

Supplementary Information

Biological determinants of bladder cancer gene expression subtypes

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Supplementary Figure Legends

Supplementary Figure 1 | Substratification of the three main subgroups of tumors. (a-c) Heatmap visualization of sample coclustering frequencies for two-group splits of the CC1 (a), CC2 (b), and CC3 (c) subgroups generated using ConsensusClusterPlus in R. (d-e) Heatmap visualization of the UNC- (d) and MDA (e) classifier genes accross the six consensus subgroups.

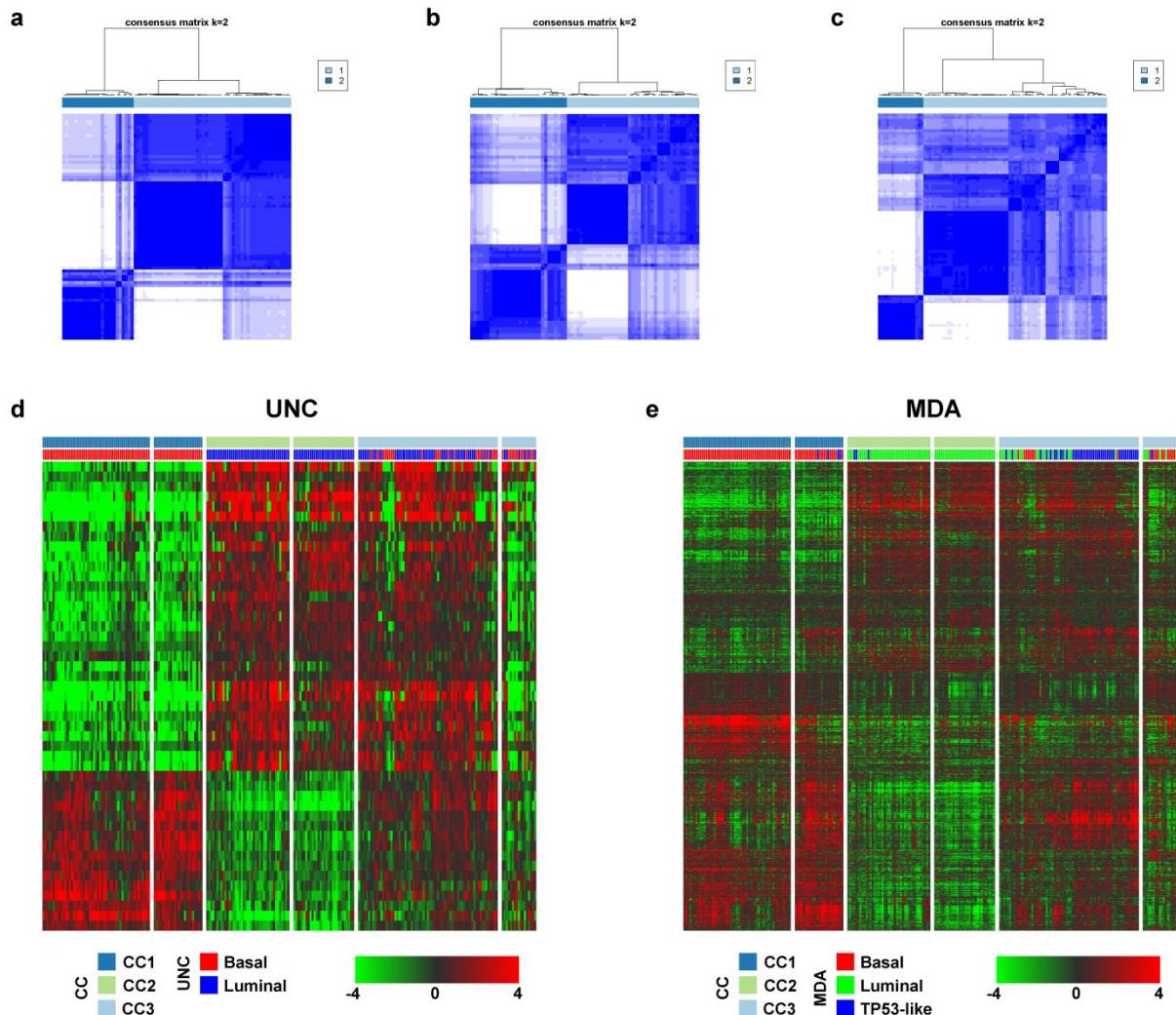
Supplementary Figure 2 |CC1-2 subgroup tumors exhibit high VIM and variable CDH1 expression.

Uncentered mRNA expression levels of the genes *VIM* (Vimentin) and *CDH1* (E-cadherin) accross the consensus cluster subgroups with Lund molecular subtype indicated (a). Boxplots showing relative difference in mRNA exprssion between the CC1-2 and CC3-1 subgroups for genes related to EMT (b), epithelial differentiation (c) and urothelial differentiation (d).

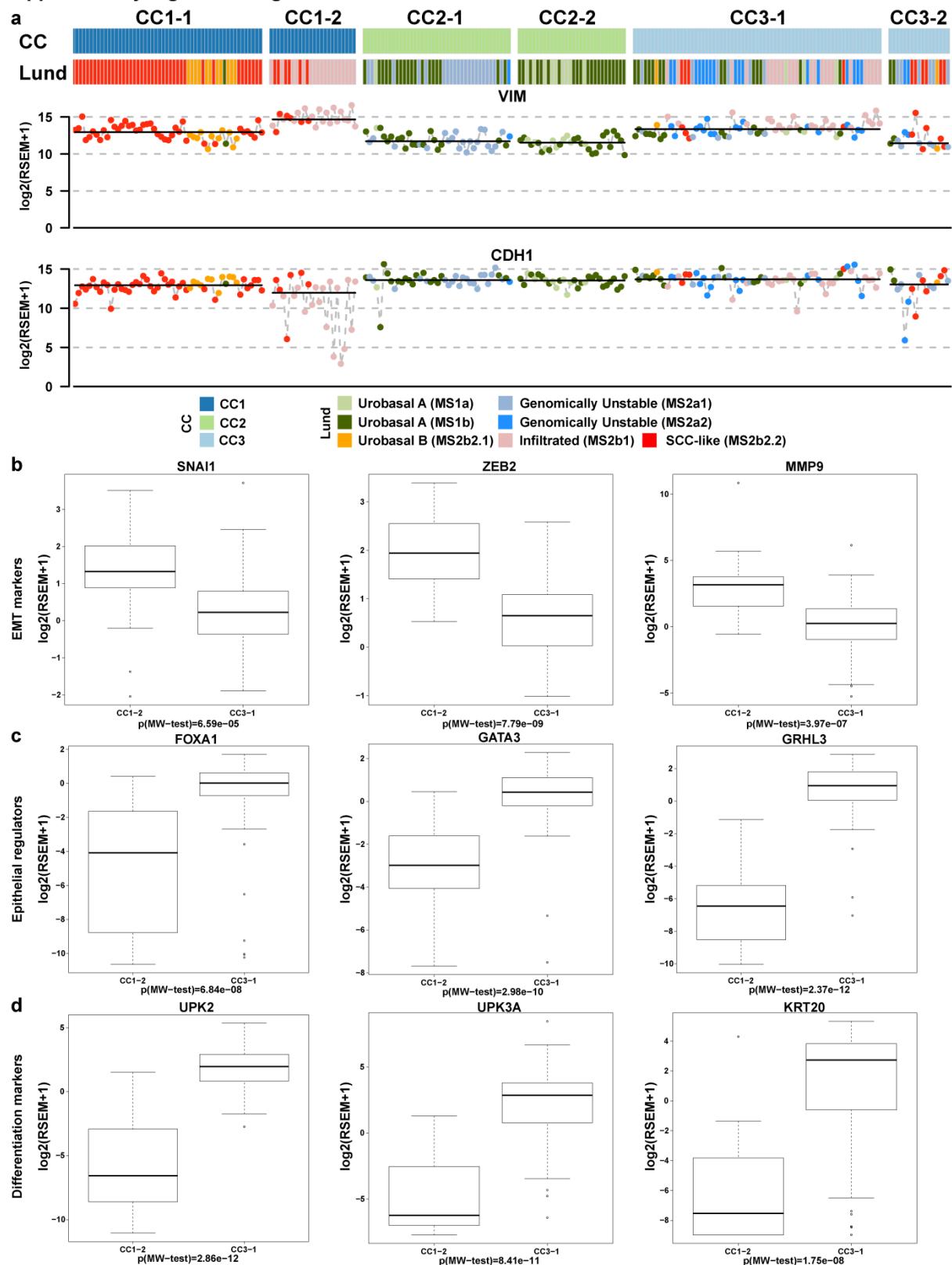
Supplementary Figure 3 | UC gene expression classifier calls accross TCGA tumor samples. TCGA samples were classified using UNC, MDA and Lund gene experssion centroids wiht Pearson correlation as the similarity metric. Final sample-level classifier calls and correlations to the respective centroids are shown in heatmap format for the three classification systems and consensus cluster subgroups.

