Table 1. Clustered common genes showing deregulated pattern of expression in docetaxel resistant PC-3 cell clones maintained without or with docetaxel in media as compared to untreated parental cells. The gene list shows values obtained with RankProd method. FC (fold change): Blank field = no change. Positive value = elevated expression. Negative value = lowered expression. FDR = false discovery rate

		8b2			**8b2 + docetaxel**			**1-INT**			**1-INT + docetaxel**		
Probe ID	**Gene**	FC	FDR	P value	FC	FDR	P value	FC	FDR	P value	FC	FDR	P value
	Regulation of cell death/apoptosis												
204777_s_at	MAL: mal, T-cell differentiation protein				3.93	0.0092	0				6.63	0.0024	0
203140_at	BCL6: B-cell CLL/lymphoma 6	3.42	0.0162	0	3.37	0.0042	0	4.66	0.0139	0	5.26	0.0025	0
225912_at	TP53INP1: Tumor protein p53 inducible nuclear protein 1	2.81	0.0328	1.00E-04	3.12	0.0209	1.00E-04	2.74	0.0092	0	3.48	0.0168	0
224917_at	MIR21: microRNA 21				2.88	0.0297	1.00E-04				2.78	0.0353	1.00E-04
218858_at	DEPDC6: DEP domain containing 6				2.75	0.035	1.00E-04				2.51	0.0488	3.00E-04
202643_s_at	TNFAIP3: tumor necrosis factor, alpha-induced protein 3	-2.56	0.0309	1.00E-04	-2.84	0.0215	1.00E-04	-3.45	0.0047	0	-3.99	0.0034	0
226142_at	GLIPR1: GLI pathogenesis-related 1	-3.90	0.0063	0	-3.93	0.0086	0	-4.17	0.0023	0	-4.07	0.0033	0
204614_at	SERPINB2: serpin peptidase inhibitor, clade B (ovalbumin), member 2	-8.91	0.0012	0	-7.57	0.001	0	-11.22	0.001	0	-10.89	0.002	0
	Regulation of cell cycle												
202769_at	CCNG2: cyclin G2	2.52	0.047	3.00E-04	2.98	0.0259	1.00E-04	3.51	0.0106	0	4.01	0.0102	0
	Regulation of cell growth/proliferation												
210095_s_at	IGFBP3: insulin-like growth factor binding protein 3	15.82	0	0	14.17	8.00E-04	0	2.62	0.0291	1.00E-04	2.54	0.0485	3.00E-04
205081_at	CRIP1: cysteine-rich protein 1 (intestinal)	5.44	0.0043	0	5.66	0	0	9.67	0	0	9.50	0	0
224797_at	ARRDC3; arrestin domain containing 3	3.42	0.0163	0	3.46	0.0149	0	4.73	0.0044	0	6.08	0.0028	0
213548_s_at	CDV3: CDV3 homolog (mouse)				-2.41	0.0402	2.00E-04				-2.59	0.0115	0
207850_at	CXCL3: chemokine (C-X-C motif) ligand 3				-2.51	0.0329	1.00E-04				-2.06	0.0266	1.00E-04
223710_at	CCL26: chemokine (C-C motif) ligand 26				-2.56	0.036	1.00E-04				-2.34	0.0196	0
210310_s_at	FGF5: fibroblast growth factor 5	-2.88	0.0182	0	-2.72	0.0239	1.00E-04	-3.33	0.0052	0	-3.34	0.0054	0
206924_at	IL11: interleukin 11	-3.03	0.0147	0	-3.14	0.0156	0	-3.25	0.0054	0	-3.62	0.0034	0
1552721_a_at	FGF1: fibroblast growth factor 1	-3.50	0.0091	0	-4.28	0.0065	0	-4.40	0.0019	0	-6.03	0.0016	0
215101_s_at	CXCL5: chemokine (C-X-C motif) ligand 5	-4.04	0.0063	0	-5.11	0.0037	0	-3.11	0.0058	0	-4.30	0.0035	0
208394_x_at	ESM1: endothelial cell-specific molecule 1	-4.21	0.0057	0	-5.60	0.0031	0	-4.16	0.0024	0	-4.48	0.0038	0
39402_at	IL1B: Interleukin 1, beta	-4.38	0.0054	0	-4.64	0.0047	0	-2.66	0.0121	0	-3.10	0.0063	0
	Extracellular matrix/adhesion												
212158_at	SDC2: syndecan 2	3.32	0.0175	0	3.10	0.0222	1.00E-04	5.03	0.003	0	4.76	0.0053	0
202291_s_at	MGP: matrix Gla protein	2.70	0.0367	1.00E-04	2.90	0.0277	1.00E-04	6.28	0.0019	0	7.26	0.0019	0
228640_at	PCDH7: protocadherin 7	-2.64	0.0304	1.00E-04	-2.51	0.0414	2.00E-04	-2.30	0.0237	1.00E-04	-2.01	0.0454	2.00E-04
202638_s_at	ICAM1: intercellular adhesion molecule 1	-3.24	0.0109	0	-3.61	0.0111	0	-2.30	0.0201	0	-2.18	0.021	1.00E-04

236179_at	CDH11: cadherin 11, type 2, OB-cadherin (osteoblast)	-3.94	0.0065	0	-5.04	0.0039	0	-10.35	0	0	-9.50	0.0014	0
237411_at	ADAMTS6: ADAM metallopeptidase with thrombospondin type 1 motif, 6	-5.17	0.0026	0	-6.18	0.0031	0	-3.84	0.0031	0	-3.84	0.0031	0
205959_at	MMP13: matrix metalloeptidase 13 (collagenase 3)	-5.49	0.0026	0	-5.16	0.0038	0	-4.67	0.0018	0	-5.13	0.0032	0
207517_at	LAMC2: laminin, gamma 2	-5.72	0.0026	0	-6.02	0.0024	0	-2.54	0.0136	0	-2.63	0.0113	0
201506_at	TGFBI: transforming growth factor beta-induced	-7.38	0.0019	0	-8.38	9.00E-04	0	-2.25	0.0217	1.00E-04	-2.45	0.0103	0
	Cytoskeleton (other than microtubule)												
227949_at	PHACTR3: phosphatse and actin regulator 3	3.41	0.016	0	4.58	0.006	0	2.69	0.0272	1.00E-04	3.60	0.0154	0
212328_at	LIMCH1: LIM and calponin homology domains 1				2.78	0.0334	1.00E-04				2.89	0.0319	1.00E-04
201310_s_at	C5orf13: chromosome 5 open reading frame 13	2.64	0.0404	2.00E-04	2.57	0.0432	2.00E-04	2.83	0.0219	1.00E-04	2.83	0.0332	1.00E-04
222457_s_at	LIMA1: LIM domain and actin binding 1				-2.40	0.0404	2.00E-04				-2.56	0.0117	0
227529_s_at	AKAP12:A kinase: A kinase (PRKA) anchor protein 12	-2.55	0.0311	1.00E-04	-2.65	0.027	1.00E-04	-2.53	0.0137	0	-2.52	0.0126	0
219165_at	PDLIM2: PDZ and LIM domain 2 (mystique)	-2.65	0.026	1.00E-04	-2.63	0.0275	1.00E-04	-2.15	0.0258	1.00E-04	-2.08	0.0261	1.00E-04
213684_s_at	PDLIM5: PDZ and LIM 5	-2.83	0.0191	0	-2.77	0.0226	1.00E-04	-3.45	0.0045	0	-2.90	0.0072	0
1567107_s_at	TPM4: tropomyosin 4	-3.03	0.0145	0	-3.30	0.0134	0	-2.43	0.0166	0	-2.10	0.0247	1.00E-04
