKHA7	pleckstrin homology domain containing A7
ZNF555	-1.13773223	0.45	1.69E-10	2.98E-12	ZNF555	zinc finger protein 555
NQO1	-1.13816463	0.45	6.53E-05	1.00E-05	NQO1	NAD(P)H quinone dehydrogenase 1
C4orf3	-1.13834606	0.45	1.73E-10	3.06E-12	C4orf3	chromosome 4 open reading frame 3
HIF3A	-1.13867307	0.45	1.79E-07	1.10E-08	HIF3A	hypoxia inducible factor 3 alpha subunit
SVIP	-1.13889266	0.45	2.89E-09	8.63E-11	SVIP	small VCP interacting protein
SUGT1	-1.13939752	0.45	6.43E-12	4.87E-14	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone
EMCN	-1.1401813	0.45	6.77E-08	3.56E-09	EMCN	endomucin
COBLL1	-1.14019552	0.45	9.52E-08	5.30E-09	COBLL1	cordon-bleu WH2 repeat protein like 1

FKBP1A-SDCBP2///SDCBP2	-1.14031806	0.45	1.54E-10	2.65E-12	FKBP1A-SDCBP2///SDCBP2	FKBP1A-SDCBP2 readthrough (NMD candidate)///syndecan binding protein 2
ANXA1	-1.1430629	0.45	6.42E-07	4.85E-08	ANXA1	annexin A1
STATH	-1.14315431	0.45	8.96E-02	4.42E-02	STATH	statherin
RGN	-1.14407539	0.45	1.12E-11	9.93E-14	RGN	regucalcin
LOC101929373///SLC9B1	-1.14436376	0.45	8.12E-10	1.94E-11	LOC101929373///SLC9B1	uncharacterized LOC101929373///solute carrier family 9 member B1
CLU	-1.14516571	0.45	2.09E-05	2.70E-06	CLU	clusterin
LOC100507311	-1.14622347	0.45	1.32E-09	3.43E-11	LOC100507311	uncharacterized LOC100507311
CARMN	-1.14664563	0.45	1.45E-06	1.26E-07	CARMN	cardiac mesoderm enhancer-associated non-coding RNA
2-Mar	-1.14686422	0.45	4.60E-08	2.27E-09	2-Mar	mitochondrial amidoxime reducing component 2
MTMR10	-1.14701392	0.45	1.83E-08	7.71E-10	MTMR10	myotubularin related protein 10
USP53	-1.14772914	0.45	1.22E-10	1.98E-12	USP53	ubiquitin specific peptidase 53
TPM1	-1.14799426	0.45	1.11E-08	4.33E-10	TPM1	tropomyosin 1 (alpha)
CPED1	-1.14811574	0.45	5.00E-08	2.50E-09	CPED1	cadherin like and PC-esterase domain containing 1
ANXA2	-1.14879955	0.45	1.13E-04	1.86E-05	ANXA2	annexin A2
SLC24A3	-1.14987544	0.45	6.22E-08	3.23E-09	SLC24A3	solute carrier family 24 member 3
WNK4	-1.15046291	0.45	1.01E-04	1.65E-05	WNK4	WNK lysine deficient protein kinase 4
NRXN1	-1.1506594	0.45	1.52E-07	9.12E-09	NRXN1	neurexin 1
IL17D	-1.15137984	0.45	3.71E-09	1.18E-10	IL17D	interleukin 17D
PTN	-1.15170752	0.45	1.86E-05	2.35E-06	PTN	pleiotrophin
PPP1R9A	-1.15300722	0.45	1.00E-08	3.83E-10	PPP1R9A	protein phosphatase 1 regulatory subunit 9A
ACOX3	-1.15573432	0.45	2.68E-09	7.87E-11	ACOX3	acyl-CoA oxidase 3, pristanoyl
AKAP12	-1.15615359	0.45	5.66E-08	2.89E-09	AKAP12	A-kinase anchoring protein 12
CFL2	-1.15626071	0.45	1.62E-07	9.82E-09	CFL2	cofilin 2
FRMD4B	-1.15652019	0.45	1.74E-11	1.73E-13	FRMD4B	FERM domain containing 4B
PHLDA1	-1.1573835	0.45	1.00E-05	1.16E-06	PHLDA1	pleckstrin homology like domain family A member 1
RASEF	-1.15738662	0.45	8.34E-06	9.41E-07	RASEF	RAS and EF-hand domain containing
ARHGAP6	-1.15795146	0.45	1.91E-11	1.97E-13	ARHGAP6	Rho GTPase activating protein 6
LOC101928274///VSIG10	-1.15976306	0.45	2.78E-11	3.12E-13	LOC101928274///VSIG10	uncharacterized LOC101928274///V-set and immunoglobulin domain containing 10
ESPL1	-1.15979615	0.45	2.13E-07	1.34E-08	ESPL1	extra spindle pole bodies like 1, separase
SFRP1	-1.15984065	0.45	9.10E-07	7.30E-08	SFRP1	secreted frizzled related protein 1
LOC101928635///ALDH1A2	-1.16003341	0.45	2.57E-08	1.14E-09	LOC101928635///ALDH1A2	uncharacterized LOC101928635///aldehyde dehydrogenase 1 family member A2
ERO1A	-1.16015702	0.45	2.96E-09	8.90E-11	ERO1A	endoplasmic reticulum oxidoreductase 1 alpha
ACPP	-1.16202552	0.45	5.46E-06	5.78E-07	ACPP	acid phosphatase, prostate
BPIFB2	-1.16241149	0.45	4.32E-03	1.23E-03	BPIFB2	BPI fold containing family B member 2

CSRP1	-1.16457633	0.45	5.92E-10	1.33E-11	CSRP1	cysteine and glycine rich protein 1
KCTD6	-1.16488582	0.45	6.06E-11	8.10E-13	KCTD6	potassium channel tetramerization domain containing 6
RASAL2	-1.16524291	0.45	3.83E-07	2.66E-08	RASAL2	RAS protein activator like 2
ARHGAP32	-1.16589124	0.45	4.57E-10	9.81E-12	ARHGAP32	Rho GTPase activating protein 32
FLJ35700	-1.16640032	0.45	1.15E-03	2.68E-04	FLJ35700	uncharacterized protein FLJ35700
ARHGAP32	-1.16667353	0.45	2.08E-11	2.22E-13	ARHGAP32	Rho GTPase activating protein 32
USP46	-1.16692298	0.45	4.47E-10	9.51E-12	USP46	ubiquitin specific peptidase 46
GNG11	-1.16806291	0.45	5.88E-11	7.72E-13	GNG11	G protein subunit gamma 11
HSDL2	-1.16862749	0.44	1.41E-10	2.36E-12	HSDL2	hydroxysteroid dehydrogenase like 2
CH25H	-1.16900421	0.44	7.23E-05	1.12E-05	CH25H	cholesterol 25-hydroxylase
DSC2	-1.16901596	0.44	7.64E-07	5.97E-08	DSC2	desmocollin 2
ZNF101	-1.1731552	0.44	1.25E-10	2.05E-12	ZNF101	zinc finger protein 101
ACACB	-1.17424285	0.44	8.12E-08	4.40E-09	ACACB	acetyl-CoA carboxylase beta
SNX9	-1.17448203	0.44	7.50E-13	2.76E-15	SNX9	sorting nexin 9
PIK3C2G	-1.17488781	0.44	3.38E-07	2.30E-08	PIK3C2G	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma
PIGN	-1.17603859	0.44	3.31E-08	1.53E-09	PIGN	phosphatidylinositol glycan anchor biosynthesis class N
GSTM5	-1.1763542	0.44	3.68E-12	2.39E-14	GSTM5	glutathione S-transferase mu 5
SNX24	-1.17702256	0.44	6.63E-12	5.09E-14	SNX24	sorting nexin 24
ACADM	-1.17709541	0.44	1.78E-10	3.15E-12	ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain
LINC01082	-1.17718292	0.44	2.55E-08	1.13E-09	LINC01082	long intergenic non-protein coding RNA 1082
UGT1A1///UGT1A4///UGT1A9///UGT1A6///UGT1A8///UGT1A10	-1.17771662	0.44	1.31E-03	3.13E-04	UGT1A1///UGT1A4///UGT1A9///UGT1A6///UGT1A8///UGT1A10	UDP glucuronosyltransferase family 1 member A1///UDP glucuronosyltransferase family 1 member A4///UDP glucuronosyltransferase family 1 member A9///UDP glucuronosyltransferase family 1 member A6///UDP glucuronosyltransferase family 1 member A8///UDP glucuronosyltransferase family 1 member A10
CAST	-1.17973675	0.44	6.71E-12	5.19E-14	CAST	calpastatin
BHMT2	-1.17981399	0.44	1.22E-09	3.13E-11	BHMT2	betaine--homocysteine S-methyltransferase 2
FAM46B	-1.17990459	0.44	9.28E-06	1.06E-06	FAM46B	family with sequence similarity 46 member B
TRPC1	-1.18103829	0.44	4.35E-06	4.44E-07	TRPC1	transient receptor potential cation channel subfamily C member 1
C1orf21	-1.1811248	0.44	3.99E-12	2.67E-14	C1orf21	chromosome 1 open reading frame 21
MICU3	-1.18136876	0.44	3.67E-09	1.16E-10	MICU3	mitochondrial calcium uptake family member 3
RANBP9	-1.18280378	0.44	1.25E-12	5.93E-15	RANBP9	RAN binding protein 9
DCLK1	-1.18301463	0.44	8.00E-08	4.33E-09	DCLK1	doublecortin like kinase 1

LINC00702	-1.18324389	0.44	1.46E-07	8.71E-09	LINC00702	long intergenic non-protein coding RNA 702
KCNAB1	-1.1836342	0.44	2.89E-09	8.62E-11	KCNAB1	potassium voltage-gated channel subfamily A member regulatory beta subunit 1
PAIP2B	-1.18444346	0.44	2.08E-11	2.21E-13	PAIP2B	poly(A) binding protein interacting protein 2B
RIOK3	-1.18476261	0.44	2.30E-07	1.47E-08	RIOK3	RIO kinase 3
DPT	-1.18554963	0.44	5.16E-09	1.77E-10	DPT	dermatopontin
MIR100HG	-1.18570119	0.44	6.68E-07	5.09E-08	MIR100HG	mir-100-let-7a-2 cluster host gene
PWAR6	-1.18575918	0.44	4.40E-07	3.13E-08	PWAR6	Prader Willi/Angelman region RNA 6
ESRRG	-1.18838269	0.44	8.79E-05	1.40E-05	ESRRG	estrogen related receptor gamma
GMDS	-1.18983007	0.44	2.88E-07	1.91E-08	GMDS	GDP-mannose 4,6-dehydratase
RANBP9	-1.19088573	0.44	1.01E-11	8.76E-14	RANBP9	RAN binding protein 9
EIF4E3	-1.19118439	0.44	1.21E-10	1.96E-12	EIF4E3	eukaryotic translation initiation factor 4E family member 3
NFIA	-1.19127886	0.44	5.56E-10	1.23E-11	NFIA	nuclear factor I A
PTN	-1.19143365	0.44	5.35E-06	5.64E-07	PTN	pleiotrophin
SVIP	-1.19146428	0.44	1.57E-08	6.45E-10	SVIP	small VCP interacting protein
RNF150	-1.19173628	0.44	1.87E-08	7.90E-10	RNF150	ring finger protein 150
REEP1	-1.19214469	0.44	3.13E-07	2.11E-08	REEP1	receptor accessory protein 1
RNASE7	-1.19419049	0.44	2.14E-04	3.89E-05	RNASE7	ribonuclease A family member 7
KLK12	-1.19477715	0.44	5.24E-04	1.08E-04	KLK12	kallikrein related peptidase 12
FMO9P	-1.19497839	0.44	4.80E-04	9.79E-05	FMO9P	flavin containing monooxygenase 9 pseudogene
PDE1C	-1.19571122	0.44	1.36E-09	3.55E-11	PDE1C	phosphodiesterase 1C
ITGA9	-1.19584228	0.44	5.31E-08	2.69E-09	ITGA9	integrin subunit alpha 9
AGFG2	-1.19640367	0.44	9.87E-13	4.12E-15	AGFG2	ArfGAP with FG repeats 2
PAX9	-1.19728829	0.44	6.82E-03	2.10E-03	PAX9	paired box 9
CDKN2AIP	-1.19783999	0.44	1.90E-09	5.31E-11	CDKN2AIP	CDKN2A interacting protein
LOC100130476	-1.19976935	0.44	6.59E-08	3.45E-09	LOC100130476	uncharacterized LOC100130476
PLEKHH2	-1.20063413	0.44	7.76E-07	6.07E-08	PLEKHH2	pleckstrin homology, MyTH4 and FERM domain containing H2
TMOD1	-1.20163268	0.43	1.26E-10	2.07E-12	TMOD1	tropomodulin 1
GRHL1	-1.20257146	0.43	2.27E-05	2.96E-06	GRHL1	grainyhead like transcription factor 1
SMTN	-1.20347752	0.43	7.29E-08	3.90E-09	SMTN	smoothelin
TMEM108	-1.20391577	0.43	1.20E-07	6.91E-09	TMEM108	transmembrane protein 108
ELOVL6	-1.20485743	0.43	2.53E-07	1.64E-08	ELOVL6	ELOVL fatty acid elongase 6
GIPC2	-1.20508651	0.43	3.10E-07	2.08E-08	GIPC2	GIPC PDZ domain containing family member 2
ZNF471	-1.20556395	0.43	7.46E-11	1.06E-12	ZNF471	zinc finger protein 471
PRR15L	-1.20623468	0.43	6.40E-07	4.84E-08	PRR15L	proline rich 15 like
CD24	-1.20637982	0.43	6.21E-11	8.43E-13	CD24	CD24 molecule
EIF4E3	-1.20638373	0.43	1.82E-12	9.95E-15	EIF4E3	eukaryotic translation initiation factor 4E family member 3

