

Identification of genes whose expression is significantly modulated by VPA (comparison VAC+VPA versus VAC)

Gene Name	P-value	fold change	Common	Genbank	Description
A_32_P136351	0.000239	3.83	LRRC12; KIAA0918; KIAA1910; RP11-395N17.1	NM_052910	SLIT and NTRK-like family, member 1
A_23_P145995	0.000752	2.807	PAELR; EDNRBL; hET(B)R-LP	NM_005302	G protein-coupled receptor 37 (endothelin receptor type B-like)
A_23_P382775	0.000752	4.515	JFY1; PUMA; PUMA/JFY1	NM_014417	BCL2 binding component 3
A_23_P52552	0.00103	2.191	BIS; BAG-3; CAIR-1; MGC104307	NM_004281	BCL2-associated athanogene 3
A_23_P152955	0.00103	2.014	PRO2472; FLJ20014	NM_017622	chromosome 17 open reading frame 59
A_23_P359738	0.00149	0.397	DKFZP566F2124	NM_015630	enhancer of polycomb homolog 2 (Drosophila)
A_23_P322	0.00149	3.698	EFL4; EPLG4; LERKA; MGC125826	NM_005227	ephrin-A4
A_23_P82814	0.00156	2.17	Fbx32; MAFbx; FLJ32424; MGC33610	NM_058229	F-box protein 32
A_23_P57137	0.00156	0.385	FLJ11168	NM_018347	chromosome 20 open reading frame 29
A_32_P90709	0.00156	2.09	C6orf204	BC045657	Chromosome 6 open reading frame 204
A_23_P151426	0.00156	3.347	FKH1; FKHR; FOXO1A	NM_002015	forkhead box O1
A_32_P205859	0.00175	3.472	ISY1; RAB41; RAB11B; MGC90481	NM_198490	RAB43, member RAS oncogene family
A_24_P56310	0.00191	3.485	TAJ; TROY; TRADE; TAJ-alpha	NM_148957	tumor necrosis factor receptor superfamily, member 19
A_23_P28598	0.00193	3.341	TES1; TES-1	NM_004445	distal-less homeobox 2
A_23_P86330	0.00193	2.314	SBB148; MGC102760	NM_016545	immediate early response 5
A_23_P27265	0.00193	3.73	C18orf4	NM_032160	dermatan sulfate epimerase-like
A_23_P141394	0.00193	2.568	Atg18; WIP149; FLJ10055	NM_017983	WD repeat domain, phosphoinositide interacting 1
A_32_P235796	0.00193	3.103	C4orf24; FLJ35630; FLJ41559	NM_152618	Bardet-Biedl syndrome 12
A_23_P209449	0.002	5.246	FzE3	NM_003507	frizzled homolog 7 (Drosophila)
A_23_P411772	0.002	0.422	MGC126854; PCDH-GAMMA-B2	NM_032096	protocadherin gamma subfamily B, 2
A_23_P28595	0.002	3.162	TES1; TES-1	NM_004405	distal-less homeobox 2
A_23_P42626	0.002	0.494	FLJ20257	NM_019606	bin3, bicoid-interacting 3, homolog (Drosophila)
A_23_P40847	0.002	2.096	C6ST	NM_004267	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
A_32_P83845	0.002	2.049	CHF2; OAF1; HERP2; HESR1; HRT-1; MGC1274	NM_012258	hairy/enhancer-of-split related with YRPW motif 1
A_23_P112241	0.002	2.534	Hsc40; KIAA1045	NM_012266	DnaJ (Hsp40) homolog, subfamily B, member 5
A_23_P145841	0.002	4.39	USAG1; CDA019; ECTODIN; DKFZp564D206	NM_015464	sclerostin domain containing 1
A_23_P205724	0.00255	0.326	FLJ10008; FLJ14051	NM_199043	chromosome 14 open reading frame 102
A_23_P1722	0.00255	0.464	FLJ25219; MGC14839; MGC131888	NM_080659	chromosome 11 open reading frame 52
A_23_P16523	0.00255	0.468	PDF; MIC1; PLAB; MIC-1; NAG-1; PTGFB; GDF-15	NM_004864	growth differentiation factor 15
A_23_P83007	0.00255	2.243	baA3L8.2; FLJ38505; FLJ90271; HYST0841; MGC46502	NM_203403	chromosome 9 open reading frame 150
A_23_P42375	0.00255	0.156	RAB32	NM_006834	RAB32, member RAS oncogene family
A_23_P254165	0.00255	2.756	RAI2	NM_021785	retinoic acid induced 2
A_24_P529168	0.00258	0.314	NM_213724	NM_213724	Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 1, mRNA [NM_213724]
A_23_P53891	0.00258	2.405	CKLF; IKLF; BTEB2	NM_001730	Kruppel-like factor 5 (intestinal)
A_23_P2041	0.00258	0.319	FLJ14966	NM_032867	MICAL C-terminal like
A_32_P18440	0.00258	3.824	MRF2; FLJ21150; RP11-341A19.1	BX641020	AT rich interactive domain 5B (MRF1-like)
A_23_P428738	0.00258	3.215	RNASE4; RNASE5; MGC22466; MGC171966	NM_001145	angiogenin, ribonuclease, RNase A family, 5
A_32_P57013	0.00258	2.196	BU540282	BU540282	Transcribed locus
A_23_P210763	0.00285	2.449	AGS; AHD; AWS; HJ1; CD339; JAGL1; MGC104644	NM_000214	jagged 1 (Alagille syndrome)
A_23_P390504	0.00289	6.475	ARA; IGDA; IHG1; FKHL7; IRID1; FREAC3	NM_001453	forkhead box C1
