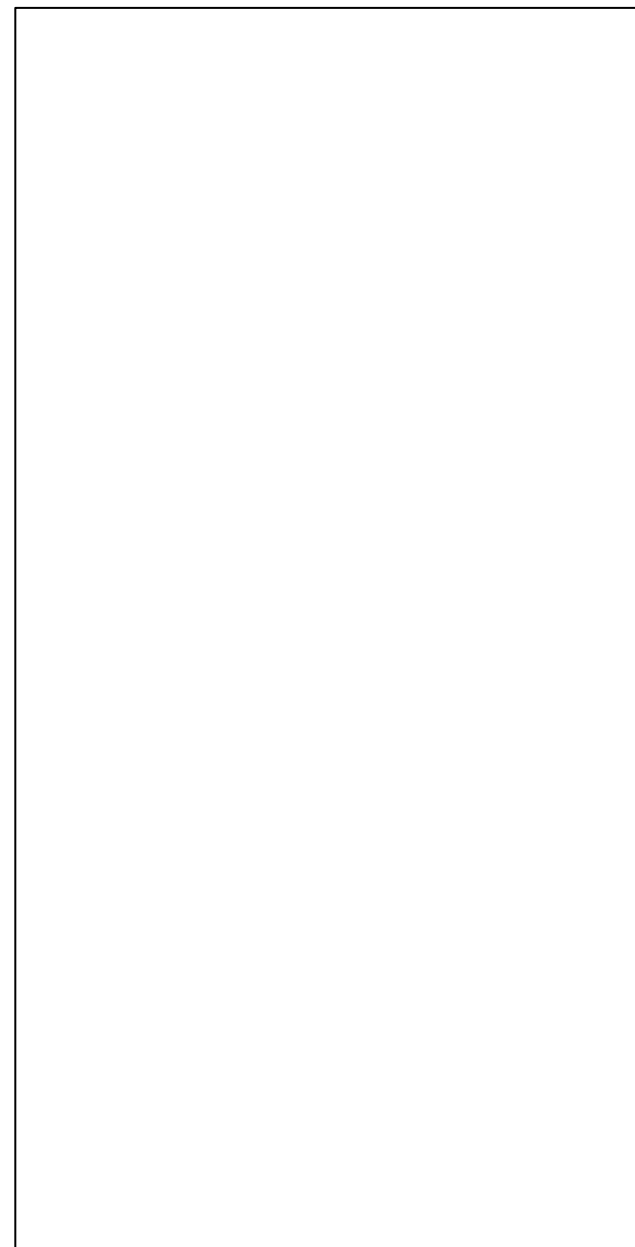
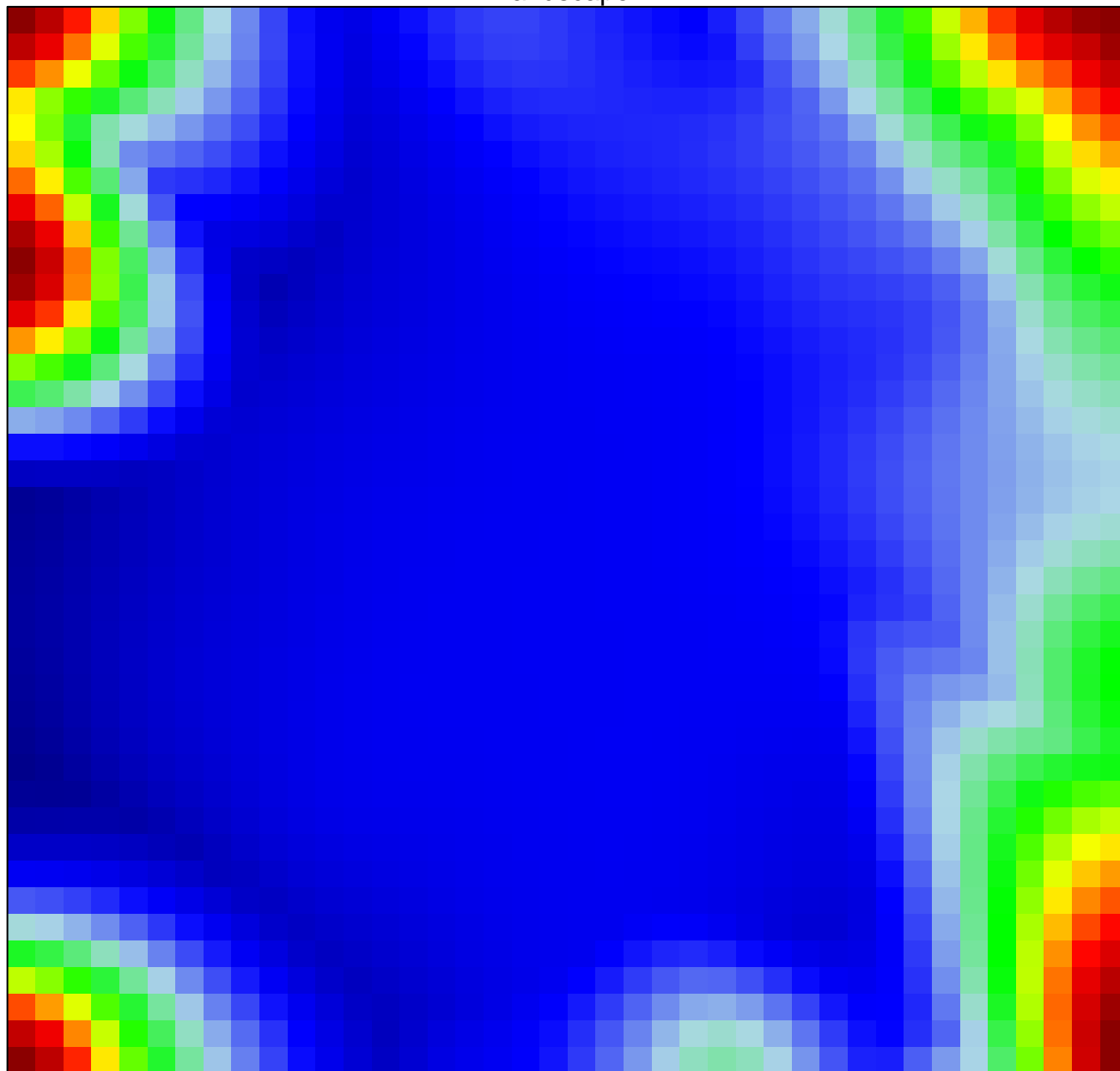