DYNLT3	-1.20768334	0.43	1.39E-09	3.62E-11	<i>DYNLT3</i>	dynein light chain Tctex-type 3
DENND2C	-1.2083653	0.43	3.73E-07	2.58E-08	<i>DENND2C</i>	DENN domain containing 2C
CCNG2	-1.20846036	0.43	7.18E-15	4.46E-18	<i>CCNG2</i>	cyclin G2
NTRK3	-1.20854643	0.43	6.84E-08	3.61E-09	<i>NTRK3</i>	neurotrophic receptor tyrosine kinase 3
TFF2	-1.2086287	0.43	3.74E-02	1.56E-02	<i>TFF2</i>	trefoil factor 2
TCP11L2	-1.20913223	0.43	5.37E-08	2.73E-09	<i>TCP11L2</i>	t-complex 11 like 2
RNF180	-1.21122869	0.43	1.19E-10	1.91E-12	<i>RNF180</i>	ring finger protein 180
AGTR1	-1.21142803	0.43	4.37E-07	3.11E-08	<i>AGTR1</i>	angiotensin II receptor type 1
PDE1A	-1.21338464	0.43	1.12E-06	9.27E-08	<i>PDE1A</i>	phosphodiesterase 1A
ABI3BP	-1.2136388	0.43	5.54E-04	1.16E-04	<i>ABI3BP</i>	ABI family member 3 binding protein
P2RY14	-1.2140398	0.43	2.80E-07	1.84E-08	<i>P2RY14</i>	purinergic receptor P2Y14
ZNF823	-1.21425489	0.43	8.51E-14	1.56E-16	<i>ZNF823</i>	zinc finger protein 823
DUOX1	-1.21512196	0.43	2.14E-06	1.96E-07	<i>DUOX1</i>	dual oxidase 1
LEPROT///LEPR	-1.21516447	0.43	4.30E-10	9.03E-12	<i>LEPROT///LEPR</i>	leptin receptor overlapping transcript///leptin receptor
UACA	-1.21529404	0.43	1.62E-12	8.33E-15	<i>UACA</i>	uveal autoantigen with coiled-coil domains and ankyrin repeats
ADAMTSL1	-1.21598261	0.43	7.99E-12	6.49E-14	<i>ADAMTSL1</i>	ADAMTS like 1
C18orf25	-1.2168021	0.43	1.04E-09	2.57E-11	<i>C18orf25</i>	chromosome 18 open reading frame 25
CLDN11	-1.21764905	0.43	1.37E-05	1.66E-06	<i>CLDN11</i>	claudin 11
CDS1	-1.21766235	0.43	1.42E-11	1.33E-13	<i>CDS1</i>	CDP-diacylglycerol synthase 1
ARHGAP32	-1.21775425	0.43	1.76E-11	1.76E-13	<i>ARHGAP32</i>	Rho GTPase activating protein 32
SH3D19	-1.21800008	0.43	1.09E-10	1.71E-12	<i>SH3D19</i>	SH3 domain containing 19
CEACAM1	-1.21955658	0.43	1.07E-11	9.38E-14	<i>CEACAM1</i>	carcinoembryonic antigen related cell adhesion molecule 1
PRH1-PRR4///PRH2///PRH1	-1.22002084	0.43	1.19E-02	4.02E-03	<i>PRH1-PRR4///PRH2///PRH1</i>	PRH1-PRR4 readthrough///proline rich protein HaellI subfamily 2///proline rich protein HaellI subfamily 1
TLR3	-1.2216081	0.43	7.48E-07	5.82E-08	<i>TLR3</i>	toll like receptor 3
TSPAN6	-1.22175514	0.43	1.47E-07	8.77E-09	<i>TSPAN6</i>	tetraspanin 6
ME1	-1.22372904	0.43	1.33E-07	7.83E-09	<i>ME1</i>	malic enzyme 1
DAPL1	-1.22576851	0.43	5.66E-03	1.69E-03	<i>DAPL1</i>	death associated protein like 1
C15orf52	-1.22643011	0.43	8.30E-11	1.22E-12	<i>C15orf52</i>	chromosome 15 open reading frame 52
ZMAT1	-1.22648964	0.43	2.76E-07	1.81E-08	<i>ZMAT1</i>	zinc finger matrin-type 1
RHBDL2	-1.22822003	0.43	1.46E-08	5.95E-10	<i>RHBDL2</i>	rhomboid like 2
TLR3	-1.22901556	0.43	6.24E-06	6.75E-07	<i>TLR3</i>	toll like receptor 3
ZNF415	-1.22958888	0.43	2.51E-08	1.11E-09	<i>ZNF415</i>	zinc finger protein 415
HCG11	-1.23080859	0.43	9.13E-08	5.06E-09	<i>HCG11</i>	HLA complex group 11 (non-protein coding)
CXCL17	-1.23135976	0.43	5.38E-06	5.68E-07	<i>CXCL17</i>	C-X-C motif chemokine ligand 17
PDK4	-1.23396405	0.43	3.70E-04	7.28E-05	<i>PDK4</i>	pyruvate dehydrogenase kinase 4
XKR4	-1.23403114	0.43	2.65E-11	2.96E-13	<i>XKR4</i>	XK related 4

HMGCS2	-1.2345884	0.42	8.33E-05	1.32E-05	HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2
ANKRD22	-1.23540215	0.42	7.32E-09	2.65E-10	ANKRD22	ankyrin repeat domain 22
BEX4	-1.23603125	0.42	1.76E-10	3.12E-12	BEX4	brain expressed X-linked 4
GALNT12	-1.23607505	0.42	4.41E-10	9.32E-12	GALNT12	polypeptide N-acetylgalactosaminyltransferase 12
IL33	-1.23658413	0.42	1.34E-05	1.61E-06	IL33	interleukin 33
KANK1	-1.23684893	0.42	2.21E-08	9.53E-10	KANK1	KN motif and ankyrin repeat domains 1
AR	-1.23757952	0.42	5.76E-13	1.99E-15	AR	androgen receptor
SLC16A9	-1.23765018	0.42	1.88E-07	1.17E-08	SLC16A9	solute carrier family 16 member 9
FAM189A2	-1.23949959	0.42	5.35E-11	6.91E-13	FAM189A2	family with sequence similarity 189 member A2
GMDS	-1.24077321	0.42	1.68E-10	2.95E-12	GMDS	GDP-mannose 4,6-dehydratase
GPAT3	-1.24109039	0.42	4.44E-08	2.17E-09	GPAT3	glycerol-3-phosphate acyltransferase 3
KIAA2022	-1.24190362	0.42	3.30E-07	2.24E-08	KIAA2022	KIAA2022
CEACAM1	-1.24302486	0.42	8.88E-14	1.69E-16	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1
TPM2	-1.24312331	0.42	3.70E-08	1.76E-09	TPM2	tropomyosin 2 (beta)
BTBD11	-1.24351483	0.42	7.24E-07	5.60E-08	BTBD11	BTB domain containing 11
TPM1	-1.24410854	0.42	3.03E-06	2.91E-07	TPM1	tropomyosin 1 (alpha)
TMEM178A	-1.24443129	0.42	2.54E-06	2.38E-07	TMEM178A	transmembrane protein 178A
CAST	-1.24520163	0.42	2.04E-11	2.14E-13	CAST	calpastatin
FIBIN	-1.24585411	0.42	6.94E-07	5.33E-08	FIBIN	fin bud initiation factor homolog (zebrafish)
ADAMTS9-AS2	-1.24665541	0.42	2.55E-10	4.89E-12	ADAMTS9-AS2	ADAMTS9 antisense RNA 2
PRKAR2B	-1.24839775	0.42	2.62E-07	1.71E-08	PRKAR2B	protein kinase cAMP-dependent type II regulatory subunit beta
PDZD2	-1.24869613	0.42	8.18E-08	4.44E-09	PDZD2	PDZ domain containing 2
PP14571	-1.24887818	0.42	1.23E-10	2.00E-12	PP14571	uncharacterized LOC100130449
TOX3	-1.25375979	0.42	5.90E-03	1.78E-03	TOX3	TOX high mobility group box family member 3
SLIT2	-1.25470634	0.42	3.89E-07	2.71E-08	SLIT2	slit guidance ligand 2
RRAGD	-1.2547597	0.42	1.32E-07	7.73E-09	RRAGD	Ras related GTP binding D
MUC7	-1.25677982	0.42	3.40E-04	6.62E-05	MUC7	mucin 7, secreted
ZNF536	-1.25923698	0.42	6.26E-10	1.43E-11	ZNF536	zinc finger protein 536
MUC20	-1.25945259	0.42	1.31E-04	2.20E-05	MUC20	mucin 20, cell surface associated
ZBTB16	-1.25969235	0.42	1.42E-04	2.42E-05	ZBTB16	zinc finger and BTB domain containing 16
PKIB	-1.25978437	0.42	3.71E-06	3.70E-07	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta
SLC27A6	-1.25986703	0.42	2.59E-09	7.57E-11	SLC27A6	solute carrier family 27 member 6
FILIP1	-1.26003829	0.42	4.63E-08	2.29E-09	FILIP1	filamin A interacting protein 1
SLK	-1.26045273	0.42	5.85E-09	2.04E-10	SLK	STE20 like kinase
RBPM5	-1.26063833	0.42	3.47E-11	4.11E-13	RBPM5	RNA binding protein with multiple splicing
ELOVL4	-1.2616542	0.42	1.23E-05	1.47E-06	ELOVL4	ELOVL fatty acid elongase 4
PLAC9	-1.26202839	0.42	1.36E-09	3.53E-11	PLAC9	placenta specific 9

C4orf3	-1.26348686	0.42	5.18E-13	1.76E-15	<i>C4orf3</i>	chromosome 4 open reading frame 3
KCNB1	-1.26420009	0.42	1.33E-09	3.45E-11	<i>KCNB1</i>	potassium voltage-gated channel subfamily B member 1
OCLN	-1.2645169	0.42	3.24E-12	2.03E-14	<i>OCLN</i>	occludin
SPAG17	-1.26643766	0.42	2.75E-06	2.61E-07	<i>SPAG17</i>	sperm associated antigen 17
ZNF844	-1.26647152	0.42	2.97E-10	5.87E-12	<i>ZNF844</i>	zinc finger protein 844
SLC8A1-AS1	-1.26877477	0.42	2.46E-09	7.13E-11	<i>SLC8A1-AS1</i>	SLC8A1 antisense RNA 1
STK39	-1.26897495	0.41	2.38E-12	1.43E-14	<i>STK39</i>	serine/threonine kinase 39
CLGN	-1.26919888	0.41	2.36E-05	3.09E-06	<i>CLGN</i>	calmegin
ATP6V0A4	-1.27031203	0.41	4.29E-07	3.05E-08	<i>ATP6V0A4</i>	ATPase H+ transporting V0 subunit a4
TTL7	-1.27139312	0.41	2.24E-09	6.44E-11	<i>TTL7</i>	tubulin tyrosine ligase like 7
HLF	-1.27208138	0.41	6.13E-05	9.31E-06	<i>HLF</i>	HLF, PAR bZIP transcription factor
EIF3F	-1.27218634	0.41	1.62E-12	8.30E-15	<i>EIF3F</i>	eukaryotic translation initiation factor 3 subunit F
C6orf132	-1.2728362	0.41	9.11E-11	1.37E-12	<i>C6orf132</i>	chromosome 6 open reading frame 132
NEXN	-1.27319536	0.41	1.48E-08	6.03E-10	<i>NEXN</i>	nexilin F-actin binding protein
MYO5C	-1.27413568	0.41	1.59E-07	9.60E-09	<i>MYO5C</i>	myosin VC
ITM2A	-1.27474764	0.41	3.97E-11	4.89E-13	<i>ITM2A</i>	integral membrane protein 2A
THSD4	-1.27503158	0.41	1.32E-09	3.40E-11	<i>THSD4</i>	thrombospondin type 1 domain containing 4
ANK2	-1.27734374	0.41	8.68E-06	9.83E-07	<i>ANK2</i>	ankyrin 2, neuronal
GATM	-1.27899564	0.41	1.88E-08	7.95E-10	<i>GATM</i>	glycine amidinotransferase
FAM135A	-1.27988753	0.41	1.43E-10	2.40E-12	<i>FAM135A</i>	family with sequence similarity 135 member A
THRB	-1.28013059	0.41	1.19E-12	5.43E-15	<i>THRB</i>	thyroid hormone receptor beta
EMP1	-1.28063221	0.41	4.42E-07	3.15E-08	<i>EMP1</i>	epithelial membrane protein 1
THSD4	-1.28187784	0.41	1.59E-08	6.59E-10	<i>THSD4</i>	thrombospondin type 1 domain containing 4
UBL3	-1.28229146	0.41	1.74E-14	1.59E-17	<i>UBL3</i>	ubiquitin like 3
RAB11A	-1.28430877	0.41	5.05E-13	1.71E-15	<i>RAB11A</i>	RAB11A, member RAS oncogene family
RRAGD	-1.28550468	0.41	4.20E-08	2.04E-09	<i>RRAGD</i>	Ras related GTP binding D
KLK12	-1.2858477	0.41	3.79E-04	7.49E-05	<i>KLK12</i>	kallikrein related peptidase 12
MSRB3	-1.28939228	0.41	4.73E-08	2.34E-09	<i>MSRB3</i>	methionine sulfoxide reductase B3
RUNDC3B	-1.29553816	0.41	4.77E-10	1.03E-11	<i>RUNDC3B</i>	RUN domain containing 3B
C18orf25	-1.29709078	0.41	3.01E-09	9.10E-11	<i>C18orf25</i>	chromosome 18 open reading frame 25
NCAM1	-1.29854822	0.41	1.99E-07	1.24E-08	<i>NCAM1</i>	neural cell adhesion molecule 1
CYP2C9	-1.29860503	0.41	4.87E-10	1.05E-11	<i>CYP2C9</i>	cytochrome P450 family 2 subfamily C member 9
NEXN	-1.29869738	0.41	7.04E-08	3.75E-09	<i>NEXN</i>	nexilin F-actin binding protein
ETFDH	-1.2999477	0.41	8.98E-13	3.53E-15	<i>ETFDH</i>	electron transfer flavoprotein dehydrogenase
SORT1	-1.30094239	0.41	1.83E-13	4.41E-16	<i>SORT1</i>	sortilin 1
APOD	-1.30319072	0.41	2.07E-05	2.66E-06	<i>APOD</i>	apolipoprotein D
SPRR3	-1.30330095	0.41	1.99E-02	7.40E-03	<i>SPRR3</i>	small proline rich protein 3
PTGR1	-1.30422398	0.40	4.19E-08	2.04E-09	<i>PTGR1</i>	prostaglandin reductase 1