Supplementary Figures

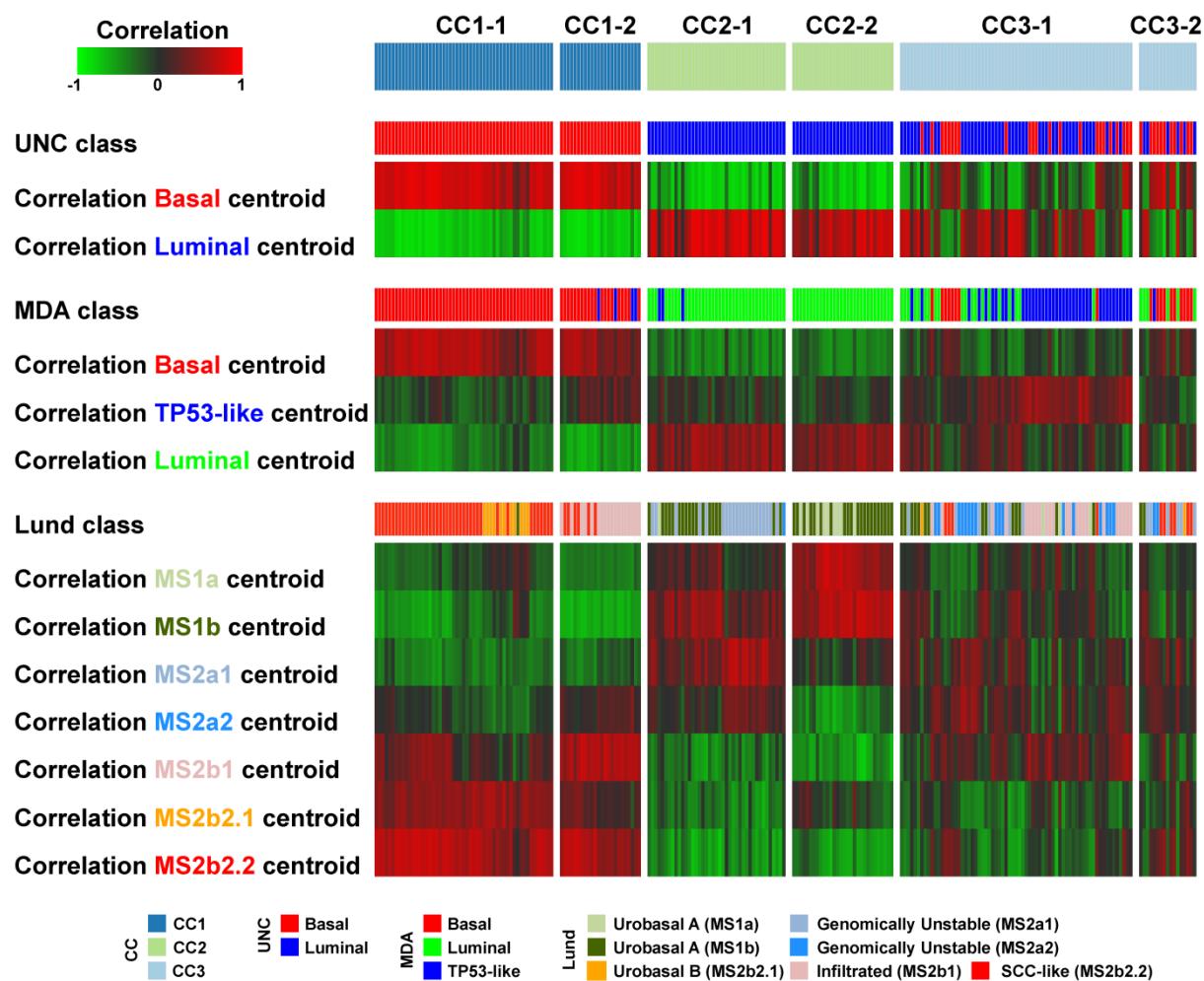
Supplementary Figure 1 - Höglund



Supplementary Figure 2 - Höglund



Supplementary Figure 3 - Höglund



Supplementary table 1
AmiGO analysis (amigo.geneontology.org/rte) output for differentially expressed genes between CC1 and CC2, table derived using PANTHER (go.pantherdb.org)

Significant GO-terms for CC1 upregulated- (N=2886) and downregulated (N=3233) genes, output truncated at p(bonferroni)<0.05 or top 25 GO-terms

Analysis Type: PANTHER Overrepresentation Test (release 20141219)
Annotation Version and Release Date: GO Ontology database Released 2015-02-17
Reference List: Homo sapiens (all genes in database)
Bonferroni correction: TRUE

CC1 upregulated genes

GO biological process complete	Enrichment/Depletion	p(bonferroni)
immune system process	+	7.48E-117
biological_process	+	5.99E-105
single-organism process	+	1.32E-97
response to stimulus	+	5.31E-96
immune response	+	2.15E-93
single-organism cellular process	+	9.64E-92
defense response	+	1.95E-89
response to stress	+	1.14E-82
biological regulation	+	1.12E-75
regulation of immune system process	+	2.44E-73
regulation of response to stimulus	+	7.02E-73
positive regulation of biological process	+	5.98E-69
regulation of biological process	+	1.27E-65
positive regulation of response to stimulus	+	1.31E-61
cellular response to stimulus	+	2.14E-60
positive regulation of immune system process	+	1.71E-59
regulation of cellular process	+	3.37E-59
cellular process	+	4.65E-57
signal transduction	+	5.87E-57
single organism signaling	+	1.34E-56
signaling	+	1.34E-56
cell communication	+	4.22E-56
response to external stimulus	+	1.36E-55
positive regulation of cellular process	+	1.93E-51
biological adhesion	+	5.29E-51

CC1 downregulated genes

GO biological process complete	Enrichment/Depletion	p(bonferroni)
biological_process	+	2.11E-33
cellular process	+	2.83E-18
biological regulation	+	9.50E-15
transcription, DNA-templated	+	9.35E-12
nucleic acid-templated transcription	+	9.97E-12
lipid metabolic process	+	1.88E-11
regulation of biological process	+	1.49E-10
detection of chemical stimulus involved in sensory perception of smell	-	3.27E-10
regulation of transcription, DNA-templated	+	3.49E-10
regulation of nucleic acid-templated transcription	+	8.93E-10
regulation of cellular process	+	9.35E-10
translation	-	1.11E-09
regulation of RNA biosynthetic process	+	2.25E-09
biosynthetic process	+	2.29E-09
RNA biosynthetic process	+	3.37E-09
cellular lipid metabolic process	+	3.97E-09
regulation of RNA metabolic process	+	5.51E-09
organic substance biosynthetic process	+	5.55E-09
cellular macromolecule catabolic process	-	5.99E-09
small molecule metabolic process	+	2.16E-08
sensory perception of smell	-	2.38E-08
detection of chemical stimulus involved in sensory perception	-	2.49E-08
xenobiotic metabolic process	+	3.29E-08
cellular response to xenobiotic stimulus	+	4.15E-08
single-organism process	+	4.50E-08

Supplementary table 2AmiGO analysis (amigo.geneontology.org/rte) output for genes upregulated in CC3-1 vs CC1-2, table derived using PANTHER (go.pantherdb.org)

Significant GO-terms for CC3-1 upregulated genes (N=1984), output truncated at p(bonferroni)<0.05 or top 25 GO-terms

Analysis Type: PANTHER Overrepresentation Test (release 20141219)

Annotation Version and Release Date: GO Ontology database Released 2015-02-17

Reference List: Homo sapiens (all genes in database)

Bonferroni correction: TRUE

GO biological process complete	Enrichment/Depletion	p(bonferroni)
biological_process	+	4.95E-24
lipid metabolic process	+	5.86E-19
cellular lipid metabolic process	+	2.14E-14
cellular process	+	8.22E-11
organic hydroxy compound metabolic process	+	1.60E-09
small molecule metabolic process	+	1.56E-08
fatty acid metabolic process	+	1.70E-08
biosynthetic process	+	3.51E-08
lipid biosynthetic process	+	5.20E-08
carboxylic acid metabolic process	+	6.16E-08
single-organism process	+	1.46E-07
oxoacid metabolic process	+	1.66E-07
organic acid metabolic process	+	1.71E-07
organic substance biosynthetic process	+	1.87E-07
monocarboxylic acid metabolic process	+	1.94E-07
metabolic process	+	1.78E-06
epithelial cell differentiation	+	2.29E-06
organic acid catabolic process	+	3.57E-06
carboxylic acid catabolic process	+	3.57E-06
cellular biosynthetic process	+	4.66E-06
organic substance metabolic process	+	1.04E-05
biological regulation	+	1.11E-05
primary metabolic process	+	1.24E-05
small molecule catabolic process	+	1.36E-05
monocarboxylic acid catabolic process	+	1.42E-05

