disease state	age	stage	grade
Prostate hyperplasia	73		
Urolithiasis	76		
normal	40		
Prostate hyperplasia	61		
Prostate hyperplasia	78		
Neurogenic bladder	72		
Prostate hyperplasia	68		
Urolithiasis	63		
normal	40		
Neurogenic bladder	76		
Prostate hyperplasia	69		
normal	24		
Prostate hyperplasia	65		
normal	24		
normal	37		
Urolithiasis	48		
normal	28		
Urolithiasis	23		
Neurogenic bladder	69		
normal	28		
normal	25		
Neurogenic bladder	78		
Normal	50		
normal	36		
normal	34		
Urolithiasis	85		
Neurogenic bladder	54		
Normal	53		
Prostate hyperplasia	55		
Prostate hyperplasia	76		
Infection	19		
Normal	64		
Normal	62		
Infection	62		
Neurogenic bladder	83		
normal lab	35		
Urolithiasis	76		
normal lab	40		
Urolithiasis	80		
Prostate hyperplasia	72		
Normal	70		
Urolithiasis	63		
TCC	82	-	-
TCC	69	2	3
TCC	52	a	1-2
Ureteral ca	77	3a	2~3
TCC	67	a	3
TCC	57	a	3
TCC	64	1	1
TCC	87	a	2
TCC	77	a	3
TCC	37	a	2
TCC	73	0	0
TCC	72	2	3

Fig. 1

disease state	age	stage	grade
TCC	76	a	2
TCC	74	a	3
TCC	38	a	2
TCC	86	a	2
TCC	77	a	3
TCC	78	1	3
TCC	72	-	-
TCC	72	1	2
TCC	71	a	2
TCC	64	1	1
TCC	81	a	1
TCC	67	a	2
TCC	75	a	2
TCC	76	a	2
TCC	70	a	3
TCC	78	is	3
TCC	76	2a	3
TCC	76	?ureteral	2=3
TCC	68	2	3
TCC	78	0	0
TCC	78	1	3
TCC	70	a	2>3
TCC	77	1	3>2
TCC	83	a	2
TCC	83	a	1

Fig. 1 (continued)

Name	Symbol	Forward Primer	Seq ID #	Reverse Primer	Seq ID #	Probe	Seq ID #
insulin-like growth factor binding protein 5	IGFBP5	AATTGTGACCGCAAAGGAT TCT	1	CAGCAGATGCCACGCTTG	2	AAGAGAAAGCAGTGCAAA CCTTCCCGT	3
homeo box A13	HOXA13	Taqman(R) Gene Expression Assay Hs00426284_m1					
midkine (neurite growth-promoting factor 2)	MDK	Taqman(R) Gene Expression Assay Hs00171064_m1					
Leukotriene B4 12-dehydrogenase	LTB4DH	TATAACAGAACCGGCCCA CTTC	4	CCCATTTCAGCAAGTCCTT CA	5	CCAGGCCCACCCCCAGAG ATTG	6
cell division cycle 2, G1 to S and G2 to M	[redacted]		7	TGT CTA CCC TTA TAC ACA ACT CCA TAG G	8	AGC CGG GAT CTA CCA TAC CCA TTG ACT AAC T	9
Topoisomerase (DNA) II alpha	TOP2A	CCG CCC AGA CAC CTA CAT TG	10	TGT ACA AAC CAG GAA CAA AAG TGA CT	11	TTC TGT GGA ATT AGT GAC CCA GCA AAT GTG	12
BCL2-associated athanogene	BAG1	Taqman(R) Gene Expression Assay Hs00185390_m1					
hypothetical protein FLJ21511	FLJ21511	Taqman(R) Gene Expression Assay Hs00228221_m1					

Fig. 2

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
ras homolog gene family, member B (RHOB), mRNA	NP_004031.1	NM_004040.2	mwghuman30K#A:08114	-2.684592	2.13794E-10	2.25758E-09	-10.53678	38	8789.5	4176	23
hypothetical protein FLJ21511 (FLJ21511), mRNA	NP_079363.1	NM_025087.1	mwghuman30K#A:00410	-2.080908	2.54894E-11	3.22908E-08	-6.925773	68	14455	9272.5	0
paired box gene 8 (PAX8), transcript variant PAX8A, mRNA	NP_003457.1	NM_003466.3	mwghuman30K#B:3648	-1.961896	4.71674E-11	4.07014E-08	-6.806281	82	19419	12999.5	0
UPF3 regulator of nonsense transcripts homolog A (yeast) (UPF3A), transcript variant 1, mRNA	NP_075387.1	NM_023011.2	mwghuman30K#A:06295	-3.84007	1.03703E-13	3.34027E-08	-7.811653	96.5	5663.5	1825	0
leukotriene B4 12-hydroxydehydrogenase (LTB4DH), mRNA	NP_036344.1	NM_012212.2	mwghuman30K#B:8686	-5.034613	3.08873E-10	1.41836E-07	-6.436167	122.5	11340.5	3138	0

Fig. 3

Gene name/ symbol	protein accession	mRNA ref seq accession.	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
RAB11 family interacting protein 2 (class I) (RAB11FIP2), mRNA	NP_055719.1	NM_014904.1	mwghuman30K#A:10479	-1.993629	4.57925E-09	5.83951E-08	-7.711624	156	19636.5	12951	0
TSC22 domain family, member 1 (TSC22D1), transcript variant 2, mRNA	NP_006013.1	NM_006022.2	mwghuman30K#A:00577	-2.133065	1.12033E-07	1.8543E-07	-7.698568	156.5	8415	6130	1
sulfite oxidase (SUOX), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	NP_000447.2	NM_000456.2	mwghuman30K#A:05512	-1.622803	4.52404E-10	5.29156E-09	-6.728892	223	11312.5	8789.5	0
tetratricopeptide repeat domain 21A (TTC21A), mRNA	NP_665698.1	NM_145755.1	mwghuman30K#B:6976	-2.976809	2.11314E-07	4.28806E-07	-6.286432	225	8375.5	3870.5	1

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 2, mRNA	NP_072179.1	NM_022650.1	mwghuman30K#A:08292	-1.947454	3.74564E-09	2.68048E-06	-5.99299	235	6895.5	5277.5	7
ensembl genscan prediction		AC024384.3.107975.119435.1	mwghuman30K#C:6641	-2.471322	4.47058E-08	1.54585E-06	-6.085076	255.5	3327.5	1537	
ensembl genscan prediction		AL031669.28.1.94224.1	mwghuman30K#C:0930	-1.774123	6.77812E-09	1.13272E-06	-5.56116	288.5	4367	3218	
geminin, DNA replication inhibitor (GMNN), mRNA	NP_056979.1	NM_015895.3	mwghuman30K#A:03435	-2.046753	1.94846E-07	4.07898E-06	-5.99032	311	11844	8413.75	2
fatty acid binding protein 1, liver (FABP1), mRNA	NP_001434.1	NM_001443.1	mwghuman30K#A:09506	-1.985247	2.20148E-06	6.83453E-07	-6.750782	312.5	25595	19500.75	0
v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), mRNA	NP_002219.1	NM_002228.3	mwghuman30K#A:04848	-3.222311	6.2171E-07	4.59274E-06	-6.383849	318.5	12139	5321.5	11

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
transmembrane and coiled-coil domains 4 (TMCO4), mRNA	NP_859070.2	NM_181719.2	mwghuman30K#B:3094	-1.799143	8.41415E-09	3.21175E-06	-5.702577	322.5	4584.5	3158	5
ensembl genscan prediction		AP002080.2.37398.74587.1	mwghuman30K#C:4035	-1.860121	5.75299E-08	1.01121E-07	-7.300326	332.5	4972.5	2643	
synaptotagmin-like 2 (SYTL2), transcript variant b, mRNA	NP_115755.2	NM_032379.3	mwghuman30K#B:9411	-2.343357	4.07526E-10	9.87494E-09	-7.993821	342	19920	12053.5	0
cyclin G1 (CCNG1), transcript variant 1, mRNA	NP_004051.1	NM_004060.3	mwghuman30K#B:5261	-1.83737	2.79204E-08	4.64998E-07	-6.214776	365	9269.5	4453	7
F-box protein 34 (FBXO34), mRNA	NP_060413.2	NM_017943.2	mwghuman30K#B:4885	-1.801846	1.15594E-06	1.13272E-06	-7.165506	365.5	17957.5	13192.75	5
hypothetical protein xp_097916 loc150582		XM_097916	mwghuman30K#B:6228	-2.291304	2.69775E-08	3.84322E-06	-5.299383	375	3591	1276	
RNA pseudouridylate synthase domain containing 4 (RPUSD4), mRNA	NP_116184.1	NM_032795.1	mwghuman30K#B:6888	-1.588438	2.0145E-10	1.14227E-08	-8.404434	407	15747.5	11247	5

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
WD repeat domain 33 (WDR33), transcript variant 2, mRNA	NP_001006623.1	NM_001006622.1	mwghuman30K#A:08115	-1.765322	1.47232E-07	1.45307E-06	-6.190057	413	14876	13787.5	8
FLJ20859 gene (FLJ20859), transcript variant 1, mRNA	NP_001025162.1	NM_001029991.1	mwghuman30K#A:10470	-1.708985	8.133E-08	1.13272E-06	-6.182853	420.5	3781	2693.75	
activating transcription factor 3 (ATF3), transcript variant 2, mRNA	NP_004015.3	NM_004024.3	mwghuman30K#A:00568	-3.134291	8.40437E-06	1.51698E-07	-7.446028	421	13832.5	5301.25	3
cytochrome P450, family 3, subfamily A, polypeptide 5 (CYP3A5), mRNA	NP_000768.1	NM_000777.2	mwghuman30K#A:04559	-2.482162	7.0225E-08	1.9772E-06	-4.813425	451.5	20350.5	12190.5	2
ensembl genscan prediction		AL161725.13.1.181179.3	mwghuman30K#C:3443	-1.955495	1.19555E-09	9.24336E-06	-5.681512	455	2738.5	1799	
KIT ligand (KITLG), transcript variant b, mRNA	NP_000890.1	NM_000899.3	mwghuman30K#A:07355	-4.28251	3.8867E-06	7.23184E-07	-5.884133	470	19497	10599.75	2

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA	NP_000565.1	NM_000574.2	mwghuman30K#A:06760	-2.146033	1.44112E-06	6.53282E-06	-5.668164	471.5	9806.5	4753.25	10
solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23 (SLC25A23), mRNA	NP_077008.2	NM_024103.2	mwghuman30K#A:05530	-1.465915	7.79426E-09	8.80903E-07	-5.741772	497	16285.5	12418.75	4
wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, mRNA	NP_004176.2	NM_004185.2	mwghuman30K#A:05696	-10.745275	2.92382E-12	3.19726E-07	-6.175471	501	10716	2016.25	0
protocadherin gamma subfamily A, 12 (PCDHGA12), transcript variant 1, mRNA	NP_003726.1	NM_003735.2	mwghuman30K#A:03393	-2.070447	2.89557E-07	6.92439E-06	-4.982742	511	2537	1931.5	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
ensembl genscan prediction		AC010828.3.125573.158193.2	mwghuman30K#C:4737	-1.679465	2.34945E-07	6.18322E-07	-5.341693	511	26962	25287.75	
olfactory receptor, family 1, subfamily D, member 5 (OR1D5), mRNA	NP_055381.1	NM_014566.1	mwghuman30K#A:08766	-1.640751	5.38884E-08	4.32856E-06	-5.134756	539.5	1644	1134	0
G protein-coupled receptor 126 (GPR126), transcript variant b1, mRNA	NP_940971.1	NM_198569.1	mwghuman30K#B:2989	-2.181735	3.9002E-07	1.05021E-05	-5.047901	549	15965.5	8040.75	0
similar to ba408e5.4 novel protein dmpk-like cdc42-binding kinase beta cdc42bpb loc144850		XM_090553	mwghuman30K#B:9158	-4.265957	2.3863E-08	5.29006E-07	-6.259229	573	1784	632	
ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila) (USP9Y), mRNA	NP_004645.2	NM_004654.3	mwghuman30K#A:10655	-1.584065	3.40815E-07	8.23838E-06	-5.287284	587	10035.5	7858.25	1

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
ensembl genscan prediction		AC022554.2.11725.14597.1	mwghuman30K#C:7523	-2.800527	1.74508E-07	6.41199E-07	-5.902891	597	3330	1296	
solute carrier family 35 (CMP-sialic acid transporter), member A1 (SLC35A1), mRNA	NP_006407.1	NM_006416.2	mwghuman30K#B:6203	-1.879113	1.20877E-06	5.48118E-06	-5.297694	606	20639	15436.75	1
cell line sc30 t receptor alpha chain v-j junctional region tcr v 29.1 j 11 coding sequence reported spans from nucleotide position		U14083	mwghuman30K#B:9790	-2.442854	9.94216E-08	1.14277E-08	-7.365379	617	6673	2661.5	
chromosome 2 open reading frame 33 (C2orf33), mRNA	NP_064579.3	NM_020194.4	mwghuman30K#A:06988	-1.615311	3.24982E-07	9.24336E-06	-5.392632	624	11555.5	8868.25	4
ensembl genscan prediction		AC073108.7.114033.192530.1	mwghuman30K#C:4991	-2.137812	1.453E-05	1.06394E-06	-6.345675	650.5	9963.5	5676.75	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA	NP_059119.1	NM_017423.1	mwghuman30K#A:01420	-1.401046	7.53042E-08	1.13272E-06	-6.143981	656.5	10573	8997.75	2
chromosome 11 open reading frame 1 (C11orf1), mRNA	NP_073598.1	NM_022761.1	mwghuman30K#A:01834	-1.81726	1.38032E-06	1.22937E-05	-5.104229	673.5	12025.5	9585.25	0
heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), transcript variant 1, mRNA	NP_062543.1	NM_019597.3	mwghuman30K#A:08547	-2.03901	2.40065E-06	6.16248E-06	-5.465662	684	777	472	9
Werner syndrome (WRN), mRNA	NP_000544.1	NM_000553.2	mwghuman30K#A:03163	-1.605462	7.49706E-08	6.16248E-06	-4.681771	696	4585	4351.25	3
ensembl genscan prediction		AC040160.3.61245.138821.5	mwghuman30K#C:7317	-4.953847	7.54477E-12	1.43666E-08	-6.602968	706.5	4523.5	744.5	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
adducin 3 (gamma) (ADD3), transcript variant 1, mRNA	NP_058432.1	NM_016824.3	mwghuman30K#B:5211	-2.092475	1.34331E-05	1.16156E-05	-5.883251	716	7668.5	4808.75	8
hydroxysteroid dehydrogenase like 2 (HSDL2), mRNA	NP_115679.2	NM_032303.2	mwghuman30K#B:3888	-2.1317	9.39999E-07	5.81228E-06	-5.58267	732.5	7276.5	5055	2
DNA-damage-inducible transcript 4 (DDIT4), mRNA	NP_061931.1	NM_019058.2	mwghuman30K#B:2115	-2.660775	6.68834E-05	5.16818E-06	-5.969252	750	10960.5	5062.75	12
RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse)) (RALY), transcript variant 1, mRNA	NP_057951.1	NM_016732.1	mwghuman30K#A:06376	-1.901576	1.7076E-07	4.32856E-06	-4.392163	750.5	977	386.5	26

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
acyl-CoA synthetase medium-chain family member 3 (ACSM3), transcript variant 1, mRNA	NP_005613.2	NM_005622.3	mwghuman30K#B:9076	-1.967123	1.7751E-05	7.33836E-06	-5.050721	765.5	18906.5	12252.25	3
BCL2-associated athanogene (BAG1), mRNA	NP_004314.3	NM_004323.3	mwghuman30K#A:09581	-2.525417	2.13163E-08	5.29006E-07	-5.934904	776	9031	4503.5	1
neural precursor cell expressed, developmentally down-regulated 4 (NEDD4), transcript variant 1, mRNA	NP_006145.1	NM_006154.1	mwghuman30K#B:7862	-1.900818	3.7763E-06	8.23334E-06	-5.249282	781	15497	12075	2
chromosome 7 open reading frame 19 (C7orf19), mRNA	NP_116220.1	NM_032831.1	mwghuman30K#B:2324	-1.780735	4.63759E-06	0.000016624	-5.43532	783	11586.5	6704.75	16
calpain 13 (CAPN13), mRNA	NP_653176.2	NM_144575.2	mwghuman30K#B:6754	-1.542431	4.41704E-06	5.81228E-06	-4.843249	808.5	23318	19953.5	0
homeo box B2 (HOXB2), mRNA	NP_002136.1	NM_002145.2	mwghuman30K#A:01639	-2.702649	2.94498E-11	5.08294E-08	-6.774876	814.5	11537.5	6408	3

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
coiled-coil domain containing 28A (CCDC28A), mRNA	NP_056254.1	NM_015439.2	mwghuman30K#B:3128	-1.960606	1.97345E-06	5.48118E-06	-5.330597	826	19022	14223.75	4
myofibrillogenesis regulator 1 (MR-1), transcript variant 1, mRNA	NP_056303.2	NM_015488.3	mwghuman30K#B:3179	-1.526799	1.22924E-05	6.92439E-06	-5.874478	832	13007	10755.75	6
guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA	NP_006089.1	NM_006098.4	mwghuman30K#C:0841	-1.789085	2.16356E-06	4.35419E-05	-4.900058	844.5	1710	1178	106
spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant beta, mRNA	NP_056108.1	NM_015293.1	mwghuman30K#B:9104	-1.414534	7.52733E-07	3.02433E-06	-5.983107	851	20159.5	17233.75	64
ensembl genscan prediction		AL021155.1.1.107603.5	mwghuman30K#C:7334	-1.766409	2.12121E-06	2.01355E-05	-4.468876	853	1264	847.5	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
bone morphogenetic protein receptor, type IA (BMPR1A), mRNA	NP_004320.2	NM_004329.2	mwghuman30K#A:02484	-1.558632	2.22237E-07	1.22937E-05	-4.618211	874.5	5116	5037.5	4
IQ motif containing B1 (IQCB1), transcript variant 1, mRNA	NP_001018864.1	NM_001023570.1	mwghuman30K#B:4020	-1.646698	2.79495E-05	1.62908E-05	-5.169855	882.5	10922	8773.5	2
ensembl genscan prediction		AC069502.9.1.18380.1	mwghuman30K#C:3663	-1.464573	6.94397E-07	2.53657E-05	-4.951029	901	21078	19035	
similar to death-associated protein (LOC92196), mRNA	NP_001017920.1	NM_001017920.1	mwghuman30K#B:6718	-2.553467	5.76345E-07	7.76152E-07	-5.221107	907	23255	15868	0
ensembl genscan prediction		AC012203.4.105191.123571.1	mwghuman30K#C:4578	-1.438718	3.21936E-05	4.85862E-07	-5.989899	907	27071.5	25867.5	
ensembl genscan prediction mwg oligo matches these RefSeq numbers NM_000986		AL158153.8.45139.113162.3	mwghuman30K#C:2173	-2.089238	4.80586E-07	4.32856E-06	-5.395407	909.5	1290	1010.25	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA	NP_001915.1	NM_001924.2	mwghuman30K#A:04346	-1.68216	7.53906E-06	2.67916E-05	-4.924921	916.5	11634.5	8596.75	3
stress 70 protein chaperone, microsome-associated, 60kDa (STCH), mRNA	NP_008879.3	NM_006948.4	mwghuman30K#A:05064	-1.761334	4.58163E-05	1.72268E-05	-5.784774	916.5	10794	6231.25	5
ensembl genscan prediction		Z84474.1.1.107526.2	mwghuman30K#C:0911	-1.884499	1.62444E-08	2.23413E-06	-5.434325	933.5	1974	1488.5	
family with sequence similarity 44, member B (FAM44B), mRNA	NP_612378.1	NM_138369.1	mwghuman30K#B:4192	-1.357114	7.91633E-07	1.64431E-06	-6.047548	942.5	15308.5	13004.75	1
ensembl genscan prediction		AC078789.15.1.55074.2	mwghuman30K#C:6283	-1.786484	1.80836E-06	3.70831E-05	-4.861731	948	25553.5	22990.75	
citrate lyase beta like (CLYBL), transcript variant 1, mRNA	NP_612124.3	NM_138280.3	mwghuman30K#B:8855	-1.444822	1.17336E-06	5.16818E-06	-5.775319	953	21231	19330.25	1

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
ensembl genscan prediction		AP001015.3.66054.115655.1	mwghuman30K#C:3998	-1.709242	1.48259E-07	7.36585E-05	-4.504002	972.5	3374.5	2739.5	
ensembl genscan prediction		AL159169.14.1.86155.2	mwghuman30K#C:4465	-1.474035	8.96434E-07	3.25437E-06	-5.020854	998.5	28575	28030	
chromosome 6 open reading frame 130 (C6orf130), mRNA	NP_659500.1	NM_145063.2	mwghuman30K#B:4652	-1.674296	1.77778E-05	3.32944E-05	-4.846371	1011.5	14804	10754.75	3
methyltransferase like 1 (METTL1), transcript variant 1, mRNA	NP_005362.1	NM_005371.3	mwghuman30K#A:00607	-1.464425	1.73108E-07	5.48118E-06	-5.447819	1026	943	645.5	2
nucleosome assembly protein 1-like 4 (NAP1L4), mRNA	NP_005960.1	NM_005969.3	mwghuman30K#A:00706	-1.902267	1.44614E-05	6.99321E-05	-4.962357	1042.5	10336.5	8978.5	12
tumor protein D52 (TPD52), transcript variant 3, mRNA	NP_005070.1	NM_005079.2	mwghuman30K#A:05633	-1.55805	1.79544E-06	3.15409E-05	-4.599069	1070	19033	14646.75	4
EH-domain containing 4 (EHD4), mRNA	NP_644670.1	NM_139265.2	mwghuman30K#B:5911	-1.64935	1.97896E-05	3.70831E-05	-4.903865	1077	12134	9187.5	4

