Supplemental Table S1. F3 Generation Ventral Prostate Regulated Genes (954 Genes)

Apoptosis

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Anxa1*	643.0	259.1	0.40	AI236455	annexin 1
2	*Apip_predicted*	178.0	342.3	1.92	BE103273	APAF1 interacting protein (predicted)
3	*Bag4*	154.6	93.7	0.61	AA818127	BCL2-associated athanogene 4
4	*Cflar*	377.2	227.3	0.60	AI578435	CASP8 and FADD-like apoptosis regulator
5	*Casp7*	119.1	198.1	1.66	BF283754	caspase 7
6	*Clu*	837.8	1687.8	2.01	AF314657	clusterin
7	*Ddx58_predicted*	67.6	134.6	1.99	AI575264	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)
8	*Eaf2*	5668.7	2681.0	0.47	BI285131	ELL associated factor 2
9	*Bat5*	424.6	674.8	1.59	BE097389	HLA-B associated transcript 5
10	*Itgb3bp*	162.2	82.4	0.51	BM387863	integrin beta 3 binding protein (beta3-endonexin)
11	*Itgb3bp_predicted*	79.5	39.1	0.49	BM387863	integrin beta 3 binding protein (beta3-endonexin) (predicted)
12	*Lsp1_predicted*	49.1	112.3	2.29	AI012109	lymphocyte specific 1 (predicted)
13	*Nradd*	59.4	163.1	2.75	AI598730	neurotrophin receptor associated death domain
14	*LOC500348*	226.9	143.5	0.63	BF403992	Similar to Apoptosis facilitator Bcl-2-like protein 14
15	*MGC105647*	1856.5	2858.0	1.54	BI282332	similar to Nur77 downstream protein 2

Cell Cycle

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Cdkn1a*	123.0	240.0	1.95	AI010427	Cyclin-dependent kinase inhibitor 1A
2	*Ccnd1*	104.6	202.8	1.94	BI295861	cyclin D1
3	*Dnajc10_predicted*	1047.3	1982.4	1.89	BM388610	DnaJ (Hsp40) homolog, subfamily C, member 10 (predicted)
4	*Kif5b*	61.5	113.3	1.84	AA924572	kinesin family member 5B
5	*Gadd45a*	214.4	379.0	1.77	NM_024127	growth arrest and DNA-damage-inducible 45 alpha
6	*Pak2*	53.3	92.6	1.74	BF420805	p21 (CDKN1A)-activated kinase 2
7	*Pak6_predicted*	51.8	86.4	1.67	AI764741	P21 (CDKN1A)-activated kinase 6 (predicted)
8	*Fcho2_predicted*	52.0	84.1	1.62	BF288361	FCH domain only 2 (predicted)
9	*Dnajb6_predicted*	1058.2	1711.1	1.62	AA899326	DnaJ (Hsp40) homolog, subfamily B, member 6 (predicted)
10	*Ptms*	354.1	550.3	1.55	NM_031975	parathymosin
11	*LOC680006*	103.3	155.1	1.50	AI044868	Similar to Mitotic spindle assembly checkpoint protein MAD1
12	*Mcm2_predicted*	288.1	188.2	0.65	AI229508	minichromosome maintenance deficient 2 mitotin
13	*Rbbp7*	103.4	67.5	0.65	AI175594	retinoblastoma binding protein 7
14	*Rbbp5_predicted*	113.8	73.0	0.64	AA946518	Retinoblastoma binding protein 5 (predicted)
15	*LOC361849*	329.8	210.8	0.64	AW534965	similar to cell division cycle and apoptosis regulator 1
16	*Trp53bp2_predicted*	630.8	377.6	0.60	BE102377	transformation related protein 53 binding protein 2 (predicted)
17	*Pmp22*	1134.0	676.7	0.60	AA943163	peripheral myelin protein 22
18	*Cep27_predicted*	252.6	149.5	0.59	BI295883	centrosomal protein 27 (predicted)
19	*LOC363849*	171.8	100.0	0.58	BE118866	similar to histone cell cycle regulation defective homolog A
20	*RGD1308872_predic*	166.8	96.1	0.58	AA997052	similar to Retinoblastoma-binding protein 8 (RBBP-8)
21	*Cdc23*	98.3	52.2	0.53	BI291309	CDC23 (cell division cycle 23, yeast, homolog)
22	*Cdc73*	650.6	330.8	0.51	BI290578	Cell division cycle 73, Paf1/RNA polymerase II complex
23	*Rbbp9*	82.3	27.3	0.33	AA956258	retinoblastoma-binding protein 9

Cytoskeleton & Extra Cellular Matrix

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Acta1*	618.1	290.7	0.47	NM_019212	actin alpha 1
2	*Actb*	1742.9	2672.5	1.53	NM_031144	actin, beta
3	*Actn3*	95.9	19.3	0.20	NM_133424	actinin alpha 3
4	*Alcam*	682.8	312.5	0.46	NM_031753	activated leukocyte cell adhesion molecule
5	*Asam*	96.4	56.3	0.58	BI303342	adipocyte-specific adhesion molecule
6	*Als2cr3*	82.4	147.4	1.79	BG378620	amyotrophic lateral sclerosis 2 (juvenile) chromosome region
7	*Ceacam1*	155.6	63.2	0.41	BM392373	carcinoembryonic antigen-related cell adhesion molecule 1
8	*Ceacam1*	75.5	18.1	0.24	BE097239	carcinoembryonic antigen-related cell adhesion molecule 1
9	*Cldn8*	1289.0	836.3	0.65	BI292090	Claudin 8 (predicted)
10	*Cotl1_predicted*	63.9	115.2	1.80	AI411057	coactosin-like 1 (Dictyostelium) (predicted)
11	*Cfl1*	543.8	897.1	1.65	BG666614	cofilin 1
12	*Coro1a*	59.2	159.6	2.70	NM_130411	coronin, actin binding protein 1A
13	*Ckap4_predicted*	112.0	204.3	1.82	BM384259	cytoskeleton-associated protein 4 (predicted)
14	*Dpt_predicted*	77.7	128.3	1.65	BI278545	dermatopontin (predicted)
15	*Dmn*	1058.7	698.9	0.66	BG373779	desmuslin
16	*Dnm2*	109.5	176.5	1.61	L24562	dynamin 2
17	*Dst_predicted*	183.7	120.0	0.65	BF549679	Dystonin (predicted)
18	*Emb*	279.7	667.5	2.39	NM_053719	embigin
19	*RGD:1303286*	42.0	82.7	1.97	BF285026	endothelial cell adhesion molecule

20	*Elmo1_predicted*	58.3	160.4	2.75	AI101913	engulfment and cell motility 1, ced-12 homolog (C. elegans)
21	*Epb4.1l3*	92.5	140.8	1.52	AB032828	erythrocyte protein band 4.1-like 3
22	*Epb4.1l5_predicted*	335.0	199.8	0.60	AA858925	erythrocyte protein band 4.1-like 5 (predicted)
23	*Fam3c*	209.0	139.0	0.66	AW920562	family with sequence similarity 3, member C
24	*RGD:620885*	375.1	32.2	0.09	NM_020104	fast myosin alkali light chain
25	*Fndc3_predicted*	216.7	137.1	0.63	AA894079	fibronectin type III domain containing 3 (predicted)
26	*Fgl1*	240.4	590.9	2.46	BM386541	fibronigen-like protein 1
27	*Grifin*	43.9	100.1	2.28	NM_057187	galectin-related inter-fiber protein
28	*Gpnmb*	55.0	110.5	2.01	NM_133298	glycoprotein (transmembrane) nmb
29	*Gpc1*	81.0	193.1	2.38	NM_030828	glypican 1
30	*Klhl2_predicted*	232.8	392.2	1.68	BI298657	kelch-like 2, Mayven (Drosophila) (predicted)
31	*Krt2-5*	73.8	122.1	1.65	BF283692	keratin complex 2, basic, gene 5
32	*Kif3c*	107.6	161.9	1.51	NM_053486	kinesin family member 3C
33	*Klc2_predicted*	239.0	370.5	1.55	AW915749	kinesin light chain 2 (predicted)
34	*Lamc2*	170.3	490.2	2.88	BM385282	lamimin, gamma 2
35	*Lamb2*	172.1	112.0	0.65	NM_012974	laminin, beta 2
36	*Lgals3*	2355.8	1290.4	0.55	NM_031832	lectin, galactose binding, soluble 3
37	*Lgals8*	325.2	210.5	0.65	AI411914	lectin, galactose binding, soluble 8
38	*Lgals9*	31.6	94.1	2.98	U72741	lectin, galactose binding, soluble 9
39	*Lgals3bp*	48.8	117.4	2.41	AF065438	lectin, galactoside-binding, soluble, 3 binding protein
40	*Lamp3_predicted*	391.5	165.8	0.42	BF283924	lysosomal-associated membrane protein 3 (predicted)
41	*Map1lc3a*	388.3	785.9	2.02	AI177372	microtubule-associated protein 1 light chain 3 alpha
42	*Map1b*	98.1	64.4	0.66	BI281702	microtubule-associated protein 1b
43	*Mcoln2*	82.6	15.0	0.18	AI555000	Mucolipin 2 (predicted)
44	*Myh9*	594.5	999.4	1.68	BM392410	myosin, heavy polypeptide 9
45	*Myl2*	301.3	17.3	0.06	NM_012605	myosin, light polypeptide 2
46	*Mtmr1_predicted*	157.4	32.4	0.21	AI029734	Myotubularin related protein 1 (predicted)
47	*Marcks*	158.5	248.1	1.56	BE108178	Myristoylated alanine-rich C-kinase substrate (MARCKS)
48	*Ncdn*	75.8	114.2	1.51	NM_053543	neurochondrin
49	*Nfasc*	237.2	370.1	1.56	BI285436	neurofascin
50	*Ogn_predicted*	81.5	49.0	0.60	AA945955	osteoglycin (predicted)
51	*Ppl_predicted*	490.7	308.9	0.63	BI303019	Periplakin (predicted)
52	*Pls3*	202.4	134.5	0.66	BG672591	plastin 3 (T-isoform)
53	*Plekhb2_predicted*	414.3	786.9	1.90	AI177176	pleckstrin homology domain containing, family B (evectins)
54	*LOC641520*	169.9	289.2	1.70	AI716912	Popeye domain-containing 3
55	*Ank*	45.0	108.4	2.41	NM_053714	progressive ankylosis
56	*Rpa3_predicted*	426.0	261.9	0.61	BM383451	replication protein A3 (predicted)
57	*Rcn2*	119.0	40.4	0.34	BI291272	Reticulocalbin 2
58	*LOC689240*	242.2	128.0	0.53	AI146108	Similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome
59	*LOC500105*	181.8	118.5	0.65	BG666397	Similar to contactin associated protein-like 2 isoform a
60	*LOC313934*	83.7	47.4	0.57	BF417645	similar to Intersectin 2 (SH3 domain-containing protein 1B)
61	*LOC498440*	94.1	36.9	0.39	AI716887	similar to myozenin 1
62	*LOC311772*	723.9	1238.6	1.71	AW253721	similar to nidogen 2
63	*LOC317070*	56.0	232.3	4.15	BG672418	similar to nidogen 2 protein
64	*LOC302457 /// LOC3*	84.0	152.4	1.81	AW253967	similar to nidogen 2 protein /// similar to nidogen 2 ///
65	*Nid67*	230.8	86.1	0.37	AF313411	putative small membrane protein NID67
66	*RGD1563148_predic*	832.3	548.4	0.66	AI237685	Similar to osteoclast inhibitory lectin
67	*Sdc2*	271.5	131.3	0.48	AI574779	syndecan 2
68	*Sdc2*	334.5	152.0	0.45	BG668421	syndecan 2
69	*Tmsbl1*	274.6	121.6	0.44	U25684	thymosin beta-like protein 1
70	*Tpm1*	3924.7	2296.4	0.59	M23764	tropomyosin 1, alpha
71	*Tnni2*	88.4	26.3	0.30	NM_017185	troponin 1, type 2
72	*Tnnc2_predicted*	369.3	75.3	0.20	BG663128	troponin C2, fast (predicted)
73	*Tnnt3*	83.3	16.8	0.20	BF521859	troponin T3, skeletal, fast
74	*Tubb5*	82.1	160.7	1.96	AB011679	tubulin, beta 5

Development

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*AP3B1*	132.4	86.0	0.65	AW528106	Adaptor-related protein complex 3, sigma 1 subunit
2	*Andpro /// RGD:7278*	2482.5	5353.2	2.16	BM388042	androgen regulated 20 kDa protein
3	*Amot12*	214.6	132.0	0.62	BF418582	angiomotin like 2
4	*Amotl1_predicted*	557.5	325.4	0.58	BI277433	Angiomotin-like 1 (predicted)
5	*Bbs4_predicted*	90.3	42.6	0.47	AW531530	Bardet-Biedl syndrome 4 homolog (human) (predicted)
6	*RGD:620495*	52.9	117.4	2.22	AI409634	Best5 protein
7	*Msmb*	5728.2	2273.1	0.40	NM_019188	beta-microseminoprotein
8	*Blm_predicted*	84.1	53.6	0.64	BF408187	Bloom syndrome (predicted)
9	*Bex4*	91.1	33.7	0.37	BI289546	Brain expressed X-linked 4
10	*Clptm1_predicted*	1456.0	2207.6	1.52	BI284472	cleft lip and palate associated transmembrane protein 1
11	*Cohh1_predicted*	478.3	312.4	0.65	BI295640	Cohen syndrome homolog 1 (predicted)

