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DEFINITION  Homo sapiens chemokine (C-X-C motif) receptor 2 (CXCR2), transcript variant
1, mRNA.
ACCESSION   NM_001557
VERSION     NM_001557.3  GI:269973857

Protein sequence:  "MEDFNMESDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPESL
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Figure 1

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Figure 1 (cont)

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Figure 1 (cont)

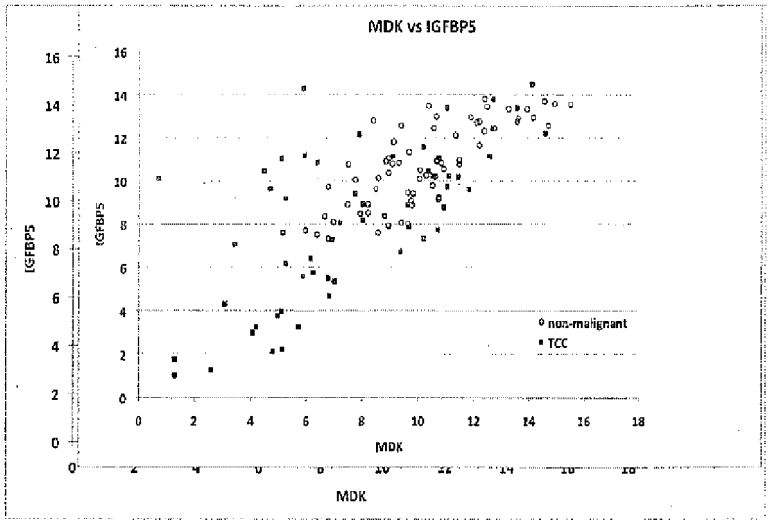


Fig. 2a

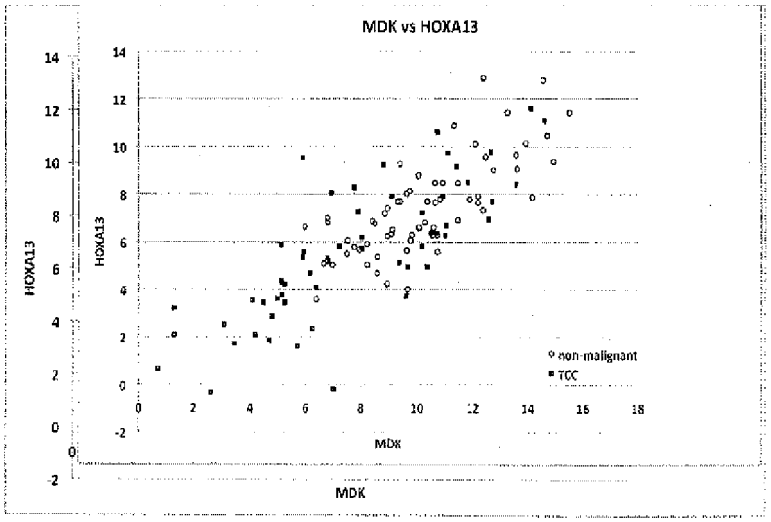


Fig. 2b

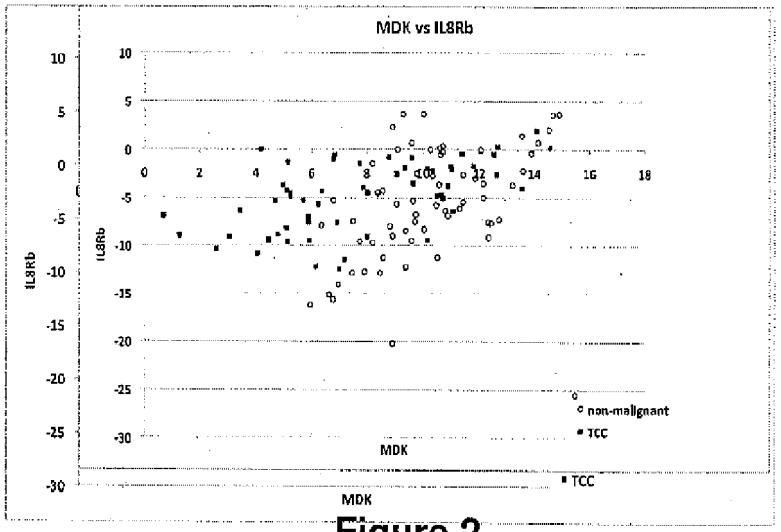


Fig. 2c

Figure 2.

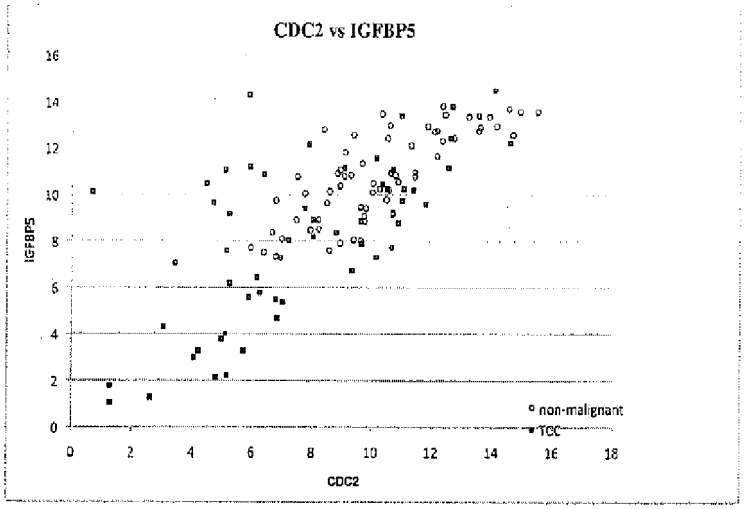


Fig. 2d

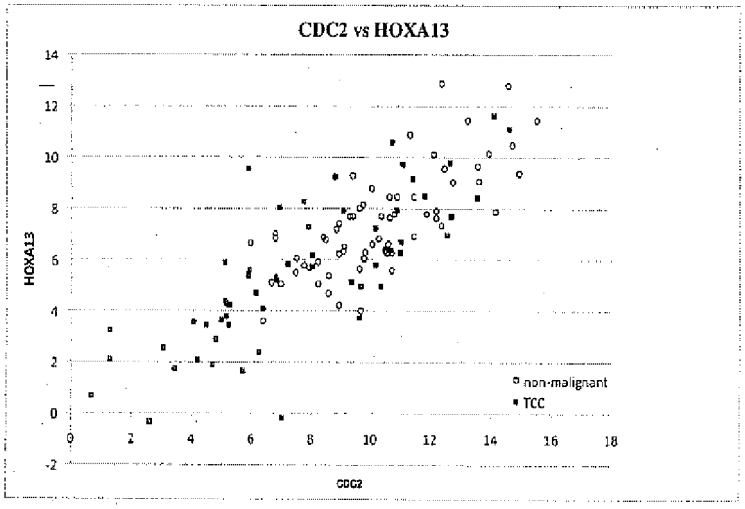


Fig. 2e

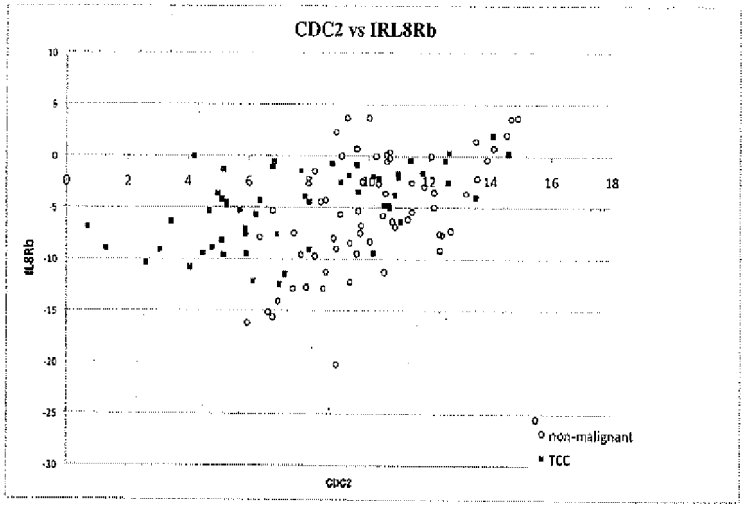


Fig. 2f

Figure 2 cont.

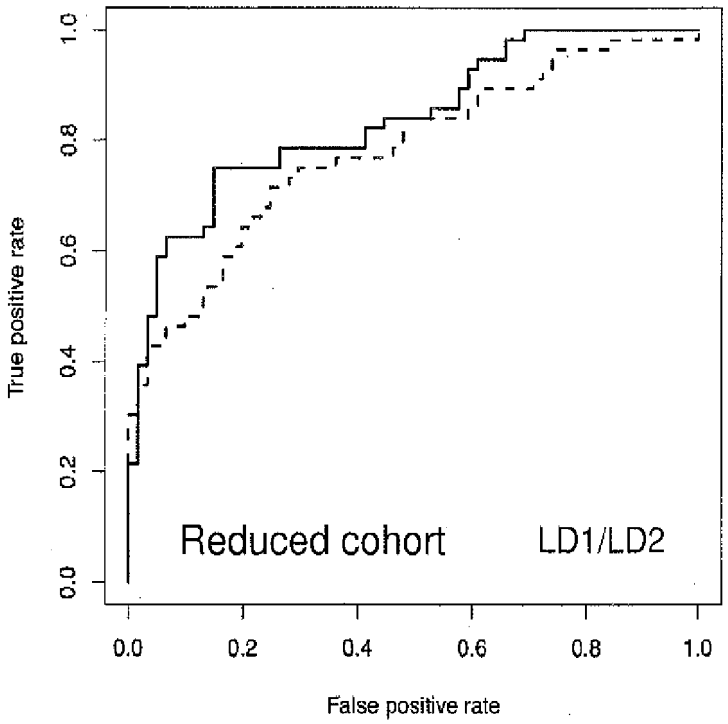


Fig. 3a

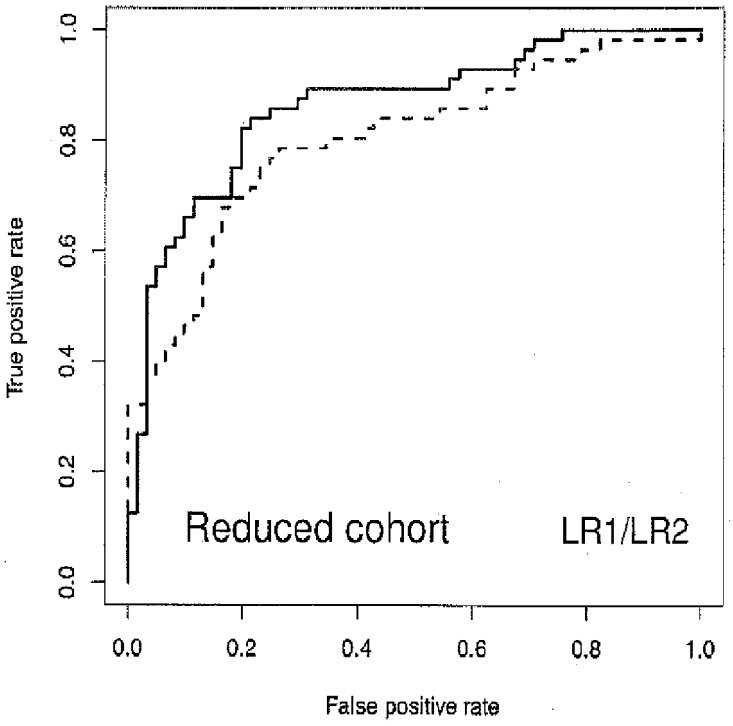


Fig. 3b

Figure 3a-b.

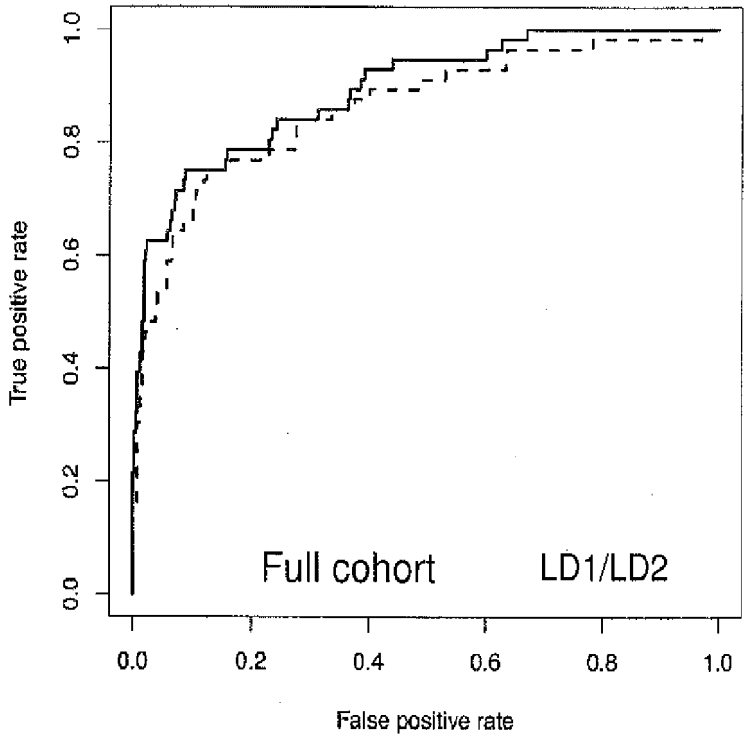


Fig. 4a

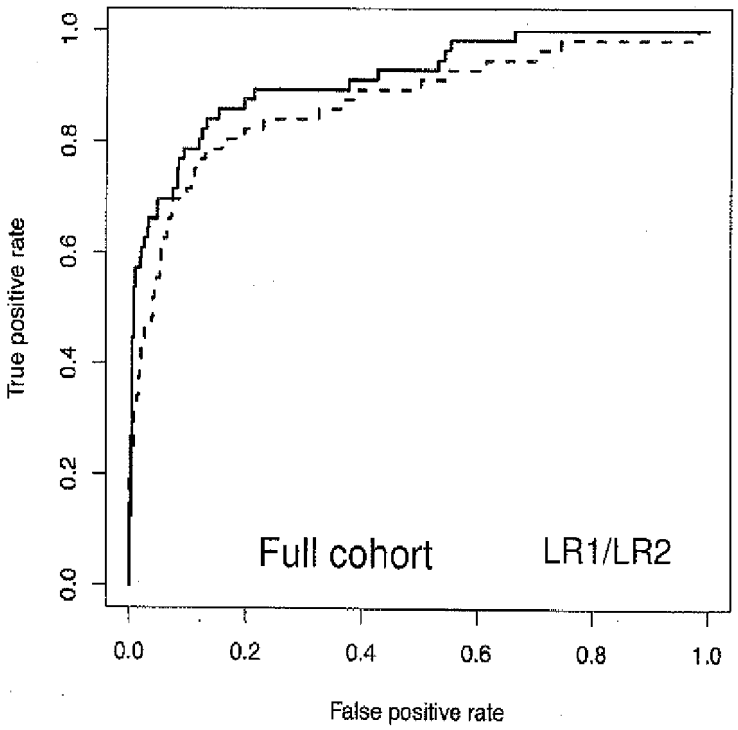


Fig. 4b

Figure 4a-b.

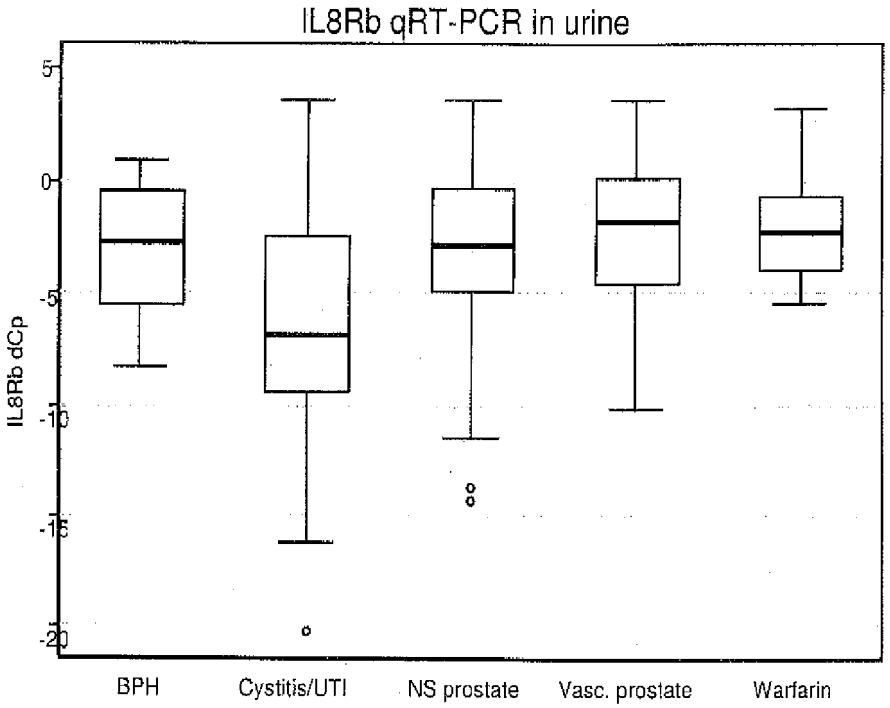

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IL8Rb dCp
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0
-5
-10
-15
-20
BPH
Cystitis/UTI
NS prostate
Vasc. prostate
Warfarin

Figure 5.