221801_x_at	NEFL: neurofilament, light polypeptide				-3.07	0.0167	0				-1.89	0.0418	2.00E-04
215189_at	KRT86 /// LOC100134394: keratin 86 /// hypothetical protein LOC100134394	-3.10	0.0138	0	-3.08	0.0164	0	-2.85	0.0089	0	-3.12	0.0063	0
201430_s_at	DPYSL3: dihydropyrimidinase-like 3	-3.39	0.0098	0	-4.13	0.0069	0	-2.11	0.0283	1.00E-04	-2.01	0.0301	1.00E-04
1555673_at	KAP2.1B: keratinassociated protein 2.1B	-3.64	0.0075	0	-4.13	0.0069	0	-6.48	0.001	0	-6.57	0.0012	0
204455_at	DST: dystonin	-4.27	0.0052	0	-4.74	0.0043	0	-3.25	0.0055	0	-3.11	0.0064	0
205547_s_at	TAGLN: transgelin	-15.72	0	0	-16.95	0	0	-10.77	0	0	-14.33	0	0
	Microtubule cytoskeleton												
209118_s_at	TUBA1A: tubulin, alpha 1a	4.75	0.0048	0	4.98	0.0049	0	3.54	0.0105	0	3.49	0.0164	0
212675_s_at	CEP68: centrosomal protein 68kDa				2.67	0.0382	2.00E-04				3.10	0.0253	1.00E-04
226757_at	IFIT2: interferon-induced protein with tetratricopeptide repeats 2				2.46	0.0498	3.00E-04				4.93	0.0051	0
1552658_a_at	NAV3: neuron navigator 3	-4.29	0.0052	0	-4.96	0.0037	0	-4.91	0.0015	0	-4.14	0.0033	0
	Response to stress/chemical stimulus												
206857_s_at	FKBP1B: FK506 binding protein 1B, 12.6kDa	5.86	0.0036	0	5.57	0.0023	0	2.97	0.0186	0	2.98	0.029	1.00E-04
227803_at	ENPP5: ectonucleotide pyrophosphatase/phosphodiesterase 5	5.47	0.0041	0	5.33	0.0031	0	3.20	0.014	0	4.08	0.0089	0
201626_at	INSIG1: insulin induced gene	2.61	0.0423	2.00E-04	2.75	0.035	1.00E-04	2.85	0.0225	1.00E-04	2.97	0.029	1.00E-04
203828_s_at	IL32: interleukin 32				-2.39	0.0408	2.00E-04				-2.21	0.0198	0
210001_s_at	SOCS1: suppressor of cytokine signaling 1	-2.70	0.0246	1.00E-04	-2.52	0.0331	1.00E-04	-2.25	0.0215	1.00E-04	-2.35	0.0157	0
221667_s_at	HSPB8: heat shock 22kDa protein 8	-3.66	0.0075	0	-3.65	0.0109	0	-2.41	0.0175	0	-2.77	0.0093	0
217767_at	C3: complement component 3	-4.17	0.0055	0	-3.89	0.0085	0	-2.35	0.0178	0	-2.16	0.0216	1.00E-04
231240_at	DIO2: deiodinase, iodothyronine, type II	-4.96	0.0035	0	-4.25	0.0062	0	-2.90	0.0081	0	-2.62	0.0114	0
204363_at	F3: coagulation factor III (thromboplastin, tissue factor)	-5.02	0.0027	0	-5.16	0.003	0	-5.46	8.00E-04	0	-5.92	0.0015	0
202627_s_at	SERPINE1: serpine petidase inhibitor, clade E (nexin), member 1	-11.20	0.0012	0	-15.62	0	0	-8.04	9.00E-04	0	-12.75	0	0

	Receptors												
211924_s_at	PLAUR: plasminogen activator, urokinase receptor	-2.86	0.0189	0	-3.15	0.0155	0	-2.19	0.0235	1.00E-04	-2.27	0.0175	0
227997_at	IL17RD: interleukin 17 receptor D	3.68	0.0128	0	3.51	0.0138	0	3.08	0.0158	0	3.33	0.0202	0
	Signal transducer activity												
205990_s_at	WNT5A: wingless-type MMTV integration site family, member 5A	3.49	0.0155	0	3.44	0.015	0	5.02	0.003	0	5.43	0.0044	0
205387_s_at	CGB: chorionic gonadotropin, beta polypeptide	-2.63	0.028	1.00E-04	-2.35	0.0433	2.00E-04	-2.12	0.0276	1.00E-04	-2.29	0.0172	0
224215_s_at	DLL1: delta-like 1 (Drosophila)	-2.83	0.0197	1.00E-04	-3.57	0.0115	0	-2.24	0.0216	1.00E-04	-2.09	0.026	1.00E-04
	GTPase binding activity												
202748_at	GBP2: guanylate binding protein 2, interferon-inducible	-5.29	0.0028	0	-5.07	0.0038	0	-3.77	0.0033	0	-3.30	0.0054	0
231577_s_at	GBP1: guanylate binding protein 1, interferon-inducible, 67kDa	-8.81	0.0014	0	-9.54	0.0012	0	-7.36	0.001	0	-7.54	0.001	0
	GTPase regulator activity												
225056_at	SIPA1L2: signal-induced proliferation-associated 1 like 2	3.38	0.0166	0	3.67	0.0126	0	3.74	0.0088	0	4.52	0.0061	0
206636_at	RASA2: RAS p21 protein activator 2				-2.39	0.0412	2.00E-04				-2.15	0.0235	1.00E-04
	Transporter activity and metabolic process												
221583_s_at	KCNMA1: potassium large conductance calcium-activated channel	6.80	0.0022	0	6.59	0.0012	0	9.53	0	0	9.19	5.00E-04	0
205513_at	TCN1: transcobalamin I (vitamin B12 binding protein, R binder family)	5.37	0.0043	0	5.75	0.0012	0	6.66	0.0012	0	7.60	0.0015	0
223044_at	SLC40A1: solute carrier family 40 (iron-regulated transporter), member 1	3.28	0.0229	1.00E-04	3.46	0.0134	0	2.85	0.022	1.00E-04	3.53	0.0165	0
244353_s_at	SLC2A12: solute carrier family 2 (facilitated glucose transporter), member 12	3.15	0.0229	1.00E-04	3.13	0.0198	1.00E-04	2.62	0.0289	1.00E-04	3.23	0.021	1.00E-04
204401_at	KCNN4: potassium intermediate/small conductance calcium-activated channel	3.05	0.0258	1.00E-04	3.10	0.0218	1.00E-04	2.85	0.0225	1.00E-04	2.83	0.0332	1.00E-04
243711_at	DDAH1: dimethylarginine dimethylaminohydrolase 1	-2.50	0.0337	1.00E-04	-2.38	0.0433	2.00E-04	-2.29	0.0207	0	-2.44	0.0144	0
206566_at	SLC7A1: solute carrier family 7 (cationic amino acid transporter, y+ system)				-2.96	0.0188	0				-2.50	0.0131	0
225782_at	MSRB3: methionine sulfoxide reductase B3	-3.05	0.0159	0	-3.19	0.0153	0	-2.09	0.0283	1.00E-04	-2.03	0.029	1.00E-04
	Lipid metabolic process												
202436_s_at	CYP1B1: cytochrome P450, family 1, subfamily B, polypeptide 1	12.43	8.00E-04	0	18.55	0	0	5.99	0.0018	0	13.21	0	0
203913_s_at	HPGD: hydroxyprostaglandin dehydrogenase 15-(NAD)	5.17	0.0041	0	6.31	0.0019	0	2.80	0.0254	1.00E-04	4.31	0.0078	0
