

Supplementary Table 5.

Significant signaling pathways and gene sets that may be affected by changed expression of genes connected with two clusters with distinct overall survival.

GSEA analysis was done on all genes connected with two clusters, using c2: curated gene set collections from MSigDB (3724 gene sets). We applied two independent tests: the LS permutation test and Efron-Tibshirani GSA test to identify gene sets differentiating two clusters of ovarian cancer samples. LS permutation test finds gene sets which have more genes differentially expressed among the classes than expected by chance. Efron-Tibshirani's test uses 'maxmean' statistics to identify gene sets differentially expressed.

We considered a GSEA category significantly differentially regulated if significance level in either of the tests was less than 0.05 after Benjamini-Hochberg False Discovery Rate (FDR) multiple test correction.

No	Gene set / Signaling pathway	No of genes	FDR corrected LS permutation p-value	FDR corrected Efron-Tibshirani's GSA test p-value
1	ALONSO METASTASIS EMT UP	82	0,00005	< 0.005 (+)
2	ANASTASSIOU CANCER MESENCHYMAL TRANSITION SIGNATURE	161	0,00005	< 0.005 (+)
3	AZARE NEOPLASTIC TRANSFORMATION BY STAT3 DN	336	0,00005	< 0.005 (+)
4	BEGUM TARGETS OF PAX3 FOXO1 FUSION AND PAX3	25	0,00005	< 0.005 (+)
5	BEGUM TARGETS OF PAX3 FOXO1 FUSION DN	111	0,00005	< 0.005 (+)
6	BHATI G2M ARREST BY 2METHOXYESTRADIOL DN	238	0,00005	< 0.005 (-)
7	BIOCARTA CTL PATHWAY	26	0,00005	0.05783 (+)
8	BIOCARTA FIBRINOLYSIS PATHWAY	21	0,00005	< 0.005 (+)
9	BIOCARTA LYM PATHWAY	29	0,00005	0.05783 (+)
10	BIOCARTA TCRA PATHWAY	20	0,00005	0.05783 (+)
11	BIOCARTA TCYTOTOXIC PATHWAY	25	0,00005	0.05783 (+)
12	BOQUEST STEM CELL UP	623	0,00005	< 0.005 (+)
13	BRUECKNER TARGETS OF MIRLET7A3 DN	183	0,00005	< 0.005 (+)
14	CHANG POU5F1 TARGETS UP	44	0,00005	< 0.005 (+)
15	CHARAFE BREAST CANCER BASAL VS MESENCHYMAL DN	123	0,00005	< 0.005 (+)
16	CHIANG LIVER CANCER SUBCLASS CTNNB1 DN	345	0,00005	< 0.005 (+)
17	CHIBA RESPONSE TO TSA UP	120	0,00005	< 0.005 (+)
18	CLAUS PGR POSITIVE MENINGIOMA DN	42	0,00005	< 0.005 (+)
19	CORRE MULTIPLE MYELOMA DN	141	0,00005	< 0.005 (+)
20	COWLING MYCN TARGETS	88	0,00005	< 0.005 (+)
21	CREIGHTON ENDOCRINE THERAPY RESISTANCE 4	697	0,00005	< 0.005 (-)