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

Figure 6

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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		AC010828.3.125573.1581 93.2	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

Figure 6 (cont)

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		AC022554.2.1 1725.14597.1	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#A:06988	-1.615311	3.24982E-07	9.24336E-06	-5.392632	624	11555.5	8868.25	4
ensembl genscan prediction		AC073108.7.1 14033.192530 .1	mwghuman3 0K#C:4991	-2.137812	1.453E-05	1.06394E-06	-6.345675	650.5	9963.5	5676.75	

Figure 6 (cont)

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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	

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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	bloo d
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

Figure 6 (cont)

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

Figure 6 (cont)

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	

Figure 6 (cont)

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_0010188 64.1	NM_0010235 70.1	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_0010179 20.1	NM_0010179 20.1	mwghuman30K#B:6718	-2.553467	5.76345E-07	7.76152E-07	-5.221107	907	23255	15868	0
ensembl genscan prediction		AC012203.4.1 05191.123571.1	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	

Figure 6 (cont)

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	3.70631E-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

Figure 6 (cont)

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		AP001015.3.6 6054.115655. 1	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#B:4652	-1.674296	1.77778E-05	3.32944E-05	-4.846371	1011.5	14804	10754.75	3
methyltransfera se like 1 (METTL1), transcript variant 1, mRNA	NP_005362.1	NM_005371.3	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#B:5911	-1.64935	1.97896E-05	3.70831E-05	-4.903865	1077	12134	9187.5	4

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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		AC079456.15.119608.150490.1	mwghuman30K#C:3309	-1.39662	6.38081E-06	4.32856E-06	-6.439308	1169.5	26755.5	26493.5		

Figure 6 (cont)

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:429841 4		BC007768	mwghuman3 0K#B:4242	-1.518362	5.21322E-06	3.51403E-05	-4.463332	1171	21159	20375	
ensembl genscan prediction		AC027086.2.2 3033.31927.1	mwghuman3 0K#C:6982	-1.659003	1.16113E-11	3.82785E-07	-6.295271	1172.5	2757	2062.75	
hyaluronogluco saminidase 3 (HYAL3), mRNA	NP_003540.2	NM_003549.2	mwghuman3 0K#A:09529	-2.01277	6.70905E-08	1.16156E-05	-4.684969	1175	4326	3464.5	4
ensembl genscan prediction		AC083822.10. 126464.12912 2.1	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#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	mwghuman3 0K#B:3465	-1.41555	6.70306E-08	2.1019E-06	-5.674131	1206	9672.5	7512.25	0

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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

Figure 6 (cont)

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 flb5634 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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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-mallgnant 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

Figure 6 (cont)

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

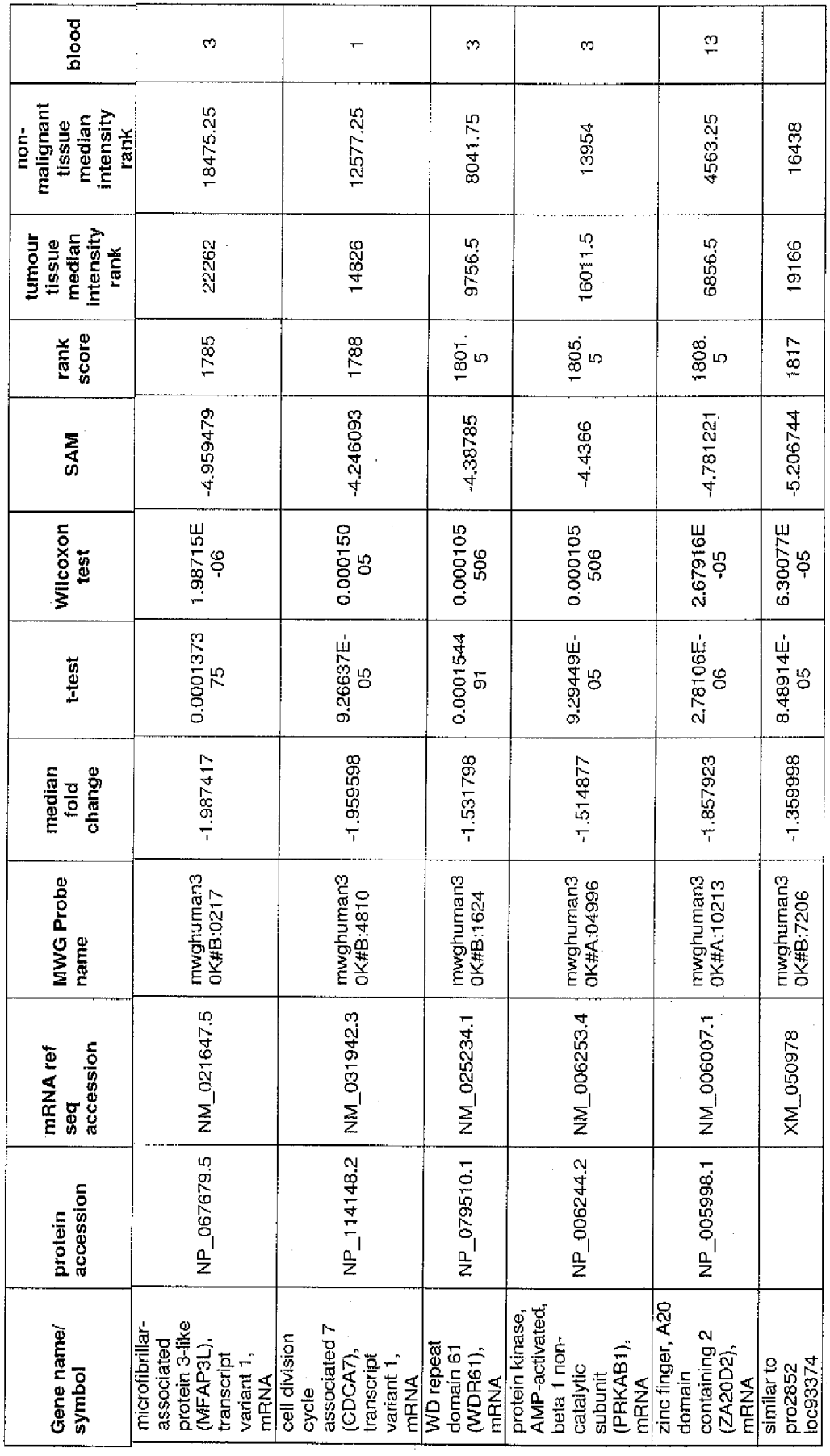
Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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	

Figure 6 (cont)

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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	0.00010550 6	-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	0.00010550 6	-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	

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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		AP001487.3.85282.114407.1	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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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	0.00023353 7	-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	0.00017411 7	-4.521635	1992	16805	15440.5	4

Figure 6 (cont)

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	0.000257 25	-4.423897	2004	10052	9080	11

Figure 6 (cont)

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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:8060	-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	

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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.f14103.1	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

Figure 6 (cont)

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

Figure 6 (cont)

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

Figure 6 (cont)

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

Figure 6 (cont)

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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	

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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	

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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	

Figure 6 (cont)

SUBSTITUTE SHEET (RULE 26)

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

Figure 6 (cont)

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

Figure 6 (cont)

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

Figure 6 (cont)

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

Figure 7

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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

Figure 7 (cont)

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

Figure 7 (cont)

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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

Figure 7 (cont)

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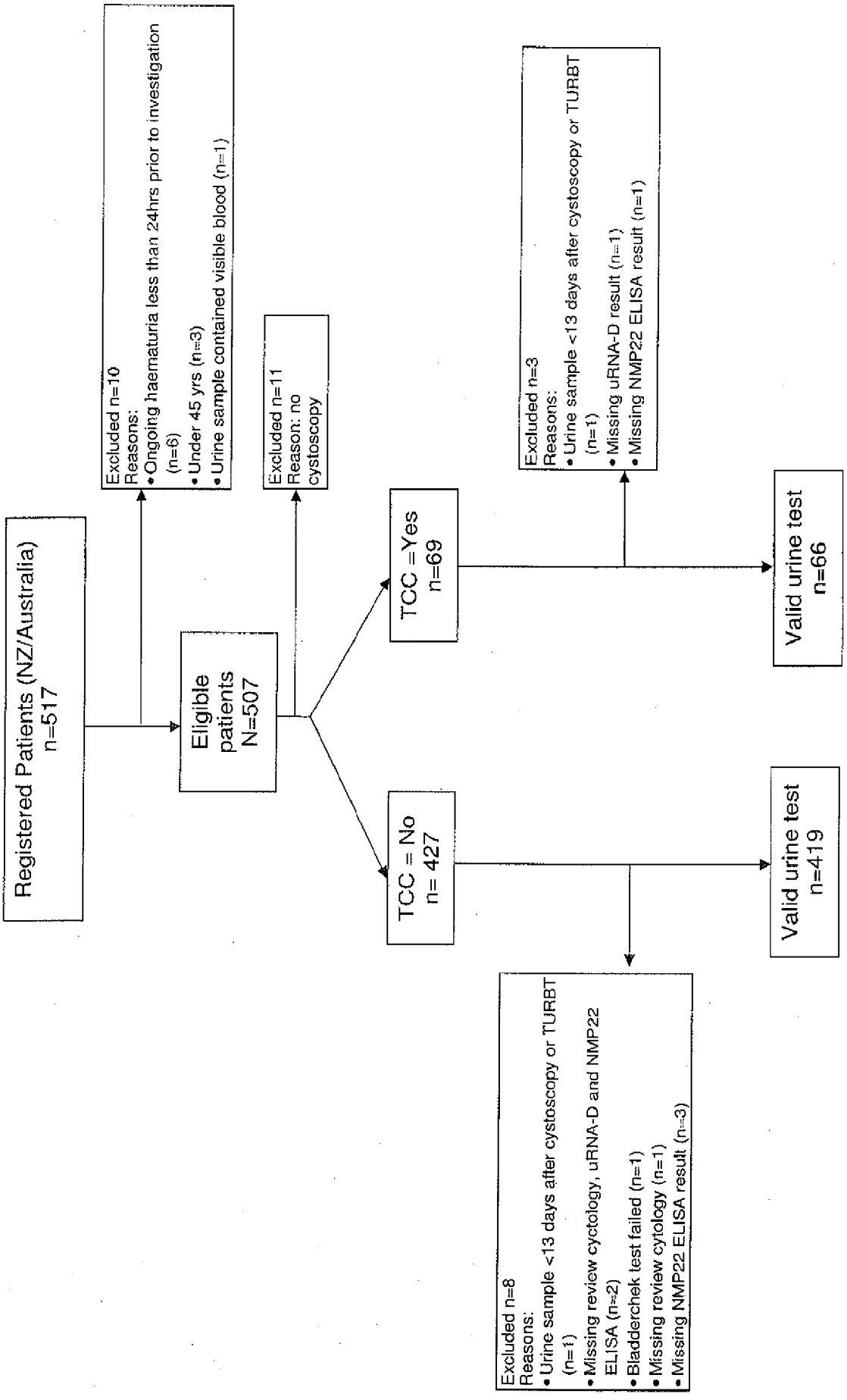

Registered Patients (NZ/Australia) n=517
Excluded n=10
Reasons:
• Ongoing haematuria less than 24hrs prior to investigation (n=6)
• Under 45 yrs (n=3)
• Urine sample contained visible blood (n=1)
Eligible patients N=507
Excluded n=11
Reason: no cystoscopy
TCC =Yes n=69
Excluded n=3
Reasons:
• Urine sample <13 days after cystoscopy or TURBT (n=1)
• Missing uRNA-D result (n=1)
• Missing NMP22 ELISA result (n=1)
Valid urine test n=66
TCC = No n= 427
Valid urine test n=419
Excluded n=8
Reasons:
• Urine sample <13 days after cystoscopy or TURBT (n=1)
• Missing review cytology, uRNA-D and NMP22 ELISA (n=2)
• Bladderchek test failed (n=1)
• Missing review cytology (n=1)
• Missing NMP22 ELISA result (n=3)

Figure 8

	No specific diagnosis (N=164)	Non-malignant disease (N=255)	TCC (N=66)	Overall (N=485)
Country, n (%)				
New Zealand	147 (89.6)	239 (93.7)	64 (97.0)	450 (92.8)
Australia	17 (10.4)	16 (6.27)	2 (3.0)	35 (7.2)
Age, median (IQ range)	64 (55, 75)	71 (62, 78)	71 (63, 80)	69 (59, 77)
Sex, n (%)				
Male	112 (68.3)	216 (84.7)	61 (92.4)	389 (80.2)
Female	52 (31.7)	39 (15.3)	5 (7.5)	96 (19.8)
Ethnicity, n (%)				
European	133 (81.1)	228 (89.4)	62 (93.9)	423 (87.2)
Maori	15 (9.1)	17 (6.7)	1 (1.5)	33 (6.8)
Other	16 (9.8)	10 (3.9)	3 (4.5)	29 (6.0)
Haematuria, n (%)				
Years since onset				
<6 mths	131 (79.9)	198 (77.6)	57 (86.4)	386 (79.6)
6 mths-1 yr	11 (6.7)	25 (9.8)	6 (9.1)	42 (8.7)
1-2 yrs	11 (6.7)	18 (7.1)	3 (4.5)	32 (6.6)
3-5 yrs	5 (3.0)	5 (2.0)	0 (0.0)	10 (2.1)
> 5 yrs	6 (3.7)	9 (3.5)	0 (0.0)	15 (3.1)
End of last episode				
1-7 days	9 (5.5)	26 (10.2)	20 (30.3)	55 (11.3)
8-28 days	14 (8.5)	27 (10.6)	13 (19.7)	54 (11.1)
1-2 Months	60 (36.6)	86 (33.7)	14 (21.2)	160 (33.0)
3-6 Months	70 (42.7)	100 (39.2)	19 (28.8)	189 (39.0)
> 6 months	11 (6.7)	15 (5.9)	0 (0.0)	26 (5.4)
Unknown	0 (0.0)	1 (0.4)	0 (0.0)	1 (0.2)
Frequency				
<=1 per day	104 (63.4)	160 (62.7)	30 (45.5)	294 (60.6)
>1 per day	59 (36.0)	95 (37.3)	36 (54.5)	190 (39.2)
Unknown	1 (0.6)	0 (0.0)	0 (0.0)	1 (0.2)
Smoking status, n (%)				
Current smoker	34 (20.7)	28 (11.0)	14 (21.2)	76 (15.7)
Ex-smoker	66 (40.2)	114 (44.7)	35 (53.0)	215 (44.3)
Never smoker	64 (39.0)	113 (44.3)	17 (25.8)	194 (40.0)

Figure 9

Test	Overall Sensitivity	Overall Specificity
uRNA-D	62.1% (49.3 73.8)	85.2% (fixed)
NMP22 Elisa	50.0% (37.4, 62.6)	88.0% (84.6, 91.0)
NMP22 BladderChek	37.9% (26.2, 50.7)	96.4% (94.2, 98.0)
Cytology*	56.1% (43.3, 68,3)	94.5 (91.9, 96.5)
Five Genes (including IL8BRb)†	81.8%	85.1% (fixed)
Five Genes (including IL8BRb)† (90% specificity)	72.7%	89.9% (fixed)

* Included in determination of TCC for some patients
† Determined on study data so confidence intervals are not presented

Figure 10

Fig 11a.

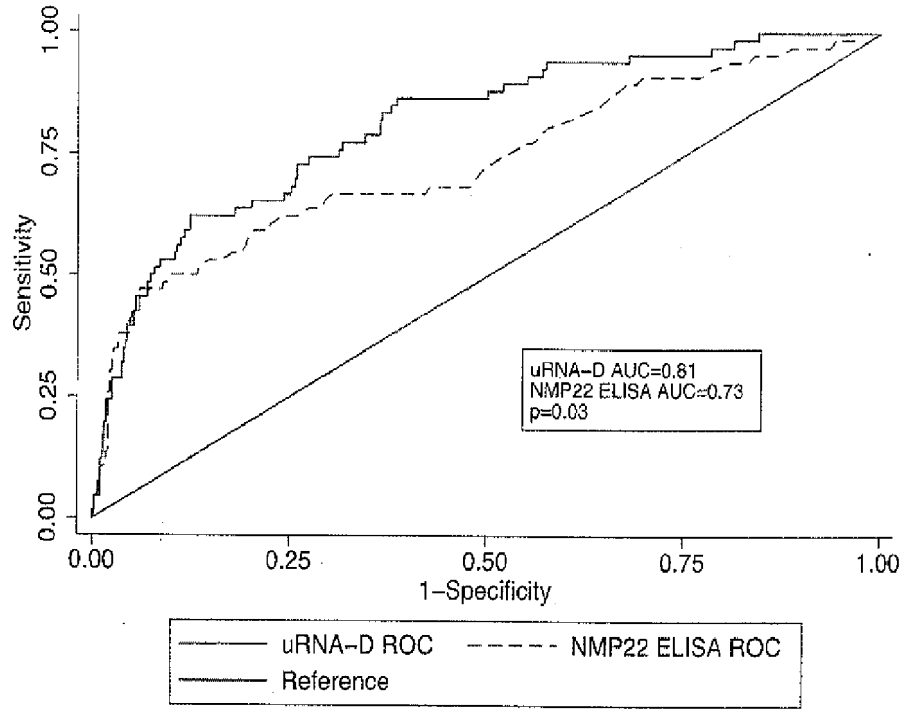


Fig 11b.

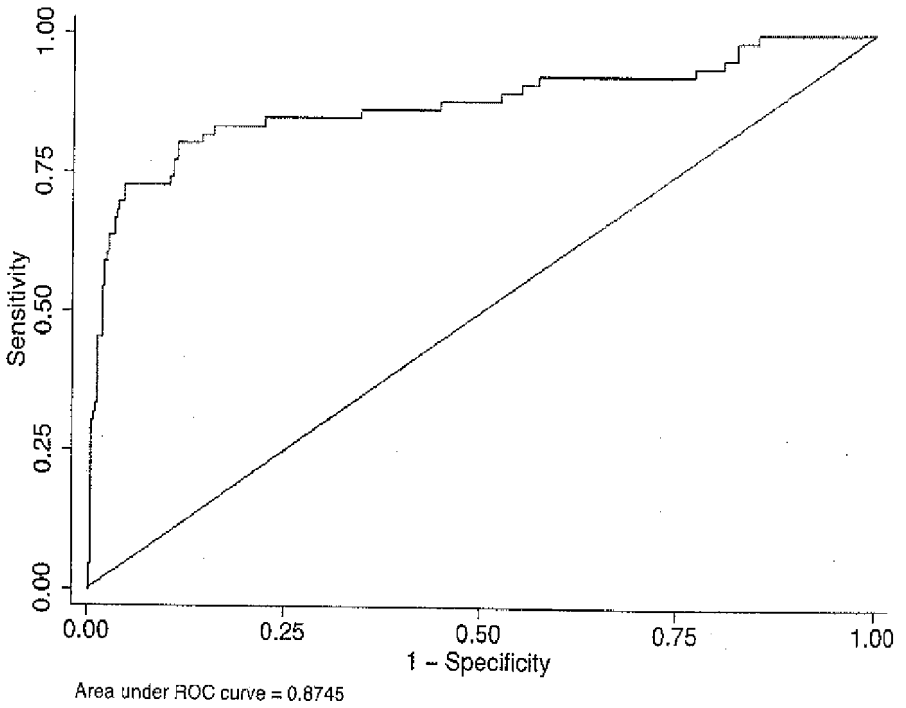


Figure 11

	Cytology	NMP22 Elisa	BladderChek	uRNA-D	Five Markers
Stage (n=66)	**n, % (95% CI)**	**n, % (95% CI)**	**n, % (95% CI)**	**n, % (95% CI)**	**n, %**
Tis (n=2)	2, 100% (16, 100)	0, 0% (0, 84)	0, 0% (0, 84)	1, 50% (1, 99)	2, 100%
Ta (n=37)	13, 35% (20, 53)	13, 35% (20, 53)	14, 38% (22, 55)	15, 41% (25, 58)	25, 68%
T1 (n=16)	11, 69% (41, 89)	12, 75% (48, 93)	8, 50% (25, 75)	15, 94 (70, 100)	16, 100%
T2 (n=9)	9, 100% (66, 100)	6, 67% (30, 93)	2, 22% (3, 60)	9, 100 (66, 100)	9, 100%
≥T3 (n=2)	2, 100% (16, 100)	2, 100% (16, 100)	1, 50% (11, 99)	1, 50% (1.3, 99)	2, 100%
Grade WHO 73 (n=65)					*p*=0.019*
1 (n=3)	1, 33% (1, 91)	1, 33% (1, 91)	1, 33% (1, 91))	1, 33% (1, 91))	1, 33%
2 (n=38)	17, 44% (29, 62)	15, 39% (24, 57)	13, 34% (20, 51)	21, 55% (38, 71)	29, 76%
3 (n=24)	19, 79% (58, 93)	17, 71% (49, 87)	11, 46% (26, 67)	19, 79% (58, 93)	23, 96%
Grade WHO ISUP 1998 (n=65)					*p*=0.016*
Low (n=32)	9, 28% (14, 47)	10, 31% (16, 50)	13, 41% (24, 59)	13, 41% (24, 59)	22, 69%
Mixed (n=4)	4, 100% (40, 100)	3, 75% (19, 99)	1, 25% (1, 81)	4, 100 (40,100)	4, 100%
High (n=29)	24, 83% (64, 94)	20, 69% (49, 85)	11, 38% (21, 58)	24, 83% (64, 94)	28, 97%
Tumour location (n=66)					*p*=0.012*
Bladder (n=62)	35, 56% (43, 69)	30, 48% (35, 61)	25, 40% (28. 54)	39, 63% (50, 75)	50, 81%
Up. tract (n=4)	2, 50% (7, 93)	3, 75% (19, 99)	0, 0% (0, 60)	2, 50% (7, 93)	4, 100%
Multiplicity (n=66)					*p*=0.33*
Single (n=52)	27, 52% (38. 66)	23, 44% (30. 59)	17, 33% (20, 47)	30, 58% (43, 71)	41, 79%
Multifocal (n=13)	10, 77% (46, 95)	10, 77% (46, 95)	8, 62% (32, 86)	11, 85% (55, 98)	12, 92%
Microhaematuria (n=65)					*p*=0.43*
Yes (n=43)	27, 63% (47, 77)	27, 63% (47, 77)	20, 47% (31, 62)	31, 72% (56, 85)	41, 95%
No (n=22)	9, 41% (21, 64))	5, 23% (8, 45)	4, 18% (5, 40)	9, 41% (21, 64)	12, 55%
Creatinine (n=55)					*p*<0.0005*
0–4.3 (n=11)	5, 45 (17, 77)	3, 27% (6,61)	4, 36% (11, 69)	4, 36% (11, 69)	7, 64%
4.3–7.1 (n=14)	9, 64% (35, 87)	6, 43% (18,71)	4, 29% (8, 58)	8, 57% (29, 82)	12, 86%
7.1–11.2 (n=22)	11, 50% (28. 72)	14, 64% (41, 83)	11, 50% (28. 72)	16, 73% (50, 89)	18, 82%
≥11.2 (n=8)	6, 75% (35, 97)	3, 38% (9, 76)	2, 25% (3, 65)	6, 75% (35, 97)	8, 100%
Sex (n=66)					*p*=0.29*
Male (n=61)	35, 57% (44, 70)	29, 48% (35, 61)	23, 38% (26, 51)	37, 61% (47, 73)	49, 80%
Female (n=5)	2, 40% (5, 85)	4, 80% (28, 99)	2, 40% (5, 85)	4, 80% (28, 99)	5, 100%
					p=0.58*