238681_at	GDPD1: glycerophosphodiester phosphodiesterase domaine containing 1	4.07	0.0106	0	3.87	0.0097	0	2.98	0.0186	0	3.56	0.0164	0
215723_s_at	PLD1: phospholipase D1, phosphatidylcholine-specific	3.01	0.026	1.00E-04	3.10	0.0218	1.00E-04	2.65	0.0288	1.00E-04	2.78	0.0356	1.00E-04

202054_s_at	ALDH3A2: aldehyde dehydrogenase 3 family, member A2	2.63	0.0406	2.00E-04	2.66	0.0391	2.00E-04	2.26	0.0489	3.00E-04	2.76	0.0354	1.00E-04
209160_at	AKR1C3: aldo-keto reductase family 1, member C3				2.55	0.0444	2.00E-04				6.04	0.0029	0
242963_at	SGMS2: sphingomyelin synthase 2				-2.30	0.0473	2.00E-04				-1.83	0.0498	2.00E-04
1554997_a_at	PTGS2: prostaglandin-endoperoxide synthase 2	-3.81	0.0074	0	-3.56	0.0114	0	-10.32	0	0	-11.09	0	0
	Chromatin organization												
218729_at	LXN: latexin				3.69	0.0117	0				2.85	0.0325	1.00E-04
210255_at	RAD51L1: RAD51-like 1 (S. cerevisiae)	3.38	0.0163	0	3.09	0.0217	1.00E-04	2.46	0.037	2.00E-04	2.52	0.049	3.00E-04
214455_at	HIST1H2BC: histone cluster 1, H2bc	2.93	0.0291	1.00E-04	2.73	0.0353	1.00E-04	4.14	0.0061	0	4.16	0.009	0
214472_at	HIST1H2AD: histone cluster 1, H2ad				2.62	0.04	2.00E-04				3.25	0.0213	1.00E-04
215071_s_at	HIST1H2AC: histone cluster 1, H2ac	2.59	0.0434	2.00E-04	2.59	0.0422	2.00E-04	3.26	0.014	0	3.63	0.0147	0
208180_s_at	HIST1H4A: histone cluster 1, H4a	2.53	0.0465	3.00E-04	2.47	0.0497	3.00E-04	3.60	0.0094	0	3.71	0.0138	0
	Transcription regulation												
227404_s_at	EGR1: early growth response 1	14.74	0	0	11.25	0	0	18.48	0	0	11.78	0	0
206059_at	ZNF91: zinc finger protein 91	10.78	7.00E-04	0	11.65	0.0014	0	9.21	0	0	11.39	0	0
215729_s_at	VGLL1: vestigial like 1 (Drosophila)				7.53	7.00E-04	0				3.09	0.0259	1.00E-04
236429_at	ZNF83: zinc finger protein 83	7.25	0.0017	0	9.36	8.00E-04	0	4.39	0.0053	0	4.95	0.0052	0
230720_at	RNF182: ring finger protein 182	5.49	0.0044	0	5.27	0.0031	0	4.39	0.0057	0	4.57	0.0054	0
223714_at	ZNF256: zinc finger protein 256	4.56	0.007	0	4.58	0.0063	0	4.08	0.006	0	4.22	0.0081	0
221911_at	ETV1: ets variant 1	3.35	0.0106	0	3.80	0.0105	0	4.96	0.0036	0	5.79	0.0031	0
207120_at	ZNF667: zinc finger protein 667	3.33	0.0172	0	3.01	0.0239	1.00E-04	3.07	0.0156	0	3.89	0.0118	0
201565_s_at	ID2: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3.76	0.0119	0	3.39	0.0154	0	2.33	0.0435	2.00E-04	2.53	0.049	3.00E-04
229614_at	ZNF320: zinc finger protein 320	3.35	0.0169	0	3.35	0.0167	0	2.98	0.0185	0	3.19	0.0231	1.00E-04
242463_x_at	ZNF600: zinc finger protein 600	3.75	0.0119	0	3.72	0.0118	0	2.51	0.0341	1.00E-04	3.24	0.0216	1.00E-04
204917_s_at	MLLT3: myeloid/lymphoid or mixed-lineage leukemia	3.21	0.0209	1.00E-04	2.76	0.0337	1.00E-04	2.69	0.027	1.00E-04	2.56	0.048	3.00E-04
231786_at	HOXA13: homeobox A13				3.07	0.0227	1.00E-04				2.63	0.0434	2.00E-04
203232_s_at	ATXN1: ataxin 1				3.07	0.0223	1.00E-04				2.87	0.0317	1.00E-04
1567032_s_at	ZNF160: zinc finger protein 160	3.04	0.025	1.00E-04	2.72	0.0354	1.00E-04	2.53	0.0324	1.00E-04	2.72	0.0371	2.00E-04
203394_s_at	HES1: hairy and enhancer of split 1 (Drosophila)	2.65	0.0405	2.00E-04	2.38	0.0457	3.00E-04	2.56	0.0323	1.00E-04	2.43	0.0444	3.00E-04
39549_at	NPAS2: neuronal PAS domain protein 2	2.53	0.0467	3.00E-04	2.74	0.0349	1.00E-04	3.02	0.0176	0	3.98	0.011	0
215505_s_at	STRN3: striatin, calmodulin binding protein 3				-2.46	0.0375	2.00E-04				-2.03	0.029	1.00E-04
206127_at	ELK3: ELK3, ETS-domain protein (SRF accessory protein 2)				-2.67	0.0265	1.00E-04				-1.86	0.0485	2.00E-04
205205_at	RELB: v-rel reticuloendotheliosis viral oncogene homo;og B	-2.64	0.027	1.00E-04	-2.74	0.0044	0	-3.44	0.0452	1.00E-04	-3.04	0.0068	0
207535_s_at	NFKB2: nuclear factor of kappa light polypeptide gene enhancer in B-cells	-3.06	0.0143	0	-3.30	0.0136	0	-3.29	0.0053	0	-2.86	0.0075	0
207109_at	POU2F3: POU class 2 homeobox 3	-3.07	0.0143	0	-3.07	0.0165	0	-3.17	0.0057	0	-2.50	0.0132	0
235417_at	SPOCD1: SPOC domain containing 1	-3.16	0.0124	0	-2.75	0.0235	1.00E-04	-2.23	0.0238	1.00E-04	-2.16	0.0223	1.00E-04
213667_at	SRCAP: Snf2-related CREBBP activator protein	-3.45	0.0094	0	-3.62	0.0111	0	-2.81	0.0091	0	-2.49	0.0129	0
224341_x_at	TLR4: toll-like receptor 4	-4.65	0.005	0	-5.00	0.0038	0	-5.61	9.00E-04	0	-5.22	0.0027	0

223642_at	ZIC2: Zic family member 2 (odd-paired homolog, Drosophila)	-15.43	0	0	-13.46	0.0012	0	-8.58	0	0	-8.18	0.0011	0
	Translation initiation												
227930_at	EIF2C4: MRNA; cDNA DKFZp547H229 (from clone DKFZp547H229)				2.47	0.0499	3.00E-04				2.86	0.0317	1.00E-04
	Other												
221986_s_at	KLHL24: kelch-like 24 (Drosophila)	5.07	0.0042	0	4.79	0.006	0	4.25	0.006	0	4.69	0.0054	0
209763_at	CHRDL1: chordin-like 1	4.28	0.0088	0	4.13	0.0086	0	9.52	0	0	10.21	0	0
1555279_at	ARMC8: armadillo repeat containing 8	-2.57	0.0309	1.00E-04	-2.60	0.0292	1.00E-04	-2.49	0.0143	0	-2.41	0.0146	0
	Unknown function												
235874_at	PRSS35: protease, serine, 35				9.93	9.00E-04	0				2.95	0.0294	1.00E-04