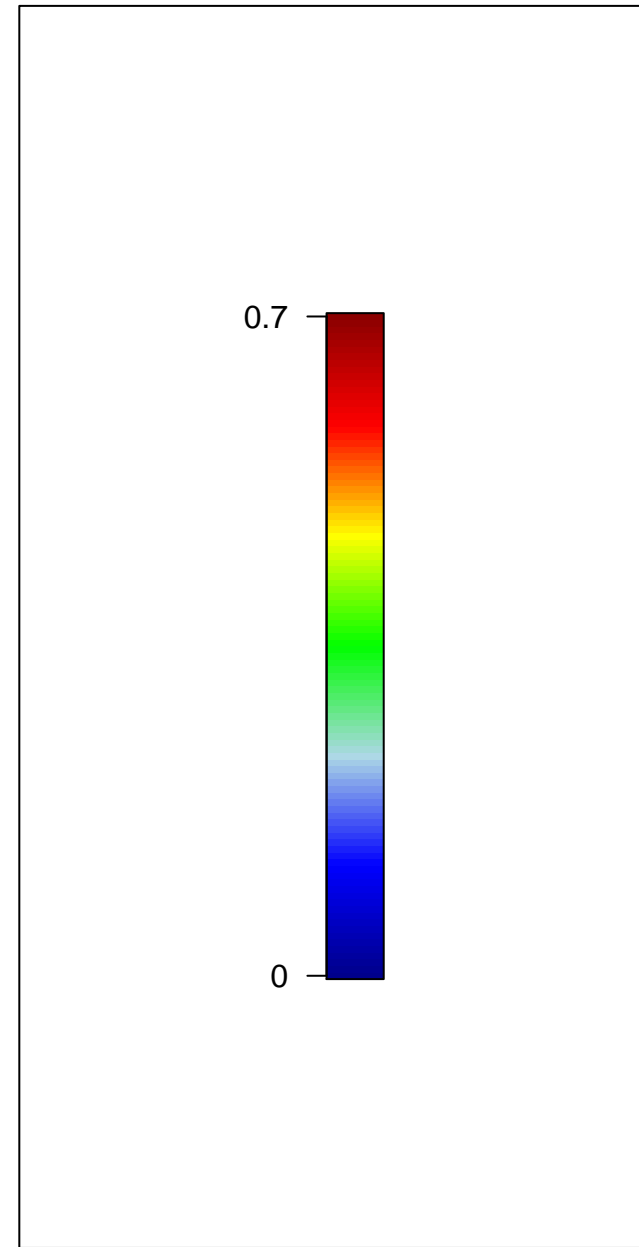
Group Overexpression Spots

landscape



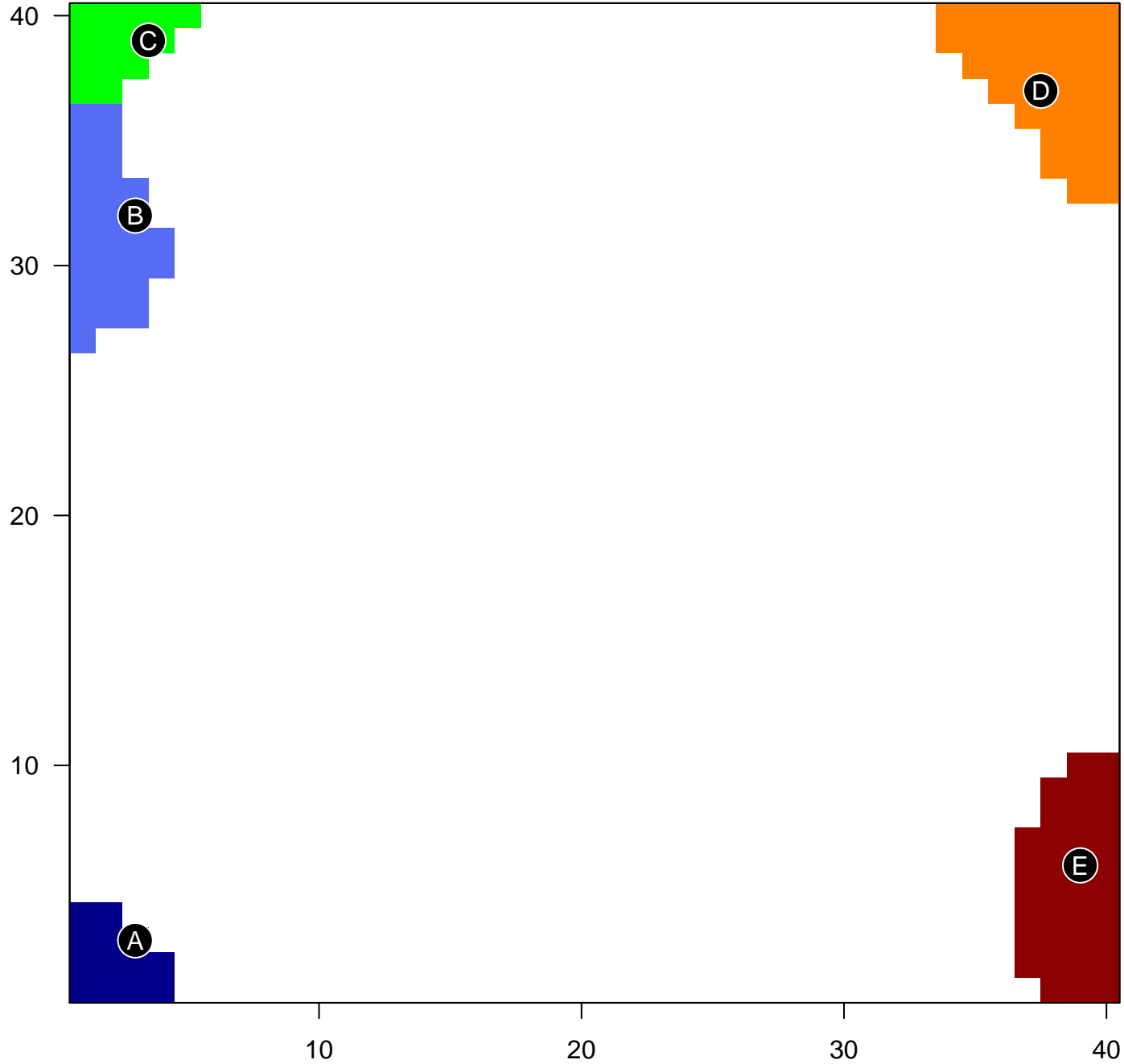
Group Overexpression Spots

beta-scores



Group Overexpression Spots

annotation



- A ■ Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_0
WIRTH_Immune system
SMID_BREAST_CANCER_NORMAL_LIKE_UP
- B ■ SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
LINDGREN_BLADDER_CANCER_CLUSTER_2B
extracellular space
- C ■ LIU_PROSTATE_CANCER_DN
Marisa_CRC-cluster-b
LIM_MAMMARY_STEM_CELL_UP
- D ■ GRADE_COLON_CANCER_UP
structural constituent of ribosome
translation
- E ■ WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCH
Pentrack_CRC_TCGA_group.over_A_normal_UP



A

B

C

D

E

Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN

WIRTH_Immune system

SMID_BREAST_CANCER_NORMAL_LIKE_UP

SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP

LINDGREN_BLADDER_CANCER_CLUSTER_2B

extracellular space

LIU_PROSTATE_CANCER_DN

Marisa_CRC-cluster-b

LIM_MAMMARY_STEM_CELL_UP

GRADE_COLON_CANCER_UP

structural constituent of ribosome

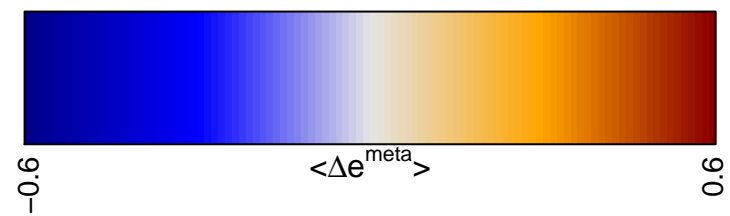
translation

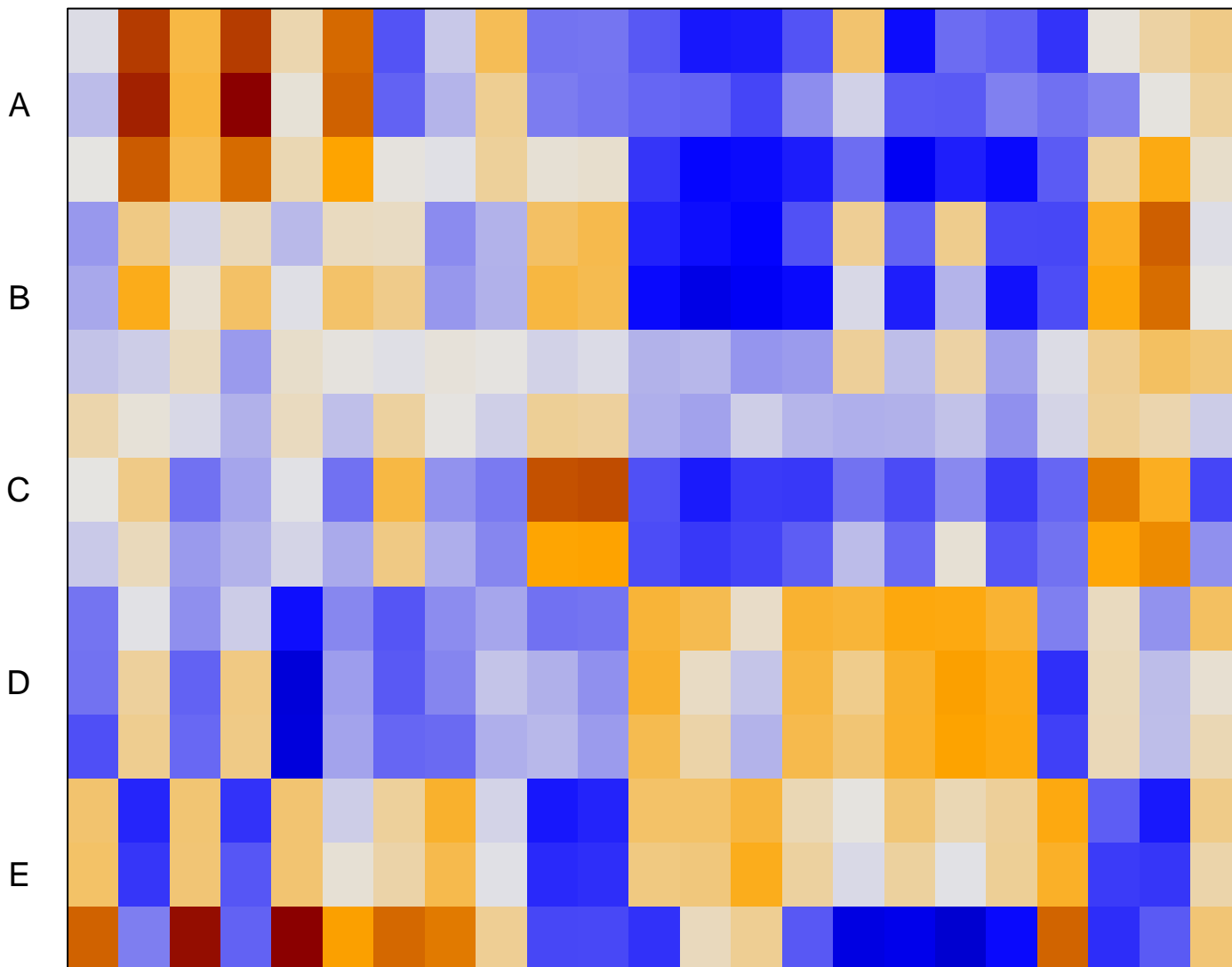
WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP

CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP

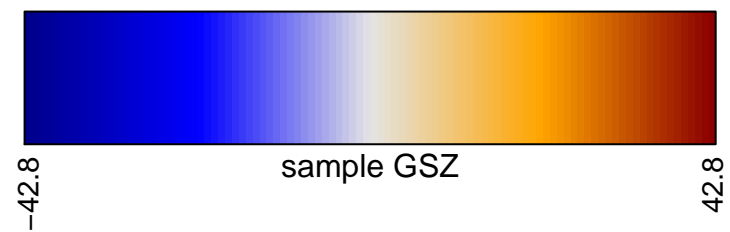
Pentrack_CRC_TCGA_group.over_A_normal_UP

02.0015.002_nH
 02.4535.001_nH
 02.4615.001_nH
 04.1134.015_nH
 04.1195.001_nH
 C31921_nH
 02.2351.003_nH
 02.4920.001_nH
 04.1045.021_nH
 04.3047.001_nH
 11_nH
 02.0015.002_aH
 04.1195.001_aH
 04.1045.021_aH
 02.4535.001_cH
 02.4615.001_cH
 04.1134.015_cH
 04.1195.001_cH
 C31921_cH
 02.2351.003_cH
 02.4920.001_cH
 04.3047.001_cH
 11_cH





- Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
- WIRTH_Immune system
- SMID_BREAST_CANCER_NORMAL_LIKE_UP
- SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
- LINDGREN_BLADDER_CANCER_CLUSTER_2B
- extracellular space
- LIU_PROSTATE_CANCER_DN
- Marisa_CRC-cluster-b
- LIM_MAMMARY_STEM_CELL_UP
- GRADE_COLON_CANCER_UP
- structural constituent of ribosome
- translation
- WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
- CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
- Pentrack_CRC_TCGA_group.over_A_normal_UP



Group Overexpression Spot

Spot Summary: A

metagenes = 13
genes = 262

<r> metagenes = 0.99

<r> genes = 0.77

beta: r2= 0.44 / log p= -3.23

samples with spot = 3 (13 %)

MLH1_normHNPCC : 3 (50 %)

Spot Genelist

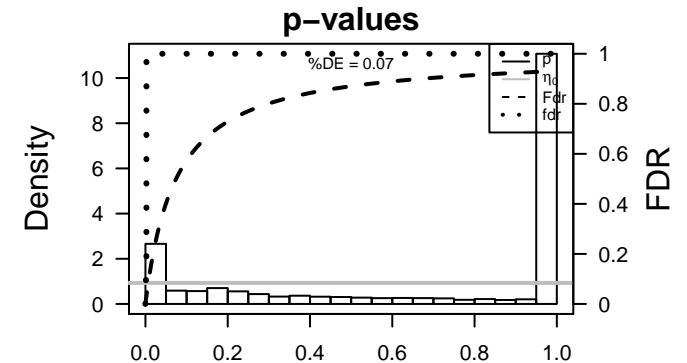
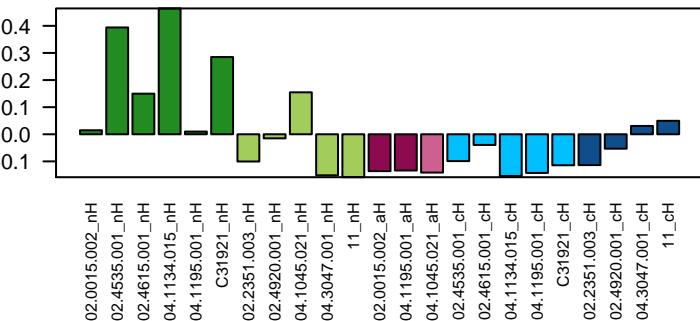
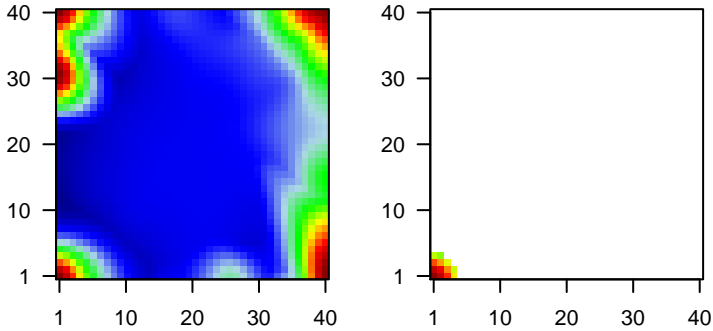
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG0000001	1.4	-0.53	0.84	FDCSP follicular dendritic cell secreted protein [Source:HGNC Symbc
2	ENSG0000001	1.34	-0.7	0.91	CCL21 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc
3	ENSG0000001	1.14	-0.59	0.93	CCL19 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
4	ENSG0000001	1.14	-0.52	0.93	CXCL13 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;f
5	ENSG0000002	1.11	-0.68	0.47	UBD ubiquitin D [Source:HGNC Symbol;Acc:HGNC:18795]
6	ENSG0000001	1.01	-0.54	0.94	CD52 CD52 molecule [Source:HGNC Symbol;Acc:HGNC:1804]
7	ENSG0000001	0.95	-0.25	0.94	CR2 complement component (3d/Epstein Barr virus) receptor 2 [S
8	ENSG0000002	0.95	-0.72	0.5	MT-RNR2-like 2 [Source:HGNC Symbol;Acc:HGNC:37156]
9	ENSG0000001	0.93	-0.22	0.98	CCR7 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac
10	ENSG0000001	0.89	-0.51	0.94	CXCR4 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
11	ENSG0000001	0.85	-0.35	0.97	LCP1 lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Syr
12	ENSG0000002	0.85	-0.8	0.45	MT-RNR2-like 9 [Source:HGNC Symbol;Acc:HGNC:37166]
13	ENSG0000001	0.85	-0.2	0.92	IL7R interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:602
14	ENSG0000001	0.84	-0.29	0.97	MS4A1 membrane-spanning 4-domains, subfamily A, member 1 [So
15	ENSG0000001	0.83	-0.25	0.94	GIMAP7 GTPase, IMAP family member 7 [Source:HGNC Symbol;Acc:
16	ENSG0000001	0.82	-0.25	0.93	ETS1 v-ets avian erythroblastosis virus E26 oncogene homolog 1 [
17	ENSG0000001	0.82	-0.39	0.93	CD79A CD79a molecule, immunoglobulin-associated alpha [Source:
18	ENSG0000001	0.81	-0.24	0.98	FCMR Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGf
19	ENSG0000000	0.8	-0.2	0.97	PTPRC protein tyrosine phosphatase, receptor type, C [Source:HGNC
20	ENSG0000001	0.79	-0.35	0.98	CD53 CD53 molecule [Source:HGNC Symbol;Acc:HGNC:1686]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	142 / 844	Colon Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	4e-94	97 / 427	Tissu WIRTH_Immune system
3	3e-81	89 / 436	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
4	4e-70	89 / 574	Canci Lembcke_Colonc Inflammation
5	9e-69	68 / 263	GSE/ WALLACE_PROSTATE_CANCER_RACE_UP
6	6e-59	54 / 175	GSE/ LEE_DIFFERENTIATING_T_LYMPHOCYTE
7	2e-51	53 / 220	GSE/ MCLACHLAN_DENTAL_CARIES_UP
8	4e-50	55 / 259	GSE/ POOLA_INVASIVE_BREAST_CANCER_UP
9	1e-48	69 / 522	GSE/ SMID_BREAST_CANCER_LUMINAL_B_DN
10	6e-44	47 / 210	GSE/ MCLACHLAN_DENTAL_CARIES_DN
11	6e-42	54 / 343	BP immune response
12	7e-38	45 / 246	GSE/ QI_PLASMACYTOMA_UP
13	8e-35	199 / 7592	Lymp HOPP_Strong_enhancer
14	3e-33	48 / 368	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_2B
15	5e-30	23 / 51	GSE/ MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
16	4e-29	34 / 181	HM HALLMARK_ALLOGRAFT_REJECTION
17	7e-29	47 / 435	GSE/ RODWELL_AGING_KIDNEY_UP
18	3e-28	39 / 279	Glio WILLSCHER_GBM_Verhaak-CL & MES_up
19	8e-28	25 / 79	GSE/ FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
20	1e-27	15 / 16	CC MHC class II protein complex
21	5e-26	21 / 53	GSE/ KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN
22	8e-26	33 / 208	Tissu PALMER_B-Cell signature up
23	9e-24	23 / 86	GSE/ WIELAND_UP_BY_HBV_INFECTION
24	1e-23	23 / 87	GSE/ BASSO_CD40_SIGNALING_UP
25	1e-23	38 / 346	GSE/ SANSOM_APC_TARGETS_DN
26	5e-23	28 / 163	GSE/ PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
27	8e-23	31 / 218	GSE/ HOSHIDA_LIVER_CANCER_SUBCLASS_S1
28	1e-22	30 / 201	CC external side of plasma membrane
29	2e-22	18 / 45	GSE/ YU_MYC_TARGETS_DN
30	2e-22	20 / 64	BP T cell costimulation
31	4e-22	68 / 1340	GSE/ PUJANA_ATM_PCC_NETWORK
32	1e-21	22 / 92	BP T cell receptor signaling pathway
33	2e-21	21 / 82	GSE/ MORI_MATURE_B_LYMPHOCYTE_UP
34	3e-21	19 / 61	BP antigen processing and presentation
35	2e-20	61 / 1165	GSE/ CHEN_METABOLIC_SYNDROM_NETWORK
36	4e-20	51 / 823	GSE/ REACTOME_IMMUNE_SYSTEM
37	1e-19	28 / 215	GSE/ JAATINEN_HEMATOPOIETIC_STEM_CELL_DN
38	3e-19	35 / 381	GSE/ KUMAR_TARGETS_OF_MLL_AF9_FUSION
39	3e-19	145 / 5643	Lymp HOPP_Txn_transition
40	4e-19	38 / 466	Lymp SPANG_CD40 6hrs DN