*p-values from Fisher's exact test of association between each TCC characteristic and Cxbladder test result

Figure 12

	Cytology	NMP22 Elisa	NMP22 BladderChek	uRNA-D*	Five Markers*
	n, % 95% CI)	n, % 95% CI)	n, % 95% CI)	n, %	n ,%
Diagnosis					
No diagnosis (n=164)					
	154, 94% (89, 97)	144, 88% (82, 92)	160, 98% (94, 99)	144, 88%	144, 88%
Non-malignant diagnosis					
Benign prostatic hypertrophy/prostatitis (n=130)					
	123, 95% (89, 98)	117, 90.% (84, 95)	127, 98% (93, 100)	113, 87%	109/128=85%
Cystitis/infection or inflammation of the urinary tract (n=39)					
	36, 92% (79, 98)	34, 87% (73, 96)	34, 87% (73, 96)	28, 72%	32,.82%
Calculi (n=28)					
	25, 89% (72, 98)	23, 82% (63, 94)	27, 96% (82, 100)	20. 71%	19, 68%
Haematuria secondary to warfarin (n=10)					
	10, 100% (69, 100)	9, 90% (55, 100)	10, 100% (69, 100)	8, 80%	8, 80%
Other urological cancer (n=5)					
	5, 100% (48, 100)	4, 80% (28, 99)	5, 100% (48, 100)	5, 100%	4, 80%
Microhaematuria (n=417)					*p†=0.12*
Yes n=99	87, 88% (80, 94)	81, 82% (73, 89)	91, 92% (85, 96)	74, 75%	73/97=75%
No n=318	307, 97% (94, 98)	287, 90% (86, 93)	311, 98% (96, 99)	281, 88%	279/317=88%
Creatinine (n=386)					*p†=0.002*
0 – 4.3, n=97	95, 98% (93, 100)	90, 93% (86, 97)	95, 98% (93, 100)	87, 90%	83/96=86%
4.3 – 7.1, n=94	92, 98% (93, 100)	81, 86% (78, 92)	90, 96% (89, 99)	81, 86%	84/93=90%
7.1 – 11.2, n=92	79, 86% (77, 92)	83, 90% (82, 95)	90, 98% (92, 100)	76, 83%	76/92=83%
≥11.2, n=103	101 98% (93, 100)	91, 88% (81, 94)	101, 98% (93, 100)	88, 85%	82/102=80%
Sex (n=419)					*p†=0.32*
Male n=328	311, 95% (92, 97)	290, 88% (84, 92)	316, 96% (94, 98)	291, 89%	280/325=86%
Female, n=91	85, 93% (86, 98)	79, 87% (78, 93)	88 97% (91, 99)	65, 71%	74/91=81%
					p†=0.25

*overall specificity fixed at 85%

†p-value from Chi square test of association between each characteristic (diagnosis, microhaematuria, creatinine sex) and Cxbladder test result

Figure 13

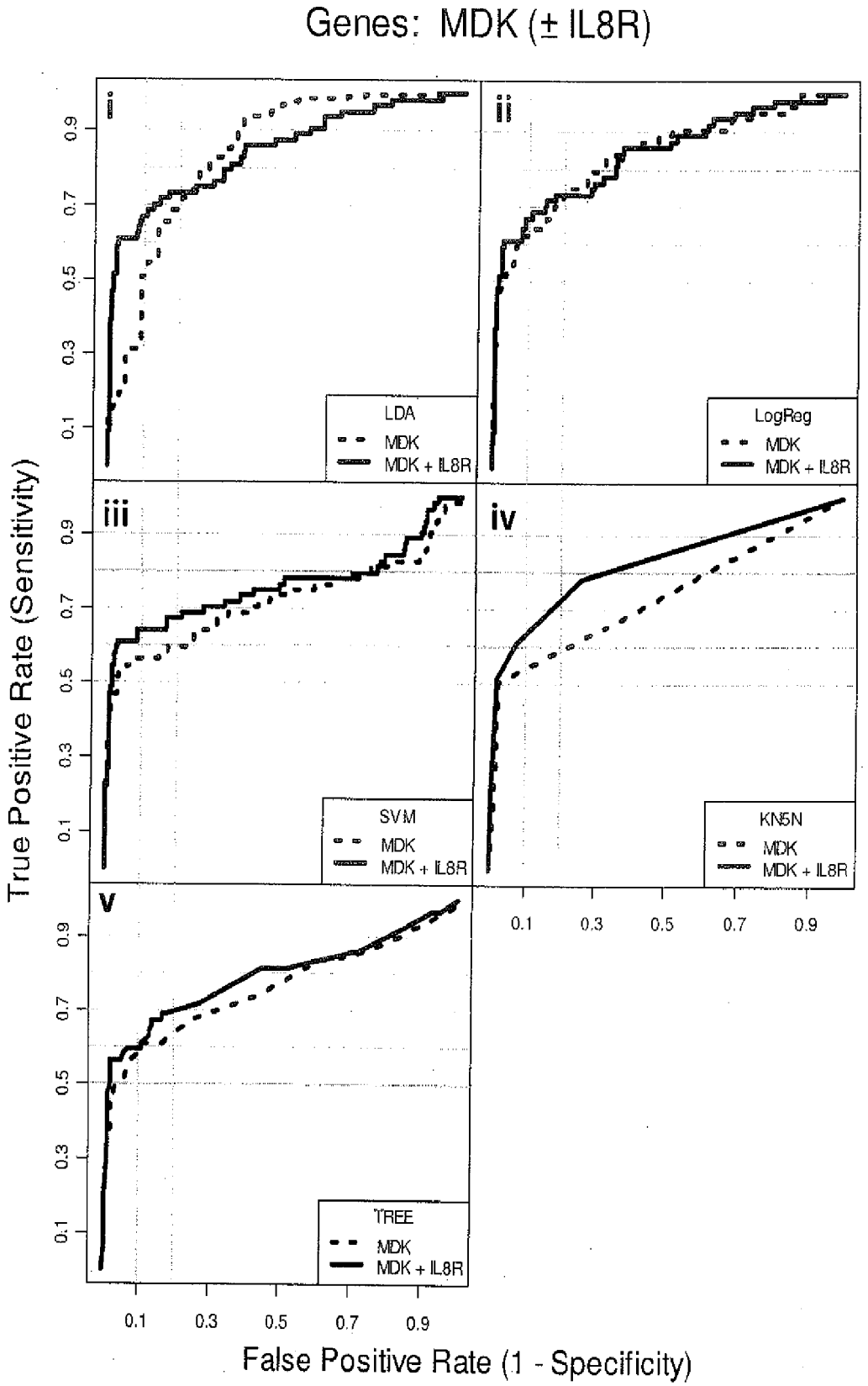

Genes: MDK (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KNN
TREE
MDK
MDK + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14a

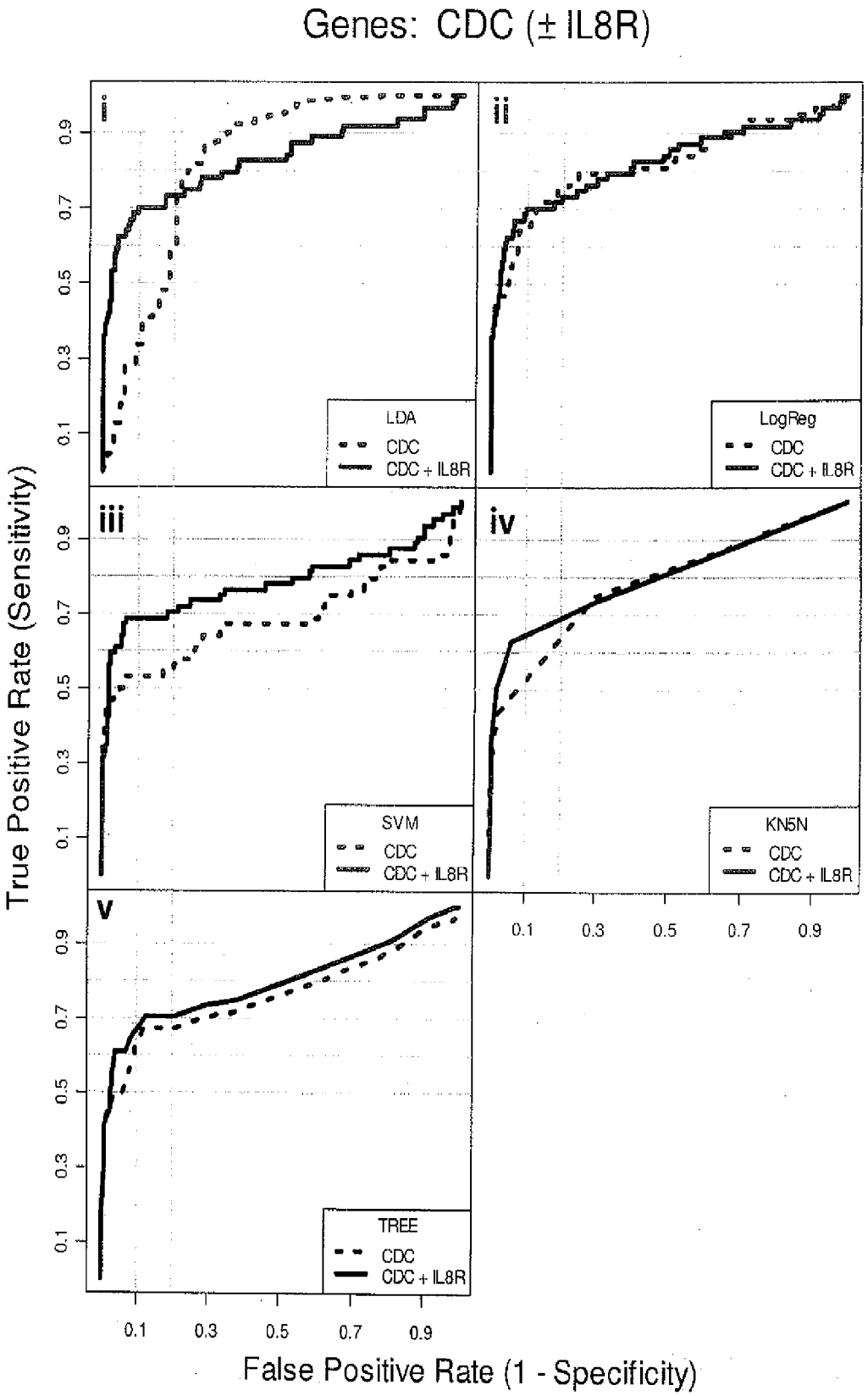

Genes: CDC (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
CDC
CDC + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14b

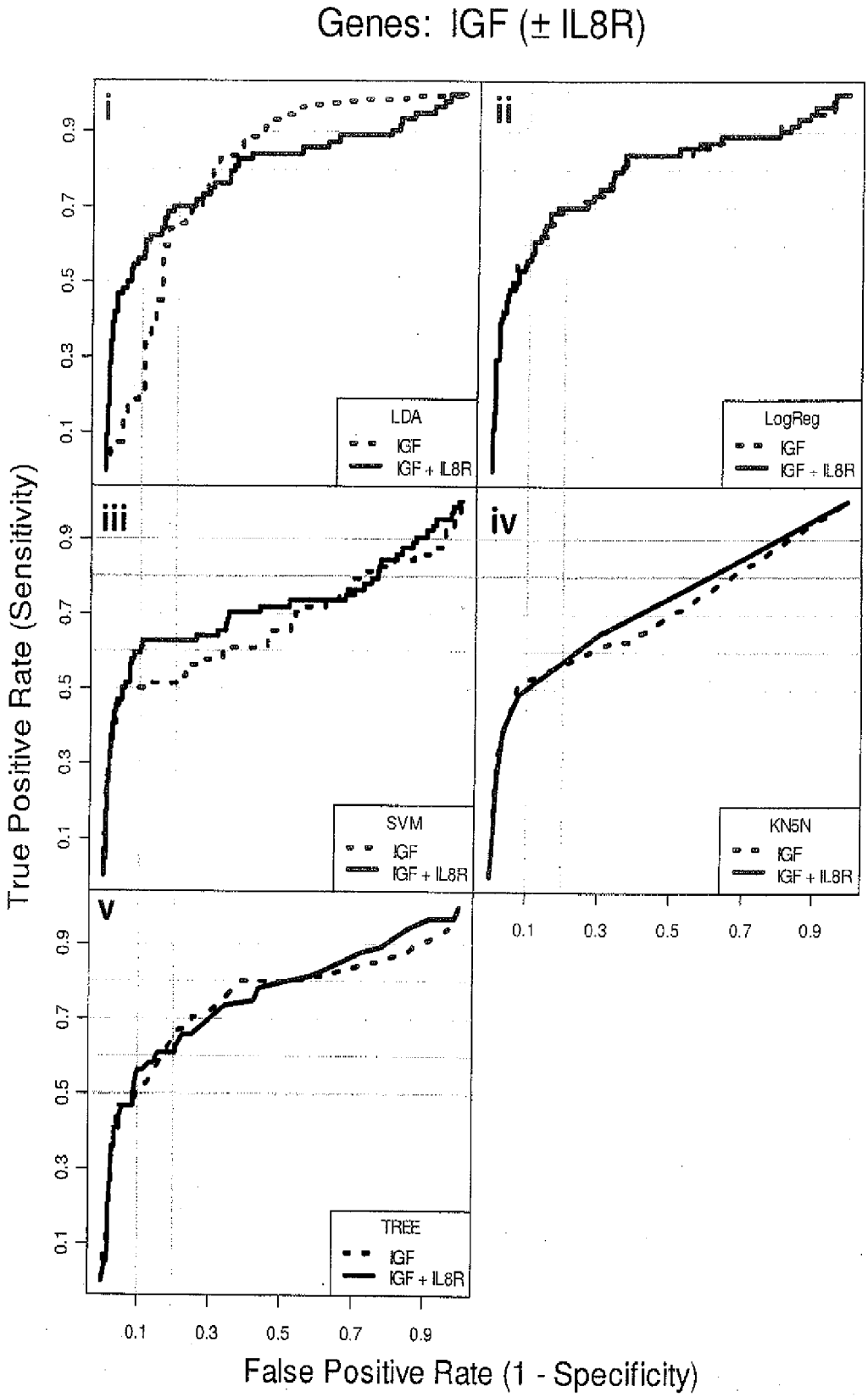

Genes: IGF (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
IGF
IGF + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14c

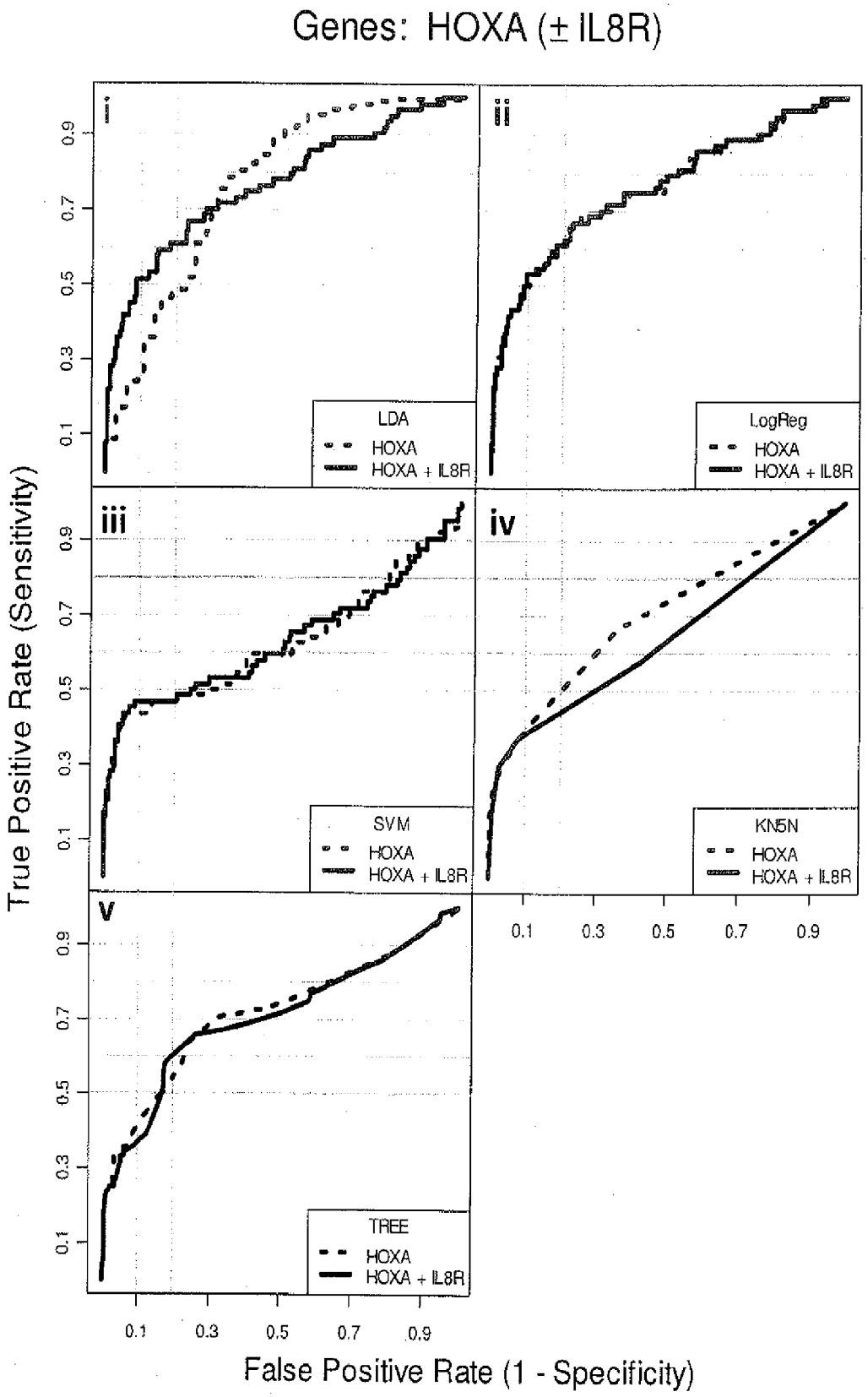

Genes: HOXA (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
LDA
HOXA
HOXA + IL8R
ii
LogReg
HOXA
HOXA + IL8R
iii
SVM
HOXA
HOXA + IL8R
iv
KN5N
HOXA
HOXA + IL8R
v
TREE
HOXA
HOXA + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14d