12	*RGD:708577*	446.7	102.7	0.23	NM_133622	common salivary protein 1
13	*Cops2*	180.6	120.2	0.67	BI292866	COP9 (constitutive photomorphogenic) homolog
14	*Cops7a_predicted*	213.8	133.4	0.62	BM386508	COP9 (constitutive photomorphogenic) homolog
15	*Cops7b_predicted*	111.0	167.5	1.51	AA818645	COP9 (constitutive photomorphogenic) homolog
16	*Cpne3_predicted*	106.0	66.1	0.62	BG671686	copine III (predicted)
17	*Cutl1*	175.4	116.7	0.67	AA963272	Cut-like 1 (Drosophila)
18	*Crim1_predicted*	359.5	169.9	0.47	AI703807	Cysteine-rich motor neuron 1 (predicted)
19	*Drg1_predicted*	103.1	65.8	0.64	AW527113	developmentally regulated GTP binding protein 1 (predicted)
20	*Tpo1*	539.4	329.3	0.61	NM_133395	developmentally regulated protein TPO1
21	*Dscr6_predicted*	81.1	35.4	0.44	BF545697	Down syndrome critical region homolog 6 (human)
22	*Elavl1_predicted*	128.6	196.5	1.53	AA925921	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1
23	*Efna5*	76.9	125.7	1.64	BF392634	Ephrin A5
24	*RGD:708426 /// LOC*	267.8	426.4	1.59	AI105044	estrous-specific protein, 250 kDa /// similar to RIKEN
25	*Ethe1_predicted*	44.7	91.3	2.04	BM384018	ethylmalonic encephalopathy 1 (predicted)
26	*Grhl1_predicted*	383.2	243.9	0.64	BM386731	Grainyhead-like 1 (Drosophila) (predicted)
27	*RGD:1302992*	80.1	50.5	0.63	BI293046	HCR (a-helix coiled-coil rod homolog)
28	*Kidins220*	50.1	90.6	1.81	AF313464	kinase D-interacting substance of 220 kDa
29	*Mkks_predicted*	98.4	151.0	1.54	BI298816	McKusick-Kaufman syndrome protein (predicted)
30	*Met*	131.2	56.4	0.43	BG378920	Met proto-oncogene
31	*Nov*	42.1	159.7	3.79	NM_030868	NOV protein
32	*Nap1l2*	85.8	55.8	0.65	BI288925	Nucleosome assembly protein 1-like 2
33	*Pcnx_predicted*	242.1	154.5	0.64	AI009650	pecanex homolog (Drosophila) (predicted)
34	*Postn_predicted*	106.6	67.7	0.64	BM389026	periostin, osteoblast specific factor (predicted)
35	*Pmp22*	113.7	69.8	0.61	AW252810	peripheral myelin protein 22
36	*Plac8_predicted*	185.3	369.6	1.99	BG378630	placenta-specific 8 (predicted)
37	*Popdc2*	170.7	89.2	0.52	BF285164	popeye domain containing 2
38	*Rb1cc1_predicted*	420.1	262.3	0.62	BG671668	RB1-inducible coiled-coil 1 (predicted)
39	*Svp4*	283.3	109.2	0.39	M25590	seminal vesicle protein 4
40	*LOC302671*	51.0	116.1	2.28	AI045228	similar to Adapter-related protein complex 1 sigma 1B subunit
41	*RGD1561188_predic*	86.6	43.3	0.50	BF397988	Similar to autism susceptibility candidate 2 (predicted)
42	*RGD1305557_predic*	27.1	194.4	7.17	BG380515	similar to Brain specific membrane-anchored protein
43	*RGD1565144_predic*	121.0	281.2	2.32	AA945915	Similar to deltex 3-like (predicted)
44	*LOC501625*	133.7	49.7	0.37	AI579422	similar to EG2RVC
45	*LOC497986*	359.1	226.8	0.63	BI303863	similar to homeotic protein Hox 2.2 - mouse
46	*LOC691379*	84.8	55.3	0.65	BM387050	Similar to NMDA receptor-regulated gene 2
47	*RGD1306323_predic*	89.3	58.1	0.65	BM390497	similar to Protein C8orf1 (hT41) (predicted)
48	*LOC685899*	137.7	244.7	1.78	AI029494	Similar to sushi, von Willebrand factor type A, EGF
49	*LOC499702*	98.7	43.7	0.44	BE113393	similar to Synaptopodin-2 (Myopodin)
50	*LOC311078*	45.4	76.2	1.68	AI043800	Similar to T-Brain-1
51	*LOC288105*	246.8	150.8	0.61	BF415114	similar to Zbtb20 protein
52	*Sox9*	364.2	80.0	0.22	AI454332	SRY-box containing gene 9
53	*Tcp11l2*	376.7	185.0	0.49	AA800197	T-complex 11 (mouse) like 2
54	*Vasp_predicted*	885.1	1359.6	1.54	AW520792	vasodilator-stimulated phosphoprotein (predicted)
55	*Whsc1l1_predicted*	257.1	145.3	0.57	AI234807	Wolf-Hirschhorn syndrome candidate 1-like 1 (predicted)

Electron Transport

		Control	Vinc	Vinc/Cont		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix
1	*Cyba*	60.5	129.5	2.14	AI232788	cytochrome b558 alpha-subunit
2	*Cox6a1*	96.9	155.8	1.61	X72759	cytochrome c oxidase, subunit VIa, polypeptide 1
3	*Ucp2*	697.3	1087.4	1.56	NM_019354	uncoupling protein 2

Growth Factors, Cyto-, and Chemokines

		Control	Vinc	Vinc/Cont		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix
1	*Bmp6*	207.1	36.8	0.18	AI230985	bone morphogenetic protein 6
2	*Csf1*	310.8	470.3	1.51	AW535553	colony stimulating factor 1(macrophage)
3	*Egf*	551.1	366.4	0.66	NM_012842	epidermal growth factor
4	*Eps8_predicted*	143.8	93.9	0.65	AI408597	epidermal growth factor receptor pathway substrate 8
5	*Efemp1_predicted*	1734.4	510.3	0.29	BF284634	epidermal growth factor-containing fibulin-like extracellular
6	*Eps8l1_predicted*	265.5	162.8	0.61	AI715477	EPS8-like 1 (predicted)
7	*Gab1_predicted*	224.8	129.3	0.58	BI278183	Growth factor receptor bound protein 2-associated protein 1
8	*RGD1561846_predic*	97.2	63.7	0.66	AA955251	similar to Cytokine-like protein C17 precursor
9	*LOC498335*	84.7	241.0	2.85	AA892854	similar to Small inducible cytokine B13 precursor (CXCL13)
10	*LOC498545*	178.7	98.4	0.55	BF410219	similar to Transforming growth factor beta 1 induced transcript 4

Golgi Apparatus

		Control	Vinc	Vinc/Cont		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix

1	*Copz1_predicted*	389.9	594.4	1.52	BF406339	coatomer protein complex, subunit zeta 1 (predicted)
2	*Dpm1_predicted*	120.3	57.1	0.47	BF405555	dolichol-phosphate (beta-D) mannosyltransferase 1
3	*Golph3*	199.0	317.4	1.59	NM_023977	golgi phosphoprotein 3
4	*Gopc_predicted*	98.1	52.6	0.54	BI290796	Golgi associated PDZ and coiled-coil motif containing
5	*Hs3st3b1_predicted*	231.9	136.0	0.59	AA926037	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1

Immune Response

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Abo*	1251.2	2144.3	1.71	BM386404	ABO blood group (transferase A, alpha 1-3-N-
2	*Aif1*	51.1	101.7	1.99	NM_017196	allograft inflammatory factor 1
3	*Azgp1*	125.0	15.7	0.13	NM_012826	alpha-2-glycoprotein 1, zinc
4	*Cd3g_predicted*	59.0	101.8	1.72	AI044631	CD3 antigen, gamma polypeptide (predicted)
5	*Cd38*	126.7	282.1	2.23	BI289418	CD38 antigen
6	*Cd52*	138.0	55.5	0.40	NM_053983	CD52 antigen
7	*Cd74*	815.1	1645.0	2.02	NM_013069	CD74 antigen (invariant polpypeptide of major
8	*C1qa_predicted*	180.5	284.1	1.57	BF418957	complement component 1, q subcomponent, alpha
9	*C1qb*	82.1	159.0	1.94	AW434057	complement component 1, q subcomponent, beta
10	*C1qg_predicted*	89.6	164.1	1.83	AI411618	complement component 1, q subcomponent, gamma
11	*C2*	44.8	92.0	2.06	AI716125	complement component 2
12	*Cfh*	501.1	325.5	0.65	NM_130409	complement component factor h
13	*Eraf_predicted*	33.8	110.9	3.28	AI230287	erythroid associated factor (predicted)
14	*Fcgr3a*	48.7	137.0	2.82	AI011757	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)
15	*Fcgr1_predicted*	53.8	90.0	1.67	BM391631	Fc receptor, IgG, high affinity I (predicted)
16	*IgG-2a /// LOC50072*	34.9	215.2	6.18	L22654	gamma-2a immunoglobulin heavy chain /// similar to gamma-
17	*Igha*	37.1	159.2	4.29	AI412189	immunoglobulin heavy chain (alpha polypeptide)
18	*Igh-1a_predicted*	90.1	385.8	4.28	AI411947	immunoglobulin heavy chain 1a (serum IgG2a) (predicted)
19	*Igj_predicted*	77.3	148.7	1.92	AA817898	immunoglobulin joining chain (predicted)
20	*Isgf3g_predicted*	84.8	192.5	2.27	AI029121	interferon dependent positive acting transcription factor 3 gamma
21	*Ifitm1_predicted*	139.5	228.1	1.63	BG380285	interferon induced transmembrane protein 1 (predicted)
22	*Ifitm2*	856.3	1438.7	1.68	NM_030833	interferon induced transmembrane protein 2 (1-8D)
23	*Irf8*	27.8	113.6	4.09	BF284262	interferon regulatory factor 8
24	*Ifi35_predicted*	79.1	147.6	1.86	BM388891	interferon-induced protein 35 (predicted)
25	*Ifi44_predicted*	161.9	254.4	1.57	BI274623	interferon-induced protein 44 (predicted)
26	*Isg20_predicted*	881.9	1348.8	1.53	BI296097	interferon-stimulated protein (predicted)
27	*Ly6c*	47.8	121.6	2.55	NM_020103	Ly6-C antigen
28	*Mpeg1*	154.6	303.2	1.96	AI170394	macrophage expressed gene 1
29	*RGD:735096*	75.9	144.2	1.90	AI171966	major histocompatibility complex, class II, DM beta
30	*Mx1*	67.6	208.0	3.08	X52711	myxovirus (influenza virus) resistance
31	*Mx2*	212.4	10.5	0.05	NM_017028	myxovirus (influenza virus) resistance 2
32	*Mx2*	48.9	133.6	2.73	NM_134350	myxovirus (influenza virus) resistance 2
33	*RT1-CE12*	465.4	930.3	2.00	M24026	RT1 class I, CE12
34	*RT1-Aw2*	109.3	346.2	3.17	AI233121	RT1 class Ib, locus Aw2
35	*RT1-Aw2 /// RT1-A2 /*	220.7	914.2	4.14	AJ249701	RT1 class Ib, locus Aw2 /// RT1 class Ia, locus A2
36	*RT1-S3*	149.8	470.4	3.14	AJ243974	RT1 class Ib, locus S3
37	*RT1-Ba*	99.0	547.5	5.53	BG378249	RT1 class II, locus Ba
38	*RT1-Bb*	73.5	199.5	2.71	BM389513	RT1 class II, locus Bb
39	*RT1-Da*	524.0	997.8	1.90	Y00480	RT1 class II, locus Da
40	*RT1-Db1*	151.7	270.7	1.79	BI279526	RT1 class II, locus Db1
41	*Slpi /// LOC296356*	146.4	470.5	3.21	NM_053372	secretory leukocyte peptidase inhibitor /// similar to secretory
42	*Sema4a_predicted*	233.3	132.6	0.57	AI228417	sema domain, immunoglobulin domain (Ig), transmembrane
43	*RGD1305133_predic*	314.0	200.8	0.64	BI296154	similar to Ab2-008 (predicted)
44	*RGD1565161_predic*	61.1	209.6	3.43	AA817993	Similar to dendritic cell-derived immunoglobulin(Ig)-like receptor 1
45	*LOC500180*	431.6	2106.0	4.88	L22655	similar to IG KAPPA CHAIN V-V REGION K2 PRECURSOR
46	*LOC299357 /// LOC2*	114.4	249.7	2.18	AI411693	similar to Igh-6 protein /// similar to Ig H-chain V-region precursor
47	*LOC362934*	257.2	489.1	1.90	AI233210	similar to lymphocyte antigen 6 complex, locus E
48	*LOC687144*	18.7	81.8	4.37	AI029637	similar to RT1 class I, CE4
49	*Slamf9_predicted*	46.5	83.5	1.79	BI295964	SLAM family member 9 (predicted)
50	*Xpa_predicted*	161.5	102.6	0.64	BF554085	xeroderma pigmentosum, complementation group A

Metabolism & Transport

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Bpgm*	66.9	133.1	1.99	BI294941	2,3-bisphosphoglycerate mutase
2	*Oas1i*	39.0	155.5	3.99	BM391818	2'-5' oligoadenylate synthetase 1I
3	*Pte1*	365.8	151.0	0.41	BF282933	4,8-dimethylnonanoyl-CoA thioesterase
4	*Pfkfb4*	177.4	270.2	1.52	BE329273	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
5	*Abhd2_predicted*	166.0	281.1	1.69	AI013474	abhydrolase domain containing 2 (predicted)
6	*Acaa2*	249.4	442.1	1.77	NM_130433	acetyl-Coenzyme A acyltransferase 2
7	*Smpdl3a*	357.7	216.8	0.61	BM389498	acid sphingomyelinase-like phosphodiesterase 3A

8	*Acsl5*	333.6	563.5	1.69	BM384537	Acyl-CoA synthetase long-chain family member 5
9	*Acad11_predicted*	207.0	453.2	2.19	BI296347	Acyl-Coenzyme A dehydrogenase family, member 11
10	*Arf1*	139.7	88.0	0.63	BF389686	ADP-ribosylation factor 1
11	*Arf6*	354.3	582.0	1.64	NM_024152	ADP-ribosylation factor 6
12	*Akr1c12_predicted*	85.4	35.0	0.41	BM383010	aldo-keto reductase family 1, member C12 (predicted)
13	*Agl_predicted*	196.8	112.8	0.57	BG374196	Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase
14	*Aqp9*	111.4	69.6	0.63	NM_022960	aquaporin 9
15	*Rere*	78.4	43.6	0.56	BF412271	Arginine-glutamic acid dipeptide (RE) repeats
16	*Rarsl_predicted*	238.6	153.4	0.64	BE118562	arginyl-tRNA synthetase-like (predicted)
17	*Atp5j*	139.1	65.0	0.47	BG372192	ATP synthase, H+ transporting, mitochondrial F0 complex
18	*Atp8a1_predicted*	75.2	43.5	0.58	BF406182	ATPase, aminophospholipid transporter (APLT), class I,
19	*Atp2a1*	114.1	27.6	0.24	NM_058213	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1
20	*Atp2b1*	694.7	460.1	0.66	NM_053311	ATPase, Ca++ transporting, plasma membrane 1
21	*Atp6v1c2*	1034.5	293.0	0.28	BF283053	ATPase, H+ transporting, V1 subunit C, isoform 2
22	*Atp1a1*	1163.9	1950.6	1.68	M74494	ATPase, Na+K+ transporting, alpha 1
23	*RGD:1303241*	84.0	51.7	0.62	BG381587	beta-site APP-cleaving enzyme 2
24	*Bach*	237.9	469.8	1.97	D88891	brain acyl-CoA hydrolase
25	*Kcnmb4*	58.9	139.8	2.37	AY028605	calcium activated potassium channel beta 4 subunit
26	*Cald1*	351.6	182.7	0.52	BI291848	caldesmon 1
27	*Ca2*	989.8	307.1	0.31	NM_019291	carbonic anhydrase 2
28	*Ca3*	153.0	344.5	2.25	NM_019292	carbonic anhydrase 3
29	*Ca5b*	258.3	144.7	0.56	BG375352	carbonic anhydrase VB, mitochondrial
30	*Cbr4*	121.8	73.5	0.60	BF404908	carbonyl reductase 4
31	*Cpa6_predicted*	318.8	164.0	0.51	AA819425	Carboxypeptidase A6 (predicted)
32	*Csnk1a1*	53.7	147.6	2.75	BE117217	Casein kinase 1, alpha 1
33	*Csnk2b*	722.1	472.4	0.65	NM_031021	casein kinase II beta subunit
34	*Csnk2a1*	112.4	36.9	0.33	AI059349	Casein kinase II subunit alpha (EC 2.7.1.37) (CK II).
35	*Comt*	334.5	137.7	0.41	NM_012531	catechol-O-methyltransferase
36	*Clic4*	85.1	184.2	2.17	BE098848	Chloride intracellular channel 4
37	*Cobll1_predicted*	302.9	197.2	0.65	BM389293	Cobl-like 1 (predicted)
38	*Ckm*	127.2	14.4	0.11	NM_012530	creatine kinase, muscle
39	*Cmah_predicted*	3666.0	312.3	0.09	AI014030	cytidine monophospho-N-acetylneuraminic acid hydroxylase
40	*Dhrs1*	88.5	40.6	0.46	BE104618	Dehydrogenase/reductase (SDR family) member 1
41	*Dguok_predicted*	161.9	91.0	0.56	BF285179	deoxyguanosine kinase (predicted)
42	*Dnttip2_predicted*	550.8	199.2	0.36	BF410997	Deoxynucleotidyltransferase, terminal, interacting protein 2
43	*Dbi*	1361.0	2106.3	1.55	AI175009	diazepam binding inhibitor
44	*Dusp6*	94.8	159.8	1.69	NM_053883	dual specificity phosphatase 6
45	*Enpp2*	99.2	149.6	1.51	AI104846	ectonucleotide pyrophosphatase/phosphodiesterase 2
46	*Elovl6*	188.0	301.6	1.60	BE116152	ELOVL family member 6
47	*Eno3*	83.4	32.7	0.39	NM_012949	enolase 3, beta
48	*Fads1*	94.4	47.0	0.50	NM_053445	fatty acid desaturase 1
49	*Fmo5*	344.6	57.2	0.17	AI454611	flavin containing monooxygenase
50	*Fut2*	68.1	240.0	3.53	NM_031635	fucosyltransferase 2
51	*Gja1*	199.6	130.5	0.65	AI411352	gap junction membrane channel protein alpha 1
52	*Got2*	87.1	37.9	0.43	BI296539	glutamate oxaloacetate transaminase 2
53	*Glrp1_predicted*	116.2	77.5	0.67	AI501417	Glutamine repeat protein 1 (predicted)
54	*Glul*	191.1	342.3	1.79	AW528806	glutamine synthetase 1
55	*Gstm6_predicted*	688.2	183.5	0.27	BF289090	glutathione S-transferase, mu 6 (predicted)
56	*Gstm3*	679.4	396.4	0.58	NM_031154	glutathione S-transferase, mu type 3 (Yb3)
57	*Gsk3a*	85.1	171.5	2.02	NM_017344	glycogen synthase kinase 3 alpha
58	*Gda*	265.2	167.7	0.63	AF245172	guanine deaminase
59	*Hyal2*	126.3	192.5	1.52	AF034218	hyaluronidase 2
60	*Hcn2*	56.5	116.8	2.07	AW532988	hyperpolarization activated cyclic nucleotide-gated
61	*Idh1*	881.0	516.8	0.59	NM_031510	isocitrate dehydrogenase 1
62	*Kat3*	219.8	113.5	0.52	BI295878	kynurenine aminotransferase III
63	*Lyz*	5900.3	3805.0	0.64	L12458	lysozyme
64	*Mt1a*	901.9	453.1	0.50	AF411318	Metallothionein
65	*Mgst1*	3374.2	1714.0	0.51	NM_134349	microsomal glutathione S-transferase 1
66	*Ndufa12_predicted*	1334.6	2172.8	1.63	AI710281	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
67	*Nnt*	859.5	528.1	0.61	AA891872	nicotinamide nucleotide transhydrogenase
68	*Ogt*	906.9	503.1	0.55	AI009074	O linked N-acetylglucosamine transferase
69	*Oact2_predicted*	1002.2	585.1	0.58	AI501287	O-acyltransferase (membrane bound) domain containing 2
70	*Pctk1*	234.7	374.2	1.59	U36444	PCTAIRE-1 protein kinase, alternatively spliced
71	*Pxmp4*	85.3	135.8	1.59	BG664011	peroxisomal membrane protein 4
72	*Pik3r1*	429.9	742.3	1.73	AA819268	phosphatidylinositol 3-kinase, regulatory subunit
73	*Pck2_predicted*	49.1	124.9	2.55	AI228633	Phosphoenolpyruvate carboxykinase 2
74	*Pck2_predicted*	239.0	511.9	2.14	BM384604	phosphoenolpyruvate carboxykinase 2
75	*Pla2g2a*	77.1	6.2	0.08	NM_031598	phospholipase A2, group IIA (platelets, synovial fluid)
76	*Pla2g12a_predicted*	199.4	329.6	1.65	BF284175	phospholipase A2, group XIIA (predicted)
77	*Plcb1*	199.1	82.2	0.41	BF409213	Phospholipase C, beta 1