Overview Map

Spot



Group Overexpression Spot

Spot Summary: B

metagenes = 27
genes = 348

<r> metagenes = 0.9

<r> genes = 0.6

beta: r2= 0.17 / log p= -1.27

samples with spot = 1 (4.3 %)

other_cancerHNPCC : 1 (25 %)

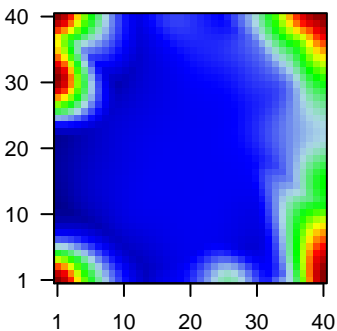
Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG000001	1.82	-0.23	0.87	FABP4 fatty acid binding protein 4, adipocyte [Source:HGNC Symbol]
2	ENSG000002	1.31	-0.26	0.9	GPX3 glutathione peroxidase 3 [Source:HGNC Symbol;Acc:HGNC:1044]
3	ENSG000002	1.17	-0.14	0.31	HBB hemoglobin, beta [Source:HGNC Symbol;Acc:HGNC:4827]
4	ENSG000001	1.11	-0.22	0.91	SFRP2 secreted frizzled-related protein 2 [Source:HGNC Symbol;Acc:HGNC:1044]
5	ENSG000001	1.02	-0.41	0.88	CTGF connective tissue growth factor [Source:HGNC Symbol;Acc:HGNC:1044]
6	ENSG000001	1.01	-0.27	0.73	BGN biglycan [Source:HGNC Symbol;Acc:HGNC:1044]
7	ENSG000001	1	-0.16	0.94	ADAMTS1 metalloproteinase with thrombospondin type 1 motif, 1
8	ENSG000000	0.98	-0.1	0.44	CHRDL2 chordin-like 2 [Source:HGNC Symbol;Acc:HGNC:24168]
9	ENSG000001	0.98	-0.25	0.59	SAA1 serum amyloid A1 [Source:HGNC Symbol;Acc:HGNC:10513]
10	ENSG000000	0.97	-0.57	0.81	VIM vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
11	ENSG000001	0.95	-0.62	0.77	DUSP1 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:1044]
12	ENSG000001	0.9	-0.24	0.81	FOSB FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:HGNC:1044]
13	ENSG000001	0.89	-0.09	0.81	ADIPOQ adiponectin, C1Q and collagen domain containing [Source:HGNC Symbol;Acc:HGNC:1044]
14	ENSG000001	0.87	-0.18	0.94	C11orf96 chromosome 11 open reading frame 96 [Source:HGNC Symbol;Acc:HGNC:1044]
15	ENSG000001	0.86	-0.22	0.77	C10orf10 chromosome 10 open reading frame 10 [Source:HGNC Symbol;Acc:HGNC:1044]
16	ENSG000001	0.86	-0.19	0.79	G0S2 G0/G1 switch 2 [Source:HGNC Symbol;Acc:HGNC:30229]
17	ENSG000001	0.84	-0.09	0.92	RBP7 retinol binding protein 7, cellular [Source:HGNC Symbol;Acc:HGNC:1044]
18	ENSG000001	0.83	-0.15	0.83	SERPINE1 serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1)
19	ENSG000001	0.83	-0.21	0.83	ADH1B alcohol dehydrogenase 1B (class I), beta polypeptide [Source:HGNC Symbol;Acc:HGNC:1044]
20	ENSG000002	0.82	-0.11	0.88	MUSTN1 musculoskeletal, embryonic nuclear protein 1 [Source:HGNC Symbol;Acc:HGNC:1044]

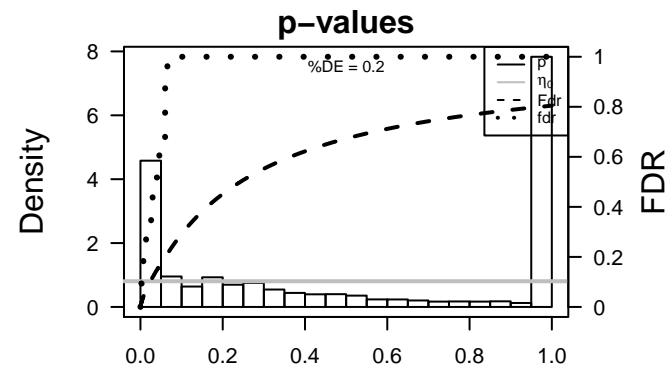
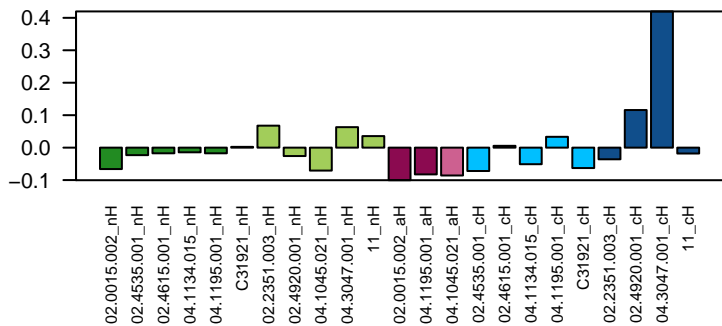
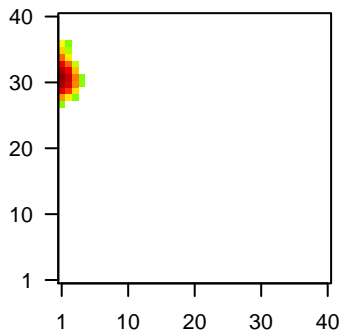
Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-50	66 / 326	GSE/ SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	7e-42	62 / 368	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_2B
3	2e-37	96 / 1176	CC extracellular space
4	3e-37	46 / 202	CC extracellular matrix
5	6e-36	85 / 945	GSE/ NABA_MATRISOME
6	3e-35	73 / 692	GSE/ WONG_ADULT_TISSUE_STEM_MODULE
7	1e-34	53 / 332	Color Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
8	3e-34	48 / 261	Lymph LENZ_Stromal signature 1
9	6e-34	43 / 198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
10	4e-33	65 / 574	Cancer Lembocke_Colonc Inflammation
11	6e-33	42 / 196	GSE/ PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
12	9e-33	62 / 522	GSE/ SMID_BREAST_CANCER_LUMINAL_B_DN
13	1e-32	56 / 413	GSE/ BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP
14	3e-30	57 / 478	GSE/ LIM_MAMMARY_STEM_CELL_UP
15	2e-29	47 / 314	Lymph Hopp_June14_MMML937_tumors+controls_group.overexpression_E_GC-DN
16	3e-29	47 / 315	Lymph WIRTH_lymphoma937_spot E
17	6e-29	58 / 525	GSE/ WEST_ADRENOCORTICAL_TUMOR_DN
18	2e-28	38 / 192	HM HALLMARK_TNFA_SIGNALING_VIA_NFKB
19	2e-28	42 / 249	GSE/ BOQUEST_STEM_CELL_UP
20	1e-27	42 / 261	GSE/ NABA_CORE_MATRISOME
21	1e-27	52 / 436	GSE/ SMID_BREAST_CANCER_NORMAL_LIKE_UP
22	2e-27	51 / 418	GSE/ SWEET_LUNG_CANCER_KRAS_DN
23	6e-27	89 / 1374	CC extracellular region
24	4e-26	24 / 62	GSE/ ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
25	1e-24	47 / 401	GSE/ REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
26	3e-24	27 / 101	GSE/ CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP
27	4e-24	35 / 204	GSE/ BOQUEST_STEM_CELL_DN
28	1e-23	22 / 59	Lymph LENZ_Stromal signature 2
29	2e-23	52 / 535	GSE/ CHICAS_RB1_TARGETS_CONFLUENT
30	3e-23	37 / 248	GSE/ ONDER_CDH1_TARGETS_2_UP
31	4e-23	42 / 337	Color Pentrack_CRC_TCGA_group.over_B_msi-h_UP
32	5e-23	30 / 148	Color Marisa_CRC-cluster-a
33	7e-23	38 / 270	CC proteinaceous extracellular matrix
34	1e-22	35 / 224	BP angiogenesis
35	1e-22	47 / 445	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
36	6e-22	23 / 78	GSE/ NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_DN
37	2e-21	27 / 126	GSE/ ZHU_CMV_ALL_DN
38	9e-21	21 / 67	GSE/ TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP
39	3e-19	54 / 711	GSE/ LEE_BMP2_TARGETS_UP
40	4e-19	36 / 306	BP extracellular matrix organization