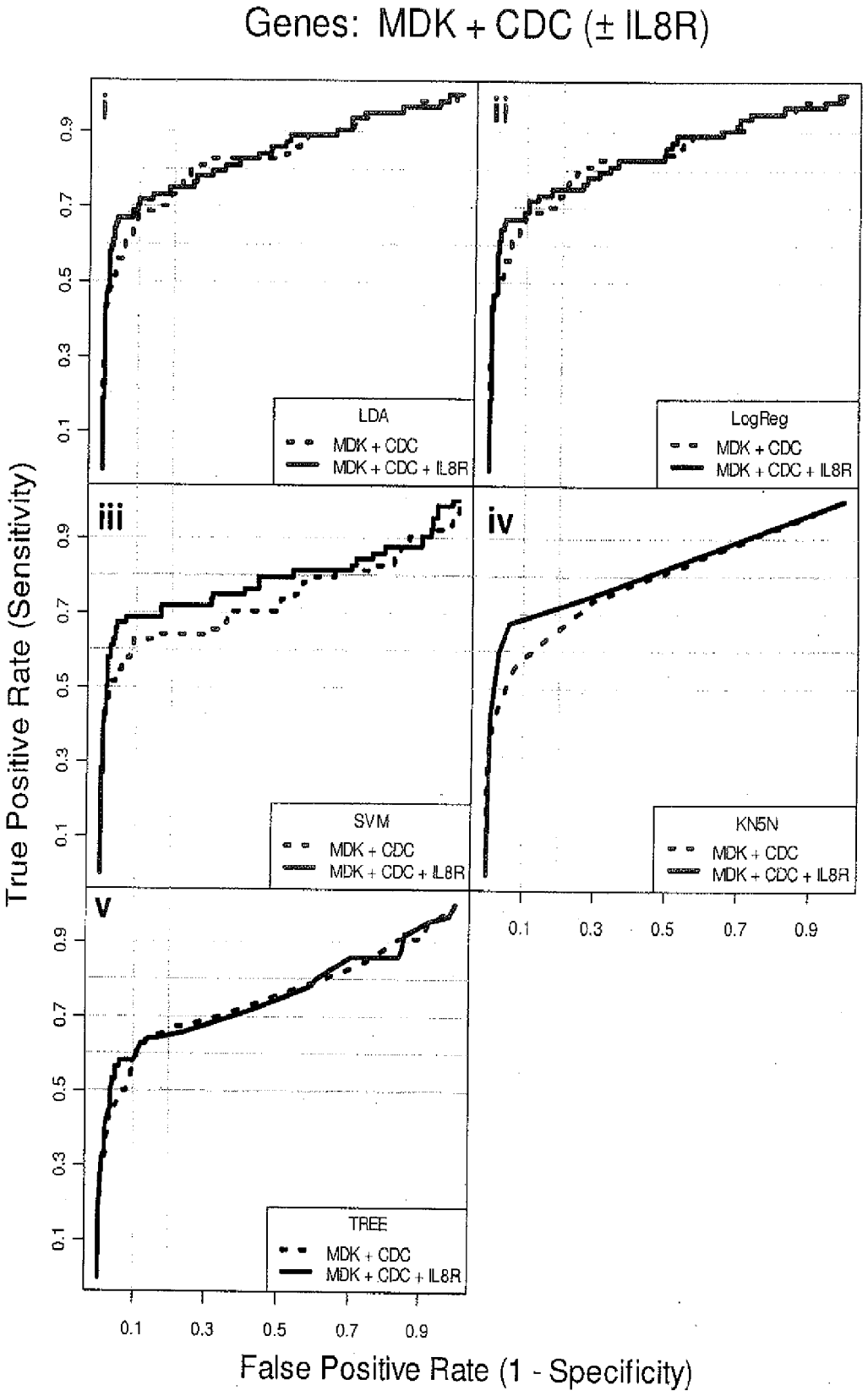

Genes: MDK + CDC (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
MDK + CDC
MDK + CDC + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14e

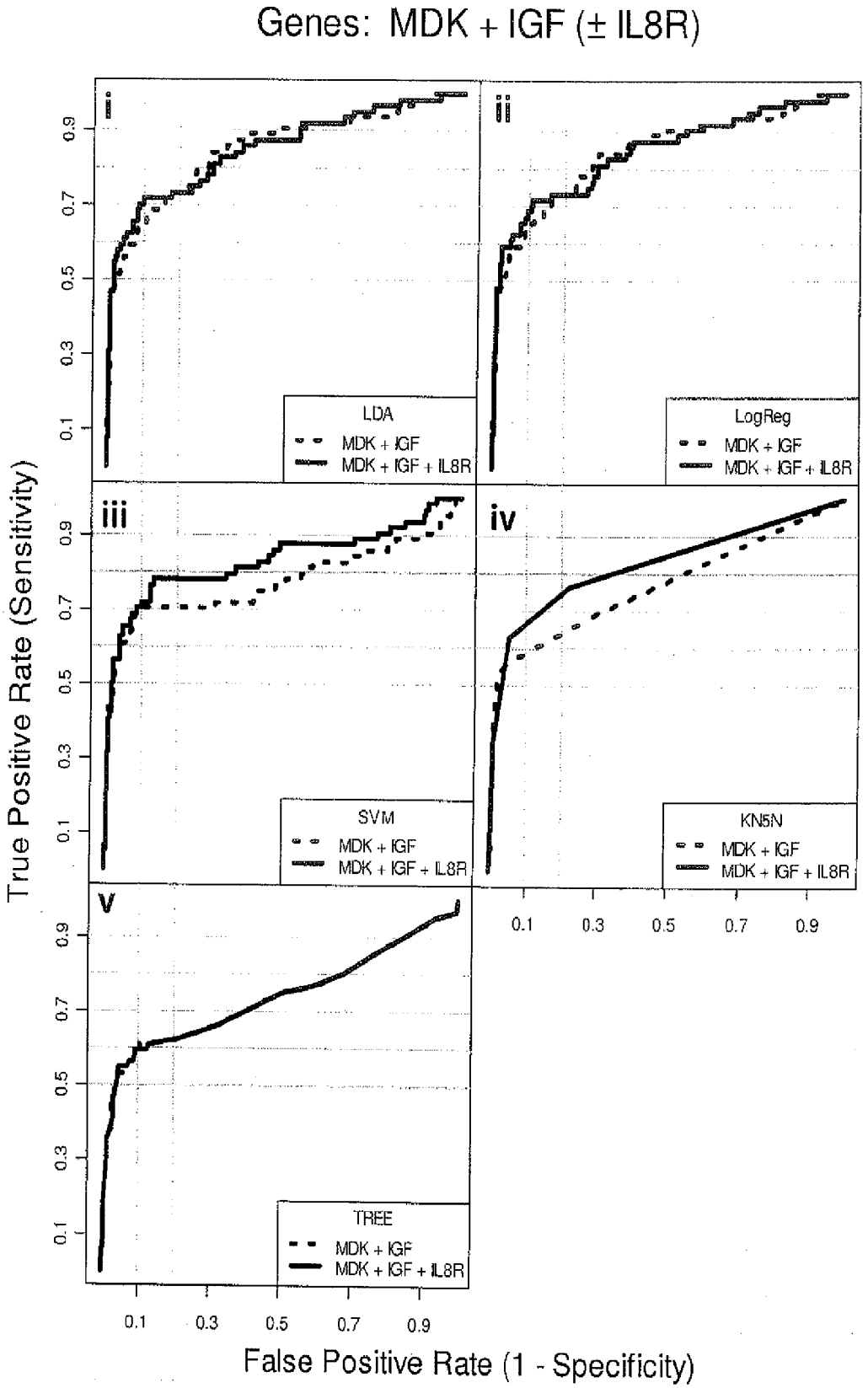

Genes: MDK + IGF (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
MDK + IGF
MDK + IGF + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14f

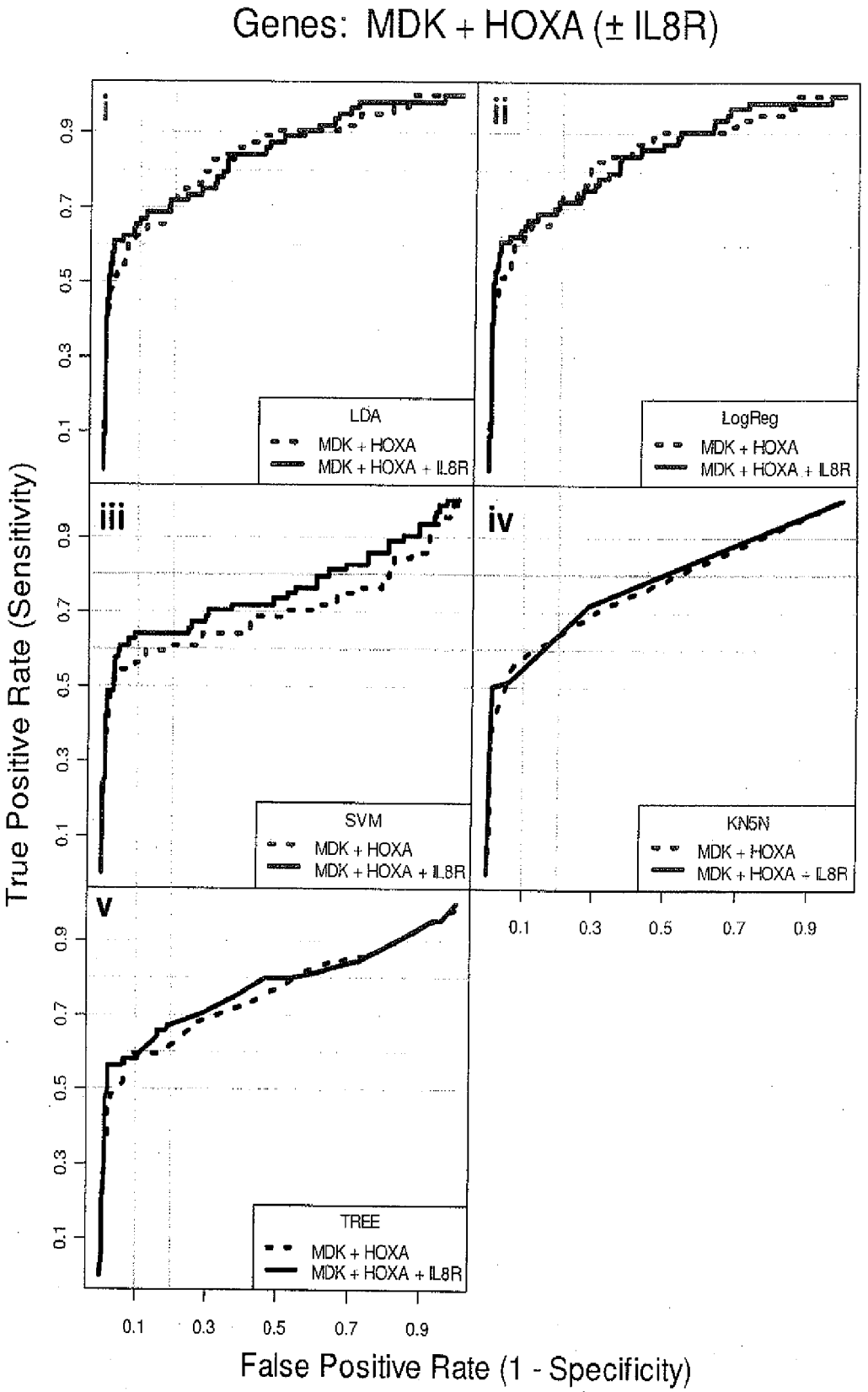

Genes: MDK + HOXA (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
ii
iii
iv
v
LDA
LogReg
SVM
KNSN
TREE
MDK + HOXA
MDK + HOXA + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14g

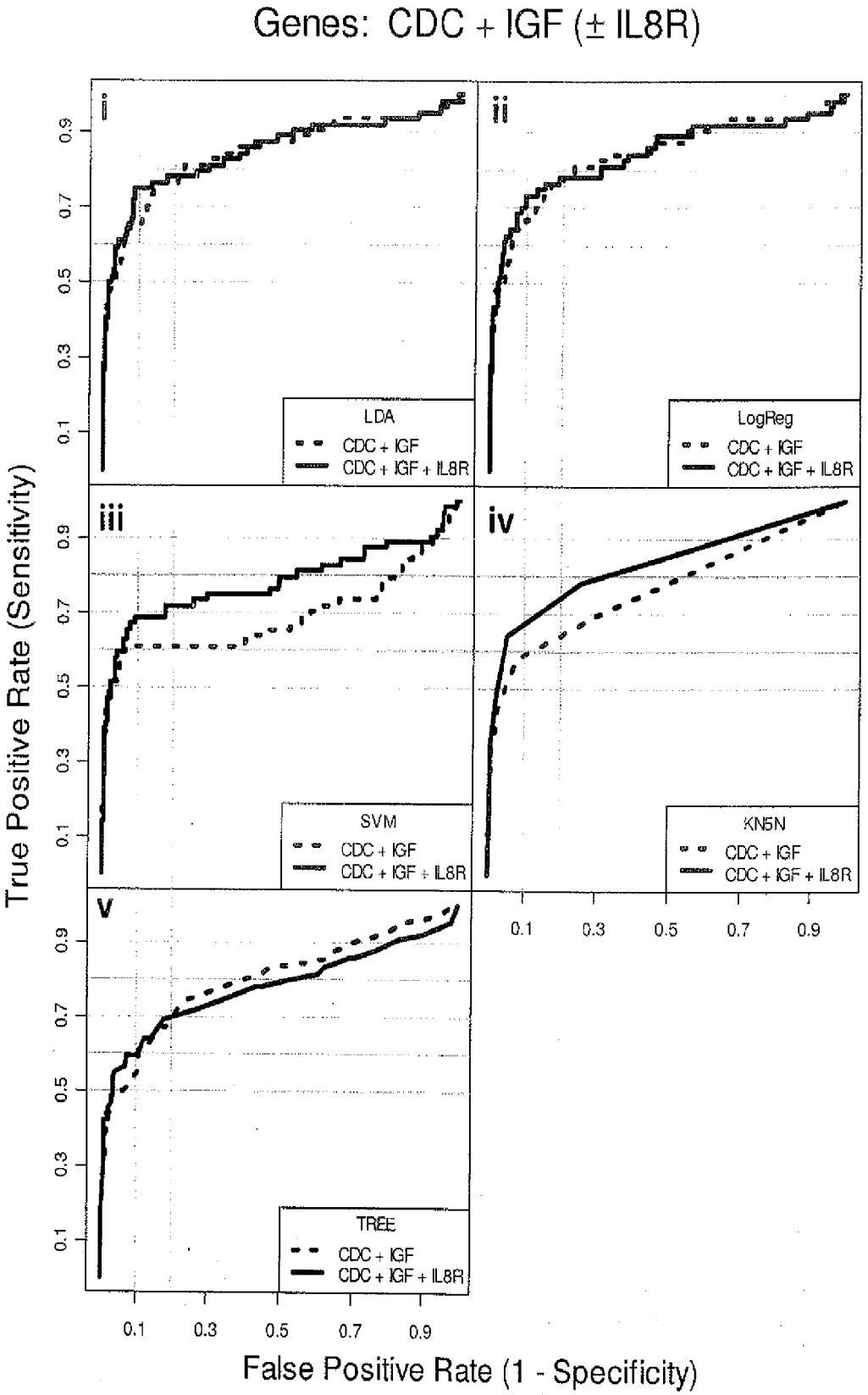

Genes: CDC + IGF (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
CDC + IGF
CDC + IGF + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14h

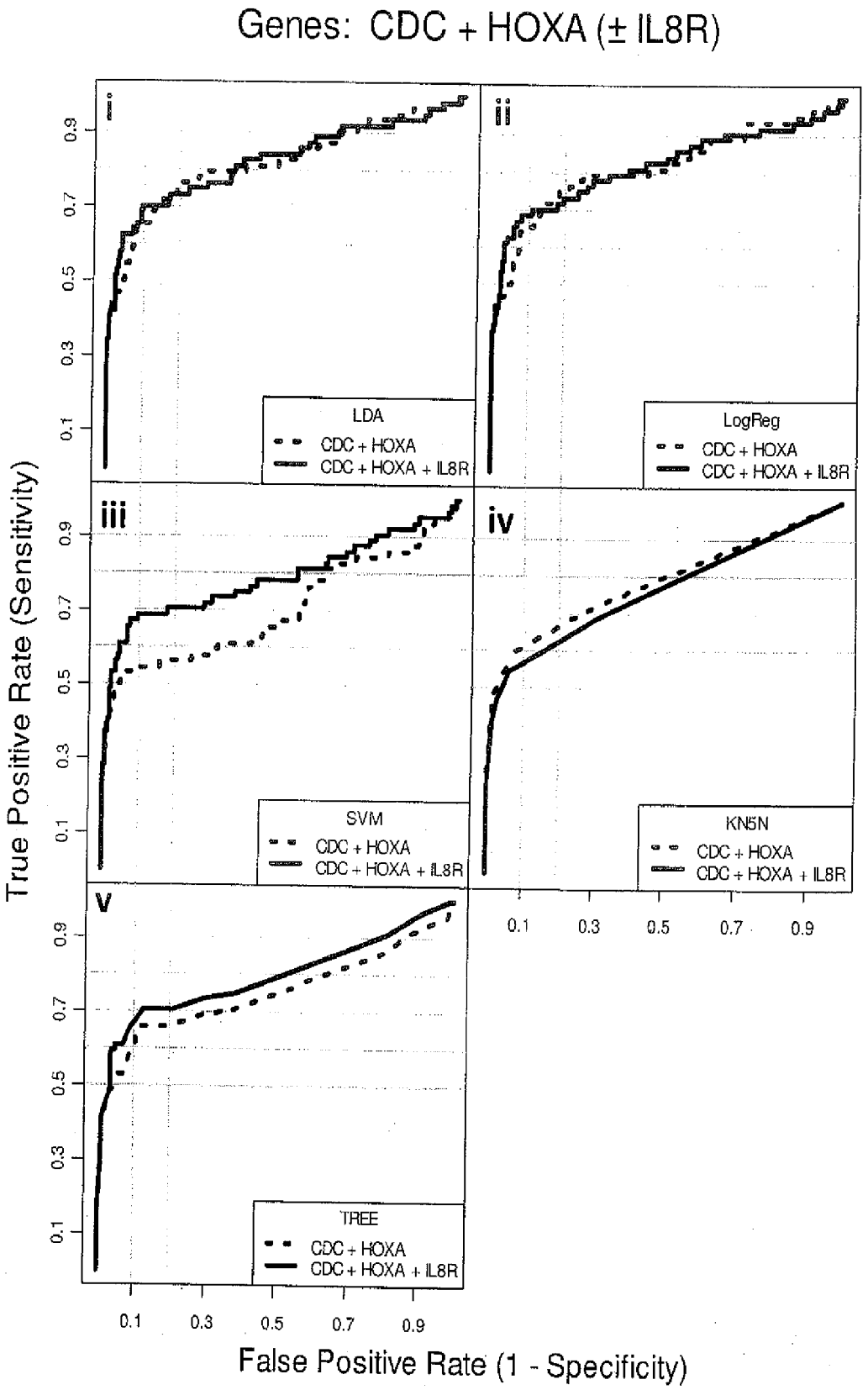

Genes: CDC + HOXA (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
ii
iii
iv
v
LDA
LogReg
SVM
KNN
TREE
CDC + HOXA
CDC + HOXA + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14i