78	*Prps2*	188.6	105.3	0.56	BF284677	phosphoribosyl pyrophosphate synthetase 2
79	*Psat1*	417.0	706.2	1.69	AI230228	phosphoserine aminotransferase 1
80	*Kcnrg_predicted*	155.2	51.9	0.33	BF411815	Potassium channel regulator (predicted)
81	*Kcnq1*	86.7	49.5	0.57	BF290181	potassium voltage-gated channel, subfamily Q, member 1
82	*Ykt6*	368.9	567.2	1.54	BM391393	prenylated SNARE protein
83	*RGD:727895*	120.7	54.4	0.45	BM384073	promethin
84	*Erp70*	198.5	320.8	1.62	NM_053849	protein disulfide isomerase related protein
85	*Pdia5*	927.6	195.4	0.21	AI045590	protein disulfide isomerase-associated 5
86	*Prkaca*	167.4	295.4	1.76	AW915101	protein kinase, cAMP-dependent, catalytic, alpha
87	*Ppp6c*	126.4	81.2	0.64	AI030892	Protein phosphatase V
88	*Ptpn1*	130.1	220.9	1.70	AA924431	protein tyrosine phosphatase, non-receptor type 1
89	*P2rx4*	642.5	1177.6	1.83	U32497	purinergic receptor P2X, ligand-gated ion channel, 4
90	*Kcnk1*	251.9	383.3	1.52	NM_021688	putative potassium channel TWIK
91	*Pc*	52.1	95.0	1.82	NM_012744	Pyruvate carboxylase
92	*Sec61a1*	328.2	499.1	1.52	BI284366	SEC61, alpha subunit (S. cerevisiae)
93	*Sec61a2_predicted*	152.5	79.7	0.52	BF406754	Sec61, alpha subunit 2 (S. cerevisiae) (predicted)
94	*Scamp1*	250.3	161.4	0.64	AW524864	Secretory carrier membrane protein 1
95	*Scamp2*	61.1	92.7	1.52	BM387006	secretory carrier membrane protein 2
96	*Shmt1_predicted*	369.8	234.1	0.63	AI412012	serine hydroxymethyl transferase 1 (soluble) (predicted)
97	*LOC688311*	40.0	93.1	2.33	BI288882	similar to ADP-ribosylation factor-like 1
98	*RGD1309808_predic*	103.9	317.8	3.06	BI289459	similar to apolipoprotein L2; apolipoprotein L-II (predicted)
99	*LOC296516 /// LOC5*	91.9	2456.7	26.75	BE329202	similar to Cystatin S precursor (LM protein)
100	*LOC313837*	359.4	184.9	0.51	BM390001	similar to Glutaminyl-peptide cyclotransferase precursor (QC)
101	*RGD1307525_predic*	660.4	375.8	0.57	AI574688	Similar to intracellular protein transport like (XM453)
102	*LOC295241*	146.8	248.4	1.69	AA964836	Similar to Metaxin 1, isoform 2
103	*LOC680036*	106.0	69.5	0.66	AI575248	Similar to methionine sulfoxide reductase B3 isoform 2
104	*MGC105753*	1252.0	805.1	0.64	AI409380	Similar to Methionine-R-sulfoxide reductase
105	*LOC498279*	177.3	399.1	2.25	BE111722	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2
106	*LOC498331*	90.2	50.9	0.56	AA818197	similar to protein Tyr phosphatase
107	*LOC360668*	164.6	264.2	1.61	AI176849	similar to SEC14-like 1
108	*RGD1566319_predic*	46.4	85.7	1.85	BE109653	Similar to Sestrin 2 (Hi95)
109	*RGD1564876_predic*	214.5	128.4	0.60	AI411981	Similar to Solute carrier family 35, member E3
110	*LOC368066*	106.1	56.9	0.54	AI232716	similar to thioether S-methyltransferase
111	*Slc1a1*	79.7	51.2	0.64	U39555	solute carrier family 1, member 1
112	*Slc20a2*	77.8	49.8	0.64	AI409899	solute carrier family 20, member 2
113	*Slc25a4*	275.3	152.3	0.55	BG666999	solute carrier family 25
114	*Slc25a22*	162.5	277.9	1.71	AI407908	Solute carrier family 25
115	*Slc25a30*	126.8	194.3	1.53	AW530647	solute carrier family 25, member 30
116	*Slc29a3*	130.5	208.4	1.60	BM385468	solute carrier family 29 (nucleoside transporters), member 3
117	*Slc3a1*	112.8	220.6	1.96	NM_017216	solute carrier family 3, member 1
118	*Slc30a2*	99.3	42.8	0.43	BI277879	Solute carrier family 30 (zinc transporter), member 2
119	*Slc39a10_predicted*	184.9	120.1	0.65	AI598315	Solute carrier family 39 (zinc transporter), member 10
120	*Slc44a4*	845.2	1393.4	1.65	BI289103	Solute carrier family 44, member 4
121	*Slc5a3*	349.1	135.9	0.39	BE116021	solute carrier family 5 (inositol transporters), member 3
122	*Slc5a11*	7.5	87.8	11.71	BG377720	solute carrier family 5 (sodium/glucose cotransporter)
123	*Slc5a2*	89.3	162.4	1.82	AA894060	Solute carrier family 5 (sodium/glucose cotransporter)
124	*Slc7a8 /// Syngap1*	126.7	192.3	1.52	NM_053442	solute carrier family 7
125	*Sc5d*	275.2	489.4	1.78	AI710051	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)-like
126	*Sumf2*	62.9	99.3	1.58	AA964066	sulfatase modifying factor 2
127	*Tasp1_predicted*	114.0	61.3	0.54	AA925658	Taspase, threonine aspartase 1 (predicted)
128	*Ugt2b10_predicted*	81.0	52.8	0.65	AI169671	UDP glycosyltransferase 2 family, polypeptide B10
129	*Ugcgl1*	239.0	480.5	2.01	AI169490	UDP-glucose ceramide glucosyltransferase-like 1
130	*Unc93b_predicted*	102.6	167.3	1.63	AI234533	unc-93 homolog B (C. elegans) (predicted)
131	*Vdac1*	224.5	346.1	1.54	AF268467	voltage-dependent anion channel 1
132	*Zadh2_predicted*	75.1	44.9	0.60	AA850919	zinc binding alcohol dehydrogenase, domain containing 2

Proteolysis

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Atg7*	251.2	148.3	0.59	BI300794	Autophagy 7-like (S. cerevisiae) (predicted)
2	*Ctsd*	772.4	1161.1	1.50	NM_134334	cathepsin D
3	*Ctss*	210.1	344.8	1.64	NM_017320	cathepsin S
4	*Ctsz*	64.3	116.0	1.80	AA849399	cathepsin Z
5	*RGD:735160*	79.6	168.9	2.12	M75281	cystatin S
6	*Fts_predicted*	348.7	616.1	1.77	BF390999	fused toes (predicted)
7	*Josd3*	216.6	134.7	0.62	AA900775	Josephin domain containing 3
8	*Laptm5*	71.8	120.0	1.67	BF406601	lysosomal-associated protein transmembrane 5
9	*Mcpt1*	20.4	170.7	8.37	U67915	mast cell protease 1
10	*Mmp7*	94.9	35.5	0.37	NM_012864	matrix metalloproteinase 7
11	*Mep1b*	167.3	81.9	0.49	NM_013183	meprin 1 beta

12	*Mon1a_predicted*	83.1	148.9	1.79	BE111711	MON1 homolog A (yeast) (predicted)
13	*Plau*	32.3	91.3	2.83	X63434	plasminogen activator, urokinase
14	*Psmb5*	1826.5	2740.8	1.50	BI285627	proteasome (prosome, macropain) subunit, beta type 5
15	*Prkcsh_predicted*	763.2	1167.3	1.53	AI008784	Protein kinase C substrate 80K-H (predicted)
16	*Psmb8*	90.1	170.3	1.89	NM_080767	proteosome (prosome, macropain) subunit, beta type 8
17	*Psmb9*	61.7	142.7	2.31	AI599350	proteosome (prosome, macropain) subunit, beta type 9
18	*Rnf146*	82.3	43.8	0.53	AI535431	Ring finger protein 146
19	*Rnf149_predicted*	374.9	239.9	0.64	AI171788	ring finger protein 149 (predicted)
20	*Rnf30_predicted*	54.8	84.1	1.54	AA800245	ring finger protein 30 (predicted)
21	*Spin2c*	88.6	55.0	0.62	NM_031531	Serine protease inhibitor
22	*LOC498690*	497.7	140.1	0.28	AI230591	similar to ctla-2-beta protein (141 AA)
23	*LOC296516*	55.3	425.1	7.69	BM386499	similar to Cystatin S precursor (LM protein)
24	*RGD1310067_predic*	116.9	46.8	0.40	BF393807	Similar to E3 ubiquitin ligase SMURF2 (predicted)
25	*LOC312688*	112.7	689.1	6.11	BI295179	similar to ubiquitin specific protease UBP43
26	*RGD1564014_predic*	159.9	26.3	0.16	AI712728	Similar to ubiquitin-conjugating enzyme E2 variant 1 (predicted)
27	*RGD1560364_predic*	477.3	261.7	0.55	BM384685	Similar to vacuolar protein sorting 13C protein
28	*Snx12_predicted*	91.6	165.3	1.80	AI599411	Sorting nexin 12 (predicted)
29	*Senp5_predicted /// L*	56.3	119.1	2.12	BE105606	SUMO/sentrin specific protease 5 (predicted)
30	*Senp7_predicted*	137.2	89.7	0.65	AI069981	SUMO1/sentrin specific protease 7 (predicted)
31	*Uchl1*	122.0	540.8	4.43	NM_017237	ubiquitin carboxy-terminal hydrolase L1
32	*LOC81816*	151.0	91.8	0.61	BE119409	Ubiquitin conjugating enzyme
33	*Usp1_predicted*	211.6	139.3	0.66	AI010241	ubiquitin specific protease 1 (predicted)
34	*Usp2*	137.3	212.8	1.55	BM385405	ubiquitin specific protease 2
35	*Usp30_predicted*	101.5	182.8	1.80	AI145892	ubiquitin specific protease 30 (predicted)
36	*Usp33*	270.2	160.4	0.59	BE108244	Ubiquitin specific protease 33 (predicted)
37	*Usp43_predicted*	49.4	82.5	1.67	BE098463	Ubiquitin specific protease 43 (predicted)
38	*Ube1dc1_predicted*	533.1	206.3	0.39	AI408025	ubiquitin-activating enzyme E1-domain containing 1
39	*Ube2l6_predicted*	61.0	98.8	1.62	BI279216	ubiquitin-conjugating enzyme E2L 6 (predicted)
40	*LOC296230 /// LOC2*	2053.5	3801.9	1.85	BI285110	similar to Cystatin-related protein 2 precursor

Receptor & Binding Proteins

		Control	Vinc	Vincl/Contr		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix
1	*Htr5b*	28.5	105.9	3.72	L10073	5-hydroxytryptamine (serotonin) receptor 5B
2	*LOC494538*	41.4	141.0	3.40	BI279486	ABP beta
3	*Acrbp*	895.3	526.3	0.59	BG381450	acrosin binding protein
4	*Aebp2_predicted*	116.6	77.0	0.66	AW526794	AE binding protein 2 (predicted)
5	*Abca5*	68.0	126.3	1.86	AI502224	ATP-binding cassette, sub-family A (ABC1), member 5
6	*RGD:1303134*	200.4	304.1	1.52	BE103071	ATP-binding cassette, sub-family A, member 7
7	*Bmpr2*	489.1	308.2	0.63	BF398206	Bone morphogenic protein receptor, type II
8	*Cab39l*	108.3	180.8	1.67	BF408129	Calcium binding protein 39-like (predicted)
9	*CSF1R_RAT*	51.7	136.7	2.64	BI285793	Colony stimulating factor 1 receptor
10	*Csf2rb1*	49.7	89.2	1.80	BI279816	colony stimulating factor 2 receptor,beta 1
11	*Ctbp2*	475.3	301.1	0.63	NM_053335	C-terminal binding protein 2
12	*Dcir3*	53.0	119.5	2.25	BF393825	dendritic cell inhibitory receptor 3
13	*Dear*	124.5	76.6	0.62	BF544968	Dual endothelin 1, angiotensin II receptor
14	*Ebpl_predicted*	91.9	138.7	1.51	AI179635	emopamil binding protein-like (predicted)
15	*Fubp3*	84.1	53.5	0.64	BF282112	Far upstream element (FUSE) binding protein 3 (predicted)
16	*Fkbp2_predicted*	129.9	209.5	1.61	BF561706	FK506 binding protein 2 (predicted)
17	*Fst*	118.5	41.8	0.35	NM_012561	follistatin
18	*Gnb1*	95.6	55.5	0.58	AI230669	Guanine nucleotide binding protein, beta 1
19	*Sned1*	91.1	60.5	0.66	AI013978	Insulin responsive sequence DNA binding protein-1
20	*Itgal*	52.9	111.4	2.11	BI289767	Integrin alpha L
21	*Il6r*	457.5	257.9	0.56	NM_017020	interleukin 6 receptor
22	*Ms4a6b*	55.6	97.2	1.75	BI294706	membrane-spanning 4-domains, subfamily A, member 6B
23	*Grm8*	26.3	95.8	3.65	Y11153	metabotropic glutamate receptor 8
24	*Ng3*	83.4	55.3	0.66	AW530272	Ng3 protein
25	*Nsbp1_predicted /// L*	197.5	116.1	0.59	BE108745	nucleosome binding protein 1 (predicted)
26	*Osbpl2*	89.4	44.5	0.50	BF387902	Oxysterol binding protein-like 2
27	*Ptbp2*	106.0	65.7	0.62	BF393884	Polypyrimidine tract binding protein 2
28	*Prlr*	446.1	270.8	0.61	NM_012630	prolactin receptor
29	*P2ry2*	389.5	251.5	0.65	NM_017255	purinergic receptor P2Y, G-protein coupled 2
30	*LOC292498*	188.6	93.8	0.50	BI300511	Putative pheromone receptor V2R4
31	*Rora_predicted*	97.1	53.5	0.55	AI235414	RAR-related orphan receptor alpha (predicted)
32	*LOC682457*	81.5	195.8	2.40	AA998007	similar to Alpha-taxilin
33	*LOC498153*	113.1	194.6	1.72	AI500893	similar to G protein-coupled receptor 146
34	*LOC686280*	215.2	122.2	0.57	BM389422	similar to integrin alpha M
35	*LOC299828*	116.6	70.1	0.60	BI295313	similar to Ku70-binding protein 3
36	*LOC367153*	90.6	44.5	0.49	BF562621	Similar to p10-binding protein
37	*LOC501026*	85.6	44.5	0.52	BF419651	similar to SH3 domain binding glutamic acid-rich protein