CAST	-1.3046032	0.40	4.39E-11	5.50E-13	CAST	calpastatin
RAB27B	-1.30539985	0.40	2.47E-11	2.73E-13	RAB27B	RAB27B, member RAS oncogene family
AGR3	-1.30726743	0.40	8.42E-02	4.10E-02	AGR3	anterior gradient 3, protein disulphide isomerase family member
IL1RN	-1.30865783	0.40	3.39E-08	1.58E-09	IL1RN	interleukin 1 receptor antagonist
UGT1A3///UGT1A1///UGT1A4///UGT1A9///UGT1A5///UGT1A6///UGT1A7///UGT1A8///UGT1A10	-1.30952488	0.40	2.20E-03	5.69E-04	UGT1A3///UGT1A1///UGT1A4///UGT1A9///UGT1A5///UGT1A6///UGT1A7///UGT1A8///UGT1A10	UDP glucuronosyltransferase family 1 member A3///UDP glucuronosyltransferase family 1 member A1///UDP glucuronosyltransferase family 1 member A4///UDP glucuronosyltransferase family 1 member A9///UDP glucuronosyltransferase family 1 member A5///UDP glucuronosyltransferase family 1 member A6///UDP glucuronosyltransferase family 1 member A7///UDP glucuronosyltransferase family 1 member A8///UDP glucuronosyltransferase family 1 member A10
ETFDH	-1.31057434	0.40	8.97E-13	3.51E-15	ETFDH	electron transfer flavoprotein dehydrogenase
LINC00675	-1.31060951	0.40	8.77E-07	7.00E-08	LINC00675	long intergenic non-protein coding RNA 675
CD24	-1.31079532	0.40	6.27E-11	8.55E-13	CD24	CD24 molecule
PLEKHA7	-1.31432071	0.40	8.51E-14	1.57E-16	PLEKHA7	pleckstrin homology domain containing A7
MYO6	-1.31671984	0.40	4.11E-13	1.35E-15	MYO6	myosin VI
CMA1	-1.31867536	0.40	2.16E-06	1.97E-07	CMA1	chymase 1
TMPRSS11D	-1.32204232	0.40	3.25E-04	6.28E-05	TMPRSS11D	transmembrane protease, serine 11D
FAM107A	-1.32297197	0.40	1.03E-08	3.96E-10	FAM107A	family with sequence similarity 107 member A
IVL	-1.32308506	0.40	2.16E-04	3.93E-05	IVL	involucrin
MTURN	-1.32412178	0.40	1.62E-11	1.59E-13	MTURN	maturin, neural progenitor differentiation regulator homolog (Xenopus)
CDS1	-1.32419509	0.40	2.02E-10	3.71E-12	CDS1	CDP-diacylglycerol synthase 1
MAB21L2	-1.32449764	0.40	4.56E-07	3.27E-08	MAB21L2	mab-21 like 2
ALDH3A1	-1.32638106	0.40	2.89E-04	5.48E-05	ALDH3A1	aldehyde dehydrogenase 3 family member A1
CDA	-1.32643656	0.40	6.12E-05	9.28E-06	CDA	cytidine deaminase
GIPC2	-1.32859128	0.40	3.14E-07	2.11E-08	GIPC2	GIPC PDZ domain containing family member 2
ERBB3	-1.32953119	0.40	5.55E-12	4.05E-14	ERBB3	erb-b2 receptor tyrosine kinase 3
ADGRF1	-1.32996536	0.40	1.32E-08	5.28E-10	ADGRF1	adhesion G protein-coupled receptor F1
DIXDC1	-1.33055981	0.40	2.94E-08	1.34E-09	DIXDC1	DIX domain containing 1
ZNF431	-1.33059676	0.40	7.97E-11	1.16E-12	ZNF431	zinc finger protein 431
GULP1	-1.334042	0.40	8.97E-12	7.60E-14	GULP1	GULP, engulfment adaptor PTB domain

						containing 1
TRIM2	-1.33498421	0.40	4.07E-05	5.79E-06	TRIM2	tripartite motif containing 2
PAQR5	-1.3354248	0.40	9.61E-12	8.22E-14	PAQR5	progesterone and adiponectin receptor family member 5
GAB1	-1.33616621	0.40	9.01E-13	3.56E-15	GAB1	GRB2 associated binding protein 1
ADGRG6	-1.33649291	0.40	3.41E-09	1.06E-10	ADGRG6	adhesion G protein-coupled receptor G6
KALRN	-1.33746679	0.40	2.42E-11	2.66E-13	KALRN	kalirin, RhoGEF kinase
SMIM5	-1.3377311	0.40	4.82E-13	1.60E-15	SMIM5	small integral membrane protein 5
ABLIM3	-1.3400612	0.40	1.83E-13	4.42E-16	ABLIM3	actin binding LIM protein family member 3
LYVE1	-1.340826	0.39	1.12E-08	4.34E-10	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1
SEL1L2///GPR37	-1.34319491	0.39	4.39E-08	2.15E-09	SEL1L2///GPR37	SEL1L2 ERAD E3 ligase adaptor subunit///G protein-coupled receptor 37
GNG7	-1.34389523	0.39	8.26E-11	1.21E-12	GNG7	G protein subunit gamma 7
CHRM3	-1.34393352	0.39	4.96E-08	2.48E-09	CHRM3	cholinergic receptor muscarinic 3
MPZL2	-1.34410255	0.39	5.11E-07	3.72E-08	MPZL2	myelin protein zero like 2
SOX6	-1.34432115	0.39	6.59E-07	5.00E-08	SOX6	SRY-box 6
LOC101927263	-1.34468707	0.39	1.51E-09	4.03E-11	LOC101927263	uncharacterized LOC101927263
RNF150	-1.34506552	0.39	1.76E-08	7.37E-10	RNF150	ring finger protein 150
TPM1	-1.34645547	0.39	2.45E-08	1.08E-09	TPM1	tropomyosin 1 (alpha)
PTCHD1	-1.34646952	0.39	4.30E-07	3.05E-08	PTCHD1	patched domain containing 1
DHRS9	-1.34688947	0.39	1.69E-08	7.07E-10	DHRS9	dehydrogenase/reductase 9
STYK1	-1.34723927	0.39	2.76E-09	8.12E-11	STYK1	serine/threonine/tyrosine kinase 1
ZDHHC13	-1.34810882	0.39	3.79E-11	4.61E-13	ZDHHC13	zinc finger DHHC-type containing 13
LOC105377134	-1.3496179	0.39	4.48E-10	9.55E-12	LOC105377134	uncharacterized LOC105377134
KLK13	-1.34991046	0.39	3.48E-10	7.06E-12	KLK13	kallikrein related peptidase 13
KCNMA1	-1.35017408	0.39	4.91E-07	3.56E-08	KCNMA1	potassium calcium-activated channel subfamily M alpha 1
EPHX3	-1.35092	0.39	1.39E-04	2.37E-05	EPHX3	epoxide hydrolase 3
TP53INP2	-1.35141988	0.39	5.93E-10	1.34E-11	TP53INP2	tumor protein p53 inducible nuclear protein 2
GREM2	-1.35299932	0.39	1.06E-10	1.65E-12	GREM2	gremlin 2, DAN family BMP antagonist
SLIT2	-1.35481094	0.39	2.71E-06	2.57E-07	SLIT2	slit guidance ligand 2
FUT6	-1.35608994	0.39	1.14E-12	5.00E-15	FUT6	fucosyltransferase 6
FBXO3	-1.35654496	0.39	1.19E-12	5.28E-15	FBXO3	F-box protein 3
GPM6A	-1.3569157	0.39	9.93E-11	1.52E-12	GPM6A	glycoprotein M6A
USP6NL	-1.35700634	0.39	3.52E-13	1.07E-15	USP6NL	USP6 N-terminal like
GRHL3	-1.35889196	0.39	6.34E-05	9.66E-06	GRHL3	grainyhead like transcription factor 3
AR	-1.36121821	0.39	5.41E-12	3.90E-14	AR	androgen receptor
ABHD5	-1.36195084	0.39	4.48E-10	9.54E-12	ABHD5	abhydrolase domain containing 5
MGLL	-1.36299387	0.39	1.55E-09	4.14E-11	MGLL	monoglyceride lipase

S100P	-1.36366877	0.39	3.87E-05	5.48E-06	S100P	S100 calcium binding protein P
ZG16B	-1.36374271	0.39	2.55E-02	9.91E-03	ZG16B	zymogen granule protein 16B
ZNF431	-1.36424511	0.39	1.82E-08	7.67E-10	ZNF431	zinc finger protein 431
PTK6	-1.36457192	0.39	7.80E-11	1.13E-12	PTK6	protein tyrosine kinase 6
CES2	-1.36543627	0.39	4.99E-12	3.53E-14	CES2	carboxylesterase 2
SPATA18	-1.3689755	0.39	7.02E-12	5.58E-14	SPATA18	spermatogenesis associated 18
SBSN	-1.36905918	0.39	1.13E-03	2.63E-04	SBSN	suprabasin
DDAH1	-1.37032284	0.39	3.97E-11	4.88E-13	DDAH1	dimethylarginine dimethylaminohydrolase 1
KLF8	-1.37055406	0.39	2.59E-07	1.68E-08	KLF8	Kruppel like factor 8
CACNB2	-1.37209962	0.39	1.65E-07	1.00E-08	CACNB2	calcium voltage-gated channel auxiliary subunit beta 2
KLK12	-1.37293118	0.39	6.67E-04	1.43E-04	KLK12	kallikrein related peptidase 12
HMGNS	-1.37460523	0.39	1.33E-10	2.20E-12	HMGNS	high mobility group nucleosome binding domain 5
TNXB///TNXA	-1.37605741	0.39	1.51E-10	2.59E-12	TNXB///TNXA	tenascin XB///tenascin XA (pseudogene)
RANBP9	-1.37610166	0.39	2.61E-09	7.63E-11	RANBP9	RAN binding protein 9
MPZL3	-1.37660307	0.39	5.93E-10	1.33E-11	MPZL3	myelin protein zero like 3
BSPRY	-1.37663012	0.39	5.05E-13	1.71E-15	BSPRY	B-box and SPRY domain containing
TF	-1.37793046	0.38	1.58E-03	3.89E-04	TF	transferrin
SLMAP	-1.37812712	0.38	4.68E-11	5.95E-13	SLMAP	sarcolemma associated protein
EPHX2	-1.37879259	0.38	5.01E-13	1.68E-15	EPHX2	epoxide hydrolase 2
MSMB	-1.37957032	0.38	9.91E-02	5.00E-02	MSMB	microseminoprotein beta
GPRASP1	-1.38005997	0.38	1.45E-09	3.82E-11	GPRASP1	G protein-coupled receptor associated sorting protein 1
TPRG1	-1.38036637	0.38	2.90E-04	5.50E-05	TPRG1	tumor protein p63 regulated 1
ANKRD35	-1.38133022	0.38	1.70E-09	4.61E-11	ANKRD35	ankyrin repeat domain 35
CES2	-1.38151544	0.38	1.62E-11	1.59E-13	CES2	carboxylesterase 2
PTGR1	-1.38196645	0.38	1.66E-09	4.48E-11	PTGR1	prostaglandin reductase 1
CPEB3	-1.38245682	0.38	2.70E-14	3.31E-17	CPEB3	cytoplasmic polyadenylation element binding protein 3
RMND5A	-1.38279454	0.38	2.66E-08	1.19E-09	RMND5A	required for meiotic nuclear division 5 homolog A
C16orf89	-1.38316121	0.38	2.35E-07	1.51E-08	C16orf89	chromosome 16 open reading frame 89
SERPINB4///SERPINB3	-1.38339695	0.38	7.82E-04	1.72E-04	SERPINB4///SERPINB3	serpin family B member 4///serpin family B member 3
PCBP1-AS1	-1.38346391	0.38	7.16E-15	4.32E-18	PCBP1-AS1	PCBP1 antisense RNA 1
GCNT3	-1.38440156	0.38	3.67E-07	2.53E-08	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type
DOPEY2	-1.3846297	0.38	3.20E-13	9.40E-16	DOPEY2	dopey family member 2
TTC39A	-1.38573237	0.38	9.77E-09	3.71E-10	TTC39A	tetratricopeptide repeat domain 39A
LOC101927972	-1.3891095	0.38	1.07E-06	8.82E-08	LOC101927972	uncharacterized LOC101927972
TNXB///TNXA	-1.39098222	0.38	8.12E-10	1.94E-11	TNXB///TNXA	tenascin XB///tenascin XA (pseudogene)
DHRS9	-1.39235219	0.38	6.28E-09	2.22E-10	DHRS9	dehydrogenase/reductase 9