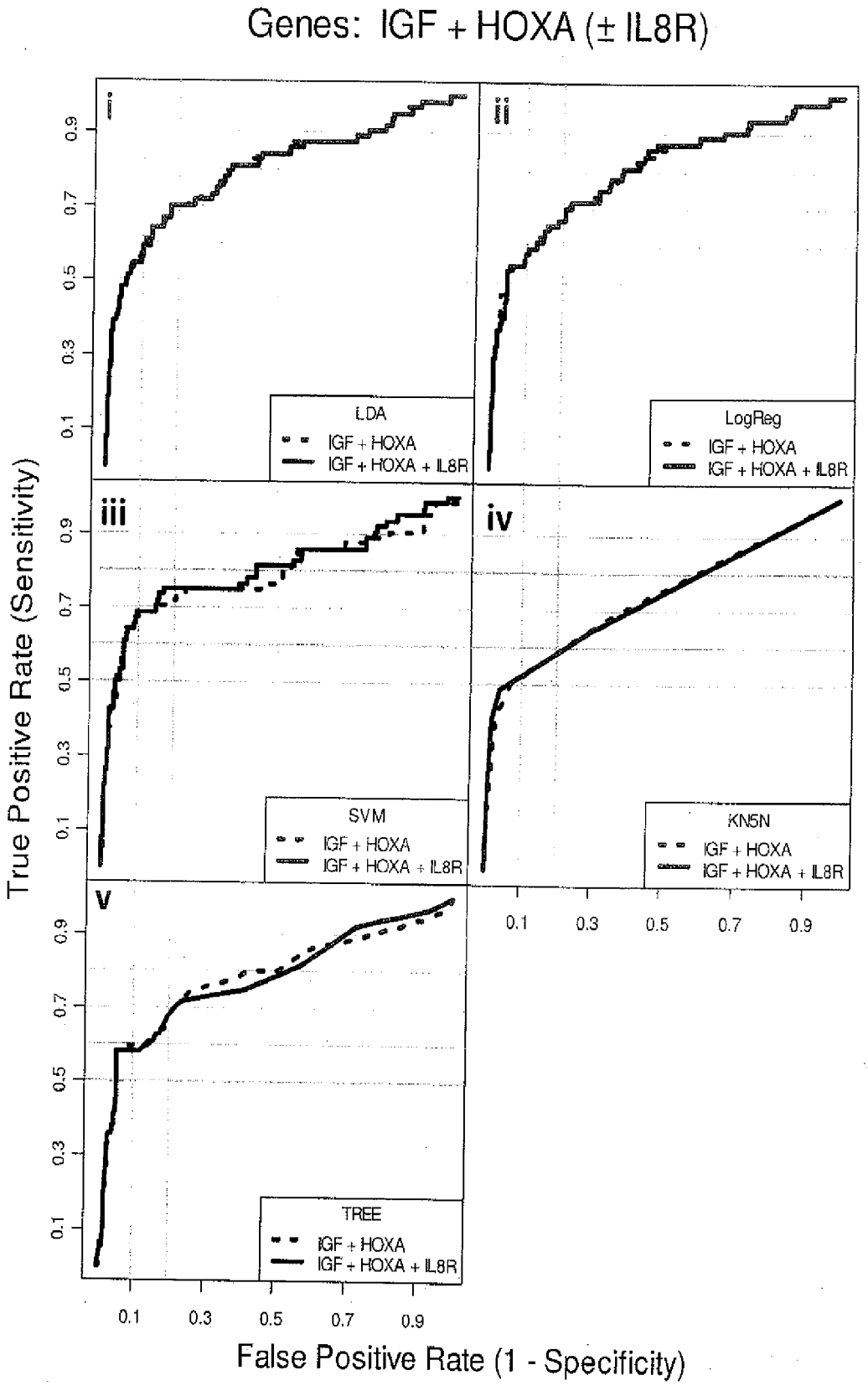

Genes: IGF + HOXA (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
LDA
IGF + HOXA
IGF + HOXA + IL8R
ii
LogReg
IGF + HOXA
IGF + HOXA + IL8R
iii
SVM
IGF + HOXA
IGF + HOXA + IL8R
iv
KN5N
IGF + HOXA
IGF + HOXA + IL8R
v
TREE
IGF + HOXA
IGF + HOXA + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14j

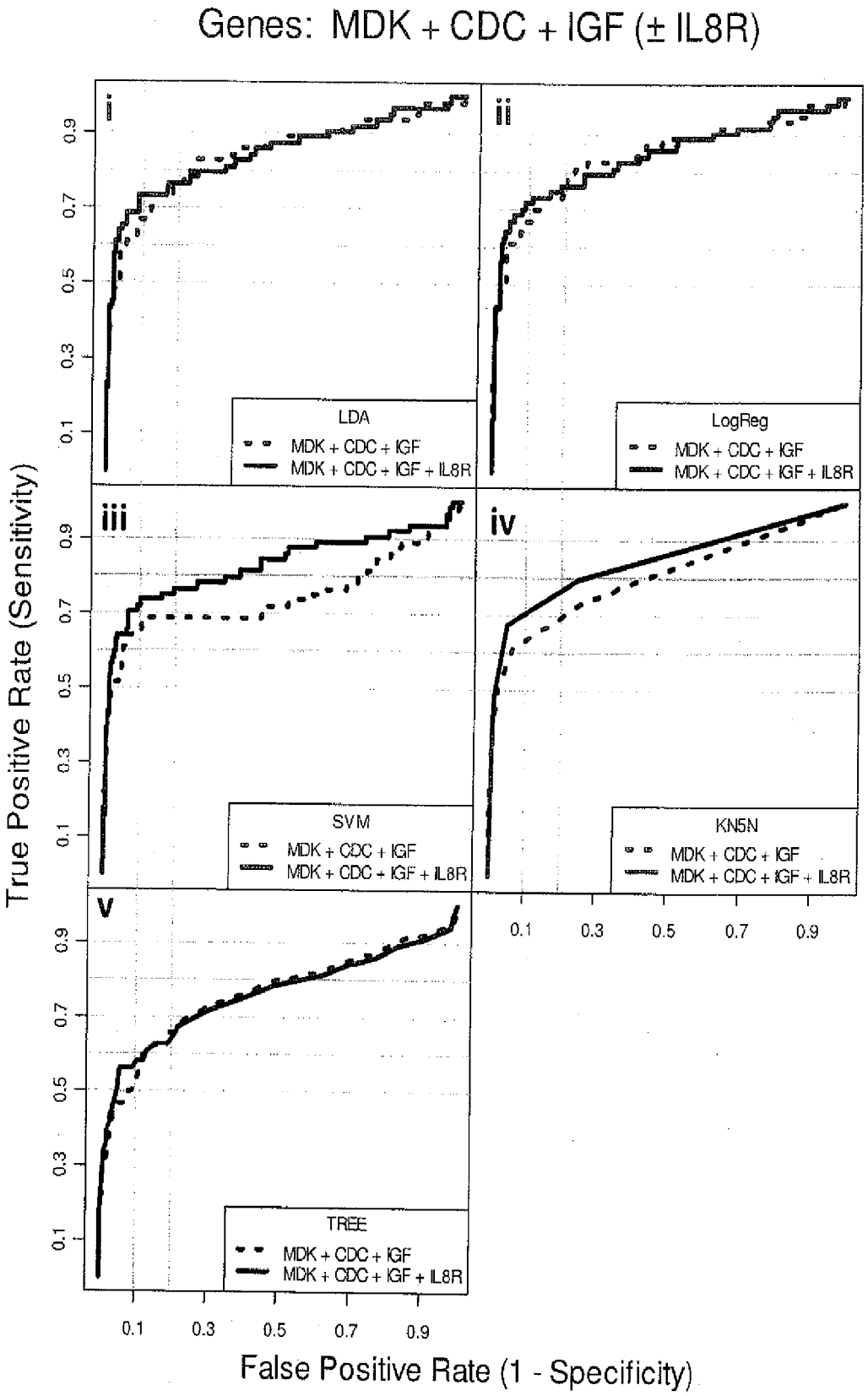

Genes: MDK + CDC + IGF (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
MDK + CDC + IGF
MDK + CDC + IGF + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14k

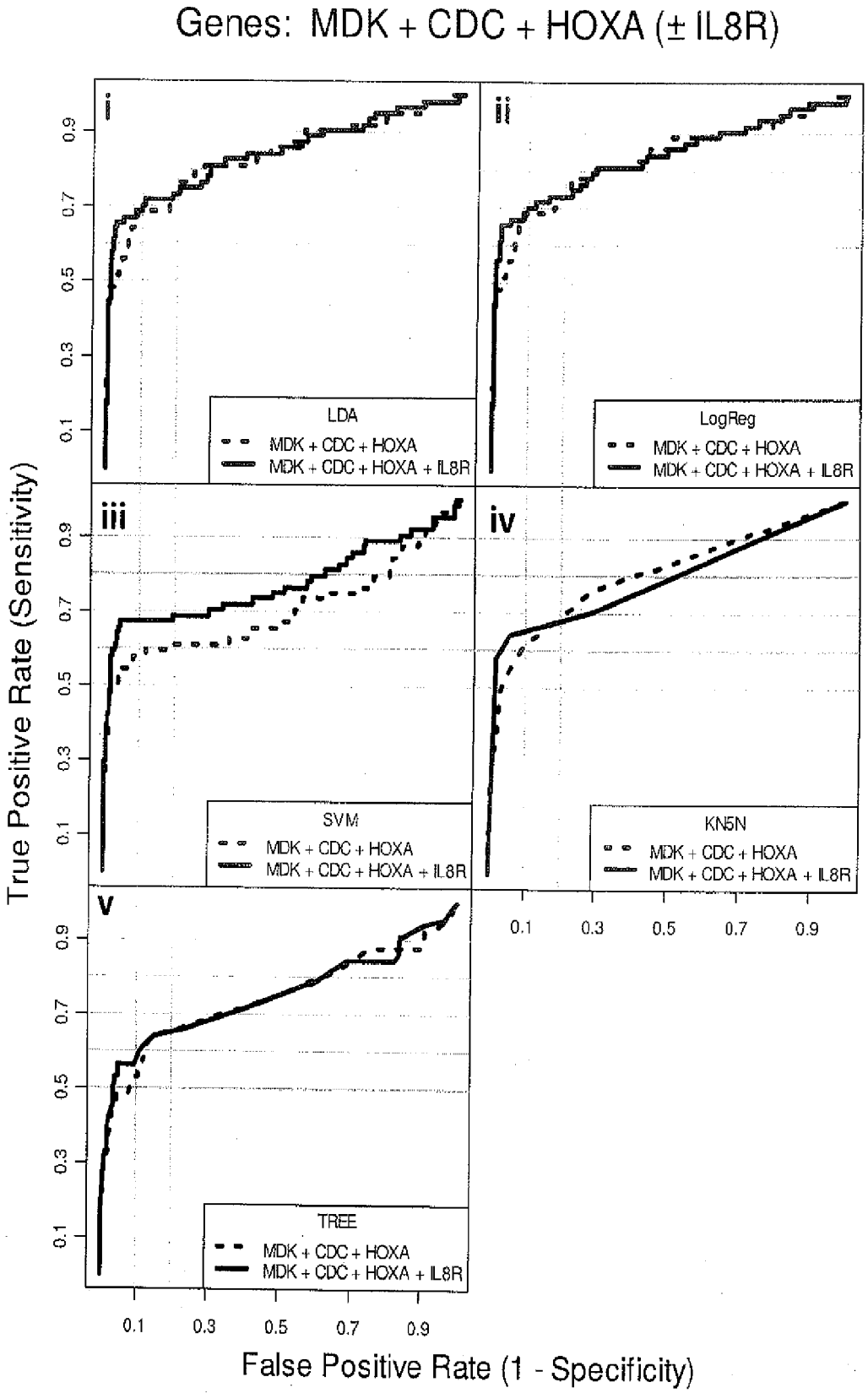

Genes: MDK + CDC + HOXA (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
LDA
MDK + CDC + HOXA
MDK + CDC + HOXA + IL8R
ii
LogReg
MDK + CDC + HOXA
MDK + CDC + HOXA + IL8R
iii
SVM
MDK + CDC + HOXA
MDK + CDC + HOXA + IL8R
iv
KN5N
MDK + CDC + HOXA
MDK + CDC + HOXA + IL8R
v
TREE
MDK + CDC + HOXA
MDK + CDC + HOXA + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14I

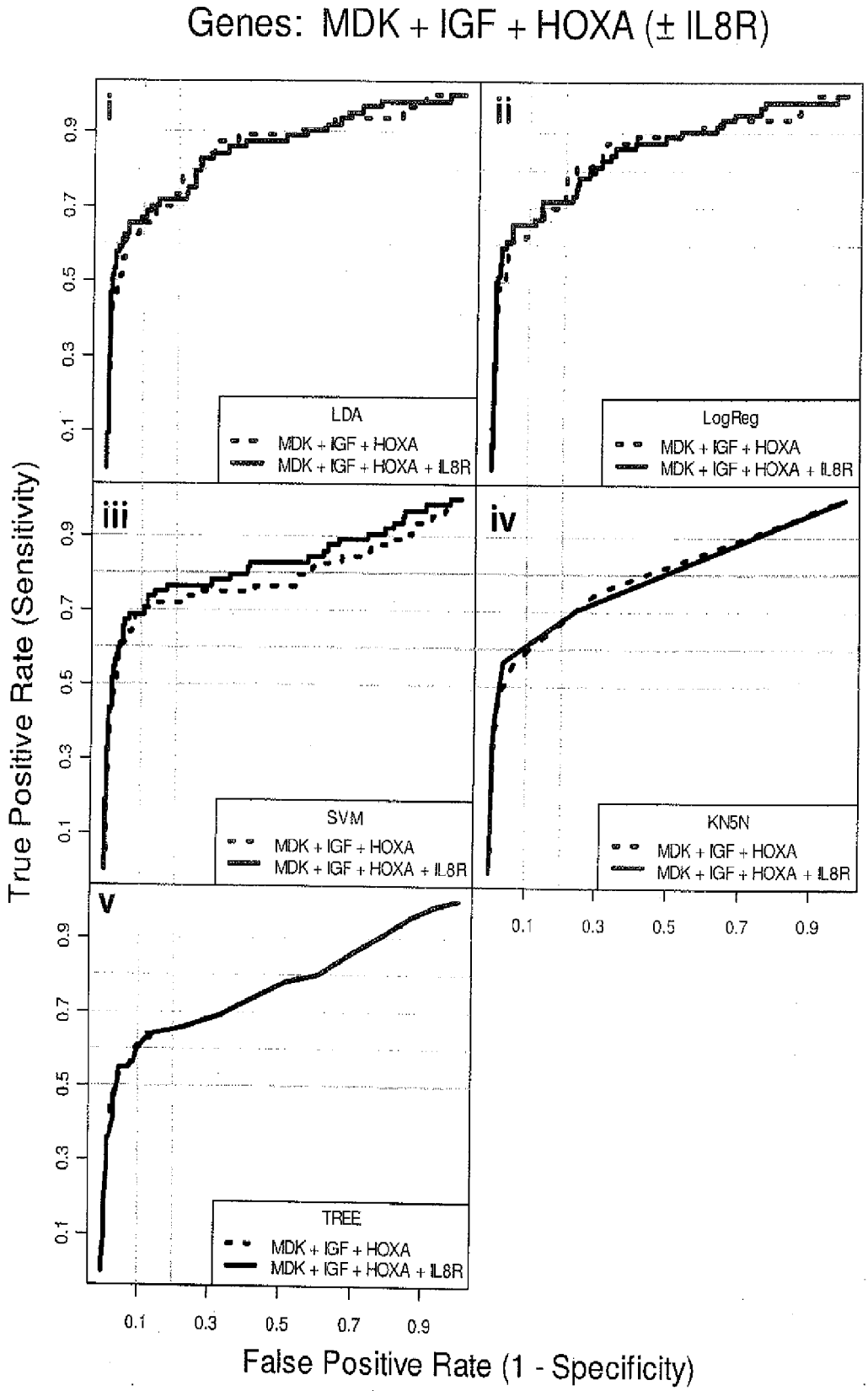

Genes: MDK + IGF + HOXA (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
MDK + IGF + HOXA
MDK + IGF + HOXA + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14m