A_32_P67533	0.00292	2.067	MBT1; MBT-1; RP11-73O6.1	NM_032438	I(3)mbt-like 3 (Drosophila)
A_23_P70660	0.00294	2.103	XTP11; C6orf37; FLJ20037; FLJ31495	NM_017633	family with sequence similarity 46, member A
A_23_P328652	0.00294	2.355	NPH3; FLJ30691; FLJ36696; KIAA2000; DKFZp667K242; DKFZp781K1312	NM_153240	nephronophthisis 3 (adolescent)
A_23_P396765	0.00313	3.066	BM32A; FLJ32029	NM_173582	phosphoglucosyltransferase 2-like 1
A_32_P74409	0.00313	3.011	ENST00000339446		Homo sapiens hypothetical LOC387763, mRNA (cDNA clone IMAGE:6272440), partial cds. [BC052560]
A_24_P940524	0.00335	0.408	ZFX	NM_003410	zinc finger protein, X-linked
A_23_P42257	0.00357	2.041	DIF2; IEX1; PRG1; DIF-2; GLY96; IEX-1; IEX-1L	NM_003897	immediate early response 3
A_23_P4561	0.00357	0.436	PI8; CAP2	NM_198833	serpin peptidase inhibitor, clade B (ovalbumin), member 8
A_23_P89589	0.00364	3.641	PER; hPER; RIGUI; MGC88021	NM_002616	period homolog 1 (Drosophila)
A_23_P23102	0.00397	0.389	KOX29; ZNF31; ZFP-31; ZNF360	NM_145238	zinc finger and SCAN domain containing 20
A_23_P49610	0.00397	4.23	MGC14376; MGC149751; DKFZp686O06159	NM_032895	hypothetical protein MGC14376
A_24_P252718	0.00397	0.335	Epl1; DKFZp781P2312	BC036529	enhancer of polycomb homolog 1 (Drosophila)
A_23_P365738	0.00397	2.519	KIAA0278	NM_015193	activity-regulated cytoskeleton-associated protein
A_23_P201837	0.00397	0.446	HLALS	AF031469	major histocompatibility complex, class I-related
A_23_P39237	0.00455	2.11	TTP; G0S24; GOS24; TIS11; NUP475; RNF162A	NM_003407	zinc finger protein 36, C3H type, homolog (mouse)
A_24_P402588	0.00455	2.061	EV19; CTIP1; BCL11A-L; BCL11A-S; FLJ10173; FLJ34997; KIAA1809; BCL11A-XL	NM_138553	B-cell CLL/lymphoma 11A (zinc finger protein)
A_24_P944640	0.00455	2.653	BE37; FLJ12957; KIAA1548	NM_020909	erythrocyte membrane protein band 4.1 like 5
A_23_P13137	0.00455	2.413	AY358815	AY358815	Clone DNA108923 SFVP2550 (UNQ2550)
A_24_P54900	0.00455	2.033	LNX; MPDZ; PDZRN2	NM_032622	ligand of numb-protein X 1
A_24_P389415	0.00455	2.054	MA2; MM2; RGAG2; KIAA0883	NM_007257	paraneoplastic antigen MA2
A_32_P166693	0.00455	2.127	THC2265769		Q9GEJ2 (Q9GEJ2) NADH dehydrogenase subunit F (Fragment), partial (5%) [THC2265769]

A_23_P411723	0.00455	2.127 PSA; SGPA	NM_002655	pleiomorphic adenoma gene 1
A_24_P411186	0.00455	2.167 EVI9; CTIP1; BCL11A-L; BCL11A-S; FLJ10173; FLJ34997; KIAA1809; BCL11A-XL	NM_022893	B-cell CLL/lymphoma 11A (zinc finger protein)
A_23_P66481	0.00455	2.134 NgR3; NGRH2; DKFZp547J144	NM_178568	reticulon 4 receptor-like 1
A_23_P207058	0.00455	3.719 CIS3; SSI3; ATOD4; Cish3; SSI-3; SOCS-3; MGC71791	NM_003955	suppressor of cytokine signaling 3
A_23_P39263	0.00455	2.336 ZNF424	NM_173480	zinc finger protein 57
A_24_P615462	0.00455	2.369 A_24_P615462		
A_23_P384748	0.00455	2.335 KIAA2028; PLEKHH1L	NM_172069	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2
A_24_P565496	0.00455	0.449 A_24_P565496		
A_23_P143016	0.00483	2.113 NM_006673	NM_006673	Homo sapiens AT rich interactive domain 5A (MRF1-like) (ARID5A), transcript variant 2, mRNA [NM_006673]
A_24_P277295	0.00483	3.06 ISY1; RAB41; RAB11B; MGC90481	NM_198490	RAB43, member RAS oncogene family
A_23_P112950	0.00487	0.47 MCAF; p621; FLJ10139; FLJ10688	NM_018179	activating transcription factor 7 interacting protein
A_23_P1602	0.0049	2.125 CEP2; BORG1	NM_006779	CDC42 effector protein (Rho GTPase binding) 2
A_24_P71280	0.0049	4.38 FLJ12132	BC018691	G protein-coupled receptor 157
A_23_P317200	0.00495	0.439 FLJ00381; MGC46534	NM_153340	ataxin 7-like 2
A_24_P96403	0.00516	2.256 AML1; CBFA2; EVI-1; AMLCR1; PEBP2aB; AML1-EVI-1	NM_001001890	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
A_23_P35082	0.00516	2.031 HI95; SES2; SEST2; DKFZp761M0212; DKFZp761M02121	NM_031459	sestrin 2
A_23_P57856	0.00516	9.368 BCL5; LAZ3; BCL6A; ZNF51; ZBTB27	NM_138931	B-cell CLL/lymphoma 6 (zinc finger protein 51)
A_23_P10591	0.00519	2.205 MGC99788	NM_001004431	meteorin, glial cell differentiation regulator-like