38	*LOC362350*	24.7	82.0	3.32	BG378607	similar to T-cell receptor beta-2 chain C region
39	*LOC503420*	214.1	57.3	0.27	AI600030	Similar to vomeronasal V1r-type receptor V1rc43
40	*Stxbp6_predicted*	509.5	333.5	0.65	BI294716	syntaxin binding protein 6 (amisyn)
41	*Tapbp*	154.7	252.6	1.63	NM_033098	TAP binding protein
42	*Tcrb*	24.2	75.4	3.12	AW919577	T-cell receptor beta chain
43	*Thrap1_predicted*	101.9	66.6	0.65	AA849989	Thyroid hormone receptor associated protein 1 (predicted)
44	*Topors_predicted*	204.0	115.4	0.57	AI176588	topoisomerase I binding, arginine/serine-rich (predicted)
45	*RGD:619831*	88.2	54.3	0.62	AI231531	Tumor necrosis factor receptor superfamily, member 6
46	*Tyrobp*	53.9	87.3	1.62	AI102519	Tyro protein tyrosine kinase binding protein

Signaling

	Common	Control Raw	Vinc Raw	Vincl/Contr Ratio	Genbank	Gene Title_Affymetrix
1	*Ascc3l1*	40.5	98.9	2.44	AI502051	Activating signal cointegrator 1 complex subunit 3-like 1
2	*Anxa3*	185.3	119.4	0.64	NM_012823	annexin A3
3	*Arrdc2_predicted*	387.5	179.1	0.46	AI145231	arrestin domain containing 2 (predicted)
4	*Bf*	103.5	236.3	2.28	AI639117	B-factor, properdin
5	*Cav2*	1093.3	405.1	0.37	BE349669	caveolin 2
6	*Rasd1*	528.4	249.7	0.47	AF239157	DEXRAS1 (Dexras1)
7	*Dyrk2_predicted*	25.4	88.7	3.49	AI501693	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase
8	*Dyrk2_predicted*	171.3	74.7	0.44	BF559746	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase
9	*Slc9a3r1*	1075.1	1654.3	1.54	NM_021594	ERM-binding phosphoprotein
10	*Ebag9_predicted*	761.4	464.0	0.61	BG372835	estrogen receptor-binding fragment-associated gene 9
11	*Frag1*	749.8	1255.4	1.67	BG373817	FGF receptor activating protein 1
12	*Fxyd3*	170.0	82.1	0.48	AI009597	FXYD domain-containing ion transport regulator 3
13	*Fxyd5*	376.7	117.2	0.31	NM_021909	FXYD domain-containing ion transport regulator 5
14	*Hspb6*	228.4	349.7	1.53	D29960	heat shock protein, alpha-crystallin-related, B6
15	*Hyou1*	747.9	1240.8	1.66	BI282904	hypoxia up-regulated 1
16	*Irf7_predicted*	213.0	534.6	2.51	BF411036	interferon regulatory factor 7 (predicted)
17	*G1p2_predicted*	89.1	354.5	3.98	BE096523	interferon, alpha-inducible protein (clone IFI-15K) (predicted)
18	*Iqcb1_predicted*	1499.4	460.4	0.31	AI234142	IQ calmodulin-binding motif containing 1 (predicted)
19	*Lancl1*	136.3	252.3	1.85	AI710389	lanC (bacterial lantibiotic synthetase component C)-like 1
20	*Lck*	54.1	103.4	1.91	AI137137	lymphocyte-specific protein tyrosine kinase
21	*Mapk8*	75.3	123.5	1.64	AI511007	Mitogen-activated protein kinase 8
22	*Mx2*	212.4	10.5	0.05	NM_017028	myxovirus (influenza virus) resistance 2
23	*Nek7_predicted*	1242.8	1889.8	1.52	AA955361	NIMA (never in mitosis gene a)-related expressed kinase 7
24	*Omp*	20.1	86.6	4.31	NM_012616	olfactory marker protein
25	*Ocm*	225.2	1082.1	4.81	J02705	oncomodulin
26	*Perc64*	94.9	61.6	0.65	BI278571	PE responsive protein c64
27	*Plekhh1_predicted*	207.7	91.2	0.44	BI275435	pleckstrin homology domain containing, family H
28	*Ptn*	1185.4	674.3	0.57	NM_017066	pleiotrophin
29	*Prkcn*	207.7	128.0	0.62	AA945751	Protein kinase C, nu
30	*Pkn1*	40.7	99.7	2.45	BE099509	Protein kinase N1
31	*Prkr*	110.3	178.5	1.62	NM_019335	Protein kinase, interferon-inducible double stranded RNA
32	*RGD:1303168*	1618.9	5325.2	3.29	NM_130743	putative ISG12(a) protein
33	*Rabl3_predicted*	75.2	115.5	1.54	BF417476	RAB, member of RAS oncogene family-like 3 (predicted)
34	*Rabl3_predicted*	124.2	57.6	0.46	AA859277	RAB, member of RAS oncogene family-like 3 (predicted)
35	*Rab15*	96.6	45.9	0.48	BF554320	RAB15, member RAS onocogene family
36	*RGD:1302985*	720.8	1451.8	2.01	BI295991	RAB2, member RAS oncogene family-like
37	*Rab3c*	51.9	174.2	3.36	NM_133536	RAB3C, member RAS oncogene family
38	*Rab3d*	747.4	1192.4	1.60	BF391905	RAB3D, member RAS oncogene family
39	*Rab40b_predicted*	105.6	70.0	0.66	AA924620	Rab40b, member RAS oncogene family (predicted)
40	*Rasd2*	154.5	92.6	0.60	AF134409	RASD family, member 2
41	*Rac2_predicted*	95.1	184.8	1.94	AI010476	RAS-related C3 botulinum substrate 2 (predicted)
42	*Ramp1*	69.0	106.4	1.54	NM_031645	receptor (calcitonin) activity modifying protein 1
43	*Rgs2*	2270.1	3942.3	1.74	AY043246	regulator of G-protein signaling protein 2
44	*Arhgap1_predicted*	36.3	100.2	2.76	AI535143	Rho GTPase activating protein 1 (predicted)
45	*Arhgdib_predicted*	122.1	220.8	1.81	BF285771	Rho, GDP dissociation inhibitor (GDI) beta (predicted)
46	*Rspo1_predicted*	117.7	280.7	2.38	AI044916	R-spondin homolog (Xenopus laevis) (predicted)
47	*RT1-Bb*	182.0	8.9	0.05	AI715202	RT1 class II, locus Bb
48	*---*	91.1	39.4	0.43	AI502069	Similar to MAPK-interacting and spindle-stabilizing protein
49	*RGD1307599_predic*	111.6	68.0	0.61	AI169756	similar to Mitogen-inducible gene 6 protein homolog
50	*LOC497961*	131.8	67.2	0.51	BE101792	similar to nemo like kinase
51	*RGD1565811_predic*	386.4	199.3	0.52	AW530163	Similar to OL-protocadherin isoform
52	*LOC362166*	788.6	507.2	0.64	BI295133	similar to PHF21A protein
53	*RGD1562474_predic*	125.5	78.4	0.62	BF396950	Similar to Rap1-interacting factor 1 (predicted)
54	*LOC364885*	135.1	61.4	0.45	BF283621	similar to Ras GTPase-activating-like protein IQGAP2
55	*MGC105830*	160.8	289.5	1.80	AI711306	similar to Ras-related protein Rab-1B
56	*LOC500988*	130.5	84.6	0.65	AA850780	similar to RCK
57	*Stra6*	78.4	46.4	0.59	AI030451	Similar to retinoic acid-responsive protein; STRA6 (predicted)

58	*LOC288689*	74.2	125.3	1.69	BI287326	similar to Tescalcin
59	*RGD1561380_predic*	123.9	66.6	0.54	AW524703	Similar to V2r2 protein (predicted)
60	*LOC363087*	102.0	30.6	0.30	BF393567	similar to vacuolar protein sorting 13C protein
61	*LOC315843*	99.2	63.8	0.64	BE116698	similar to WD repeat domain 11 protein
62	*Smo*	220.0	142.2	0.65	BF398112	smoothened homolog (Drosophila)
63	*Snx24_predicted*	125.8	83.6	0.66	BF284123	sorting nexing 24 (predicted)
64	*Tbc1d1_predicted*	217.5	123.5	0.57	BM383480	TBC1 domain family, member 1 (predicted)
65	*Tns*	168.2	108.5	0.65	BF290193	Tensin
66	*Tns4*	82.2	35.8	0.44	AI179390	Tensin 4
67	*Tspan6*	211.8	114.8	0.54	BI295929	Tetraspanin 6
68	*Tieg3_predicted*	122.2	318.5	2.61	BI289045	TGFB inducible early growth response 3 (predicted)
69	*Trp53rk_predicted ///*	75.4	154.3	2.05	AI711481	TP53 regulating kinase (predicted) /// TP53 regulating kinase
70	*Trio*	259.1	137.9	0.53	AI577848	triple functional domain (PTPRF interacting)
71	*Trio_predicted*	285.9	74.8	0.26	BF554226	triple functional domain (PTPRF interacting) (predicted)
72	*Tacstd2*	1655.5	947.2	0.57	AA891826	tumor-associated calcium signal transducer 2

Transcription

	Common	Control Raw	Vinc Raw	Vincl/Contr Ratio	Genbank	Gene Title_Affymetrix
1	*Atf5*	159.4	241.2	1.51	BM391471	activating transcription factor 5
2	*Ahdc1_predicted*	250.3	133.2	0.53	BE120316	AT hook, DNA binding motif, containing 1 (predicted)
3	*Arid2_predicted*	187.3	123.9	0.66	AA900891	AT rich interactive domain 2 (Arid-rfx like) (predicted)
4	*Baz2b_predicted*	56.7	175.1	3.09	BF404567	Bromodomain adjacent to zinc finger domain, 2B (predicted)
5	*Baz2b_predicted*	198.6	87.5	0.44	AA944574	BS69 protein
6	*Banp_predicted*	71.5	125.2	1.75	AI575458	Btg3 associated nuclear protein (predicted)
7	*Cnot7_predicted*	309.6	200.3	0.65	BE111850	CCR4-NOT transcription complex, subunit 7 (predicted)
8	*RGD1308111_predic*	103.6	64.7	0.62	BF396260	cellular zinc finger anti-NF-kappaB Cezanne (predicted)
9	*Chd1_predicted*	91.6	60.9	0.67	AI060045	chromodomain helicase DNA binding protein 1 (predicted)
10	*Chd1l_predicted*	227.2	98.5	0.43	AA858645	chromodomain helicase DNA binding protein 1-like
11	*Chd2_predicted*	165.6	107.4	0.65	BF396633	Chromodomain helicase DNA binding protein 2 (predicted)
12	*Chd6_predicted*	164.2	101.6	0.62	BF398050	chromodomain helicase DNA binding protein 6 (predicted)
13	*Crebbp*	290.4	173.8	0.60	AI714243	CREB binding protein
14	*Dpf2_predicted*	76.1	116.7	1.53	BE111797	D4, zinc and double PHD fingers family 2 (predicted)
15	*Dhx36_predicted*	490.8	178.4	0.36	AA859982	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)
16	*Dre1*	117.4	71.4	0.61	BM385908	Dre1 protein
17	*Egr1*	395.9	121.1	0.31	NM_012551	early growth response 1
18	*Fos*	804.0	193.3	0.24	BF415939	FBJ murine osteosarcoma viral oncogene homolog
19	*Fhl2*	164.9	369.2	2.24	AA800031	Four and a half LIM domains 2
20	*Fmr1*	207.9	134.8	0.65	AI705393	fragile X mental retardation syndrome 1 homolog
21	*Gfm*	130.6	204.9	1.57	NM_053625	G elongation factor
22	*Gnaq*	66.6	104.9	1.58	AI029833	heterotrimeric guanine nucleotide-binding protein alpha
23	*Foxq1 /// LOC49771*	47.7	79.0	1.66	NM_022858	HNF-3/forkhead homolog-1 /// hypothetical gene supported
24	*Hod*	3411.9	2111.5	0.62	NM_133621	homeobox only domain
25	*Hivep2*	157.5	102.0	0.65	NM_024137	human immunodeficiency virus type 1 enhancer-binding
26	*Hip1r*	103.6	65.6	0.63	BI295536	Huntingtin interacting protein 1 related
27	*Isgf3g_predicted*	68.7	209.8	3.06	BF283727	Interferon dependent positive acting transcription factor 3
28	*Khdrbs3*	248.4	142.5	0.57	NM_022249	KH domain containing, RNA binding, signal transduction
29	*Klf5*	308.0	142.5	0.46	BM382886	Kruppel-like factor 5 (intestinal)
30	*MGC116147*	237.7	364.3	1.53	BI296304	leucine zipper domain protein
31	*Mdc1*	79.8	40.3	0.50	BE120346	mediator of DNA damage checkpoint 1
32	*Med25_predicted*	143.0	221.1	1.55	AA892531	Mediator of RNA polymerase II transcription
33	*Mageh1*	178.3	91.9	0.52	H32543	melanoma antigen, family H, 1
34	*LOC362156*	72.6	123.8	1.70	BI294693	Membrane-associated DHHC5 zinc finger protein
35	*"March7"*	132.2	76.8	0.58	BE100638	membrane-associated ring finger (C3HC4) 7
36	*Mgea5*	156.4	241.8	1.55	BF548107	meningioma expressed antigen 5 (hyaluronidase)
37	*Mtf2*	137.1	90.8	0.66	BI294718	Metal response element binding transcription factor 2
38	*SMAD3_RAT*	103.7	66.7	0.64	BF552908	Mothers against decapentaplegic homolog 3 (SMAD 3)
39	*Mina*	146.5	92.0	0.63	BI278157	myc induced nuclear antigen
40	*Mnda_predicted*	50.4	86.9	1.72	AA901151	myeloid cell nuclear differentiation antigen (predicted)
41	*Mllt6_predicted*	243.5	145.2	0.60	AI555336	Myeloid/lymphoid or mixed lineage-leukemia translocation
42	*Mll_mapp*	140.1	78.1	0.56	BE114473	myeloid/lymphoid or mixed-lineage leukemia (mapped)
43	*Mllt5_predicted*	130.3	73.2	0.56	BE120038	Myeloid/lymphoid or mixed-lineage leukemia 5
44	*Nkx3-1_predicted*	155.2	46.1	0.30	BM386415	NK-3 transcription factor, locus 1 (Drosophila) (predicted)
45	*Nfib*	1360.0	852.5	0.63	AW253720	Nuclear factor I/B
46	*Nfkbiz_predicted*	93.3	40.0	0.43	AI176265	nuclear factor of kappa light polypeptide gene enhancer
47	*Nupr1*	4242.1	7221.3	1.70	NM_053611	nuclear protein 1
48	*Ncor1*	99.6	55.9	0.56	BE100543	nuclear receptor co-repressor 1
49	*Nr1d2*	168.9	80.5	0.48	BF284190	Nuclear receptor subfamily 1, group D, member 2
50	*Nr3c1*	127.9	73.5	0.57	BF394158	Nuclear receptor subfamily 3, group C, member 1
51	*Phf11_predicted*	42.1	82.5	1.96	AW920026	PHD finger protein 11 (predicted)