Supplementary table 3AmiGO analysis (amigo.geneontology.org/rte) output for genes upregulated in CC3-2 vs rest, table derived using PANTHER (go.pantherdb.org)

Significant GO-terms for CC3-2 upregulated genes (N=289), output truncated at p(bonferroni)<0.05 or top 25 GO-terms

Analysis Type: PANTHER Overrepresentation Test (release 20141219)

Annotation Version and Release Date: GO Ontology database Released 2015-02-17

Reference List: Homo sapiens (all genes in database)

Bonferroni correction: TRUE

GO biological process complete	Enrichment/Depletion	p(bonferroni)
cell cycle	+	6.50E-12
mitotic cell cycle	+	2.89E-10
mitotic cell cycle process	+	7.00E-09
cell cycle process	+	9.19E-08
single-organism process	+	1.95E-07
organelle fission	+	5.11E-07
cellular process	+	5.64E-07
biological_process	+	6.73E-07
nuclear division	+	8.19E-07
single-organism cellular process	+	5.10E-06
DNA metabolic process	+	1.31E-05
mitotic nuclear division	+	2.75E-05
organelle organization	+	6.73E-05
biological regulation	+	3.50E-04
single-organism organelle organization	+	3.73E-04
chromosome organization	+	6.32E-04
regulation of biological process	+	8.57E-04
cell division	+	9.95E-04
regulation of cellular process	+	1.03E-03
chromosome segregation	+	1.13E-03
nucleic acid metabolic process	+	1.27E-03
nucleobase-containing compound metabolic process	+	1.82E-03
cellular component organization	+	1.88E-03
anatomical structure development	+	3.17E-03
meiotic cell cycle	+	4.56E-03

Supplementary table 4AmiGO analysis (amigo.geneontology.org/rte) output for genes upregulated in CC2-2 vs rest, table derived using PANTHER (go.pantherdb.org)

Significant GO-terms for CC2-2 upregulated- (N=511) and downregulated (N=1030) genes, output truncated at p(bonferroni)<0.05 or top 25 GO-terms

Analysis Type: PANTHER Overrepresentation Test (release 20141219)

Annotation Version and Release Date: GO Ontology database Released 2015-02-17

Reference List: Homo sapiens (all genes in database)

Bonferroni correction: TRUE

CC2-2 upregulated genes

GO biological process complete	Enrichment/Depletion	p(bonferroni)
SRP-dependent cotranslational protein targeting to membrane	+	3.83E-29
cotranslational protein targeting to membrane	+	7.37E-29
protein targeting to ER	+	1.02E-28
establishment of protein localization to endoplasmic reticulum	+	3.59E-28
viral transcription	+	2.51E-27
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	+	1.13E-26
protein localization to endoplasmic reticulum	+	4.70E-26
viral gene expression	+	4.79E-26
translational termination	+	2.03E-25
multi-organism metabolic process	+	2.49E-25
cellular protein complex disassembly	+	5.02E-24
protein targeting to membrane	+	3.84E-23
translational elongation	+	5.38E-23
protein complex disassembly	+	1.55E-22
macromolecular complex disassembly	+	5.96E-22
nuclear-transcribed mRNA catabolic process	+	3.20E-21
RNA catabolic process	+	1.33E-20
viral life cycle	+	1.52E-20
mRNA catabolic process	+	1.97E-20
translational initiation	+	2.97E-20
establishment of protein localization to membrane	+	2.55E-19
aromatic compound catabolic process	+	5.64E-17
nucleobase-containing compound catabolic process	+	1.39E-16
organic cyclic compound catabolic process	+	2.16E-16
cellular nitrogen compound catabolic process	+	2.80E-16

CC2-2 downregulated genes

GO biological process complete	Enrichment/Depletion	p(bonferroni)
single-organism process	+	4.40E-43
biological_process	+	1.15E-40
single-organism cellular process	+	9.97E-40
mitotic cell cycle	+	4.73E-33
cellular process	+	1.05E-31
cell cycle	+	6.22E-31
cell cycle process	+	1.28E-27
mitotic cell cycle process	+	6.73E-27
biological phase	+	1.84E-26
mitotic cell cycle phase	+	4.84E-26
cell cycle phase	+	4.84E-26
nuclear division	+	4.01E-22
organelle fission	+	3.45E-21
biological regulation	+	6.92E-21
response to stress	+	1.22E-19
cellular component organization	+	2.23E-19
response to stimulus	+	1.32E-18
mitotic nuclear division	+	3.01E-18
cellular component organization or biogenesis	+	6.95E-18
cellular response to stimulus	+	7.54E-18
mitotic prometaphase	+	2.25E-17
regulation of cellular process	+	4.64E-17
regulation of biological process	+	7.67E-17
cell division	+	3.83E-16
positive regulation of biological process	+	9.45E-16

Supplementary table 5Files downloaded through the TCGA public ftp-site available at "https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftputers/anonymous/tumor/blca/"TCGA sample clusters file according to TCGA, Nature, Volume 507 Number 7492, 315-322, Mar. 20, 2014 [doi:10.1038]
BLCA_cluster-assign-k4.tsv**TCGA somatic variant annotation file**

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TCGA gene expression files

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AMAZE_p_TCGASNP_b86_87_88_N_GenomeWideSNP_6_F05_735440
BISON_p_TCGA_164_173_175_SNP_N_GenomeWideSNP_6_F09_863298
WHIPS_p_TCGA_220_235_N_GenomeWideSNP_6_F06_1230930
XYLEM_p_TCGASNP_207_212_N_GenomeWideSNP_6_E04_1051190
GLIAS_p_TCGA_204_205_206_207_N_GenomeWideSNP_6_E10_1051830
DLP_RED0_FROM_CONGA_B03
FRUIT_p_TCGAb_327_328_329_NSP_GenomeWideSNP_6_E06_1367852
SNOWS_p_TCGA_Batch_309_310_NSP_GenomeWideSNP_6_B12_1362068
CODON_p_TCGA_293_294_295_N_GenomeWideSNP_6_F05_1343540
COPAL_p_TCGAb_337_338_339_NSP_GenomeWideSNP_6_B06_1373642
GLIAS_p_TCGA_204_205_206_207_N_GenomeWideSNP_6_E01_1051786
ENDUE_p_TCGA_271_76_79_280_81_N_GenomeWideSNP_6_E05_1346908
SNOWS_p_TCGA_Batch_309_310_NSP_GenomeWideSNP_6_B06_1362010
AVISO_p_4TCGA_242_238_250_mN_GenomeWideSNP_6_A12_1231568
SNOWS_p_TCGA_Batch_309_310_NSP_GenomeWideSNP_6_B10_1362078
XYLEM_p_TCGASNP_207_212_N_GenomeWideSNP_6_B08_1051166
BISON_p_TCGA_164_173_175_SNP_N_GenomeWideSNP_6_C11_863354
COPAL_p_TCGAb_337_338_339_NSP_GenomeWideSNP_6_C12_1373596
SNOWS_p_TCGA_Batch_309_310_NSP_GenomeWideSNP_6_C09_1362008
LOLLS_p_TCGASNP_223_225_N_GenomeWideSNP_6_H04_1151988
XYLEM_p_TCGASNP_207_212_N_GenomeWideSNP_6_E05_1051216
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CODON_p_TCGA_293_294_295_N_GenomeWideSNP_6_D05_1343632
BASIC_p_TCGASNP_219_221_223_N_GenomeWideSNP_6_D02_1148644
HORNS_p_TCGA_b110_113_SNP_N_GenomeWideSNP_6_C04_772308