A_23_P164946	0.00531	0.47 MDC1C; LGMD2I; MGC2991; FLJ12576	NM_024301	fukutin related protein
A_23_P118392	0.00531	2.376 AGS1; DEXRAS1; MGC:26290	NM_016084	RAS, dexamethasone-induced 1
A_23_P69100	0.00531	2.628 SGEF; CSGEF; HMFN1864; DKFZp434D146	NM_015595	Src homology 3 domain-containing guanine nucleotide exchange factor
A_32_P34003	0.00533	2.644 THC2313453		
A_32_P104334	0.00534	3.292 AW972815	AW972815	Transcribed locus
A_24_P182494	0.00534	4.053 MKP5; MKP-5	NM_007207	dual specificity phosphatase 10
A_32_P102428	0.00534	2.192 AK129982	AK129982	CDNA clone IMAGE:5285282
A_24_P101314	0.00566	2.229 MGC126650; MGC126652	NM_138356	Src homology 2 domain containing F
A_24_P382489	0.00568	2.077 FATP; FATP1; ACSVL5; FLJ00336; MGC71751	NM_198580	solute carrier family 27 (fatty acid transporter), member 1
A_23_P84555	0.00568	2.616 KCTD21	NM_001029859	potassium channel tetramerisation domain containing 21
A_32_P122715	0.00573	0.34 THC2280867		
A_23_P28485	0.00573	2.013 GCL	NM_012198	grancalcin, EF-hand calcium binding protein
A_23_P105088	0.00578	0.434 ASH2; HASH2; MASH2	NM_005170	achaete-scute complex homolog 2 (Drosophila)
A_23_P216664	0.00585	0.443 TTF2; FOXE2; HFKH4; HFKL5; TITF2; TTF-2; FKHL15	NM_004473	forkhead box E1 (thyroid transcription factor 2)
A_32_P215669	0.00585	2.122 AK124803	AK124803	Clone 23695 mRNA sequence
A_23_P102706	0.00585	2.061 KIAA0374; MGC46096; bA314N13.5	NM_014723	syntrophin
A_23_P499	0.0063	0.396 GLCT2; BETA3GALT2; beta3Gal-T2	NM_003783	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
A_32_P86318	0.00647	3.582 ISY1; RAB41; RAB11B; MGC90481	NM_198490	RAB43, member RAS oncogene family
A_24_P741023	0.00647	0.464 BC008476	BC008476	CDNA clone IMAGE:4290767
A_24_P918147	0.00651	2.79 AK023391	AK023391	CDNA FLJ39585 fis, clone SKMUS2006633
A_23_P167920	0.00654	2.031 Delta; DELTA1	NM_005618	delta-like 1 (Drosophila)
A_23_P92349	0.00694	3.063 FHFR; FGFR5	NM_001004356	fibroblast growth factor receptor-like 1
A_24_P350796	0.00696	0.424 MGC44931; DKFZp434D0421	BC040695	Williams-Beuren syndrome chromosome region 16
A_32_P5276	0.00697	2.34 SGEF; CSGEF; HMFN1864; DKFZp434D146	AB073386	Src homology 3 domain-containing guanine nucleotide exchange factor
A_23_P78405	0.00697	2.955 EL; EDL; PRO719	NM_006033	lipase, endothelial
A_23_P49338	0.007	4.676 FN14; CD266; TWEAKR	NM_016639	tumor necrosis factor receptor superfamily, member 12A
A_23_P145978	0.007	2.026 VPAC2; FLJ16511	NM_003382	vasoactive intestinal peptide receptor 2
A_23_P218584	0.007	2.83 EVI9; CTIP1; BCL11A-L; BCL11A-S; FLJ10173; FLJ34997; KIAA1809; BCL11A-XL	NM_022893	B-cell CLL/lymphoma 11A (zinc finger protein)
A_23_P21785	0.007	0.497 MST077; MSTP077; FLJ22109; FLJ22609	NM_022072	NOL1/NOP2/Sun domain family, member 3
A_24_P380022	0.007	3.887 EIF-5A2; eIF5AII	NM_020390	eukaryotic translation initiation factor 5A2
A_32_P79966	0.007	0.36 THC2364821		
A_24_P125469	0.00722	2.151 EL; EDL; PRO719	NM_006033	lipase, endothelial
A_23_P160598	0.00724	0.486 FLJ13949	CR591540	target of EGR1, member 1 (nuclear)
A_32_P3431	0.00732	2.391 AK129542	AK129542	CDNA FLJ26031 fis, clone PNC08078
A_23_P39454	0.00742	2.483 FLJ11637	NM_024967	zinc finger protein 556
A_23_P46725	0.00742	0.355 Epl1; DKFZp781P2312	NM_025209	enhancer of polycomb homolog 1 (Drosophila)
A_24_P290527	0.00743	0.468 ZFX	NM_003410	zinc finger protein, X-linked
A_32_P151244	0.00743	0.464 AK022268	AK022268	CDNA FLJ12206 fis, clone MAMMA1000941
A_32_P194372	0.00772	2.387 AK129547	AK129547	CDNA FLJ26036 fis, clone PRS00145
A_24_P118011	0.00785	0.268 ENST00000295112		PREDICTED: Homo sapiens similar to RIKEN cDNA 2010316F05 (LOC344405), mRNA [XM_293034]
A_23_P161428	0.00838	2.26 MGC22805	NM_144590	ankyrin repeat domain 22
A_32_P69930	0.00849	3.204 FLJ90575; MGC138479	NM_153376	coiled-coil domain containing 96
A_23_P51856	0.00849	4.395 MKP5; MKP-5	NM_007207	dual specificity phosphatase 10