52	*Poldip2_predicted*	88.7	160.0	1.80	AI232159	polymerase (DNA-directed), delta interacting protein 2
53	*Rag1ap1_predicted*	230.0	149.9	0.65	AI138061	Recombination activating gene 1 activating protein 1
54	*SDCCAG3*	164.0	94.6	0.58	BE117444	Serologically defined colon cancer antigen 33 (predicted)
55	*Stat2_predicted*	189.1	383.8	2.03	BG666368	signal transducer and activator of transcription 2 (predicted)
56	*Stat2*	135.0	239.0	1.77	AA799569	Signal transducer and activator of transcription 2 (predicted)
57	*LOC689197*	95.4	53.5	0.56	BE114414	Similar to antigenic determinant of rec-A protein
58	*LOC680231*	144.8	89.4	0.62	BM383983	similar to chromodomain helicase DNA binding protein 9
59	*LOC499851*	128.5	82.9	0.64	AA875129	similar to elongation protein 4 homolog
60	*RGD1305741_predic*	47.6	88.8	1.87	AW921463	similar to glioma-amplified sequence-41 (predicted)
61	*RGD1306721_predic*	99.8	65.6	0.66	BI300993	similar to helicase-like protein NHL isoform 2 (predicted)
62	*RGD1305020_predic*	395.7	203.3	0.51	BG380736	similar to Hepatocellular carcinoma-associated antigen 58
63	*LOC367956*	417.2	1997.0	4.79	AW535518	similar to leucine zipper, down-regulated in cancer 1
64	*LOC688133*	608.7	368.3	0.61	BE114154	Similar to Mbt domain containing 1
65	*RGD1307526*	299.2	172.1	0.58	BE114469	similar to modulator of estrogen induced transcription
66	*RGD1564912_predic*	464.2	284.4	0.61	AI145481	Similar to Mut protein (predicted)
67	*LOC679623*	30.6	76.6	2.50	AA923865	Similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa)
68	*LOC691703*	632.5	1202.5	1.90	BM384963	similar to nuclear localized factor 1
69	*LOC501015*	84.7	178.0	2.10	AI229218	Similar to nuclear localized factor 2
70	*LOC682058*	419.6	246.0	0.59	BG380672	similar to nucleolar protein with MIF4G domain 1
71	*LOC500011*	62.4	117.3	1.88	AA998964	similar to OEF2
72	*LOC500030*	309.0	188.5	0.61	BE107536	similar to PHD finger protein 14 isoform 1
73	*LOC306254*	164.9	103.1	0.63	AW532414	similar to polybromo-1
74	*LOC361669*	60.5	105.4	1.74	AW523472	similar to transcription elongation regulator 1-like
75	*LOC679869*	90.5	51.2	0.57	AI137045	similar to transcription factor 7-like 2, T-cell specific
76	*MGC125073*	122.6	281.7	2.30	BF412297	Similar to TSC22 domain family protein 4
77	*LOC293112*	189.7	121.8	0.64	BI292899	similar to tyrosine kinase-associated leucine zipper protein
78	*LOC685865*	132.5	67.5	0.51	BG371744	Similar to zinc finger protein 458
79	*RGD1562434_predic*	247.4	152.8	0.62	AW252020	similar to zinc finger protein 651 (predicted)
80	*LOC499508*	83.5	47.1	0.56	AI029732	similar to Zinc finger, FYVE domain containing 16
81	*Sirt6_predicted*	63.1	103.4	1.64	AW525725	sirtuin 6
82	*Tbpl1_predicted*	393.1	226.5	0.58	AW434020	TATA box binding protein-like 1 (predicted)
83	---	137.1	80.9	0.59	BF389889	Transcribed locus, strongly similar to NP_009039.1
84	---	491.5	188.8	0.38	BI278967	Transcribed locus, weakly similar to XP_537399.1
85	*Tcfdp2_predicted*	260.6	161.7	0.62	AI177322	transcription factor Dp 2 (predicted)
86	*Tsc22d3*	180.2	96.6	0.54	BF399517	TSC22 domain family 3
87	*Ubn1_predicted*	96.2	50.2	0.52	AI578566	ubinuclein 1 (predicted)
88	*Zbtb4_predicted*	338.8	212.3	0.63	BM384146	zinc finger and BTB domain containing 4 (predicted)
89	*Znf22*	80.1	34.5	0.43	AI232806	zinc finger protein 22 (KOX 15)
90	*Znf292*	241.2	138.7	0.58	BE116321	Zinc finger protein 292
91	*Zfp295_predicted*	139.8	75.7	0.54	AI233009	zinc finger protein 295 (predicted)
92	*Zfp307_predicted*	153.8	98.4	0.64	BE098868	zinc finger protein 307 (predicted)
93	*Zfp395_predicted*	218.5	139.8	0.64	BM388100	Zinc finger protein 395 (predicted)
94	*Zfp503_predicted*	272.9	171.8	0.63	BF560938	zinc finger protein 503 (predicted)
95	*Zfp592_predicted*	277.1	167.4	0.60	AW529067	Zinc finger protein 592 (predicted)
96	*Zfp622*	600.2	948.7	1.58	BE109520	Zinc finger protein 622 (predicted)
97	*Zfp629*	88.6	58.7	0.66	BG380675	Zinc finger protein 629
98	*Zfp68_predicted*	138.3	82.3	0.59	AI555743	zinc finger protein 68 (predicted)
99	*Zfx_predicted*	107.9	71.9	0.67	BI293943	Zinc finger protein X-linked (predicted)
100	*Zfand2a*	110.3	168.5	1.53	AI406908	Zinc finger, AN1-type domain 2A
101	*Zcsl3_predicted*	109.5	56.7	0.52	BI289564	Zinc finger, CSL-type containing 3 (predicted)
102	*Zmat2*	86.9	57.6	0.66	BI291360	Zinc finger, matrin type 2
103	*Zswim3_predicted*	112.8	71.3	0.63	BM385609	zinc finger, SWIM domain containing 3 (predicted)

Translation & Protein Modification

	Sample	F3-Contr	Vincl	Vincl/Contr		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix
1	*Rnr2*	442.6	258.2	0.58	BG671790	16S ribosomal RNA
2	*Oas1*	121.4	311.7	2.57	Z18877	25 oligoadenylate synthetase
3	*Ate1_predicted*	409.6	264.5	0.65	BE117273	arginine-tRNA-protein transferase 1 (predicted)
4	*Cdk105*	2274.5	1435.1	0.63	NM_134415	CDK105 protein
5	*Cct8_predicted*	88.0	57.5	0.65	BF409759	chaperonin subunit 8 (theta) (predicted)
6	*Dhx36_predicted*	316.8	178.5	0.56	BE114021	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)
7	*Strbp*	102.0	46.9	0.46	BF415963	Double-stranded RNA-binding protein p74
8	*Dkc1*	103.6	171.8	1.66	NM_133419	dyskeratosis congenita 1, dyskerin
9	*Erp29*	432.3	672.4	1.56	U36482	endoplasmic retuclum protein 29
10	*Eif2s3x*	324.2	164.6	0.51	AI577833	eukaryotic translation initiation factor 2
11	*Hnrpa2b1_predicted*	184.8	112.3	0.61	BE108222	heterogeneous nuclear ribonucleoprotein A2/B1 (predicted)
12	*Hnrpd*	310.8	201.3	0.65	AI180251	Heterogeneous nuclear ribonucleoprotein D-like
13	*Hnrph3_predicted*	164.3	102.2	0.62	AI101886	heterogeneous nuclear ribonucleoprotein H3 (2H9)
14	*Imp3_predicted*	400.6	675.3	1.69	BG378108	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)

15	*Lars_predicted*	118.8	198.4	1.67	BE119004	leucyl-tRNA synthetase (predicted)
16	*Mrpl48_predicted*	366.4	219.5	0.60	AF209972	mitochondrial ribosomal protein L48 (predicted)
17	*Mrpl50_predicted*	155.5	249.5	1.61	AA891839	mitochondrial ribosomal protein L50 (predicted)
18	*Pabpn1*	497.5	326.9	0.66	AW525563	poly(A) binding protein, nuclear 1
19	*Paip1_predicted*	44.0	89.6	2.04	AA963084	Polyadenylate binding protein-interacting protein 1
20	*RBM22_RAT*	119.3	69.1	0.58	BE100371	Pre-mRNA-splicing factor RBM22
21	*Prpf39_predicted*	326.7	188.7	0.58	AA850679	PRP39 pre-mRNA processing factor 39 homolog (yeast)
22	*Qtrt1*	236.3	135.2	0.57	AI060136	queuine tRNA-ribosyltransferase 1
23		470.8	186.6	0.40	AFFX_rat_5S_	Rat 5sS rRNA
24	*Rrm2_mapped*	79.3	176.1	2.22	BG379338	ribonucleotide reductase M2 (mapped)
25	*Rbm14*	188.0	299.5	1.59	BF284573	RNA binding motif protein 14
26	*Rbm27_predicted*	78.1	48.3	0.62	BE116889	RNA binding motif protein 27 (predicted)
27	*Rbm34*	101.6	62.9	0.62	BM392304	RNA binding motif protein 34
28	*Rbm5_predicted*	346.4	229.9	0.66	BI293987	RNA binding motif protein 5 (predicted)
29	*Rnpc2*	648.4	416.6	0.64	BM388276	RNA-binding region (RNP1, RRM) containing 2
30	*Slfn2_predicted*	84.5	170.3	2.02	AW915529	schlafen 2 (predicted)
31	*Slfn3*	233.9	535.3	2.29	NM_053687	schlafen 3
32	*LOC690845*	46.6	107.4	2.31	BI282024	Similar to 40S ribosomal protein S4, X isoform
33	*RGD1563213_predic*	96.6	47.6	0.49	AW526060	Similar to peptide chain release factor 3 (predicted)
34	*LOC368070*	400.5	235.1	0.59	BF549763	similar to pinin
35	*RGD1563860_predic*	145.8	80.9	0.55	BM386762	Similar to ribosomal protein S6 kinase 2 (predicted
36	*LOC680726*	135.6	89.6	0.66	AW144676	Similar to RNA binding motif, single stranded interacting protein
37	*LOC691538*	340.1	217.9	0.64	BI289966	Similar to RNA-binding region (RNP1, RRM) containing 3
38	*RGD1561347_predic*	189.1	108.8	0.58	BF393502	similar to Sfrs4 protein (predicted)
39	*Sf3b1*	210.8	121.5	0.58	BF523561	splicing factor 3b, subunit 1
40	*Sf3b1*	535.8	336.4	0.63	BM384277	splicing factor 3b, subunit 1, 155kD
41	*Taf13_predicted*	298.9	468.8	1.57	BE120513	TAF13 RNA polymerase II, TATA box binding protein
42	*Tsn*	73.8	114.8	1.56	NM_021762	translin
43	*Unc45a*	277.0	428.8	1.55	BI296209	Unc-45 homolog A (C. elegans)

Miscelneous & Unknown

	Common	Control Raw	Vinc Raw	Vincl/Contr Ratio	Genbank	Gene Title_Affymetrix
1	*Dnmt2*	78.0	45.8	0.59	AI145497	DNA methyltransferase 2
2	*Tmem101*	86.8	138.6	1.60	H31535	transmembrane protein 101
3	*Brd1_predicted*	131.6	85.9	0.65	BI301225	bromodomain containing 1 (predicted)
4	---	153.6	92.1	0.60	AI717510	CDNA clone IMAGE:7368370
5	*Ccdc2*	153.7	96.7	0.63	BG376705	coiled-coil domain containing 2
6	*Gramd3*	41.3	85.9	2.08	BI281497	GRAM domain containing 3
7	*Mfhas1_predicted*	546.0	281.8	0.52	AI136864	malignant fibrous histiocytoma amplified sequence 1
8	*Map17*	100.8	208.2	2.06	NM_130401	membrane-associated protein 17
9	*MGC105691*	323.1	156.9	0.49	BF283798	NIPSNAP-related protein
10	*Nudcd1_predicted*	142.3	90.6	0.64	AI408455	NudC domain containing 1 (predicted)
11	*Ociad1*	98.3	51.9	0.53	BI275477	OCIA domain containing 1
12	*Oxr1*	3901.8	2500.5	0.64	NM_057153	oxidation resistance 1
13	*RGD:1303168*	1618.9	5325.2	3.29	NM_130743	putative ISG12(a) protein
14	*Rwdd3*	102.0	64.8	0.64	BE121336	RWD domain containing 3
15	*Sel1h*	212.0	323.2	1.52	BI285936	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)
16	*Sdccag10_predicted*	220.1	97.9	0.44	BF416387	serologically defined colon cancer antigen 10 (predicted)
17	*Sh3yl1_predicted*	862.9	424.0	0.49	AW527403	Sh3 domain YSC-like 1 (predicted)
18	*RGD1565969_predic*	261.7	423.7	1.62	AI236621	Similar to 5730405I09Rik protein
19	*RGD1306974_predic*	63.9	139.3	2.18	AA819788	similar to 5830458K16Rik protein (predicted)
20	*RGD1311925_predic*	190.3	117.0	0.61	AI008077	similar to BC003940 protein (predicted)
21	*LOC689397*	131.8	201.7	1.53	BM390235	Similar to C184L-22
22	*LOC690000*	94.9	142.4	1.50	AI228291	similar to CG3740-PA
23	*LOC688867*	92.6	60.7	0.66	BF408881	similar to cisplatin resistance-associated overexpressed
24	*LOC691657*	353.9	581.1	1.64	BF550246	similar to Cysteine-rich protein 1
25	---	134.0	233.5	1.74	AA965075	Similar to D15Wsu75e protein (predicted)
26	*LOC681647*	78.9	121.5	1.54	AW522260	similar to F43G9.2
27	*RGD1563869_predic*	208.7	133.0	0.64	BI295240	Similar to glucocorticoid induced gene 1 (predicted)
28	*LOC362736*	527.9	336.9	0.64	AI059295	similar to HECT domain containing 1
29	---	108.5	46.8	0.43	BM389654	Similar to hypothetical protein FLJ11342 (predicted)
30	*LOC315327*	137.6	216.5	1.57	BM390695	similar to hypothetical protein FLJ14800
31	*LOC292780*	146.1	79.4	0.54	BI279648	similar to hypothetical protein MGC15677
32	*LOC683071*	196.3	44.0	0.22	AI599250	similar to La-related protein 4
33	*LOC295961*	167.4	259.7	1.55	AI172106	similar to MMRP19
34	*LOC498803*	101.8	58.1	0.57	AI717553	similar to OTU domain containing 1
35	*LOC309557*	143.4	229.1	1.60	BE110569	similar to protein 4.1G
36	*LOC501231*	688.9	212.8	0.31	AW528611	similar to PSST739 protein
37	*LOC498066*	89.3	55.2	0.62	AA800892	similar to putative SH3BGR protein