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
fibroblast growth factor receptor 4 (FGFR4), transcript variant 2, mRNA	NP_075252.2	NM_022963.2	mwghuman30K#B:8174	-2.638426	2.02402E-06	3.21175E-06	-6.251766	1087.5	17096	9762.5	0
KIAA0674 (KIAA0674), mRNA	XP_376903.2	XM_376903.2	mwghuman30K#B:0240	-1.362276	3.68739E-06	3.62055E-06	-5.432041	1092.5	10744	9097.25	4
chromosome 16 bac clone cit987sk-a-363e6		U91321	mwghuman30K#B:5375	-1.568388	5.91844E-05	6.53282E-06	-6.349455	1114.5	10576.5	6083.25	
ensembl genscan prediction		AC073610.11.63494.102478.3	mwghuman30K#C:1337	-1.828108	1.68631E-06	1.30096E-05	-5.253574	1114.5	1434.5	737	
androgen receptor (AR), transcript variant 1, mRNA	NP_000035.2	NM_000044.2	mwghuman30K#A:01003	-1.575215	1.18973E-07	1.54035E-05	-4.291628	1120.5	18067.5	15252.5	0
thyroid transcription factor 1 (TITF1), mRNA	NP_003308.1	NM_003317.3	mwghuman30K#A:07197	-1.466987	8.57665E-07	1.54585E-06	-6.023277	1124.5	2139	1026.25	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant longest, mRNA	NP_892006.1	NM_182961.1	mwghuman30K#C:2340	-1.440164	6.37872E-05	2.15085E-05	-5.805222	1124.5	26092.5	21681.5	64
ensembl genscan prediction		AC019084.7.93515.134992.2	mwghuman30K#C:5482	-1.55364	1.48892E-06	7.77593E-06	-5.043927	1126.5	8785.5	8789.5	
ensembl genscan prediction		AC026235.12.9210.157122.4	mwghuman30K#C:3969	-1.693854	8.74991E-08	0.000122803	-4.393663	1136.5	804	493.5	
ensembl genscan prediction		AP002840.1.99623.121675.1	mwghuman30K#C:5950	-1.784079	2.96992E-05	7.75722E-05	-4.69759	1156	16693.5	14033.25	
CDC-like kinase 1 (CLK1), transcript variant 1, mRNA	NP_004062.2	NM_004071.2	mwghuman30K#A:07840	-2.034707	6.15281E-05	6.99321E-05	-5.146308	1157.5	12199	7934.75	4
lipin 1 (LPIN1), mRNA	NP_663731.1	NM_145693.1	mwghuman30K#B:8172	-1.851742	1.40757E-07	2.98753E-05	-4.301729	1159.5	3757	2609	2
lamin A/C (LMNA), transcript variant 2, mRNA	NP_005563.1	NM_005572.2	mwghuman30K#A:08943	-1.724223	9.63727E-05	5.67358E-05	-5.305029	1162.5	4447	3295	10
ensembl genscan prediction		AC079456.15.119608.151490.1	mwghuman30K#C:3309	-1.39662	6.38081E-06	4.32856E-06	-6.439308	1169.5	26755.5	26493.5	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
similar to riken cdna 1500002b03 clone mgc:12928 image:4298414		BC007768	mwghuman30K#B:4242	-1.518362	5.21322E-06	3.51403E-05	-4.463332	1171	21159	20375	
ensembl genscan prediction		AC027086.2.23033.31927.1	mwghuman30K#C:6982	-1.659003	1.16113E-11	3.82785E-07	-6.295271	1172.5	2757	2062.75	
hyaluronoglucosaminidase 3 (HYAL3), mRNA	NP_003540.2	NM_003549.2	mwghuman30K#A:09529	-2.01277	6.70905E-08	1.16156E-05	-4.684969	1175	4326	3464.5	4
ensembl genscan prediction		AC083822.10.126464.129122.1	mwghuman30K#C:9101	-1.479602	6.01319E-06	2.53657E-05	-4.526959	1177	22091.5	20578.5	
VprBP protein (VprBP), mRNA	NP_055518.1	NM_014703.1	mwghuman30K#B:0332	-1.720326	3.28082E-05	2.40122E-05	-5.246863	1178	17312.5	14031	0
nuclear RNA export factor 1 (NXF1), mRNA	NP_006353.2	NM_006362.3	mwghuman30K#B:1047	-1.485619	7.48559E-05	1.62908E-05	-5.176445	1195.5	15210	14049.75	20
empty spiracles homolog 2 (Drosophila) (EMX2), mRNA	NP_004089.1	NM_004098.2	mwghuman30K#B:9279	-1.745086	9.4996E-09	5.64117E-07	-5.709572	1199.5	19380	10749.25	0
homeo box D8 (HOXD8), mRNA	NP_062458.1	NM_019558.2	mwghuman30K#B:3465	-1.41555	6.70306E-08	2.1019E-06	-5.674131	1206	9672.5	7512.25	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
pro2591 predicted protein of hq2591		AF119886	mwghuman30K#B:1001	-1.487408	7.83971E-05	1.30297E-05	-4.929888	1212	27543.5	26699	0
ensembl genscan prediction		AC016432.3.16946.19371.1	mwghuman30K#C:6058	-3.528975	4.33482E-13	5.08294E-08	-6.731611	1216.5	3962.5	1303	
ensembl genscan prediction		AF286885.1.76372.115954.3	mwghuman30K#C:7800	-1.83051	1.14443E-05	5.11795E-05	-4.359199	1218	21163.5	21224.5	
zinc finger protein 25 (KOX 19) (ZNF25), mRNA	NP_659448.1	NM_145011.2	mwghuman30K#C:1648	-1.473477	6.43814E-09	4.35863E-07	-5.84264	1253.5	21026.5	19171	1
zinc finger protein 626 (ZNF626), mRNA	NP_660340.1	NM_145297.2	mwghuman30K#B:4148	-1.773183	2.31455E-06	6.63845E-05	-4.294361	1266	14806.5	10341	1
growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA	NP_056490.1	NM_015675.1	mwghuman30K#A:00537	-1.950707	0.000200032	2.03519E-05	-5.558029	1270.5	13309	8615.5	5
nebulette (NEBL), transcript variant 1, mRNA	NP_006384.1	NM_006393.1	mwghuman30K#A:10459	-1.513391	1.95755E-05	3.15409E-05	-4.789714	1276	22936	20052.5	1

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
hypothetical protein pro2832 pro2832		NM_018541	mwghuman30K#A:00371	-1.457098	3.06355E-05	6.99321E-05	-5.164495	1289.5	16692.5	14266.5	
ring finger protein 44 (RNF44), mRNA	NP_055716.1	NM_014901.4	mwghuman30K#A:10680	-1.353366	7.76079E-07	2.37433E-06	-5.842265	1292	6288.5	4664.5	1
REX1, RNA exonuclease 1 homolog (S. cerevisiae) (REXO1), mRNA	NP_065746.2	NM_020695.2	mwghuman30K#B:8218	-1.36867	1.73225E-05	2.38069E-05	-5.111364	1305.5	4933	3309.5	6
pyrimidinergic receptor P2Y, G-protein coupled, 4 (P2RY4), mRNA	NP_002556.1	NM_002565.3	mwghuman30K#A:00433	-1.732075	5.0193E-08	2.68048E-06	-5.510614	1309	18307	12139.5	0
ensembl genscan prediction		AL023804.2.1.96460.1	mwghuman30K#C:5405	-1.533348	1.03637E-06	2.806E-05	-4.693772	1313	28610	27980.5	
ensembl genscan prediction		AL139823.3.49422.51911.1	mwghuman30K#C:8800	-1.894452	4.41409E-05	0.00012914	-4.650026	1320	11214.5	7548	
similar to hypothetical protein (LOC440804), mRNA	XP_036936.3	XM_036936.3	mwghuman30K#B:4832	-4.049648	5.38047E-11	1.51698E-07	-6.579174	1332	3647	996.5	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
chromosome X open reading frame 41 (CXorf41), mRNA	NP_775765.1	NM_173494.1	mwghuman30K#C:1526	-1.448331	1.77872E-05	2.53657E-05	-5.140193	1334	27414	24062.75	0
chromosome 20 open reading frame 152 (C20orf152), mRNA	NP_543024.1	NM_080834.1	mwghuman30K#B:3251	-1.948612	6.84261E-06	1.82138E-05	-4.987586	1349	10775	8652.5	0
ensembl genscan prediction		AL390766.11.35686.142382.1	mwghuman30K#C:4546	-1.516487	5.60986E-05	4.81914E-05	-4.642986	1352	28469.5	27078.25	
phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA	NP_002854.3	NM_002863.3	mwghuman30K#A:04342	-2.190281	5.14475E-06	0.000269936	-4.316788	1388.5	10289.5	7222	21
ensembl genscan prediction		AC013764.3.117501.157349.1	mwghuman30K#C:3627	-1.671949	8.77886E-06	7.36585E-05	-4.28185	1395.5	1205	826.5	
follistatin-like 4 (FSTL4), mRNA	NP_055897.1	NM_015082.1	mwghuman30K#B:0510	-1.544042	4.79688E-05	4.35419E-05	-4.607654	1405.5	17051	12319	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
chromosome 14 open reading frame 168 (C14orf168), mRNA	NP_113615.1	NM_031427.1	mwghuman30K#B:4011	-1.512002	1.56095E-05	5.97939E-05	-4.695177	1414	15738	14705.75	1
aldehyde dehydrogenase 7 family, member A1 (ALDH7A1), mRNA	NP_001173.1	NM_001182.2	mwghuman30K#A:08361	-1.837545	4.80787E-07	0.000105506	-3.903403	1433	20103.5	14345.5	2
ensembl genscan prediction		AC010904.9.383.204857.4	mwghuman30K#C:7433	-1.40403	4.74755E-05	3.07694E-05	-4.852328	1444	27423.5	25979.25	
kallikrein 8 (neuropsin/ovasin) (KLK8), transcript variant 2, mRNA	NP_653088.1	NM_144505.1	mwghuman30K#B:0129	-2.091505	3.56009E-06	2.61655E-06	-5.991679	1449.5	8391	6488	0
leucine zipper, down-regulated in cancer 1-like (LDOC1L), mRNA	NP_115663.2	NM_032287.2	mwghuman30K#B:8710	-1.501021	2.6566E-06	1.22937E-05	-4.280727	1454.5	16509.5	14157	0
two pore segment channel 1 (TPCN1), mRNA	NP_060371.2	NM_017901.3	mwghuman30K#B:7759	-1.497443	4.32588E-06	3.32944E-05	-4.567011	1460.5	17545	11635.75	8

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
hypothetical protein MGC11242 (MGC11242), mRNA	NP_077296.1	NM_024320.2	mwghuman30K#A:05130	-1.527839	2.70218E-05	1.72268E-05	-4.004461	1463.5	17565	13134.5	0
phosphofurin acidic cluster sorting protein 1 (PACS1), mRNA	NP_060496.2	NM_018026.2	mwghuman30K#B:7703	-1.494259	5.23361E-05	7.36585E-05	-4.899266	1482.5	9352	7757.75	19
hypothetical protein xp_036406 loc91138		XM_036406	mwghuman30K#B:8080	-1.533764	1.02161E-05	4.59223E-05	-4.93538	1486.5	15372.5	14652	
KIAA1274 (KIAA1274), mRNA	NP_055246.1	NM_014431.1	mwghuman30K#B:8047	-1.41942	7.87044E-05	2.27276E-05	-5.659345	1488.5	8059	5065	0
ensembl genscan prediction		AC090651.1.9901.36661.2	mwghuman30K#C:6027	-1.525691	2.39913E-05	7.36585E-05	-4.620984	1489.5	21092	20253	
hypothetical protein FLJ13111 (FLJ13111), mRNA	NP_079358.1	NM_025082.1	mwghuman30K#A:02690	-1.496988	3.69096E-05	7.08197E-05	-4.489468	1494	4861	7579.25	10
glycophorin C (Gerbich blood group) (GYPC), transcript variant 1, mRNA	NP_002092.1	NM_002101.3	mwghuman30K#A:01278	-1.628829	9.49623E-06	0.000135784	-4.110107	1502	8042	6771	2

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
hypothetical LOC401510 (LOC401510), mRNA	XP_376843.2	XM_376843.2	mwghuman30K#B:6807	-1.402922	3.03035E-06	0.000105506	-4.471835	1504	13882.5	11233.25	0
ensembl genscan prediction		AC068282.4.168870.201224.1	mwghuman30K#C:1421	-1.273265	1.4683E-06	4.32856E-06	-5.673395	1505.5	4650	3232.25	
phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA	NP_077734.1	NM_024420.1	mwghuman30K#C:2726	-1.656839	1.32347E-05	2.82936E-05	-4.522341	1508.5	17687.5	14140.5	5
plastin 1 (I isoform) (PLS1), mRNA	NP_002661.1	NM_002670.1	mwghuman30K#A:06551	-1.626206	5.67628E-05	2.98753E-05	-4.952263	1509.5	20943	14040.5	1
neurobeachin-like 1 (NBEAL1), mRNA	NP_945183.1	NM_198945.1	mwghuman30K#C:8646	-1.528665	7.51176E-06	2.82936E-05	-5.005478	1511.5	23554.5	20060	3
alcohol dehydrogenase 4 (class II), pi polypeptide (ADH4), mRNA	NP_000661.2	NM_000670.3	mwghuman30K#A:04002	-1.485933	6.40488E-05	7.36585E-05	-4.608649	1520.5	22288	20240.75	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
clone rp5-947l8 on chromosome 1p34.1-36.11. contains ests gsss and stss. part of novel cub sushi scr repeat domain containing p		AL355178	mwghuman30K#B:9614	-1.466888	8.43097E-06	3.15409E-05	-4.397922	1529	4947.5	4650.25	
cytochrome b5 reductase 3 (CYB5R3), transcript variant M, mRNA	NP_000389.1	NM_000398.4	mwghuman30K#A:01423	-1.497796	0.000121606	9.05266E-05	-5.28459	1531.5	9574.5	6353.5	9
clone fib5634 pro1477 predicted protein of hq1477		AF130059	mwghuman30K#B:1074	-1.699661	1.17568E-05	3.32944E-05	-4.802532	1535	5685	3946.75	10
zinc finger, DHHC-type containing 2 (ZDHHC2), mRNA	NP_057437.1	NM_016353.2	mwghuman30K#A:03494	-1.588633	8.03858E-06	0.000105506	-4.741236	1536	13684.5	10087.5	0
cone-rod homeobox (CRX), mRNA	NP_000545.1	NM_000554.2	mwghuman30K#A:09219	-3.022299	2.51326E-05	9.24336E-06	-5.849282	1548	16588.5	7500.5	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
chromosome 14 open reading frame 154 (C14orf154), transcript variant 1, mRNA	NP_115609.2	NM_032233.2	mwghuman30K#B:2665	-1.704609	8.00302E-05	0.000166293	-4.427372	1561.5	16629	15080.75	5
hypothetical protein xp_098665 loc155085		XM_098665	mwghuman30K#B:6056	-1.672814	4.27782E-05	0.000142749	-4.312941	1566.5	8795	6847.25	
clone hq0117 pro0117		AF090895	mwghuman30K#B:0914	-1.888405	1.18377E-05	9.05266E-05	-4.735768	1570.5	20158	14933.5	4
prostate and breast cancer overexpressed 1 (PBOV1), mRNA	NP_067648.1	NM_021635.1	mwghuman30K#A:05114	-1.610345	5.40979E-06	8.1682E-05	-4.437567	1571.5	22494.5	19845.75	0
esterase D/formylglutathione hydrolase (ESD), mRNA	NP_001975.1	NM_001984.1	mwghuman30K#C:2641	-1.535083	6.75303E-06	4.84259E-05	-4.777065	1574	8049	4838.75	6
ATG4 autophagy related 4 homolog B (S. cerevisiae) (ATG4B), transcript variant 1, mRNA	NP_037457.3	NM_013325.4	mwghuman30K#B:2748	-1.348856	8.59727E-06	1.6224E-05	-4.71932	1575	15166	16712.25	13

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
NADPH oxidase 1 (NOX1), transcript variant NOH-1Lv, mRNA	NP_039249.1	NM_013955.1	mwghuman30K#B:1370	-1.903809	5.04367E-06	2.65189E-05	-3.799677	1585.5	18807.5	17371.5	0
ensembl genscan prediction		AL445675.9.1.171985.3	mwghuman30K#C:8741	-1.774793	2.60881E-05	0.000182916	-4.133137	1598	22483.5	18071.5	
putative nuclear protein ORF1-FL49 (ORF1-FL49), mRNA	NP_115788.1	NM_032412.2	mwghuman30K#B:7958	-1.499659	6.10749E-05	3.32944E-05	-4.457256	1610.5	8598	4986	8
THUMP domain containing 1 (THUMPD1), mRNA	NP_060206.2	NM_017736.3	mwghuman30K#B:2088	-1.313257	4.11592E-07	6.53282E-06	-5.325518	1651.5	14877	15313.5	0
glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA	NP_036545.1	NM_012413.3	mwghuman30K#A:09422	-1.769571	4.69509E-07	0.000122803	-3.882851	1651.5	11960	8357.75	2
PHD finger protein 23 (PHF23), mRNA	NP_077273.1	NM_024297.1	mwghuman30K#A:02678	-1.398461	1.43961E-05	0.000109884	-4.356774	1657.5	10656.5	9355.75	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
nasopharyngeal carcinoma associated gene protein-8 (NAG8), mRNA	NP_055226.1	NM_014411.2	mwghuman30K#B:1482	-1.388055	2.38325E-05	5.10584E-05	-4.601658	1660	15731.5	12161	0
ensembl genscan prediction		AC013487.5.102379.117540.1	mwghuman30K#C:3348	-1.465932	0.000144857	2.37433E-06	-6.225756	1662	14711	9423	
ensembl genscan prediction		AC079757.5.54037.62672.1	mwghuman30K#C:3844	-1.486502	2.69625E-05	4.12788E-05	-4.765229	1684.5	25678.5	23575.5	
hypothetical protein FLJ22313 (FLJ22313), mRNA	NP_071768.2	NM_022373.3	mwghuman30K#B:3974	-1.47429	0.000104725	5.67358E-05	-4.784258	1688.5	8360.5	9165.25	2
holocytochrome c synthase (cytochrome c heme-lyase) (HCCS), mRNA	NP_005324.2	NM_005333.2	mwghuman30K#A:04510	-2.084412	0.000332632	0.000211886	-5.979649	1692.5	10130.5	5488.25	4
dual specificity phosphatase 5 (DUSP5), mRNA	NP_004410.3	NM_004419.3	mwghuman30K#A:04028	-1.866767	5.52516E-05	2.27276E-05	-5.708882	1694.5	16243.5	8885	2
hypothetical protein FLJ20245 (FLJ20245), mRNA	NP_060193.1	NM_017723.1	mwghuman30K#B:2083	-1.525601	6.09068E-05	0.00011676	-4.325617	1697	16122	13101	3

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
protein kinase, AMP-activated, gamma 2 non-catalytic subunit (PRKAG2), mRNA	NP_057287.2	NM_016203.2	mwghuman30K#A:00771	-1.408092	1.41299E-05	8.59969E-05	-4.435082	1697.5	16315.5	13437.25	5
clone rp11-314a4 on chromosome 20. contains part of the eya2 eyes absent drosophila homolog 2 ests an sts and gsss starts i		AL359434	mwghuman30K#B:9638	-1.591958	1.67257E-05	6.56055E-05	-4.203762	1702	25348.5	23840.75	
hypothetical protein pro1598 pro1598		NM_018503	mwghuman30K#B:0983	-1.446989	3.89533E-06	1.30096E-05	-5.339446	1716.5	24112.5	22618.75	
NIMA (never in mitosis gene a)- related kinase 9 (NEK9), mRNA	NP_149107.3	NM_033116.3	mwghuman30K#C:0238	-1.359292	3.922E-05	4.35419E-05	-4.78725	1722.5	10134.5	7455.5	5
glycine receptor, alpha 3 (GLRA3), mRNA	NP_006520.1	NM_006529.1	mwghuman30K#A:03690	-1.412224	0.000103763	8.1682E-05	-4.59741	1726	9472.5	8083.25	2

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
ensembl genscan prediction		AC004408.1.1.113252.2	mwghuman30K#C:9512	-1.54073	2.55537E-06	1.54035E-05	-3.618774	1727	2977	2622.75	
ensembl genscan prediction		AP001655.2.148977.153525.1	mwghuman30K#C:7868	-1.285997	2.64478E-05	1.96829E-05	-4.601991	1746	28566	28245.5	
HERV-H LTR-associating 3 (HHLA3), transcript variant 3, mRNA	NP_001031722.1	NM_001036645.1	mwghuman30K#B:1046	-2.043346	8.67677E-05	9.52067E-05	-3.941702	1759	13925.5	11798	0
ensembl genscan prediction		AL355497.14.1.215397.9	mwghuman30K#C:7911	-3.056765	1.10766E-06	3.82785E-07	-6.916789	1760	5672.5	2481.25	
fibronectin *leucine rich* transmembrane protein 3 (FLRT3), transcript variant 1, mRNA	NP_037413.1	NM_013281.2	mwghuman30K#A:05822	-4.204569	1.4941E-08	9.99201E-07	-6.042443	1770	18156	9231.25	0
cyp3a5 allele cyp3a5*3 alternatively spliced		AF355802	mwghuman30K#B:1830	-1.371576	7.33293E-06	1.91497E-05	-4.362299	1784	26198.5	24518.25	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
microfibrillar-associated protein 3-like (MFAP3L), transcript variant 1, mRNA	NP_067679.5	NM_021647.5	mwghuman30K#B:0217	-1.987417	0.000137375	1.98715E-06	-4.959479	1785	22262	18475.25	3
cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA	NP_114148.2	NM_031942.3	mwghuman30K#B:4810	-1.959598	9.26637E-05	0.00015005	-4.246093	1788	14826	12577.25	1
WD repeat domain 61 (WDR61), mRNA	NP_079510.1	NM_025234.1	mwghuman30K#B:1624	-1.531798	0.000154491	0.000105506	-4.38785	1801.5	9756.5	8041.75	3
protein kinase, AMP-activated, beta 1 non-catalytic subunit (PRKAB1), mRNA	NP_006244.2	NM_006253.4	mwghuman30K#A:04996	-1.514877	9.29449E-05	0.000105506	-4.4366	1805.5	16011.5	13954	3
zinc finger, A20 domain containing 2 (ZA20D2), mRNA	NP_005998.1	NM_006007.1	mwghuman30K#A:10213	-1.857923	2.78106E-06	2.67916E-05	-4.781221	1808.5	6856.5	4563.25	13
similar to pro2852 loc93374		XM_050978	mwghuman30K#B:7206	-1.359998	8.48914E-05	6.30077E-05	-5.206744	1817	19166	16438	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
catalase (CAT), mRNA	NP_001743.1	NM_001752.2	mwghuman30K#C:3530	-2.225675	8.1938E-07	6.92439E-06	-4.777325	1820	7219.5	4208.75	31
peptidylprolyl isomerase (cyclophilin)-like 2 (PPIL2), transcript variant 2, mRNA	NP_680480.1	NM_148175.1	mwghuman30K#B:6262	-1.384263	4.77437E-07	4.59274E-06	-5.396075	1834.5	3806	3514	5
periaxin (PRX), transcript variant 2, mRNA	NP_870998.1	NM_181882.1	mwghuman30K#A:01781	-1.399169	1.03356E-05	6.63845E-05	-4.549994	1838	19643.5	17122.5	0
breast carcinoma amplified sequence 3 (BCAS3), mRNA	NP_060149.2	NM_017679.2	mwghuman30K#A:01576	-1.41274	2.55423E-07	3.64015E-06	-4.03611	1839	15754.5	17960.25	2
HtrA serine peptidase 2 HTRA2	AAF66598.1	AF141307.1	mwghuman30K#B:1170	-1.284282	2.27894E-05	1.86362E-05	-4.071282	1850	22760.5	20044.75	
ensembl genscan prediction		AC012095.13.12848.17419.1	mwghuman30K#C:7012	-1.517696	0.000134314	0.000172435	-4.407333	1854	26139.5	25010.5	
formin binding protein 4 (FNBP4), mRNA	NP_056123.1	NM_015308.1	mwghuman30K#B:8897	-1.360042	0.000119422	2.15085E-05	-5.532889	1855	17142	14814.25	11

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
aldehyde dehydrogenase 1 family, member L1 (ALDH1L1), mRNA	NP_036322.2	NM_012190.2	mwghuman30K#A:07479	-2.396851	2.32809E-05	0.000157701	-3.740555	1856.5	13469	8189.5	3
ensembl genscan prediction		AP001487.35282.114407.1	mwghuman30K#C:8733	-1.603991	4.09016E-06	5.97939E-05	-4.353485	1870	3882	3994.75	
ensembl genscan prediction		AC015651.18.1.191583.4	mwghuman30K#C:2191	-1.392136	5.55423E-07	1.72268E-05	-4.562358	1873.5	2463	1928.25	
OTU domain containing 5 (OTUD5), mRNA	NP_060072.1	NM_017602.2	mwghuman30K#B:7999	-1.721318	3.42749E-06	1.37651E-05	-5.356883	1894.5	1453	1011	14
ensembl genscan prediction		AC026668.5.84589.93793.1	mwghuman30K#C:5546	-1.668723	3.74924E-06	2.40122E-05	-5.209366	1899	3201	1676.5	
chromosome 20 open reading frame 121 (C20orf121), mRNA	NP_077307.1	NM_024331.2	mwghuman30K#A:03031	-1.520517	5.93503E-08	1.82138E-05	-4.163768	1906	8788	6894	2
pyruvate dehydrogenase kinase, isozyme 4 (PDK4), mRNA	NP_002603.1	NM_002612.2	mwghuman30K#A:07564	-1.735687	1.72294E-05	1.22937E-05	-5.445156	1911.5	18067	13997.25	1