A_24_P595877	0.00849	0.398 SRrp86; SRrp508; MGC133045; DKFZp564B176	AB209694	splicing factor, arginine/serine-rich 12
A_23_P82065	0.00866	2.109 ADMD; STGD2; STGD3	NM_022726	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4

A_23_P216667	0.00866	0.483 TTF2; FOXE2; HFKH4; HFKL5; TTF2; TTF-2; FKHL15	NM_004473	forkhead box E1 (thyroid transcription factor 2)
A_24_P305312	0.00886	2.524 JFY1; PUMA; PUMA/JFY1	NM_014417	BCL2 binding component 3
A_23_P62465	0.00886	0.402 MGC138710	NM_003411	zinc finger protein, Y-linked
A_23_P46149	0.00892	2.49 TM7SF1	NM_003272	G protein-coupled receptor 137B
A_24_P204971	0.00894	2.052 FLJ16340	NM_012257	HMG-box transcription factor 1
A_23_P14083	0.00894	4.051 ALI1; DEGA	NM_181847	adhesion molecule with Ig-like domain 2
A_23_P327370	0.00916	2.514 ENST00000269919		Homo sapiens hypothetical protein MGC10812, mRNA (cDNA clone MGC:10812 IMAGE:3612949), complete cds. [BC004942]
A_23_P94403	0.00916	0.433 TRP; CAS2; CATB; GP75; TYRP; b-PROTEIN	NM_000550	tyrosinase-related protein 1
A_24_P928272	0.00953	0.393 AF086376	AF086376	Full length insert cDNA clone ZD68D12
A_23_P102160	0.00955	0.487 BLOCK18; FLJ32954; FLJ38143; MGC33318; PRO34163; PYST9371	AF435956	family with sequence similarity 82, member A
A_23_P151098	0.00955	2.661 SSB2; GRCC9; SSB-2; MGC2519	NM_032641	splA/ryanodine receptor domain and SOCS box containing 2
A_24_P762886	0.00955	3.901 KIAA0485	AB007954	KIAA0485 protein
A_23_P339818	0.00955	2.954 FLJ36045	NM_183376	arrestin domain containing 4
A_23_P318800	0.00955	2.908 SSTR2	NM_001050	somatostatin receptor 2
A_32_P19716	0.00955	2.01 MGC45731	AK027019	zinc finger protein 697
A_32_P134167	0.00964	0.474 BG031574	BG031574	Transcribed locus, strongly similar to XP_522173.1 Vasopressin-activated calcium-mobilizing receptor-1 [Pan troglodytes]
A_24_P934435	0.00964	3.45 AF086077	AF086077	Full length insert cDNA clone YZ60H05
A_24_P22079	0.00964	2.36 FKH1; FKHR; FOXO1A	NM_002015	forkhead box O1
A_32_P119348	0.00964	0.309 AK130049	AK130049	CDNA FLJ26539 fis, clone KDN09310
A_24_P367804	0.00969	2.79 BC024651	BC024651	Homo sapiens cDNA clone MGC:25116 IMAGE:4509288, complete cds.
A_23_P349398	0.01	0.402 ZAR1	NM_175619	zygote arrest 1
A_32_P24140	0.0102	2.282 MGC32610	NM_005256	growth arrest-specific 2
A_23_P335958	0.0102	2.112 DEP.7; PGR22; DEPDC3; FLJ31819; FLJ39346	NM_152529	G protein-coupled receptor 155
A_23_P369666	0.0102	0.473 RACK7; PRKCBP1; PRO2893; MGC31836	AL137703	zinc finger, MYND-type containing 8
A_24_P695306	0.0103	0.346 XM_294353	XM_294353	PREDICTED: Homo sapiens similar to RIKEN cDNA 6332401O19 gene (LOC340344), mRNA [XM_294353]
A_23_P311885	0.0103	2.229 MBT1; MBT-1; RP11-7306.1	NM_032438	l(3)mbt-like 3 (Drosophila)
A_23_P52161	0.0103	2.394 BCA3; AKIP1	NM_182901	chromosome 11 open reading frame 17
A_23_P61945	0.0103	2.844 WS2A	NM_198159	microphthalmia-associated transcription factor
A_23_P75260	0.0103	2.887 AD037; MGC44914	NM_032023	Ras association (RalGDS/AF-6) domain family 4
A_32_P198791	0.0103	2.513 THC2397265		ALU2_HUMAN (P39189) Alu subfamily SB sequence contamination warning entry, partial (10%) [THC2397265]
A_24_P573514	0.0105	0.488 BC033528	BC033528	CDNA clone IMAGE:4822684
A_32_P11	0.0106	0.489 THC2373805		
A_24_P919230	0.0107	0.319 AI340058	AI340058	Transcribed locus
A_23_P47885	0.0107	2.155 FLJ26573; FLJ90440; KIAA3016	NM_153377	leucine-rich repeats and immunoglobulin-like domains 3
A_32_P104432	0.0107	3.547 NM_203306	NM_203306	Homo sapiens hypothetical protein MGC39606 (MGC39606), mRNA [NM_203306]
A_24_P570049	0.0108	2.254 NM_001001930	NM_001001930	Homo sapiens peroxisome proliferative activated receptor, alpha (PPARA), transcript variant 6, mRNA [NM_001001930]
A_23_P26729	0.0109	0.439 CLN80; p80-coilin	NM_004645	coilin
A_32_P213091	0.0113	3.725 LOC440338	AK094972	Hypothetical gene supported by AJ002784
A_24_P253003	0.0113	3.369 HWNT11; MGC141946; MGC141948	NM_004626	wingless-type MMTV integration site family, member 11