Overview Map



Spot



Group Overexpression Spot

Spot Summary: C

metagenes = 14
genes = 300

<r> metagenes = 0.99

<r> genes = 0.81

beta: r2= 0.69 / log p= -6.02

samples with spot = 4 (17.4 %)

other_normHNPCC : 2 (40 %)

other_cancerHNPCC : 2 (50 %)

Spot Genelist

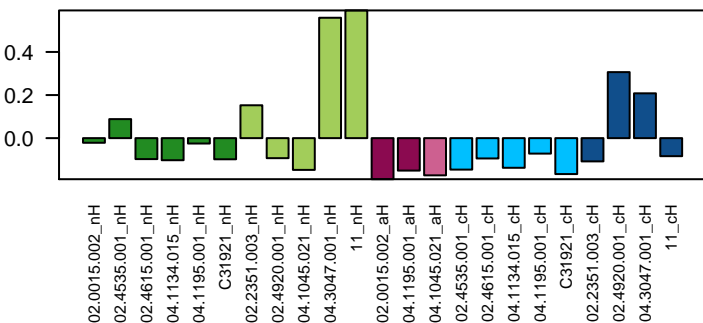
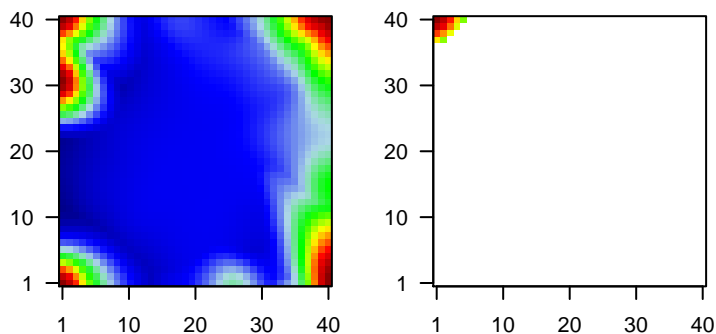
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG0000001	1.59	-0.8	0.87	DES desmin [Source:HGNC Symbol;Acc:HGNC:2770]
2	ENSG0000001	1.46	-0.53	0.95	MYH11 myosin, heavy chain 11, smooth muscle [Source:HGNC Syml
3	ENSG0000001	1.44	-0.52	0.94	CNN1 calponin 1, basic, smooth muscle [Source:HGNC Symbol;Acc
4	ENSG0000001	1.42	-0.68	0.92	ACTG2 actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
5	ENSG0000002	1.37	-0.24	0.43	MTRNR2MF-RNR2-like 1 [Source:HGNC Symbol;Acc:HGNC:37155]
6	ENSG0000001	1.35	-0.91	0.9	MYL9 myosin, light chain 9, regulatory [Source:HGNC Symbol;Acc:I
7	ENSG0000001	1.32	-0.37	0.97	SYNM synemin, intermediate filament protein [Source:HGNC Symbc
8	ENSG0000001	1.3	-0.58	0.96	FLNA filamin A, alpha [Source:HGNC Symbol;Acc:HGNC:3754]
9	ENSG0000001	1.29	-0.49	0.95	TPM2 tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:120
10	ENSG0000001	1.24	-0.52	0.72	IGFBP7 insulin-like growth factor binding protein 7 [Source:HGNC Sy
11	ENSG0000001	1.21	-0.38	0.98	CSRP1 cysteine and glycine-rich protein 1 [Source:HGNC Symbol;A
12	ENSG0000001	1.2	-0.74	0.92	TAGLN transgelin [Source:HGNC Symbol;Acc:HGNC:11553]
13	ENSG0000000	1.17	-0.45	0.95	HSPB6 heat shock protein, alpha-crystallin-related, B6 [Source:HG
14	ENSG0000000	1.17	-0.25	0.96	NDE1 nudE neurodevelopment protein 1 [Source:HGNC Symbol;Ac
15	ENSG0000001	1.17	-0.39	0.99	CALD1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
16	ENSG0000000	1.17	-0.4	0.97	FHL1 four and a half LIM domains 1 [Source:HGNC Symbol;Acc:HK
17	ENSG0000001	1.17	-0.36	0.98	LMOD1 leiomodin (smooth muscle) [Source:HGNC Symbol;Acc:HG
18	ENSG0000001	1.14	-0.57	0.94	ACTA2 actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;
19	ENSG0000000	1.14	-0.3	0.98	MYLK myosin light chain kinase [Source:HGNC Symbol;Acc:HGNC:
20	ENSG0000001	1.12	-0.31	0.98	PLN phospholamban [Source:HGNC Symbol;Acc:HGNC:9080]