22	CROMER_TUMORIGENESIS_UP	137	0,00005	< 0.005 (+)
23	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_DN	213	0,00005	< 0.005 (+)
24	CROONQUIST_STROMAL_STIMULATION_UP	148	0,00005	< 0.005 (+)
25	DANG_REGULATED_BY_MYC_DN	691	0,00005	< 0.005 (+)
26	DASU_IL6_SIGNALING_DN	22	0,00005	< 0.005 (+)
27	DASU_IL6_SIGNALING_SCAR_DN	45	0,00005	< 0.005 (+)
28	DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_DN	41	0,00005	< 0.005 (+)
29	DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN	162	0,00005	< 0.005 (+)
30	DELYS_THYROID_CANCER_UP	996	0,00005	< 0.005 (+)
31	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN	56	0,00005	< 0.005 (+)
32	ELVIDGE_HIF2A_TARGETS_UP	16	0,00005	< 0.005 (+)
33	FARMER_BREAST_CANCER_CLUSTER_5	42	0,00005	< 0.005 (+)
34	FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_UP	128	0,00005	< 0.005 (-)
35	FRIDMAN_SENESCENCE_DN	28	0,00005	< 0.005 (+)
36	FRIDMAN_SENESCENCE_UP	203	0,00005	< 0.005 (+)
37	GILDEA_METASTASIS	85	0,00005	< 0.005 (+)
38	GRANDVAUX_IRF3_TARGETS_DN	59	0,00005	< 0.005 (+)
39	GRUETZMANN_PANCREATIC_CANCER_UP	887	0,00005	< 0.005 (+)
40	GU_PDEF_TARGETS_UP	214	0,00005	< 0.005 (+)
41	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN	128	0,00005	< 0.005 (+)
42	HAEGERSTRAND_RESPONSE_TO_IMATINIB	24	0,00005	< 0.005 (+)
43	HAHTOLA_CTCL_PATHOGENESIS	29	0,00005	< 0.005 (+)
44	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP	209	0,00005	< 0.005 (+)
45	HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP	47	0,00005	< 0.005 (+)
46	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_DN	45	0,00005	< 0.005 (+)
47	HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	142	0,00005	< 0.005 (+)
48	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP	164	0,00005	< 0.005 (+)
49	HOSHIDA_LIVER_CANCER_SUBCLASS_S1	552	0,00005	< 0.005 (+)
50	HOSHIDA_LIVER_CANCER_SURVIVAL_UP	195	0,00005	< 0.005 (+)
51	JAEGER_METASTASIS_UP	115	0,00005	< 0.005 (+)
52	KARAKAS_TGFB1_SIGNALING	44	0,00005	< 0.005 (+)
53	KEGG_ECM_RECEPTOR_INTERACTION	235	0,00005	< 0.005 (+)
54	KEGG_FOCAL_ADHESION	595	0,00005	0.05783 (+)

55	KEGG_RIBOSOME	144	0,00005	< 0.005 (-)
56	KOYAMA_SEMA3B_TARGETS_DN	924	0,00005	< 0.005 (-)
57	KYNG_DNA_DAMAGE_DN	522	0,00005	< 0.005 (+)
58	LI_AMPLIFIED_IN_LUNG_CANCER	369	0,00005	< 0.005 (-)
59	LI_WILMS_TUMOR_VS_FETAL_KIDNEY_2_DN	145	0,00005	< 0.005 (+)
60	LIANG_SILENCED_BY_METHYLATION_UP	65	0,00005	< 0.005 (+)
61	LIEN_BREAST_CARCINOMA_METAPLASTIC	107	0,00005	< 0.005 (+)
62	LINDGREN_BLADDER_CANCER_CLUSTER_2B	959	0,00005	< 0.005 (+)
63	LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	137	0,00005	< 0.005 (+)
64	LINDVALL_IMMORTALIZED_BY_TERT_DN	217	0,00005	< 0.005 (+)
65	LIU_TARGETS_OF_VMYB_VS_CMYB_DN	110	0,00005	< 0.005 (+)
66	LU_TUMOR_ENDOTHELIAL_MARKERS_UP	52	0,00005	< 0.005 (+)
67	LU_TUMOR_VASCULATURE_UP	64	0,00005	< 0.005 (+)
68	LUCAS_HNF4A_TARGETS_DN	22	0,00005	< 0.005 (+)
69	MAHAJAN_RESPONSE_TO_IL1A_DN	210	0,00005	< 0.005 (+)
70	MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS	96	0,00005	< 0.005 (+)
71	MIKKELSEN_MEF_LCP_WITH_H3K4ME3	267	0,00005	< 0.005 (+)
72	MIPS_60S_RIBOSOMAL_SUBUNIT_CYTOPLASMIC	78	0,00005	< 0.005 (-)
73	MIPS_NOP56P_ASSOCIATED_PRE_RRNA_COMPLEX	218	0,00005	< 0.005 (-)
74	MIPS_RIBOSOME_CYTOPLASMIC	136	0,00005	< 0.005 (-)
75	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP	51	0,00005	< 0.005 (+)
76	MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN	604	0,00005	< 0.005 (+)
77	MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_UP	37	0,00005	< 0.005 (+)
78	MULLIGHAN_MLL_SIGNATURE_1_DN	611	0,00005	< 0.005 (-)
79	NAKAMURA_ADIPOGENESIS_EARLY_DN	114	0,00005	< 0.005 (+)
80	NAKAMURA_ADIPOGENESIS_LATE_DN	111	0,00005	< 0.005 (+)
81	NAKAMURA_CANCER_MICROENVIRONMENT_UP	65	0,00005	< 0.005 (+)
82	NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_UP	725	0,00005	< 0.005 (+)
83	NEWMAN_ERCC6_TARGETS_DN	107	0,00005	< 0.005 (+)
84	NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_DN	42	0,00005	< 0.005 (+)
85	NIELSEN_MALIGNANT_FIBROUS_HISTIOCYTOMA_UP	25	0,00005	< 0.005 (+)
86	OHM_EMBRYONIC_CARCINOMA_DN	22	0,00005	< 0.005 (+)
87	OHM_METHYLATED_IN_ADULT_CANCERS	74	0,00005	< 0.005 (+)