A_23_P97218	0.0116	2.085 ERO1LB	CR596670	ERO1-like beta (S. cerevisiae)
A_32_P173023	0.0117	0.473 A_32_P173023		
A_23_P360964	0.0119	2.074 RRR1; MGC15476	NM_145056	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)
A_24_P636882	0.0119	2.341 THC2337176		ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (30%) [THC2337176]
A_32_P174572	0.0119	2.821 THC2438039		
A_32_P34064	0.0119	0.435 A_32_P34064		
A_32_P221590	0.0119	2.306 A_32_P221590		
A_32_P58029	0.0122	3.976 A_32_P58029		
A_24_P345209	0.0122	2.014 RED; REDK; DYRK5; hYAK3-2	NM_001004023	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
A_23_P317465	0.0123	2.114 FLJ38125	NM_016530	RAB8B, member RAS oncogene family
A_23_P215787	0.0124	2.156 FLJ16340	NM_012257	HMG-box transcription factor 1
A_23_P90542	0.0124	3.27 FLJ16004; Nbla10512; DKFZp313K2238; DKFZp547B0714	NM_152606	zinc finger protein 540
A_24_P931755	0.0127	0.471 ZNF675	D70835	Zinc finger protein 675
A_23_P141960	0.0127	2.285 RBT1	NM_203344	SERTA domain containing 3
A_23_P80763	0.0127	2.42 PPR3; PRR3; PVRR3; CDw113; FLJ90624; nectin-3; DKFZP566B0846	BC017572	poliovirus receptor-related 3
A_32_P216566	0.0127	0.493 dJ237115.1	NM_001009994	chromosome 6 open reading frame 159
A_32_P214860	0.0136	2.349 A_32_P214860		
A_23_P73264	0.0136	0.494 hoxA7	AJ005814	Homo sapiens mRNA for hoxA7 protein.
A_24_P330309	0.0138	2.139 RBP1; RBBP1; RBP-1	NM_002892	AT rich interactive domain 4A (RBP1-like)
A_23_P386254	0.0139	2.018 NKX3B; NKX3-2; NKX3.2; MGC138171	NM_001189	bagpipe homeobox homolog 1 (Drosophila)
A_32_P88262	0.0142	2.314 FLJ37228	AK094547	hypothetical protein FLJ37228
A_32_P190181	0.0146	2.388 THC2345075		
A_32_P26956	0.0148	0.452 C19orf7	AW090036	Chromosome 19 open reading frame 7
A_23_P107350	0.0148	2.543 GLUT4	NM_001042	solute carrier family 2 (facilitated glucose transporter), member 4

A_23_P105251	0.0148	7.053 GLI	NM_005269	glioma-associated oncogene homolog 1 (zinc finger protein)
A_23_P214080	0.0148	2.448 TIS8; AT225; G0S30; NGFI-A; ZNF225; KROX-24; ZIF-268	NM_001964	early growth response 1
A_23_P41824	0.015	0.368 A_23_P41824		
A_32_P61708	0.0151	3.131 A_32_P61708		
A_32_P164203	0.0151	0.499 THC2436337		
A_23_P210210	0.0154	2.484 HLF; MOP2; HIF2A; PASD2	NM_001430	endothelial PAS domain protein 1
A_23_P363174	0.0154	2.188 H2A.i; H2A.f; H2A.FI; HIST1H2AM; dJ193B12.9	NM_003511	histone cluster 1, H2al
A_24_P10137	0.0155	2.454 RGC32; RGC-32; KIAA0564; MGC87338; bA157L14.2	NM_014059	chromosome 13 open reading frame 15
A_23_P48530	0.0155	2.334 IA-6; mit1	NM_032594	insulinoma-associated 2
A_24_P102293	0.0156	3.297 LRRC11; KIAA0918; bA364G4.2	NM_015567	SLIT and NTRK-like family, member 5
A_24_P4816	0.016	2.027 ATG8; GEC1; APG8L	NM_031412	GABA(A) receptor-associated protein like 1
A_23_P162165	0.0167	0.279 MGC2376	NM_023930	potassium channel tetramerisation domain containing 14
A_23_P380954	0.0167	0.451 FLJ13839; FLJ20307; KIAA1703	NM_017757	zinc finger protein 407
A_32_P179131	0.017	0.411 THC2449383		Q96E07 (Q96E07) CCBL1 protein, partial (32%) [THC2449383]
A_23_P347623	0.017	2.378 ERO1LB	NM_019891	ERO1-like beta (S. cerevisiae)
A_23_P254863	0.017	3.921 MGC42105	NM_153361	hypothetical protein MGC42105
A_23_P39294	0.017	2.545 ENST00000312785		Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1759349. [AL365412]
A_23_P119196	0.017	4.031 LKLF	NM_016270	Kruppel-like factor 2 (lung)
A_24_P295590	0.0172	2.474 AD037; MGC44914	NM_032023	Ras association (RalGDS/AF-6) domain family 4
A_32_P3342	0.0176	0.401 THC2315555		ALU7_HUMAN (P39194) Alu subfamily SQ sequence contamination warning entry, partial (21%) [THC2315555]
A_24_P417036	0.0176	2.664 NM_001001930	NM_001001930	Homo sapiens peroxisome proliferative activated receptor, alpha (PPARA), transcript variant 6, mRNA [NM_001001930]
A_23_P418031	0.0178	3.205 ENST00000304963		Homo sapiens mRNA for FLJ00074 protein, partial cds. [AK024480]
A_23_P208579	0.0184	0.445 A_23_P208579		