38	*RGD1565023_predic*	62.4	128.3	2.06	BF398016	Similar to Suppressor of S. cerevisiae gcr2
39	*LOC498112*	164.0	101.2	0.62	BE103152	similar to YEATS domain containing 2
40	*Tom1l2_predicted*	95.8	48.7	0.51	BE101876	Target of myb1-like 2 (chicken) (predicted)
41	*Ttc23*	102.9	67.6	0.66	BF284579	Tetratricopeptide repeat domain 23
42	*Ttc9c*	135.8	86.8	0.64	BG668930	Tetratricopeptide repeat domain 9C
43	*Tmed4_predicted*	166.6	259.7	1.56	AI235294	transmembrane emp24 protein transport domain containing
44	*Tmem2_predicted*	45.8	112.1	2.45	AI101945	Transmembrane protein 2 (predicted)
45	*Tmem24_predicted*	49.6	85.0	1.71	BI279622	transmembrane protein 24 (predicted)
46	*Tmem97*	101.5	155.7	1.53	H31931	Transmembrane protein 97
47	*Tnrc6_predicted*	248.2	431.5	1.74	BI294732	Trinucleotide repeat containing 6 (predicted)
48	*Trim33_predicted*	91.5	137.3	1.50	AI103408	tripartite motif protein 33 (predicted)
49	*Wfdc5_predicted*	175.0	48.9	0.28	AW529736	WAP four-disulfide core domain 5 (predicted)
50	*Wdr36_predicted*	468.3	306.3	0.65	AI407932	WD repeat domain 36 (predicted)
51	*Yipf3*	129.3	253.4	1.96	AI102932	Yip1 domain family, member 3
52	*Zwint*	870.8	1440.6	1.65	AF439397	ZW10 interactor

EST's

Matt-Vinc-Ven-Prostate-031606-Norm to Contr

	Common	Control Raw	Vinc Raw	Vincl/Contr Ratio	Genbank	Gene Title_Affymetrix
1	*LOC304497*	396.9	104.7	0.26	BE103975	Hypothetical LOC304497 (predicted)
2	*LOC360478*	681.5	1031.9	1.51	BG378463	hypothetical LOC360478
3	*LOC498154*	281.5	554.6	1.97	AI170446	hypothetical protein LOC498154
4	*LOC500855*	1572.8	1025.8	0.65	BF289183	hypothetical protein LOC500855
5	*LOC502414*	88.0	153.5	1.74	AI410886	hypothetical protein LOC502414
6	*LOC680254*	124.7	55.2	0.44	BE115842	Hypothetical protein LOC680254
7	*LOC680422*	618.7	329.2	0.53	BM385170	hypothetical protein LOC680422
8	*LOC684964*	112.7	73.9	0.66	AI136134	Hypothetical protein LOC684964
9	*LOC685578*	215.6	137.3	0.64	AI175531	hypothetical protein LOC685578
10	*LOC689836*	74.3	127.6	1.72	AI235586	hypothetical protein LOC689836
11	*LOC691821*	93.1	41.2	0.44	BF417784	hypothetical protein LOC691821
12	*RGD1306116_predic*	688.8	437.4	0.63	BI294742	LOC361774 (predicted)
13	*RGD1310444_predic*	135.7	231.1	1.70	BF546148	LOC363015 (predicted)
14	*LOC498261*	56.5	116.1	2.06	AI177743	LOC498261
15	*LOC499304*	755.1	379.7	0.50	AI008409	LOC499304
16	*LOC499318*	152.2	447.4	2.94	BM388445	LOC499318
17	*RGD:1303214*	222.5	347.4	1.56	AI410096	similar to 2310044H10Rik protein
18	*RGD1307658_predic*	105.7	69.8	0.66	BI291427	similar to 3000004N20Rik protein (predicted)
19	*RGD1306674_predic*	50.8	85.0	1.67	BF412970	similar to 4930566A11Rik protein (predicted)
20	*LOC361261*	122.8	219.0	1.78	AI599176	similar to 5730405I09Rik protein
21	*RGD1304810_predic*	45.9	89.4	1.95	AI044301	similar to 6430573F11Rik protein (predicted)
22	*LOC498404*	198.0	113.5	0.57	AI013005	Similar to cDNA sequence BC018601
23	*LOC302987*	208.0	108.6	0.52	AI548527	similar to chromosome 16 open reading frame 28
24	*LOC501559*	230.8	140.4	0.61	BE117291	similar to chromosome X open reading frame 23
25	*RGD1307696_predic*	76.5	156.9	2.05	BI289554	similar to dJ881L22.2 (novel protein) (predicted)
26	*LOC499322*	16.7	3558.5	213.72	AA799328	similar to expressed sequence AW413625
27	*LOC315646*	97.5	59.7	0.61	BI275569	similar to hypothetical gene supported by AK085276
28	*RGD1311294_predic*	32.0	122.1	3.82	BI296237	similar to Hypothetical protein C6orf60 (predicted)
29	*LOC498228*	697.2	1101.5	1.58	AI709793	similar to hypothetical protein DKFZp761N1114
30	---	111.0	64.8	0.58	AI059937	Similar to hypothetical protein FLJ14007 (predicted)
31	*RGD1311381_predic*	180.4	288.6	1.60	AI136660	similar to hypothetical protein FLJ20037 (predicted)
32	---	195.3	302.7	1.55	BE111700	Similar to hypothetical protein FLJ20037 (predicted)
33	*RGD1311092_predic*	114.6	69.3	0.60	BI291880	similar to hypothetical protein FLJ20604 (predicted)
34	*RGD1565800_predic*	92.3	50.3	0.55	BI292079	Similar to hypothetical protein FLJ20674 (predicted)
35	---	186.1	106.8	0.57	BF549700	Similar to hypothetical protein FLJ30596 (predicted)
36	*LOC500595*	43.4	76.2	1.76	AI556333	similar to hypothetical protein FLJ32825
37	---	130.5	86.2	0.66	BI291413	Similar to hypothetical protein HSPC129 (predicted)
38	*RGD1307374_predic*	118.3	74.5	0.63	AI709802	similar to hypothetical protein MGC36325 (predicted)
39	*RGD1309263_predic*	97.8	150.0	1.54	BE109510	similar to hypothetical protein PRO1580 (predicted)
40	*RGD1306148_predic*	142.3	53.2	0.37	BF404837	similar to KIAA0368 (predicted)
41	*RGD1311429_predic*	395.0	222.7	0.56	AI177115	similar to KIAA1267 protein (predicted)
42	*RGD1311595_predic*	211.0	140.4	0.67	BF390453	similar to KIAA2026 protein (predicted)
43	---	206.3	108.2	0.52	AA924312	Similar to LOC443645 protein
44	---	117.9	65.1	0.55	BF398450	Similar to Mbt domain containing 1
45	*LOC299317*	309.9	601.5	1.94	AW527316	similar to MGC4645 protein
46	*LOC297504*	268.7	416.5	1.55	BF418342	Similar to mKIAA0212 protein
47	*RGD1309570_predic*	92.2	141.2	1.53	BF281872	similar to mKIAA0376 protein (predicted)
48	*RGD1310066*	82.3	51.1	0.62	AA817889	similar to mKIAA1002 protein
49	*LOC362153*	129.8	82.8	0.64	BF394282	similar to mKIAA1604 protein
50	*LOC498368*	115.6	75.7	0.65	BE113616	similar to RIKEN cDNA 0610040J01

51	*RGD1311122*	173.0	83.8	0.48	AI029476	similar to RIKEN cDNA 1110003E01
52	*RGD1305156_predic*	159.1	93.5	0.59	BG374333	similar to RIKEN cDNA 1110014D18 (predicted)
53	*RGD1309809_predic*	89.1	58.5	0.66	BF414252	similar to RIKEN cDNA 1110061L23 (predicted)
54	*RGD1310507_predic*	2634.6	1514.2	0.57	BI297744	similar to RIKEN cDNA 1300017J02 (predicted)
55	*RGD1310224_predic*	478.1	275.8	0.58	BM390774	similar to RIKEN cDNA 1810022C23 (predicted)
56	*RGD1311946_predic*	82.7	128.8	1.56	BM388441	similar to RIKEN cDNA 1810055G02 (predicted)
57	*LOC498586*	261.5	150.7	0.58	BI285092	similar to RIKEN cDNA 2200001I15
58	*LOC362040*	1524.0	2404.8	1.58	BE098941	similar to RIKEN cDNA 2310008M10
59	*LOC300472*	90.0	50.5	0.56	H33428	similar to RIKEN cDNA 2310075A12
60	---	212.5	112.7	0.53	AI172278	Similar to RIKEN cDNA 2610318K02 (predicted)
61	*LOC498145*	124.3	80.9	0.65	BE111635	similar to RIKEN cDNA 2810453I06
62	*RGD1305276_predic*	79.7	125.8	1.58	BI281651	similar to RIKEN cDNA 4631403P03 (predicted)
63	*RGD1310810_predic*	127.6	83.1	0.65	BG377386	similar to RIKEN cDNA 4930444A02 (predicted)
64	*LOC497860*	90.5	7.9	0.09	AI111983	Similar to RIKEN cDNA 4930517K11
65	*LOC499731*	109.8	68.8	0.63	AI410336	similar to RIKEN cDNA 5230400J09
66	*MGC125002*	82.6	33.1	0.40	BF287691	similar to RIKEN cDNA 5830433M19
67	*RGD1305918_predic*	372.3	175.7	0.47	AI137309	similar to RIKEN cDNA 6030443O07 (predicted)
68	*LOC364357*	146.3	5463.2	37.34	BI278952	similar to RIKEN cDNA A430107P09 gene
69	*RGD1310958_predic*	885.0	2014.4	2.28	BE328934	similar to RIKEN cDNA C130090K23 (predicted)
70	*RGD1310199_predic*	155.2	85.5	0.55	BM390240	similar to RIKEN cDNA D030070L09 (predicted)
71	*RGD1310722_predic*	125.5	71.8	0.57	AW534218	similar to RIKEN cDNA D130059P03 gene (predicted)
72	*LOC315911*	315.3	529.3	1.68	BE112948	similar to RIKEN cDNA D330045A20
73	*LOC315911*	168.8	278.7	1.65	AW142796	similar to RIKEN cDNA D330045A20
74	*RGD1560873_predic*	167.5	83.7	0.50	BF281860	Similar to RIKEN cDNA E230015L20 gene
75	*RGD1304846_predic*	137.4	208.2	1.52	BI289802	similar to X83328 protein (predicted)
76	---	197.2	106.4	0.54	BF289017	Transcribed locus, moderately similar to NP_076356.1
77	---	90.4	58.0	0.64	BE106331	Transcribed locus, moderately similar to NP_598791.1
78	---	149.4	82.1	0.55	BE118116	Transcribed locus, moderately similar to XP_225891.2
79	---	440.1	259.9	0.59	AI029285	Transcribed locus, moderately similar to XP_484071.1
80	---	354.7	226.9	0.64	BI282296	Transcribed locus, strongly similar to NP_076005.1
81	---	479.7	315.7	0.66	AA996970	Transcribed locus, strongly similar to NP_954666.1
82	---	195.2	129.2	0.66	BI285035	Transcribed locus, weakly similar to NP_062289.1
83	---	208.5	126.1	0.60	AI236841	Transcribed locus, weakly similar to XP_142546.4
84	---	801.0	487.3	0.61	AI172362	Transcribed locus, weakly similar to XP_376339.2
85	---	53.8	10371.2	192.95	BI275261	Transcribed locus, weakly similar to XP_574280.1
86	---	82.7	50.0	0.60	BF416395	Transcribed locus, weakly similar to XP_576460.1
87	*RGD:735147*	1461.9	963.9	0.66	BM385898	Unknown (protein for MGC:72974)
88	*MGC72974*	708.4	430.0	0.61	BI275851	Unknown (protein for MGC:72974)
89	*RGD:735106*	85.6	142.9	1.67	AI712625	Unknown (protein for MGC:73017)
90	---	37.5	92.9	2.48	BG670246	Transcribed locus
91	---	112.2	70.1	0.63	BF404539	Transcribed locus
92	---	63.4	97.6	1.54	BI296489	Transcribed locus
93	---	80.0	50.1	0.63	AI175820	Transcribed locus
94	---	179.3	104.4	0.58	AI406341	Transcribed locus
95	---	271.8	170.3	0.63	BM382988	Transcribed locus
96	---	168.0	86.8	0.52	BM384279	Transcribed locus
97	---	228.9	129.6	0.57	AI408734	Transcribed locus
98	---	85.0	46.1	0.54	AI714124	Transcribed locus
99	---	619.9	402.7	0.65	BF397951	Transcribed locus
100	---	91.9	50.3	0.55	AW531412	Transcribed locus
101	---	85.2	51.2	0.60	BM388895	Transcribed locus
102	---	57.4	91.2	1.59	BF567763	Transcribed locus
103	---	112.1	17.8	0.16	BE100973	Transcribed locus
104	---	419.2	248.0	0.59	BI290077	Transcribed locus
105	---	108.8	37.0	0.34	BE118580	Transcribed locus
106	---	203.5	124.3	0.61	BF389087	Transcribed locus
107	---	105.3	57.5	0.55	BE349836	Transcribed locus
108	---	309.8	168.7	0.54	AI071538	Transcribed locus
109	---	60.1	142.7	2.38	BM385853	Transcribed locus
110	---	76.6	36.5	0.48	BF388747	Transcribed locus
111	---	56.2	91.9	1.64	BF391155	Transcribed locus
112	---	175.3	83.5	0.48	AI639521	Transcribed locus
113	---	85.2	28.9	0.34	AI137052	Transcribed locus
114	---	223.7	144.2	0.64	AI111735	Transcribed locus
115	---	79.6	42.6	0.54	BF290937	Transcribed locus
116	---	154.4	100.2	0.65	AA955691	Transcribed locus
117	---	1002.4	590.0	0.59	AI410438	Transcribed locus
118	---	118.0	65.0	0.55	BG672201	Transcribed locus
119	---	162.0	243.5	1.50	BE114751	Transcribed locus
120	---	673.6	447.1	0.66	AI030349	Transcribed locus