Geneset Overrepresentation

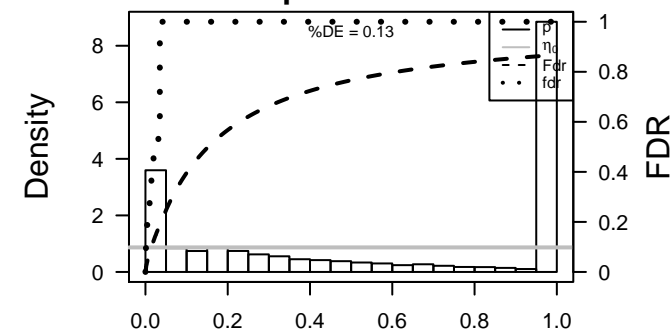
Rank	p-value	#in/all	Geneset
1	3e-68	5 / 16	Cancer LIU_PROSTATE_CANCER_DN
2	3e-63	54 / 132	Colon Marisa_CRC-cluster-b
3	1e-45	68 / 478	GSE# LIM_MAMMARY_STEM_CELL_UP
4	4e-45	57 / 303	GSE# PASINI_SUZ12_TARGETS_DN
5	1e-42	59 / 368	GSE# LINDGREN_BLADDER_CANCER_CLUSTER_2B
6	2e-42	68 / 535	GSE# CHICAS_RB1_TARGETS_CONFLUENT
7	5e-37	43 / 196	GSE# PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
8	1e-32	46 / 294	GSE# ACEVEDO_FGFR1_TARGETS_IN_PROSTATE_CANCER_MODEL_DN
9	2e-31	36 / 160	GSE# BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN
10	2e-30	52 / 445	GSE# CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
11	9e-30	62 / 692	GSE# WONG_ADULT_TISSUE_STEM_MODULE
12	2e-29	45 / 326	GSE# SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
13	4e-28	40 / 261	Lymp LENZ_Stromal signature 1
14	5e-28	36 / 198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
15	5e-27	42 / 314	Lymp Hopp_June14_MMML937_tumors+controls_group.overexpression_E_GC-
16	6e-27	42 / 315	Lymp WIRTH_lymphoma937_spot E
17	1e-26	45 / 378	CC focal adhesion
18	8e-26	46 / 418	GSE# SWEET_LUNG_CANCER_KRAS_DN
19	1e-24	33 / 195	HM HALLMARK_MYOGENESIS
20	3e-24	19 / 40	GSE# TOMLINS_PROSTATE_CANCER_DN
21	8e-24	43 / 399	Disea GUDJ_pсориаzis down
22	2e-23	48 / 525	GSE# WEST_ADRENOCORTICAL_TUMOR_DN
23	5e-23	37 / 292	GSE# CHANDRAN_METASTASIS_DN
24	2e-22	54 / 711	GSE# LEE_BMP2_TARGETS_UP
25	2e-22	34 / 248	GSE# ONDER_CDH1_TARGETS_2_UP
26	1e-20	14 / 22	GSE# REACTOME_SMOOTH_MUSCLE_CONTRACTION
27	3e-20	33 / 267	GSE# WANG_SMARCE1_TARGETS_UP
28	4e-19	16 / 40	GSE# PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_DN
29	6e-19	22 / 105	BP muscle contraction
30	8e-18	24 / 148	Color Marisa_CRC-cluster-a
31	5e-17	26 / 195	GSE# KEGG_FOCAL_ADHESION
32	5e-17	29 / 254	GSE# LU_AGING_BRAIN_UP
33	6e-17	23 / 144	GSE# IGLESIAS_E2F_TARGETS_UP
34	8e-17	145 / 5039	Lymp HOPP_Repressed
35	8e-17	15 / 44	GSE# REACTOME_MUSCLE_CONTRACTION
36	1e-16	31 / 306	BP extracellular matrix organization
37	2e-16	28 / 246	GSE# DANG_REGULATED_BY_MYC_DN
38	2e-16	31 / 313	GSE# KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
39	3e-16	11 / 18	GSE# NIELSEN_LEIOMYOSARCOMA_CNN1_UP
40	3e-16	35 / 413	GSE# BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP

Overview Map

Spot



p-values



Group Overexpression Spot

Spot Summary: D

metagenes = 37
genes = 753

<r> metagenes = 0.93
<r> genes = 0.55
beta: r2= 0.2 / log p= -1.48

samples with spot = 3 (13 %)
MLH1_adenomaHNPCC : 1 (50 %)
MLH1_cancerHNPCC : 2 (40 %)

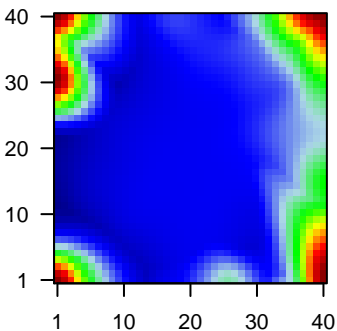
Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG00000001	1.84	-0.57	0.58	REG1A regenerating islet-derived 1 alpha [Source:HGNC Symbol;Acc:HGNC:17190]
2	ENSG00000001	1.71	-0.34	0.47	ITLN1 intelectin 1 (galactofuranose binding) [Source:HGNC Symbol;Acc:HGNC:17190]
3	ENSG00000001	1.65	-0.75	0.58	OLFM4 olfactomedin 4 [Source:HGNC Symbol;Acc:HGNC:17190]
4	ENSG00000001	1.57	-0.24	0.59	REG3A regenerating islet-derived 3 alpha [Source:HGNC Symbol;Acc:HGNC:17190]
5	ENSG00000001	1.47	-0.28	0.64	MMP1 matrix metalloproteinase 1 [Source:HGNC Symbol;Acc:HGNC:17190]
6	ENSG00000001	1.33	-0.75	0.34	PLA2G2A phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:17190]
7	ENSG00000001	1.31	-0.29	0.4	CXCL8 chemokine (C-X-C motif) ligand 8 [Source:HGNC Symbol;Acc:HGNC:17190]
8	ENSG00000001	1.27	-0.21	0.53	REG1B regenerating islet-derived 1 beta [Source:HGNC Symbol;Acc:HGNC:17190]
9	ENSG00000001	1.25	-0.21	0.56	DMBT1 deleted in malignant brain tumors 1 [Source:HGNC Symbol;Acc:HGNC:17190]
10	ENSG00000001	1.17	-0.36	0.44	REG4 regenerating islet-derived family, member 4 [Source:HGNC Symbol;Acc:HGNC:17190]
11	ENSG00000001	1.16	-0.2	0.63	MMP3 matrix metalloproteinase 3 [Source:HGNC Symbol;Acc:HGNC:17190]
12	ENSG00000001	1.15	-0.44	0.7	SPINK1 serine peptidase inhibitor, Kazal type 1 [Source:HGNC Symbol;Acc:HGNC:17190]
13	ENSG00000000	1.15	-0.35	0.46	CLCA1 chloride channel accessory 1 [Source:HGNC Symbol;Acc:HGNC:17190]
14	ENSG00000002	1.1	-0.18	0.56	TNFRSF6B tumor necrosis factor receptor superfamily, member 6b, decoy [Source:HGNC Symbol;Acc:HGNC:17190]
15	ENSG00000001	1.05	-0.66	0.81	LCN2 lipocalin 2 [Source:HGNC Symbol;Acc:HGNC:6526]
16	ENSG00000001	1.05	-0.87	0.71	AGR2 anterior gradient 2, protein disulphide isomerase family member 2 [Source:HGNC Symbol;Acc:HGNC:17190]
17	ENSG00000001	0.98	-0.17	0.41	SPP1 secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:17190]
18	ENSG00000001	0.97	-0.41	0.59	SPINK4 serine peptidase inhibitor, Kazal type 4 [Source:HGNC Symbol;Acc:HGNC:17190]
19	ENSG00000001	0.91	-1	0.68	GPX2 glutathione peroxidase 2 [Source:HGNC Symbol;Acc:HGNC:17190]
20	ENSG00000001	0.87	-0.25	0.5	CYP2S1 cytochrome P450, family 2, subfamily S, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:17190]