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
KIAA1049 protein (KIAA1049), mRNA	NP_055787.1	NM_014972.1	mwghuman30K#B:2555	-1.400381	1.30483E-05	7.36585E-05	-4.350759	1913.5	10972	8868.5	12
DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA	NP_490647.1	NM_058246.3	mwghuman30K#A:04664	-1.455502	9.60314E-05	0.00015005	-4.286094	1917	3609	2895.5	14
lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3), mRNA	NP_002297.1	NM_002306.1	mwghuman30K#A:10306	-1.93733	6.69527E-06	2.55121E-05	-4.690215	1923	2753	1803.5	6
PTPRF interacting protein, binding protein 2 (liprin beta 2) (PPFIBP2), mRNA	NP_003612.1	NM_003621.1	mwghuman30K#B:0552	-1.881545	1.28489E-06	2.98753E-05	-4.14602	1937.5	6372.5	4594.5	2
polymerase (DNA directed), lambda (POLL), mRNA	NP_037406.1	NM_013274.2	mwghuman30K#B:1279	-1.399567	3.5582E-05	2.98753E-05	-4.793654	1938	15108.5	11461.25	8

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
growth differentiation factor 15 (GDF15), mRNA	NP_004855.1	NM_004864.1	mwghuman30K#A:07217	-2.483648	0.000224134	0.00025725	-4.296268	1944	6377	3127.5	2
hypothetical protein xp_089809 loc159765		XM_089809	mwghuman30K#B:6474	-1.381507	9.90157E-07	2.40122E-05	-4.093057	1949	11626.5	11522.5	
leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, mRNA	NP_612370.3	NM_138361.3	mwghuman30K#B:4416	-2.034574	0.000184031	0.000233537	-4.13512	1959.5	7671.5	4421.75	1
trafficking protein particle complex 6A (TRAPPC6A), mRNA	NP_077013.1	NM_024108.1	mwghuman30K#A:02117	-1.452954	2.44741E-06	2.53657E-05	-3.509555	1985	1279	1294	8
ensembl genscan prediction		AL357146.10.1.82494.1	mwghuman30K#C:3608	-1.287782	1.49736E-05	6.05474E-05	-4.826559	1989	28444.5	26083.25	
hypothetical protein MGC14327 (MGC14327), mRNA	NP_444273.1	NM_053045.1	mwghuman30K#B:4427	-1.504495	0.000150258	0.000174117	-4.521635	1992	16805	15440.5	4

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
similar to kinesin family member 5b clone mgc:15265 image:4297793		BC009353	mwghuman30K#B:4438	-1.51682	0.000188214	0.000192131	-4.531075	1992	23071.5	21809.75	
potassium channel tetramerisation domain containing 3 (KCTD3), mRNA	NP_057205.2	NM_016121.3	mwghuman30K#A:04386	-1.358006	1.34593E-05	5.38262E-05	-4.810824	1994.5	17479.5	13203.75	3
ensembl genscan prediction		AC018425.3.153134.186975.1	mwghuman30K#C:3925	-1.496534	0.000149525	0.000192131	-4.315259	1997	25336	25414.75	
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), mRNA	NP_002060.4	NM_002069.4	mwghuman30K#A:10201	-1.631361	5.34686E-06	0.000433377	-3.885346	2003	16803.5	14082	1
microtubule-associated protein 4 (MAP4), transcript variant 1, mRNA	NP_002366.2	NM_002375.3	mwghuman30K#B:4355	-1.468752	0.000155187	0.000257025	-4.423897	2004	10052	9080	11

Fig. 3 (continued

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant alpha, mRNA	NP_075068.2	NM_022917.4	mwghuman30K#A:07182	-1.30257	1.12604E-06	3.70831E-05	-4.767639	2009	10513	8821	7
cerebral endothelial cell adhesion molecule 1 (CEECAM1), mRNA	NP_057258.2	NM_016174.3	mwghuman30K#A:10231	-1.516413	4.80848E-05	0.000109198	-3.667581	2014	16662.5	13757.75	0
ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa (UQCRQ), nuclear gene encoding mitochondrial protein, mRNA	NP_055217.2	NM_014402.3	mwghuman30K#B:6060	-1.71221	4.79681E-05	4.35419E-05	-5.049156	2014	4199.5	2985.25	14
hypothetical protein xp_092745 loc164337		XM_092745	mwghuman30K#B:3255	-1.386871	3.26973E-05	0.000165718	-4.513374	2041	19510	15741.25	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
hypothetical protein FLJ22965 (FLJ22965), mRNA	NP_071384.1	NM_022101.2	mwghuman30K#A:09776	-1.903469	7.16955E-05	0.000475592	-4.078844	2041.5	2596	2337	0
chromosome 9 open reading frame 102 (C9orf102), transcript variant 1, mRNA	NP_064592.1	NM_020207.2	mwghuman30K#B:6956	-1.369819	3.05523E-05	0.000105506	-4.676244	2049	16457.5	13970	0
sphingosine-1-phosphate phosphatase 1 (SGPP1), mRNA	NP_110418.1	NM_030791.2	mwghuman30K#B:1809	-1.477332	4.90035E-05	0.000142749	-4.328137	2062.5	20094	17541.5	1
pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 1, mRNA	NP_056125.2	NM_015310.2	mwghuman30K#B:9515	-1.395381	2.70551E-05	0.000142896	-3.953529	2072	14023	13223.25	1
hypothetical protein LOC283874 (LOC283874), mRNA	NP_001012749.1	NM_001012731.1	mwghuman30K#B:2101	-1.376341	1.45793E-05	2.67916E-05	-5.079903	2090.5	23511.5	23000	1

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
zinc finger, FYVE domain containing 21 (ZFYVE21), mRNA	NP_076976.1	NM_024071.2	mwghuman30K#A:05642	-1.579562	0.000114253	0.000342648	-4.238027	2094	2994.5	2740.25	0
forkhead box E1 (thyroid transcription factor 2) (FOXE1), mRNA	NP_004464.2	NM_004473.3	mwghuman30K#A:07899	-1.678652	1.3104E-05	0.000192131	-3.837954	2107	7269	5293.75	0
ensembl genscan prediction		AL158168.17.82811.114103.1	mwghuman30K#C:5892	-1.54059	5.72345E-05	8.88591E-06	-4.136599	2114	28578	27753.75	
similar to per-hexamer repeat protein 5 loc149135		XM_089208	mwghuman30K#B:9694	-1.363387	0.000105564	3.77672E-05	-3.9371	2131	27002.5	27249.5	
zinc finger, matrin type 1 (ZMAT1), transcript variant 3, mRNA	NP_115817.1	NM_032441.1	mwghuman30K#C:0106	-1.423696	0.000156267	0.000211886	-4.538065	2134.5	20339.5	17190.25	2
endoplasmic reticulum to nucleus signalling 2 (ERN2), mRNA	NP_150296.2	NM_033266.2	mwghuman30K#B:9444	-1.735187	1.98165E-05	2.70994E-05	-4.509363	2135	24789	18903	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
ring finger protein 38 (RNF38), transcript variant 1, mRNA	NP_073618.3	NM_022781.3	mwghuman30K#B:5588	-1.302965	2.50283E-06	2.15085E-05	-4.986001	2138	24546.5	22148.75	1
Myc-induced mitochondria protein (mimitin), mRNA	NP_777549.1	NM_174889.2	mwghuman30K#B:3716	-1.474873	8.439E-05	0.000359234	-4.207401	2151.5	9215	7030.25	1
TGF beta-inducible nuclear protein 1 (TINP1), mRNA	NP_055701.1	NM_014886.2	mwghuman30K#A:06520	-1.655993	0.000318759	0.000571767	-4.796546	2153	7530	5545.5	6
similar to developmental pluripotency associated 5; embryonal stem cell specific gene 1 (LOC341912), mRNA	XP_292301.3	XM_292301.3	mwghuman30K#B:8134	-1.639786	7.64251E-07	4.32856E-06	-5.437632	2155	18581.5	12815.25	1
dehydrogenase/reductase (SDR family) member 3 (DHRS3), mRNA	NP_004744.2	NM_004753.4	mwghuman30K#B:0738	-1.439285	4.39582E-05	0.000222464	-3.974197	2166.5	4626	3570	3

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
flavin containing monooxygenase 4 (FMO4), mRNA	NP_002013.1	NM_002022.1	mwghuman30K#B:2927	-1.804252	0.000195967	0.000222464	-4.159771	2173.5	21428	18241	1
ensembl genscan prediction		AC022526.4.9087.13827.1	mwghuman30K#C:9081	-1.518222	0.000126409	0.000174117	-4.437239	2174	25713.5	23316	
serologically defined colon cancer antigen 8 (SDCCAG8), mRNA	NP_006633.1	NM_006642.1	mwghuman30K#B:4992	-1.359218	5.81032E-06	1.22937E-05	-4.628131	2177.5	18648	16566	4
CDC14 cell division cycle 14 homolog B (S. cerevisiae) (*CDC14B*), transcript variant 2, mRNA	NP_201588.1	NM_033331.1	mwghuman30K#B:0753	-1.438486	0.000150076	0.000245124	-4.702655	2178.5	23322	22971	2
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA	NP_004520.1	NM_004529.1	mwghuman30K#A:00725	-1.503791	3.87447E-05	0.000311603	-4.282874	2188	20164.5	17462	4

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1), nuclear gene encoding mitochondrial protein, mRNA	NP_000775.1	NM_000784.2	mwghuman30K#A:07422	-1.399906	4.05019E-05	3.91276E-05	-4.065883	2197	20714	13781.5	10
pre-tnk cell associated protein 1f6 3' end		L17326	mwghuman30K#B:9025	-1.643879	5.92984E-08	3.84322E-06	-5.055927	2201	6449.5	4787.5	
hepcidin antimicrobial peptide (HAMP), mRNA	NP_066998.1	NM_021175.2	mwghuman30K#A:06397	-1.279742	2.53831E-05	1.72268E-05	-4.893297	2205.5	3722.5	3385.25	0
ensembl genscan prediction		AC078819.13.1.41283.1	mwghuman30K#C:7792	-1.349603	2.94705E-06	7.88194E-05	-4.262185	2213	21381.5	17800.75	
hypothetical protein BC009862 (LOC90113), mRNA	XP_291077.3	XM_291077.3	mwghuman30K#B:3668	-1.769275	0.000340569	0.000454027	-4.413577	2221.5	6261.5	5176	0
elongation factor, RNA polymerase II, 2 (ELL2), mRNA	NP_036213.1	NM_012081.3	mwghuman30K#A:00356	-1.499648	5.40285E-05	0.000157701	-4.384409	2223.5	14138	11702.5	4

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
FGFR1 oncogene partner (FGFR1OP), transcript variant 1, mRNA	NP_008976.1	NM_007045.2	mwghuman30K#B:4675	-1.513357	9.11409E-05	0.000233537	-4.085108	2228.5	19894	19145.25	0
ensembl genscan prediction		AC025953.2.116948.127472.1	mwghuman30K#C:6647	-2.043219	0.000155145	0.000283207	-3.955032	2231	21041	17429.5	
EH domain binding protein 1 (EHBP1), mRNA	NP_056067.1	NM_015252.2	mwghuman30K#B:0385	-1.35833	2.50342E-06	6.99321E-05	-4.628579	2249.5	13151.5	12131	5
propionyl Coenzyme A carboxylase, alpha polypeptide (PCCA), mRNA	NP_000273.2	NM_000282.2	mwghuman30K#B:3551	-1.505038	6.411E-05	0.000110999	-4.042034	2251	16323	13459	5
ensembl genscan prediction		AL138499.4.1.185713.1	mwghuman30K#C:4137	-1.655664	1.65577E-05	8.59969E-05	-3.700791	2252.5	6728	6542.5	
ensembl genscan prediction		AC025937.3.28407.38498.1	mwghuman30K#C:9420	-5.821331	1.29566E-11	3.14688E-07	-6.568115	2255.5	3524	1068.5	

Fig. 3 (continued)

Gene name/ symbol	*protein* accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
myocilin, trabecular meshwork inducible glucocorticoid response (MYOC), mRNA	NP_000252.1	NM_000261.1	mwghuman30K#A:09642	-1.364785	4.61814E-05	2.61402E-05	-4.638227	2263	23815.5	22357.25	0
hspc074		AF161337	mwghuman30K#B:1281	-1.61806	1.54965E-06	1.54035E-05	-4.426706	2264.5	1792	1727	3
epoxide hydrolase 2, cytoplasmic (EPHX2), mRNA	NP_001970.2	NM_001979.4	mwghuman30K#A:08300	-1.416398	5.8666E-06	5.81228E-06	-4.695716	2267.5	19752.5	16857	3
centromere protein C 1 (CENPC1), mRNA	NP_001803.2	NM_001812.2	mwghuman30K#A:10535	-1.578112	0.000183356	0.000192131	-4.258306	2275	19346.5	14107.25	4
poly(A) polymerase beta (testis specific) (PAPOLB), mRNA	NP_064529.4	NM_020144.4	mwghuman30K#A:00034	-1.533242	0.000179394	0.000311603	-4.111646	2284	24777	23772.75	1
oligonucleotide /oligosaccharide-binding fold containing 1 (OBFC1), mRNA	NP_079204.1	NM_024928.3	mwghuman30K#A:07366	-1.597262	0.000151906	0.00015005	-4.339099	2292	15940.5	11655	4

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
tripartite motif-containing 10 (TRIM10), transcript variant 1, mRNA	NP_006769.1	NM_006778.2	mwghuman30K#A:10515	-1.750912	5.52205E-05	0.000135784	-4.621742	2296.5	4089.5	1565.5	0
Rap2-binding protein 9 (RPIB9), mRNA	NP_612147.1	NM_138290.1	mwghuman30K#B:7696	-1.451227	1.03873E-06	1.37651E-05	-5.068475	2297	24136.5	22036.5	1
fksg17		NM_032031	mwghuman30K#B:1656	-1.576144	0.000141834	0.000233537	-4.037961	2320.5	2050	1701.75	1
G protein-coupled receptor 83 (GPR83), mRNA	NP_057624.2	NM_016540.2	mwghuman30K#A:05359	-1.472466	6.54909E-05	0.000182916	-3.811779	2322.5	18971.5	15879.25	0
ensembl genscan prediction		AC078987.9.135718.144151.1	mwghuman30K#C:4632	-1.300374	2.50018E-05	1.72268E-05	-4.918105	2322.5	25018.5	21332.5	
LIM homeobox 9 (LHX9), transcript variant 1, mRNA	NP_064589.2	NM_020204.2	mwghuman30K#B:8634	-1.374971	4.6951E-06	9.24336E-06	-5.312469	2333.5	16158	13872.25	0
pellino homolog 1 (Drosophila) (PELI1), mRNA	NP_065702.2	NM_020651.2	mwghuman30K#A:10770	-1.492094	8.8328E-06	8.23838E-06	-5.23835	2336	22421.5	17524.5	7

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
hypothetical LOC401500 (LOC401500), mRNA	XP_379629.1	XM_379629.1	mwghuman30K#B:6223	-1.325858	2.27785E-05	4.12788E-05	-4.402696	2336.5	26315	25320.25	0
TSC22 domain family, member 3 (TSC22D3), transcript variant 2, mRNA	NP_004080.2	NM_004089.3	mwghuman30K#B:0462	-1.491298	5.41371E-05	1.72268E-05	-5.010311	2350.5	18693.5	13200.5	43
G protein-coupled receptor 51 (GPR51), mRNA	NP_005449.5	NM_005458.5	mwghuman30K#A:04815	-1.389185	0.000101706	2.98753E-05	-4.845168	2361	3420	2489.25	0
chromosome 10 open reading frame 61 (C10orf61), transcript variant 2, mRNA	NP_056446.1	NM_015631.2	mwghuman30K#B:3105	-1.555923	0.000177095	0.000297088	-4.510054	2366.5	10134	8091.5	3.
jumonji domain containing 2C (JMJD2C), mRNA	NP_055876.1	NM_015061.1	mwghuman30K#B:8433	-1.317474	6.41124E-05	0.000142749	-4.870495	2366.5	24516.5	22272.75	11
zinc finger protein 547 (ZNF547), mRNA	NP_775902.2	NM_173631.2	mwghuman30K#B:6716	-1.63256	0.000251174	0.00025725	-3.984452	2370	19484	19537	2

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
hypothetical protein FLJ20032 (FLJ20032), mRNA	NP_060098.2	NM_017628.2	mwghuman30K#B:2068	-1.74414	6.61052E-05	0.000105506	-4.166213	2374	15233.5	9767.75	16
ensembl genscan prediction		AC064877.3.121131.166993.1	mwghuman30K#C:7466	-1.319284	4.28953E-05	2.03519E-05	-4.802131	2374	27348	26740.25	
ensembl genscan prediction		AC027755.2.81287.97090.1	mwghuman30K#C:3411	-1.439071	0.000125901	0.000331474	-4.145868	2378.5	14385.5	10781.5	
KIAA0690 (KIAA0690), mRNA	NP_055994.1	NM_015179.2	mwghuman30K#B:7202	-1.642414	0.000173936	0.000433377	-4.08872	2380	14459	11844.25	10
SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA	NP_113657.1	NM_031469.1	mwghuman30K#B:1794	-1.995457	0.000279676	0.000376568	-4.033794	2381	9893.5	6985.75	3
cdna: flj21394 fis clone col03536 unnamed protein product		AK025047	mwghuman30K#B:2580	-2.258109	0.000447376	0.000359234	-4.071961	2387.5	17288	11926.75	0
hypothetical protein xp_039231 loc91565		XM_039231	mwghuman30K#B:6431	-1.337232	2.70835E-05	0.000174117	-4.141157	2398	24099.5	20885	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
GPI anchored molecule like protein (GML), mRNA	NP_002057.1	NM_002066.1	mwghuman30K#A:02108	-1.438045	0.000072493	0.00012914	-4.162956	2405	16818	14265.75	0
small nuclear RNA activating complex, polypeptide 5, 19kDa (SNAPC5), mRNA	NP_006040.1	NM_006049.1	mwghuman30K#B:0945	-1.323754	1.74702E-05	0.000184787	-4.006319	2444	17556.5	17969.25	6
ensembl genscan prediction		AC027689.10.1.180573.5	mwghuman30K#C:9758	-1.644263	0.000255065	2.98753E-05	-3.674603	2451	16829.5	10684.25	
mitochondrial tumor suppressor 1 (MTUS1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	NP_001001924.1	NM_001001924.1	mwghuman30K#B:7775	-1.715161	0.000303663	0.000269936	-4.435392	2461.5	17489	15873	0
ensembl genscan prediction		AL049829.4.1.196292.3	mwghuman30K#C:4548	-1.402914	1.70061E-06	2.49927E-06	-5.01844	2471	28131	26784	
ensembl genscan prediction		AC084842.1.7903.10639.1	mwghuman30K#C:7638	-1.400793	0.000812094	7.36585E-05	-5.107784	2475.5	14235.5	11061.25	

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
SAFB-like, transcription modulator (SLTM), transcript variant 1, mRNA	NP_079031.2	NM_024755.2	mwghuman30K#B:2154	-1.309539	2.00445E-05	0.000122803	-4.680439	2477.5	12490	12280	12
guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), transcript variant 2, mRNA	NP_002062.1	NM_002071.1	mwghuman30K#A:06286	-1.836112	0.00030026	0.000498109	-4.10637	2478	19959	16690.75	0
similar to cg14182 product loc146175		XM_085352	mwghuman30K#B:7365	-1.746066	0.000194923	0.000433377	-3.812815	2487	14791.5	9814.5	
PH domain and leucine rich repeat protein phosphatase (PHLPP), mRNA	NP_919431.1	NM_194449.1	mwghuman30K#B:2242	-2.043619	0.000307945	0.000498109	-4.006924	2500	15125	10009.75	7

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
autism susceptibility candidate 2 (AUTS2), mRNA	NP_056385.1	NM_015570.1	mwghuman30K#B:0110	-1.807633	0.000369299	0.000382814	-4.213775	2503	18404	14412.75	8
hypothetical protein xp_097338 loc147909		XM_097338	mwghuman30K#B:5652	-1.428873	1.32234E-06	2.67916E-05	-4.387947	2513	4388	2991.75	
leucine-rich repeat-containing G protein-coupled receptor 4 (LGR4), mRNA	NP_060960.1	NM_018490.1	mwghuman30K#A:06106	-1.519205	7.81416E-05	0.000122803	-3.810559	2514.5	21417.5	19684	2
ensembl prediction		ENSG00000113407	mwghuman30K#C:2560	-1.740805	1.93346E-05	9.52811E-05	-4.388894	2525	8797.5	6359.5	
programmed cell death 1 (PDCD1), mRNA	NP_005009.1	NM_005018.1	mwghuman30K#B:9147	-1.519488	1.50412E-06	3.41028E-06	-5.713059	2537	8575	7118.5	0
cadherin 20, type 2 (CDH20), mRNA	NP_114097.2	NM_031891.2	mwghuman30K#B:7584	-1.393019	1.91884E-05	2.73302E-05	-4.362445	2538	15588	12275.75	0

Fig. 3 (continued)

Gene name/ symbol	protein accession	mRNA ref seq accession	MWG Probe name	median fold change	t-test	Wilcoxon test	SAM	rank score	tumour tissue median intensity rank	non-malignant tissue median intensity rank	blood
glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P) (GLDC), mRNA	NP_000161.1	NM_000170.1	mwghuman30K#B:8959	-1.405054	9.33312E-05	0.00011676	-4.398207	2542.5	6039	4550.5	1
protease, serine, 35 (PRSS35), mRNA	NP_699193.1	NM_153362.1	mwghuman30K#B:3364	-1.451818	0.000237039	0.00025725	-4.319803	2545	16909	14109	0
ensembl genscan prediction		AC008134.3.1.175132.1	mwghuman30K#C:3643	-1.601839	0.00037884	0.000286633	-4.042534	2545	27071.5	25825	
ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), transcript variant 1, mRNA	NP_775099.2	NM_173076.2	mwghuman30K#B:3505	-1.653773	0.000237178	0.000475592	-3.927921	2561.5	19931	18593.5	0
suppressor of hairy wing homolog 3 (Drosophila) (SUHW3), mRNA	NP_060136.1	NM_017666.2	mwghuman30K#B:2904	-1.678106	0.000186359	0.000546156	-3.864729	2568	17527	15364.5	1

Fig. 3 (continued)