CAMK2N1	-1.39376066	0.38	2.29E-09	6.58E-11	CAMK2N1	calcium/calmodulin dependent protein kinase II inhibitor 1
ZNF677	-1.39398687	0.38	1.21E-10	1.97E-12	ZNF677	zinc finger protein 677
RUNDC3B	-1.39484477	0.38	4.39E-09	1.45E-10	RUNDC3B	RUN domain containing 3B
COL14A1	-1.39582817	0.38	2.53E-07	1.64E-08	COL14A1	collagen type XIV alpha 1 chain
EPB41L3	-1.39688749	0.38	9.27E-11	1.40E-12	EPB41L3	erythrocyte membrane protein band 4.1 like 3
SLC16A7	-1.39955238	0.38	7.63E-09	2.79E-10	SLC16A7	solute carrier family 16 member 7
NMU	-1.39975743	0.38	1.19E-05	1.41E-06	NMU	neuromedin U
SLC6A4	-1.4005248	0.38	1.89E-09	5.24E-11	SLC6A4	solute carrier family 6 member 4
VSIG2	-1.40117204	0.38	4.14E-07	2.92E-08	VSIG2	V-set and immunoglobulin domain containing 2
MYOCD	-1.40258515	0.38	3.15E-09	9.59E-11	MYOCD	myocardin
TSPAN6	-1.40266689	0.38	1.34E-09	3.49E-11	TSPAN6	tetraspanin 6
ATG9B	-1.40285335	0.38	8.73E-09	3.26E-10	ATG9B	autophagy related 9B
RAB25	-1.40369336	0.38	4.41E-12	3.03E-14	RAB25	RAB25, member RAS oncogene family
GULP1	-1.40431765	0.38	5.63E-12	4.13E-14	GULP1	GULP, engulfment adaptor PTB domain containing 1
AHNAK	-1.40545153	0.38	6.12E-11	8.21E-13	AHNAK	AHNAK nucleoprotein
FAM149A	-1.40578208	0.38	1.36E-10	2.26E-12	FAM149A	family with sequence similarity 149 member A
FUT6	-1.40650386	0.38	2.14E-11	2.30E-13	FUT6	fucosyltransferase 6
C6orf58	-1.40657051	0.38	6.28E-04	1.33E-04	C6orf58	chromosome 6 open reading frame 58
RYR2	-1.40798754	0.38	8.09E-09	2.99E-10	RYR2	ryanodine receptor 2
FAM214A	-1.40895418	0.38	2.83E-13	8.01E-16	FAM214A	family with sequence similarity 214 member A
PLAC8	-1.40930738	0.38	2.52E-05	3.32E-06	PLAC8	placenta specific 8
GRPEL2	-1.41251584	0.38	6.18E-11	8.35E-13	GRPEL2	GrpE like 2, mitochondrial
EHD3	-1.41315079	0.38	6.74E-08	3.54E-09	EHD3	EH domain containing 3
ZNF662	-1.41354034	0.38	3.36E-14	4.23E-17	ZNF662	zinc finger protein 662
EHF	-1.41413927	0.38	3.69E-06	3.66E-07	EHF	ETS homologous factor
TNXB///TNXA	-1.41433811	0.38	1.21E-10	1.97E-12	TNXB///TNXA	tenascin XB///tenascin XA (pseudogene)
LOC105376081	-1.41464344	0.38	3.73E-10	7.66E-12	LOC105376081	uncharacterized LOC105376081
NMRK1	-1.41571427	0.37	2.42E-11	2.66E-13	NMRK1	nicotinamide riboside kinase 1
NFIA	-1.41692645	0.37	1.32E-10	2.18E-12	NFIA	nuclear factor I A
MMRN1	-1.41884675	0.37	2.21E-07	1.40E-08	MMRN1	multimerin 1
EPB41L4A	-1.42072091	0.37	3.21E-11	3.70E-13	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A
PLS1	-1.42170277	0.37	2.95E-06	2.83E-07	PLS1	plastin 1
NDFIP2	-1.42295004	0.37	1.31E-08	5.20E-10	NDFIP2	Nedd4 family interacting protein 2
ATP13A4	-1.42373215	0.37	8.85E-09	3.32E-10	ATP13A4	ATPase 13A4
RNF141	-1.42482854	0.37	5.29E-12	3.78E-14	RNF141	ring finger protein 141
FAM214A	-1.42513253	0.37	1.01E-08	3.87E-10	FAM214A	family with sequence similarity 214 member A
RBFOX3	-1.42572513	0.37	7.37E-11	1.05E-12	RBFOX3	RNA binding protein, fox-1 homolog 3
MYO5B	-1.42839521	0.37	4.64E-11	5.86E-13	MYO5B	myosin VB

PRELP	-1.42857036	0.37	6.75E-09	2.41E-10	PRELP	proline and arginine rich end leucine rich repeat protein
SVIP	-1.43106376	0.37	1.90E-09	5.31E-11	SVIP	small VCP interacting protein
CILP	-1.43128104	0.37	9.50E-06	1.09E-06	CILP	cartilage intermediate layer protein
DLG2	-1.43435405	0.37	3.37E-12	2.15E-14	DLG2	discs large MAGUK scaffold protein 2
TMOD3	-1.43440251	0.37	1.08E-13	2.30E-16	TMOD3	tropomodulin 3
DEPTOR	-1.4347483	0.37	2.34E-06	2.17E-07	DEPTOR	DEP domain containing MTOR-interacting protein
EHD3	-1.43564876	0.37	1.34E-09	3.49E-11	EHD3	EH domain containing 3
CEACAM6	-1.43648793	0.37	4.00E-07	2.80E-08	CEACAM6	carcinoembryonic antigen related cell adhesion molecule 6
DMD	-1.43654315	0.37	1.84E-08	7.73E-10	DMD	dystrophin
TJP3	-1.43666329	0.37	1.42E-12	7.11E-15	TJP3	tight junction protein 3
AFDN	-1.437282	0.37	4.89E-11	6.23E-13	AFDN	afadin, adherens junction formation factor
CFH	-1.43859043	0.37	6.84E-08	3.61E-09	CFH	complement factor H
LOC101928429	-1.44055677	0.37	8.66E-06	9.81E-07	LOC101928429	uncharacterized LOC101928429
CCNG2	-1.44121655	0.37	4.44E-06	4.53E-07	CCNG2	cyclin G2
KIAA1211L	-1.44227791	0.37	1.77E-11	1.76E-13	KIAA1211L	KIAA1211 like
LINC01088	-1.44353986	0.37	5.19E-05	7.68E-06	LINC01088	long intergenic non-protein coding RNA 1088
CARD18	-1.44593736	0.37	4.95E-04	1.01E-04	CARD18	caspase recruitment domain family member 18
AZGP1	-1.44622292	0.37	2.81E-02	1.11E-02	AZGP1	alpha-2-glycoprotein 1, zinc-binding
GFRA1	-1.44651991	0.37	2.09E-09	5.92E-11	GFRA1	GDNF family receptor alpha 1
ZNF536	-1.44881706	0.37	1.15E-09	2.88E-11	ZNF536	zinc finger protein 536
FAM149A	-1.44890511	0.37	1.71E-11	1.68E-13	FAM149A	family with sequence similarity 149 member A
NFASC	-1.45065625	0.37	1.18E-10	1.89E-12	NFASC	neurofascin
PAQR8	-1.45137361	0.37	4.17E-10	8.69E-12	PAQR8	progesterin and adipoQ receptor family member 8
MALL	-1.45171402	0.37	1.24E-07	7.18E-09	MALL	mal, T-cell differentiation protein like
EHF	-1.45233931	0.37	2.26E-06	2.08E-07	EHF	ETS homologous factor
C19orf33	-1.45259519	0.37	3.78E-08	1.81E-09	C19orf33	chromosome 19 open reading frame 33
RBFOX3	-1.45295204	0.37	3.87E-11	4.73E-13	RBFOX3	RNA binding protein, fox-1 homolog 3
DHRS9	-1.45414852	0.36	1.24E-08	4.90E-10	DHRS9	dehydrogenase/reductase 9
MSMB	-1.45677267	0.36	7.92E-02	3.80E-02	MSMB	microseminoprotein beta
SSBP2	-1.45687329	0.36	1.15E-11	1.04E-13	SSBP2	single stranded DNA binding protein 2
PID1	-1.45778308	0.36	8.27E-08	4.50E-09	PID1	phosphotyrosine interaction domain containing 1
PEG3	-1.45906003	0.36	1.73E-09	4.74E-11	PEG3	paternally expressed 3
KLB	-1.45962126	0.36	1.31E-11	1.21E-13	KLB	klotho beta
MBD2	-1.46117693	0.36	4.05E-10	8.42E-12	MBD2	methyl-CpG binding domain protein 2
GPM6A	-1.46614894	0.36	5.31E-08	2.69E-09	GPM6A	glycoprotein M6A
SLC16A6	-1.46677668	0.36	2.04E-10	3.77E-12	SLC16A6	solute carrier family 16 member 6
KLK11	-1.46759561	0.36	2.00E-06	1.81E-07	KLK11	kallikrein related peptidase 11

PPID	-1.46760511	0.36	6.50E-12	4.97E-14	PPID	peptidylprolyl isomerase D
PRSS2	-1.4694612	0.36	3.31E-07	2.25E-08	PRSS2	protease, serine 2
FOLR1	-1.47217602	0.36	5.46E-03	1.62E-03	FOLR1	folate receptor 1
RASEF	-1.47262284	0.36	3.24E-07	2.20E-08	RASEF	RAS and EF-hand domain containing
MAOB	-1.47500411	0.36	4.53E-10	9.68E-12	MAOB	monoamine oxidase B
STRADB	-1.47564523	0.36	1.14E-11	1.02E-13	STRADB	STE20-related kinase adaptor beta
MT1M	-1.47582116	0.36	5.50E-05	8.21E-06	MT1M	metallothionein 1M
SYTL4	-1.47626207	0.36	3.46E-09	1.08E-10	SYTL4	synaptotagmin like 4
TMEM35A	-1.4820204	0.36	1.00E-06	8.18E-08	TMEM35A	transmembrane protein 35A
CASQ2	-1.48262887	0.36	2.19E-09	6.25E-11	CASQ2	calsequestrin 2
RNASE4	-1.48271316	0.36	1.55E-08	6.36E-10	RNASE4	ribonuclease A family member 4
LINC01214	-1.48412772	0.36	3.92E-12	2.60E-14	LINC01214	long intergenic non-protein coding RNA 1214
FILIP1	-1.48496556	0.36	6.61E-07	5.03E-08	FILIP1	filamin A interacting protein 1
AIM1	-1.48563327	0.36	1.13E-12	4.95E-15	AIM1	absent in melanoma 1
LOC101928274//VSIG10	-1.48670349	0.36	1.31E-11	1.22E-13	LOC101928274//V SIG10	uncharacterized LOC101928274//V-set and immunoglobulin domain containing 10
CEACAM1	-1.48894595	0.36	6.63E-12	5.11E-14	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1
SULT2B1	-1.48948128	0.36	5.38E-07	3.95E-08	SULT2B1	sulfotransferase family 2B member 1
IKZF2	-1.48988006	0.36	8.09E-09	2.99E-10	IKZF2	IKAROS family zinc finger 2
AOC3	-1.48999339	0.36	2.68E-09	7.87E-11	AOC3	amine oxidase, copper containing 3
PTGIS	-1.49112645	0.36	7.17E-06	7.90E-07	PTGIS	prostaglandin I2 (prostacyclin) synthase
SERPINB3	-1.49249857	0.36	1.75E-03	4.35E-04	SERPINB3	serpin family B member 3
LRRK2	-1.49367506	0.36	7.04E-09	2.54E-10	LRRK2	leucine rich repeat kinase 2
GBP6	-1.49405445	0.36	1.69E-05	2.10E-06	GBP6	guanylate binding protein family member 6
CST6	-1.49538439	0.35	6.88E-07	5.27E-08	CST6	cystatin E/M
RAB11FIP1	-1.49643295	0.35	7.68E-13	2.84E-15	RAB11FIP1	RAB11 family interacting protein 1
NEBL	-1.49643531	0.35	5.52E-08	2.81E-09	NEBL	nebullette
TOX3	-1.49738872	0.35	2.55E-03	6.73E-04	TOX3	TOX high mobility group box family member 3
TF	-1.49759857	0.35	7.49E-04	1.63E-04	TF	transferrin
SPNS2	-1.4994563	0.35	1.19E-12	5.45E-15	SPNS2	sphingolipid transporter 2
CD24	-1.49953126	0.35	1.26E-10	2.06E-12	CD24	CD24 molecule
NFIA	-1.50027635	0.35	3.08E-12	1.92E-14	NFIA	nuclear factor I A
TOX3	-1.50407908	0.35	2.10E-03	5.38E-04	TOX3	TOX high mobility group box family member 3
MXD1	-1.50439603	0.35	6.63E-11	9.15E-13	MXD1	MAX dimerization protein 1
ABLIM1	-1.50858445	0.35	6.71E-12	5.22E-14	ABLIM1	actin binding LIM protein 1
AFF3	-1.50863027	0.35	5.35E-08	2.72E-09	AFF3	AF4/FMR2 family member 3
DSTN	-1.51090552	0.35	6.35E-11	8.69E-13	DSTN	destrin, actin depolymerizing factor
ADAMTSL3	-1.51357028	0.35	3.23E-07	2.18E-08	ADAMTSL3	ADAMTS like 3
ATP6V1C2	-1.51391298	0.35	3.21E-08	1.48E-09	ATP6V1C2	ATPase H+ transporting V1 subunit C2