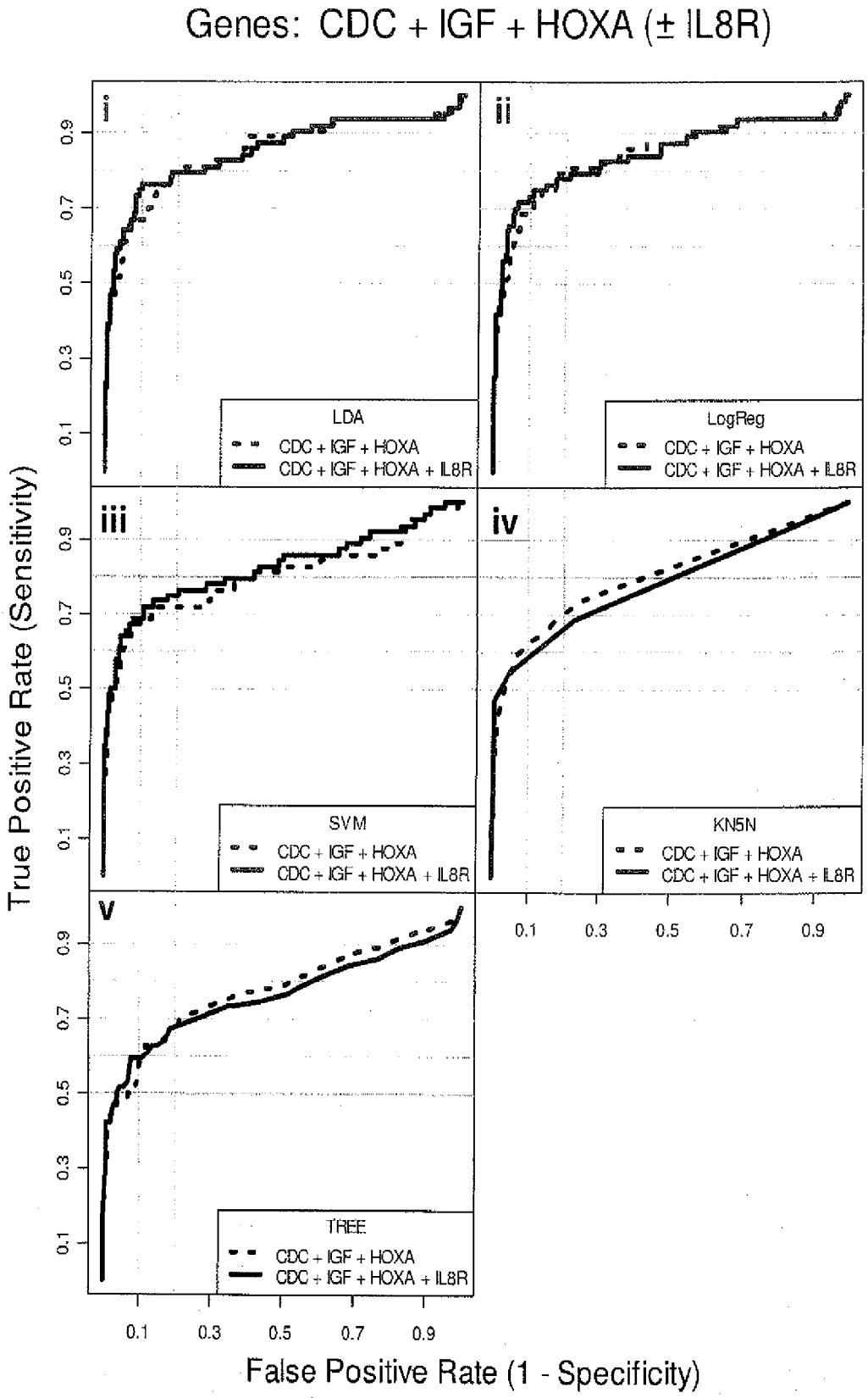

Genes: CDC + IGF + HOXA (± IL8R)
i
ii
iii
iv
v
LDA
LogReg
SVM
KN5N
TREE
CDC + IGF + HOXA
CDC + IGF + HOXA + IL8R
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
0.1
0.3
0.5
0.7
0.9

Figure 14n

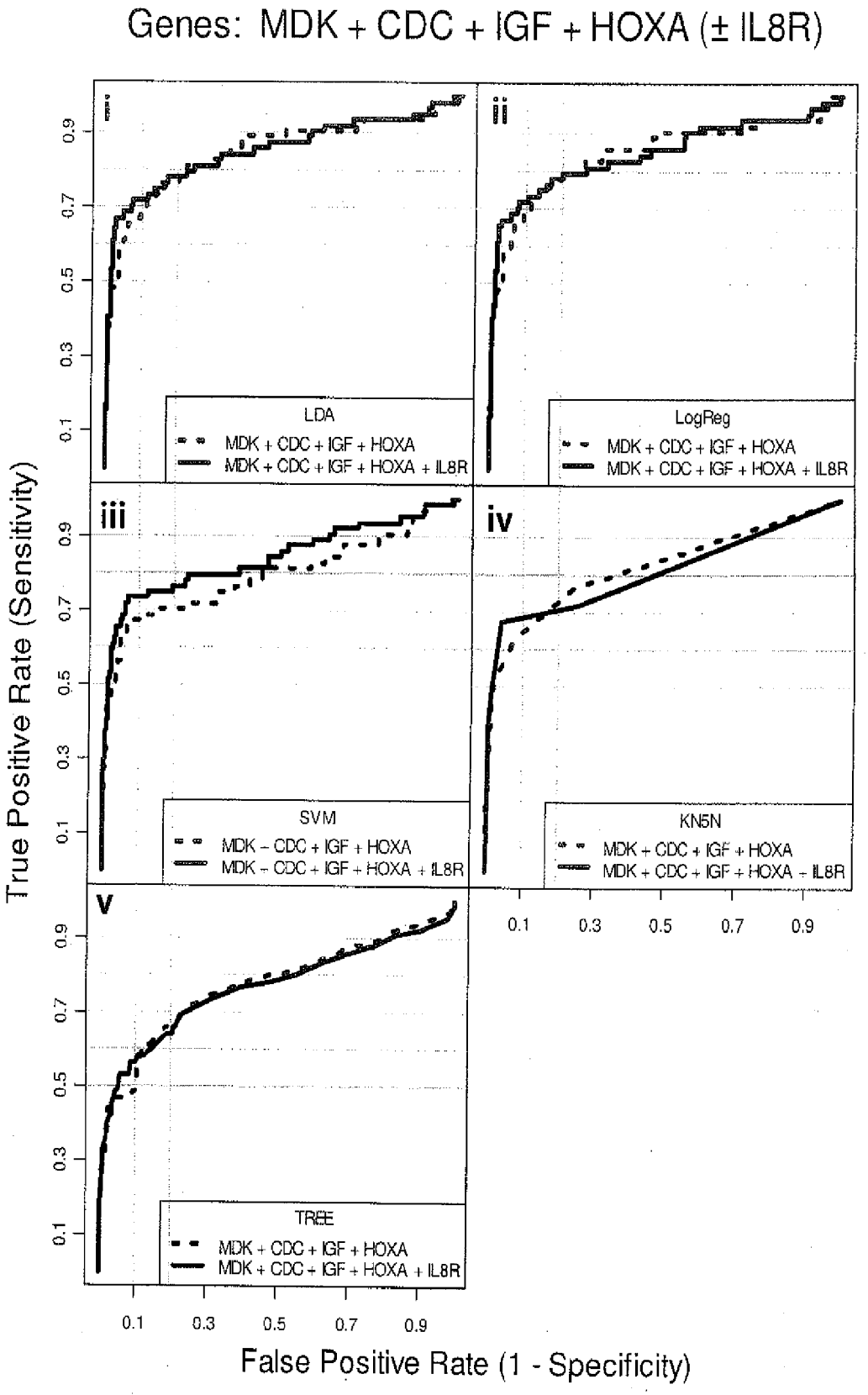

Genes: MDK + CDC + IGF + HOXA (± IL8R)
True Positive Rate (Sensitivity)
False Positive Rate (1 - Specificity)
i
ii
iii
iv
v
LDA
LogReg
SVM
KNSN
TREE
MDK + CDC + IGF + HOXA
MDK + CDC + IGF + HOXA + IL8R
0.1
0.3
0.5
0.7
0.9

Figure 14o

Model	LDA		LogReg		SVM		KN5N		TREE	
	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb
MDK	0.087	0.127	0.119	0.127	0.107	0.121	0.100	0.120	0.107	0.117
CDC2	0.062	0.129	0.124	0.129	0.102	0.127	0.102	0.121	0.114	0.124
IGFBP5	0.060	0.108	0.109	0.108	0.094	0.107	0.093	0.090	0.093	0.096
HOXA13	0.058	0.094	0.094	0.094	0.082	0.084	0.075	0.071	0.078	0.075
MDK + CDC2	0.124	0.134	0.124	0.133	0.115	0.131	0.109	0.128	0.107	0.111
MDK + IGFBP5	0.122	0.129	0.121	0.129	0.125	0.133	0.111	0.122	0.107	0.107
MDK + HOXA13	0.119	0.126	0.118	0.125	0.108	0.118	0.107	0.107	0.107	0.114
CDC2 + IGFBP5	0.128	0.134	0.127	0.133	0.114	0.125	0.109	0.125	0.109	0.115
CDC + HOXA13	0.122	0.128	0.123	0.129	0.103	0.125	0.116	0.108	0.113	0.123
IGF + HOXA13	0.109	0.109	0.108	0.107	0.119	0.121	0.096	0.098	0.102	0.101
MDK + CDC2 + IGFBP5	0.127	0.135	0.127	0.135	0.123	0.134	0.119	0.132	0.103	0.108
MDK + CDC2 + HOXA13	0.125	0.133	0.125	0.134	0.109	0.127	0.113	0.122	0.104	0.111
MDK + IGFBP5 + HOXA13	0.122	0.128	0.121	0.127	0.126	0.132	0.111	0.115	0.110	0.109
CDC2 + IGFBP5 + HOXA13	0.129	0.136	0.131	0.136	0.126	0.131	0.117	0.114	0.108	0.111
MDK+CDC2+IGFBP5+HOXA13	0.130	0.137	0.130	0.138	0.124	0.137	0.122	0.129	0.103	0.106

Area Under the ROC Curve (AUC) for False Positive Rate from 0.00 to 0.20

Figure 15a

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.040	0.008	0.014	0.019	0.010
CDC2	0.067	0.005	0.025	0.018	0.009
IGFBP5	0.048	-0.001	0.013	-0.003	0.002
HOXA13	0.036	0.000	0.001	-0.004	-0.003
MDK + CDC2	0.009	0.009	0.015	0.019	0.005
MDK + IGFBP5	0.007	0.007	0.008	0.011	-0.000
MDK + HOXA13	0.007	0.007	0.010	0.000	0.007
CDC2 + IGFBP5	0.007	0.006	0.012	0.016	0.006
CDC + HOXA13	0.006	0.006	0.022	-0.007	0.010
IGF + HOXA13	0.000	-0.001	0.002	0.002	-0.000
MDK + CDC2 + IGFBP5	0.009	0.008	0.012	0.013	0.004
MDK + CDC2 + HOXA13	0.008	0.008	0.018	0.009	0.006
MDK + IGFBP5 + HOXA13	0.006	0.006	0.006	0.004	-0.001
CDC2 + IGFBP5 + HOXA13	0.006	0.006	0.005	-0.003	0.004
MDK+CDC2+IGFBP5+HOXA13	0.007	0.007	0.013	0.007	0.002
Gain in AUC (over FPR from 0.0 to 0.2)					

Figure 15b

a

Model	LDA		LogReg		SVM		KNSN		TREE	
	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb
MDK	0.721	0.734	0.734	0.734	0.594	0.672	0.531	0.781	0.625	0.688
CDC2	0.753	0.734	0.750	0.734	0.562	0.703	0.750	0.734	0.672	0.703
IGFBP5	0.657	0.703	0.688	0.703	0.516	0.625	0.516	0.656	0.656	0.609
HOXA13	0.486	0.609	0.625	0.609	0.484	0.469	0.406	0.375	0.547	0.578
MDK + CDC2	0.734	0.750	0.734	0.750	0.641	0.719	0.734	0.750	0.672	0.641
MDK + IGFBP5	0.734	0.734	0.734	0.734	0.703	0.781	0.688	0.766	0.625	0.625
MDK + HOXA13	0.719	0.719	0.734	0.719	0.609	0.641	0.703	0.719	0.609	0.672
CDC2 + IGFBP5	0.766	0.781	0.766	0.781	0.609	0.719	0.688	0.781	0.672	0.688
CDC + HOXA13	0.750	0.734	0.750	0.734	0.562	0.703	0.703	0.688	0.656	0.703
IGF + HOXA13	0.703	0.703	0.672	0.672	0.719	0.750	0.500	0.641	0.688	0.672
MDK + CDC2 + IGFBP5	0.766	0.766	0.766	0.766	0.688	0.766	0.734	0.797	0.656	0.625
MDK + CDC2 + HOXA13	0.734	0.734	0.734	0.734	0.609	0.688	0.766	0.703	0.656	0.656
MDK + IGFBP5 + HOXA13	0.734	0.719	0.734	0.719	0.719	0.766	0.750	0.703	0.656	0.656
CDC2 + IGFBP5 + HOXA13	0.797	0.797	0.812	0.781	0.719	0.750	0.734	0.688	0.672	0.672
MDK+CDC2+IGFBP5+HOXA13	0.766	0.781	0.781	0.797	0.703	0.766	0.766	0.719	0.656	0.641

Sensitivity at Specificity: Sp.80

Figure 16a

b

Model	LDA		LogReg		SVM		KN5N		TREE	
	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb
MDK	0.657	0.719	0.672	0.719	0.578	0.641	0.531	0.609	0.609	0.672
CDC2	0.481	0.703	0.719	0.703	0.531	0.688	0.500	0.625	0.672	0.703
IGFBP5	0.595	0.641	0.625	0.656	0.516	0.625	0.516	0.484	0.562	0.578
HOXA13	0.462	0.594	0.562	0.562	0.469	0.469	0.406	0.375	0.500	0.406
MDK + CDC2	0.688	0.734	0.688	0.734	0.641	0.688	0.562	0.672	0.641	0.641
MDK + IGFBP5	0.703	0.719	0.703	0.719	0.703	0.781	0.562	0.766	0.609	0.609
MDK + HOXA13	0.656	0.688	0.656	0.688	0.594	0.641	0.562	0.516	0.594	0.625
CDC2 + IGFBP5	0.750	0.766	0.750	0.766	0.609	0.688	0.578	0.641	0.625	0.641
CDC + HOXA13	0.719	0.703	0.719	0.703	0.547	0.688	0.594	0.547	0.656	0.703
IGF + HOXA13	0.641	0.641	0.641	0.641	0.688	0.719	0.500	0.484	0.609	0.609
MDK + CDC2 + IGFBP5	0.734	0.734	0.734	0.734	0.688	0.734	0.609	0.797	0.609	0.625
MDK + CDC2 + HOXA13	0.688	0.719	0.688	0.719	0.594	0.672	0.609	0.641	0.641	0.641
MDK + IGFBP5 + HOXA13	0.703	0.719	0.703	0.719	0.719	0.750	0.562	0.703	0.641	0.641
CDC2 + IGFBP5 + HOXA13	0.750	0.766	0.750	0.766	0.719	0.734	0.594	0.688	0.625	0.625
MDK+CDC2+IGFBP5+HOXA13	0.766	0.750	0.750	0.750	0.688	0.750	0.625	0.719	0.609	0.594

Sensitivity at Specificity: Sp.85

Figure 16b

c	Model	LDA		LogReg		SVM		KNSN		TREE	
		-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb
	MDK	0.511	0.672	0.625	0.672	0.562	0.641	0.531	0.609	0.609	0.594
	CDC2	0.338	0.703	0.656	0.703	0.531	0.688	0.500	0.625	0.625	0.672
	IGFBP5	0.212	0.562	0.562	0.562	0.500	0.594	0.516	0.484	0.500	0.562
	HOXA13	0.257	0.516	0.500	0.531	0.438	0.469	0.406	0.375	0.391	0.359
	MDK + CDC2	0.688	0.703	0.688	0.688	0.625	0.688	0.562	0.672	0.562	0.578
	MDK + IGFBP5	0.641	0.719	0.641	0.688	0.703	0.719	0.562	0.625	0.578	0.594
	MDK + HOXA13	0.641	0.672	0.625	0.656	0.562	0.641	0.562	0.516	0.594	0.578
	CDC2 + IGFBP5	0.656	0.750	0.672	0.734	0.609	0.688	0.578	0.641	0.547	0.594
	CDC + HOXA13	0.641	0.703	0.656	0.688	0.547	0.688	0.594	0.547	0.594	0.672
	IGF + HOXA13	0.594	0.594	0.578	0.578	0.672	0.688	0.500	0.484	0.594	0.578
	MDK + CDC2 + IGFBP5	0.672	0.734	0.672	0.719	0.656	0.734	0.609	0.672	0.531	0.578
	MDK + CDC2 + HOXA13	0.688	0.688	0.688	0.703	0.578	0.672	0.609	0.641	0.531	0.562
	MDK + IGFBP5 + HOXA13	0.641	0.672	0.625	0.656	0.688	0.688	0.562	0.562	0.609	0.594
	CDC2 + IGFBP5 + HOXA13	0.672	0.766	0.703	0.734	0.672	0.688	0.594	0.547	0.578	0.594
	MDK+CDC2+IGFBP5+HOXA13	0.688	0.719	0.703	0.719	0.672	0.734	0.625	0.672	0.500	0.562
	Sensitivity at Specificity: Sp.90										

Figure 16c

d	Model	LDA		LogReg		SVM		KN5N		TREE	
		-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb
	MDK	0.304	0.609	0.547	0.609	0.531	0.609	0.500	0.609	0.500	0.562
	CDC2	0.180	0.625	0.516	0.625	0.500	0.609	0.438	0.625	0.500	0.609
	IGFBP5	0.148	0.484	0.484	0.484	0.500	0.500	0.359	0.391	0.469	0.438
	HOXA13	0.173	0.422	0.438	0.422	0.422	0.406	0.297	0.297	0.344	0.297
	MDK + CDC2	0.562	0.672	0.562	0.672	0.547	0.672	0.453	0.672	0.453	0.562
	MDK + IGFBP5	0.562	0.609	0.578	0.609	0.609	0.656	0.562	0.625	0.531	0.547
	MDK + HOXA13	0.531	0.609	0.531	0.609	0.531	0.609	0.562	0.516	0.500	0.562
	CDC2 + IGFBP5	0.562	0.609	0.562	0.625	0.562	0.594	0.453	0.641	0.500	0.547
	CDC + HOXA13	0.516	0.625	0.500	0.625	0.516	0.609	0.594	0.547	0.516	0.609
	IGF + HOXA13	0.484	0.484	0.531	0.531	0.547	0.531	0.500	0.484	0.406	0.406
	MDK + CDC2 + IGFBP5	0.594	0.656	0.609	0.672	0.578	0.641	0.609	0.672	0.469	0.500
	MDK + CDC2 + HOXA13	0.562	0.672	0.562	0.672	0.547	0.672	0.516	0.641	0.484	0.562
	MDK + IGFBP5 + HOXA13	0.609	0.625	0.609	0.609	0.609	0.656	0.562	0.562	0.531	0.547
	CDC2 + IGFBP5 + HOXA13	0.609	0.641	0.578	0.656	0.594	0.641	0.594	0.547	0.484	0.516
	MDK+CDC2+IGFBP5+HOXA13	0.609	0.688	0.594	0.672	0.625	0.672	0.625	0.672	0.469	0.484
	Sensitivity at Specificity: Sp.95										

Figure 16d

e

Model	LDA		LogReg		SVM		KN5N		TREE	
	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb	-IL8Rb	+IL8Rb
MDK	0.163	0.516	0.484	0.516	0.469	0.547	0.312	0.516	0.359	0.562
CDC2	0.047	0.453	0.469	0.469	0.453	0.562	0.438	0.500	0.469	0.422
IGFBP5	0.054	0.391	0.391	0.391	0.359	0.375	0.234	0.266	0.219	0.266
HOXA13	0.089	0.281	0.312	0.281	0.297	0.281	0.203	0.297	0.234	0.234
MDK + CDC2	0.484	0.578	0.500	0.578	0.469	0.578	0.375	0.422	0.359	0.391
MDK + IGFBP5	0.484	0.547	0.484	0.547	0.469	0.500	0.531	0.344	0.359	0.359
MDK + HOXA13	0.484	0.547	0.469	0.547	0.469	0.484	0.422	0.500	0.359	0.562
CDC2 + IGFBP5	0.484	0.500	0.484	0.500	0.469	0.484	0.453	0.484	0.438	0.422
CDC + HOXA13	0.469	0.422	0.453	0.469	0.422	0.484	0.484	0.406	0.453	0.453
IGF + HOXA13	0.391	0.391	0.375	0.375	0.375	0.422	0.234	0.406	0.219	0.250
MDK + CDC2 + IGFBP5	0.484	0.578	0.484	0.562	0.500	0.562	0.500	0.484	0.312	0.391
MDK + CDC2 + HOXA13	0.484	0.609	0.484	0.609	0.484	0.578	0.344	0.578	0.359	0.391
MDK + IGFBP5 + HOXA13	0.469	0.531	0.500	0.547	0.469	0.516	0.469	0.406	0.359	0.359
CDC2 + IGFBP5 + HOXA13	0.469	0.484	0.469	0.484	0.469	0.500	0.469	0.469	0.453	0.422
MDK+CDC2+IGFBP5+HOXA13	0.484	0.609	0.484	0.609	0.469	0.531	0.516	0.484	0.344	0.391