Gene name/symbol	protein accession	mRNA ref seq accession	median fold change	rank score	tumour issue median intensity rank	non-malignant tissue median intensity rank	blood EST number
hypothetical protein FLJ21511 (FLJ21511), mRNA	NP_079363.1	NM_025087.1	-2.080908	68	14455	9272.5	0
paired box gene 8 (PAX8), transcript variant PAX8A, mRNA	NP_003457.1	NM_003466.3	-1.961896	82	19419	12999.5	0
UPF3 regulator of nonsense transcripts homolog A (yeast) (UPF3A), transcript variant 1, mRNA	NP_075387.1	NM_023011.2	-3.84007	96.5	5663.5	1825	0
leukotriene B4 12-hydroxydehydrogenase (LTB4DH), mRNA	NP_036344.1	NM_012212.2	-5.034613	122.5	11340.5	3138	0
RAB11 family interacting protein 2 (class I) (RAB11FIP2), mRNA	NP_055719.1	NM_014904.1	-1.993629	156	19636.5	12951	0
TSC22 domain family, member 1 (TSC22D1), transcript variant 2, mRNA	NP_006013.1	NM_006022.2	-2.133065	156.5	8415	6130	1
sulfite oxidase (SUOX), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	NP_000447.2	NM_000456.2	-1.622803	223	11312.5	8789.5	0
tetratricopeptide repeat domain 21A (TTC21A), mRNA	NP_665698.1	NM_145755.1	-2.976809	225	8375.5	3870.5	1
synaptotagmin-like 2 (SYTL2), transcript variant b, mRNA	NP_115755.2	NM_032379.3	-2.343357	342	19920	12053.5	0
wingless-type MMTV integration site family, member 2B (WNT2B), transcript variant WNT-2B1, mRNA	NP_004176.2	NM_004185.2	-10.745275	501	10716	2016.25	0
protocadherin gamma subfamily A, 12 (PCDHGA12), transcript variant 1, mRNA	NP_003726.1	NM_003735.2	-2.070447	511	2537	1931.5	0
olfactory receptor, family 1, subfamily D, member 5 (OR1D5), mRNA	NP_055381.1	NM_014566.1	-1.640751	539.5	1644	1134	0
G protein-coupled receptor 126 (GPR126), transcript variant b1, mRNA	NP_940971.1	NM_198569.1	-2.181735	549	15965.5	8040.75	0
ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila) (USP9Y), mRNA	NP_004645.2	NM_004654.3	-1.584065	587	10035.5	7858.25	1

Fig. 4

Gene name/symbol	protein accession	mRNA ref seq accession	median fold change	rank score	tumour issue median intensity rank	non-malignant tissue median intensity rank	blood EST number
chromosome 11 open reading frame 1 (C11orf1), mRNA	NP_073598.1	NM_022761.1	-1.81726	673.5	12025.5	9585.25	0
BCL2-associated athanogene (BAG1), mRNA	NP_004314.3	NM_004323.3	-2.525417	776	9031	4503.5	1
family with sequence similarity 44, member B (FAM44B), mRNA	NP_612378.1	NM_138369.1	-1.357114	942.5	15308.5	13004.75	1
fibroblast growth factor receptor 4 (FGFR4), transcript variant 2, mRNA	NP_075252.2	NM_022963.2	-2.638426	1087.5	17096	9762.5	0
thyroid transcription factor 1 (TITF1), mRNA	NP_003308.1	NM_003317.3	-1.466987	1124.5	2139	1026.25	0
VprBP protein (VprBP), mRNA	NP_055518.1	NM_014703.1	-1.720326	1178	17312.5	14031	0
empty spiracles homolog 2 (Drosophila) (EMX2), mRNA	NP_004089.1	NM_004098.2	-1.745086	1199.5	19380	10749.25	0
homeo box D8 (HOXD8), mRNA	NP_062458.1	NM_019558.2	-1.41555	1206	9672.5	7512.25	0
zinc finger protein 626 (ZNF626), mRNA	NP_660340.1	NM_145297.2	-1.773183	1266	14806.5	10341	1
ring finger protein 44 (RNF44), mRNA	NP_055716.1	NM_014901.4	-1.353366	1292	6288.5	4664.5	1
pyrimidinergic receptor P2Y, G-protein coupled, 4 (P2RY4), mRNA	NP_002556.1	NM_002565.3	-1.732075	1309	18307	12139.5	0
similar to hypothetical protein (LOC440804), mRNA	XP_036936.3	XM_036936.3	-4.049648	1332	3647	996.5	0
chromosome 20 open reading frame 152 (C20orf152), mRNA	NP_543024.1	NM_080834.1	-1.948612	1349	10775	8652.5	0
follistatin-like 4 (FSTL4), mRNA	NP_055897.1	NM_015082.1	-1.544042	1405.5	17051	12319	0
chromosome 14 open reading frame 168 (C14orf168), mRNA	NP_113615.1	NM_031427.1	-1.512002	1414	15738	14705.75	1
kallikrein 8 (neuropsin/ovasin) (KLK8), transcript variant 2, mRNA	NP_653088.1	NM_144505.1	-2.091505	1449.5	8391	6488	0
leucine zipper, down-regulated in cancer 1-like (LDOC1L), mRNA	NP_115663.2	NM_032287.2	-1.501021	1454.5	16509.5	14157	0
hypothetical protein MGC11242 (MGC11242), mRNA	NP_077296.1	NM_024320.2	-1.527839	1463.5	17565	13134.5	0
KIAA1274 (KIAA1274), mRNA	NP_055246.1	NM_014431.1	-1.41942	1488.5	8059	5065	0
hypothetical LOC401510 (LOC401510), mRNA	XP_376843.2	XM_376843.2	-1.402922	1504	13882.5	11233.25	0

Fig. 4 (continued)

Gene name/symbol	protein accession	mRNA ref seq accession	median fold change	rank score	tumour issue median intensity rank	non-malignant tissue median intensity rank	blood EST number
plastin 1 (I isoform) (PLS1), mRNA	NP_002661.1	NM_002670.1	-1.626206	1509.5	20943	14040.5	1
zinc finger, DHHC-type containing 2 (ZDHHC2), mRNA	NP_057437.1	NM_016353.2	-1.588633	1536	13684.5	10087.5	0
cone-rod homeobox (CRX), mRNA	NP_000545.1	NM_000554.2	-3.022299	1548	16588.5	7500.5	0
PHD finger protein 23 (PHF23), mRNA	NP_077273.1	NM_024297.1	-1.398461	1657.5	10656.5	9355.75	0
nasopharyngeal carcinoma associated gene protein-8 (NAG8), mRNA	NP_055226.1	NM_014411.2	-1.388055	1660	15731.5	12161	0
HERV-H LTR-associating 3 (HHLA3), transcript variant 3, mRNA	NP_001031722.1	NM_001036645.1	-2.043346	1759	13925.5	11798	0
fibronectin leucine rich transmembrane protein 3 (FLRT3), transcript variant 1, mRNA	NP_037413.1	NM_013281.2	-4.204569	1770	18156	9231.25	0
cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA	NP_114148.2	NM_031942.3	-1.959598	1788	14826	12577.25	1
pyruvate dehydrogenase kinase, isozyme 4 (PDK4), mRNA	NP_002603.1	NM_002612.2	-1.735687	1911.5	18067	13997.25	1
leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, mRNA	NP_612370.3	NM_138361.3	-2.034574	1959.5	7671.5	4421.75	1
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 (GNAI1), mRNA	NP_002060.4	NM_002069.4	-1.631361	2003	16803.5	14082	1
cerebral endothelial cell adhesion molecule 1 (CEECAM1), mRNA	NP_057258.2	NM_016174.3	-1.516413	2014	16662.5	13757.75	0
hypothetical protein FLJ22965 (FLJ22965), mRNA	NP_071384.1	NM_022101.2	-1.903469	2041.5	2596	2337	0
chromosome 9 open reading frame 102 (C9orf102), transcript variant 1, mRNA	NP_064592.1	NM_020207.2	-1.369819	2049	16457.5	13970	0
pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 1, mRNA	NP_056125.2	NM_015310.2	-1.395381	2072	14023	13223.25	1
zinc finger, FYVE domain containing 21 (ZFYVE21), mRNA	NP_076976.1	NM_024071.2	-1.579562	2094	2994.5	2740.25	0
forkhead box E1 (thyroid transcription factor 2) (FOXE1), mRNA	NP_004464.2	NM_004473.3	-1.678652	2107	7269	5293.75	0

Fig. 4 (continued)

Gene name/symbol	protein accession	mRNA ref seq accession	median fold change	rank score	tumour issue median intensity rank	non-malignant tissue median intensity rank	blood EST number
Myc-induced mitochondria protein (mimitin), mRNA	NP_777549.1	NM_174889.2	-1.474873	2151.5	9215	7030.25	1
similar to developmental pluripotency associated 5; embryonal stem cell specific gene 1 (LOC341912), mRNA	XP_292301.3	XM_292301.3	-1.639786	2155	18581.5	12815.25	1
hepcidin antimicrobial peptide (HAMP), mRNA	NP_066998.1	NM_021175.2	-1.279742	2205.5	3722.5	3385.25	0
hypothetical protein BC009862 (LOC90113), mRNA	XP_291077.3	XM_291077.3	-1.769275	2221.5	6261.5	5176	0
tripartite motif-containing 10 (TRIM10), transcript variant 1, mRNA	NP_006769.1	NM_006778.2	-1.750912	2296.5	4089.5	1565.5	0
fksg17 fksg17		NM_032031	-1.576144	2320.5	2050	1701.75	1
LIM homeobox 9 (LHX9), transcript variant 1, mRNA	NP_064589.2	NM_020204.2	-1.374971	2333.5	16158	13872.25	0
G protein-coupled receptor 51 (GPR51), mRNA	NP_005449.5	NM_005458.5	-1.389185	2361	3420	2489.25	0
cdna: flj21394 fis clone col03536 unnamed protein product		AK025047	-2.258109	2387.5	17288	11926.75	0
GPI anchored molecule like protein (GML), mRNA	NP_002057.1	NM_002066.1	-1.438045	2405	16818	14265.75	0
programmed cell death 1 (PDCD1), mRNA	NP_005009.1	NM_005018.1	-1.519488	2537	8575	7118.5	0
cadherin 20, type 2 (CDH20), mRNA	NP_114097.2	NM_031891.2	-1.393019	2538	15588	12275.75	0
glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P) (GLDC), mRNA	NP_000161.1	NM_000170.1	-1.405054	2542.5	6039	4550.5	1
protease, serine, 35 (PRSS35), mRNA	NP_699193.1	NM_153362.1	-1.451818	2545	16909	14109	0

Fig. 4 (continued)

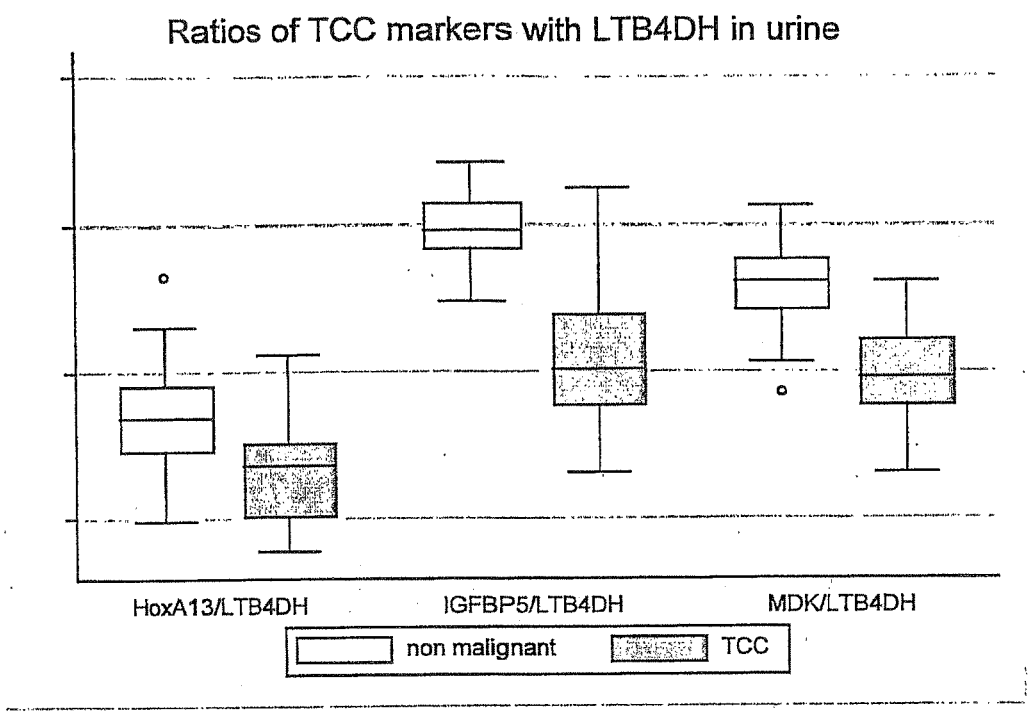

Ratios of TCC markers with LTB4DH in urine
HoxA13/LTB4DH
IGFBP5/LTB4DH
MDK/LTB4DH
non malignant
TCC

Fig. 5

a.

ratio	sensitivity (%)	specificity (%)
MDK/LTB4DH	87	81
IGFBP5/LTB4DH	87	88
HoxA13/LTB4DH	65	81

b.

combination test	sensitivity (%)	specificity (%)
MDK/LTB4DH and IGFBP5/LTB4DH	92	98
MDK/LTB4DH and HoxA13/LTB4DH	88	86
IGFBP5/LTB4DH and HoxA13/LTB4DH	83	98

Fig. 6

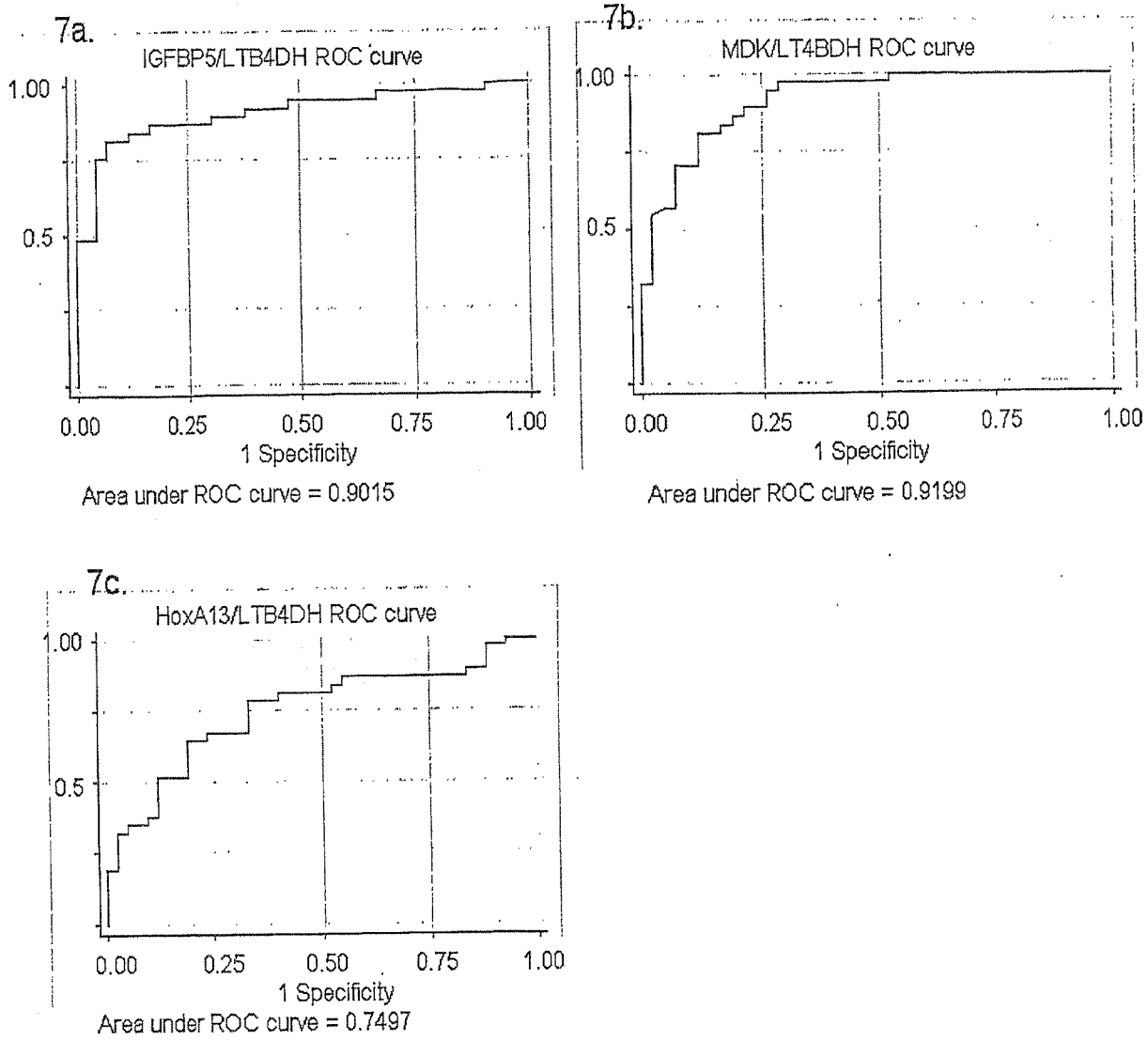


Figure 7. ROC curves showing the sensitivity and specificity of detection of TCC in urine samples from TCC patients and non-malignant controls using ratios with LTB4DH.

7a. IGFBP5/LTB4DH; 7b. MDK/LT4BDH; 7c. HoxA13/LTB4DH.