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WHIRR_p_TCGA_168_169_170_redo_N_GenomeWideSNP_6_A07_845096
AVISO_p_4TCGA_242_238_250_mN_GenomeWideSNP_6_A08_1231504
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COPAL_p_TCGAb_337_338_339_NS_P_GenomeWideSNP_6_B02_1373644
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WAXEN_p_TCGA_252_253_N_GenomeWideSNP_6_A07_1270578
TYPED_p_TCGA_188_192_Mirn_SNP_N_GenomeWideSNP_6_C12_913854
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LOLLS_p_TCGASNP_223_225_N_GenomeWideSNP_6_C06_1152032
TYPED_p_TCGA_188_192_Mirn_SNP_N_GenomeWideSNP_6_C11_913922
OKRAS_p_TCGA_198_199_200_SNP_N_GenomeWideSNP_6_C08_955374
WHIRR_p_TCGA_168_169_170_redo_N_GenomeWideSNP_6_C08_845224
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OKRAS_p_TCGA_198_199_200_SNP_N_GenomeWideSNP_6_F10_955324
SNOWS_p_TCGA_Batch_309_310_NS_P_GenomeWideSNP_6_A12_1362074
XYLEM_p_TCGASNP_207_212_N_GenomeWideSNP_6_A06_1051212
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AVISO_p_4TCGA_242_238_250_mN_GenomeWideSNP_6_A03_1231578
WHIPS_p_1TCGA_220_235_N_GenomeWideSNP_6_H02_1230922
AVISO_p_4TCGA_242_238_250_mN_GenomeWideSNP_6_A07_1231484
CONGA_p_TCGA_b_317_318_319_NS_P_GenomeWideSNP_6_B06_1365250
WAXEN_p_TCGA_252_253_N_GenomeWideSNP_6_A11_1270596
SNOWS_p_TCGA_Batch_309_310_NS_P_GenomeWideSNP_6_B02_1362062
COPAL_p_TCGAb_337_338_339_NS_P_GenomeWideSNP_6_C08_1373618
WHIRR_p_TCGA_168_169_170_redo_N_GenomeWideSNP_6_C12_845256
WAXEN_p_TCGA_252_253_N_GenomeWideSNP_6_C01_1270618
HORNS_p_TCGA_b110_113_SNP_N_GenomeWideSNP_6_F07_772336
COPAL_p_TCGAb_337_338_339_NS_P_GenomeWideSNP_6_A07_1373574
XYLEM_p_TCGASNP_207_212_N_GenomeWideSNP_6_E01_1051160
FRUIT_p_TCGAb_327_328_329_NS_P_GenomeWideSNP_6_D08_1367900
FOXED_p_TCGA_b122_128_SNP_N_GenomeWideSNP_6_D10_781864
CONGA_p_TCGA_b_317_318_319_NS_P_GenomeWideSNP_6_A08_1365346

Supplementary table 6

Sample annotations for all tumors included in Aine et al.

Gene mutations (m) indicated as 0 (WT) and 1 (Mutant)

Gene copy-number status (cna) indicated as -2 (deletion), -1 (loss), 0 (Neutral), 1 (gain) and 2 (amplification)

Centroid correlations were calculated using Pearson correlation

Cells with NA indicate that the sample was not included in the TCGA publication on BLCA (Nature, Volume 507 Number 7492, 315-322, Mar. 20, 2014 [doi:10.1038/nature13046])

SampleID	Histology	TCGAclass	Two_group	Three_group	Six_group	UNC	MDA	Lund	FGFR3m	FGFR3ns	PIK3CAm	RASm	chr9pDel	chr9qDel	CDKN2Acn	TP53m	MDM2cn	R81cm	E2F3ns	cor.UNC.Basal	cor.UNC.Luminal	cor.MDA.Basal	cor.MDA.Luminal	cor.lund.M51m	cor.lund.M51b	cor.lund.M52m	cor.lund.M52b1	cor.lund.M52b2			
TCGA-DK-A6AV	Non-papillary	NA	2	2	21	Luminal	Luminal	MS51b	0	0	0	0	0	0	0	0	0	0	-0.537	-0.796	-0.315	-0.189	0.487	0.205	0.475	0.107	-0.214				
TCGA-DK-A8WV	Non-papillary	3	1	1	11	Basal	Basal	MS52b2	0	0	0	0	0	-1	0	0	0	0	0.943	-0.795	-0.241	-0.141	-0.517	-0.293	-0.532	-0.411	-0.389				
TCGA-FD-A35Q	Non-papillary	2	2	3	31	Basal	TP53-like	MS51b	0	0	0	0	0	0	0	0	0	0.066	-0.286	-0.062	0.583	0.269	0.139	0.046	-0.358	-0.196	0.444	-0.09			
TCGA-FD-A3AC	Non-papillary	2	2	3	31	Luminal	Luminal	MS52b2	0	0	1	0	0	0	1	1	0	0	-1	0.075	-0.296	-0.136	-0.057	0.119	-0.414	-0.292	0.421	0.532	0.214	0.342	-0.039
TCGA-FD-A43N	NA	NA	2	3	31	Luminal	Luminal	MS51b	0	0	1	0	0	0	0	1	0	0	0	-0.62	0.757	-0.183	0.157	0.286	0.014	0.222	0.221	0.16	-0.051	-0.296	-0.424
TCGA-FD-A5BU	NA	NA	1	1	11	Basal	Basal	MS52b2	0	0	0	0	0	-1	0	0	0	0	0.889	-0.822	0.696	0.095	-0.568	-0.173	-0.493	-0.536	-0.203	0.449	0.532	0.709	
TCGA-FD-A6TG	NA	NA	2	3	31	Luminal	TP53-like	MS52b1	0	0	0	0	0	0	0	1	0	0	1	0.096	0.231	-0.174	0.454	0.019	-0.073	-0.018	-0.021	0.134	0.293	0.227	-0.209
TCGA-BT-A20J	Non-papillary	4	1	1	12	Basal	Basal	MS52b1	0	0	0	0	0	0	-2	1	0	0	0	0.701	-0.639	0.241	0.031	-0.319	-0.312	-0.488	-0.137	0.177	0.43	0.118	0.414
TCGA-E7-A67T	NA	NA	2	2	21	Luminal	TP53-like	MS51b	0	0	0	0	1	1	-2	0	0	0	0	-0.092	0.007	-0.086	0.101	0.08	0.267	0.39	-0.129	-0.275	-0.219	-0.059	-0.202
TCGA-CF-A47Y	NA	NA	2	2	22	Luminal	Luminal	MS51a	1	0	0	0	0	0	0	1	0	0	0	-0.631	0.562	-0.48	0.15	0.296	0.758	0.681	-0.147	-0.589	-0.395	0.202	-0.578
TCGA-FD-A43P	NA	NA	2	3	31	Luminal	Luminal	MS52a	0	0	0	1	0	0	0	1	0	2	-0.33	0.409	-0.182	-0.007	0.189	-0.368	-0.257	0.361	0.544	0.245	-0.367	-0.118	