A_23_P43175	0.0187	2.032 FLJ11619	NM_144710	septin 10
A_23_P422144	0.0187	5.837 FLJ90022	NM_153690	family with sequence similarity 43, member A
A_32_P372337	0.0187	2.127 ENST00000333010		Homo sapiens mRNA for KIAA0555 protein, partial cds. [AB011127]
A_23_P360797	0.0187	0.485 NT3; HDNF; NGF2; NGF-2; MGC129711	NM_002527	neurotrophin 3
A_23_P16673	0.0187	2.538 CNN2	NM_004368	calponin 2
A_23_P141035	0.0188	0.389 LSST	NM_005769	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
A_32_P124538	0.0188	0.485 THC2342810		
A_32_P90740	0.019	0.493 AF086427	AF086427	Full length insert cDNA clone ZD79D11
A_23_P404902	0.0192	0.39 APXL2; KIAA1960	AB075840	shroom family member 1
A_32_P47027	0.0192	0.249 THC2282701		
A_24_P931443	0.0198	0.499 OGR1; MGC111379	BC098567	G protein-coupled receptor 68
A_23_P121987	0.0198	3.844 TSLP	NM_033035	thymic stromal lymphopoietin
A_23_P411188	0.0198	0.473 CHRNA10	NM_020402	cholinergic receptor, nicotinic, alpha 10
A_23_P108835	0.0198	2.255 CGI-127	NM_016061	yippee-like 5 (Drosophila)
A_24_P418250	0.0198	2.61 NM_203306	NM_203306	Homo sapiens hypothetical protein MGC39606 (MGC39606), mRNA [NM_203306]
A_23_P89621	0.0198	2.088 PC2; hPC2; NBP16	NM_003655	chromobox homolog 4 (Pc class homolog, Drosophila)
A_24_P243749	0.0198	3.909 FLJ40832	NM_002612	pyruvate dehydrogenase kinase, isozyme 4
A_23_P99226	0.0202	2.685 SIR2L4; MGC57437; MGC130046; MGC130047; sirtuin 4	NM_012240	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)
A_24_P254079	0.0202	2.174 TLN; TLCN	NM_003259	intercellular adhesion molecule 5, telencephalin
A_23_P23748	0.0204	2.508 FLJ90135; KIAA0893	NM_014969	WD repeat domain 47
A_23_P204958	0.0204	2.78 KPM; FLJ13161	NM_014572	LATS, large tumor suppressor, homolog 2 (Drosophila)
A_23_P85941	0.0204	0.5 MGC138212; MGC141988	NM_006492	aristaless-like homeobox 3
A_24_P634530	0.0204	0.471 THC2281463		
A_24_P937691	0.0204	2.569 AL050204	AL050204	CDNA clone IMAGE:4733238
A_32_P139196	0.0211	0.285 NM_213723	NM_213723	Homo sapiens chromosome 13 open reading frame 25 (C13orf25), transcript variant 2, mRNA [NM_213723]
A_23_P24004	0.0212	0.442 G10P2; IFI54; ISG54; cig42; IFI-54; GARG-39; ISG-54K	NM_001547	interferon-induced protein with tetratricopeptide repeats 2
A_23_P19673	0.0212	2.392 SGK1	NM_005627	serum/glucocorticoid regulated kinase
A_23_P85682	0.0212	2.196 NFI-L; KIAA1439; DKFZp434L0422	NM_005595	nuclear factor I/A
A_24_P367576	0.0212	0.374 AK125170	AK125170	CDNA FLJ25310 fis, clone SYN00991
A_32_P780817	0.0214	3.676 CT45-1	NM_001017417	cancer/testis antigen CT45-1
A_32_P119744	0.0215	2.009 LOC344595; FLJ31372	BC039550	hypothetical LOC344595
A_32_P42313	0.0217	0.495 THC2438994		
A_23_P405216	0.0219	0.446 FLJ90764	NM_173656	zinc finger protein 619
A_32_P46154	0.0219	0.422 KOX8; ZNF15; ZNF15L1; FLJ16755; FLJ46310; DKFZp686L10267	NM_021269	zinc finger protein 708
A_23_P52266	0.0219	2.204 G10P1; IFI56; ISG56; IFI-56; IFNAI1; RNM561; GARG-16	NM_001548	interferon-induced protein with tetratricopeptide repeats 1
A_23_P204937	0.0219	2.211 RGC32; RGC-32; KIAA0564; MGC87338; bA157L14.2	NM_014059	chromosome 13 open reading frame 15
A_32_P12372	0.0222	2.102 THC2355348		ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (7%) [THC2355348]
A_32_P230326	0.0222	0.382 THC2416677		
A_23_P344400	0.0225	0.377 AHH; AHR; KIAA1234	NM_020731	aryl-hydrocarbon receptor repressor
A_23_P120103	0.0225	2.402 KV9.3; MGC9481	NM_002252	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3

A_24_P148503	0.0227	2.177 HFZ5; C2orf31; MGC129692; DKFZP434E2135	AK024850	frizzled homolog 5 (Drosophila)
A_24_P363278	0.0233	6.406 dJ417M14.2	NM_005906	male germ cell-associated kinase
A_32_P15544	0.0238	0.381 THC2337501		PRMA_HUMAN (Q86XR5) Proline rich membrane anchor 1 precursor (PRiMA), partial (15%) [THC2337501]
A_24_P203696	0.0244	0.498 ENST00000301171		Human cytochrome P450 (CYP2A7PT) pseudogene mRNA, partial cds. [U22030]