Fig. 7

Fig. 8a: Combination test with MDK/LTB4DH and IGFBP5/LTB4DH

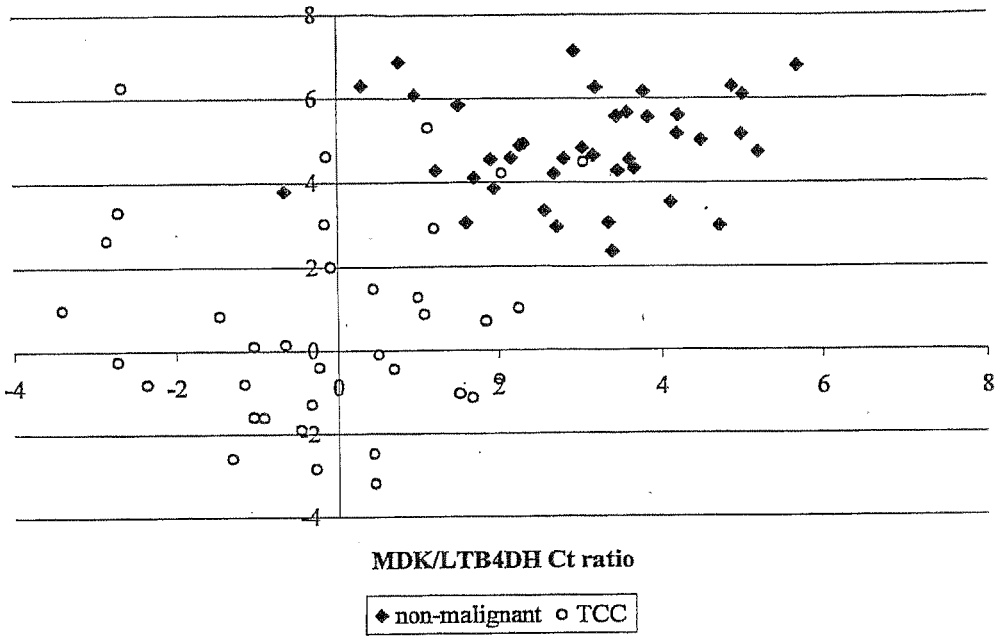


Fig. 8b: Combination test with MDK/LTB4DH and HoxA13/LTB4DH

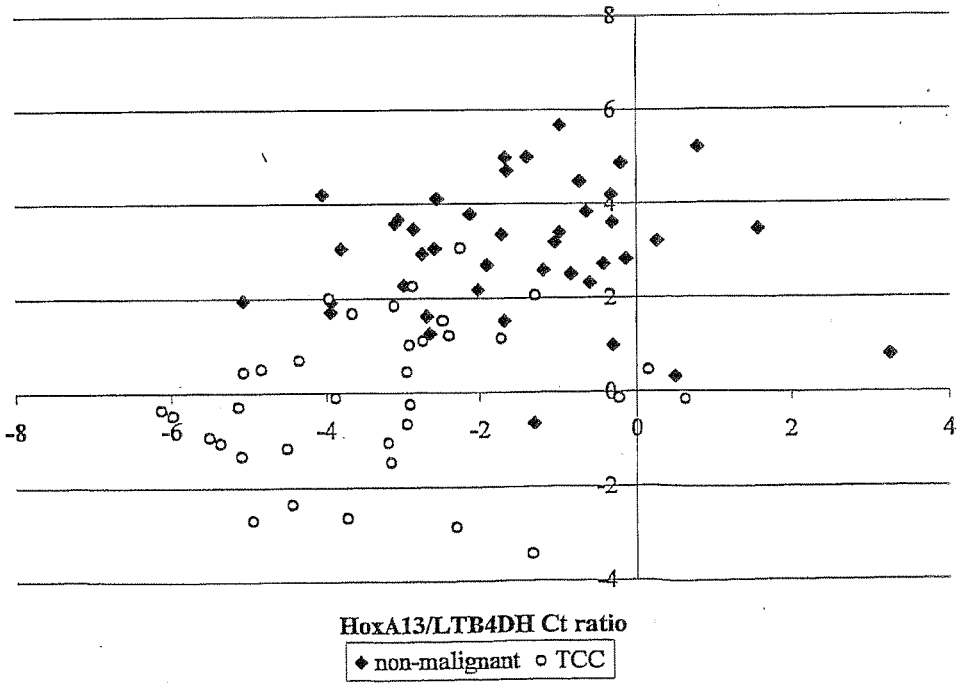


Fig. 8c: Combination test with IGFBP5/LTB4DH and HoxA13/LTB4DH

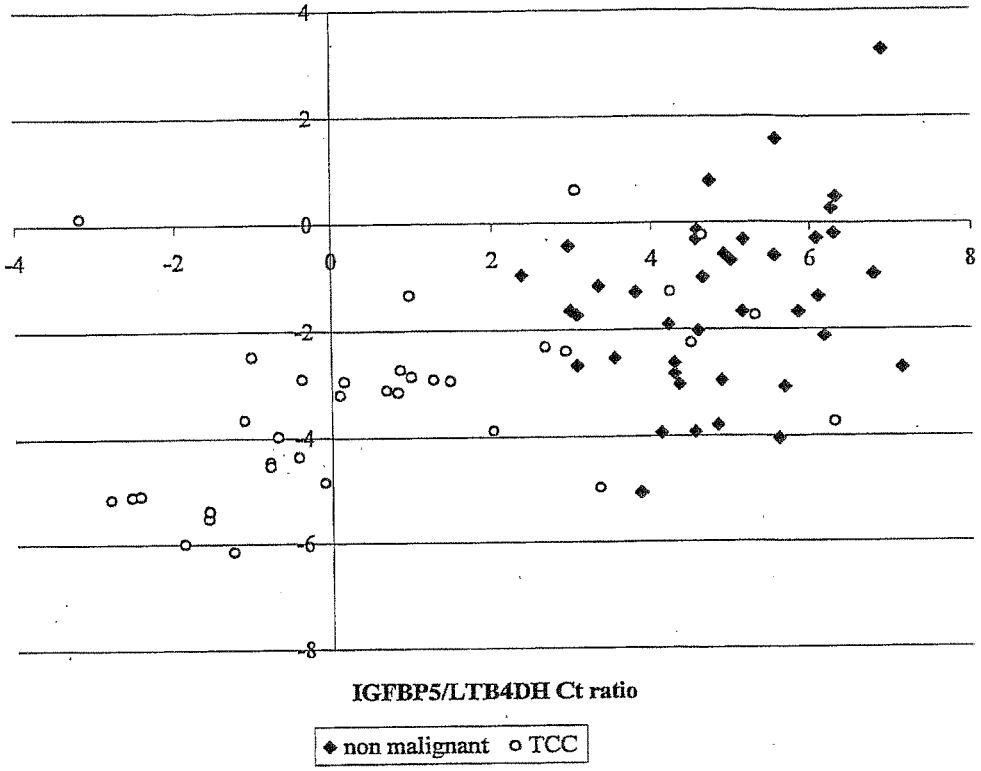


Fig 8d: Combination Test with MDK/BAG1 and IGFBP5/BAG1

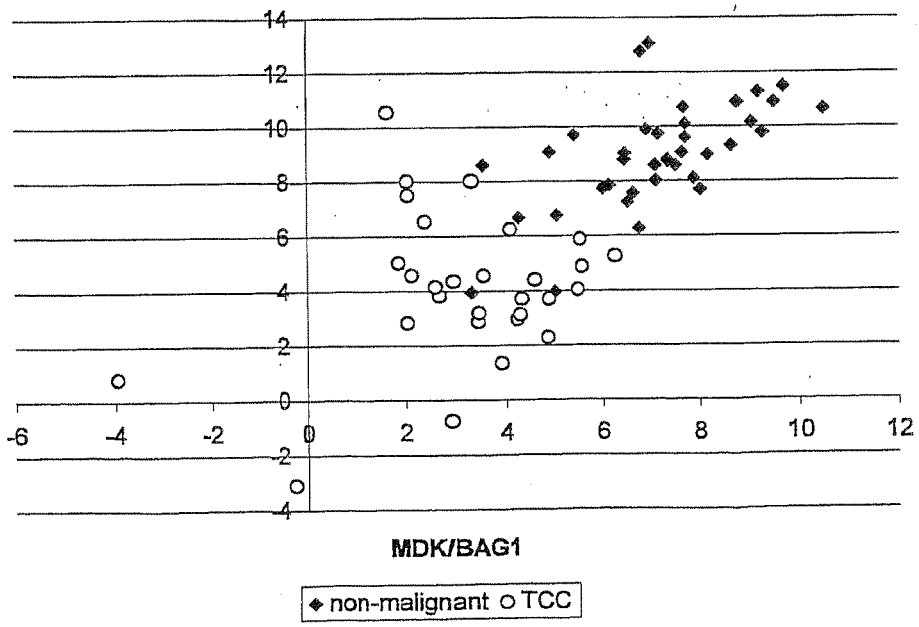


Fig. 8e: Combination test with MDK/BAG1 and HoxA13/BAG1

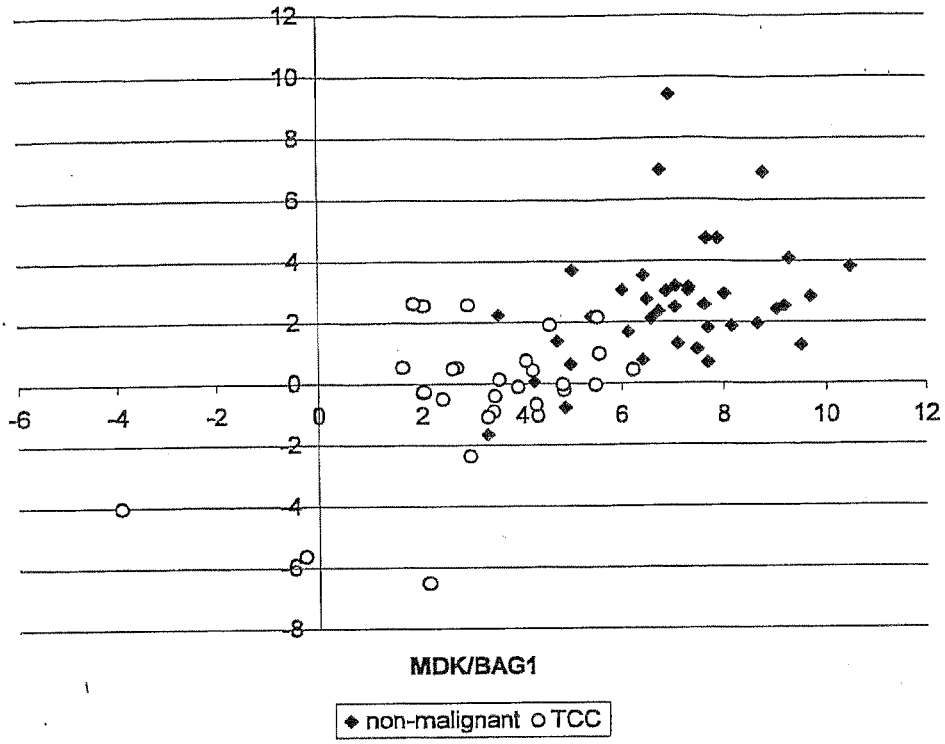


Fig. 8f: Combination test with IGFBP5/BAG1 and HoxA13/BAG1

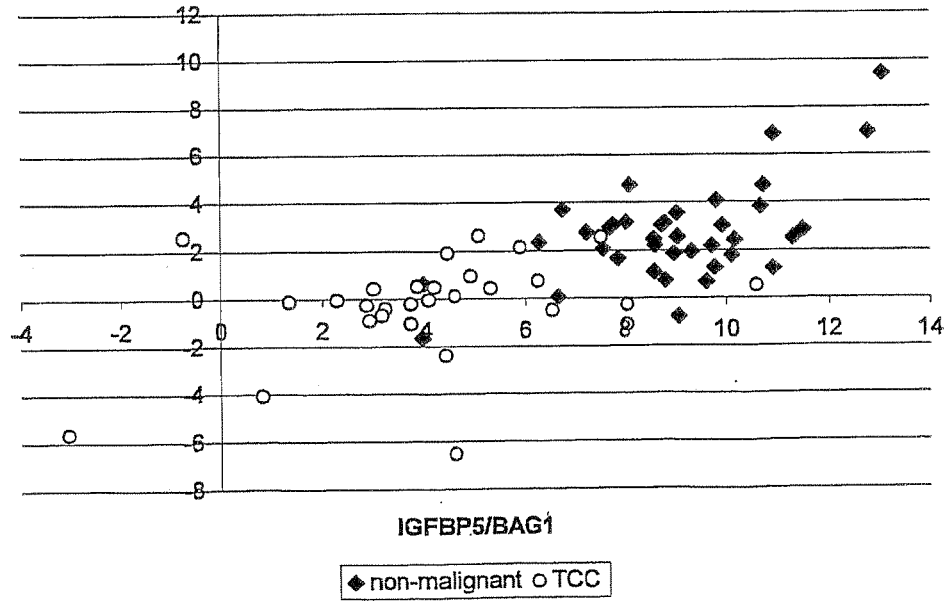
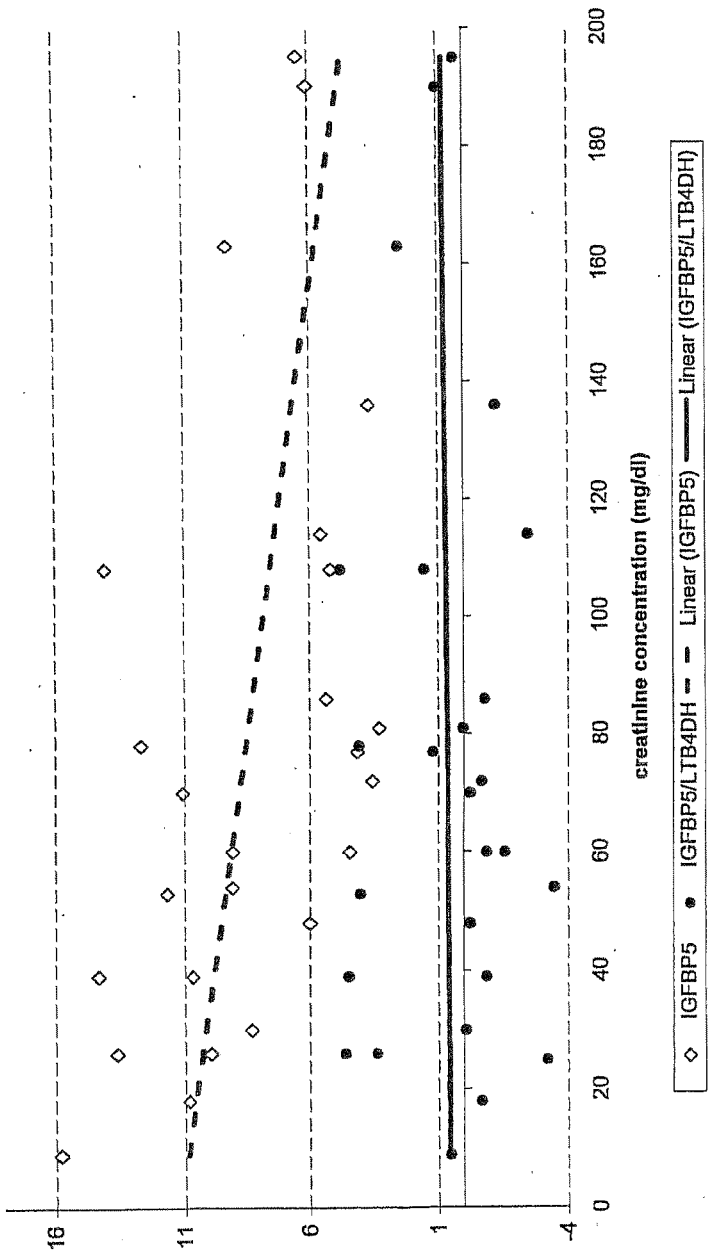


Figure 8. Scatter plots showing the use of test combinations to discriminate between urine samples from TCC patients and controls with non-malignant disease.8a. MDK/LTB4DH and IGFBP5/LTB4DH; 8b. MDK/LTB4DH and HoxA13/LTB4DH; 8c. IGFBP5/LTB4DH and HoxA13/LTB4DH; 8d. MDK/BAG1 and IGFBP5/BAG1; 8e. MDK/BAG1 and HoxA13/BAG1; 8f. IGFBP5/BAG1 and HoxA13/BAG1.

Fig. 9a: IGFBP5 and IGFBP5/LTB4DH vs creatinine concentration: TCC samples



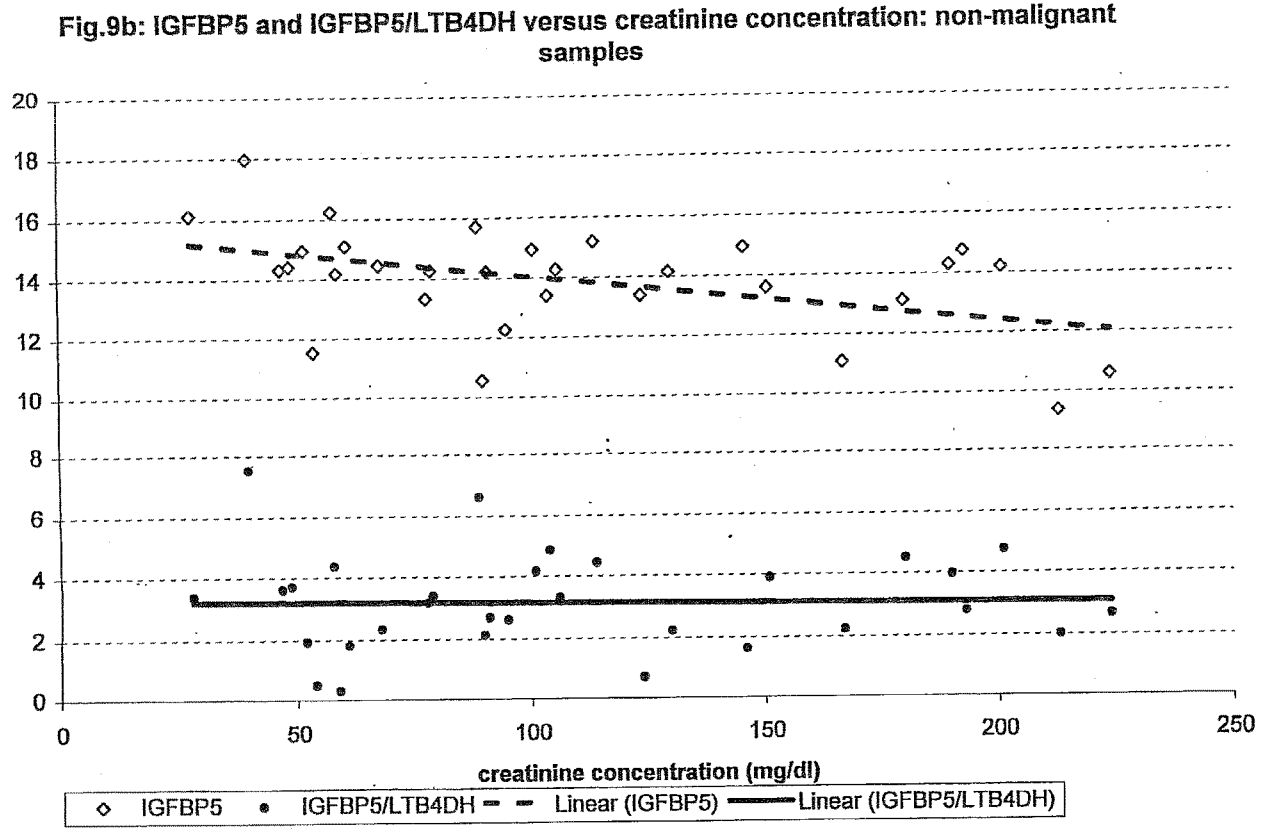


Figure 9. Scatter plots showing the correlation between ΔCt for IGFBP5 and ΔCt ratios for IGFBP5/LTB4DH and urine creatinine concentration.
9a. Urine samples from patients with TCC.
9b. Urine samples from patients with non-malignant disease.

Fig. 10a: MDK - catheterised and voided samples

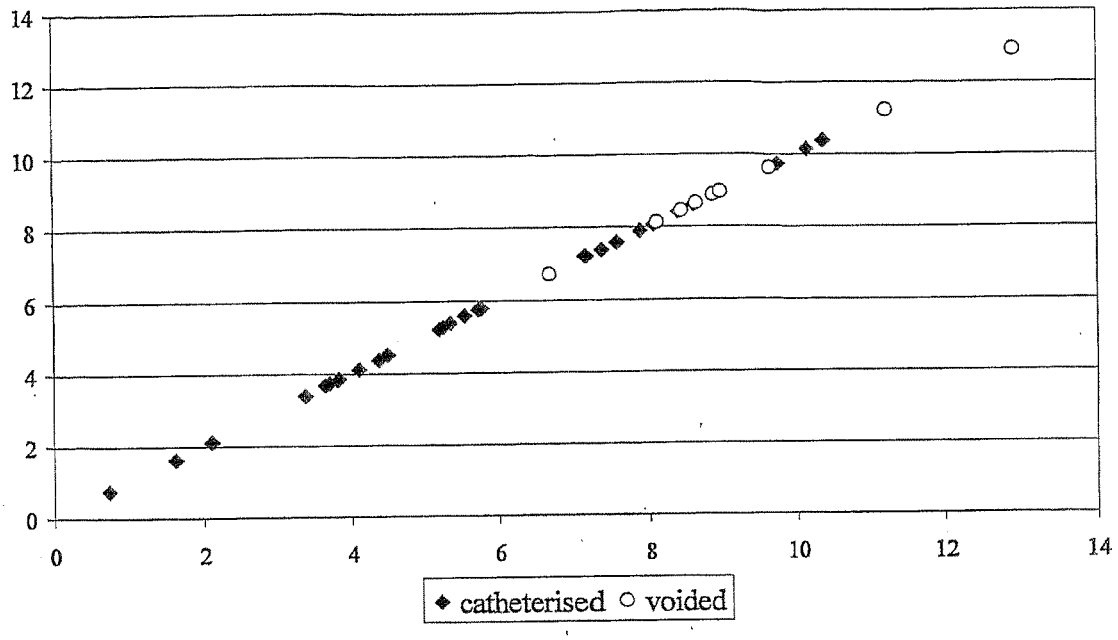


Fig. 10b: MDK/LTB4DH -catheterised and voided samples

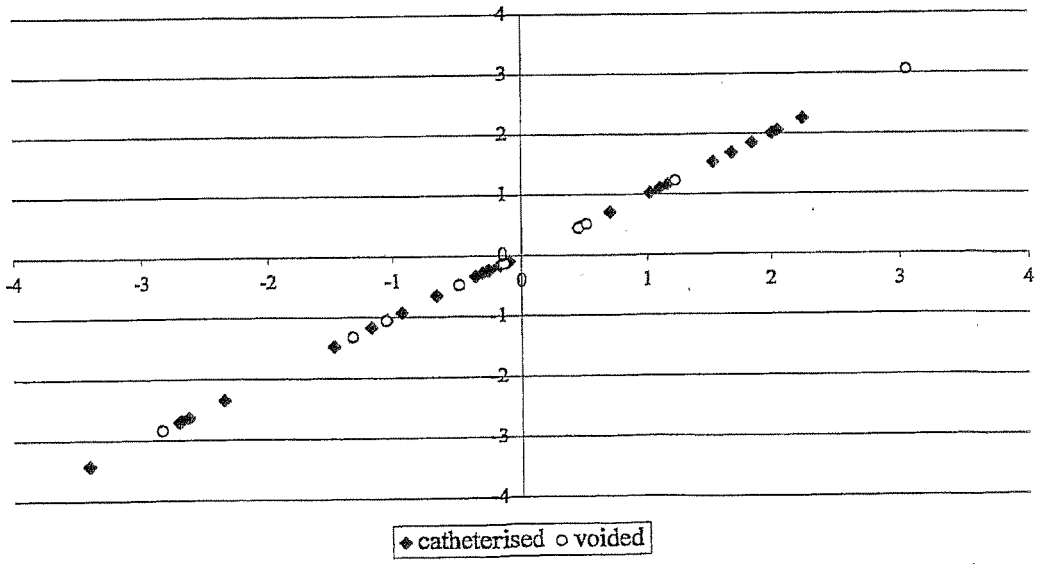


Fig. 10c: IGFBP5 - catheterised and voided samples

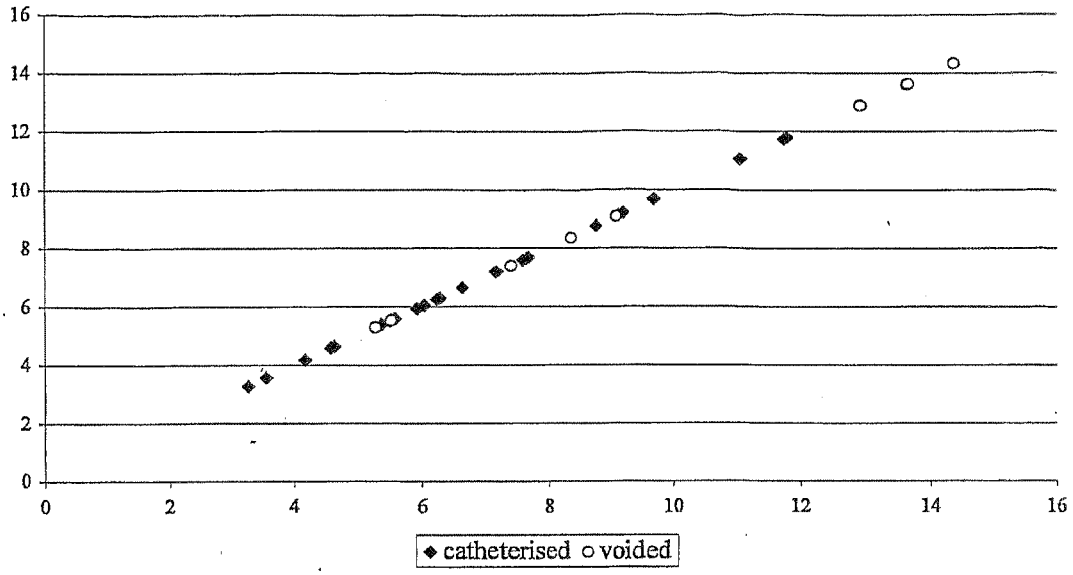


Fig. 10d: IGFBP5/LTB4DH -catheterised and voided samples

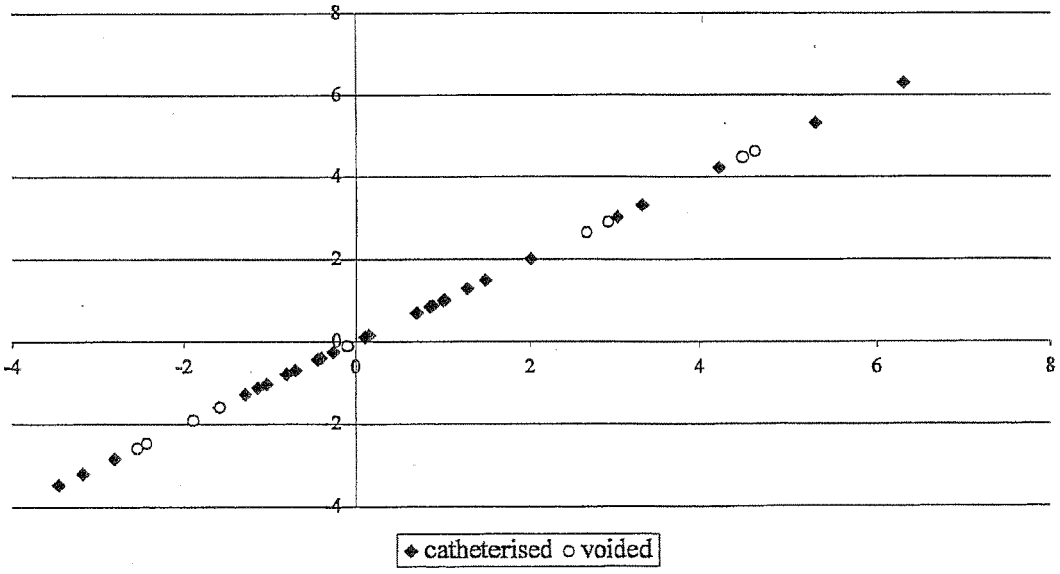


Fig. 10e: HoxA13 - catheterised and voided samples

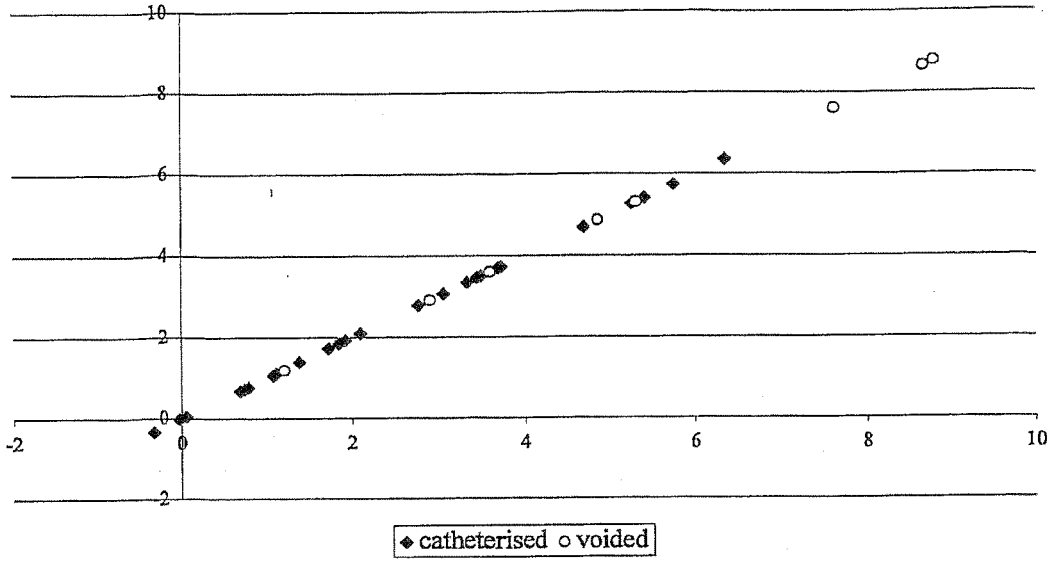


Fig. 10f: HoxA13/LTB4DH -catheterised and voided samples

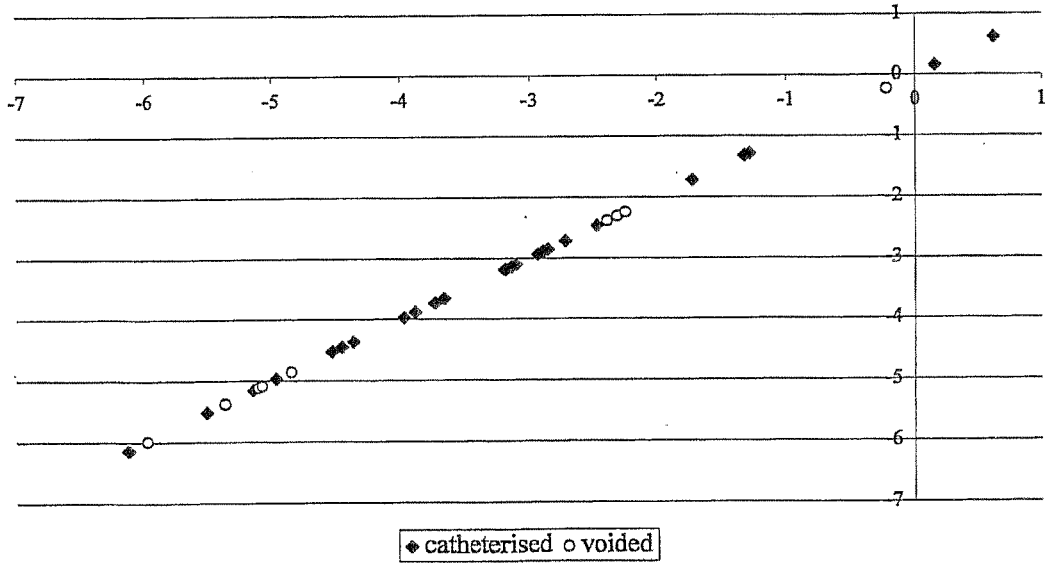


Figure 10a. Self-self scatter plots showing the distribution of voided and catheterised samples from TCC patients analysed using BTMs alone and BTMs in ratios with LTB4DH. 10a. MDK; 10b. MDK/LTB4DH; 10c. IGFBP5; 10d. IGFBP5/LTB4DH; 10e. HoxA13; 10f. HoxA13/LTB4DH.