TCGA-LT-A5Z6	NA	NA	2	2	21	Luminal	Luminal	MS52a1	0	0	0	0	0	0	0	1	0	0	-0.725	0.787	-0.382	-0.152	0.588	-0.062	0.258	0.647	0.353	0.405	-0.485		
TCGA-GV-A3YS	Non-papillary	3	1	1	11	Basal	Basal	MS52b2	0	0	0	0	0	0	0	1	0	1	-0.588	-0.845	0.651	-0.038	-0.573	0.4	-0.035	0.439	0.559	0.747			
TCGA-SG-A50W	NA	NA	2	3	31	Luminal	TP53-like	MS52a	0	0	0	0	0	0	2	0	1	0	0	-0.41	0.395	-0.305	-0.102	-0.274	-0.205	0.305	0.299	-0.308	-0.102	-0.002	
TCGA-BL-A0C8	Papillary	1	2	2	21	Luminal	Luminal	MS51a1	0	1	0	0	0	0	1	0	0	0	0.579	0.729	-0.438	0.14	0.346	0.106	0.169	0.471	0.349	0.12	-0.485	-0.433	
TCGA-GC-A61I	NA	NA	1	1	11	Basal	Basal	MS52b2	0	0	0	0	0	0	1	0	0	0	0.841	-0.854	0.727	-0.212	-0.515	-0.247	-0.56	-0.455	-0.069	0.449	0.73		
TCGA-CU-A55W	NA	NA	2	3	31	Luminal	Luminal	MS51b	0	1	1	0	0	0	-2	0	0	0	0	0.713	0.644	-0.146	-0.033	0.39	0.034	0.261	0.176	0.072	-0.251	0.019	-0.302
TCGA-DK-A3WY	Non-papillary	4	1	1	12	Basal	TP53-like	MS52b1	0	0	0	0	0	0	0	0	0	0	0.824	-0.826	0.29	0.296	-0.528	-0.413	-0.61	-0.179	0.244	0.667	0.019	0.444	
TCGA-FD-A5B5	NA	NA	1	1	12	Basal	Basal	MS52b2	0	0	1	0	0	0	0	0	0	0	0.787	-0.819	0.365	0.324	-0.571	-0.355	-0.626	-0.293	0.164	0.75	0.045		
TCGA-FD-A3B6	Papillary	4	1	1	12	Basal	Basal	MS52b2	0	0	1	0	0	0	1	0	1	0	0.752	-0.758	0.582	-0.227	0.449	-0.413	0.608	-0.197	0.143	0.411	0.316	0.687	
TCGA-FD-A3B5	Non-papillary	3	1	1	11	Basal	Basal	MS52b2	0	0	1	0	0	0	-2	0	0	0	0.721	0.642	-0.625	-0.164	-0.299	-0.034	-0.216	-0.324	-0.244	-0.003	0.509	0.556	
TCGA-FT-A3EE	Papillary	1	1	11	Basal	Basal	MS51b	0	0	0	1	0	0	0	0	0	1	0.181	-0.343	0.032	-0.13	0.015	0.211	0.247	-0.236	-0.331	-0.14	0.169	-0.002		
TCGA-FD-A3B3	Papillary	3	1	1	11	Basal	Basal	MS52b2	0	0	0	0	0	0	0	0	0	1	0.918	-0.837	0.76	0.046	-0.569	-0.376	-0.622	-0.417	0.022	0.555	0.433	-0.788	
TCGA-FD-A43U	NA	NA	2	3	31	Luminal	TP53-like	MS52b1	0	0	0	0	0	-1	0	0	0	0	-0.015	0.345	-0.131	-0.166	-0.146	-0.106	-0.106	0.131	0.448	-0.166	-0.114		
TCGA-FD-A43P	Papillary	3	1	1	11	Basal	TP53-like	MS52b2	0	0	0	0	0	0	0	0	0	0	0.814	-0.745	0.154	-0.054	-0.333	-0.375	-0.459	-0.369	0.002	0.469	0.711		
TCGA-FD-A5C1	NA	NA	1	1	11	Basal	MS52b2	0	0	0	0	0	0	0	1	0	0	0	0.79	-0.658	0.609	-0.025	-0.256	-0.327	-0.407	-0.506	0.015	0.547	0.727		
TCGA-FD-A5U	NA	NA	2	2	21	Luminal	Luminal	MS51a	0	0	1	0	0	0	0	0	0	0	0.658	0.762	-0.383	-0.117	0.425	0.408	0.257	0.45	0.191	-0.31	0.354	-0.448	
TCGA-FD-A40E	Non-papillary	3	1	1	11	Basal	Basal	MS52b2	0	0	0	0	0	0	0	0	0	0	0.731	-0.708	0.571	-0.236	0.38	-0.356	0.459	-0.208	0.098	0.221	0.313	0.678	
TCGA-GD-A76B	NA	NA	2	2	21	Luminal	Luminal	MS52a1	0	0	1	0	0	0	-1	0	0	0	0	0.74	-0.708	0.387	-0.154	0.472	-0.387	0.237	-0.444	-0.044	-0.504	-0.504	
TCGA-BT-A20T	Non-papillary	2	2	3	31	Basal	TP53-like	MS51a	0	0	0	0	0	-2	0	0	0	0	0.054	0.046	0.063	0.183	0.018	0.214	0.138	-0.375	-0.306	0.113	-0.243	-0.07	
TCGA-UY-A78D	NA	NA	2	2	21	Luminal	Luminal	MS51b	0	0	0	0	0	0	0	1	0	0	0	0.764	0.84	-0.513	0.111	0.554	0.218	0.561	0.284	0.0	-0.341	0.403	-0.653
TCGA-BT-A05T	Non-papillary	3	2	3	32	Basal	Basal	MS52b2	1	0	0	0	0	-2	0	2	0	1	0	0.653	-0.638	0.348	-0.016	-0.303	-0.227	-0.388	-0.129	0.061	0.241	0.441	
TCGA-H4-A2H0	Non-papillary	1	2	2	22	Luminal	Luminal	MS51b	1	0	0	0	0	-2	0	2	0	0	0	0.203	0.316	-0.162	-0.276	0.289	0.328	0.331	0.016	0.268	-0.116		
TCGA-KQ-A11N	NA	NA	2	2	21	Luminal	Luminal	MS51b	0	0	0	0	0	0	0	0	0	0	0.459	0.591	-0.392	0.083	0.378	0.204	0.466	0.297	-0.011	-0.341	-0.504		
TCGA-BT-A0YX	Non-papillary	3	1	1	11	Basal	MS52b1	0	0	0	0	0	-2	0	0	0	0	0	0.713	0.661	-0.533	-0.217	-0.297	-0.042	-0.456	-0.263	0.149	0.627	0.578		
TCGA-FD-A0Y0	Non-papillary	2	2	3	31	Luminal	TP53-like	MS51a	0	0	0	0	0	-2	0	0	0	0	0.449	0.275	-0.142	0.464	0.066	0.397	0.222	-0.333	-0.094	0.148	-0.291		
TCGA-BT-A20W	Non-papillary	2	2	3	31	Luminal	Luminal	MS52a1	0	0	0	1	0	-1	0	0	0	0	0.682	0.818	-0.445	0.167	0.469	0.04	0.288	0.403	0.282	-0.095	0.562	0.543	
TCGA-CU-A0YN	Non-papillary	3	1	1	11	Basal	MS52b2	0	0	0	0	0	0	0	0	0	0	0.815	-0.799	0.695	-0.186	0.451	-0.455	-0.455	-0.332	0.0	0.291	0.463	0.699		
TCGA-G2-A2EF	Non-papillary	4	1	1	11	Basal	MS52b2	0	0	0	0	0	0	-2	0	0	0	0	0.88	-0.834	0.575	-0.207	0.451	-0.267	-0.477	-0.304	0.014	0.355	0.281	0.647	
TCGA-FD-A5N	Papillary	2	1	3	31	Basal	MS52b2	0	0	1	0	0	0	0	0	0	0	0.524	-0.505	0.306	-0.002	-0.245	-0.189	-0.191	-0.164	0.024	0.109	0.156	0.368		
TCGA-CF-A3MF	Papillary	1	2	2	22	Luminal	Luminal	MS51b	0	0	0	0	1	-1	0	1	0	0	0	-0.864	0.716	-0.436	0.137	0.418							