235976_at	SLITRK6: SLIT and NTRK-like family, member 6	2.74	0.0356	1.00E-04	3.39	0.0156	0	7.50	5.00E-04	0	10.16	0	0
1552389_at	C8orf47: chromosome 8 open reading frame 47	4.78	0.0048	0	3.83	0.0099	0	3.33	0.0134	0	2.73	0.0365	2.00E-04
238673_at	SAMD12: clone TEC_AC113188.2-001_REV mRNA sequence	4.31	0.0082	0	4.61	0.006	0	3.09	0.016	0	3.90	0.0117	0
244741_s_at	MGC9913: hypothetical protein MGC9913	3.92	0.0117	0	3.64	0.0129	0	4.22	0.0059	0	4.15	0.0082	0
53720_at	C19orf66: chromosome 19 open reading frame 66	2.64	0.0404	2.00E-04	2.94	0.0177	0	3.01	0.0177	0	3.49	0.0168	0
234989_at	NCRNA00084: non-protein coding RNA 84				2.52	0.0461	2.00E-04				2.76	0.0356	1.00E-04
239319_at	LOC728342: CDNA clone IMAGE:5297581	3.19	0.0233	1.00E-04	3.26	0.0177	0	2.67	0.029	1.00E-04	2.72	0.0372	2.00E-04
223268_at	C11orf54: chromosome 11 open reading frame 54	3.05	0.0252	1.00E-04	3.25	0.0432	2.00E-04	2.33	0.0432	2.00E-04	2.98	0.0288	1.00E-04
226811_at	FAM46C: family with similarity 46, member C	2.53	0.0466	3.00E-04	2.56	0.0432	2.00E-04	2.67	0.0282	1.00E-04	3.08	0.0258	1.00E-04
1558404_at	LOC644242: hypothetical protein LOC644242, mRNA	-3.44	0.0075	0	-3.01	0.0143	0	-2.48	0.0143	0	-2.12	0.0253	1.00E-04
224920_x_at	MYADM: myeloid-associated differentiation marker	-3.24	0.0078	0	-3.42	0.0117	0	-2.17	0.0248	1.00E-04	-1.98	0.0318	1.00E-04
238460_at	FAM83A: family with sequence similarity 83, member A	-7.04	0.0024	0	-5.51	0.003	0	-2.45	0.0175	0	-2.85	0.0075	0

Table 2. Clustered common genes showing deregulated pattern of expression in docetaxel resistant DU145 T2 cell line as compared to the parental docetaxel sensitive DU145 cells. The gene list shows values obtained with RankProd method. FC (fold change): Blank field = no change. Positive value = elevated expression. Negative value = lowered expression. FDR = false discovery rate

PROBE SET	**GENE**	**FC**	**FDR**	**P value**
	Regulation of cell death/apotosis			
210145_at	PLA2G4A: phospholipase A2, group IVA (cytosolic, calcium-dependent)	3.31	0.0028	0
204684_at	NPTX1: neuronal pentaxin 1	2.61	0.0067	0
219257_s_at	SPHK1: sphingosine kinase 1	2.26	0.0132	0
203381_s_at	APOE: apolipoprotein E	2.19	0.0167	0
204224_s_at	GCH1: GTP cyclohydrolase 1	2.1	0.0277	0
242138_at	DLX1: distal-less homeobox1	1.99	0.0415	1.00E-04
217999_s_at	PHLDA1: pleckstrin homology-like domain, familyA, member 1	1.92	0.0415	1.00E-04
203508_at	TNFRSF1B: tumor necrosis factor receptor superfamily, member 1B	1.9	0.0421	1.00E-04
223333_s_at	ANGPTL4: angiopoietin-like 4	1.9	0.042	1.00E-04
202086_at	MX1: myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	1.89	0.0444	1.00E-04
208792_s_at	CLU: clusterin	-2.06	0.0455	2.00E-04
206814_at	NGF: nerve growth factor (beta polypeptide)	-2.14	0.0386	2.00E-04
206569_at	IL24: interleukin 24	-2.18	0.0366	1.00E-04
215990_s_at	BCL6: B-cell CLL/lymphoma 6	-2.21	0.0017	1.00E-04
212609_s_at	AKT3: A-akt murine thymona viral oncogene homolog 3 (protein kinase B, gamma)	-2.21	0.0348	1.00E-04
212063_at	CD44: CD44 molecule (Indian blood group)	-2.37	0.0255	1.00E-04
227961_at	CTSB: cathepsin B	-2.53	0.0211	0
214203_s_at	PRODH: proline dehydrogenase (oxydase) 1	-2.54	0.0208	0
208965_s_at	IFI16: interferon, gamma-inducible protein 16	-2.6	0.0194	0
225606_at	BCL2L11: BCL2-like 11 (apaptosis facilitator)	-2.8	0.0143	0
215719_x_at	FAS: fas (TNFreceptor superfamily, member 6)	-2.91	0.0121	0
209772_s_at	CD24: CD24 molecule	-4.68	0.0014	0
227828_s_at	FAM176A: family with sequence similarity 176< member A	-6.56	0	0
	Regulation of cell cycle			
1555772_a_at	CDC25A: cell division cycle 25 homolog A (S.pombe)	2.29	0.0136	0
231769_at	FBXO6: F-boxprotein 6	2.22	0.0145	0
229671_s_at	C21orf45: Chromosome 21 open reading frame 45	2.06	0.0277	1.00E-04
217010_s_at	CDC25C: cell division cycle 25 homolog C (S.Pombe)	1.98	0.0335	1.00E-04
211088_s_at	PLK4: Polo-like kinase 4 (Drosophila)	1.93	0.0396	1.00E-04
209891_at	SPC25: SPC25, NDC80 kinetochore complex component, homolog (S.cerevisiae)	1.89	0.0452	2.00E-04
203323_at	CAV2: calveolin 2	-2.04	0.0484	2.00E-04
1553055_a_at	SLFN5: schlafen family member 5	-2.9	0.0125	0
235683_at	SESN3: sestrin 3	-3.15	0.0098	0
	Regulation of cell growth/proliferation			
214974_x_at	CXCL5: chemokonie (C-X-C motif) ligand 5	7.53	0	0
201667_at	GJA1: gap junction protein, alpha 1, 43 kDa	4.34	5.00E-04	0
231798_at	NOG: noggin	3.19	0.0031	0
242996_at	MTRF1: mitochondrial translational release factor 1	2.11	0.0211	0
211017_s_at	NF2: neurofibromim 2 (merlin)	2.04	0.0313	1.00E-04
205032_at	ITGA2: integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	2.02	0.0296	1.00E-04
228834_at	TOB1: transducer of ERBB2, 1	-2.1	0.0424	2.00E-04
226016_at	CD47: CD47 molecule	-2.17	0.0366	1.00E-04
201508_at	IGFBP4: insulin-like growth factor binding protein 4	-2.27	0.0316	1.00E-04
213010_at	PRKCDBP: protein kinase C, delta binding protein	-2.28	0.0318	1.00E-04
201324_at	EMP1: epithelial membrane protein 1	-2.44	0.0227	1.00E-04
205792_at	WISP2: WINT1 inducible signaling pathway protein 2	-2.53	0.0208	0