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
gamma-glutamyl hydrolase	GGH	mwghuman3 0K#A:03601	NM_003878.1	NP_003869.1	2.7	7.5	2.78E-08	3.63E-09	102	S
secreted phosphoprotein 1	SPP1	mwghuman3 0K#A:09441	NM_000582.2	NP_000573.1	5.1	28.6	3.04E-08	0.000000525	143.5	S
neuritin 1	NRN1	mwghuman3 0K#A:00658	NM_016588.2	NP_057672.1	3.9	54.8	1.93E-07	0.000000265	232	S
secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	mwghuman3 0K#A:08092	NM_003118.2	NP_003109.1	2.5	6.9	2.9E-07	0.00000013	352.5	S
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif	ADAMTS10	mwghuman3 0K#B:1355	NM_030957.1	NP_112219.2	2.7	25.8	2.27E-06	0.000000856	465	S
contactin 1	CNTN1	mwghuman3 0K#A:01591	NM_175038.1	NP_778203.1	1.9	5.3	2.61E-06	0.00000196	805	S
tolloid-like 2	TLL2	mwghuman3 0K#A:02932	NM_012465.2	NP_036597.1	3.9	35.6	0.0000207	0.0000466	1019	S
protein disulfide isomerase-related	PDIR	mwghuman3 0K#A:03506	NM_006810.1	NP_006801.1	1.6	3.3	0.0000228	0.00000785	1044.5	S
fibrillin 1	FBN1	mwghuman3 0K#A:07105	NM_000138.2	NP_000129.2	2.1	7.9	2.822E-06	1.37393E-06	1072.5	S
KIAA0100 gene product		mwghuman3 0K#A:10762	NM_014680.2	NP_055495.2	1.5	2.3	1.65E-06	0.00000187	1100.5	S
calreticulin	CALR	mwghuman3 0K#A:10360	NM_004343.2	NP_004334.1	1.7	3.4	5.39E-06	0.00000518	1123.5	S
integrin, beta-like 1	ITGBL1	mwghuman3 0K#A:07933	NM_004791.1	NP_004782.1	1.9	10.5	0.0000293	0.0000224	1186	S
elastase 3B, pancreatic	ELA3B	mwghuman3 0K#B:3993	NM_007352.1	NP_031378.1	1.4	2.1	1.65E-06	0.00000785	1239.5	S
SPARC related modular calcium binding 2	SMOC2	mwghuman3 0K#B:0260	NM_022138.1	NP_071421.1	1.6	4.3	0.0000069	0.00000547	1280	S

Fig. 11

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
hexosaminidase A (alpha polypeptide)	HEXA	mwghuman3 0K#B:9777	NM_000520.2	NP_000511.1	1.9	14.6	0.0000183	0.0000325	1318.5	S
insulin-like growth factor binding protein 7	IGFBP7	mwghuman3 0K#A:03385	NM_001553.1	NP_001544.1	2.0	6.5	0.0000614	0.000059	1554.5	S
microfibrillar-associated protein 2	MFAP2	mwghuman3 0K#B:3055	NM_017459.1	NP_059453.1	1.6	4.9	0.0000388	0.0000466	1565.5	S
cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	CILP	mwghuman3 0K#A:00019	NM_003613.1	NP_003604.2	1.5	2.7	0.0000323	0.0000254	1582	S
olfactomedin 1	OLFM1	mwghuman3 0K#B:3555	NM_058199.2	NP_478106.1	2.3	20.7	0.0000508	0.0000254	1704	S
lumican	LUM	mwghuman3 0K#A:09199	NM_002345.2	NP_002336.1	2.6	25.0	0.0002509	6.62502E-05	1953	S
midkine (neurite growth-promoting factor 2)	MDK	mwghuman3 0K#A:01650	NM_002391.2	NP_002382.1	1.8	8.9	0.0002901	5.24719E-05	2897	S
semaphorin (LOC56920)	SEM2	mwghuman3 0K#A:05073	NM_020163.1	NP_064548.1	1.4	2.2	7.236E-05	0.000116474	2920	S
protease, serine, 11	PRSS11	mwghuman3 0K#B:1274	NM_002775.2	NP_002766.1	1.5	5.4	0.0002849	9.32339E-05	3896.5	S
sulfatase 1	SULF1	mwghuman3 0K#B:8770	NM_015170.1	NP_055985.1	3.2	60.9	0.0025727	0.000797894	4138.5	S
serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1	SERPINH1	mwghuman3 0K#A:08615	NM_001235.2	NP_001226.2	1.5	2.7	5.232E-05	0.000221711	4391	S
matrix Gla protein	MGP	mwghuman3 0K#B:4003	NM_000900.2	NP_000891.2	2.6	47.9	0.0011611	0.001781907	5134	S

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
tissue inhibitor of metalloproteinase 1	TIMP1	mwghuman3 0K#A:08048	NM_003254.1	NP_003245.1	1.8	4.4	0.0010783	0.006400169	7533	S
EGF-like-domain, multiple 6	EGFL6	mwghuman3 0K#A:07688	NM_015507.2	NP_056322.2	1.5	3.4	0.0042021	0.00857023	8467	S
sperm associated antigen 11	SPAG11	mwghuman3 0K#B:1373	NM_058203.1	NP_478110.1	1.3	4.2	0.0015737	0.001050446	10950	S
insulin-like growth factor binding protein 5	IGFBP5	mwghuman3 0K#C:1077	NM_000599.2	NP_000590.1	1.7	6.5	0.0097847	0.03366216	10980.5	S
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEMA3F	mwghuman3 0K#A:07262	NM_004186.2	NP_004177.2	-1.1	17.2	0.4328626	0.5041839	NA	S
cell division cycle 2, G1 to S and G2 to M	CDC2	mwghuman3 0K#A:05382	NM_033379.2	NP_203698.1	5.3	16.5	1.67E-12	6.12E-11	8	
topoisomerase (DNA) II alpha	TOP2A	mwghuman3 0K#B:7144	NM_001067.2	NP_001058.2	3.6	7.5	5.33E-11	1.32E-09	28.5	
ubiquitin-conjugating enzyme E2C	UBE2C	mwghuman3 0K#A:01776	NM_181803.1	NP_861519.1	4.6	34.3	6.82E-10	1.01E-09	29.5	
stathmin 1	STMN1	mwghuman3 0K#A:00925	NM_203401.1	NP_981946.1	3.2	11.4	7.66E-10	3.63E-09	44	
tubulin, alpha 4	TUBA4	mwghuman3 0K#B:2461	NM_025019.1	NP_079295.1	2.6	4.5	3.1E-09	1.32E-09	82.5	
histone 1, H1b	HIST1H1B	mwghuman3 0K#A:05716	NM_005322.2	NP_005313.1	2.3	5.7	1.77E-11	4.42E-12	93	
high-mobility group box 2	HMGB2	mwghuman3 0K#B:3649	NM_002129.2	NP_002120.1	2.6	5.6	7.85E-09	1.44E-08	95.5	
cyclin A2	CCNA2	mwghuman3 0K#A:04253	NM_001237.2	NP_001228.1	2.9	8.4	3.87E-08	5.85E-09	129.5	
cell division cycle associated 1	CDCA1	mwghuman3 0K#B:9471	NM_145697.1	NP_663735.1	2.4	8.2	1.85E-09	5.85E-09	151.5	

Fig. 11 (continued)

WO 2007/091904 PCT/NZ2007/000029

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
hypothetical protein MGC5576		mwghuman3 0K#A:06786	NM_024056.2	NP_076961.1	2.1	4.6	6.35E-09	9.25E-09	171	
DEK oncogene	DEK	mwghuman3 0K#B:2969	NM_003472.2	NP_003463.1	2.4	6.2	1.11E-07	1.44E-08	173.5	
MLF1 interacting protein	MLF1IP	mwghuman3 0K#C:8850	NM_024629.2	NP_078905.2	2.3	4.6	2.22E-07	6.07E-08	209.5	
cell division cycle associated 8	CDCA8	mwghuman3 0K#A:07906	NM_018101.1	NP_060571.1	2.3	4.1	2.8E-07	4.99E-08	212	
hypothetical protein FLJ20647		mwghuman3 0K#A:03566	NM_017918.3	NP_060388.1	2.2	4.6	1.5E-07	0.000000109	216	
thymidylate synthetase	TYMS	mwghuman3 0K#A:10045	NM_001071.1	NP_001062.1	2.2	5.0	1.48E-07	2.72E-08	232.5	
SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	SMC4L1	mwghuman3 0K#A:05648	NM_001002799.1	NP_001002799.1	2.4	5.7	5.7E-07	0.000000525	264.5	
v-yes-1 Yamaguchi sarcoma viral related oncogene *homolog*	LYN	mwghuman3 0K#C:2653	NM_002350.1	NP_002341.1	1.9	4.5	8.07E-08	0.000000265	267	
high-mobility group box 3	HMGB3	mwghuman3 0K#A:01602	NM_005342.1	NP_005333.1	1.9	5.0	2.13E-10	6.12E-11	268	
prostaglandin I2 (prostacyclin) receptor	PTGIR	mwghuman3 0K#A:00268	NM_000960.3	NP_000951.1	3.2	31.5	3.59E-07	4.09E-08	270.5	
downstream neighbor of SON (DONSON)	DONSON	mwghuman3 0K#A:05883	NM_145795.1	NP_665738.1	1.8	3.3	2.74E-08	4.09E-08	279.5	
hyaluronan-mediated motility receptor	HMMR	mwghuman3 0K#A:02702	NM_012485.1	NP_036617.1	2.7	6.8	1.84E-06	0.000000729	291	
claudin 6	CLDN6	mwghuman3 0K#A:08357	NM_021195.3	NP_067018.1	3.2	39.1	7.89E-07	6.07E-08	296.5	
histone 1, H1d	HIST1H1D	mwghuman3 0K#C:1892	NM_005320.2	NP_005311.1	2.1	4.8	4.46E-08	7.37E-08	306.5	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
chromosome 10 open reading frame 3	C10orf3	mwghuman3 0K#A:01678	NM_018131.3	NP_060601.2	2.1	4.3	9.03E-08	6.07E-08	308.5	
kinetochore associated 1	KNTC1	mwghuman3 0K#A:05391	NM_014708.3	NP_055523.1	2.2	4.2	2.32E-07	0.000000265	325	
CDC28 protein kinase regulatory subunit 1B	CKS1B	mwghuman3 0K#C:0649	NM_001826.1	NP_001817.1	2.1	3.4	1.7E-08	4.99E-08	332	
ribonucleotide reductase M2 polypeptide	RRM2	mwghuman3 0K#B:3501	NM_001034.1	NP_001025.1	2.6	16.6	0.0000015	0.000000856	344	
histone 1, H2bh	HIST1H2BH	mwghuman3 0K#B:2977	NM_003524.2	NP_003515.1	3.1	15.3	0.0000011	0.000000794	349	
serine/threonine kinase 6	STK6	mwghuman3 0K#A:04814	NM_198437.1	NP_940839.1	2.6	26.9	1.67E-06	7.37E-08	349.5	
M-phase phosphoprotein 1	MPHOSPH1	mwghuman3 0K#A:09885	NM_016195.2	NP_057279.2	1.9	3.8	3.29E-07	0.00000137	359.5	
cyclin B2	CCNB2	mwghuman3 0K#A:03606	NM_004701.2	NP_004692.1	2.0	3.4	6.19E-07	7.37E-09	373.5	
G protein-coupled receptor 32	GPR32	mwghuman3 0K#A:03297	NM_001506.1	NP_001497.1	3.4	42.0	1.26E-06	0.000000856	390	
endoglin	ENG	mwghuman3 0K#A:05668	NM_000118.1	NP_000109.1	1.9	5.3	4.49E-07	0.000000525	418.5	
malignant fibrous histiocytoma amplified sequence 1 MFHAS1	MFHAS1	mwghuman3 0K#A:04639	NM_004225.1	NP_004216.1	2.4	11.0	2.17E-07	0.000000243	425	
histone 1, H1c	HIST1H1C	mwghuman3 0K#A:07773	NM_005319.3	NP_005310.1	2.3	10.0	3.71E-07	0.000000375	425	
arginine vasopressin receptor 2	AVPR2	mwghuman3 0K#A:01219	NM_000054.2	NP_000045.1	2.3	22.3	8.93E-07	6.07E-08	427.5	
centromere protein F	CENPF	mwghuman3 0K#A:06471	NM_016343.2	NP_057427.3	1.7	2.6	2.51E-07	1.17564E-06	435.5	
homeo box A13	HOXA13	mwghuman3 0K#A:08971	NM_000522.2	NP_000513.2	1.7	3.5	2.61E-07	0.000000619	439.5	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
h4 histone family, member g		mwghuman3 0K#A:01329	XM_030144	-	3.0	13.2	2.33E-06	0.00000179	463	
MGC27121 gene		mwghuman3 0K#C:3953	NM_0010013 43.1	NP_0010013 43.1	3.6	46.3	1.891E-06	5.18452E-06	481.5	
nucleoside phosphorylase	NP	mwghuman3 0K#A:03762	NM_000270.1	NP_000261.1	1.9	4.2	2.7E-07	0.000000375	497	
asp (abnormal spindle)-like, microcephaly associated	ASPM	mwghuman3 0K#A:01367	NM_018136.2	NP_060606.2	2.4	14.5	7.55E-07	0.00000187	504.5	
hypothetical protein flj11871		mwghuman3 0K#A:10682	NM_025117		2.0	13.2	1.96E-06	0.000001	511	
likely ortholog of mouse limb-bud and heart gene	LBH	mwghuman3 0K#B:7280	NM_030915.1	NP_112177.1	1.7	4.7	2.64E-07	0.000000223	528	
nudix (nucleoside diphosphate linked moiety X)-type motif 1	NUDT1	mwghuman3 0K#A:05916	NM_198954.1	NP_945192.1	1.9	3.7	5.12E-08	0.000000444	546.5	
helicase, lymphoid-specific	HELLS	mwghuman3 0K#A:00387	NM_018063.3	NP_060533.2	1.8	4.3	5.874E-07	3.74678E-07	550	
ankyrin repeat and SOCS box-containing 9	ASB9	mwghuman3 0K#A:01131	NM_024087.1	NP_076992.1	1.7	5.9	1.27E-06	0.0000016	556	
MCM5 minichromosome maintenance deficient 5	MCM5	mwghuman3 0K#A:07747	NM_006739.2	NP_006730.2	1.7	3.3	7.631E-08	1.55499E-07	557.5	
IGF-II mRNA-binding protein 2	IMP-2	mwghuman3 0K#A:09784	NM_006548.3	NP_006539.2	2.1	4.9	3.964E-06	1.17464E-05	575	
hypothetical protein DKFZp566M1046	DKFZP566 M1046	mwghuman3 0K#B:8751	NM_032127.1	NP_115503.1	1.8	5.7	2.214E-06	1.37393E-06	594.5	
tubulin, alpha 2	TUBA2	mwghuman3 0K#B:4654	NM_079836.1	NP_524575.1	1.8	3.9	6.73E-07	0.00000217	602	
growth arrest-specific 2 like 3	GAS2L3	mwghuman3 0K#C:3659	NM_174942.1	NP_777602.1	2.0	5.6	7.484E-07	2.91943E-06	604	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
hypothetical protein FLJ12442		mwghuman3 0K#B:2460	NM_022908.1	NP_075059.1	1.7	2.9	1.54E-08	3.63E-09	614	
MCM6 minichromosome maintenance deficient 6	MCM6	mwghuman3 0K#B:8147	NM_005915.4	NP_005906.2	2.2	5.7	5.43E-07	0.000000232	653.5	
docking protein 3	DOK3	mwghuman3 0K#B:2635	NM_024872.1	NP_079148.1	2.2	12.6	1.75E-06	4.99E-08	655	
WD repeat domain 18	WDR18	mwghuman3 0K#B:3546	NM_024100.2	NP_077005.2	2.0	8.7	9.89E-07	4.99E-08	677	
cytoskeleton associated protein 2	CKAP2	mwghuman3 0K#A:00670	NM_018204.2	NP_060674.2	1.8	4.3	3.106E-06	1.93626E-05	701.5	
kinesin family member 20A	KIF20A	mwghuman3 0K#A:07989	NM_005733.1	NP_005724.1	1.9	2.8	1.045E-06	1.07593E-07	707.5	
putative fap protein		mwghuman3 0K#B:5292	U63542		2.1	18.9	4.98E-06	0.0000045	718	
chromosome 6 open reading frame 32	C6orf32	mwghuman3 0K#A:04643	NM_015864.2	NP_056948.2	1.8	11.4	1.527E-07	1.29514E-07	721.5	
NIMA (never in mitosis gene a)-related kinase 2	NEK2	mwghuman3 0K#A:00847	NM_002497.2	NP_002488.1	2.0	3.5	1.023E-05	3.37794E-06	732	
cryptochrome 1 (photolyase-like)	CRY1	mwghuman3 0K#A:06219	NM_004075.2	NP_004066.1	1.8	3.0	6.04E-06	0.000001	744	
transglutaminase 2	TGM2	mwghuman3 0K#A:08571	NM_004613.2	NP_004604.2	2.0	6.3	1.498E-05	3.37794E-06	747	
discs, large homolog 7	DLG7	mwghuman3 0K#B:7380	NM_014750.3	NP_055565.2	2.0	5.9	1.353E-05	1.17464E-05	748	
eukaryotic translation initiation factor 2C	EIF2C2	mwghuman3 0K#C:2287	NM_012154.2	NP_036286.2	1.7	2.7	1.73E-08	9.25E-09	766	
DEP domain containing 1	DEPDC1	mwghuman3 0K#B:7337	NM_017779.3	NP_060249.2	2.0	4.6	1.722E-06	3.15648E-07	776	
histone 2, H4	HIST2H4	mwghuman3 0K#C:1932	NM_003548.2	NP_003539.1	1.7	2.7	3.279E-06	2.91943E-06	823	

Fig. 11 (continued)