Sensitivity at Specificity: Sp.98

Figure 16e

Model	LDA	LogReg	SVM	KNSN	TREE
MDK	0.013	0.000	0.078	0.250	0.062
CDC2	-0.019	-0.016	0.141	-0.016	0.031
IGFBP5	0.046	0.016	0.109	0.141	-0.047
HOXA13	0.123	-0.016	-0.016	-0.031	0.031
MDK + CDC2	0.016	0.016	0.078	0.016	-0.031
MDK + IGFBP5	0.000	0.000	0.078	0.078	0.000
MDK + HOXA13	0.000	-0.016	0.031	0.016	0.062
CDC2 + IGFBP5	0.016	0.016	0.109	0.094	0.016
CDC + HOXA13	-0.016	-0.016	0.141	-0.016	0.047
IGF + HOXA13	0.000	0.000	0.031	0.141	-0.016
MDK + CDC2 + IGFBP5	0.000	0.000	0.078	0.062	-0.031
MDK + CDC2 + HOXA13	0.000	0.000	0.078	-0.062	0.000
MDK + IGFBP5 + HOXA13	-0.016	-0.016	0.047	-0.047	0.000
CDC2 + IGFBP5 + HOXA13	0.000	-0.031	0.031	-0.047	0.000
MDK+CDC2+IGFBP5+HOXA13	0.016	0.016	0.062	-0.047	-0.016
Gain in sensitivity, starting at specificity=0.80					

Figure 17a

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.062	0.047	0.047	0.078	0.062
CDC2	0.222	-0.016	-0.016	0.125	0.031
IGFBP5	0.046	0.031	0.031	-0.031	0.016
HOXA13	0.132	0.000	0.031	-0.031	-0.094
MDK + CDC2	0.047	0.047	0.016	0.109	0.000
MDK + IGFBP5	0.016	0.016	0.016	0.203	0.000
MDK + HOXA13	0.031	0.031	0.016	-0.047	0.031
CDC2 + IGFBP5	0.016	0.016	0.016	0.062	0.016
CDC + HOXA13	-0.016	-0.016	-0.016	-0.047	0.047
IGF + HOXA13	0.000	0.000	0.062	-0.016	0.000
MDK + CDC2 + IGFBP5	0.000	0.000	0.016	0.188	0.016
MDK + CDC2 + HOXA13	0.031	0.031	0.000	0.031	0.000
MDK + IGFBP5 + HOXA13	0.016	0.016	0.047	0.141	0.000
CDC2 + IGFBP5 + HOXA13	0.016	0.016	0.031	0.094	0.000
MDK+CDC2+IGFBP5+HOXA13	-0.016	0.000	-0.016	0.094	-0.016

Gain in sensitivity, starting at specificity=0.85

Figure 17b

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.161	0.047	0.078	0.078	-0.016
CDC2	0.365	0.047	0.156	0.125	0.047
IGFBP5	0.350	0.000	0.094	-0.031	0.062
HOXA13	0.259	0.031	0.031	-0.031	-0.031
MDK + CDC2	0.016	0.000	0.062	0.109	0.016
MDK + IGFBP5	0.078	0.047	0.016	0.062	0.016
MDK + HOXA13	0.031	0.031	0.078	-0.047	-0.016
CDC2 + IGFBP5	0.094	0.062	0.078	0.062	0.047
CDC + HOXA13	0.062	0.031	0.141	-0.047	0.078
IGF + HOXA13	0.000	0.000	0.016	-0.016	-0.016
MDK + CDC2 + IGFBP5	0.062	0.047	0.078	0.062	0.047
MDK + CDC2 + HOXA13	0.000	0.016	0.094	0.031	0.031
MDK + IGFBP5 + HOXA13	0.031	0.031	0.000	0.000	-0.016
CDC2 + IGFBP5 + HOXA13	0.094	0.031	0.016	-0.047	0.016
MDK+CDC2+IGFBP5+HOXA13	0.031	0.016	0.062	0.047	0.062

Gain in sensitivity, starting at specificity=0.90

Figure 17c

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.306	0.062	0.078	0.109	0.062
CDC2	0.445	0.109	0.109	0.188	0.109
IGFBP5	0.336	0.000	0.000	0.031	-0.031
HOXA13	0.249	-0.016	-0.016	0.000	-0.047
MDK + CDC2	0.109	0.109	0.125	0.219	0.109
MDK + IGFBP5	0.047	0.031	0.047	0.062	0.016
MDK + HOXA13	0.078	0.078	0.078	-0.047	0.062
CDC2 + IGFBP5	0.047	0.062	0.031	0.188	0.047
CDC + HOXA13	0.109	0.125	0.094	-0.047	0.094
IGF + HOXA13	0.000	0.000	-0.016	-0.016	0.000
MDK + CDC2 + IGFBP5	0.062	0.062	0.062	0.062	0.031
MDK + CDC2 + HOXA13	0.109	0.109	0.125	0.125	0.078
MDK + IGFBP5 + HOXA13	0.016	0.000	0.047	0.000	0.016
CDC2 + IGFBP5 + HOXA13	0.031	0.078	0.047	-0.047	0.031
MDK+CDC2+IGFBP5+HOXA13	0.078	0.078	0.047	0.047	0.016

Gain in sensitivity, starting at specificity=0.95

Figure 17d

Model	LDA	LogReg	SVM	KNSN	TREE
MDK	0.353	0.031	0.078	0.203	0.203
CDC2	0.406	0.000	0.109	0.062	-0.047
IGFBP5	0.336	0.000	0.016	0.031	0.047
HOXA13	0.192	-0.031	-0.016	0.094	0.000
MDK + CDC2	0.094	0.078	0.109	0.047	0.031
MDK + IGFBP5	0.062	0.062	0.031	-0.188	0.000
MDK + HOXA13	0.062	0.078	0.016	0.078	0.203
CDC2 + IGFBP5	0.016	0.016	0.016	0.031	-0.016
CDC + HOXA13	-0.047	0.016	0.062	-0.078	0.000
IGF + HOXA13	0.000	0.000	0.047	0.172	0.031
MDK + CDC2 + IGFBP5	0.094	0.078	0.062	-0.016	0.078
MDK + CDC2 + HOXA13	0.125	0.125	0.094	0.234	0.031
MDK + IGFBP5 + HOXA13	0.062	0.047	0.047	-0.062	0.000
CDC2 + IGFBP5 + HOXA13	0.016	0.016	0.031	0.000	-0.031
MDK+CDC2+IGFBP5+HOXA13	0.125	0.125	0.062	-0.031	0.047

Gain in sensitivity, starting at specificity=0.98

Figure 17e

Model	LDA	LogReg	SVM	KNSN	TREE
MDK	0.030	0.000	0.168	0.180	0.069
CDC2	-0.025	-0.040	0.178	-0.104	0.094
IGFBP5	0.037	0.022	0.131	0.119	-0.025
HOXA13	0.114	-0.007	-0.002	0.116	0.027
MDK + CDC2	0.012	0.030	0.158	-0.101	-0.049
MDK + IGFBP5	0.000	0.000	0.101	0.146	-0.022
MDK + HOXA13	0.000	-0.054	0.126	-0.089	0.072
CDC2 + IGFBP5	0.022	0.012	0.143	0.146	0.035
CDC + HOXA13	-0.025	-0.040	0.158	-0.109	0.106
IGF + HOXA13	0.000	0.000	0.042	0.158	0.005
MDK + CDC2 + IGFBP5	0.000	0.000	0.133	0.151	-0.012
MDK + CDC2 + HOXA13	0.000	0.000	0.165	-0.091	-0.035
MDK + IGFBP5 + HOXA13	-0.022	-0.022	0.081	-0.042	-0.032
CDC2 + IGFBP5 + HOXA13	0.000	-0.094	0.064	-0.032	0.015
MDK+CDC2+IGFBP5+HOXA13	0.027	0.000	0.138	-0.057	-0.010

Gain in specificity, starting at specificity=0.80

Figure 17f

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.059	0.041	0.123	0.130	0.039
CDC2	0.125	-0.023	0.130	0.130	0.044
IGFBP5	0.041	0.009	0.081	0.069	0.036
HOXA13	0.064	-0.001	-0.001	0.066	-0.015
MDK + CDC2	0.054	0.046	0.108	0.118	-0.001
MDK + IGFBP5	0.051	0.041	0.051	0.096	0.019
MDK + HOXA13	0.051	0.044	0.103	0.086	0.041
CDC2 + IGFBP5	0.017	0.002	0.093	0.096	0.031
CDC + HOXA13	-0.018	-0.028	0.113	0.086	0.056
IGF + HOXA13	-0.001	-0.001	0.002	0.108	-0.008
MDK + CDC2 + IGFBP5	-0.001	-0.001	0.083	0.101	0.014
MDK + CDC2 + HOXA13	0.049	0.054	0.118	0.130	-0.001
MDK + IGFBP5 + HOXA13	0.007	0.014	0.031	0.113	0.009
CDC2 + IGFBP5 + HOXA13	0.051	0.007	0.014	0.101	-0.003
MDK+CDC2+IGFBP5+HOXA13	-0.015	-0.001	0.088	0.110	0.004

Gain in specificity, starting at specificity=0.85

Figure 17g

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.078	0.021	0.075	0.080	-0.011
CDC2	0.098	0.038	0.080	0.080	0.028
IGFBP5	0.090	0.001	0.043	0.019	0.011
HOXA13	0.088	0.004	0.028	0.016	-0.026
MDK + CDC2	0.004	0.001	0.058	0.068	0.043
MDK + IGFBP5	0.028	0.026	0.001	0.046	0.009
MDK + HOXA13	0.011	0.016	0.063	0.036	-0.009
CDC2 + IGFBP5	0.021	0.028	0.043	0.046	0.058
CDC + HOXA13	0.019	0.033	0.063	0.036	0.053
IGF + HOXA13	0.001	0.001	0.004	0.058	-0.031
MDK + CDC2 + IGFBP5	0.048	0.043	0.036	0.051	0.048
MDK + CDC2 + HOXA13	0.001	0.004	0.075	0.080	0.053
MDK + IGFBP5 + HOXA13	0.041	0.046	0.001	0.063	0.004
CDC2 + IGFBP5 + HOXA13	0.021	0.033	0.021	0.051	-0.001
MDK+CDC2+IGFBP5+HOXA13	0.031	0.021	0.048	0.060	0.046

Gain in specificity, starting at specificity=0.90

Figure 17h

Model	LDA	LogReg	SVM	KNSN	TREE
MDK	0.043	0.025	0.030	0.030	0.028
CDC2	0.050	0.025	0.030	0.030	0.023
IGFBP5	0.043	0.001	0.001	0.015	-0.007
HOXA13	0.045	-0.002	-0.004	0.020	-0.012
MDK + CDC2	0.030	0.030	0.033	0.038	0.013
MDK + IGFBP5	0.023	0.025	0.010	-0.004	0.006
MDK + HOXA13	0.030	0.030	0.013	-0.014	0.028
CDC2 + IGFBP5	0.020	0.018	0.015	0.025	0.015
CDC + HOXA13	0.023	0.025	0.025	-0.014	0.015
IGF + HOXA13	0.001	0.001	-0.007	0.008	0.003
MDK + CDC2 + IGFBP5	0.025	0.023	0.023	0.001	0.010
MDK + CDC2 + HOXA13	0.035	0.033	0.033	0.030	0.013
MDK + IGFBP5 + HOXA13	0.006	0.001	0.003	0.013	0.006
CDC2 + IGFBP5 + HOXA13	0.003	0.015	0.008	0.001	0.008
MDK+CDC2+IGFBP5+HOXA13	0.028	0.030	0.015	0.010	0.010

Gain in specificity, starting at specificity=0.95

Figure 17i

Model	LDA	LogReg	SVM	KN5N	TREE
MDK	0.015	0.005	0.008	0.005	0.008
CDC2	0.020	0.000	0.000	0.000	-0.007
IGFBP5	0.018	0.000	0.000	0.000	0.003
HOXA13	0.015	-0.007	-0.007	0.010	0.000
MDK + CDC2	0.003	0.003	0.005	0.008	0.003
MDK + IGFBP5	0.000	0.000	0.000	-0.010	0.000
MDK + HOXA13	0.008	0.008	0.008	0.010	0.008
CDC2 + IGFBP5	0.005	0.000	0.003	-0.005	0.000
CDC + HOXA13	-0.002	0.000	0.000	-0.010	-0.002
IGF + HOXA13	0.000	0.000	0.003	0.008	0.003
MDK + CDC2 + IGFBP5	0.003	0.003	0.005	0.005	0.010
MDK + CDC2 + HOXA13	0.008	0.008	0.003	0.005	0.003
MDK + IGFBP5 + HOXA13	0.008	0.005	0.000	0.005	0.000
CDC2 + IGFBP5 + HOXA13	0.000	0.000	0.008	0.013	-0.007
MDK+CDC2+IGFBP5+HOXA13	0.005	0.005	0.005	0.005	0.010
Gain in specificity, starting at specificity=0.98					

Figure 17j

SUBSTITUTE SHEET (RULE 26)

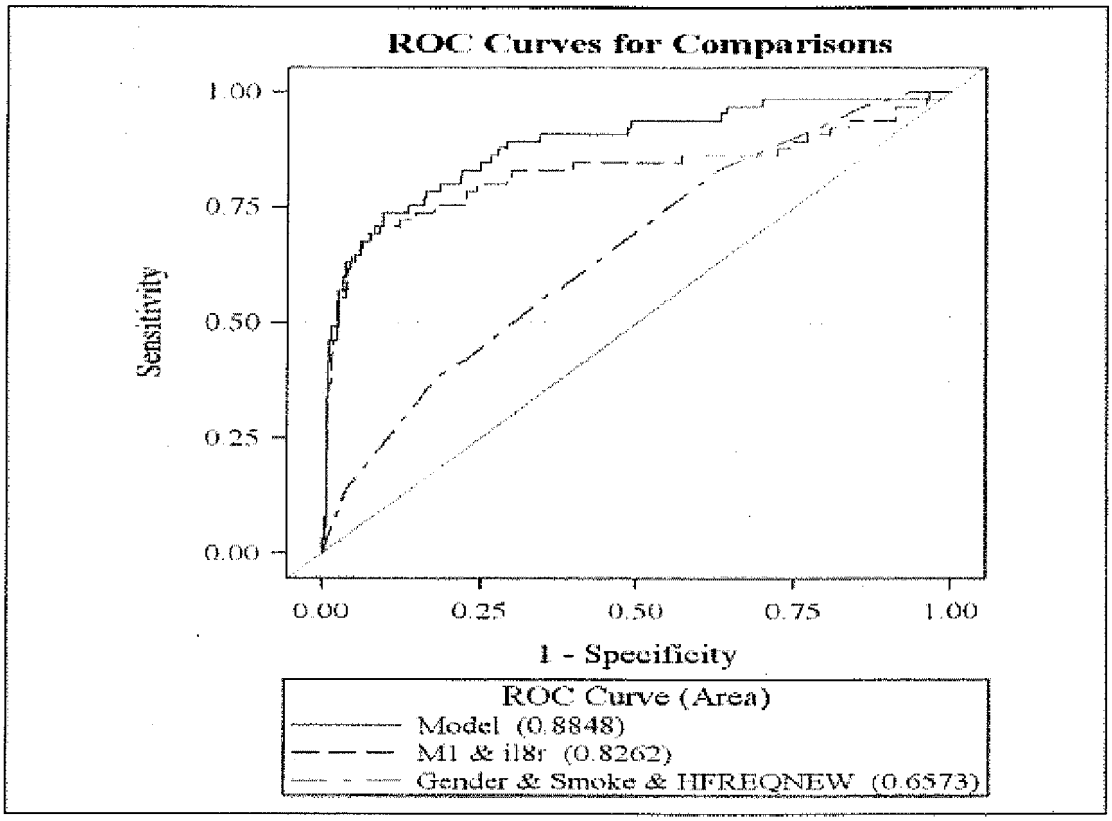

ROC Curves for Comparisons
1.00
0.75
0.50
0.25
0.00
Sensitivity
0.00
0.25
0.50
0.75
1.00
1 - Specificity
ROC Curve (Area)
Model (0.8848)
M1 & il8r (0.8262)
Gender & Smoke & HFREQNEW (0.6573)

FIG. 18

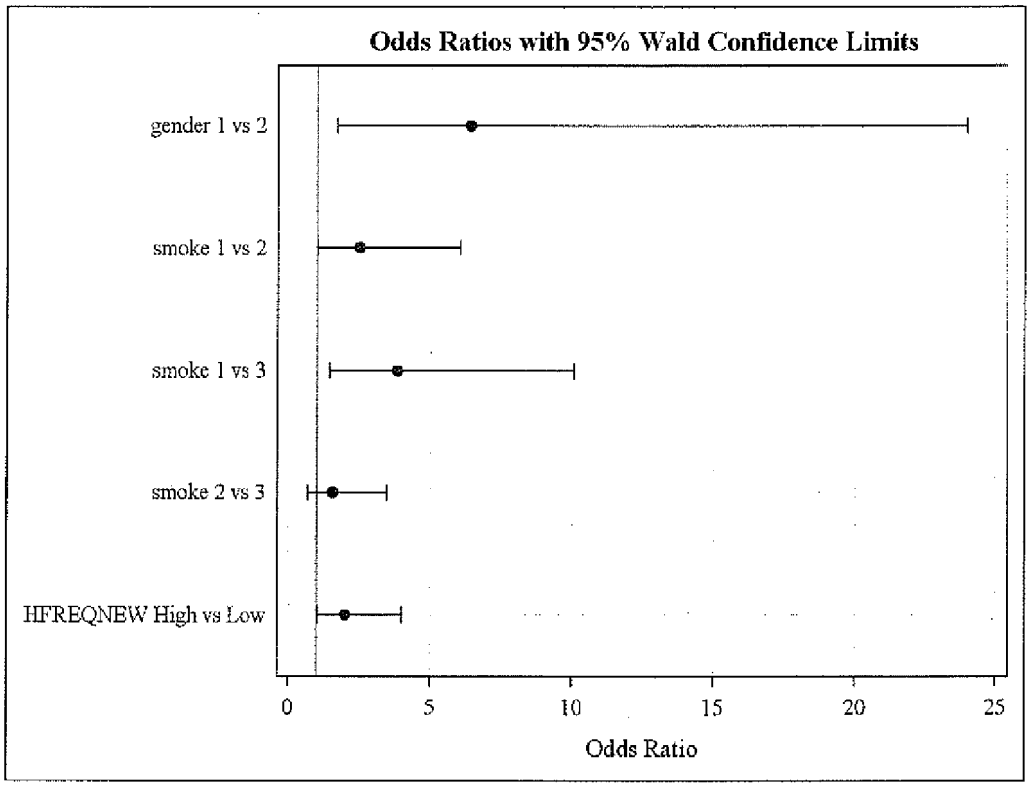

Odds Ratios with 95% Wald Confidence Limits
gender 1 vs 2
smoke 1 vs 2
smoke 1 vs 3
smoke 2 vs 3
HFREQNEW High vs Low
0
5
10
15
20
25
Odds Ratio