206343_s_at	NRG1: neuregulin 1	-2.67	0.0181	0
222802_at	EDN1: endothelin 1	-3.44	0.0067	0
205627_at	CDA: cytidine deaminase	-3.55	0.0056	0

205014_at	FGFBP1: fibroblast growth factor binding protein 1	-4.32	0.0022	0
205207_at	IL6: interleukin 6 (interferon, beta 2)	-4.82	0.0015	0
	Extracellular matrix/cell adhesion and junctions			
218435_at	DNAJC15: DnaJ (HSP40) homolog, subfamily C, member 15	7.55	0	0
202790_at	CLDN7: claudin 7	2.89	0.0039	0
201839_s_at	EPCAM: epithelial cell adhesion molecule	2.59	0.0068	0
218182_s_at	CLDN1: claudin 1	2.45	0.0083	0
203417_at	MFAP2: microfibrillar-associated protein 2	2.13	0.0241	0
209277_at	TFPI2: tissue factor pathway inhibitor 2	2.13	0.0132	0
211340_s_at	MCAM: melanoma cell adhesion molecule	2.03	0.0302	1.00E-04
235955_at	MARVEL domain containing 2	1.97	0.0342	1.00E-04
207517_at	LAMC2: laminin, gamma 2	1.92	0.0416	1.00E-04
211719_x_at	FN1: fibronectin 1	-2.11	0.0401	2.00E-04
212830_at	MEGF9: multiple EGF-like-domains 9	-2.15	0.0383	1.00E-04
217478_s_at	HLA-DMA////HLA-DMB: major histocompatibility complex, class II, DM alpha	-2.17	0.0366	1.00E-04
200923_at	LGALS3BP: lectin, galactoside-binding soluble, 3 binding protein	-2.21	0.035	1.00E-04
202363_at	SPOCK1: spart/osteonectin, cwcv and katal-like domain proteoglycan (testican) 1	-2.24	0.0335	1.00E-04
225242_s_at	CCDC80: coiled-coil domain containing 80	-2.27	0.0319	1.00E-04
242722_at	LMO7: LIM domain 7	-2.31	0.0281	1.00E-04
206033_s_at	DSC3: desmocolin 3	-2.33	0.0281	1.00E-04
226145_s_at	FRAS1: Fraser syndrome 1	-2.54	0.0212	0
225189_s_at	RAPH1: Ras associated (RalGDS/AF-6) and pleckstrin homology domain 1	-2.58	0.0193	0
201645_at	TNC: tenascin C	-3.28	0.0076	0
215446_s_at	LOX: lysyl oxydase	-3.5	0.0063	0
226189_at	ITBG8: integrin, beta 8	-4.67	0.0015	0
203757_s_at	CEACAM6: carcinoembryonic antigen-related cell adhesion molecule 6	-6.77	0	0
203779_s_at	MPZL2: myelin protein zero-like 2	-6.87	0	0
	Cytoskeleton (other than microtubule)			
204465_s_at	INA: internexin neuronal intermediate filament protein, alpha	4.81	7.00E-04	0
231248_at	CST6: Cystatin E/M	2.63	0.0065	0
229292_at	EPB41L5: erythrocyte membrane protein band 4.1 like 5	2.25	0.0143	0
212339_at	EPB41L1: erythrocyte membrane protein band 4.1 like 1	-2.04	0.0482	2.00E-04
202555_s_at	MYLK: myosin light chain kinase	-2.04	0.0482	2.00E-04
205428_s_at	CALB2: calbindin 2	-2.12	0.0399	2.00E-04
221870_at	EHD2: EH-domain containing 2	-2.13	0.0397	2.00E-04
202668_at	EFNB2: ephrin-B2	-2.19	0.0366	1.00E-04
205347_s_at	TMSB15A: thymosin beta 15a	-2.23	0.0341	1.00E-04
200696_s_at	GSN: gelsolin (amyloidosis, Finnish type)	-2.32	0.0283	1.00E-04
206884_s_at	SCEL: scielin	-2.47	0.0225	1.00E-04
228256_s_at	EPB41L4A: erythrocyte membrane protein band 4.1 like 4A	-2.87	0.0126	0
201976_s_at	MYO10: myosin X	-3.27	0.0076	0
	Microtubule cytoskeleton			
202890_at	MAP7: microtubule-associated protein 7	3.11	0.0029	0
242283_at	DNAH14: dynein, axonemal, heavy chain 14	2.41	0.0098	0
1568678_s_at	FGFR1OP: FGFR1 oncogene partner	1.98	0.0145	1.00E-04
202275_at	G6PD: glucose-6-phosphate dehydrogenase	-2.06	0.0427	2.00E-04
204610_s_at	CCDC85B: coiled-coil domain containing 85B	-2.12	0.0399	2.00E-04
228905_at	PCM1: pericentriolar material 1	-2.16	0.0383	2.00E-04
207526_s_at	IL1RL1: interleukin 1 receptor-like	-2.41	0.0242	1.00E-04
225540_at	MAP2: microtubule-associated protein 2	-3.3	0.0072	0
224772_at	NAV1: neuron navigator 1	-3.83	0.0039	0
	Response to stress/chemical stimulus			
203399_x_at	PSG3: pregnancy specific beta-1-glycoprotein 3	5.2	0	0
206029_at	ANKRD1: ankyrin repeat domain 1 (cardiac muscle)	4.48	6.00E-04	0
219936_s_at	GPR87: G protein coupled receptor 87	3.47	6.00E-04	0
221667_s_at	HSPB8: heat shock 22kDa protein 8	3.01	0.0029	0
209594_x_at	PSG9: pregnancy specific beta-1-glycoprotein 9	2.36	0.0103	0
209738_x_at	PSG6: pregnancy specific beta-1-glycoprotein 6	2.36	0.01	0

204935_at	PTPN2: protein tyroine phosphatase, non-receptor type 2	2.04	0.0367	1.00E-04
209301_at	CA2: carbonic anhydrase II	1.97	0.0324	1.00E-04
206023_at	NMU: neuromedin U	1.94	0.0382	1.00E-04
210187_at	FKBP1A: FK506 binding protein 1A, 12kDa	1.94	0.0381	1.00E-04
204363_at	F3: coagulation factor IIII (thromboplastin, tissue factor)	-2.01	0.0498	2.00E-04
202180_s_at	MVP: major vault protein	-2.39	0.0246	1.00E-04
200632_s_at	NDRG1: N-mycdownstream regulated 1	-2.45	0.0227	1.00E-04
204014_at	DUSP4: dual specificity phosphatase 4	-2.45	0.0223	1.00E-04
204396_s_at	GRK5: G protein-coupled receptor kinase 5	-2.5	0.0217	0
201739_at	SGK1: serum/glucocorticoid regulated kinase 1	-3.09	0.0104	0
205756_s_at	F8: coagulation factor VIII, procoagulant component	-3.1	0.0104	0
213693_s_at	MUC1: mucin1, cell surface associated	-3.23	0.0081	0
202833_s_at	SERPINA1: serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-4.65	0.0014	0
209392_at	ENPP2: ectonucleotide pyrophosphatase/phosphodiesterase 2	-6.39	0	0
	Receptors			
240042_at	FIBCD1: fibrinogen C domain containing 1	3.32	0.0011	0