TCGA-GC-A3RD	Non-papillary	1	2	3	32 Lumin	Luminal	MS51b	0	0	0	0	0	0	0	0	0	-0.499	0.642	-0.109	-0.192	0.443	0.184	0.387	0.175	-0.063	-0.397	-0.119	-0.31			
TCGA-HO-ASNE	NA	NA	1	1	11 Basal	Basal	MS2b.1	0	0	1	0	0	0	0	1	0.49	0.68	0.502	-0.049	-0.231	0.058	-0.016	-0.317	-0.301	-0.013	0.397	0.306				
TCGA-CU-A3YL	Papillary	1	2	2	21 Lumin	Luminal	MS1b	0	0	0	0	1	0	-2	0	0	0	0	0.845	0.817	-0.482	0.218	0.431	0.296	0.486	0.203	-0.043	-0.265	0.359	-0.629	
TCGA-CU-A72E	NA	NA	1	1	11 Basal	Basal	MS2b.1	1	0	1	0	1	1	-2	0	0	0	0	0.501	-0.463	0.335	0.101	-0.185	0.18	-0.056	-0.474	-0.431	0.063	0.612	0.297	
TCGA-CF-ASUA	NA	NA	2	2	22 Lumin	Luminal	MS1b	0	1	1	1	0	0	-2	0	2	0	0	1	-0.599	0.538	-0.359	-0.073	0.26	0.434	0.469	-0.003	-0.301	-0.022	-0.354	
TCGA-FD-A35S	Non-papillary	2	1	3	31 Basal	Basal	MS2a1	0	0	0	0	0	0	0	1	-1	-2	0	0	0.308	-0.13	0.197	0.021	-0.048	-0.314	-0.229	0.313	0.313	-0.068	-0.101	0.229
TCGA-DK-A21I	Papillary	2	2	3	31 Lumin	TP53-like	MS2a2	0	0	0	0	0	0	-2	1	0	0	0	-0.424	0.6	-0.282	0.36	0.23	-0.122	0.079	0.192	0.258	0.223	-0.432	-0.389	
TCGA-K4-A3WU	Non-papillary	2	2	3	31 Lumin	TP53-like	MS2b1	0	0	0	0	0	0	0	0	0	1	0.396	0.56	-0.126	0.611	0.087	-0.061	-0.044	0.041	0.147	0.352	-0.269	-0.28		
TCGA-BT-A2QD	Non-papillary	4	1	3	31 Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	1	0	0	0	0.436	-0.463	0.225	0.11	-0.226	-0.409	-0.406	0.094	0.338	0.254	0.062	0.353	
TCGA-CF-A3H5	Non-papillary	3	1	1	11 Basal	Basal	MS2b.2	0	0	0	0	0	0	0	0	0	1	0	0.735	-0.783	-0.247	-0.152	0.365	-0.077	0	0.428	0.301	-0.119	-0.223	-0.274	
TCGA-FD-A3WV	Non-papillary	3	1	1	31 Lumin	Luminal	MS1b	0	0	0	0	0	0	0	1	0	0	0	0.748	-0.792	-0.393	0.045	0.553	0.149	0.379	0.036	0.023	0.353	-0.346	-0.427	
TCGA-GV-A0G	Non-papillary	2	2	2	21 Lumin	Luminal	MS2a1	0	-1	0	0	0	0	1	0	1	0	0	0.501	-0.583	-0.429	0.191	0.269	0.718	0.501	-0.184	-0.547	-0.304	0.012	-0.479	
TCGA-PD-A5F1	NA	NA	1	1	11 Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	1	0	0	0	-0.165	-0.021	-0.252	0.105	0.109	0.647	0.36	-0.221	-0.534	-0.17	0.079		
TCGA-GU-A4Q2	NA	NA	1	1	11 Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	1	0	0	0	0.802	0.648	-0.119	0.475	0.106	0.236	0.618	0.219	-0.055	0.736			
TCGA-CF-A3Mg	Papillary	1	2	2	22 Lumin	Luminal	MS1b	0	0	0	0	1	1	-2	0	0	0	0	-0.876	0.867	-0.453	-0.267	0.611	0.369	0.744	0.261	-0.206	-0.743	0.166	-0.53	
TCGA-FD-A5CO	NA	NA	2	3	31 Lumin	TP53-like	MS2a2	0	0	0	0	0	0	-1	0	0	1	0	-0.029	0.125	-0.111	0.199	0.12	-0.176	-0.026	0.174	0.19	-0.001	0.064	-0.04	
TCGA-E7-A3Y1	Papillary	1	2	2	22 Lumin	Luminal	MS1a	1	0	0	0	0	0	0	0	0	0	0	-0.587	0.583	-0.429	0.191	0.269	0.718	0.501	-0.184	-0.547	-0.304	0.012	-0.479	
TCGA-E7-A6MF	NA	NA	2	2	22 Lumin	Luminal	MS1a	0	0	0	1	0	0	0	0	0	0	-0.165	-0.021	-0.252	0.105	0.109	0.647	0.36	-0.221	-0.534	-0.17	0.079			
TCGA-G2-A3VY	Non-papillary	1	2	2	21 Lumin	Luminal	MS2a1	0	0	1	0	1	0	-1	1	0	0	0	-0.775	0.873	-0.524	-0.142	0.618	0.125	0.458	0.618	-0.268	0.528	-0.085		
TCGA-K4-A6MB	NA	NA	2	3	31 Lumin	Luminal	MS2a1	0	1	0	0	1	0	-1	1	0	0	0	0.612	-0.75	-0.114	0.17	0.317	-0.045	0.233	0.327	0.227	-0.19	0.324		
TCGA-FD-A6TB	NA	NA	1	1	11 Basal	TP53-like	MS2b1	0	0	0	0	0	0	0	1	0	0	0	0.529	-0.749	-0.562	-0.16	-0.382	-0.026	-0.203	-0.278	-0.233	-0.053	0.428		
TCGA-FD-A3OS	Non-papillary	4	2	3	32 Basal	Basal	MS2b2.2	0	0	0	0	0	0	1	-2	1	0	0	0	0.848	-0.765	-0.441	0.191	-0.508	-0.275	-0.469	-0.128	0.11	0.388	0.602	
TCGA-K4-A3WV	Non-papillary	3	2	3	32 Basal	Basal	MS2b2.2	0	-1	0	0	0	0	0	0	0	0	0	-0.409	0.675	-0.175	-0.233	0.717	-0.147	0.078	-0.083	0.055	0.325			
TCGA-FD-A3B8	NA	NA	1	1	11 Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	0	0	0	0.887	-0.853	-0.74	0.083	-0.585	-0.227	-0.525	-0.462	-0.141	0.421	0.742			
TCGA-GU-A4ZP	NA	NA	2	2	22 Lumin	Luminal	MS2a1	0	0	0	0	0	0	0	0	1	0	-0.751	0.844	-0.457	0.002	0.447	-0.114	0.233	0.693	0.412	-0.381	0.532	-0.441		
TCGA-FI-A3Z9	NA	NA	2	2	22 Lumin	Luminal	MS1b	0	0	0	1	0	0	0	0	0	0	-0.742	0.761	-0.328	0.015	0.566	0.406	0.736	0.184	-0.211	0.665	0.273	-0.528		
TCGA-FD-A6TK	NA	NA	1	1	11 Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	0	0	0	0.769	-0.759	-0.54	0.155	-0.575	-0.334	0.056	0.579	0.226	0.613				
TCGA-FJ-A3Z7	Non-papillary	2	2	3	31 Lumin	TP53-like	MS2a2	0	0	0	0	0	0	0	0	0	0	-0.097	0.283	-0.202	0.28	0.02	-0.148	0.133	0.284	0.322	-0.256	-0.422			
TCGA-FD-A5BR	NA	NA	2	3	31 Lumin	TP53-like	MS2b1	0	0	0	0	0	0	-2	1	0	0	0	-0.352	0.447	-0.02	0.441	0.076	0.114	-0.112	-0.073	0.213	-0.11	-0.242		
TCGA-C4-A6EZ	NA	NA	2	3	32 Basal	Basal	MS2a2	0	0	0	0	0	0	0	1	0	0	-0.664	-0.528	0.194	0.126	-0.17	-0.288	-0.268	0.233	0.277	0.04	-0.118	0.237		
TCGA-K4-A3BM	Non-papillary	1	2	2	22 Lumin	Luminal	MS1a	1	0	0	0	0	0	-1	0	0	0	-0.162	0.287	-0.112	-0.153	0.353	-0.231	-0.536	-0.364	0.116	-0.36	-0.125			
TCGA-K4-A3AC	NA	NA	1	1	11 Basal	Basal	MS2b2.2	0	0	0	0	0	0	-1	1	0	0	-0.812	-0.863	-0.686	-0.178	-0.446	-0.239	-0.443	-0.372	-0.092	0.233	0.487			
TCGA-FD-A3ZD	Non-papillary	2	3	31 Basal	TP53-like	MS2b1	1	0	1	0	0	0	0	0	1	0	0	-0.079	-0.025	-0.131	0.084	-0.226	-0.212	-0.084	0.295	0.033	0.018				
TCGA-FD-A3ZU	NA	NA	2	3	32 Basal	TP53-like	MS2b2	0	-1	0	1	0	1	2	0	0	0	0.533	-0.57	0.379	-0.165	0.51	-0.091	0.119	-0.024	0.118	-0.452	-0.444			
TCGA-FD-A3ZV	NA	NA	2	3	32 Basal	TP53-like	MS2b2	0	-1	0	1	0	1	2	0	0	0	0.533	-0.57	0.379	-0.165	0.51	-0.091	0.119	-0.024	0.118	-0.452	-0.444			
TCGA-K4-A5BL	NA	NA	1	1	11 Basal	Basal	MS2b2	0	0	0	0	0	0	-1	0	0	0	-0.802	0.811	-0.514	0.043	-0.424	0.054	0.206	0.563	0.345	-0.558				
TCGA-K4-A5RH	NA	NA	1	1	12 Basal	Basal	MS2b1	0	0	0	0	0	0	0	1	0	0	-0.848	-0.809	-0.413	0.144	-0.572	-0.398	-0.647	-0.162	0.218	0.628				
TCGA-K4-A5ZZ	NA	NA	1	1	12 Basal	Basal	MS2b1	0	0	0	0	0	0	-1	0	0	0	-0.339	0.349	-0.313	-0.267	0.552	-0.033	0.142	-0.245	0.441	0.396				
TCGA-GC-A3QO	Non-papillary	2	2	3	31 Lumin	TP53-like	MS2b1	0	0	1	0	0	0	0	0	0	-0.109	0.118	-0.011	0.468	-0.148	-0.023	-0.052	0.043	0.174	-0.034					
TCGA-DK-A216	Non-papillary	3	1	1	11 Basal	Basal	MS2b2.2	0	0	0	0	0	0	-1	0	0	0	-0.109	0.118	-0.011	0.468	-0.148	-0.023	-0.052	0.043	0.174	-0.034				
TCGA-FD-A3SM	Papillary	2	2	3	31 Lumin	TP53-like	MS2b1	0	0	0	0	0	0	0	1	0	0	-0.073	0.073	-0.017	0.222	-0.041	-0.021	-0.052	0.031	0.111	-0.034				
TCGA-C4-A6F6	Non-papillary	2	2	3	31 Lumin	TP53-like	MS1b	0	0	0	0	0	0	0	1	0	0	-0.466	0.504	-0.192	0.045	-0.423	-0.29	-0.086	0.173	-0.025	0.058	0.078			
TCGA-E5-MT2	Non-papillary	2	2	3	32 Lumin	Basal	MS2b2.1	0	-1	0	0	0	0	0	1	0	0	-0.099	0.122	-0.2	0.099	-0.358	-0.192	-0.026	0.276	0.066	0.172				
TCGA-FD-A35I	Non-papillary	2	2	3	31 Lumin	TP53-like	MS2a2	0	0	1	0	0	0	-2	0	0	0	-0.383	0.568	-0.343	0.422	-0.168	-0.094	0.08	0.432	0.335	0.035	0.552	-0.422		
TCGA-GD-A2C5	Papillary	2	2	3	31 Lumin	Luminal	MS1b	0	-1	0	0	0	0	0	1	0															