EPS8L2	-1.51588038	0.35	1.19E-12	5.45E-15	<i>EPS8L2</i>	EPS8 like 2
UBL3	-1.5178152	0.35	1.29E-14	1.04E-17	<i>UBL3</i>	ubiquitin like 3
KAT2B	-1.51907279	0.35	3.37E-13	1.01E-15	<i>KAT2B</i>	lysine acetyltransferase 2B
EME2	-1.5211855	0.35	7.29E-11	1.04E-12	<i>EME2</i>	essential meiotic structure-specific endonuclease subunit 2
GATM	-1.52157433	0.35	2.16E-09	6.17E-11	<i>GATM</i>	glycine amidinotransferase
RNASE7	-1.52219831	0.35	4.20E-04	8.41E-05	<i>RNASE7</i>	ribonuclease A family member 7
DOCK9	-1.52224311	0.35	2.72E-07	1.78E-08	<i>DOCK9</i>	dedicator of cytokinesis 9
SUPT20H///DES	-1.52259009	0.35	5.33E-09	1.83E-10	<i>SUPT20H///DES</i>	SPT20 homolog, SAGA complex component///desmin
LPIN1	-1.52471581	0.35	7.75E-13	2.89E-15	<i>LPIN1</i>	lipin 1
NFIA	-1.52510151	0.35	2.61E-08	1.16E-09	<i>NFIA</i>	nuclear factor I A
SASH1	-1.52598741	0.35	1.51E-12	7.69E-15	<i>SASH1</i>	SAM and SH3 domain containing 1
CAMK2N1	-1.5292802	0.35	6.60E-10	1.52E-11	<i>CAMK2N1</i>	calcium/calmodulin dependent protein kinase II inhibitor 1
STX19	-1.53177385	0.35	3.77E-11	4.57E-13	<i>STX19</i>	syntaxin 19
DHRS1	-1.5318584	0.35	6.39E-11	8.76E-13	<i>DHRS1</i>	dehydrogenase/reductase 1
CEACAM6	-1.53228476	0.35	1.86E-06	1.67E-07	<i>CEACAM6</i>	carcinoembryonic antigen related cell adhesion molecule 6
RECK	-1.53281737	0.35	1.46E-10	2.47E-12	<i>RECK</i>	reversion inducing cysteine rich protein with kazal motifs
BTBD11	-1.53320643	0.35	3.39E-07	2.31E-08	<i>BTBD11</i>	BTB domain containing 11
CD24	-1.53538179	0.34	2.80E-09	8.29E-11	<i>CD24</i>	CD24 molecule
MPP7	-1.53721519	0.34	6.71E-12	5.23E-14	<i>MPP7</i>	membrane palmitoylated protein 7
CES2	-1.537547	0.34	1.42E-12	7.12E-15	<i>CES2</i>	carboxylesterase 2
VSIG2	-1.5375722	0.34	1.08E-10	1.69E-12	<i>VSIG2</i>	V-set and immunoglobulin domain containing 2
RBPMS2	-1.53971603	0.34	3.72E-09	1.18E-10	<i>RBPMS2</i>	RNA binding protein with multiple splicing 2
PTGR1	-1.54025709	0.34	2.03E-09	5.71E-11	<i>PTGR1</i>	prostaglandin reductase 1
ROR1	-1.54072854	0.34	2.08E-11	2.22E-13	<i>ROR1</i>	receptor tyrosine kinase like orphan receptor 1
LIMCH1	-1.54212794	0.34	1.81E-11	1.83E-13	<i>LIMCH1</i>	LIM and calponin homology domains 1
CD207	-1.54240951	0.34	1.64E-10	2.86E-12	<i>CD207</i>	CD207 molecule
LIMCH1	-1.54329277	0.34	2.82E-11	3.18E-13	<i>LIMCH1</i>	LIM and calponin homology domains 1
C5orf66-AS1	-1.54337606	0.34	3.21E-09	9.81E-11	<i>C5orf66-AS1</i>	C5orf66 antisense RNA 1
ZBED2	-1.5434411	0.34	5.32E-05	7.91E-06	<i>ZBED2</i>	zinc finger BED-type containing 2
TCN1	-1.54360066	0.34	9.80E-04	2.23E-04	<i>TCN1</i>	transcobalamin 1
PTGS1	-1.54373008	0.34	7.56E-09	2.75E-10	<i>PTGS1</i>	prostaglandin-endoperoxide synthase 1
MYRIP	-1.5457228	0.34	4.94E-10	1.07E-11	<i>MYRIP</i>	myosin VIIA and Rab interacting protein
SCGB3A1	-1.54596728	0.34	1.26E-02	4.33E-03	<i>SCGB3A1</i>	secretoglobulin family 3A member 1
LOC101927157///NIPAL1	-1.54722742	0.34	1.83E-13	4.49E-16	<i>LOC101927157///NIPAL1</i>	uncharacterized LOC101927157///NIPAL1 like domain containing 1
SORT1	-1.54854726	0.34	7.08E-11	1.00E-12	<i>SORT1</i>	sortilin 1
GREM2	-1.55038665	0.34	4.17E-10	8.68E-12	<i>GREM2</i>	gremlin 2, DAN family BMP antagonist

ANKRD37	-1.55596551	0.34	1.28E-07	7.47E-09	ANKRD37	ankyrin repeat domain 37
ANKRD20A12P///ANKRD20A8P///ANKRD20A4///ANKRD20A2///ANKRD20A3///ANKRD20A5P///ANKRD20A1	-1.55622957	0.34	2.56E-12	1.55E-14	ANKRD20A12P///ANKRD20A8P///ANKRD20A4///ANKRD20A2///ANKRD20A3///ANKRD20A5P///ANKRD20A1	ankyrin repeat domain 20 family member A12, pseudogene///ankyrin repeat domain 20 family member A8, pseudogene///ankyrin repeat domain 20 family member A4///ankyrin repeat domain 20 family member A2///ankyrin repeat domain 20 family member A3///ankyrin repeat domain 20 family member A5, pseudogene///ankyrin repeat domain 20 family member A1
PLEKHA6	-1.55740988	0.34	7.99E-12	6.56E-14	PLEKHA6	pleckstrin homology domain containing A6
EXOSC7///CLEC3B	-1.55999851	0.34	4.82E-08	2.40E-09	EXOSC7///CLEC3B	exosome component 7///C-type lectin domain family 3 member B
STXBP6	-1.56075679	0.34	5.77E-07	4.29E-08	STXBP6	syntaxin binding protein 6
CYP2E1	-1.56374777	0.34	6.38E-08	3.33E-09	CYP2E1	cytochrome P450 family 2 subfamily E member 1
TGM1	-1.56506223	0.34	2.32E-05	3.02E-06	TGM1	transglutaminase 1
ANXA9	-1.56518266	0.34	3.41E-10	6.87E-12	ANXA9	annexin A9
FUT3	-1.56540932	0.34	4.83E-12	3.39E-14	FUT3	fucosyltransferase 3 (Lewis blood group)
SMAGP	-1.56752933	0.34	3.38E-15	1.31E-18	SMAGP	small cell adhesion glycoprotein
SYTL5	-1.57129694	0.34	9.72E-07	7.88E-08	SYTL5	synaptotagmin like 5
FMO2	-1.57265181	0.34	1.33E-06	1.14E-07	FMO2	flavin containing monooxygenase 2
CCL15-CCL14///CCL14	-1.57651754	0.34	7.38E-08	3.96E-09	CCL15-CCL14///CCL14	CCL15-CCL14 readthrough (NMD candidate)///C-C motif chemokine ligand 14
DES	-1.58040813	0.33	2.60E-06	2.45E-07	DES	desmin
LPIN1	-1.58056093	0.33	1.14E-11	1.02E-13	LPIN1	lipin 1
JAM2	-1.58114745	0.33	3.39E-10	6.81E-12	JAM2	junctional adhesion molecule 2
HLF	-1.58198079	0.33	1.04E-07	5.91E-09	HLF	HLF, PAR bZIP transcription factor
SERPINB3	-1.58572199	0.33	4.83E-04	9.84E-05	SERPINB3	serpin family B member 3
CEACAM1	-1.58666479	0.33	1.68E-10	2.95E-12	CEACAM1	carcinoembryonic antigen related cell adhesion molecule 1
LOC100507258///CA13	-1.5880866	0.33	7.26E-12	5.80E-14	LOC100507258///CA13	uncharacterized LOC100507258///carbonic anhydrase 13
MUC1	-1.59109433	0.33	3.58E-09	1.13E-10	MUC1	mucin 1, cell surface associated
CAB39L	-1.59234339	0.33	2.62E-14	3.12E-17	CAB39L	calcium binding protein 39 like
RDH12	-1.59553718	0.33	1.28E-08	5.07E-10	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)
SCGB1D2	-1.59831558	0.33	2.68E-04	5.04E-05	SCGB1D2	secretoglobin family 1D member 2
ANGPTL1	-1.59896141	0.33	1.19E-10	1.93E-12	ANGPTL1	angiotensin like 1
LONRF2	-1.60006268	0.33	4.12E-09	1.33E-10	LONRF2	LON peptidase N-terminal domain and ring finger 2
PRUNE2	-1.60343102	0.33	6.18E-07	4.64E-08	PRUNE2	prune homolog 2
TMEFF2	-1.60771874	0.33	8.76E-08	4.81E-09	TMEFF2	transmembrane protein with EGF like and two follistatin like domains 2
NUCB2	-1.6086836	0.33	9.87E-14	1.95E-16	NUCB2	nucleobindin 2

SPAG16	-1.60943346	0.33	9.03E-13	3.59E-15	SPAG16	sperm associated antigen 16
LOC101928274//V/SIG10	-1.61172359	0.33	6.45E-15	3.51E-18	LOC101928274//V/SIG10	uncharacterized LOC101928274//V-set and immunoglobulin domain containing 10
COBL	-1.6124902	0.33	1.80E-12	9.78E-15	COBL	cordon-bleu WH2 repeat protein
TTC22	-1.61444797	0.33	2.05E-12	1.16E-14	TTC22	tetratricopeptide repeat domain 22
NEBL	-1.61573477	0.33	3.00E-09	9.05E-11	NEBL	nebullette
RAB9B	-1.61596023	0.33	5.98E-11	7.92E-13	RAB9B	RAB9B, member RAS oncogene family
YOD1	-1.6176899	0.33	1.60E-10	2.77E-12	YOD1	YOD1 deubiquitinase
MYH11	-1.61773771	0.33	1.54E-07	9.25E-09	MYH11	myosin heavy chain 11
SORBS1	-1.61810689	0.33	1.41E-09	3.69E-11	SORBS1	sorbin and SH3 domain containing 1
RAB11A	-1.62039122	0.33	5.50E-15	2.51E-18	RAB11A	RAB11A, member RAS oncogene family
SLC4A4	-1.6225453	0.32	5.30E-07	3.89E-08	SLC4A4	solute carrier family 4 member 4
SERPINB11	-1.62326604	0.32	7.23E-05	1.12E-05	SERPINB11	serpin family B member 11 (gene/pseudogene)
ATP1A2	-1.62649302	0.32	2.05E-12	1.17E-14	ATP1A2	ATPase Na ⁺ /K ⁺ transporting subunit alpha 2
HCG22	-1.62879899	0.32	1.16E-10	1.86E-12	HCG22	HLA complex group 22
TMEM45B	-1.6331324	0.32	1.25E-11	1.15E-13	TMEM45B	transmembrane protein 45B
HSPB8	-1.63360386	0.32	1.22E-09	3.12E-11	HSPB8	heat shock protein family B (small) member 8
TFF1	-1.63790041	0.32	1.00E-02	3.29E-03	TFF1	trefoil factor 1
LOC105379426	-1.64027868	0.32	3.15E-11	3.62E-13	LOC105379426	ankyrin repeat domain-containing protein 20A2
MGLL	-1.64035972	0.32	3.87E-12	2.56E-14	MGLL	monoglyceride lipase
WIF1	-1.64111439	0.32	1.07E-02	3.54E-03	WIF1	WNT inhibitory factor 1
SDPR	-1.64267911	0.32	3.36E-08	1.56E-09	SDPR	serum deprivation response
GLTP	-1.64276158	0.32	2.96E-08	1.35E-09	GLTP	glycolipid transfer protein
NBEA	-1.64681818	0.32	5.50E-09	1.90E-10	NBEA	neurobeachin
MYOCD	-1.64705902	0.32	6.86E-10	1.59E-11	MYOCD	myocardin
ERO1A	-1.64815011	0.32	1.02E-10	1.57E-12	ERO1A	endoplasmic reticulum oxidoreductase 1 alpha
GGT6	-1.65118903	0.32	1.19E-11	1.08E-13	GGT6	gamma-glutamyltransferase 6
ELOVL6	-1.65305747	0.32	5.79E-11	7.59E-13	ELOVL6	ELOVL fatty acid elongase 6
SERPINB13	-1.65362121	0.32	2.35E-04	4.31E-05	SERPINB13	serpin family B member 13
PIGR	-1.65406921	0.32	5.52E-02	2.48E-02	PIGR	polymeric immunoglobulin receptor
C6orf132	-1.65738974	0.32	3.39E-12	2.16E-14	C6orf132	chromosome 6 open reading frame 132
ERBB3	-1.65915892	0.32	1.50E-13	3.30E-16	ERBB3	erb-b2 receptor tyrosine kinase 3
PDZRN4	-1.66016952	0.32	2.47E-08	1.09E-09	PDZRN4	PDZ domain containing ring finger 4
BLNK	-1.66569828	0.32	3.38E-15	1.36E-18	BLNK	B-cell linker
CITED2	-1.66628919	0.32	1.78E-11	1.78E-13	CITED2	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2
CYP2J2	-1.66630113	0.32	1.61E-10	2.81E-12	CYP2J2	cytochrome P450 family 2 subfamily J member 2
RBP7	-1.6663216	0.32	4.30E-09	1.41E-10	RBP7	retinol binding protein 7
THSD4	-1.666539	0.32	1.89E-08	7.98E-10	THSD4	thrombospondin type 1 domain containing 4