121	---	121.4	225.5	1.86	BI298932	Transcribed locus
122	---	88.6	51.0	0.57	AW254703	Transcribed locus
123	---	390.1	183.2	0.47	AI102821	Transcribed locus
124	---	50.8	83.6	1.65	BF411062	Transcribed locus
125	---	262.2	167.4	0.64	BF290416	Transcribed locus
126	---	140.6	45.4	0.32	AA818098	Transcribed locus
127	---	107.5	62.7	0.58	AI535467	Transcribed locus
128	---	96.1	50.4	0.52	AW529791	Transcribed locus
129	---	117.6	67.9	0.58	AI072068	Transcribed locus
130	---	192.2	325.9	1.70	AI029796	Transcribed locus
131	---	114.3	74.9	0.66	AA893004	Transcribed locus
132	---	88.0	132.0	1.50	AA900322	Transcribed locus
133	---	109.8	68.8	0.63	AI169118	Transcribed locus
134	---	241.7	460.7	1.91	BI279587	Transcribed locus
135	---	37.0	81.7	2.21	AI408955	Transcribed locus
136	---	366.4	178.1	0.49	AI179665	Transcribed locus
137	---	85.6	26.7	0.31	BE107173	Transcribed locus
138	---	93.6	53.1	0.57	AI102429	Transcribed locus
139	---	90.0	36.7	0.41	BF551311	Transcribed locus
140	---	110.8	64.8	0.58	AI175259	Transcribed locus
141	---	175.5	97.3	0.55	AA956982	Transcribed locus
142	---	62.1	107.1	1.72	BG371591	Transcribed locus
143	---	224.4	148.9	0.66	BI275419	Transcribed locus
144	---	31.8	99.2	3.11	BF417625	Transcribed locus
145	---	94.8	145.8	1.54	BI275559	Transcribed locus
146	---	156.5	55.2	0.35	AA818098	Transcribed locus
147	---	157.9	100.3	0.64	BE101321	Transcribed locus
148	---	106.3	171.3	1.61	BI293249	Transcribed locus
149	---	267.4	109.0	0.41	BF549929	Transcribed locus
150	---	148.0	90.9	0.61	BF410644	Transcribed locus
151	---	117.5	182.4	1.55	BE096056	Transcribed locus
152	---	87.7	34.4	0.39	BF392155	Transcribed locus
153	---	426.9	212.3	0.50	BM386743	Transcribed locus
154	---	236.0	145.9	0.62	BG377356	Transcribed locus
155	---	96.7	53.0	0.55	BF393962	Transcribed locus
156	---	207.6	64.7	0.31	BM383081	Transcribed locus
157	---	425.4	185.2	0.44	AW532489	Transcribed locus
158	---	191.7	78.2	0.41	BE103021	Transcribed locus
159	---	276.1	132.0	0.48	BF400811	Transcribed locus
160	---	1501.5	562.3	0.37	AW917731	Transcribed locus
161	---	60.7	151.0	2.49	AI714115	Transcribed locus
162	---	117.9	71.8	0.61	AW523217	Transcribed locus
163	---	74.3	114.5	1.54	AI408264	Transcribed locus
164	---	130.6	81.5	0.62	BM389611	Transcribed locus
165	---	86.0	16.1	0.19	BF415514	Transcribed locus
166	---	292.1	184.4	0.63	AA858696	Transcribed locus
167	---	95.9	55.1	0.57	BE105979	Transcribed locus
168	---	105.9	179.8	1.70	H31701	Transcribed locus
169	---	139.3	78.2	0.56	AI112993	Transcribed locus
170	---	413.2	637.9	1.54	BF408431	Transcribed locus
171	---	130.2	86.6	0.67	BF387289	Transcribed locus
172	---	109.2	64.2	0.59	BG372832	Transcribed locus
173	---	125.1	77.5	0.62	BF285297	Transcribed locus
174	---	96.9	63.7	0.66	AA998150	Transcribed locus
175	---	165.0	73.1	0.44	BE098025	---
176	---	110.2	73.5	0.67	AI178495	---
177	---	197.4	112.4	0.57	AI012884	---
178	---	121.6	209.6	1.72	AW434139	---
179	---	774.7	514.5	0.66	BI290799	---
180	---	93.3	153.5	1.65	BI296287	---
181	---	952.0	536.5	0.56	BM383995	---
182	---	225.0	342.1	1.52	BE110241	---
183	---	138.8	360.2	2.59	AI413056	---
184	---	161.8	105.1	0.65	AI071602	---
185	---	156.3	104.1	0.67	BF397911	---
186	---	340.7	528.9	1.55	AA849027	---
187	---	183.1	365.0	1.99	BM385840	---
188	---	188.5	119.9	0.64	BE116508	---
189	---	139.3	76.0	0.55	AW536039	---
190	---	4913.1	7506.6	1.53	BE349658	---

191	---	89.3	154.4	1.73	BF419130	---
192	---	130.0	65.4	0.50	BE105488	---
193	---	78.0	48.0	0.61	BM389974	---
194	---	343.1	193.6	0.56	BI280114	---
195	---	48.3	129.1	2.67	AI177144	---
196	---	37.3	196.8	5.28	BF417649	---
197	---	309.6	466.1	1.51	AW920828	---
198	---	151.3	85.1	0.56	AW435306	---
199	---	96.0	62.4	0.65	BF397283	---
200	---	393.4	220.8	0.56	BE118753	---
201	---	103.4	189.8	1.84	AI030314	---
202	---	102.4	53.5	0.52	AA875124	---
203	---	124.6	34.0	0.27	AI177159	---
204	---	141.4	59.3	0.42	BI296990	---
205	---	104.9	175.5	1.67	BM383635	---
206	---	40.4	76.3	1.89	BG666849	---
207	---	58.5	585.2	10.00	BI275261	---
208	---	99.5	65.7	0.66	AI101416	---
209	---	88.7	52.0	0.59	BI278779	---
210	---	558.7	363.5	0.65	BE117009	---
211	---	4906.4	8122.8	1.66	BI282114	---
212	---	112.6	746.4	6.63	AW532939	---
213	---	137.9	67.5	0.49	AI502349	---
214	---	153.0	71.5	0.47	BM390812	---
215	---	163.2	94.9	0.58	AI229129	---
216	---	296.1	150.2	0.51	AI145951	---
217	---	129.5	62.9	0.49	AW524669	---
218	---	457.3	728.3	1.59	AW921279	---
219	---	149.2	298.7	2.00	AW921250	---
220	---	57.9	97.5	1.68	AW535011	---
221	---	566.6	371.1	0.65	AI145087	---
222	---	152.1	78.3	0.51	BE108415	---
223	---	168.7	348.2	2.06	AI407953	---
224	---	95.2	170.1	1.79	AI502529	---
225	---	84.0	43.0	0.51	AW530081	---
226	---	75.7	27.6	0.36	AW532375	---
227	---	209.0	101.9	0.49	BE106279	---
228	---	118.1	63.4	0.54	AW534671	---
229	---	123.6	75.8	0.61	AW535380	---

Supplemental Table S2. Prostate Epithelial Cell Regulated Genes List (243 genes)

Apoptosis

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	***Clu***	882.5	2150.1	2.44	AF314657	clusterin
2	*Cidea_predicted*	47.1	84.6	1.80	BF284899	cell death-inducing DNA fragmentation
3	***Eaf2***	2112.6	1309.1	0.62	BI285131	ELL associated factor 2
4	*Bag3_predicted*	1322.8	814.8	0.62	AI231792	Bcl2-associated athanogene 3
5	*Bcl2l1 /// LOC293190*	113.1	55.2	0.49	U72350	Bcl2-like 1 /// similar to bcl-x short
6	*Traf4af1*	98.5	163.4	1.66	BM388478	TRAF4 associated factor 1

Cell Cycle

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Gadd45b_predicted*	1044.6	509.3	0.49	BI287978	growth arrest and DNA-damage
2	***Dnajc10_predicted***	900.6	1390.8	1.54	AI172034	DnaJ (Hsp40) homolog, subfamily C
3	*Ccnl2*	59.8	94.5	1.58	AI412463	Cyclin L2
4	*Ccne2_predicted*	62.4	95.6	1.53	BM383329	Cyclin E2 (predicted)
5	*Ccnb1*	67.4	110.1	1.63	X64589	cyclin B1
6	***Cdc73***	559.7	304.0	0.54	BI290578	cell division cycle 73, Paf1

Cytoskeleton & ExtraCellular Matriz

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	***Ceacam1***	77.8	144.6	1.86	BM392373	carcinoembryonic antigen-related cell
2	***Kif3c***	87.1	141.8	1.63	NM_053486	kinesin family member 3C
3	*Kif9_predicted*	108.9	72.4	0.66	BF408879	kinesin family member 9 (predicted)
4	***Lgals3***	2866.2	1468.3	0.51	NM_031832	lectin, galactose binding, soluble 3
5	*Lrfn3_predicted*	58.2	88.9	1.53	BE101066	leucine rich repeat and fibronectin
6	*Mtap6*	50.2	82.7	1.65	AW521452	Microtubule-associated protein 6
7	***Tmsbl1***	139.9	213.7	1.53	U25684	thymosin beta-like protein 1
8	*Tpm3*	50.5	79.3	1.57	BE104273	Tropomyosin isoform 6
9	*Ttll12_predicted*	273.1	152.5	0.56	BI297049	tubulin tyrosine ligase-like family

Development

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Apc*	39.2	81.7	2.08	NM_012499	adenomatosis polyposis coli
2	*ADRP*	280.5	150.2	0.54	BI285616	adipose differentiation-related protein
3	***Als2cr3***	209.8	558.1	2.66	BG378620	amyotrophic lateral sclerosis 2
4	***Msmb***	2784.4	4538.7	1.63	NM_019188	beta-microseminoprotein
5	*Hdh*	54.7	82.4	1.51	BF548061	Huntington disease gene homolog
6	*LOC246046*	75.2	47.05	0.63	BE115262	Liver regeneration p-53 related protein
7	*Maf*	232.3	367.8	1.58	BG376037	monocyte to macrophage differentiation
8	*Rs21c6*	234.3	353.1	1.51	AY029335	RS21-C6 protein
9	***Svp4***	137.6	212.5	1.54	M25590	seminal vesicle protein 4
10	***RGD1562142_predicte***	117.7	54.15	0.46	BF396436	Similar to homeotic protein Hox 2.2
11	*LOC685814*	81.1	50	0.62	AI176027	Similar to MIR-interacting saposin-like
12	*STRA6*	301.8	191.0	0.63	BI284420	Similar to retinoic acid-responsive
13	*Spata6*	65.3	102.9	1.58	NM_134392	spermatogenesis associated 6
14	*Syn2*	47.2	75.2	1.59	AI101340	Synapsin II
15	*Sv2b*	8790.9	3008.3	0.34	BG672437	synaptic vesicle glycoprotein 2b

Electron Transport

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Cyp1a1*	99.0	21.85	0.22	X00469	cytochrome P450, 1a1
2	*RGD:628846*	54.9	98.9	1.80	NM_031605	cytochrome P450, 4a12
3	*Prdx6*	72.4	110.2	1.52	BF398290	Peroxiredoxin 6
4	*Pdia5*	1101.0	666.2	0.61	AI045590	protein disulfide isomerase-associated 5

Golgi Apparatus

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix

1	***LOC499761***	370.4	590.6	1.59	NM_023094	similar to N-acetylgalactosaminyltransferase e
2	***Fut2***	101.6	189.0	1.86	NM_031635	fucosyltransferase 2
3	*Gnpda2_predicted*	79.2	44.6	0.56	BG374650	glucosamine-6-phosphate deaminase 2

Growth Factors,Cyto-, and Chemokines

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	***Bmp6***	103.6	226.5	2.19	AI230985	bone morphogenetic protein 6
2	*Cxcr4*	292.0	186.7	0.64	AA945737	Chemokine receptor (LCR1)
3	*Cxcl2*	260.1	160.7	0.62	NM_053647	chemokine (C-X-C motif) ligand 2

Immune Response

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	***Azgp1***	104.9	55.6	0.53	NM_012826	alpha-2-glycoprotein 1, zinc
2	*Irf1*	429.1	251.2	0.59	NM_012591	interferon regulatory factor 1
3	*Ifit2_predicted*	92.8	189.1	2.04	BE118697	interferon-induced protein with tetratricopeptide
4	*RT1-Aw2*	1304.4	629.2	0.48	M24024	RT1 class Ib, locus Aw2
5	*Ighmbp2*	61.3	96.3	1.57	NM_031586	immunoglobulin mu binding protein 2

Metabolism & Transport

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Chpt1*	96.2	202.3	2.10	AI511041	choline phosphotransferase 1
2	*Nt5c3_predicted*	45.6	81.5	1.79	AI409146	5'-nucleotidase, cytosolic III (predicted)
3	*Abhd2_predicted*	82.8	131.3	1.59	BF405871	abhydrolase domain containing 2 (predicted)
4	*Ampd3*	792.8	1303.8	1.64	NM_031544	adenosine monophosphate deaminase 3
5	*Adh1*	134.1	315.2	2.35	NM_130780	alcohol dehydrogenase 1
6	***Akr1c12_predicted***	38.9	111.8	2.87	BM383010	aldo-keto reductase family 1, member C12 (predicted)
7	*Alpl*	515.4	272.5	0.53	Y00714	alkaline phosphatase, tissue-nonspecific
8	*Retsat*	312.1	511.7	1.64	AF465614	all-trans-13,14-dihydroretinol saturase
9	*Arsb*	108.3	49.8	0.46	AI101331	arylsulfatase B
10	*Alg9_predicted*	94.1	166.8	1.77	AI236397	asparagine-linked glycosylation 9 homolog
11	*Aspa*	58.0	126.5	2.18	NM_024399	aspartoacylase
12	*Atp6v1g3_predicted*	134.7	205.6	1.53	AW140864	ATPase, H+ transporting, V1 subunit G, isoform 3
13	***Ca2***	579.9	997.9	1.72	NM_019291	carbonic anhydrase 2
14	*Ca3*	194.0	125.5	0.65	AB030829	carbonic anhydrase 3
15	*Cbr1*	452.8	686.3	1.52	NM_019170	carbonyl reductase 1
16	*Colec12*	430.4	720.6	1.67	BI284441	collectin sub-family member 12
17	*Dhfr*	88.6	49.6	0.56	BE113295	dihydrofolate reductase
18	*Dpysl3*	104.1	69.35	0.67	BI294841	Dihydropyrimidinase-like 3
19	*Elovl6*	55.9	91.5	1.64	BF396857	ELOVL family member 6
20	*Glrx2*	80.2	48.6	0.61	BF558518	Glutaredoxin 2 (thioltransferase) (predicted)
21	*Gstp1 /// Gstp2*	362.7	591.4	1.63	X02904	glutathione-S-transferase, pi 1
22	*Gpd2*	197.3	126.4	0.64	U08027	glycerol-3-phosphate dehydrogenase 2
23	*Gmpr2*	78.6	132.7	1.69	BM386889	guanosine monophosphate reductase 2
24	*Hsd17b9*	722.9	303.4	0.42	U89280	hydroxysteroid (17-beta) dehydrogenase 9
25	*Mir16*	156.0	256.2	1.64	NM_032615	membrane interacting protein of RGS16
26	*Nmt1*	223.5	144.7	0.65	BE126380	N-myristoyltransferase 1
27	*Pgk1*	570.3	857.8	1.50	BI279760	phosphoglycerate kinase 1
28	*Pik3c2b_predicted*	51.7	79.4	1.54	BE105801	phosphoinositide-3-kinase, class 2, beta polypeptide
29	*Plod2*	86.9	53.95	0.62	BI279641	Procollagen lysine, 2-oxoglutarate 5-dioxygenase 2
30	***Pdia5***	1101.0	666.2	0.61	AI045590	protein disulfide isomerase-associated 5
31	*Serpine1*	194.5	123.3	0.63	NM_012620	serine (or cysteine) proteinase inhibitor, member 1
32	***Slc3a1***	84.8	154.0	1.82	NM_017216	solute carrier family 3, member 1
33	*Slc35d1_predicted*	47.2	78.05	1.65	AI177887	Solute carrier family 35
34	***Slc5a11***	9.8	121.7	12.42	BG377720	solute carrier family 5 (sodium/glucose cotransporter)
35	*Tcn2*	111.5	177.2	1.59	NM_022534	transcobalamin 2
36	*Tpcn1*	161.1	247.8	1.54	AB018253	two pore channel 1

Proteolysis

Vinc Prostate Epithelium-Norm_Exclude Control

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Plg*	90.0	158.9	1.77	NM_053491	plasminogen
2	*Rnf6_predicted*	78.8	126.7	1.61	BI296352	Ring finger protein (C3H2C3 type) 6 (predicted)

3	*Rnf134_predicted*	52.2	83.4	1.60	AA858786	ring finger protein 134 (predicted)
4	*Serpine1*	97.2	49.15	0.51	AI500951	serine (or cysteine) proteinase inhibitor, member 1
5	*LOC293844*	110.7	69.4	0.63	AI703543	similar to UCH37-interacting protein 1
6	*Snx16*	79.7	47.8	0.60	NM_022289	sorting nexin 16
7	***Uchl1***	139.3	223.2	1.60	NM_017237	ubiquitin carboxy-terminal hydrolase L1
8	*Ubd*	66.3	113.9	1.72	NM_053299	ubiquitin D
9	*Usp12_predicted*	62.0	112.3	1.81	AI639241	ubiquitin specific protease 12 (predicted)
10	*Usp43_predicted*	310.0	189.4	0.61	BE120893	ubiquitin specific protease 43 (predicted)
11	***Ube1dc1_predicted***	385.3	190.8	0.50	AI408025	ubiquitin-activating enzyme E1-domain containing 1
12	*Vps37b_predicted*	342.4	210.7	0.62	BG380336	Vacuolar protein sorting 37B (yeast) (predicted)
13	***RGD1564014_predicte***	600.6	121.3	0.20	AI712728	Similar to ubiquitin-conjugating enzyme E2 variant 1