TCGA-BT-A20R	Non-papillary	2	2	3	31	Basal	TP53-like	MS2b1	0	0	1	0	0	0	0	0	1	0	2	0.257	-0.209	-0.049	0.333	-0.16	-0.318	-0.351	0.165	0.351	0.419	-0.286	0.045		
TCGA-GV-A30G	Papillary	4	1	1	12	Basal	TP53-like	MS2b1	0	0	0	0	0	0	0	0	0	0	0.344	-0.437	0.112	0.289	-0.309	-0.451	-0.484	0.02	0.421	0.6	-0.213	0.189			
TCGA-FD-A35R	Non-papillary	2	2	3	31	Basal	TP53-like	MS2b2	0	0	0	0	0	0	-1	0	0	0	1	0.106	-0.169	0.296	-0.023	-0.314	-0.353	0.264	0.429	0.375	0.332	-0.033			
TCGA-E7-A54I	NA	NA	2	2	21	Luminal	Luminal	MS2a2	0	0	0	0	0	0	0	0	1	0	-2	0	-0.452	0.522	-0.18	0.178	-0.11	-0.052	0.176	0.204	0.007	0.089	-0.09		
TCGA-GV-A30H	Non-papillary	1	2	2	21	Luminal	Luminal	MS2a1	0	0	0	0	0	0	-2	1	0	0	0	2	-0.831	0.9	-0.409	-0.204	0.553	0.017	0.358	0.658	0.315	-0.523	0.445	-0.517	
TCGA-G2-A31B	Non-papillary	3	1	1	11	Basal	Basal	MS2b2.2	0	-1	0	0	0	1	-1	1	0	0	0	0.697	-0.638	0.589	-0.319	-0.209	-0.001	-0.114	-0.257	-0.241	-0.159	0.487	0.509		
TCGA-BT-A20N	Non-papillary	1	2	3	32	Basal	Luminal	MS1b	0	0	0	0	0	0	-1	1	0	0	-1	0	0.108	0.082	0.057	-0.31	0.19	0.08	0.176	0.129	-0.09	-0.374	0.056	0.031	
TCGA-E7-A6ME	NA	NA	2	2	32	Luminal	Luminal	MS2a1	0	0	0	0	0	0	0	0	1	0	1	-0.606	0.758	-0.291	0.077	0.369	-0.088	0.109	0.55	0.342	-0.171	-0.406	-0.405		
TCGA-DK-A31T	Non-papillary	2	2	3	31	Luminal	TP53-like	MS2a2	0	-1	0	0	0	0	0	0	0	0	0	-0.322	0.227	-0.141	0.256	0.116	-0.289	-0.034	0.215	0.347	0.122	0.246	-0.131		
TCGA-HQ-A7BL	NA	NA	1	1	11	Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	0	1	0	0	-0.699	0.485	-0.081	-0.294	0.433	-0.050	0.167	0.159	0.568	0.234	0.33			
TCGA-F-A4M7	NA	NA	2	2	22	Luminal	Luminal	MS2d	1	2	0	0	0	0	0	1	0	0	0	0.727	0.511	-0.391	0.154	0.232	0.324	0.398	-0.113	-0.368	-0.251	-0.149	-0.533		
TCGA-F1-A3ZF	Papillary	1	2	2	21	Luminal	Luminal	MS2a1	0	0	0	0	0	0	0	0	1	0	0	0	0.821	0.517	-0.094	0.099	0.343	0.703	0.378	-0.42	-0.651	0.355			
TCGA-FD-A5TH	NA	NA	1	3	31	Basal	Basal	MS2a2	0	0	0	0	0	0	0	0	0	0	0.577	-0.541	0.202	0.08	0.238	-0.385	-0.401	0.118	0.337	0.248	0.335				
TCGA-FD-A3NS	Non-papillary	3	1	1	11	Basal	Basal	MS2b2.2	0	0	0	0	0	0	1	1	0	1	-2	0	0.699	-0.663	0.669	-0.169	-0.333	-0.26	-0.374	-0.195	-0.032	0.074	0.422	0.676	
TCGA-K4-A54R	NA	NA	2	3	31	Basal	Basal	MS2b1	0	-1	1	0	0	0	0	1	0	1	-1	0	0.34	-0.478	0.103	-0.068	-0.119	-0.29	-0.262	-0.064	0.209	0.311	-0.004	0.194	
TCGA-GV-A3QJ	Papillary	1	2	3	32	Luminal	Luminal	MS2a1	0	0	0	0	0	0	0	0	0	0	-0.137	0.176	-0.201	-0.066	0.181	0.061	0.216	0.438	0.087	-0.381	0.292	-0.238			
TCGA-HQ-A20F	Papillary	1	2	2	21	Luminal	Luminal	MS1b	0	0	0	0	1	1	-1	0	1	0	-1	1	-0.623	0.464	-0.31	-0.178	0.403	0.02	0.345	0.321	0.154	-0.384	0.263		
TCGA-G2-A3JF	Non-papillary	1	2	2	21	Luminal	Luminal	MS1b	0	0	0	0	0	0	-1	1	0	0	0	-0.816	0.863	-0.563	-0.038	0.602	0.368	0.626	0.273	-0.085	-0.448	0.432	-0.685		
TCGA-H4-A2HZ	Papillary	1	2	2	21	Luminal	Luminal	MS2a1	0	0	1	0	0	0	0	0	1	0	0	-0.836	0.839	-0.553	0.226	0.426	0.069	0.251	0.37	0.199	-0.028	0.052	-0.588		
TCGA-KQ-A41S	NA	NA	2	3	31	Luminal	TP53-like	MS2b1	0	0	0	0	0	0	0	0	1	0	-1	0	-0.166	0.234	-0.208	0.35	-0.043	-0.15	-0.097	0.21	0.21	0.233	0.266	-0.186	
TCGA-DK-A3WV	Papillary	3	1	1	11	Basal	Basal	MS2b2.2	0	0	1	0	0	0	-2	0	0	0	0	0.767	-0.782	0.691	-0.309	-0.457	-0.205	-0.484	-0.427	-0.127	0.324	0.521	0.718		
TCGA-FD-A5Z2	NA	NA	2	3	31	Luminal	TP53-like	MS2b1	0	0	0	0	1	1	-2	0	2	0	0	-0.142	0.225	-0.023	0.521	-0.087	-0.08	0.079	-0.02	0.05	0.252	0.263	-0.2		
TCGA-DK-A4Z3L	Non-papillary	2	2	3	31	Luminal	TP53-like	MS2a1	0	0	0	0	0	0	0	0	1	0	0	-0.363	0.434	-0.392	0.299	0.274	-0.026	0.231	0.404	0.253	0.172	-0.435	0.425		
TCGA-DK-A4Z3	NA	NA	2	3	31	Luminal	Luminal	MS2a2	0	0	0	1	0	0	0	0	0	1	-0.19	0.513	-0.201	0.398	0.118	-0.152	0.303	0.324	0.231	0.358	-0.323				
TCGA-GV-A3JZ	Non-papillary	2	2	3	31	Luminal	Luminal	MS2a2	0	0	0	0	0	0	0	0	1	-1	0	0	-0.13	0.283	-0.217	0.038	0.133	-0.348	0.136	0.461	0.495	0.078	-0.421	0.136	
TCGA-FD-A4TD	NA	NA	1	1	11	Basal	Basal	MS2b2.2	0	0	1	0	0	0	0	1	0	0	0	-0.744	-0.774	0.632	-0.058	-0.516	-0.299	-0.564	-0.411	-0.037	0.47	0.693			
TCGA-FD-A4X3	NA	NA	2	2	22	Luminal	Luminal	MS1b	1	0	0	0	1	1	-2	0	0	0	0	-0.798	0.685	-0.463	-0.071	0.459	0.659	0.754	0.006	-0.474	-0.575	-0.16	-0.606		
TCGA-BT-A4ZC	Papillary	1	2	2	21	Luminal	Luminal	MS1b	1	0	0	0	0	0	0	1	0	0	-2	0	-0.749	0.72	-0.249	-0.165	0.475	0.241	0.537	0.198	-0.122	-0.553	0.399	-0.397	
TCGA-GV-A3QF	Papillary	1	2	2	21	Luminal	Luminal	MS2a1	0	0	0	0	0	0	-2	0	0	0	0	-0.826	0.866	-0.468	-0.144	0.561	0.08	0.457	0.46	0.178	0.502	0.289	-0.526		
TCGA-FJ-A3ZE	Non-papillary	1	2	2	22	Luminal	Luminal	MS1b	1	0	0	0	0	0	-2	1	0	0	0	-0.313	0.389	-0.236	-0.231	0.401	0.288	0.417	0.252	-0.128	-0.574	0.073			
TCGA-K4-A6ZF	NA	NA	1	1	11	Basal	Basal	MS2b1.1	0	0	0	0	0	0	0	0	1	0	1	0	0.22	-0.38	0.431	-0.191	-0.029	0.246	0.107	-0.364	-0.43	-0.121	0.502	0.168	
TCGA-BT-A4ZE	NA	NA	1	1	11	Basal	Basal	MS2b2.2	0	0	0	0	0	0	-2	0	0	0	0	0.854	-0.832	0.701	-0.248	-0.433	-0.289	-0.504	-0.41	-0.04	0.334	0.474	0.757		
TCGA-DK-A6B6	NA	NA	2	2	21	Luminal	Luminal	MS1b	0	0	0	0	0	0	0	0	1	0	0	-0.809	0.852	-0.504	-0.179	0.582	0.277	0.434	0.349	0.035	-0.325	-0.396	-0.643		
TCGA-HQ-A76Z	Non-papillary	3	1	1	12	Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	1	0	0	-1	0	0.796	-0.718	0.668	-0.23	-0.396	0.153	-0.388	-0.461	-0.203	0.238	0.670		
TCGA-F-A4Z2S	Non-papillary	3	1	1	11	Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	0	1	0	-1	0	-0.796	0.718	0.668	-0.23	-0.396	0.153	-0.388	-0.461	-0.203	0.238	0.670		
TCGA-F-A4M7	NA	NA	2	2	22	Luminal	Luminal	MS2d	0	0	0	0	0	0	0	0	2	0	0	0	0	0.748	-0.748	0.658	-0.168	-0.397	0.47	0.396	0.547	-0.305	0.437	-0.159	
TCGA-DK-A4A8	NA	NA	3	1	11	Basal	Basal	MS2b2.2	0	0	0	0	0	0	0	0	1	0	0	-0.859	-0.756	0.527	0.213	-0.513	-0.033	0.415	-0.547	-0.305	0.437	0.584			
TCGA-UJ-A7BN	NA	NA	3	1	32	Luminal	Luminal	MS2a3	1	0	0	0	0	0	0	0	1	0	-2	1	0	-0.515	0.711	-0.328	0.141	0.256	0.031	0.273	0.41	0.144	0.313	0.381	
TCGA-DK-A3JS	Papillary	1	2	2	22	Luminal	Luminal	MS1b	1	2	0	0	0	1	-1	1	0	0	0	-0.558	0.693	-0.305	0.46	-0.281	0.491	0.103	-0.236	-0.581	0.167	-0.306			
TCGA-FD-A4TF	NA	NA	2	3	31	Basal	TP53-like	MS2b1	0	0	0	0	0	0	0	0	1	0	0	0	-0.685	-0.677	0.272	0.354	-0.393	-0.4	-0.55	0.013	0.296	0.508	0.061	0.363	
TCGA-BT-A20P	Non-papillary	1	2	2	22	Luminal	Luminal	MS1b	0	2	0	0	0	0	1	-2	0	1	0	0	0	-0.484	0.45	-0.287	-0.073	0.194	0.401	0.452	0.009	-0.294	-0.431	0.066	-0.337
TCGA-E5-A4U1	NA	NA	2	2	21	Luminal	Luminal	MS1b	0	1	0	0	1	1	-1	1	0	0	0	-0.735	0.789	-0.441	-0.016	0.467	0.276	0.57	0.353	-0					