219789_at	NPR3: natriuretic peptide receptorC/guanylate cyclase C (atrionatriuretic peptide receptor C)	2.36	0.0099	0
203632_s_at	GPRC5B: G protein coupled receptor, family C, group 5, member B	2.26	0.0141	0
205945_at	IL6R: interleukin 6 receptor	2.1	0.0233	0
225661_at	IFNAR1: interferon (alpha, beta and omega) receptor 1	1.94	0.0379	1.00E-04
211924_s_at	PLAUR: plasminogen activator, urokinase receptor	1.87	0.0471	2.00E-04
204916_at	RAMP1: receptor (G protein coupled receptor) activity modifying protein 1	-2.15	0.0398	2.00E-04
1554199_at	PTPRO: protein tyrosine phosphatase, receptor type, O	-2.32	0.0279	1.00E-04
207526_s_at	IL1RL1: interleukin 1 receptor-like 1	-2.4	0.0242	1.00E-04
227449_at	EPHA4: EPH receptor A4	-2.61	0.0192	0
219476_at	C1orf116: chromosome 1 open reading frame 116	-3.5	0.0064	0
228573_at	ANTXR2: anthraxtoxin receptor 2	-5.64	4.00E-04	0
	Protein kinase regulator activity			
231120_x_at	PKIB: protein kinase (cAMP-dependent, catalytic) inhibitor beta	2.25	0.0163	0
226864_at	PKIA: protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-2.18	0.0367	1.00E-04
	Signal transducer activity			
230925_at	APBB1IP: amyloid beta (A4) precursor protein-binding family B, member 1 interacting protein	2.51	0.0079	0
228882_at	TUB: tubby homolog (mouse)	2.06	0.0271	1.00E-04
221029_s_at	WNT5B: wingless-type MMTV integration site family, member 5B	1.9	0.0422	1.00E-04
214247_s_at	DKK3: dickkopf homolog 3 (Xenopus laevis)	-2.04	0.0472	2.00E-04
202286_s_at	TACSTD2: tumor-associated calcium signal transducer 2	-2.08	0.0429	2.00E-04
	GTPase binding activity			
204803_s_at	RRAD: ras-related associated with diabetes	2.2	0.0152	0
231577_s_at	GBP1: guanylate binding protein1, interferon-inducible, 67kDa	2.11	0.0239	0
230075_at	RAB39B: RAB39B, member RAS oncogene family	-2.11	0.0426	2.00E-04
228708_at	RAB27B: RAB27B, member RAS oncogene family	-2.49	0.0223	1.00E-04
217762_s_at	RAB31: RAB31 member RAS oncogene family	-2.8	0.0142	0
	GTPase regulator activity			
233115_at	DEPDC1B: DEP domain containing 1B	2.92	0.0039	0
202388_at	RGS2: regulator of G-protein signaling2, 24kDa	2.68	0.0058	0
222173_s_at	TBC1D2: TBC1 domain family, member 2	-2.36	0.0264	1.00E-04
225496_s_at	SYTL2: synaptotagmin-like 2	-2.36	0.0255	
228171_s_at	PLEKHG4: pleckstrin homology domain containing, family G (with RhoGef domain) member 4	-2.37	0.0248	1.00E-04
226875_at	DOCK11: dedicator of cytokinesis 11	-3.02	0.0116	0
	Endocytosis			
204840_s_at	EEA1: early endosome antigen 1	2.09	0.0238	0
212990_at	SYNJ1: synaptojanin 1	1.99	0.0325	1.00E-04
1558021_at	RABEPK: Rab9 effector protein with kelch motifs	1.89	0.047	2.00E-04

203485_at	RTN1: reticulon 1	-3.51	0.0067	0
	Transporter activity and metabolic process			
238066_at	RBP7: Retinol binding protein 7, cellular	3.88	4.00E-04	0
239913_at	SLC10A4: solute carrier family 10 (sodium/bile acid cotransporter family), member 4	3.13	0.003	0
205097_at	SLC26A2: solute carrier family 26(sulfate transporter), member 2	3.08	0.0028	0
209735_at	ABCG2: ATP-binding cassette, sub-family G (WHITE), member 2	2.77	0.0057	0
218792_s_at	BSPRY: B-box and SPRY domain containing	2.39	0.0103	0
214769_at	CLCN4: chloride channel 4	2.34	0.0106	0
236420_s_at	ANO4: anoctamin 4	2.22	0.0151	0
210286_s_at	SLC4A7: solute carrier family 4, sodium bicarbonate cotransporter, member 7	2.1	0.0269	1.00E-04
206698_at	XK: X-linked Kx blood group (McLeod syndrome)	1.96	0.037	1.00E-04
242690_at	ATP11C: ATPase, classVI, type 11C	-2.02	0.0498	2.00E-04
208161_s_at	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3	-2.05	0.0482	2.00E-04
219529_at	CLIC3: chloride channel 3	-2.09	0.0427	2.00E-04
244455_at	KCNT2: potassium channel, subfamily T, member 2	-2.41	0.0258	1.00E-04
204368_at	SLCO2A1: solute carrier organic anion transporter family, member 2A1	-2.43	0.023	1.00E-04
212136_at	ATP2B4: ATPase, Ca++ transporting, plasma membrane 4	-2.63	0.0193	0
213415_at	CLIC2: chloride intracellular channel 2	-2.75	0	0
203157_s_at	GLS: glutaminase	-2.77	0.0141	0
214255_at	ATP10A: ATPase, classV, type 10A	-3.08	0.0095	0
204646_at	DPYD: dihydropyrimidine dehydrogenase	-3.48	0.0063	0
	Drug metabolism			
202967_at	GSTA4: glutathione S-transferase alpha 4	-2.09	0.0428	2.00E-04
	Lipid metabolic process			
218454_at	PLBD1: phospholipase B domain containing 1	4.4	6.00E-04	0
203180_at	ALDH1A3: aldehyde dehydrogenase 1 family, member A3	2.62	0.0066	0
227180_at	ELOVL7: ELOVL family member 7, elongation of long chain fatty acids (yeast)	2.45	0.0081	0
202982_s_at	ACOT1////ACOT2: acyl-CoA thioesterase 1//// acyl-CoA thioesterase 2	1.98	0.0321	1.00E-04
202481_at	DHRS3: dehydrogenase/reductase (SDR family) member 3	1.92	0.0417	1.00E-04
203423_at	RBP1: retinol binding protein 1, cellular	-2.27	0.0319	1.00E-04
213288_at	MBOAT2: membrane bound)-acyltransferase domain containing 2	-2.75	0.0148	0
212230_at	PPAP2B: phosphatidic acid phosphatase 2B	-2.85	0.0134	0
230076_at	PITPNM3: PITPNM family member 3	-2.97	0.0121	0