Receptors & Binding proteins

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Aebp1_predicted*	96.9	57.55	0.59	BI278482	AE binding protein 1 (predicted)
2	*Bmpr2*	209.3	333.7	1.59	BE118651	bone morphogenic protein receptor, type II
3	*Cdk5rap2*	83.5	52.75	0.63	BF564964	CDK5 activator-binding protein
4	*F2r*	223.6	122.5	0.55	NM_012950	coagulation factor II receptor
5	*Gpr116*	80.2	144.0	1.79	BI290677	G protein-coupled receptor 116
6	*MGC94555*	93.5	146.5	1.57	BM386365	Intimal thickness-related receptor
7	***Iqcb1_predicted***	364.0	228.35	0.63	AI234142	IQ calmodulin-binding motif containing 1 (predicted)
8	*Mawbp*	37.0	92.9	2.51	AY083160	MAWD binding protein
9	*Ptprg*	166.5	259.1	1.56	BF400937	Protein tyrosine phosphatase, receptor type, G
10	*Ptprj*	96.7	50.1	0.52	NM_017269	protein tyrosine phosphatase, receptor type, J
11	*RGD1306176_predicted*	84.9	48.6	0.57	AI453967	similar to FCRL (predicted)
12	*LOC686203*	333.9	215.5	0.65	BM387197	similar to S100 calcium-binding protein A14 (S114)
13	*Synj2bp*	57.0	88.25	1.55	BI285174	synaptojanin 2 binding protein
14	*Mt3*	71.3	192.5	2.70	NM_053968	metallothionein 3

Signaling

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Akap8l*	146.8	86.7	0.59	BF392577	A kinase (PRKA) anchor protein 8-like
2	*Adcy5*	87.4	48.2	0.55	AI008095	adenylate cyclase 5
3	*Arrdc3*	973.7	626.5	0.64	AA818910	Arrestin domain containing 3
4	*Aurkb*	62.9	99.8	1.59	NM_053749	aurora kinase B
5	*Camkk1*	109.6	69.9	0.64	NM_031662	calcium/calmodulin-dependent protein kinase
6	*Crem*	192.1	122.8	0.64	NM_017334	cAMP responsive element modulator
7	*Csnk1d*	40.0	75.6	1.89	L07578	casein kinase 1, delta
8	***Rasd1***	1607.7	795.0	0.49	AF239157	DEXRAS1 (Dexras1)
9	*Dyrk3_predicted*	239.3	142.2	0.59	BE103067	dual-specificity tyrosine-(Y)-phosphorylation regulated
10	*Enpp1*	546.2	330.3	0.60	NM_053535	ectonucleotide pyrophosphatase/phosphodiesterase 1
11	*Efna1*	393.4	246.7	0.63	AW531877	ephrin A1
12	*Hsf1*	59.8	92.3	1.54	AI172496	heat shock transcription factor 1
13	*Itpkb*	73.3	116.3	1.59	AI180252	Inositol 1,4,5-trisphosphate 3-kinase
14	***Nkiras2_predicted***	99.5	59.8	0.60	AI406810	NFKB inhibitor interacting Ras-like protein 2
15	***Plekhh1_predicted***	132.2	53.8	0.41	BI275435	pleckstrin homology domain containing, family H
16	***Ptn***	1029.1	637.2	0.62	NM_017066	pleiotrophin
17	***Rab3c***	50.9	101.5	2.00	NM_133536	RAB3C, member RAS oncogene family
18	*Rap2ip*	124.9	220.2	1.76	AI535169	Rap2 interacting protein
19	*Rps6ka1*	66.6	134.5	2.02	BI285433	S6 protein kinase (Rsk-1)
20	*RGD1307284_predicted*	130.3	197.0	1.51	BE104506	similar to protein kinase, lysine deficient 1
21	***LOC364885***	107.6	166.7	1.55	BF283621	similar to Ras GTPase-activating-like protein IQGAP2
22	*Scap2*	68.7	123.6	1.80	AA891732	Src family associated phosphoprotein 2
23	*Sfn_predicted*	251.9	383.2	1.52	BI286166	stratifin (predicted)
24	*Tns*	99.4	61.6	0.62	AA894192	Tensin
25	***Tieg3_predicted***	150.9	271.8	1.80	BI289045	TGFB inducible early growth response 3 (predicted)

Transcription

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	*Ascl3*	225.8	343.1	1.52	BG374992	Achaete-scute complex homolog-like 3 (Drosophila)
2	*Ankrd52_predicted*	232.8	375.7	1.61	AA964250	ankyrin repeat domain 52 (predicted)
3	*Arid2_predicted*	45.8	77.1	1.69	BF398770	AT rich interactive domain 2 (Arid-rfx like) (predicted)
4	***Chd2_predicted***	145.7	61.4	0.42	BF396633	Chromodomain helicase DNA binding protein 2
5	*Cdcp1_predicted*	123.5	72.7	0.59	BI276505	CUB domain containing protein 1 (predicted)
6	*Ddx3x*	327.8	209.35	0.64	BF391513	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked

7	*Dot1l_predicted*	89.3	58.3	0.65	BG381046	DOT1-like, histone H3 methyltransferase (S. cerevisiae)
8	*Eftud1_predicted*	90.2	59.35	0.66	BM385306	Elongation factor Tu GTP binding domain containing 1
9	*Fosl2*	274.7	148.9	0.54	BI296947	FBJ osteosarcoma oncogene B (predicted)
10	*Fosl2 /// Fosb_predicted*	204.5	123.7	0.60	NM_012954	fos-like antigen 2 /// FBJ osteosarcoma oncogene B
11	*Ftsj3_predicted*	180.5	117.6	0.65	BG374267	FtsJ homolog 3 (E. coli) (predicted)
12	*H1f4*	177.4	105.1	0.59	NM_133285	H1 histone family, member 4
13	*Hes1*	1814.0	991.8	0.55	NM_024360	hairy and enhancer of split 1 (Drosophila)
14	*RGD:619976*	295.2	453.3	1.54	AA892297	histone deacetylase 2
15	*Hdac6*	35.6	83.4	2.34	AI411391	histone deacetylase 6
16	*Jund*	501.6	278.05	0.55	NM_138875	Jun D proto-oncogene
17	*Msh3*	131.7	243.1	1.85	BF390807	mutS homolog 3 (E. coli)
18	***Nkx3-1_predicted***	103.9	160.8	1.55	BM386415	NK-3 transcription factor, locus 1 (Drosophila)
19	*Nasp*	83.7	147.8	1.77	AI137618	Nuclear autoantigenic sperm protein (histone-binding)
20	*Nrip1_predicted*	587.2	378.0	0.64	BE117278	nuclear receptor interacting protein 1 (predicted)
21	*Nr1d1*	153.2	100.7	0.66	M25804	nuclear receptor subfamily 1, group D, member 1
22	*Rev1l_predicted*	45.9	81.5	1.77	BM384011	REV1-like (S. cerevisiae) (predicted)
23	***Stat2_predicted***	158.4	240.5	1.52	BG666368	signal transducer and activator of transcription 2
24	*Stat3*	1020.3	549.8	0.54	BE113920	signal transducer and activator of transcription 3
25	*LOC499745*	80.7	52.05	0.64	AA800680	Similar to Notch-regulated ankyrin repeat protein
26	*LOC690728*	166.9	271.2	1.62	AW528215	Similar to Protein C12orf11
27	***LOC690559***	82.4	49.85	0.61	BI300511	Similar to reduced expression 2
28	*LOC685179*	213.5	133.6	0.63	BE107610	Similar to SWI/SNF-related matrix-associated
29	***LOC361669***	107.4	224.2	2.09	AW523472	similar to transcription elongation regulator 1-like
30	***Sirt6_predicted***	56.3	104.5	1.86	AW525725	sirtuin 6 (silent mating type information regulation 2
31	*Tbx5*	76.1	48.95	0.64	BE110811	T-box 5 (predicted)
32	*Tle4*	77.3	48.55	0.63	NM_019141	transducin-like enhancer of split 4, E(spl) homolog
33	*Wrb*	116.4	195.1	1.68	AI177128	tryptophan rich basic protein
34	*Txnip*	1931.6	1180.5	0.61	U30789	upregulated by 1,25-dihydroxyvitamin D-3
35	*RGD:1303128*	134.2	75.0	0.56	AI231532	zinc finger protein 183 (RING finger, C3HC4 type)
36	*Zfp212_predicted*	299.3	187.9	0.63	AI178375	Zinc finger protein 212 (predicted)
37	*Zfp655*	70.5	134.9	1.91	AI103040	Zinc finger protein 655

Translation & Protein Modification

		Control	Vinc	Vinc/Cont		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix
1	*Rpn2*	80.3	52.05	0.65	BF407155	Ribophorin II
2	*Slfn5_predicted*	43.4	97.0	2.23	BI278962	schlafen 5 (predicted)
3	*LOC309692*	109.5	68.25	0.62	BI282130	similar to Disco-interacting protein 2 homolog
4	***RGD1563213_predicte***	102.1	64.95	0.64	AW526060	Similar to peptide chain release factor 3 (predicted)
5	*Stau2*	54.5	82.6	1.52	NM_134466	staufen, RNA binding protein, homolog 2 (Drosophila)

Miscelaneous & Unknown

		Control	Vinc	Vinc/Cont		
	Common	Raw	Raw	Ratio	Genbank	Gene Title_Affymetrix
1	*Pqlc2_predicted*	35.9	100.7	2.81	BI283849	PQ loop repeat containing 2 (predicted)
2	*LOC298250 /// LOC298*	218.8	510.4	2.33	AA926048	similar to hypothetical protein FLJ10986
3	***Wfdc5_predicted***	82.8	153.0	1.85	AW529736	WAP four-disulfide core domain 5 (predicted)
4	***Map17***	87.2	156.1	1.79	NM_130401	membrane-associated protein 17
5	*LOC313535*	90.2	161.2	1.79	AA899150	similar to prion protein interacting protein 1
6	***Tmem2_predicted***	47.9	85.4	1.78	AI101945	Transmembrane protein 2 (predicted)
7	*Wbp1_predicted*	82.0	142.9	1.74	BI289053	WW domain binding protein 1 (predicted)
8	*LOC362616*	127.8	217.9	1.71	BF411837	similar to EAPG6122
9	*RGD:735075*	163.6	276.7	1.69	AI009530	Unknown (protein for MGC:72614)
10	*RGD1311873_predicted*	210.8	344.8	1.64	BG378798	similar to hypothetical protein FLJ14466 (predicted)
11	*MGC94190*	67.5	107.2	1.59	BI296614	Similar to 0610007L01Rik protein
12	***LOC502414***	73.6	116.7	1.59	AI410886	hypothetical protein LOC502414
13	*Wfdc2*	170.4	268.7	1.58	AI411527	WAP four-disulfide core domain 2
14	*LOC498014*	84.3	132.3	1.57	BG379949	similar to hypothetical protein LOC284018 isoform b
15	*RGD1307882_predicted*	65.6	99.3	1.51	AW252589	similar to CG9346-PA (predicted)
16	*RGD1309621_predicted*	305.0	193.8	0.64	BM390131	similar to hypothetical protein FLJ10652 (predicted)
17	*Rlf_predicted*	143.8	90.0	0.63	BE104395	rearranged L-myc fusion sequence (predicted)
18	*Wdr3_predicted*	96.1	59.9	0.62	BE113663	WD repeat domain 3 (predicted)
19	*Usp6nl_predicted*	123.3	61.9	0.50	AI555989	USP6 N-terminal like (predicted)
20	*LOC500057*	83.9	41.6	0.50	AW523423	similar to hypothetical protein LOC168850
21	***LOC501231***	357.1	147.2	0.41	AW528611	similar to PSST739 protein
22	*RGD1304728_predicted*	152.5	100.5	0.66	BE097947	Similar to 4933427D14Rik protein (predicted)
23	*RGD1305255_predicted*	78.1	43.8	0.56	BF407593	similar to CG3996-PA (predicted)

EST's

	Common	Control Raw	Vinc Raw	Vinc/Cont Ratio	Genbank	Gene Title_Affymetrix
1	---	67.6	109.5	1.62	BE111759	CDNA clone IMAGE:7305115
2	***---***	110.1	72.15	0.66	AI717510	CDNA clone IMAGE:7368370
3	***---***	227.9	115.0	0.50	BE103975	Hypothetical LOC304497 (predicted)
4	***RGD1306116_predicted***	669.6	394.2	0.59	BI294742	LOC361774 (predicted)
5	*ORF19_predicted*	123.7	78.5	0.63	BG376997	open reading frame 19 (predicted)
6	*RGD:1303140*	612.7	379.9	0.62	AI408907	similar to cDNA sequence BC003324
7	---	2013.1	986.3	0.49	AI028809	Similar to cDNA sequence BC006662 (predicted)
8	*RGD1308168_predicted*	59.8	95.0	1.59	AA899109	similar to chromosome 17 open reading frame 27
9	***LOC499322***	1718.6	5791.5	3.37	AA799328	similar to expressed sequence AW413625
10	*RGD1310950_predicted*	88.6	138.4	1.56	AW526683	similar to KIAA1078 protein (predicted)
11	*RGD1564821_predicted*	61.7	96.6	1.56	BI301535	Similar to mKIAA1208 protein
12	*RGD1310475_predicted*	286.8	166.7	0.58	AI232524	Similar to RIKEN cDNA 0610010D20 (predicted)
13	*MGC93924*	90.7	137.8	1.52	BF411622	similar to RIKEN cDNA 3110043O21 gene
14	*RGD1311589_predicted*	60.4	102.0	1.69	BE113624	similar to RIKEN cDNA E130201N16 (predicted)
15	***---***	321.4	131.9	0.41	BI278967	Transcribed locus, weakly similar to XP_537399.1
16	---	998.3	622.0	0.62	AI031032	Transcribed locus, weakly similar to XP_341951.1
17	---	76.1	130.3	1.71	AI579823	Transcribed locus, weakly similar to XP_580018.1
18	---	69.0	109.5	1.59	AI411971	Transcribed locus
19	***---***	148.9	35.8	0.24	AI137052	Transcribed locus
20	---	61.4	104.3	1.70	BE111057	Transcribed locus
21	---	44.6	158.3	3.55	BF398614	Transcribed locus
22	---	103.1	171.4	1.66	AI231286	Transcribed locus
23	---	88.0	135.7	1.54	BE107619	Transcribed locus
24	---	85.1	130.8	1.54	AI236580	Transcribed locus
25	---	79.4	125.0	1.57	BF562507	Transcribed locus
26	***---***	83.9	126.8	1.51	BI293249	Transcribed locus
27	---	339.9	519.4	1.53	BE117266	Transcribed locus
28	---	56.6	86.0	1.52	BG669136	Transcribed locus
29	---	36.9	89.0	2.42	BE116195	Transcribed locus
30	***---***	1241.0	747.9	0.60	AW917731	Transcribed locus
31	---	85.2	54.75	0.64	AI029580	Transcribed locus
32	---	92.6	59.95	0.65	BG373166	Transcribed locus
33	---	89.1	141.7	1.59	AI406271	---
34	***---***	1113.2	2264.6	2.03	BM383995	---
35	---	40.9	75.8	1.86	AA800782	---
36	---	81.0	130.5	1.61	BM382838	---
37	---	874.6	523.3	0.60	AI043711	---
38	---	41.9	85.4	2.04	BF398618	---
39	***---***	140.1	90.7	0.65	AW532375	---

Bolded genes are common between the total prostate list and the epithelial cell list.