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Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
baculoviral IAP repeat-containing 5 (survivin)	BIRC5	mwghuman3 0K#B:0833	NM_001168.1	NP_001159.1	2.6	54.8	4.87E-06	0.000000856	823	
MCM7 *minichromosome* maintenance deficient 7	MCM7	mwghuman3 0K#B:7620	NM_182776.1	NP_877577.1	1.9	4.0	1.13E-06	0.0000103	829	
methylthioadenosine phosphorylase	MTAP	mwghuman3 0K#B:8310	AF109294.1	AAD19641.1	2.3	13.3	1.033E-05	1.33979E-05	844.5	
kinetochore associated 2	KNTC2	mwghuman3 0K#A:10053	NM_006101.1	NP_006092.1	1.6	2.9	1.169E-06	2.17032E-06	848	
HSPC150 protein similar to ubiquitin-conjugating enzyme	HSPC150	mwghuman3 0K#A:00955	NM_014176.1	NP_054895.1	1.9	3.4	1.782E-05	1.73622E-05	849.5	
SMC6 structural maintenance of chromosomes 6-like 1	SMC6L1	mwghuman3 0K#A:05363	NM_024624.2	NP_078900.1	1.7	4.0	6.059E-06	1.28219E-05	852	
histone 1, H2bc	HIST1H2BC	mwghuman3 0K#B:9593	NM_003526.2	NP_003517.2	1.9	5.3	7.93E-06	1.73622E-05	870	
ASF1 anti-silencing function 1 homolog B	ASF1B	mwghuman3 0K#A:04415	NM_018154.1	NP_060624.1	1.7	4.1	1.04E-06	0.0000016	872	
LDL receptor adaptor protein	ARH	mwghuman3 0K#B:2491	NM_015627.1	NP_056442.1	2.0	14.0	4.01E-06	0.000000155	872	
lamin B1	LMNB1	mwghuman3 0K#A:02069	NM_005573.2	NP_005564.1	1.8	3.4	2.869E-05	1.52615E-05	891.5	
hypothetical protein FLJ10719		mwghuman3 0K#B:2212	NM_018193.1	NP_060663.1	1.7	3.4	4.715E-06	8.99315E-06	894.5	
hypothetical protein FLJ10706		mwghuman3 0K#A:00611	NM_018186.2	NP_060656.2	1.5	2.8	1.483E-06	1.00418E-06	913	
MAD2 mitotic arrest deficient-like 1	MAD2L1	mwghuman3 0K#A:06387	NM_002358.2	NP_002349.1	1.8	3.9	1.058E-05	2.87228E-05	913.5	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
solute carrier family 22	SLC22A2	mwghuman3 0K#A:02704	NM_153191.1	NP_694861.1	3.2	31.3	0.0000171	0.0000287	915.5	
hypothetical protein MGC34923		mwghuman3 0K#C:4473	NM_144717.2	NP_653318.2	1.9	8.7	6.72E-07	0.000000525	937.5	
sperm associated antigen 5	SPAG5	mwghuman3 0K#A:07691	NM_006461.2	NP_006452.2	2.8	6.6	0.0000482	0.0000171	947	
activin A receptor type II-like 1	ACVRL1	mwghuman3 0K#A:00470	NM_000020.1	NP_000011.1	1.5	2.4	6.94E-06	0.00000733	961	
Down syndrome critical region gene 1	DSCR1	mwghuman3 0K#A:09846	NM_004414.5	NP_004405.3	1.5	2.7	1.119E-06	2.91943E-06	967	
protease, serine, 15	PRSS15	mwghuman3 0K#A:03353	NM_004793.2	NP_004784.2	1.9	15.2	0.0000135	0.00000292	969	
S100 calcium binding protein A9	S100A9	mwghuman3 0K#A:07436	NM_002965.2	NP_002956.1	4.1	44.0	0.0000071	0.0000525	975	
MCM4 minichromosome maintenance deficient 4	MCM4	mwghuman3 0K#B:7581	NM_182746.1	NP_877423.1	1.6	3.9	0.0000039	0.00000785	986.5	
suppression of tumorigenicity 7 like	ST7L	mwghuman3 0K#A:01391	NM_138728.2	NP_620056.1	2.0	13.4	7.64E-06	0.00000292	1001	
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	PLEKHA4	mwghuman3 0K#B:3447	NM_020904.1	NP_065955.1	1.4	3.0	1.28E-07	0.000000444	1030.5	
EphB1	EPHB1	mwghuman3 0K#A:00465	NM_004441.2	NP_004432.1	2.2	9.5	2.334E-05	1.52615E-05	1042.5	
caldesmon 1	CALD1	mwghuman3 0K#A:07744	NM_033140.2	NP_149131.1	2.2	7.0	1.129E-05	8.32858E-05	1057	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
SMC1 structural maintenance of chromosomes 1-like 1	SMC1L1	mwghuman3 0K#A:05798	NM_006306.2	NP_006297.2	1.6	2.9	4.98E-06	0.0000134	1061.5	
Thy-1 co-transcribed		mwghuman3 0K#C:0578	NM_033209.2	NP_149986.1	1.8	4.7	1.15E-06	0.000000375	1074	
RA-regulated nuclear matrix-associated protein	RAMP	mwghuman3 0K#A:03935	NM_016448.1	NP_057532.1	1.5	2.1	4.195E-07	7.28584E-07	1076	
FK506 binding protein 11	FKBP11	mwghuman3 0K#A:07244	NM_016594.1	NP_057678.1	1.8	5.0	0.0000122	0.0000287	1088.5	
chromosome 20 open reading frame 129	C20orf129	mwghuman3 0K#B:3650	NM_030919.1	NP_112181.1	1.6	2.4	2.438E-05	2.91943E-06	1106	
histone 1, H4h	HIST1H4H	mwghuman3 0K#B:4596	NM_003543.3	NP_003534.1	2.1	6.4	0.0000344	0.000059	1117	
cyclin-dependent kinase inhibitor 3	CDKN3	mwghuman3 0K#A:05799	NM_005192.2	NP_005183.2	2.1	4.7	7.871E-05	1.93626E-05	1117.5	
melanoma cell adhesion molecule	MCAM	mwghuman3 0K#A:10599	NM_006500.1	NP_006491.1	1.6	3.0	1.81E-06	0.0000045	1135.5	
synuclein, alpha interacting protein	SNCAIP	mwghuman3 0K#A:08103	NM_005460.1	NP_005451.1	1.7	2.7	0.0000151	0.0000236	1151.5	
nipsnap homolog 1	NIPSNAP1	mwghuman3 0K#A:10699	NM_003634.1	NP_003625.1	2.4	21.5	0.0000194	0.0000153	1165.5	
adaptor-related protein complex 1, mu 1 subunit	AP1M1	mwghuman3 0K#B:1553	NM_032493.2	NP_115882.1	1.5	4.1	6.692E-06	8.99315E-06	1173.5	
anillin, actin binding protein	ANLN	mwghuman3 0K#A:05280	NM_018685.2	NP_061155.2	2.6	7.7	0.0001	0.0000716	1177	
chromosome 6 open reading frame 69	C6orf69	mwghuman3 0K#C:0854	NM_173562.3	NP_775833.2	1.6	3.6	3.55E-07	0.000000856	1187	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
transducer of regulated cAMP response element-binding protein	TORC3	mwghuman30K#A:04006	NM_022769.1	NP_073606.2	1.6	2.8	1.51E-05	1.73622E-05	1187.5	
MYC-associated zinc finger protein	MAZ	mwghuman30K#A:04363	NM_002383.1	NP_002374.1	1.6	3.5	0.0000117	0.0000325	1195.5	
thioredoxin reductase 1	TXNRD1	mwghuman30K#A:02930	NM_182743.1	NP_877420.1	2.4	16.9	0.0000377	0.0000254	1201	
hypothetical protein xp_096695		mwghuman30K#B:5965	XM_096695		1.5	3.2	5.361E-06	2.51921E-06	1211.5	
chromosome 22 open reading frame 4	C22orf4	mwghuman30K#B:9849	NM_014346.1	NP_055161.1	1.5	2.3	1.056E-05	1.33979E-05	1234	
visinin-like 1	VSNL1	mwghuman30K#A:06227	NM_003385.3	NP_003376.2	2.2	13.8	0.0000215	0.0000254	1243.5	
similar to Carboxypeptidase N 83 kDa chain		mwghuman30K#B:4922	XM_209550.5	XP_209550.4	2.0	10.5	0.0000141	0.00000899	1256.5	
KIAA1598	KIAA1598	mwghuman30K#A:10158	NM_018330.3	NP_060800.2	1.9	18.9	6.547E-05	8.56146E-07	1271	
hypothetical protein flj13501		mwghuman30K#A:06319	NM_025007		2.0	5.7	3.162E-05	2.23862E-05	1285	
DKFZP434O047 protein	DKFZP434O047	mwghuman30K#A:08783	NM_015594.1	NP_056409.1	1.8	4.5	9.622E-06	4.13751E-05	1290.5	
hypothetical protein FLJ38716		mwghuman30K#B:7389	NM_152367.1	NP_689580.1	1.9	4.0	9.5E-06	2.87228E-05	1291.5	
similar to hypothetical protein (L1H 3 region)		mwghuman30K#A:02711	XM_372039.1	XP_372039.2	1.9	3.5	3.977E-05	1.73622E-05	1295.5	
hypothetical protein KIAA1875		mwghuman30K#B:5745	XM_291269.3	XP_291269.2	1.6	2.4	2.655E-05	1.33979E-05	1313.5	
primase, polypeptide 1	PRIM1	mwghuman30K#A:07833	NM_000946.2	NP_000937.1	1.6	2.9	3.313E-05	5.24719E-05	1315	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
hypothetical protein BC001096		mwghuman30K#B:6914	NM_138389.1	NP_612398.1	1.7	3.3	0.0000359	0.0000367	1318.5	
MCM2 minichromosome maintenance deficient 2	MCM2	mwghuman30K#A:08834	NM_004526.2	NP_004517.2	1.6	2.7	1.81E-06	0.0000045	1332	
gap junction protein, alpha 3	GJA3	mwghuman30K#A:04569	NM_021954.2	NP_068773.2	1.6	2.7	1.04E-06	0.00000252	1332.5	
chromosome 11 open reading frame 30	C11orf30	mwghuman30K#A:10832	NM_020193.2	NP_064578.2	1.4	3.4	6.848E-07	1.00418E-06	1339	
similar to hypothetical protein FLJ30672		mwghuman30K#B:9577	XM_376318.1	XP_376318.1	1.6	2.3	3.03E-05	2.53726E-05	1349	
Thy-1 co-transcribed (LOC94105)	THY1	mwghuman30K#A:07498	NM_033209.2	NP_149986.1	1.5	3.4	1.262E-05	2.53726E-05	1353	
low density lipoprotein receptor-related protein 3	LRP3	mwghuman30K#A:05066	NM_002333.1	NP_002324.1	1.5	2.1	1.068E-05	1.9727E-05	1358	
LAG1 longevity assurance homolog 2	LASS2	mwghuman30K#A:00827	NM_013384.3	NP_037516.3	1.7	4.6	0.0000173	0.0000224	1365	
chromosome 18 open reading frame 8	C18orf8	mwghuman30K#A:07371	NM_013326.2	NP_037458.2	1.5	2.1	6.11E-06	0.00000899	1366.5	
zinc finger protein 81	ZNF81	mwghuman30K#B:1067	NM_007137.1	NP_009068.1	1.5	2.2	2.599E-06	1.8667E-06	1387.5	
nuclear prelamin A recognition factor	NARF	mwghuman30K#A:02301	NM_031968.1	NP_114174.1	1.5	2.5	8.752E-06	1.73622E-05	1391.5	

Fig. 11 (continued)

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Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
methylene tetrahydrofolate dehydrogenase (NAD+ dependent)	MTHFD2	mwghuman30K#A:01688	NM_006636.2	NP_006627.1	2.4	8.4	0.0000861	0.00013	1392.5	
dihydrolipoamide branched chain transacylase E2	DBT	mwghuman30K#B:6654	NM_001918.1	NP_001909.1	1.6	2.3	4.015E-05	8.99315E-06	1398.5	
sialyltransferase 7D	SIAT7D	mwghuman30K#A:03286	NM_175040.1	NP_778205.1	1.7	7.9	3.17E-06	0.00000596	1400	
matrix metalloproteinase -like 1	MMPL1	mwghuman30K#A:02674	NM_004142.1	NP_004133.1	1.5	3.4	1.36E-06	2.91943E-06	1403	
kallikrein 11	KLK11	mwghuman30K#A:09721	NM_144947.1	NP_659196.1	1.5	2.3	0.0000159	0.0000153	1415.5	
karyopherin alpha 2	KPNA2	mwghuman30K#B:4036	NM_002266.1	NP_002257.1	1.6	3.3	9.792E-05	5.89923E-05	1426.5	
FGFR1 oncogene partner 2	FGFR1OP2	mwghuman30K#B:2210	NM_015633.1	NP_056448.1	1.5	5.0	1.338E-05	1.33979E-05	1427.5	
vimentin	VIM	mwghuman30K#A:02879	NM_003380.1	NP_003371.1	3.3	19.1	0.000123	0.0002	1451	
FLJ44108 protein		mwghuman30K#B:0931	XM_379827.1	XP_379827.1	1.7	2.9	7.746E-05	2.53726E-05	1474	
poly(A) polymerase gamma	PAPOLG	mwghuman30K#A:03836	NM_022894.2	NP_075045.2	2.7	36.2	0.0000757	0.0000932	1474.5	
formin homology 2 domain containing 1	FHOD1	mwghuman30K#A:05058	NM_013241.1	NP_037373.1	1.6	4.0	9.54E-06	0.00000187	1483.5	
RAS-like, family 12 (RASL12)	RASL12	mwghuman30K#A:07221	NM_016563.2	NP_057647.1	1.4	2.1	1.179E-05	2.23862E-05	1490.5	
high-mobility group nucleosomal binding domain 2	HMGN2	mwghuman30K#B:9113	NM_005517.2	NP_005508.1	1.6	2.7	0.0000826	0.0000367	1495.5	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	mwghuman30K#B:8464	NM_020845	NP_06589	2.3	26.2	0.0000711	0.0000224	1497	
derlin-1	DER1	mwghuman30K#A:01654	NM_024295.3	NP_077271.1	1.5	3.3	4.883E-05	5.24719E-05	1527	
EphA4	EPHA4	mwghuman30K#A:04433	NM_004438.3	NP_004429.1	1.5	3.1	0.0000113	0.0000743	1527.5	
V-set and immunoglobulin domain containing 1	VSIG1	mwghuman30K#B:6454	NM_182607.3	NP_872413.1	2.0	5.8	7.831E-05	3.24766E-05	1532.5	
regulator of G-protein signalling 5	RGS5	mwghuman30K#B:0128	NM_003617.2	NP_003608.1	1.8	6.3	0.0000417	0.0000174	1534.5	
KIAA1639 protein		mwghuman30K#B:4938	XM_290923.2	XP_290923.3	1.9	11.5	2.676E-05	1.9727E-05	1540.5	
SH2-B homolog	SH2B	mwghuman30K#B:8571	NM_015503.1	NP_056318.1	2.2	13.2	0.0000252	0.0000197	1556.5	
peptidoglycan recognition protein 4	PGLYRP4	mwghuman30K#A:00688	NM_020393.1	NP_065126.1	1.5	3.2	2.991E-06	4.50136E-06	1566	
CDC45 cell division cycle 45-like	CDC45L	mwghuman30K#A:09331	NM_003504.3	NP_003495.1	1.8	2.9	6.316E-05	0.000129985	1567.5	
male sterility domain containing 1	MLSTD1	mwghuman30K#A:04600	NM_018099.3	NP_060569.3	1.9	10.0	6.279E-05	3.66781E-05	1585.5	
hypothetical protein MGC11266		mwghuman30K#A:10595	NM_024322.1	NP_077298.1	1.5	3.4	5.16E-05	6.62502E-05	1608	
tumor necrosis factor receptor superfamily, member 13B	TNFRSF13B	mwghuman30K#A:00922	NM_012452.2	NP_036584.1	1.7	3.8	2.737E-05	6.62502E-05	1643	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
neuroepithelial cell transforming gene 1	NET1	mwghuman3 0K#B:5122	S82401.1	AAB37683.1	1.4	2.1	8.678E-06	4.50136E-06	1657	
lipoma HMGIC fusion partner-like 5	LHFPL5	mwghuman3 0K#C:9217	NM_182548.2	NP_872354.1	1.7	9.5	5.419E-05	4.66206E-05	1661	
myxovirus (influenza virus) resistance 2	MX2	mwghuman3 0K#A:10346	NM_002463.1	NP_002454.1	1.6	9.3	0.0000739	0.000001	1680	
sphingosine kinase 1	SPHK1	mwghuman3 0K#C:2264	NM_182965.1	NP_892010.1	1.5	2.2	2.284E-06	5.18452E-06	1702	
ATP-binding cassette, sub-family G (WHITE), member 4	ABCG4	mwghuman3 0K#A:02044	NM_022169.3	NP_071452.2	1.7	8.3	0.000012	0.0000039	1702	
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	SERPINB2	mwghuman3 0K#A:10076	NM_002575.1	NP_002566.1	1.8	8.3	3.09E-05	2.50475E-05	1705.5	
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10	GALNT10	mwghuman3 0K#A:10048	NM_017540.3	NP_060010.3	1.6	7.1	6.432E-05	2.23862E-05	1711	
leptin receptor	LEPR	mwghuman3 0K#B:5260	NM_0010036 80.1	NP_0010036 80.1	1.6	2.8	2.176E-05	2.87228E-05	1715.5	
MAX dimerization protein 4	MXD4	mwghuman3 0K#A:08296	NM_006454.2	NP_006445.1	1.7	4.1	0.0000111	0.0000134	1719.5	
phosphoinositol 4-phosphate adaptor protein-2	FAPP2	mwghuman3 0K#A:06904	NM_032639.2	NP_116028.1	1.5	3.3	1.563E-05	3.66781E-05	1725.5	
nucleoporin 210	NUP210	mwghuman3 0K#B:7411	NM_024923.2	NP_079199.2	1.6	2.8	6.528E-05	0.000104262	1728.5	

Fig. 11 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
c-src tyrosine *kinase*	CSK	mwghuman3 0K#A:01629	NM_004383.1	NP_004374.1	1.5	5.1	7.283E-06	8.56146E-07	3601	
neuropilin 1	NRP1	mwghuman3 0K#A:03091	NM_003873.2	NP_003864.2	2.3	17.2	0.002761	0.004728544	6356	

Fig. 11 (continued)

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Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
neuritin 1	NRN1	mwghuman30K#A:00658	NM_016588.2	NP_057672.1	3.0	17.6	4.78E-07	0.000000421	63	S
mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	MGAT1	mwghuman30K#A:09187	NM_002406.2	NP_002397.1	1.7	4.1	3.51E-07	0.00000395	165.5	S
KIAA0100 gene product		mwghuman30K#A:10762	NM_014680.2	NP_055495.2	1.6	2.5	1.74E-08	0.000000085	241	S
lipocalin 7	LCN7	mwghuman30K#B:9472	NM_022164.1	NP_071447.1	1.8	5.6	0.000015	0.0000271	436.5	S
olfactomedin 1	OLFM1	mwghuman30K#B:3555	NM_058199.2	NP_478106.1	1.8	6.9	3.39E-06	0.00000178	455	S
bone morphogenetic protein 7 A	BMP7	mwghuman30K#A:09963	NM_001719.1	NP_001710.1	1.7	4.1	2.96E-06	0.00000579	473	S
midkine (neurite growth-promoting factor 2)	MDK	mwghuman30K#B:4650	NM_002391.2	NP_002382.1	1.8	4.8	4.98E-07	0.000000194	492.5	S
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 10	ADAMTS10	mwghuman30K#B:1355	NM_030957.1	NP_112219.2	1.9	6.9	0.0000442	0.0000379	569.5	S
pM5 protein	PM5	mwghuman30K#A:00608	NM_014287.2	NP_055102.3	1.6	2.5	0.000017	0.0000339	598.5	S
tissue inhibitor of metalloproteinase 1	TIMP1	mwghuman30K#A:08048	NM_003254.1	NP_003245.1	1.7	3.2	0.0000185	0.0000107	611.5	S
lumican	LUM	mwghuman30K#A:09199	NM_002345.2	NP_002336.1	2.5	19.1	0.000104	0.0000883	632	S

Fig. 12

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Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
EGF-like-domain, multiple 6	EGFL6	mwghuman30K#A:07688	NM_015507.2	NP_056322.2	1.9	4.2	0.0000747	0.0000243	712	S
NODAL modulator 3	NOMO3	mwghuman30K#A:08071	NM_173614.1	NP_775885.1	1.5	3.0	1.71E-06	0.00000395	844.5	S
insulin-like growth factor binding protein 5	IGFBP5	mwghuman30K#C:1077	NM_000599.2	NP_000590.1	2.3	15.0	0.0000791	0.000284	859.5	S
hexosaminidase A (alpha polypeptide)	HEXA	mwghuman30K#B:9777	NM_000520.2	NP_000511.1	1.5	3.1	0.0000386	0.0000718	903.5	S
serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1	SERPINH1	mwghuman30K#A:08615	NM_001235.2	NP_001226.2	1.5	3.2	0.0000043	0.0000107	1070.5	S
carboxypeptidase A6	CPA6	mwghuman30K#A:02979	NM_020361.2	NP_065094.2	1.4	3.2	0.0000154	0.0000271	1098.5	S
natriuretic peptide precursor C	NPPC	mwghuman30K#A:06602	NM_024409.1	NP_077720.1	1.5	3.1	8.17E-06	0.0000121	1134	S
protease, serine, 11	PRSS11	mwghuman30K#B:1274	NM_002775.2	NP_002766.1	1.4	2.6	0.0000125	0.0000523	1151.5	S
insulin-like growth factor binding protein 7	IGFBP7	mwghuman30K#A:03385	NM_001553.1	NP_001544.1	1.8	4.2	0.000239	0.000756	1222	S
hypothetical protein FLJ23221		mwghuman30K#A:06273	NM_024579.1	NP_078855.1	1.5	2.8	0.000598	0.000375	1277.5	S
protein disulfide isomerase related protein	ERP70	mwghuman30K#A:03979	NM_004911.3	NP_004902.1	1.5	3.9	0.000321	0.000215	1419	S

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	GALNT14	mwghuman30K#B:4583	BC010659.1	AAH10659.1	1.4	2.4	0.000215	0.000312	1450.5	S
inter-alpha (globulin) inhibitor H3	ITIH3	mwghuman30K#B:7988	NM_002217.1	NP_002208.2	1.5	3.0	0.000317	0.000972	1504	S
pappalysin 2	PAPPA2	mwghuman30K#B:1636	NM_020318.1	NP_064714.1	1.5	2.8	0.000358	0.000584	1584	S
lysyl oxidase-like 1	LOXL1	mwghuman30K#A:07055	NM_005576.1	NP_005567.1	1.6	5.5	0.0001	0.000259	1598.5	S
secreted phosphoprotein 1	SPP1	mwghuman30K#A:09441	NM_000582.2	NP_000573.1	2.7	139.1	0.000577	0.00185	1789	S
tumor necrosis factor receptor superfamily, member 6b, decoy	TNFRSF6B	mwghuman30K#A:05069	NM_032945.2	NP_116563.1	2.0	6.8	0.001594	0.001244	1901.5	S
secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	mwghuman30K#A:08092	NM_003118.2	NP_003109.1	1.7	4.5	0.000359	0.000895	2512	S
sulfatase 1	SULF1	mwghuman30K#B:8770	NM_015170.1	NP_055985.1	2.5	67.3	0.007144	0.000895	2581	S
microseminoprotein, beta	MSMB	mwghuman30K#B:4000	NM_002443.2	NP_002434.1	1.6	11.8	0.00535	0.042817	6739.5	S
tolloid-like 2	TLL2	mwghuman30K#A:02932	NM_012465.2	NP_036597.1	1.9	29.2	0.036032	0.070205	8875.5	S
semaphorin sem2 (LOC56920)	SEM2	mwghuman30K#A:05073	NM_020163.1	NP_064548.1	1.2	1.8	0.0172289	0.01761606	10677	S