A_23_P330788	0.0245	0.404 KIAA0522	NM_015075	IQ motif and Sec7 domain 2
A_32_P58201	0.0249	2.014 C9orf52	AK021570	Chromosome 9 open reading frame 52
A_32_P65067	0.0255	0.455 THC2315602		
A_23_P131394	0.0257	0.401 MCT14; FLJ30794	NM_152527	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)
A_32_P197585	0.0258	0.434 THC2377770		Q5SVL1 (Q5SVL1) Caspase 7, apoptosis-related cysteine protease, partial (12%) [THC2377770]
A_23_P401709	0.0264	0.483 FLJ25067; RP4-784N16.1	NM_152504	chromosome 20 open reading frame 196
A_23_P300033	0.0265	4.88 CD140A; PDGFR2; MGC74795; Rhe-PDGFR	NM_006206	platelet-derived growth factor receptor, alpha polypeptide
A_32_P185682	0.0266	2.283 CR613361	CR613361	Full-length cDNA clone CS0DJ002YF02 of T cells (Jurkat cell line) Cot 10-normalized of Homo sapiens (human)
A_32_P181564	0.0267	2.594 THC2411808		
A_32_P111394	0.0269	3.995 THC2441040		
A_24_P636451	0.0271	0.425 AK023559	AK023559	CDNA FLJ13497 fis, clone PLACE1004518
A_23_P145024	0.0271	2.774 BAR; B2AR; ADRBR; ADRB2R; BETA2AR	NM_000024	adrenergic, beta-2-, receptor, surface
A_32_P30717	0.0271	2.67 THC2317093		
A_24_P396327	0.0271	0.449 C1orf171; FLJ40918	NM_138467	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)
A_24_P929388	0.0279	2.015 FLJ34263; DKFZp781L2456	NM_138390	transmembrane protein 169
A_23_P358714	0.0279	2.159 MGC150624; RP11-352P4.1	AY358366	KIAA1324
A_23_P1823	0.0279	2.183 AN; AN2; MGDA; WAGR; D11S812E; MGC17209	NM_001604	paired box gene 6 (aniridia, keratitis)
A_23_P500956	0.0282	2.214 B3GNT; B3GNT1; B3GN-T1; B3GN-T2; B3GNT-2; BETA3GNT	NM_006577	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
A_23_P101380	0.0288	0.376 B3GALT7; BGALT15; beta3Gn-T8	NM_198540	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8
A_24_P944063	0.0294	0.415 FLJ32130	NM_152458	zinc finger protein 785
A_23_P216307	0.0296	0.206 CDR; ETO; MTG8; MTG8b; AML1T1; ZMYND2; CBFA2T1; MGC2796	NM_004349	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
A_23_P85726	0.0296	0.463 AsTP2; MGC9084; RP1-117P20.4	NM_033418	chromosome 1 open reading frame 156
A_24_P930391	0.0296	3.443 AK022351	AK022351	CDNA FLJ12289 fis, clone MAMMA1001788
A_23_P351148	0.0297	0.335 EAT2	NM_053282	SH2 domain containing 1B
A_24_P884376	0.0297	0.451 XM_499519	XM_499519	PREDICTED: Homo sapiens hypothetical gene supported by AK092942; NM_198284 (LOC442539), mRNA [XM_499519]
A_23_P60775	0.0297	2.077 CELF5; BRUNOL-5	NM_021938	bruno-like 5, RNA binding protein (Drosophila)
A_24_P346762	0.0297	3.395 FLJ11560; P1.11659_5; bA182N22.6; RP11-182N22.6	NM_025182	KIAA1539
A_24_P122746	0.0308	2.204 WARP; VWA-1; FLJ22215; DKFZp761O051	AL137722	von Willebrand factor A domain containing 1
A_24_P117410	0.0309	0.33 MGC16635	NM_138433	kelch domain containing 7B
A_32_P68097	0.031	0.471 C8ORFK32	CR936831	C8orfK32 protein
A_23_P210100	0.0311	2.247 CYP26A2; MGC129613; P450RAI-2; DKFZp686G0638	NM_019885	cytochrome P450, family 26, subfamily B, polypeptide 1
A_32_P81324	0.0311	0.462 THC2404993		
A_32_P56604	0.0313	0.443 CBY2; NURIT; FLJ35810	NM_152719	spermatid associated
A_23_P500381	0.0313	3.037 5-HT7	NM_019859	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)
A_23_P132378	0.0313	0.375 ME2; FMI2; CDHF9; HFMI2; DKFZp434P0729	NM_014246	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
A_32_P183718	0.0313	4.011 SP5	NM_001003845	Sp5 transcription factor
A_24_P393303	0.0317	0.473 MDS032	AK074683	uncharacterized hematopoietic stem/progenitor cells protein MDS032
A_23_P32955	0.033	2.158 MER; c-mer; MGC133349	U08023	c-mer proto-oncogene tyrosine kinase
A_32_P174385	0.0332	0.456 A_32_P174385		
A_24_P170667	0.0332	3.403 ENST00000279873		Homo sapiens AT rich interactive domain 5B (MRF1-like), mRNA (cDNA clone IMAGE:30345306), partial cds. [BC066345]
A_23_P120354	0.0332	3.589 C2orf26	NM_023016	ankyrin repeat domain 57
A_23_P137984	0.0332	2.065 42C; P11; p10; GP11; ANX2L; CAL1L; CLP11; Ca[1]; ANX2LG; MGC111133	NM_002966	S100 calcium binding protein A10
