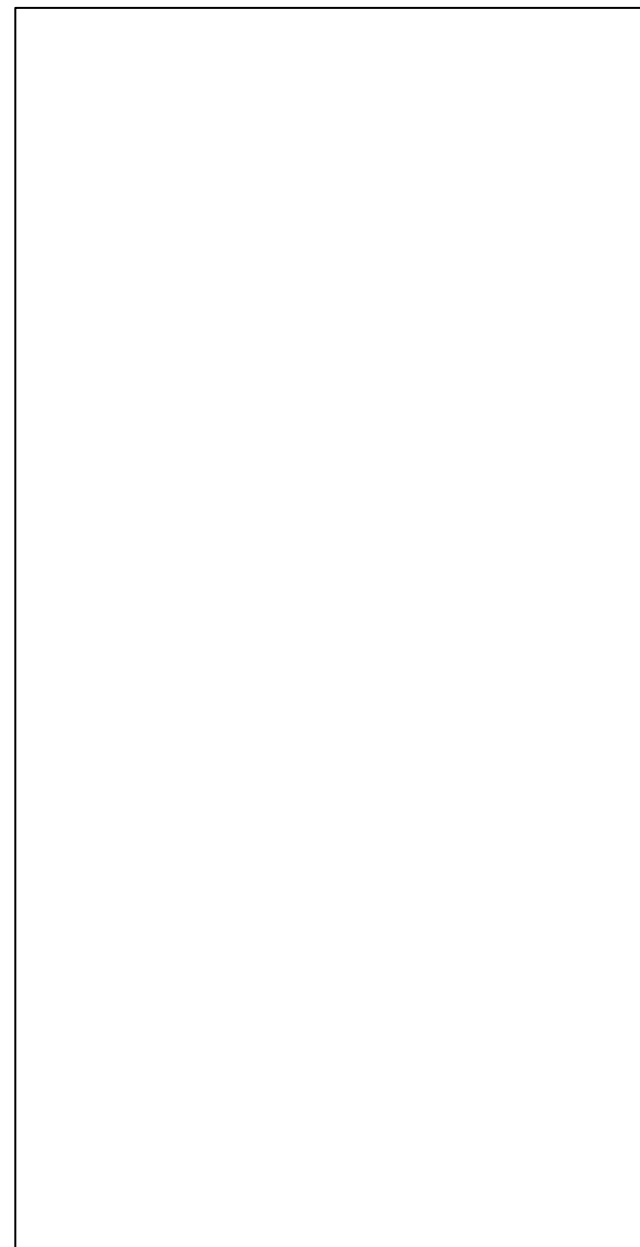
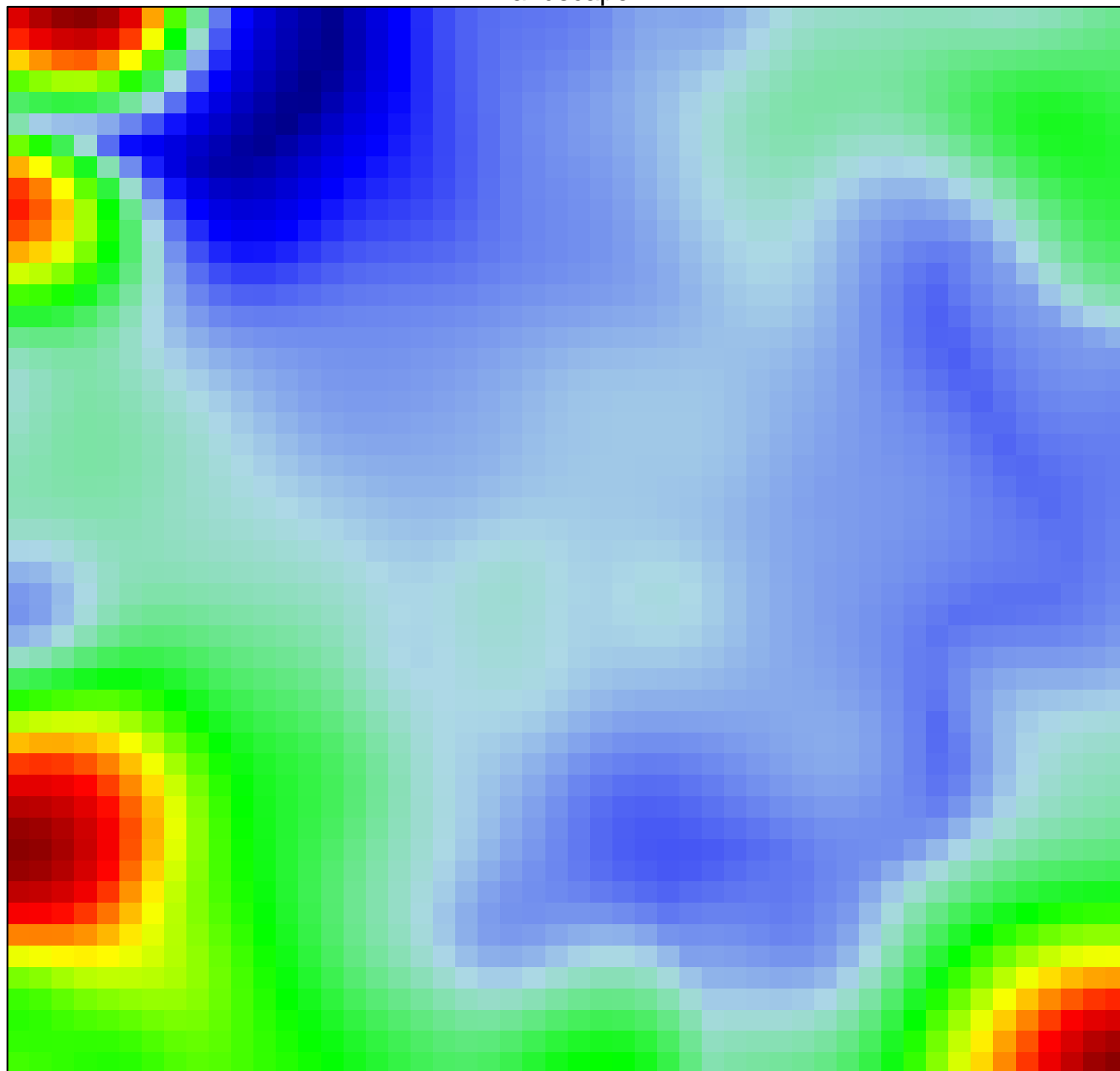