SASH1	-1.66690261	0.31	1.78E-13	4.10E-16	SASH1	SAM and SH3 domain containing 1
CXCR2	-1.67358468	0.31	2.23E-07	1.41E-08	CXCR2	C-X-C motif chemokine receptor 2
THRB	-1.67415747	0.31	1.11E-09	2.77E-11	THRB	thyroid hormone receptor beta
IL36A	-1.67457434	0.31	5.65E-12	4.18E-14	IL36A	interleukin 36, alpha
SPTLC1	-1.67881336	0.31	6.71E-12	5.22E-14	SPTLC1	serine palmitoyltransferase long chain base subunit 1
SLMAP	-1.67909098	0.31	1.02E-10	1.58E-12	SLMAP	sarcolemma associated protein
TMEM110-MUSTN1//MUSTN1//TMEM110	-1.68103445	0.31	7.06E-10	1.65E-11	TMEM110-MUSTN1//MUSTN1//TMEM110	TMEM110-MUSTN1 readthrough//musculoskeletal, embryonic nuclear protein 1//transmembrane protein 110
EPB41L3	-1.68112361	0.31	2.12E-10	3.95E-12	EPB41L3	erythrocyte membrane protein band 4.1 like 3
KRT13	-1.68228948	0.31	3.02E-03	8.14E-04	KRT13	keratin 13
ID4	-1.68435681	0.31	8.83E-11	1.32E-12	ID4	inhibitor of DNA binding 4, HLH protein
MUC1	-1.68589286	0.31	3.03E-06	2.91E-07	MUC1	mucin 1, cell surface associated
DSC2	-1.6892493	0.31	7.52E-06	8.36E-07	DSC2	desmocollin 2
EMP1	-1.68937231	0.31	6.21E-09	2.18E-10	EMP1	epithelial membrane protein 1
AKAP12	-1.69089701	0.31	9.67E-08	5.41E-09	AKAP12	A-kinase anchoring protein 12
RCAN2	-1.69215559	0.31	1.97E-11	2.05E-13	RCAN2	regulator of calcineurin 2
ADIRF	-1.69407356	0.31	1.10E-11	9.68E-14	ADIRF	adipogenesis regulatory factor
OGN	-1.69532356	0.31	1.16E-08	4.54E-10	OGN	osteoglycin
TGFBR3	-1.69773246	0.31	2.02E-10	3.71E-12	TGFBR3	transforming growth factor beta receptor 3
MXD1	-1.69785423	0.31	2.84E-09	8.47E-11	MXD1	MAX dimerization protein 1
TXNL1	-1.70124594	0.31	3.40E-12	2.18E-14	TXNL1	thioredoxin like 1
TP53I3	-1.70181375	0.31	1.26E-12	6.02E-15	TP53I3	tumor protein p53 inducible protein 3
LMOD1	-1.70289682	0.31	1.03E-09	2.55E-11	LMOD1	leiomodulin 1
SORBS2	-1.70478202	0.31	2.04E-12	1.15E-14	SORBS2	sorbin and SH3 domain containing 2
VIT	-1.70712724	0.31	1.68E-12	8.74E-15	VIT	vitron
SCNN1B	-1.70732932	0.31	1.01E-09	2.47E-11	SCNN1B	sodium channel epithelial 1 beta subunit
CAB39L	-1.71222354	0.31	1.01E-12	4.32E-15	CAB39L	calcium binding protein 39 like
OBFC1	-1.71748717	0.30	3.22E-15	1.18E-18	OBFC1	oligonucleotide/oligosaccharide binding fold containing 1
EPB41L3	-1.71988052	0.30	2.49E-11	2.76E-13	EPB41L3	erythrocyte membrane protein band 4.1 like 3
TGFBR3	-1.72253444	0.30	8.96E-10	2.17E-11	TGFBR3	transforming growth factor beta receptor 3
GGTA1P	-1.72272028	0.30	2.16E-12	1.27E-14	GGTA1P	glycoprotein, alpha-galactosyltransferase 1 pseudogene
IL1RN	-1.7240666	0.30	2.52E-09	7.31E-11	IL1RN	interleukin 1 receptor antagonist
MYO6	-1.72463978	0.30	4.96E-12	3.50E-14	MYO6	myosin VI
NPY1R	-1.72581571	0.30	1.88E-09	5.22E-11	NPY1R	neuropeptide Y receptor Y1
SRPX	-1.7278184	0.30	6.72E-10	1.55E-11	SRPX	sushi repeat containing protein, X-linked
BCHE	-1.73366408	0.30	3.02E-07	2.01E-08	BCHE	butyrylcholinesterase
HLF	-1.73445942	0.30	4.82E-10	1.04E-11	HLF	HLF, PAR bZIP transcription factor

SCNN1A	-1.73486255	0.30	3.35E-09	1.03E-10	SCNN1A	sodium channel epithelial 1 alpha subunit
TCEAL2	-1.73648632	0.30	2.80E-09	8.31E-11	TCEAL2	transcription elongation factor A like 2
C9orf152	-1.74087864	0.30	4.36E-07	3.10E-08	C9orf152	chromosome 9 open reading frame 152
RNASE4	-1.74304782	0.30	1.78E-09	4.90E-11	RNASE4	ribonuclease A family member 4
ACTA2	-1.74791907	0.30	8.88E-09	3.33E-10	ACTA2	actin, alpha 2, smooth muscle, aorta
TFF3	-1.74795727	0.30	8.18E-05	1.29E-05	TFF3	trefoil factor 3
OR7E14P	-1.74818882	0.30	1.79E-12	9.60E-15	OR7E14P	olfactory receptor family 7 subfamily E member 14 pseudogene
DUSP5	-1.75332742	0.30	1.16E-08	4.54E-10	DUSP5	dual specificity phosphatase 5
PRSS2	-1.75548374	0.30	2.90E-11	3.31E-13	PRSS2	protease, serine 2
CLDN10	-1.75611553	0.30	3.21E-04	6.20E-05	CLDN10	claudin 10
ZNF426	-1.75792308	0.30	2.83E-11	3.19E-13	ZNF426	zinc finger protein 426
FAM13C	-1.76015463	0.30	1.15E-11	1.04E-13	FAM13C	family with sequence similarity 13 member C
C1orf116	-1.77243471	0.29	7.16E-15	4.19E-18	C1orf116	chromosome 1 open reading frame 116
PLCB4	-1.77582442	0.29	5.75E-11	7.53E-13	PLCB4	phospholipase C beta 4
YOD1	-1.77828217	0.29	3.77E-07	2.62E-08	YOD1	YOD1 deubiquitinase
ABLIM1	-1.78138559	0.29	1.29E-11	1.19E-13	ABLIM1	actin binding LIM protein 1
SFRP1	-1.7824123	0.29	4.07E-08	1.97E-09	SFRP1	secreted frizzled related protein 1
CRISP2	-1.7844468	0.29	4.09E-10	8.50E-12	CRISP2	cysteine rich secretory protein 2
IL1RN	-1.78598616	0.29	4.04E-08	1.95E-09	IL1RN	interleukin 1 receptor antagonist
NR3C2	-1.79071836	0.29	5.08E-12	3.63E-14	NR3C2	nuclear receptor subfamily 3 group C member 2
OCLN	-1.79490632	0.29	4.27E-12	2.91E-14	OCLN	occludin
PLN	-1.80100679	0.29	8.16E-08	4.43E-09	PLN	phospholamban
TJP1	-1.8021826	0.29	5.03E-10	1.10E-11	TJP1	tight junction protein 1
CYP3A5	-1.80807369	0.29	9.56E-08	5.34E-09	CYP3A5	cytochrome P450 family 3 subfamily A member 5
EXPH5	-1.8107418	0.29	8.38E-08	4.56E-09	EXPH5	exophilin 5
NEGR1	-1.81219824	0.28	1.98E-11	2.06E-13	NEGR1	neuronal growth regulator 1
CDH19	-1.81468725	0.28	4.40E-10	9.30E-12	CDH19	cadherin 19
LAMB4	-1.81496052	0.28	8.58E-13	3.34E-15	LAMB4	laminin subunit beta 4
TMEM40	-1.81931816	0.28	3.84E-07	2.67E-08	TMEM40	transmembrane protein 40
SCIN	-1.81935348	0.28	1.15E-11	1.03E-13	SCIN	scinderin
IGFL1	-1.82649289	0.28	6.51E-05	9.95E-06	IGFL1	IGF like family member 1
SLC16A6	-1.82910468	0.28	5.06E-11	6.47E-13	SLC16A6	solute carrier family 16 member 6
LOC284825	-1.83415056	0.28	9.75E-10	2.39E-11	LOC284825	uncharacterized LOC284825
ANXA3	-1.83418155	0.28	1.27E-09	3.27E-11	ANXA3	annexin A3
COL14A1	-1.84047935	0.28	6.42E-09	2.27E-10	COL14A1	collagen type XIV alpha 1 chain
PLN	-1.84097519	0.28	4.69E-09	1.57E-10	PLN	phospholamban
TMOD3	-1.84290174	0.28	4.00E-12	2.69E-14	TMOD3	tropomodulin 3
CYP3A5	-1.84362945	0.28	1.94E-09	5.41E-11	CYP3A5	cytochrome P450 family 3 subfamily A member 5