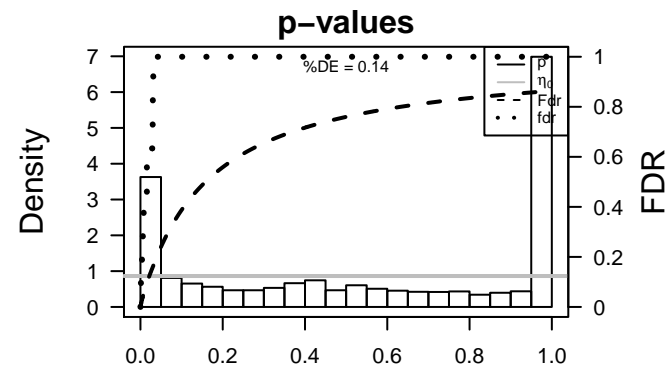
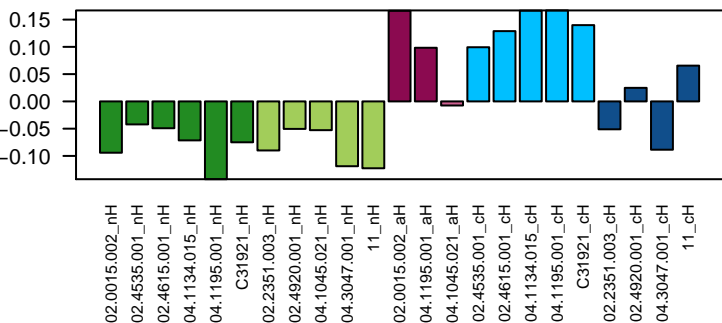
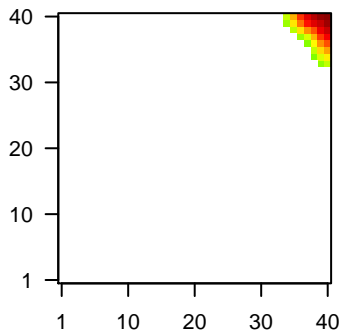
Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-99	195 / 813	GSE# GRADE_COLON_CANCER_UP
2	1e-91	95 / 162	MF structural constituent of ribosome
3	5e-90	113 / 259	BP translation
4	1e-88	171 / 713	Colon Pentrack_CRC_TCGA_group.over_C_normal_DN
5	5e-84	152 / 582	GSE# CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	2e-77	87 / 168	CC ribosome
7	4e-77	73 / 108	BP SRP-dependent cotranslational protein targeting to membrane
8	5e-77	163 / 754	GSE# MARTENS_TRETINOIN_RESPONSE_DN
9	1e-76	113 / 327	GSE# WONG_EMBRYONIC_STEM_CELL_CORE
10	6e-76	230 / 1563	GSE# PUJANA_BRCA1_PCC_NETWORK
11	4e-75	80 / 142	GSE# REACTOME_TRANSLATION
12	8e-75	66 / 88	BP translational termination
13	2e-73	69 / 101	BP translational elongation
14	2e-73	70 / 105	GSE# REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING
15	5e-73	69 / 102	GSE# REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION
16	1e-70	62 / 82	GSE# REACTOME_PEPTIDE_CHAIN_ELONGATION
17	2e-69	62 / 84	GSE# KEGG_RIBOSOME
18	2e-67	85 / 195	HM HALLMARK_MYC_TARGETS_V1
19	1e-66	110 / 370	GSE# HSIAO_HOUSEKEEPING_GENES
20	3e-66	64 / 98	GSE# REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION
21	4e-66	74 / 142	BP translational initiation
22	2e-65	114 / 412	GSE# REACTOME_METABOLISM_OF_PROTEINS
23	6e-65	179 / 1091	MF poly(A) RNA binding
24	2e-63	65 / 109	BP viral transcription
25	6e-62	153 / 830	Color Pentrack_CRC_TCGA_corr_R_normal_DN
26	3e-61	62 / 102	GSE# REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EUKARYOTIC_TRANSLATION_MACHINERY
27	2e-60	65 / 117	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
28	2e-60	76 / 174	GSE# LI_AMPLIFIED_IN_LUNG_CANCER
29	2e-60	161 / 944	GSE# KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
30	8e-59	67 / 132	GSE# REACTOME_INFLUENZA_LIFE_CYCLE
31	8e-59	131 / 633	BP cellular protein metabolic process
32	3e-58	141 / 747	GSE# PUJANA_CHEK2_PCC_NETWORK
33	5e-57	527 / 8123	Color TssF_Colon
34	6e-57	68 / 144	BP viral life cycle
35	3e-56	144 / 807	Lymp Hopp_June14_MMM1937_tumors+controls_group.overexpression_D_cell_line
36	2e-54	142 / 811	Lymp WIRTH_lymphoma937_spot_D
37	3e-52	80 / 242	GSE# REACTOME_METABOLISM_OF_RNA
38	1e-51	73 / 198	GSE# REACTOME_METABOLISM_OF_MRNA
39	2e-51	93 / 350	GSE# RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN
40	1e-50	83 / 275	GSE# GRADE_COLON_AND_RECTAL_CANCER_UP

Overview Map



Spot



Group Overexpression Spot

Spot Summary: E

metagenes = 35
genes = 581

<r> metagenes = 0.93

<r> genes = 0.57

beta: r2= 0.46 / log p= -3.46

samples with spot = 5 (21.7 %)

MLH1_normHNPCC : 2 (33.3 %)

other_normHNPCC : 1 (20 %)

other_adenomaHNPCC : 1 (100 %)

other_cancerHNPCC : 1 (25 %)

Spot Genelist

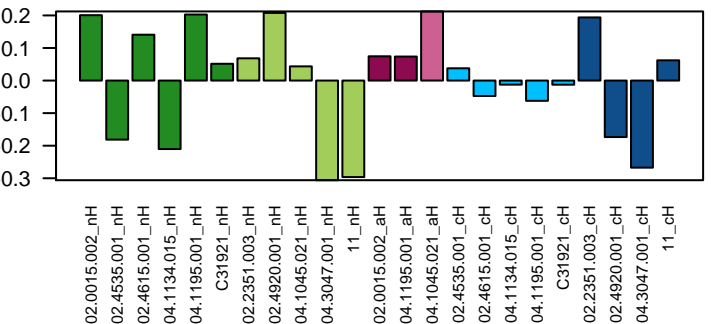
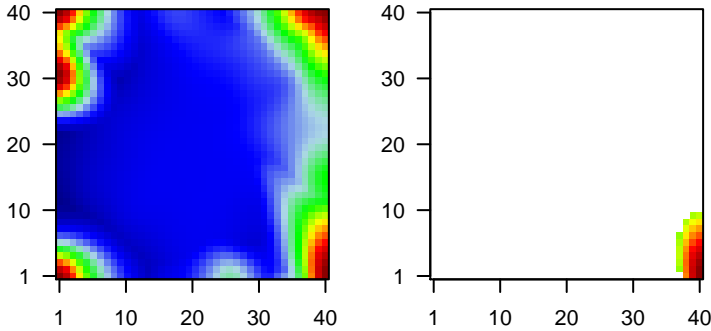
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSG000002	1.55	-0.86	0.83	PHGR1 proline/histidine/glycine-rich 1 [Source:HGNC Symbol;Acc:HGNC:11755]
2	ENSG000001	1.42	-0.99	0.76	GUCA2Aguanylate cyclase activator 2A (guanylin) [Source:HGNC Symbol;Acc:HGNC:11755]
3	ENSG000001	1.33	-0.38	0.41	PP7080 uncharacterized LOC25845 [Source:EntrezGene;Acc:25845]
4	ENSG000001	1.3	-0.63	0.61	AQP8 aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
5	ENSG000001	1.28	-0.52	0.58	ANPEP alanyl (membrane) aminopeptidase [Source:HGNC Symbol;Acc:HGNC:11755]
6	ENSG000000	1.26	-0.59	0.55	CLCA4 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:11755]
7	ENSG000000	1.24	-0.81	0.73	SLC26A3solute carrier family 26 (anion exchanger), member 3 [Source:HGNC Symbol;Acc:HGNC:11755]
8	ENSG000000	1.24	-0.99	0.73	CEACAM6carcinoembryonic antigen-related cell adhesion molecule 7 [Source:HGNC Symbol;Acc:HGNC:11755]
9	ENSG000001	1.24	-0.49	0.64	ZG16 zymogen granule protein 16 [Source:HGNC Symbol;Acc:HGNC:11755]
10	ENSG000000	1.22	-0.52	0.67	GUCA2Bguanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:11755]
11	ENSG000001	1.21	-0.51	0.71	TFF1 trefoil factor 1 [Source:HGNC Symbol;Acc:HGNC:11755]
12	ENSG000001	1.2	-0.44	0.66	PRAP1 proline-rich acidic protein 1 [Source:HGNC Symbol;Acc:HGNC:11755]
13	ENSG000002	1.15	-0.61	0.74	PHGR1 proline/histidine/glycine-rich 1 [Source:HGNC Symbol;Acc:HGNC:11755]
14	ENSG000001	1.13	-1.09	0.83	FABP1 fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:HGNC:11755]
15	ENSG000001	1.12	-0.37	0.66	AKR1B10aldo-keto reductase family 1, member B10 (aldose reductase) [Source:HGNC Symbol;Acc:HGNC:11755]
16	ENSG000001	1.1	-0.7	0.67	PI3 peptidase inhibitor 3, skin-derived [Source:HGNC Symbol;Acc:HGNC:11755]
17	ENSG000001	1.06	-1.31	0.7	PIGR polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:HGNC:11755]
18	ENSG000001	1.02	-1.15	0.72	CEACAM6carcinoembryonic antigen-related cell adhesion molecule 5 [Source:HGNC Symbol;Acc:HGNC:11755]
19	ENSG000001	1	-0.96	0.82	KRT20 keratin 20, type I [Source:HGNC Symbol;Acc:HGNC:20412]
20	ENSG000001	1	-0.35	0.68	C11orf86chromosome 11 open reading frame 86 [Source:HGNC Symt