218322_s_at	ACSL5: acyl-CoA synthetase long-chain family member 5	-3.15	0.0097	0
209160_at	AKR1C3: aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase tyoe III)	-9.62	0	0
211653_x_at	AKR1C2: aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile caid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	-10.16	0	0
204151_x_at	AKR1C1: aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	-10.18	0	0
	Carbohydrate metabolic process			
219049_at	CSGALNACT1: chondroitin sulfate N-acetylgalactosaminyltransferase 1	2.9	0.004	0
211379_x_at	B3GALNT1: beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	2.41	0.0101	0
219750_at	TMEM144: transmembrane protein 144	2.18	0.0214	0
203397_s_at	GALNT3: UDP-N-acetyl-alpha-Dgalactosamine-polypeptide N-acetylgalactosaminyltransferase 3 (GalNac-T3)	1.97	0.0367	1.00E-04
214755_at	UAP1L1: UDP-N-acteylglucosamine pyrophosphorylatse 1-like 1	1.94	0.0418	1.00E-04
209696_at	FBP1: fructose-1,6-biphosphatase 1	-2.27	0.0311	1.00E-04
230183_at	EXT1: exostoses (multiple) 1	-2.29	0.0306	1.00E-04
205100_at	GFPT2: glutamine-fructose-6-phosphate transaminase 2	-2.43	0.0228	1.00E-04
208116_s_at	MAN1A1: mannosidase, alpha, class 1A, emeber 1	-2.44	0.0233	1.00E-04
226303_at	PGM5: phosphoglutamase 5	-2.46	0.0221	1.00E-04
202242_at	TSPAN7: tetraspanin 7	-3.15	0.0099	0
	Proteolysis			
216905_s_at	ST14: suppression of tumorigenicity 14 (colon carcinoma)	3.55	7.00E-04	0
201295_s_at	WSB1: WD repeat and SOCS box-containing 1	2.36	0.0146	0
206239_s_at	SPINK1: serine peptidase inhibitor, Kazal type 1	2.34	0.0134	0

202342_s_at	TRIM2: tripartite motif-containing 2	2.22	0.0176	0
238803_at	HECTD2: HECT domain containing 2	2.06	0.0252	1.00E-04
229441_at	PRSS23: Protease, serine, 23	-2.32	0.0282	1.00E-04
204475_at	MMP1: matrix metallopeptidase 1 (intersticial collagenase)	-7.85	0	0
	Chromatin organization			
205659_at	HDAC9: histone deacetylase	2.46	0.0087	0
208025_s_at	HMGA2: high mobility group AT-hook 2	1.87	0.0472	2.00E-04
205832_at	CPA4: carboxypeptidase A4	-2.03	0.0481	2.00E-04
202708_s_at	HIST2H2BE: histone cluster 2, H2be	-2.05	0.0474	2.00E-04
	Transcription regulation			
226847_at	FST: follistatin	3.38	0.0024	0
1552946_at	ZNF114: zinc finger protein 114	3.29	0.0022	0
206683_at	ZNF165: zinc finger protein 165	2.79	0.004	0
235795_at	PAX6: paired box6	2.47	0.0088	0
236471_at	NFE2L3: nuclear factor (erythroid-derived 2)-like 3	2.35	0.0105	0
235121_at	ZNF542: zinc finger protein 542	2.32	0.0134	0
228698_at	SOX7: SRY (sex determining regionY)-box7	2.31	0.016	0
1554894_a_at	PCBD2: pterin-4-alpha-carbinolamine dehydratase	2.04	0.0309	1.00E-04
242919_at	ZNF253: zinc finger protein 253	2.02	0.0321	1.00E-04
206653_at	POLR3G: polymerase (RNA) III (DNA directed) plypeptide G (32KD)	2	0.0309	1.00E-04
231800_s_at	DMRT3: doublesex and mab-3 related transcription factor	1.97	0.0402	1.00E-04
220549_at	RAD54B: RAD54 homolg B (S.cerevisiae)	1.94	0.0385	1.00E-04
206140_at	LHX2: LIM homeobox2	1.93	0.0417	1.00E-04
219459_at	POLR3B: polymerase (RNA) III (DNA directed) polypepetide B	1.91	0.0415	1.00E-04
216305_s_at	C2orf3: chromosome 2 open reading frame 3	1.91	0.0418	1.00E-04
1552634_a_at	ZNF101: zinc finger protein 101	1.88	0.047	2.00E-04
201823_s_at	RNF14: ring finger protein 14	1.87	0.0473	2.00E-04
228483_s_at	TAF9B: TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31 kDa	-2.03	0.0499	2.00E-04
212124_at	ZMIZ1: zinc finger, MIZ-type containing 1	-2.08	0.0428	2.00E-04
203543_s_at	KLF9: Kruppel-like factor9	-2.13	0.0395	2.00E-04
219778_at	ZFPM2: zinc finger protein, multitype 2	-2.24	0.0332	1.00E-04
212614_at	ARID5B: AT rich interactive domain 5B (MRF1-like)	-2.25	0.0317	1.00E-04
213006_at	CEBPD: CCAAT/enhancer binding protein (C/EBP), delta	-2.33	0.0276	1.00E-04
205249_at	EGR2: early growth response 2	-2.4	0.0248	1.00E-04
209212_s_at	KLF5: Kruppel-like factor 5	-2.45	0.0233	1.00E-04
209189_at	FOS: FBJ murine osteosarcoma viral omcogene homolog	-2.59	0.0193	0
215111_s_at	TSC22D1: TSC22 domain family, member 1	-2.79	0.0145	0
223282_at	TSHZ1: teashirt zinc finger homeobox 1	-2.97	0.0121	0
212148_at	PBX1: pre-B-cell leukemia homeobox1	-4.28	0.0023	0
226420_at	MECOM: MDS1 and EVI1 complex locus	-3.63	0,0053	0
	Transcription coactivator activity			
236471_at	NFE2L3: nuclear factor (erythroid-derived 2)-like 3	2.35	0.0105	0
209505_at	NR2F1: Nuclear receptor subfamily2, group F, member 1	1.93	0.039	1.00E-04
	RNA (nucleotide) binding/processing			
225846_at	ESRP1: epithelial splicing regulatory protein 1	5.49	7.00E-04	0
203820_s_at	IGF2BP3: insulin-like growth factor 2 mRNA binding protein 3	3.4	0.0012	0
1566403_at	SNRPN: small nuclear ribonucleoprotein polypeptide N	2.28	0.0129	0
224828_at	CPEB4: cytoplasmic polyadenylation element protein 4	2.14	0.021	0
205228_at	RBMS2: RNA binding matif, single stranded interacting protein 2	2.09	0.0223	0
210117_at	SPAG1: sperm associated antigen 1	2.06	0.0271	1.00E-04