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	SEMA3F	mwghuman30K#A:07262	NM_004186.2	NP_004177.2	1.7	19.5	0.2804993	0.3890127	23988.5	S
endoglin	ENG	mwghuman30K#A:05668	NM_000118.1	NP_000109.1	1.9	3.7	2.76E-10	1.75E-09	37	
claudin 6	CLDN6	mwghuman30K#A:08357	NM_021195.3	NP_067018.1	2.2	6.7	1.84E-07	0.000000881	59	
prothymosin, alpha (gene sequence 28)	PTMA	mwghuman30K#B:9039	NM_002823.2	NP_002814.2	1.9	6.0	1.17E-07	0.00000031	77.5	
nipsnap homolog 1	NIPSNAP1	mwghuman30K#A:10699	NM_003634.1	NP_003625.1	2.0	4.0	3.08E-07	0.000000362	92.5	
arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)	AVPR2	mwghuman30K#A:01219	NM_000054.2	NP_000045.1	1.7	3.7	1.2E-07	0.000000227	98	
malignant fibrous histiocytoma amplified sequence 1	MFHAS1	mwghuman30K#A:04639	NM_004225.1	NP_004216.1	2.2	9.3	1.68E-09	2.62E-08	120	
homeo box A13	HOXA13	mwghuman30K#A:08971	NM_000522.2	NP_000513.2	1.9	6.4	7.15E-07	0.000000421	122	
myxovirus (influenza virus) resistance 2	MX2	mwghuman30K#A:10346	NM_002463.1	NP_002454.1	1.9	6.6	1.42E-06	0.000000659	156.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
similar to sodium- and chloride-dependent creatine transporter		mwghuman30K#C:4265	NM_198857.1	NP_942154.1	1.8	4.1	1.78E-06	0.0000051	164	
transmembrane protein 19	TMEM19	mwghuman30K#B:7083	NM_018279.2	NP_060749.2	1.8	3.0	3.14E-06	0.00000204	175	
prostaglandin I2 (prostacyclin) receptor (IP)	PTGIR	mwghuman30K#A:00268	NM_000960.3	NP_000951.1	2.1	9.9	4.88E-06	0.00000449	205	
hypothetical protein xp_047287		mwghuman30K#B:6955	XM_047287		1.6	3.9	2.89E-07	0.000000881	235	
hypothetical protein flj11871		mwghuman30K#A:10682	NM_025117		1.6	3.3	6.94E-07	0.00000102	240.5	
proline synthetase co-transcribed homolog	PROSC	mwghuman30K#B:0341	NM_007198.2	NP_009129.1	1.7	3.8	3.41E-07	0.00000233	270	
G protein-coupled receptor 32	GPR32	mwghuman30K#A:03297	NM_001506.1	NP_001497.1	2.4	21.8	0.0000154	0.0000216	322	
hypothetical protein MGC34923		mwghuman30K#C:4473	NM_144717.2	NP_653318.2	1.5	2.7	0.0000015	0.00000117	323	
MGC27121 gene		mwghuman30K#C:3953	NM_001001343.1	NP_001001343.1	2.6	10.4	0.0000214	0.0000243	333	
NAD(P)H dehydrogenase, quinone 1	NQO1	mwghuman30K#A:06176	NM_000903.1	NP_000894.1	2.6	17.7	7.17E-06	0.0000422	352.5	
cytoskeleton-associated protein 4	CKAP4	mwghuman30K#A:01860	NM_006825.2	NP_006816.2	1.8	4.9	0.0000029	0.00000233	382	
sialyltransferase 7D	SIAT7D	mwghuman30K#A:03286	NM_175040.1	NP_778205.1	1.6	2.6	4.14E-09	6.34E-09	394	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
hypothetical protein BC001096		mwghuman30K#B:6914	NM_138389.1	NP_612398.1	1.6	3.6	1.99E-07	0.000000421	394	
3-phosphoinositide dependent protein kinase-1	PDPK1	mwghuman30K#A:10300	NM_002613.2	NP_002604.1	1.5	2.1	0.0000192	0.00000135	438	
phosphatidylinositol transfer protein, membrane-associated 2	PITPNM2	mwghuman30K#B:8464	AB040890.2	BAA95981.2	2.1	7.8	0.0000309	0.00000579	448	
regulator of mitotic spindle assembly 1		mwghuman30K#A:09972	XM_040863		2.0	11.1	0.0000219	0.0000271	449.5	
molecule interacting with Rab13	MIRAB13	mwghuman30K#C:0021	NM_033386.1	NP_203744.1	1.5	3.0	2.16E-06	0.0000084	457.5	
protease, serine, 15	PRSS15	mwghuman30K#A:03353	NM_004793.2	NP_004784.2	1.5	2.7	0.0000101	0.0000136	497	
porcupine homolog	PORCN	mwghuman30K#A:00520	NM_203476.1	NP_982302.1	1.6	3.4	7.61E-06	0.0000243	528	
likely ortholog of mouse limb-bud and heart gene	LBH	mwghuman30K#B:7280	NM_030915.1	NP_112177.1	1.6	3.8	3.35E-07	0.000000266	534.5	
sine oculis homeobox homolog 6	SIX6	mwghuman30K#A:10145	NM_007374.1	NP_031400.1	1.5	2.4	0.0000131	0.00000949	538	
gap junction protein, beta 2A	GJB2	mwghuman30K#A:09852	NM_004004.3	NP_003995.2	1.6	4.1	0.0000164	0.0000977	541.5	
FLJ35784 protein		mwghuman30K#C:4803	NM_198534.1	NP_940936.1	2.0	5.2	0.0000295	0.0000304	563.5	
cell division cycle 2	CDC2	mwghuman30K#A:05382	NM_033379.2	NP_203698.1	2.4	7.8	0.0000208	0.000284	582.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
solute carrier family 37 (glycerol-3-phosphate transporter), member 3	SLC37A3	mwghuman30K#B:8722	NM_207113.1	NP_996996.1	1.5	3.8	7.99E-07	0.00000117	596	
sprouty homolog 4	SPRY4	mwghuman30K#C:0553	NM_030964.2	NP_112226.2	1.5	3.1	3.13E-06	0.0000084	597.5	
LIM homeobox 3	LHX3	mwghuman30K#A:02580	NM_178138.2	NP_835258.1	1.4	2.2	1.73E-06	0.00000049	608.5	
chromosome 7 open reading frame 27	C7orf27	mwghuman30K#B:2531	NM_152743.1	NP_689956.1	1.6	3.2	2.33E-06	0.00000102	648.5	
LDL receptor adaptor protein	ARH	mwghuman30K#B:2491	NM_015627.1	NP_056442.1	1.5	3.1	0.0000141	0.0000216	649	
solute carrier family 39 (zinc transporter), member 1	SLC39A1	mwghuman30K#A:02443	NM_014437.3	NP_055252.2	1.6	3.7	0.0000296	0.0000496	652	
zinc finger protein 307 (ZNF307)	ZNF307	mwghuman30K#A:08705	NM_019110.3	NP_061983.2	1.5	3.8	5.01E-06	0.00000743	658	
macrophage migration inhibitory factor	MIF	mwghuman30K#A:09347	NM_002415.1	NP_002406.1	1.6	3.6	0.0000719	0.0000977	681.5	
synuclein, alpha interacting protein	SNCAIP	mwghuman30K#A:08103	NM_005460.1	NP_005451.1	1.6	2.7	0.0000186	0.00000301	683	
bone marrow stromal cell antigen 2	BST2	mwghuman30K#B:4758	NM_004335.2	NP_004326.1	2.1	5.3	0.0000816	0.000236	737.5	
proline-serine-threonine phosphatase interacting protein 1	PSTPIP1	mwghuman30K#B:0578	NM_003978.2	NP_003969.2	1.6	3.3	2.22E-06	0.00000347	755	

Fig. 12 (contined)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
topoisomerase (DNA) II alpha	TOP2A	mwghuman3 0K#B:7144	NM_001067.2	NP_001058.2	2.0	5.5	0.0000799	0.000161	760.5	
MCM2 minichromosome maintenance deficient 2	MCM2	mwghuman3 0K#A:08834	NM_004526.2	NP_004517.2	1.5	2.3	4.21E-06	0.00000395	774.5	
SRY (sex determining region Y)-box 4	SOX4	mwghuman3 0K#A:07410	NM_003107.2	NP_003098.1	1.5	4.8	4.96E-06	0.00000449	789	
nuclear receptor coactivator 5	NCOA5	mwghuman3 0K#B:8592	NM_020967.1	NP_066018.1	1.6	2.8	0.0000122	0.00000223	792	
tubulin, alpha 4	TUBA4	mwghuman3 0K#B:2461	NM_025019.1	NP_079295.1	1.9	5.1	0.0000645	0.000161	793.5	
hypothetical protein FLJ31438		mwghuman3 0K#C:8001	NM_152385.1	NP_689598.1	1.5	2.9	0.0000327	0.0000121	804	
odd-skipped homolog	ODD	mwghuman3 0K#C:8737	NM_145260.1	NP_660303.1	1.6	5.9	0.000131	0.0000523	813	
solute carrier family 23 (nucleobase transporters), member 2	SLC23A2	mwghuman3 0K#A:04621	NM_203327.1	NP_976072.1	1.8	4.7	0.0000069	0.000132	819.5	
split hand/foot malformation (ectrodactyly) type 1	SHFM1	mwghuman3 0K#A:05669	NM_006304.1	NP_006295.1	1.6	3.3	0.0000306	0.0000647	823.5	
SFRS protein kinase 2	SRPK2	mwghuman3 0K#A:08606	NM_182692.1	NP_872634.1	1.6	6.4	0.0000197	0.0000339	848.5	
chromosome 18 open reading frame 8	C18orf8	mwghuman3 0K#A:07371	NM_013326.2	NP_037458.2	1.4	2.1	1.54E-06	0.00000347	856	
formin homology 2 domain containing 1	FHOD1	mwghuman3 0K#A:05058	NM_013241.1	NP_037373.1	1.5	2.3	0.0000106	0.0000153	863.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
receptor (calcitonin) activity modifying protein 2	RAMP2	mwghuman30K#A:02505	NM_005854.1	NP_005845.1	1.6	4.2	0.0000208	0.0000172	866.5	
2,3-bisphosphoglycerate mutase	BPGM	mwghuman30K#A:00673	NM_001724.3	NP_001715.1	1.6	4.1	0.000203	0.0000523	868	
SH2-B homolog	SH2B	mwghuman30K#B:8571	NM_015503.1	NP_056318.1	1.7	5.7	0.0000461	0.0000647	906	
regulator of G-protein signalling 5	RGS5	mwghuman30K#B:0128	NM_003617.2	NP_003608.1	1.8	12.8	0.0000299	0.000177	922.5	
phosphoinositol 4-phosphate adaptor protein-2	FAPP2	mwghuman30K#A:06904	NM_032639.2	NP_116028.1	1.4	2.3	0.0000188	0.0000647	932.5	
coxsackie virus and adenovirus receptor	CXADR	mwghuman30K#A:00118	NM_001338.3	NP_001329.1	1.9	4.7	0.000165	0.000177	935.5	
Meis1, myeloid ecotropic viral integration site 1 homolog 2	MEIS2	mwghuman30K#A:08006	NM_002399.2	NP_002390.1	1.5	2.8	0.0000766	0.0000883	941	
tensin-like SH2 domain containing 1	TENS1	mwghuman30K#A:01929	NM_022748.6	NP_073585.6	1.5	3.1	0.0000869	0.000132	946.5	
snail homolog 2	SNAI2	mwghuman30K#A:10656	NM_003068.3	NP_003059.1	1.8	17.9	0.0000524	0.0000339	960.5	
docking protein 3	DOK3	mwghuman30K#B:2635	NM_024872.1	NP_079148.1	1.6	4.8	7.57E-06	0.00000049	967.5	
carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	CHST2	mwghuman30K#A:06174	NM_004267.2	NP_004258.2	1.7	5.2	9.87E-07	0.00000155	983	
nucleoside phosphorylase	NP	mwghuman30K#A:03762	NM_000270.1	NP_000261.1	1.5	4.1	0.0000189	0.0000271	996.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
visinin-like 1	VSNL1	mwghuman30K#A:06227	NM_003385.3	NP_003376.2	1.7	3.5	0.0000811	0.00012	1013	
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	mwghuman30K#C:2653	NM_002350.1	NP_002341.1	1.6	3.5	0.0000593	0.000108	1013.5	
hepatocellular carcinoma-associated antigen 127	HCA127	mwghuman30K#B:7758	NM_018684.1	NP_061154.1	1.3	2.0	0.0000442	0.0000797	1017	
solute carrier family 22 (organic cation transporter), member 2	SLC22A2	mwghuman30K#A:02704	NM_153191.1	NP_694861.1	2.3	12.5	0.000298	0.000535	1021	
MAX dimerization protein 4	MXD4	mwghuman30K#A:08296	NM_006454.2	NP_006445.1	1.4	2.5	5.21E-06	0.00000656	1025	
Thy-1 co-transcribed (LOC94105)		mwghuman30K#A:07498	NM_033209.2	NP_149986.1	1.4	2.0	0.0000307	0.0000153	1032.5	
Thy-1 co-transcribed (LOC94105)	THY1	mwghuman30K#A:07498	NM_033209.2	NP_149986.1	1.4	2.0	3.072E-05	1.52973E-05	1032.5	
leucine rich repeat and fibronectin type III domain containing 3	LRFN3	mwghuman30K#A:00147	NM_024509.1	NP_078785.1	1.6	2.4	0.000225	0.0000419	1035.5	
h4 histone family, member g		mwghuman30K#A:01329	XM_030144		1.9	12.3	0.000241	0.0000883	1040	
hypothetical protein FLJ22390		mwghuman30K#A:06789	NM_022746.2	NP_073583.2	1.5	2.4	0.0000373	0.0000172	1045.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
tribbles homolog 2	TRIB2	mwghuman3 0K#A:05272	NM_021643.1	NP_067675.1	1.7	4.1	0.0000616	0.000195	1058	
keratin, hair, acidic, 3B	KRTHA3B	mwghuman3 0K#A:02682	NM_002279.3	NP_002270.1	1.3	2.1	0.0000079	0.0000271	1071.5	
kinesin family member 21A	KIF21A	mwghuman3 0K#C:0043	NM_017641.2	NP_060111.2	1.7	3.1	0.000121	0.000108	1073	
high-mobility group nucleosomal binding domain 2	HMGN2	mwghuman3 0K#B:9113	NM_005517.2	NP_005508.1	1.5	2.9	0.000199	0.0000883	1075	
ankyrin repeat domain 17	ANKRD17	mwghuman3 0K#B:0250	NM_198889.1	NP_942592.1	1.5	2.6	0.000013	0.00000743	1089.5	
recombination activating gene 1	RAG1	mwghuman3 0K#A:09856	NM_000448.1	NP_000439.1	1.4	2.7	0.000114	0.0000797	1090	
nucleotide binding protein 2	NUBP2	mwghuman3 0K#C:1908	NM_012225.1	NP_036357.1	1.4	2.3	0.0000198	0.0000193	1097	
hypothetical protein FLJ20489		mwghuman3 0K#A:07462	NM_017842.1	NP_060312.1	1.4	2.7	3.49E-06	0.00000395	1100.5	
calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK	mwghuman3 0K#A:01768	NM_003688.1	NP_003679.1	1.5	3.5	0.0000572	0.000161	1104.5	
huntingtin interacting protein 1	HIP1	mwghuman3 0K#A:05908	NM_005338.4	NP_005329.3	1.4	4.5	0.0000185	0.00000656	1110	
LAG1 longevity assurance homolog 2	LASS2	mwghuman3 0K#A:00827	NM_013384.3	NP_037516.3	1.5	2.3	0.0000311	0.000063	1111.5	
protein kinase C, delta binding protein	PRKCDBP	mwghuman3 0K#B:4639	NM_145040.2	NP_659477.2	1.6	3.5	6.96E-07	0.000000194	1123.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	TIE	mwghuman30K#A:05888	NM_005424.2	NP_005415.1	1.7	4.3	0.000266	0.000312	1126.5	
chromosome 5 open reading frame 15	C5orf15	mwghuman30K#A:10834	NM_020199.1	NP_064584.1	1.6	3.3	0.000144	0.000195	1131	
anillin, actin binding protein	ANLN	mwghuman30K#A:05280	NM_018685.2	NP_061155.2	2.2	6.5	0.000906	0.000332	1154	
derlin-1	DER1	mwghuman30K#A:01654	NM_024295.3	NP_077271.1	1.4	3.1	0.000115	0.0000422	1160.5	
CGI-72 protein	CGI-72	mwghuman30K#C:2137	NM_016018.3	NP_057102.3	1.4	2.5	0.000047	0.000195	1165	
activin A receptor type II-like 1	ACVRL1	mwghuman30K#A:00470	NM_000020.1	NP_000011.1	1.4	2.3	0.000113	0.0000618	1178	
ectonucleoside triphosphate diphosphohydrolase 8	ENTPD8	mwghuman30K#C:1422	NM_138793.2	NP_620148.1	1.4	2.2	0.0000121	0.0000379	1179.5	
SH3 domain binding glutamic acid-rich protein like 3	SH3BGRL3	mwghuman30K#B:1593	NM_031286.2	NP_112576.1	1.5	2.5	0.000062	0.000177	1185.5	
SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	SMC4L1	mwghuman30K#A:05648	NM_001002799.1	NP_001002799.1	1.7	3.4	0.000271	0.000215	1190	
NADH:ubiquinone oxidoreductase MLRQ subunit homolog		mwghuman30K#B:1359	NM_020142.3	NP_064527.1	2.2	17.8	0.000123	0.000249	1196	
angiogenic factor VG5Q	VG5Q	mwghuman30K#B:2180	NM_018046.3	NP_060516.2	1.4	2.8	0.0000245	0.0000582	1226.5	

Fig. 12 (continued)

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Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
stathmin 1	STMN1	mwghuman30K#A:00925	NM_203401.1	NP_981946.1	1.9	11.6	0.0004	0.000342	1250	
lipidosin	BG1	mwghuman30K#A:08285	NM_015162.3	NP_055977.3	1.6	8.8	0.000221	0.00017	1267	
BCL2-like 11	BCL2L11	mwghuman30K#A:08369	NM_207003.1	NP_996886.1	1.4	2.5	0.0000689	0.000108	1271	
AMP-activated protein kinase family member 5	ARK5	mwghuman30K#B:9070	NM_014840.2	NP_055655.1	1.5	3.1	0.000345	0.0000647	1273.5	
pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	PLEKHA4	mwghuman30K#B:3447	NM_020904.1	NP_065955.1	1.4	2.6	6.69E-06	0.0000107	1278.5	
kallikrein 11	KLK11	mwghuman30K#A:09721	NM_144947.1	NP_659196.1	1.4	3.3	0.00024	0.000047	1332	
suppression of tumorigenicity 7 like	ST7L	mwghuman30K#A:01391	NM_138728.2	NP_620056.1	1.5	3.3	0.000161	0.000132	1376.5	
transducin-like enhancer of split 3	TLE3	mwghuman30K#A:09092	NM_005078.1	NP_005069.1	1.3	2.1	0.0000102	0.0000084	1382.5	
inter-alpha (globulin) inhibitor H5	ITIH5	mwghuman30K#A:10153	NM_032817.2	NP_116206.2	1.4	2.4	0.000205	0.000259	1387.5	
regulator of G-protein signalling 11	RGS11	mwghuman30K#A:09250	NM_183337.1	NP_899180.1	1.5	2.8	0.0000268	0.0000379	1400.5	
ankyrin repeat and SOCS box-containing 9	ASB9	mwghuman30K#A:01131	NM_024087.1	NP_076992.1	1.4	2.5	0.000131	0.000146	1418.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
chromosome 6 open reading frame 69	C6orf69	mwghuman3 0K#C:0854	NM_173562.3	NP_775833.2	1.4	2.7	0.0000737	0.000195	1436	
transmembrane 7 superfamily member 3	TM7SF3	mwghuman3 0K#A:09485	NM_016551.1	NP_057635.1	1.6	3.0	0.000278	0.000535	1437	
secernin 3	SCRN3	mwghuman3 0K#A:00384	NM_024583.2	NP_078859.2	1.4	2.7	0.0000977	0.000215	1452	
cryptochrome 1	CRY1	mwghuman3 0K#A:06219	NM_004075.2	NP_004066.1	1.5	3.7	0.000377	0.000259	1457.5	
plexin A1	PLXNA1	mwghuman3 0K#B:8739	NM_032242.2	NP_115618.2	1.4	3.2	0.000107	0.000108	1474	
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	GALNT10	mwghuman3 0K#B:6489	NM_017540.3	NP_060010.3	1.4	2.0	4.42E-06	0.000000659	1479.5	
gap junction protein, alpha 4	GJA4	mwghuman3 0K#A:07540	NM_002060.1	NP_002051.1	1.4	2.8	0.000427	0.000284	1488.5	
hypothetical protein DKFZp434G1415		mwghuman3 0K#C:3525	NM_031292.2	NP_112582.2	1.4	2.9	0.0000627	0.000156	1501	
WD repeat and SOCS box-containing 2A	WSB2	mwghuman3 0K#B:1353	NM_018639.3	NP_061109.1	1.4	2.5	0.0000652	0.0000523	1505	
cytidine deaminase	CDA	mwghuman3 0K#A:07490	NM_001785.1	NP_001776.1	1.6	3.0	0.0000477	0.0000271	1538.5	
phosphoribosylglycinamide formyltransferase	GART	mwghuman3 0K#A:10142	NM_000819.3	NP_000810.1	1.4	2.2	0.0000428	0.000146	1560	
histone 1, H1b	HIST1H1B	mwghuman3 0K#A:05716	NM_005322.2	NP_005313.1	1.5	4.0	0.0000929	0.000236	1578.5	

Fig. 12 (continued)

Gene Name	HUGO	MWG oligo #	NCBI mRNA ref seq	Protein ref seq	mean fold change	max fold change	T-test	Wilcoxon test	Summated rank	Serum
zinc metalloproteinase (STE24 homolog, yeast)	ZMPSTE24	mwghuman30K#A:09568	NM_005857.2	NP_005848.2	1.5	3.9	0.000166	0.000236	1653.5	
transmembrane protein 33	TMEM33	mwghuman30K#A:01542	NM_018126.1	NP_060596.1	2.9	31.9	0.000365	0.002513	1669.5	
glucose phosphate isomerase	GPI	mwghuman30K#B:1465	NM_000175.2	NP_000166.2	1.4	2.6	0.000153	0.000236	1670.5	
hypothetical protein FLJ11000		mwghuman30K#B:4538	NM_018295.1	NP_060765	1.6	5.1	0.000203	0.000448	1687.5	
hypothetical protein MGC5576		mwghuman30K#A:06786	NM_024056.2	NP_076961.1	1.6	11.7	0.000735	0.000312	1710	
calcium/calmodulin-dependent protein kinase ID	CAMK1D	mwghuman30K#A:00327	NM_020397.1	NP_065130.1	1.4	2.6	0.00034	0.000423	1719	
protein tyrosine phosphatase, non-receptor type 21	PTPN21	mwghuman30K#A:09269	NM_007039.2	NP_008970.1	1.4	2.4	0.000571	0.000259	1723.5	
eukaryotic translation initiation factor 2C	EIF2C2	mwghuman30K#C:2287	NM_012154.2	NP_036286.2	1.4	2.5	0.00011	0.0000243	1730	
WD repeat domain 18	WDR18	mwghuman30K#B:3546	NM_024100.2	NP_077005.2	1.4	3.2	0.0000511	0.0000582	1748.5	
tensin	TNS	mwghuman30K#B:8493	NM_022648.2	NP_072174.2	1.3	2.0	0.0000393	0.000177	1753.5	
c-src tyrosine kinase	CSK	mwghuman30K#A:01629	NM_004383.1	NP_004374.1	1.4	1.9	1.05E-06	0.0000107	1935.5	
ubiquitin-conjugating enzyme E2C	UBE2C	mwghuman30K#A:01776	NM_181803.1	NP_861519.1	2.1	8.9	0.001146	0.003908	2155	
neuropilin 1	NRP1	mwghuman30K#A:03091	NM_003873.2	NP_003864.2	1.9	6.0	0.003291	0.003636	2941	

Fig. 12 (continued)

control	number	TCC	number
other urological cancer	35	Ta grade 1	9
benign prostate hyperplasia	10	Ta grade 2	28
miscellaneous non malignant urological disease	10	T1 stage 2	4
TCC surveillance (no cancer)	47	Tis stage 1	1
urinary tract infection	21	Tis stage 2	1

Fig. 13

	Area under curve (%)			
TCC characteristic	HoxA13	HoxA13/LTB4DH	IGFBP5	IGFBP5/LTB4DH
Stage Ta (grades 1-2)	64	67	61	70
Stage Ta (grade 1)	66	69	73	81
Grade 1 (all stages)	66	69	73	81
Grade 2 (all stages)	62	62	55	63
Grade 1-2 (all)	64	64	60	68

Fig. 14

BTM	Overall Sensitivity	stage Ta	grade 1&2	grade 3
cdc2 Hoxa13, MDK	0.61	0.41	0.42	0.86
cdc2, Hoxa13, MDK, LTB4DH	0.63	0.44	0.43	0.89
cdc2 Hoxa13, IGFBP5, MDK	0.61	0.44	0.44	0.82
cdc2 Hoxa13, IGFBP5, MDK, LTB4DH	0.62	0.46	0.45	0.84
cdc2, IGFBP5, MDK	0.61	0.44	0.45	0.82
cdc2, IGFBP5, MDK, LTB4DH	0.62	0.46	0.45	0.85
Hoxa13, IGFBP5, MDK, Top2a	0.61	0.44	0.45	0.83
Hoxa13, IGFBP5, MDK, Top2a, LTB4DH	0.63	0.47	0.46	0.85
Hoxa13, IGFBP5, MDK	0.61	0.44	0.45	0.83
Hoxa13, IGFBP5, MDK, LTB4DH	0.62	0.46	0.45	0.85
HoxA13, MDK	0.62	0.42	0.42	0.87
HoxA13, MDK, LTB4DH	0.64	0.45	0.44	0.89
IGFBP5, MDK	0.62	0.44	0.45	0.84
IGFBP5, MDK, LTB4DH	0.63	0.47	0.45	0.86
cdc2, IGFBP5, MDK, Top2a	0.62	0.45	0.45	0.84
cdc2, IGFBP5, MDK, Top2a, LTB4DH	0.64	0.48	0.46	0.87

Fig. 15