Geneset Overrepresentation

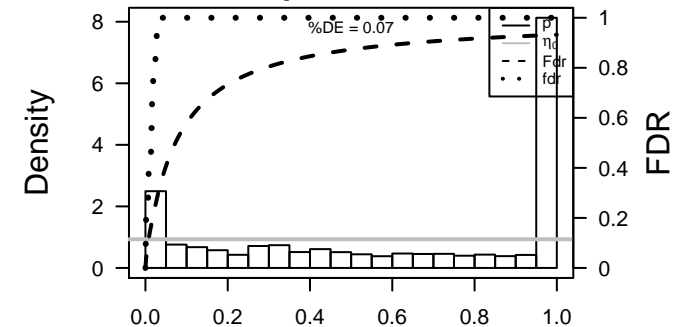
Rank	p-value	#in/all	Geneset
1	2e-52	74 / 251	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_LMP_UP
2	5e-49	89 / 429	GSE/ CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP
3	4e-48	50 / 104	Colon Pentrack_CRC_TCGA_group.over_A_normal_UP
4	6e-47	237 / 3122	Colon TxEnhG1_Colon
5	2e-45	213 / 2638	CC extracellular exosome
6	1e-44	64 / 222	GSE/ COLDREN_GEFITINIB_RESISTANCE_DN
7	7e-42	88 / 507	Colon Pentrack_CRC_TCGA_corr_C_normal_UP
8	8e-41	79 / 412	GSE/ LIM_MAMMARY_STEM_CELL_DN
9	1e-37	79 / 455	GSE/ ONDER_CDH1_TARGETS_2_DN
10	3e-32	142 / 1624	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_UP
11	4e-32	101 / 877	Colon TxEnhG2_Colon
12	3e-31	207 / 3112	Colon EnhA_Colon
13	6e-31	54 / 248	GSE/ JAEGER_METASTASIS_DN
14	5e-30	40 / 126	GSE/ VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN
15	8e-30	83 / 643	Colon Lembcke_TCGA_meth_kmeans_J_CIMP_H_DN
16	2e-29	478 / 11791	Color Enh_Colon
17	1e-28	41 / 144	Lymp WIRTH_lymphoma937_spot G
18	8e-28	40 / 142	Lymp Hopp_June14_MMML937_tumors+controls_group.overexpression_G_tonsil
19	2e-27	425 / 9930	Color Tx_Colon
20	1e-26	81 / 682	GSE/ CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_3
21	1e-24	294 / 5889	Color EnhWk1_Colon
22	4e-24	48 / 261	GSE/ MCBRYAN_PUBERTAL_BREAST_4_5WK_UP
23	6e-24	36 / 137	Tissu WIRTH_Mucosa
24	2e-23	35 / 132	GSE/ WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_UP
25	2e-23	33 / 115	GSE/ CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP
26	6e-23	32 / 110	Color Marisa_CRC-cluster-h
27	3e-22	359 / 8123	Color TssF_Colon
28	2e-21	38 / 181	GSE/ WU_CELL_MIGRATION
29	2e-19	57 / 467	GSE/ SWEET_LUNG_CANCER_KRAS_UP
30	3e-19	419 / 10475	Color TssA_Colon
31	3e-18	57 / 495	GSE/ ENK_UV_RESPONSE KERATINOCYTE_UP
32	1e-17	303 / 6761	Color TssD2_Colon
33	3e-17	51 / 424	GSE/ DELYS_THYROID_CANCER_UP
34	7e-17	62 / 616	Color Lembcke_TCGA-expr_kmeans_M_CIMP_H_DN
35	1e-16	61 / 608	Disea GUDJ_psooriasis up
36	4e-16	66 / 711	GSE/ LEE_BMP2_TARGETS_UP
37	7e-16	33 / 195	HM HALLMARK_ESTROGEN_RESPONSE_LATE
38	8e-16	100 / 1418	BP small molecule metabolic process
39	2e-15	18 / 49	Color Marisa_CRC-cluster-f
40	5e-15	15 / 32	GSE/ AIGNER_ZEB1_TARGETS

Overview Map

Spot



p-values



Rank	p-value	#in/all
1	0.000000	1/123
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Geneset
 H3K9me3_enriched_genes_meth_UP
 H3K9me3_enriched_genes_meth_DOWN
 TESCHENDORFF_age_hypermethylated

Rank	p-value	#in/all
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92	0.000000	1/191
93	0.000000	1/191
94	0.000000	1/191
95	0.000000	1/191
96	0.000000	1/191
97	0.000000	1/191
98	0.000000	1/191
99	0.000000	1/191
100	0.000000	1/191

Geneset
 LU_PROSTATE_CANCER_UP
 WANG_ES_DN
 SPANGLER_H3K9me3_CANCER_GRADE_1_VS_3_UP
 LU_PROSTATE_CANCER_DN
 LU_COMMON_CANCER_GENES
 KUIPERS_WTP_poor_survival
 GUNZ_CAR_Tumor_geneset_nanostring
 LU_LIVER_CANCER
 LU_BREAST_CANCER
 OCEN1_L101_modul16
 OCEN1_L101_modul18
 PAN_CAR_KAS_geneset_nanostring

Rank	p-value	#in/all
1	0.000000	1/122
2	0.000000	1/122
3	0.000000	1/122
4	0.000000	1/122
5	0.000000	1/122
6	0.000000	1/122
7	0.000000	1/122
8	0.000000	1/122
9	0.000000	1/122
10	0.000000	1/122
11	0.000000	1/122
12	0.000000	1/122
13	0.000000	1/122
14	0.000000	1/122
15	0.000000	1/122
16	0.000000	1/122
17	0.000000	1/122
18	0.000000	1/122
19	0.000000	1/122
20	0.000000	1/122
21	0.000000	1/122
22	0.000000	1/122
23	0.000000	1/122
24	0.000000	1/122
25	0.000000	1/122
26	0.000000	1/122
27	0.000000	1/122
28	0.000000	1/122
29	0.000000	1/122
30	0.000000	1/122
31	0.000000	1/122
32	0.000000	1/122
33	0.000000	1/122
34	0.000000	1/122
35	0.000000	1/122
36	0.000000	1/122
37	0.000000	1/122
38	0.000000	1/122
39	0.000000	1/122
40	0.000000	1/122
41	0.000000	1/122
42	0.000000	1/122
43	0.000000	1/122
44	0.000000	1/122
45	0.000000	1/122
46	0.000000	1/122
47	0.000000	1/122
48	0.000000	1/122
49	0.000000	1/122
50	0.000000	1/122
51	0.000000	1/122
52	0.000000	1/122
53	0.000000	1/122
54	0.000000	1/122
55	0.000000	1/122
56	0.000000	1/122
57	0.000000	1/122
58	0.000000	1/122
59	0.000000	1/122
60	0.000000	1/122
61	0.000000	1/122
62	0.000000	1/122
63	0.000000	1/122
64	0.000000	1/122
65	0.000000	1/122
66	0.000000	1/122
67	0.000000	1/122
68	0.000000	1/122
69	0.000000	1/122
70	0.000000	1/122
71	0.000000	1/122
72	0.000000	1/122
73	0.000000	1/122
74	0.000000	1/122
75	0.000000	1/122
76	0.000000	1/122
77	0.000000	1/122
78	0.000000	1/122
79	0.000000	1/122
80	0.000000	1/122
81	0.000000	1/122
82	0.000000	1/122
83	0.000000	1/122
84	0.000000	1/122
85	0.000000	1/122
86	0.000000	1/122
87	0.000000	1/122
88	0.000000	1/122
89	0.000000	1/122
90	0.000000	1/122
91	0.000000	1/122
92	0.000000	1/122
93	0.000000	1/122
94	0.000000	1/122
95	0.000000	1/122
96	0.000000	1/122
97	0.000000	1/122
98	0.000000	1/122
99	0.000000	1/122
100	0.000000	1/122

Geneset
 Pentrack_TCGA_group.over_A_normal_UP
 Pentrack_CRC_TCGA_corr_C_normal_UP
 Entick_Colon
 Lembecke_TCGA_meth_kmeans_J_CIMP_H_DN
 Entick_Colon
 Entick_Colon
 Lembecke_TCGA_expr_kmeans_M_CIMP_H_DN
 Mansa_CRC_cluster_F
 Lembecke_TCGA_expr_kmeans_L_CIMP_H_UP_Cluster4_DN
 LXWV_Colon
 Lembecke_TCGA_expr_kmeans_N_CIMP_H_DN
 Mansa_CRC_cluster_e

Rank	p-value	#in/all
1	0.000000	1/232
2	0.000000	1/232
3	0.000000	1/232
4	0.000000	1/232
5	0.000000	1/232
6	0.000000	1/232
7	0.000000	1/232
8	0.000000	1/232
9	0.000000	1/232
10	0.000000	1/232
11	0.000000	1/232
12	0.000000	1/232
13	0.000000	1/232
14	0.000000	1/232
15	0.000000	1/232
16	0.000000	1/232
17	0.000000	1/232
18	0.000000	1/232
19	0.000000	1/232
20	0.000000	1/232
21	0.000000	1/232
22	0.000000	1/232
23	0.000000	1/232
24	0.000000	1/232
25	0.000000	1/232
26	0.000000	1/232
27	0.000000	1/232
28	0.000000	1/232
29	0.000000	1/232
30	0.000000	1/232
31	0.000000	1/232
32	0.00000	