FIG. 19

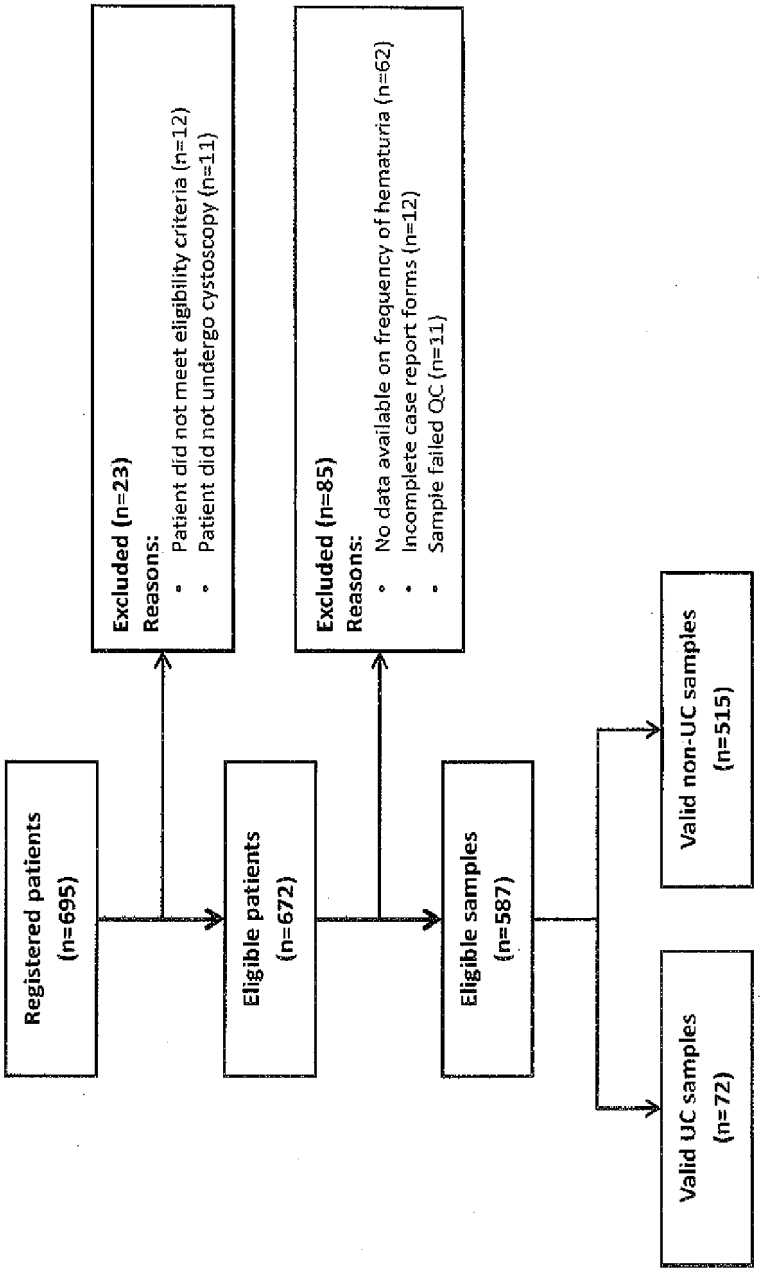

Registered patients (n=695)
Excluded (n=23)
Reasons:
Patient did not meet eligibility criteria (n=12)
Patient did not undergo cystoscopy (n=11)
Eligible patients (n=672)
Excluded (n=85)
Reasons:
No data available on frequency of hematuria (n=62)
Incomplete case report forms (n=12)
Sample failed QC (n=11)
Eligible samples (n=587)
Valid non-UC samples (n=515)
Valid UC samples (n=72)

FIG. 20A

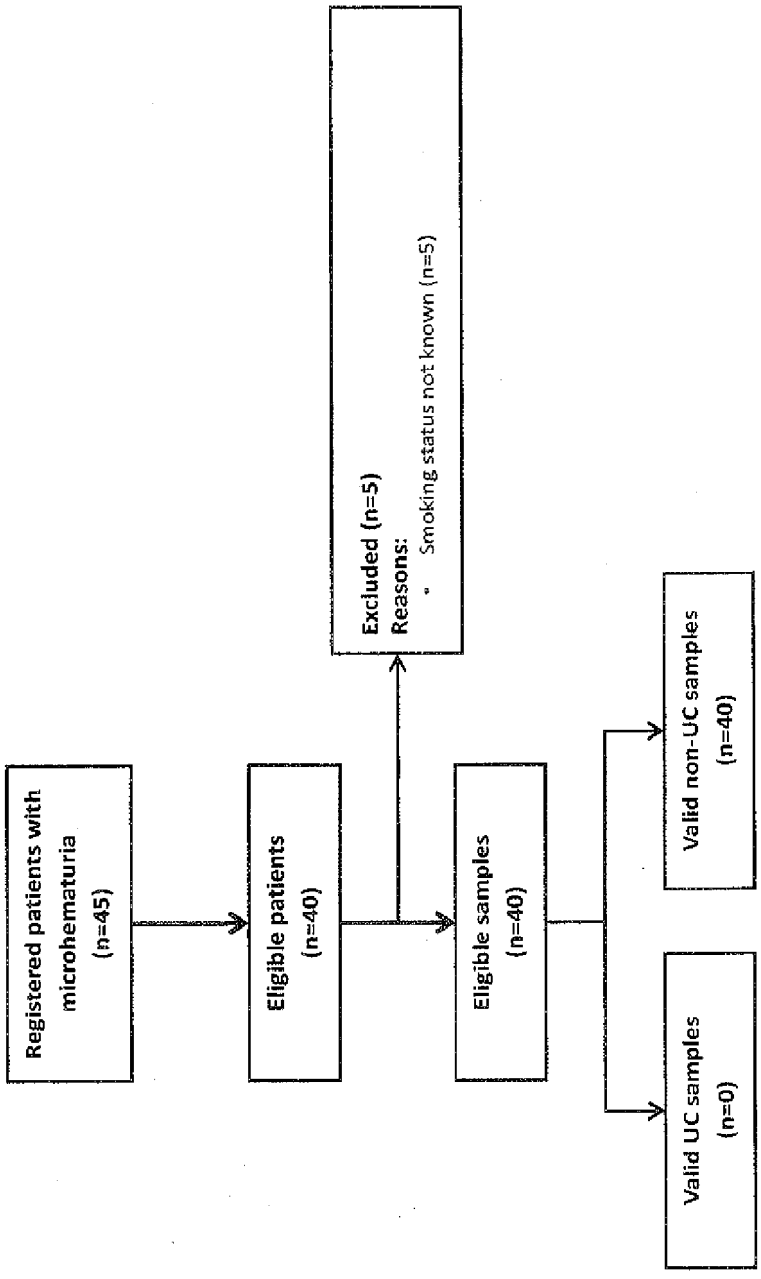

Registered patients with microhematuria (n=45)
Eligible patients (n=40)
Excluded (n=5)
Reasons:
Smoking status not known (n=5)
Eligible samples (n=40)
Valid non-UC samples (n=40)
Valid UC samples (n=0)

FIG. 20B

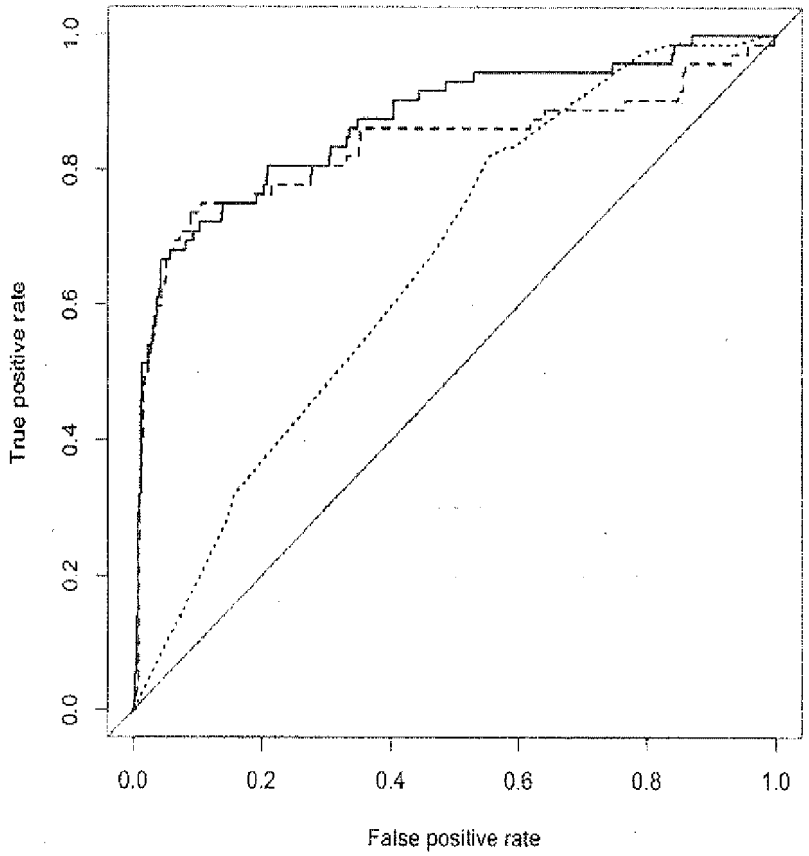

True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate
0.0
0.2
0.4
0.6
0.8
1.0

FIG. 21

30

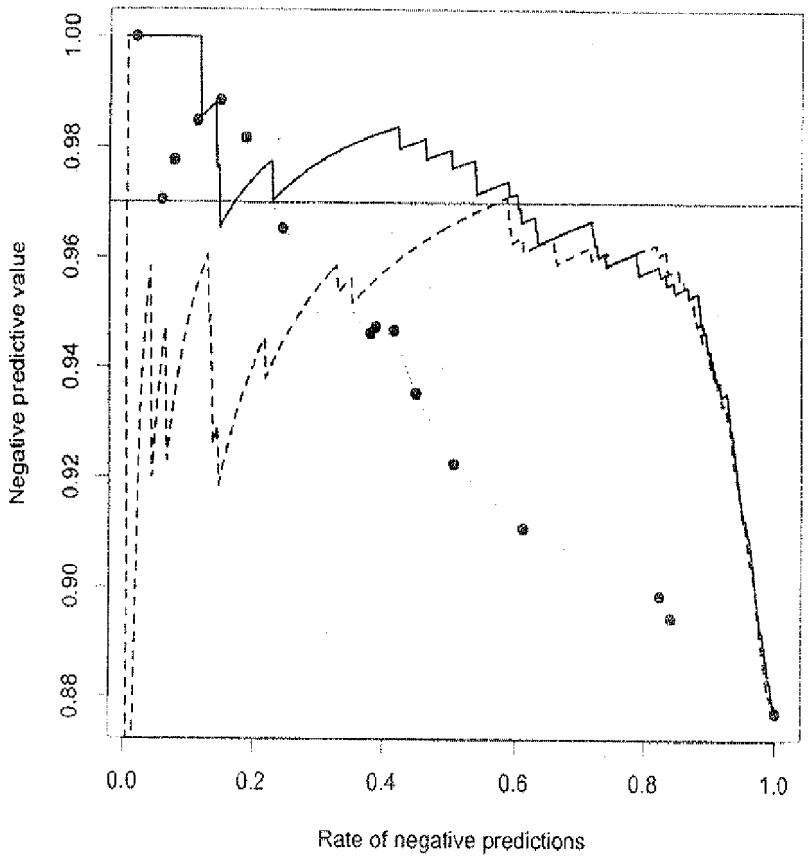

Negative predictive value
1.00
0.98
0.96
0.94
0.92
0.90
0.88
0.0
0.2
0.4
0.6
0.8
1.0
Rate of negative predictions

FIG. 22

31

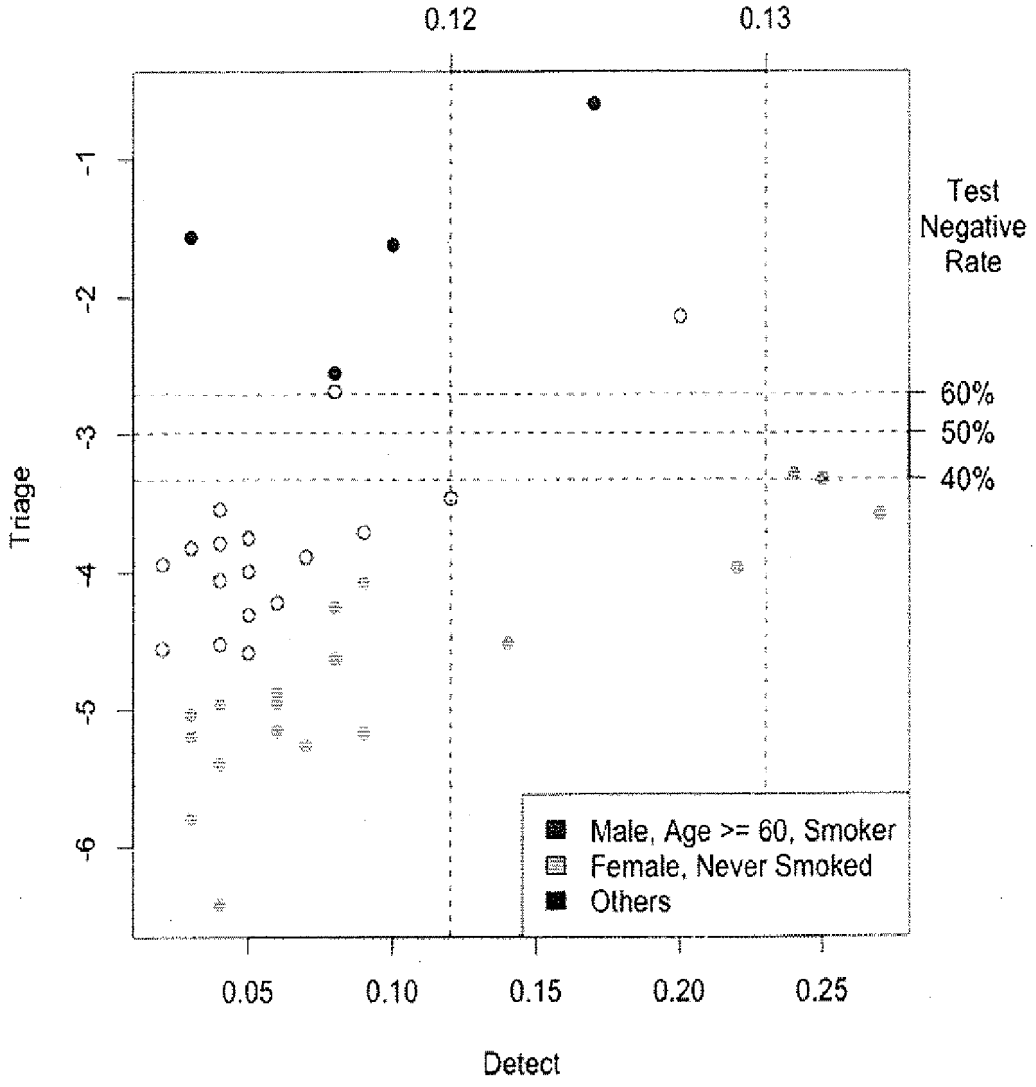

0.12
0.13
Test
Negative
Rate
60%
50%
40%
Triage
-1
-2
-3
-4
-5
-6
Male, Age >= 60, Smoker
Female, Never Smoked
Others
0.05
0.10
0.15
0.20
0.25
Detect

FIG. 23

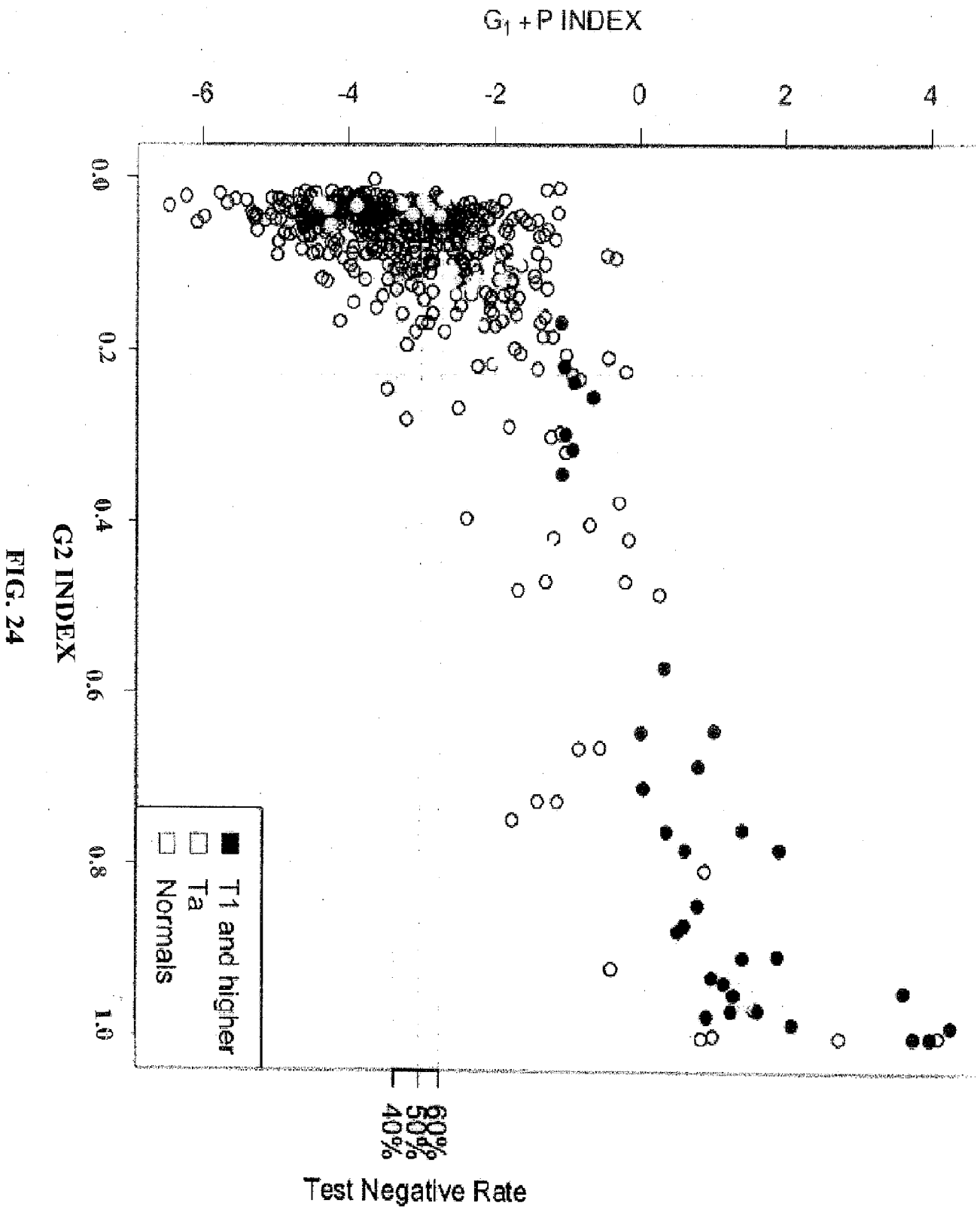

G1 + P INDEX
-6
-4
-2
0
2
4
G2 INDEX
0.0
0.2
0.4
0.6
0.8
1.0
T1 and higher
Ta
Normals
60%
50%
40%
Test Negative Rate

FIG. 24