SH3PXD2A-AS1	-1.8450262	0.28	1.42E-11	1.33E-13	<i>SH3PXD2A-AS1</i>	SH3PXD2A antisense RNA 1
SERPINB1	-1.85158228	0.28	1.83E-13	4.50E-16	<i>SERPINB1</i>	serpin family B member 1
CNN1	-1.85930904	0.28	1.17E-09	2.94E-11	<i>CNN1</i>	calponin 1
SYNPO2	-1.86082732	0.28	9.15E-08	5.08E-09	<i>SYNPO2</i>	synaptopodin 2
CYP4F3	-1.86124669	0.28	5.25E-06	5.53E-07	<i>CYP4F3</i>	cytochrome P450 family 4 subfamily F member 3
XK	-1.86125199	0.28	2.61E-10	5.04E-12	<i>XK</i>	X-linked Kx blood group
LYNX1	-1.86513918	0.27	5.26E-05	7.82E-06	<i>LYNX1</i>	Ly6/neurotoxin 1
PDE5A	-1.86689291	0.27	2.69E-10	5.26E-12	<i>PDE5A</i>	phosphodiesterase 5A
RBM20	-1.86818363	0.27	1.37E-07	8.05E-09	<i>RBM20</i>	RNA binding motif protein 20
USP6NL	-1.87012132	0.27	1.23E-12	5.79E-15	<i>USP6NL</i>	USP6 N-terminal like
PCP4	-1.8725397	0.27	4.57E-06	4.69E-07	<i>PCP4</i>	Purkinje cell protein 4
MYH11	-1.87324658	0.27	4.02E-08	1.94E-09	<i>MYH11</i>	myosin heavy chain 11
GREM2	-1.87508404	0.27	1.18E-08	4.63E-10	<i>GREM2</i>	gremlin 2, DAN family BMP antagonist
DSG1	-1.87729425	0.27	3.44E-04	6.70E-05	<i>DSG1</i>	desmoglein 1
TTC9	-1.87949623	0.27	5.72E-12	4.25E-14	<i>TTC9</i>	tetratricopeptide repeat domain 9
ATP6V1C2	-1.88096253	0.27	2.03E-09	5.71E-11	<i>ATP6V1C2</i>	ATPase H+ transporting V1 subunit C2
SIM2	-1.88533214	0.27	9.93E-10	2.44E-11	<i>SIM2</i>	single-minded family bHLH transcription factor 2
HOPX	-1.88676209	0.27	3.82E-07	2.65E-08	<i>HOPX</i>	HOP homeobox
GPT2	-1.88896954	0.27	4.24E-11	5.29E-13	<i>GPT2</i>	glutamic-pyruvic transaminase 2
DPT	-1.893001	0.27	9.79E-09	3.73E-10	<i>DPT</i>	dermatopontin
LGI1	-1.89901676	0.27	1.22E-13	2.61E-16	<i>LGI1</i>	leucine rich glioma inactivated 1
FMO2	-1.90788249	0.27	1.18E-09	2.98E-11	<i>FMO2</i>	flavin containing monooxygenase 2
TMOD3	-1.9080721	0.27	1.91E-11	1.97E-13	<i>TMOD3</i>	tropomodulin 3
ADH1B	-1.91187157	0.27	1.25E-12	5.94E-15	<i>ADH1B</i>	alcohol dehydrogenase 1B (class I), beta polypeptide
FHL1	-1.91514949	0.27	1.84E-10	3.29E-12	<i>FHL1</i>	four and a half LIM domains 1
SLC6A1	-1.91799859	0.26	7.65E-09	2.80E-10	<i>SLC6A1</i>	solute carrier family 6 member 1
ZNF185	-1.91960526	0.26	6.82E-09	2.44E-10	<i>ZNF185</i>	zinc finger protein 185 (LIM domain)
GPD1L	-1.9206768	0.26	7.99E-12	6.56E-14	<i>GPD1L</i>	glycerol-3-phosphate dehydrogenase 1-like
PROM1	-1.92149418	0.26	1.37E-04	2.33E-05	<i>PROM1</i>	prominin 1
ZNF536	-1.92751995	0.26	1.00E-11	8.67E-14	<i>ZNF536</i>	zinc finger protein 536
EPS8L1	-1.94026646	0.26	2.52E-13	6.83E-16	<i>EPS8L1</i>	EPS8 like 1
GPX3	-1.94275373	0.26	5.28E-13	1.80E-15	<i>GPX3</i>	glutathione peroxidase 3
ZNF365	-1.94470367	0.26	3.35E-08	1.55E-09	<i>ZNF365</i>	zinc finger protein 365
C15orf48	-1.94828309	0.26	5.47E-10	1.21E-11	<i>C15orf48</i>	chromosome 15 open reading frame 48
PTK6	-1.95249243	0.26	1.78E-13	4.06E-16	<i>PTK6</i>	protein tyrosine kinase 6
EMP1	-1.96113997	0.26	1.54E-10	2.65E-12	<i>EMP1</i>	epithelial membrane protein 1
SERPINB13	-1.96159293	0.26	4.98E-05	7.33E-06	<i>SERPINB13</i>	serpin family B member 13
SCARA5	-1.96581175	0.26	6.22E-10	1.42E-11	<i>SCARA5</i>	scavenger receptor class A member 5

MUC5B	-1.96765404	0.26	4.12E-04	8.25E-05	MUC5B	mucin 5B, oligomeric mucus/gel-forming
CDKN2B	-1.9687011	0.26	4.40E-07	3.13E-08	CDKN2B	cyclin dependent kinase inhibitor 2B
ASPA	-1.98045462	0.25	1.06E-10	1.64E-12	ASPA	aspartoacylase
EPS8L1	-1.98417678	0.25	2.00E-13	5.05E-16	EPS8L1	EPS8 like 1
TRNP1	-1.98528296	0.25	1.16E-11	1.05E-13	TRNP1	TMF1-regulated nuclear protein 1
PLP1	-1.99218864	0.25	5.44E-12	3.95E-14	PLP1	proteolipid protein 1
LEXM	-1.99280384	0.25	1.03E-13	2.06E-16	LEXM	lymphocyte expansion molecule
DPT	-2.00024818	0.25	1.48E-13	3.22E-16	DPT	dermatopontin
SERPINB1	-2.00164446	0.25	3.51E-13	1.06E-15	SERPINB1	serpin family B member 1
PRUNE2	-2.00824629	0.25	3.46E-09	1.08E-10	PRUNE2	prune homolog 2
IL1RN	-2.00868349	0.25	7.96E-10	1.90E-11	IL1RN	interleukin 1 receptor antagonist
C2orf54	-2.01189939	0.25	9.64E-12	8.28E-14	C2orf54	chromosome 2 open reading frame 54
TMPRSS2	-2.01190768	0.25	1.83E-13	4.38E-16	TMPRSS2	transmembrane protease, serine 2
GBP6	-2.01761739	0.25	2.78E-06	2.64E-07	GBP6	guanylate binding protein family member 6
ACTG2	-2.01853039	0.25	1.62E-09	4.35E-11	ACTG2	actin, gamma 2, smooth muscle, enteric
LOC101930349///LOC101930344///CGNL1	-2.02159567	0.25	4.76E-13	1.58E-15	LOC101930349///LOC101930344///CGNL1	uncharacterized LOC101930349///uncharacterized LOC101930344///cingulin like 1
MAB21L3	-2.02317844	0.25	3.50E-09	1.09E-10	MAB21L3	mab-21 like 3
PAQR8	-2.02781343	0.25	3.81E-13	1.21E-15	PAQR8	progesterin and adiponectin receptor family member 8
GABRP	-2.02848373	0.25	3.53E-07	2.42E-08	GABRP	gamma-aminobutyric acid type A receptor pi subunit
PPP1R3C	-2.03055963	0.24	8.80E-11	1.31E-12	PPP1R3C	protein phosphatase 1 regulatory subunit 3C
EPS8L1	-2.03440699	0.24	3.04E-13	8.74E-16	EPS8L1	EPS8 like 1
PPL	-2.03480577	0.24	8.14E-09	3.02E-10	PPL	periplakin
CEACAM7	-2.03661983	0.24	3.84E-05	5.43E-06	CEACAM7	carcinoembryonic antigen related cell adhesion molecule 7
FHL1	-2.0379027	0.24	8.28E-14	1.48E-16	FHL1	four and a half LIM domains 1
ADGRF1	-2.04765501	0.24	2.63E-12	1.60E-14	ADGRF1	adhesion G protein-coupled receptor F1
CEACAM5	-2.04844893	0.24	3.30E-07	2.24E-08	CEACAM5	carcinoembryonic antigen related cell adhesion molecule 5
PLCB4	-2.05194626	0.24	6.21E-11	8.42E-13	PLCB4	phospholipase C beta 4
LIFR	-2.05409988	0.24	4.99E-12	3.54E-14	LIFR	leukemia inhibitory factor receptor alpha
ST6GALNAC1	-2.0558649	0.24	1.83E-07	1.13E-08	ST6GALNAC1	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
ANGPTL1	-2.05681565	0.24	2.08E-13	5.44E-16	ANGPTL1	angiopoietin like 1
BPIFB1	-2.05872682	0.24	1.79E-02	6.54E-03	BPIFB1	BPI fold containing family B member 1
FLG-AS1	-2.0673946	0.24	6.13E-13	2.14E-15	FLG-AS1	FLG antisense RNA 1
TMEM45B	-2.07574616	0.24	5.70E-09	1.98E-10	TMEM45B	transmembrane protein 45B
MUC15	-2.07700152	0.24	5.19E-10	1.13E-11	MUC15	mucin 15, cell surface associated
ACPP	-2.0771494	0.24	7.75E-13	2.89E-15	ACPP	acid phosphatase, prostate

PRKAA2	-2.07942833	0.24	1.47E-10	2.50E-12	PRKAA2	protein kinase AMP-activated catalytic subunit alpha 2
SHROOM3	-2.0846304	0.24	3.33E-18	1.22E-22	SHROOM3	shroom family member 3
TFAP2B	-2.08894641	0.24	5.33E-14	8.68E-17	TFAP2B	transcription factor AP-2 beta
GPX3	-2.08993936	0.23	1.82E-12	9.94E-15	GPX3	glutathione peroxidase 3
CCNG2	-2.0944839	0.23	1.19E-12	5.44E-15	CCNG2	cyclin G2
SERPINB1	-2.09599591	0.23	1.04E-12	4.47E-15	SERPINB1	serpin family B member 1
BTC	-2.11988797	0.23	1.93E-12	1.06E-14	BTC	betacellulin
TCP11L2	-2.12051977	0.23	6.27E-11	8.56E-13	TCP11L2	t-complex 11 like 2
PRSS3	-2.12099567	0.23	1.69E-12	8.89E-15	PRSS3	protease, serine 3
PPP1R9A	-2.12229212	0.23	2.21E-10	4.14E-12	PPP1R9A	protein phosphatase 1 regulatory subunit 9A
TTC9	-2.12296436	0.23	5.56E-10	1.23E-11	TTC9	tetratricopeptide repeat domain 9
RIOK3	-2.13034813	0.23	5.16E-10	1.12E-11	RIOK3	RIO kinase 3
CSTB	-2.13313647	0.23	1.28E-08	5.06E-10	CSTB	cystatin B
SLC44A3	-2.1378179	0.23	5.24E-15	2.30E-18	SLC44A3	solute carrier family 44 member 3
MXD1	-2.14092626	0.23	5.56E-12	4.07E-14	MXD1	MAX dimerization protein 1
SASH1	-2.15648062	0.22	1.08E-13	2.26E-16	SASH1	SAM and SH3 domain containing 1
RHCG	-2.15905469	0.22	5.57E-06	5.90E-07	RHCG	Rh family C glycoprotein
CTTNBP2	-2.16450843	0.22	1.68E-12	8.78E-15	CTTNBP2	cortactin binding protein 2
ERO1A	-2.16672046	0.22	3.25E-10	6.49E-12	ERO1A	endoplasmic reticulum oxidoreductase 1 alpha
CITED2	-2.16741264	0.22	1.35E-09	3.53E-11	CITED2	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2
ID4	-2.17142047	0.22	3.79E-12	2.50E-14	ID4	inhibitor of DNA binding 4, HLH protein
C1orf116	-2.17319879	0.22	1.82E-15	5.00E-19	C1orf116	chromosome 1 open reading frame 116
LIFR	-2.17331831	0.22	1.68E-12	8.81E-15	LIFR	leukemia inhibitory factor receptor alpha
CHRD1	-2.18653085	0.22	8.62E-08	4.73E-09	CHRD1	chordin like 1
C1QTNF7	-2.19838152	0.22	2.12E-12	1.24E-14	C1QTNF7	C1q and tumor necrosis factor related protein 7
CNFN	-2.20201302	0.22	4.90E-06	5.08E-07	CNFN	cornifelin
GALNT12	-2.20401982	0.22	2.40E-11	2.63E-13	GALNT12	polypeptide N-acetylgalactosaminyltransferase 12
CLIC3	-2.20457848	0.22	2.90E-08	1.31E-09	CLIC3	chloride intracellular channel 3
GDPD3	-2.21794702	0.21	2.69E-15	7.88E-19	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3
LNX1	-2.23021595	0.21	2.68E-13	7.46E-16	LNX1	ligand of numb-protein X 1
KRT4	-2.2364285	0.21	2.73E-04	5.15E-05	KRT4	keratin 4
SCARA5	-2.23770422	0.21	2.71E-09	7.95E-11	SCARA5	scavenger receptor class A member 5
MYH11	-2.24090107	0.21	2.77E-09	8.16E-11	MYH11	myosin heavy chain 11
C18orf25	-2.24103156	0.21	1.92E-12	1.05E-14	C18orf25	chromosome 18 open reading frame 25
SORBS2	-2.24134795	0.21	1.17E-10	1.88E-12	SORBS2	sorbin and SH3 domain containing 2
SYNPO2	-2.25984015	0.21	7.78E-12	6.30E-14	SYNPO2	synaptopodin 2
TMEM100	-2.26841309	0.21	1.62E-10	2.83E-12	TMEM100	transmembrane protein 100