Supplementary table 7

Gene signatures used in Figures 1-2, Gene IDs are according to TCGA nomenclature

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CA2|760

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COL17A1|1308

DSC2|1824

ELL2|22936

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KRT5|3852

LGALS7|3963

LOC100133331|100133331

MAF|4094

MMP3|4314

MXD1|4084

PI3|5266

PTHLH|5744

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S100A8|6279

SFN|2810

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ACAP1|9744

ADAMDEC1|27299

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ALOX5AP|241

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ANXA6|309

AOAH|313

AP1S2|8905

APOE|348

ARHGAP15|55843

ARHGAP25|9938

ARHGAP9|64333

ATP8B4|79895

BATF3|55509

BIN1|274

BTK|695

C1orf162|128346

C1orf54|79630

C1QA|712

C1QB|713

C1QC|714

C1S|716

C3AR1|719

CCL2|6347

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CD163|9332

CD2|914

CD209|30835

CD247|919

CD300LF|146722

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CD38|952

CD3D|915

CD48|962

CD52|1043

CD53|963

CD6|923

CD7|924

CD74|972

CD86|942

CLEC4A|50856

CORO1A|11151
CPVL|54504
CSF1R|1436
CST7|8530
CTLA4|1493
CTSK|1513
CYBB|1536
CYTH4|27128
CYTIP|9595
DOCK10|55619
DOCK11|139818
DOCK2|1794
EMP3|2014
ENTPD1|953
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EVI2B|2124
FAM65B|9750
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FCN1|2219
FERMT3|83706
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FPR3|2359
FYB|2533
FYN|2534
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GIMAP5|55340
GIMAP7|168537
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GZMK|3003
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HLA-DQA1|3117
HLA-DRA|3122
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IFITM1|8519
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IKZF1|10320
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IL18BP|10068
IL18RAP|8807
IL2RA|3559
IL2RB|3560
IL7R|3575
IQGAP2|10788
IRF8|3394
ISG20|3669
ITGAL|3683
ITGAM|3684
ITGB2|3689
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LAT2|7462
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MFNG|4242
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NKG7|4818
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PARVG|64098
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PIK3AP1|118788
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PRF1|5551
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PTPN7|5778
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RGS2|5997
RNASE6|6039
RUNX3|864
SAMSNI|64092
SASH3|54440
SH2B3|10019
SIGLEC10|89790
SLA|6503
SLAMF1|6504
SLAMF6|114836
SLAMF8|56833
SLC7A7|9056
SLCO2B1|11309
SPI1|6688
SRGN|5552
ST6GAL1|6480
STAT4|6775
SUSD3|203328
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TBXAS1|6916
TLR8|51311
TMEM176A|55365
TNFRSF1B|7133
TNFRSF4|7293
TNFSF13B|10673
TOX2|84969
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TSPAN4|7106
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WAS|7454
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CYP4F12|66002
CYP4F22|126410
DHRS2|10202
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FAM3B|54097
GGT6|124975
HMGC52|3158
HPGD|3248
PKHD1|5314
PPARG|5468
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SNCG|6623
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TRAK1|22906

UPK1A|11045
VSIG2|23584

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FGFR3|2261
IRS1|3667
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PTPN13|5783
SEMA4B|10509
SLC2A9|56606
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CXCL2|2920
FCGR3B|2215
ITGAX|3687
MMP25|64386
MNDA|4332
OSM|5008
PHACTR1|221692
PROK2|60675
SOD2|6648
TAGAP|117289
VNN2|8875

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AURKB|9212
BIRC5|332
BUB1|699
BUB1B|701
C12orf48|55010
C15orf23|90417
C16orf59|80178
C17orf53|78995
C1orf112|55732
C1orf135|79000
CCNA2|890
CCNB1|891
CCNB2|9133
CCNE2|9134
CDC20|991
CDC25A|993
CDC25C|995
CDC45|8318
CDCA2|157313
CDCA3|83461
CDCA5|113130
CDC48|55143
CDK1|983
CDKN3|1033
CDT1|81620
CENPA|1058
CENPE|1062
CENPF|1063
CENPL|91687

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CENPN|55839
CENPW|387103
CEP55|55165
CHAF1B|8208
CHEK1|1111
CKAP2L|150468
CKS1B|1163
DEPDC1|55635
DEPDC1B|55789
DLGAP5|9787
DONSON|29980
DTL|51514
E2F2|1870
ECT2|1894
EXO1|9156
FAM64A|54478
FAM83D|81610
FANCI|55215
FEN1|2237
FOXM1|2305
GINS2|51659
H2AFZ|3015
HJURP|55355
HMGB2|3148
HMMR|3161
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KIF20B|9585
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NUF2|83540
NUSAP1|51203
OIP5|11339
PKMYT1|9088
PLK4|10733
POC1A|25886
POLA2|23649
POLE2|5427
POLQ|10721
PRC1|9055
PRR11|55771
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PTTG3P|26255
RACGAP1|29127
RAD51AP1|10635
RFC3|5983
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RNASEH2A|10535
RRM2|6241
SGOL1|151648
SGOL2|151246
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SKA3|221150
SPC25|57405
STIL|6491
TK1|7083
TOP2A|7153
TPX2|22974
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TYMS|7298
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ZWINT|11130

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C1R|715
CALD1|800
CD248|57124
CD93|22918
CDH11|1009
CHN1|1123
CLIP3|25999
COL15A1|1306
COL1A1|1277
COL1A2|1278
COL3A1|1281
COL5A1|1289
COL5A2|1290
COL6A1|1291
COL6A2|1292
COL6A3|1293
COL8A1|1295
COLEC12|81035
COX7A1|1346
CPXM1|56265
CRISPLD2|83716
CTHRC1|115908
DACT3|147906
DCN|1634
DDR2|4921
DPYSL2|1808
ECM2|1842
EDNRA|1909
EMILIN1|11117
FAM20C|56975
FERMT2|10979
FILIP1L|11259
FSTL1|11167
GEM|2669
GLT8D2|83468
GPR124|25960
GUCY1A3|2982
HEPH|9843
IGDCC4|57722
ISLR|3671
JAM3|83700
KCNMB1|3779
LAMA4|3910
LGALS1|3956
LHFP|10186
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