A_23_P2901	0.0332	0.479 FLJ20034	AK000041	chromosome 14 open reading frame 113
A_23_P95594	0.0332	0.216 AAC1; NATI	NM_000662	N-acetyltransferase 1 (arylamine N-acetyltransferase)
A_32_P182609	0.0339	0.454 LOC644422	BE008305	Similar to arginine/serine-rich splicing factor 6
A_32_P9931	0.0342	0.478 A_32_P9931		
A_24_P330303	0.0346	3.52 EX1; Willin; C14orf31; MGC17921; c14_5320	NM_152330	FERM domain containing 6
A_32_P78311	0.0349	0.484 LOC729096	CR590180	Similar to BMS1-like, ribosome assembly protein
A_24_P18270	0.0349	0.352 C10orf49	NM_145314	chromosome 10 open reading frame 49
A_24_P398790	0.0349	0.487 FLJ10008; FLJ14051	AK024113	chromosome 14 open reading frame 102
A_23_P131208	0.0351	4.494 NOT; RNR1; HZF-3; NURR1; TINUR	NM_006186	nuclear receptor subfamily 4, group A, member 2
A_24_P601511	0.0362	0.444 AK090762	AK090762	CDNA FLJ33443 fis, clone BRALZ1000103
A_32_P85131	0.0363	0.465 THC2415297		
A_24_P253723	0.0366	2.088 MGC14376; MGC149751; DKFZp686O06159	NM_032895	hypothetical protein MGC14376
A_23_P368779	0.037	0.326 MGC17986; MGC149700	NM_153608	zinc finger protein 114
A_23_P347027	0.0372	2.52 NSMASE2; FLJ22593; MGC138443	NM_018667	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
A_23_P132856	0.0376	0.313 GARPL1; UNQ3030; MGC50789	NM_198565	leucine rich repeat containing 33
A_23_P46131	0.0384	0.447 FLJ14050; RP11-96L14.5	NM_024869	glycine/arginine rich protein 1
A_23_P334271	0.0396	0.492 SMAD1	BC069781	SMAD family member 1

A_23_P71928	0.0403	2.517 CHAT; NSP3; FLJ39664; PRO34088	NM_005489	SH2 domain containing 3C
A_23_P75192	0.0412	0.432 A_23_P75192		
A_23_P18362	0.0417	5.741 KIAA0848; MGC138681	NM_014926	SLIT and NTRK-like family, member 3
A_23_P209700	0.0417	0.498 FM3; FM-3; GPC-R; GPR66; NMU1R; (FM-3)	NM_006056	neuromedin U receptor 1
A_24_P218259	0.042	3.23 AK124390	AK124390	CDNA FLJ39585 fis, clone SKMUS2006633
A_23_P200707	0.042	2.384 EK12; FLJ10761; HMFT1716; RP11-74C13.2	NM_018208	ethanolamine kinase 2
A_23_P149281	0.042	2.005 ECK	NM_004431	EPH receptor A2
A_24_P57631	0.042	0.33 SGB; DGSX; SDYS; SGBS; OCI-5; SGBS1	NM_004484	glypican 3
A_24_P179363	0.042	0.463 FAF; MGC126856	BC005077	Fanconi anemia, complementation group F
A_23_P337778	0.0433	2.932 FLJ25033	AK057762	L-threonine dehydrogenase
A_23_P16242	0.0439	2.235 KOX13; FLJ39241	NM_021143	zinc finger protein 20
A_24_P918518	0.0444	0.418 PH-4	BC018731	hypoxia-inducible factor prolyl 4-hydroxylase
A_24_P31275	0.045	2.254 AMOG	NM_001678	ATPase, Na+/K+ transporting, beta 2 polypeptide
A_23_P204947	0.0454	4.681 HID; KID; PPK; CX26; DFNA3; DFNB1; NSRD1	NM_004004	gap junction protein, beta 2, 26kDa
A_32_P224253	0.0454	4.025 DNHBL; DPL11; DNAHBL; DNAHC11; FLJ30095; FLJ37699	NM_003777	dynein, axonemal, heavy chain 11
A_23_P347541	0.046	0.46 NR3A; NMDAR-L; FLJ45414	NM_133445	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A
A_23_P380318	0.046	4.111 NGFIC; NGFI-C; PAT133	NM_001965	early growth response 4
A_32_P35205	0.0462	2.281 THC2380237		
A_32_P100206	0.0462	0.384 A_32_P100206		
A_32_P856518	0.0466	0.461 AS250; FLJ12819; KIAA1272; dJ1049G11; bA287B20.1; dJ1049G11.4; RP11-470C13.2	AB033098	chromosome 20 open reading frame 74
A_23_P356494	0.0466	0.489 NS; NETS; LEKTI; LETKI; VAKTI; FLJ21544	NM_006846	serine peptidase inhibitor, Kazal type 5
A_23_P215549	0.0467	0.447 PON3	NM_000940	paraoxonase 3
A_23_P34066	0.0467	0.469 CD129	NM_176786	interleukin 9 receptor
A_23_P257365	0.0479	2.66 ZNF163	NM_005263	growth factor independent 1
A_23_P135381	0.0483	3.692 SP5	NM_001003845	Sp5 transcription factor
A_23_P113212	0.0485	2.027 DERP7; FLJ10134	NM_018004	transmembrane protein 45A
A_24_P158314	0.0485	2.205 FLJ38360; bA356B19.1; DKFZp434O131; DKFZp761J1523; RP11-356B19.1	NM_032293	GTPase activating Rap/RanGAP domain-like 3
A_23_P329261	0.0499	2.27 IRK1; LQT7; SQT3; HHIRK1; KIR2.1; HHBIRK1	NM_000891	potassium inwardly-rectifying channel, subfamily J, member 2