210802_s_at	DIMT1L: DIM1 dimethyladenosine transferase 1-like (S.cerevisiae)	1.96	0.0353	1.00E-04
225107_at	HNRNPA2B1: heterogeneous nuclear ribonucleoprotein A2/B1	1.92	0.0473	2.00E-04
241599_at	LSM11: LSM11, U7 small nuclear RNA-associated	1.89	0.0467	2.00E-04
205115_s_at	RBM19: RNA-binding motif protein 19	1.88	0.047	2.00E-04
238447_at	RBMS3: RNA binding motif, single stranded interacting protein	-2.47	0.0227	1.00E-04
	Metal ion binding			
233819_s_at	RNF160: ring finger protein 160	2.11	0.0228	0

204525_at	PHF14: PHD finger protein 14	2.08	0.0272	1.00E-04
1553938_a_at	STK32A: serine/threonin kinase 32A	2	0.0321	1.00E-04
220144_s_at	ANKRD5: ankyrin repeat domain 5	1.93	0.0383	1.00E-04
217546_at	MT1M: metallothionein 1M	1.92	0.042	1.00E-04
233167_at	RP3.402G11.5: selenoprotein O	-2.05	0.0491	2.00E-04
238440_at	CLYBL: citrate lyase beta like	-2.22	0.034	1.00E-04
236884_at	RIMKLA: ribosomal modification protein rimk-like family member A	-3.1	0.0097	0
228855_at	NUDT7: nudix (nucleotside diphosphate linked moiety X)-type-motif 7	-3.25	0.0082	0
213069_at	HEG1: HEG homolog 1 (zebrafish)	-2.68	0.0177	0
	Unknown function			
242162_at	WDR69: WD repeat domain 69	5.71	7.00E-04	0
220057_at	XAGE1A////XAGE1B////XAGE1C////XAGE1D////XAGE1E: X antigen family, member 1A//// X antigen family, member 1B//// X antigen family, member 1C//// X antigen family, member 1D//// X antigen family, member 1E	3	0.0037	0
236917_at	LRRC34: leucine rich repeat containing 34	2.74	0.0055	0
220169_at	TMEM156: transmembrane protein 156	2.6	0.0067	0
216870_x_at	DLEU2: deleted in lymphocytic leukemia 2 (non-protein coding)	2.58	0.0087	0
239148_at	MARVELD3: MARVEL domain containing 3	2.51	0.0102	0
1554333_at	DNAJA4: DnaJ (Hsp40) homolog, subfamily A, member 4	2.47	0.0085	0
235148_at	KRTCAP3: keratinocyte associated protein 3	2.3	0.0136	0
238784_at	DPY19L2: dpy-19-like 2 (C.elegans)	2.27	0.0136	0
229759_s_at	VEPH1: ventricular zone expressed PH domain homolog 1 (zebrafish)	2.25	0.0134	0
1557636_a_at	C7orf57: chromosome 7 open reading frame 57	2.23	0.0144	0
243750_x_at	C21orf70: chromosome 21 open reading frame	2.23	0.0148	0
203595_s_at	IFIT5: interferon-induced proetin with tetratricopeptide repeats 5	2.19	0.0155	0
223241_at	SNX8: sorting nexin 8	2.17	0.017	0
1569433_at	SAMD5: sterile alpha motif domain containing 5	2.16	0.0179	0
229865_at	FNDC3B: fibronectin type III domain containing 3B	2.1	0.0228	0
218374_s_at	C12orf4; chromosome 12 open reading frame 4	2.08	0.0239	0
226490_at	NHSL1: NHS-like 1	1.99	0.0324	1.00E-04
1566403_at	SNORA68: small nuclear RNA, H/ACA box 68	1.97	0.0412	1.00E-04
226809_at	LOC100216479: hypothetical LOC100216479	1.91	0.0416	1.00E-04
208092_s_at	FAM49A: family with sequence similarity 49, member A	1.9	0.0444	2.00E-04
213285_at	TMEM30B: transmembrane protein 30B	1.9	0.0425	1.00E-04
203023_at	NOP16: NOP16 nucleolar protein homolog (yeast)	1.9	0.0418	1.00E-04
228378_at	C12orf29: chromosome 12 open reading frame 29	1.89	0.0442	1.00E-04
228875_at	FAM162B: family with sequence similarity 162, member B	1.88	0.047	2.00E-04
223059_s_at	FAM107B: family with sequence similarity 107, member B	1.86	0.0497	2.00E-04
1569283_at	hCG_1646157: hGC1646157	1.95	0.0367	1.00E-04
1559060_a_at	FNIP1: Folliculin interactin protein 1	1.89	0.047	2.00E-04
220060_s_at	C12orf48: chromosome 12 open reading frame 48	1.89	0.0449	2.00E-04
226349_at	C12orf45: chromosome 12 open reading frame 45	1.88	0.0471	2.00E-04
203830_at	C17orf75: chromosome 17 open reading frame 75	1.87	0.468	2.00E-04
233504_at	C9orf84: chromosome 9 open reading frame 84	-2.04	0.0487	2.00E-04
228979_at	SFTA3: surfactant associated 3	-2.05	0.0474	2.00E-04
236044_at	PPAPDC1A: phosphatidic acid phosphate type 2 domain containing !A	-2.1	0.042	2.00E-04
227019_at	C1orf226: chromosome open reading frame 226	-2.12	0.0393	2..00E-4
218711_s_at	SDPR: serum deprivation response (phosphatidylserine binding protein)	-2.13	0.0391	2.00E-04
228160_at	LOC339290: hypothetical LOC339290	-2.14	0.0383	1.00E-04
231175_at	BEND6: BEN containing 6	-2.18	0.0365	1.00E-04
226382_at	CAMK1D////LOC283070: calcium/calmodulin-dependent protein kinase ID	-2.26	0.0318	1.00E-04
224990_at	C4orf34: chromosome 4 open reading frame 34	-2.32	0.0281	1.00E-04
226614_s_at	FAM167A: family with sequence similarity 167, member A	-2.45	0.0224	1.00E-04
223503_at	TMEM163: transmembrane protein 163	-2.47	0.0224	1.00E-04
209183_s_at	C10orf10: chromosome 10 open reading frame 10	-2.53	0.0208	0
52837_at	KiAA1644	-2.88	0.0127	0
228325_at	KAA0146	-3.12	0.0102	0
209755_at	NMNAT2: nicotinamide nucleotide adenylyltransferase 2	-3.21	0.0081	0
238460_at	FAM83A: family with sequence similarity 83, member A	-3.33	0.007	0
203571_s_at	C10orf116: chromosome 10 open reading frame 116	-3.59	0.0057	0
230323_s_at	TMEM45B: transmembrane protein 45B	-4.09	0.0023	0

226811_at	FAM46C: family with sequence similarity 46, member C	-4.25	0.0024	0
212942_s_at	KIAA1199	-4.99	6.00E-04	0
243871_at	LOC100130476: Similar to hCG2036711	-5.68	4.00E-04	0