88	OLSSON E2F3 TARGETS DN	100	0,00005	< 0.005 (+)
89	ONDER CDH1 SIGNALING VIA CTNNB1	202	0,00005	< 0.005 (+)
90	ONDER CDH1 TARGETS 2 UP	671	0,00005	< 0.005 (+)
91	OXFORD RALA AND RALB TARGETS DN	23	0,00005	< 0.005 (+)
92	OXFORD RALB TARGETS UP	23	0,00005	< 0.005 (+)
93	OZANNE AP1 TARGETS DN	21	0,00005	< 0.005 (+)
94	PETRETTO CARDIAC HYPERTROPHY	115	0,00005	< 0.005 (+)
95	PETROVA PROX1 TARGETS DN	154	0,00005	< 0.005 (+)
96	PICCALUGA ANGIOIMMUNOBLASTIC LYMPHOMA UP	558	0,00005	< 0.005 (+)
97	PID AVB3 INTEGRIN PATHWAY	227	0,00005	< 0.005 (+)
98	PID FRA PATHWAY	95	0,00005	< 0.005 (+)
99	REACTOME 3 UTR MEDIATED TRANSLATIONAL REGULATION	193	0,00005	< 0.005 (-)
100	REACTOME A TETRASACCHARIDE LINKER SEQUENCE IS REQUIRED FOR GAG SYNTHESIS	58	0,00005	< 0.005 (+)
101	REACTOME CELL SURFACE INTERACTIONS AT THE VASCULAR WALL	223	0,00005	0.05783 (+)
102	REACTOME CHONDROITIN SULFATE BIOSYNTHESIS	45	0,00005	< 0.005 (+)
103	REACTOME CHONDROITIN SULFATE DERMATAN SULFATE METABOLISM	111	0,00005	< 0.005 (+)
104	REACTOME COLLAGEN FORMATION	136	0,00005	< 0.005 (+)
105	REACTOME CS DS DEGRADATION	42	0,00005	< 0.005 (+)
106	REACTOME DEGRADATION OF THE EXTRACELLULAR MATRIX	58	0,00005	< 0.005 (+)
107	REACTOME EXTRACELLULAR MATRIX ORGANIZATION	194	0,00005	< 0.005 (+)
108	REACTOME GLYCOSAMINOGLYCAN METABOLISM	257	0,00005	< 0.005 (+)
109	REACTOME HEPARAN SULFATE HEPARIN HS GAG METABOLISM	117	0,00005	0.05783 (+)
110	REACTOME INFLUENZA VIRAL RNA TRANSCRIPTION AND REPLICATION	183	0,00005	< 0.005 (-)
111	REACTOME INTEGRIN CELL SURFACE INTERACTIONS	222	0,00005	< 0.005 (+)
112	REACTOME KERATAN SULFATE DEGRADATION	23	0,00005	0.05783 (+)
113	REACTOME METABOLISM OF PROTEINS	857	0,00005	< 0.005 (-)
114	REACTOME NONSENSE MEDIATED DECAY ENHANCED BY THE EXON JUNCTION COMPLEX	187	0,00005	< 0.005 (-)
115	REACTOME PEPTIDE CHAIN ELONGATION	148	0,00005	< 0.005 (-)
116	REACTOME PLATELET ADHESION TO EXPOSED COLLAGEN	31	0,00005	< 0.005 (+)
117	REACTOME SIGNALING BY PDGF	340	0,00005	0.05783 (+)

118	REACTOME SRP DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO MEMBRANE	190	0,00005	< 0.005 (-)
119	BIOCARTA CARDIACEGF PATHWAY	54	0,00012	0.05783 (+)
120	REACTOME TRANSLATION	279	0,00025	< 0.005 (-)
121	REACTOME INFLUENZA LIFE CYCLE	276	0,0038	< 0.005 (-)
122	REACTOME GLYCOPROTEIN HORMONES	13	0,00809	0.05783 (+)
123	REACTOME FORMATION OF THE TERNARY COMPLEX AND SUBSEQUENTLY THE 43S COMPLEX	97	0,01713	< 0.005 (-)
124	REACTOME ACTIVATION OF THE MRNA UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS AND SUBSEQUENT BINDING TO 43S	113	0,02187	< 0.005 (-)
125	REACTOME FORMATION OF ATP BY CHEMIOSMOTIC COUPLING	30	0,03646	< 0.005 (-)