EPS8L1	-2.27415904	0.21	3.79E-13	1.19E-15	<i>EPS8L1</i>	EPS8 like 1
C1orf116	-2.28871808	0.20	2.30E-14	2.61E-17	<i>C1orf116</i>	chromosome 1 open reading frame 116
CXCL12	-2.28942024	0.20	3.47E-08	1.63E-09	<i>CXCL12</i>	C-X-C motif chemokine ligand 12
CYP2C18	-2.28971973	0.20	1.19E-12	5.43E-15	<i>CYP2C18</i>	cytochrome P450 family 2 subfamily C member 18
CYP2C18	-2.29744572	0.20	9.84E-12	8.47E-14	<i>CYP2C18</i>	cytochrome P450 family 2 subfamily C member 18
SHROOM3	-2.3109943	0.20	2.46E-16	4.49E-20	<i>SHROOM3</i>	shroom family member 3
FAM3B	-2.31468554	0.20	8.24E-08	4.48E-09	<i>FAM3B</i>	family with sequence similarity 3 member B
A2ML1	-2.32612173	0.20	4.29E-10	8.99E-12	<i>A2ML1</i>	alpha-2-macroglobulin like 1
ADH7	-2.34263876	0.20	2.08E-07	1.31E-08	<i>ADH7</i>	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
LOC441178	-2.34375648	0.20	2.68E-13	7.49E-16	<i>LOC441178</i>	uncharacterized LOC441178
BNIP1//C1orf56	-2.34472648	0.20	1.45E-08	5.84E-10	<i>BNIP1//C1orf56</i>	BCL2 interacting protein like//chromosome 1 open reading frame 56
MUC15	-2.34656873	0.20	4.50E-09	1.49E-10	<i>MUC15</i>	mucin 15, cell surface associated
PRSS3	-2.35808294	0.20	9.46E-13	3.84E-15	<i>PRSS3</i>	protease, serine 3
SAMD5	-2.37342381	0.19	4.11E-15	1.73E-18	<i>SAMD5</i>	sterile alpha motif domain containing 5
PDK4	-2.37967256	0.19	4.21E-07	2.98E-08	<i>PDK4</i>	pyruvate dehydrogenase kinase 4
EMP1	-2.37989048	0.19	1.56E-10	2.69E-12	<i>EMP1</i>	epithelial membrane protein 1
ABCA8	-2.38000132	0.19	2.96E-09	8.93E-11	<i>ABCA8</i>	ATP binding cassette subfamily A member 8
SYNPO2L	-2.38018297	0.19	7.46E-11	1.07E-12	<i>SYNPO2L</i>	synaptopodin 2 like
RERGL	-2.38440859	0.19	2.87E-13	8.20E-16	<i>RERGL</i>	RERG like
CYP3A5	-2.39404908	0.19	5.22E-08	2.64E-09	<i>CYP3A5</i>	cytochrome P450 family 3 subfamily A member 5
SORBS1	-2.39547914	0.19	1.19E-10	1.91E-12	<i>SORBS1</i>	sorbin and SH3 domain containing 1
SYNPO2	-2.3991765	0.19	5.93E-11	7.82E-13	<i>SYNPO2</i>	synaptopodin 2
ACPP	-2.40138426	0.19	8.50E-12	7.03E-14	<i>ACPP</i>	acid phosphatase, prostate
SYNM	-2.40548206	0.19	5.19E-10	1.13E-11	<i>SYNM</i>	synemin
ANKRD20A5P	-2.41158414	0.19	4.26E-14	6.39E-17	<i>ANKRD20A5P</i>	ankyrin repeat domain 20 family member A5, pseudogene
LMO7	-2.4127212	0.19	7.48E-15	5.06E-18	<i>LMO7</i>	LIM domain 7
CWH43	-2.41707868	0.19	8.82E-11	1.32E-12	<i>CWH43</i>	cell wall biogenesis 43 C-terminal homolog
PADI1	-2.42378592	0.19	3.31E-11	3.85E-13	<i>PADI1</i>	peptidyl arginine deiminase 1
LOC441178	-2.43212712	0.19	3.65E-13	1.14E-15	<i>LOC441178</i>	uncharacterized LOC441178
MYOC	-2.44364959	0.18	3.66E-14	4.89E-17	<i>MYOC</i>	myocilin
TSPAN8	-2.44394249	0.18	7.36E-05	1.15E-05	<i>TSPAN8</i>	tetraspanin 8
CFD	-2.45865496	0.18	1.76E-12	9.38E-15	<i>CFD</i>	complement factor D
HPGD	-2.47081792	0.18	6.94E-13	2.50E-15	<i>HPGD</i>	hydroxyprostaglandin dehydrogenase 15-(NAD)
SCGB2A1	-2.4806123	0.18	6.58E-04	1.41E-04	<i>SCGB2A1</i>	secretoglobin family 2A member 1
PRKAA2	-2.48131977	0.18	1.19E-12	5.24E-15	<i>PRKAA2</i>	protein kinase AMP-activated catalytic subunit alpha 2
KRTAP3-2	-2.48344732	0.18	5.64E-10	1.26E-11	<i>KRTAP3-2</i>	keratin associated protein 3-2
C6orf58	-2.48785359	0.18	8.59E-04	1.92E-04	<i>C6orf58</i>	chromosome 6 open reading frame 58

PRSS27	-2.48851061	0.18	7.06E-10	1.64E-11	PRSS27	protease, serine 27
SH3BGR12	-2.49586797	0.18	1.18E-15	2.79E-19	SH3BGR12	SH3 domain binding glutamate rich protein like 2
C7	-2.50062811	0.18	4.11E-08	1.99E-09	C7	complement component 7
CWH43	-2.5045913	0.18	5.10E-11	6.55E-13	CWH43	cell wall biogenesis 43 C-terminal homolog
ECM1	-2.50891397	0.18	6.72E-10	1.55E-11	ECM1	extracellular matrix protein 1
EMP1	-2.52343666	0.17	1.51E-10	2.59E-12	EMP1	epithelial membrane protein 1
OGN	-2.52549385	0.17	4.15E-09	1.35E-10	OGN	osteoglycin
CYP4B1	-2.52827994	0.17	1.08E-06	8.94E-08	CYP4B1	cytochrome P450 family 4 subfamily B member 1
SLC8A1-AS1	-2.52847921	0.17	3.55E-12	2.29E-14	SLC8A1-AS1	SLC8A1 antisense RNA 1
DPCR1	-2.53908295	0.17	2.62E-10	5.11E-12	DPCR1	diffuse panbronchiolitis critical region 1
VSIG10L	-2.5504506	0.17	6.99E-09	2.51E-10	VSIG10L	V-set and immunoglobulin domain containing 10 like
ANKRD20A11P	-2.56193043	0.17	1.85E-13	4.57E-16	ANKRD20A11P	ankyrin repeat domain 20 family member A11, pseudogene
SCN7A	-2.56679456	0.17	3.63E-10	7.43E-12	SCN7A	sodium voltage-gated channel alpha subunit 7
MYZAP	-2.59372398	0.17	8.03E-17	1.01E-20	MYZAP	myocardial zonula adherens protein
FAM3D	-2.59632423	0.17	3.87E-14	5.42E-17	FAM3D	family with sequence similarity 3 member D
EDN3	-2.60321854	0.16	1.29E-10	2.12E-12	EDN3	endothelin 3
ALOX12	-2.61853296	0.16	8.61E-08	4.72E-09	ALOX12	arachidonate 12-lipoxygenase, 12S type
PGM5	-2.62095575	0.16	3.77E-11	4.58E-13	PGM5	phosphoglucomutase 5
CRCT1	-2.62511688	0.16	1.37E-06	1.18E-07	CRCT1	cysteine rich C-terminal 1
SYNPO2	-2.63472636	0.16	1.20E-12	5.56E-15	SYNPO2	synaptopodin 2
SERPINB2	-2.64025948	0.16	5.05E-07	3.67E-08	SERPINB2	serpin family B member 2
LDB3	-2.6411307	0.16	5.08E-11	6.50E-13	LDB3	LIM domain binding 3
UPK1A	-2.64512792	0.16	6.72E-08	3.53E-09	UPK1A	uroplakin 1A
AIF1L	-2.64583005	0.16	7.32E-13	2.68E-15	AIF1L	allograft inflammatory factor 1 like
SYNPO2	-2.65521525	0.16	1.04E-11	9.01E-14	SYNPO2	synaptopodin 2
ATP1A2	-2.65876354	0.16	8.67E-11	1.28E-12	ATP1A2	ATPase Na ⁺ /K ⁺ transporting subunit alpha 2
FCER1A	-2.67669049	0.16	5.99E-11	7.94E-13	FCER1A	Fc fragment of IgE receptor Ia
PSCA	-2.70606304	0.15	2.36E-11	2.57E-13	PSCA	prostate stem cell antigen
LOC102725051//LOC102723891//ANKRD20A4//ANKRD20A2//ANKRD20A3//ANKRD20A5P//ANKRD20A11P//ANKRD20A9P//ANKRD20A1	-2.70953044	0.15	1.79E-12	9.59E-15	LOC102725051//LOC102723891//ANKRD20A4//ANKRD20A2//ANKRD20A3//ANKRD20A5P//ANKRD20A11P//ANKRD20A9P//ANKRD20A1	uncharacterized LOC102725051//ankyrin repeat domain-containing protein 20B-like//ankyrin repeat domain 20 family member A4//ankyrin repeat domain 20 family member A2//ankyrin repeat domain 20 family member A3//ankyrin repeat domain 20 family member A5, pseudogene//ankyrin repeat domain 20 family member A11, pseudogene//ankyrin repeat domain 20 family member A9,

						pseudogene//ankyrin repeat domain 20 family member A1
KLK13	-2.73360357	0.15	6.01E-09	2.11E-10	KLK13	kallikrein related peptidase 13
PRH1-PRR4///PRR4	-2.75556402	0.15	8.46E-04	1.88E-04	PRH1-PRR4///PRR4	PRH1-PRR4 readthrough///proline rich 4 (lacrimal)
SCEL	-2.76017393	0.15	2.09E-12	1.21E-14	SCEL	sciellin
MAMDC2	-2.76778243	0.15	1.31E-12	6.38E-15	MAMDC2	MAM domain containing 2
DPCR1	-2.81533334	0.14	1.14E-10	1.80E-12	DPCR1	diffuse panbronchiolitis critical region 1
SCGB2A2	-2.8299678	0.14	7.23E-04	1.57E-04	SCGB2A2	secretoglobin family 2A member 2
ANXA9	-2.83032332	0.14	1.51E-10	2.59E-12	ANXA9	annexin A9
BBOX1	-2.83748842	0.14	2.96E-10	5.85E-12	BBOX1	gamma-butyrobetaine hydroxylase 1
KRT78	-2.83957536	0.14	1.02E-10	1.58E-12	KRT78	keratin 78
CYSRT1	-2.88564168	0.14	3.19E-10	6.36E-12	CYSRT1	cysteine rich tail 1
IL18	-2.95497231	0.13	6.56E-13	2.30E-15	IL18	interleukin 18
C2orf40	-2.97539428	0.13	3.97E-11	4.89E-13	C2orf40	chromosome 2 open reading frame 40
HPGD	-2.98140555	0.13	1.20E-11	1.09E-13	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)
PGM5-AS1	-3.0004861	0.12	1.80E-12	9.78E-15	PGM5-AS1	PGM5 antisense RNA 1
TFAP2B	-3.04514278	0.12	4.77E-12	3.33E-14	TFAP2B	transcription factor AP-2 beta
TMPRSS11E	-3.05629159	0.12	6.93E-08	3.67E-09	TMPRSS11E	transmembrane protease, serine 11E
HPGD	-3.07029695	0.12	8.47E-12	6.99E-14	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)
ENDOU	-3.07870837	0.12	1.33E-12	6.51E-15	ENDOU	endonuclease, poly(U) specific
SLURP1	-3.0790442	0.12	2.26E-08	9.78E-10	SLURP1	secreted LY6/PLAUR domain containing 1
SORBS2	-3.09725267	0.12	1.01E-12	4.35E-15	SORBS2	sorbin and SH3 domain containing 2
PPP1R3C	-3.10025456	0.12	1.65E-14	1.45E-17	PPP1R3C	protein phosphatase 1 regulatory subunit 3C
HPGD	-3.11137278	0.12	5.84E-14	9.83E-17	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)
CLCA4	-3.11596913	0.12	5.55E-07	4.10E-08	CLCA4	chloride channel accessory 4
SPINK5	-3.21221328	0.11	2.57E-09	7.48E-11	SPINK5	serine peptidase inhibitor, Kazal type 5
SORBS2	-3.24848135	0.11	1.61E-11	1.56E-13	SORBS2	sorbin and SH3 domain containing 2
SORBS2	-3.27762477	0.10	2.62E-12	1.59E-14	SORBS2	sorbin and SH3 domain containing 2
SCIN	-3.3040394	0.10	9.31E-15	6.64E-18	SCIN	scinderin
LOC100507221	-3.30957382	0.10	7.87E-14	1.38E-16	LOC100507221	uncharacterized LOC100507221
KRT78	-3.31469961	0.10	2.29E-12	1.36E-14	KRT78	keratin 78
A2ML1	-3.31907439	0.10	2.58E-09	7.53E-11	A2ML1	alpha-2-macroglobulin like 1
SCEL	-3.34497449	0.10	3.44E-09	1.07E-10	SCEL	sciellin
CAPN14	-3.35950589	0.10	2.83E-08	1.27E-09	CAPN14	calpain 14
LOC102724689	-3.45314242	0.09	6.16E-11	8.31E-13	LOC102724689	uncharacterized LOC102724689
TGM3	-3.4675135	0.09	1.66E-08	6.92E-10	TGM3	transglutaminase 3
ADH1B	-3.50666049	0.09	1.97E-12	1.09E-14	ADH1B	alcohol dehydrogenase 1B (class I), beta

						polypeptide
SCEL	-3.56085478	0.08	3.05E-08	1.39E-09	SCEL	sciellin
GYS2	-3.56756634	0.08	5.80E-15	2.76E-18	GYS2	glycogen synthase 2
SYNPO2L	-3.5932563	0.08	3.95E-12	2.63E-14	SYNPO2L	synaptopodin 2 like
SPINK7	-3.60199594	0.08	4.64E-07	3.34E-08	SPINK7	serine peptidase inhibitor, Kazal type 7 (putative)
CRNN	-3.63161698	0.08	9.46E-07	7.64E-08	CRNN	cornulin
MAL	-3.65348715	0.08	4.61E-09	1.54E-10	MAL	mal, T-cell differentiation protein
TMPRSS11B	-3.74767842	0.07	3.26E-07	2.21E-08	TMPRSS11B	transmembrane protease, serine 11B
ADH1B	-3.90612418	0.07	4.14E-12	2.81E-14	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide
FLG	-4.0088523	0.06	2.79E-09	8.22E-11	FLG	filaggrin
SFTA2	-4.23856836	0.05	1.05E-17	5.74E-22	SFTA2	surfactant associated 2
CRISP3	-5.21969932	0.03	2.42E-11	2.67E-13	CRISP3	cysteine rich secretory protein 3