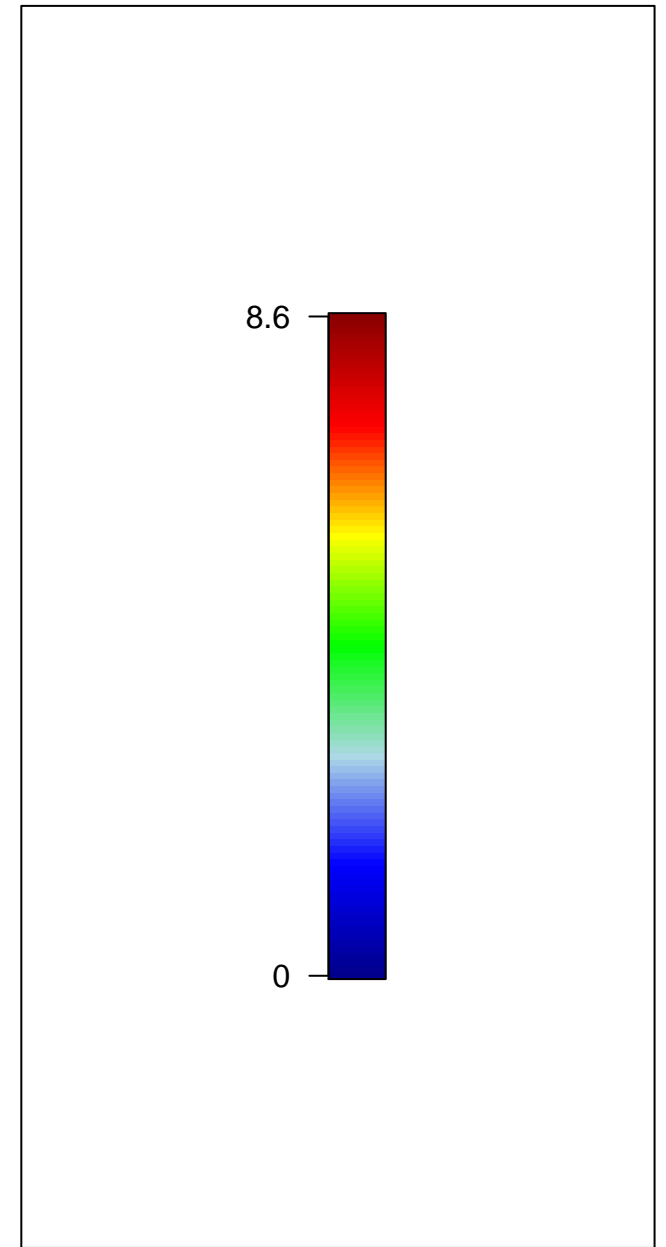
Group Overexpression Spots

landscape



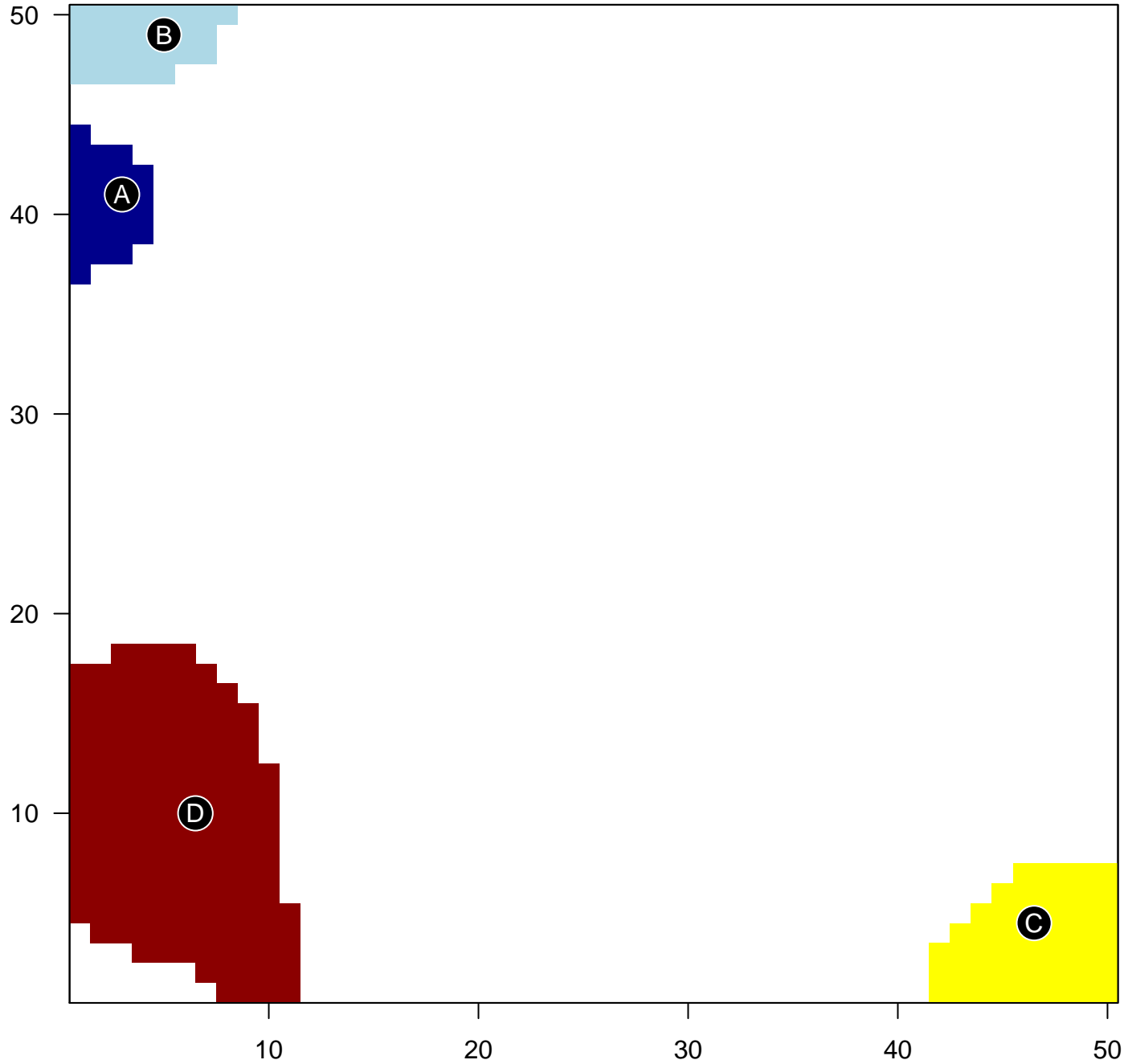
Group Overexpression Spots

beta-scores



Group Overexpression Spots

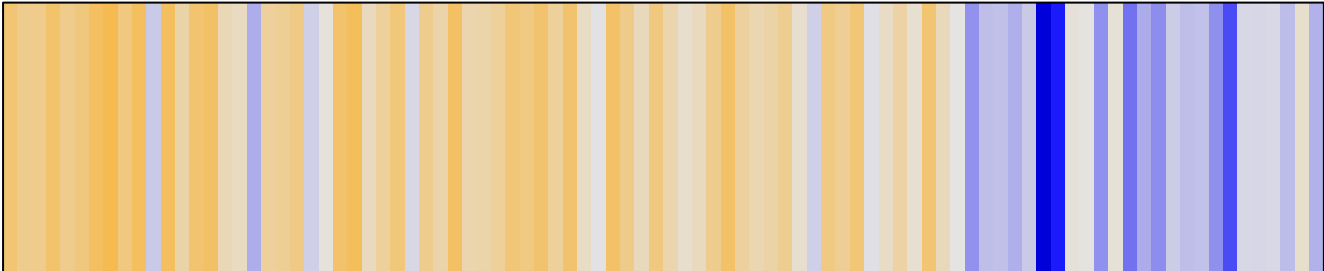
annotation



- A ■ mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP
- B ■ cell cycle
mitotic cell cycle
WILLSCHER_GBM_Verhaak-CL_up (C)
- C ■ PASINI_SUZ12_TARGETS_DN
DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
WONG_ADULT_TISSUE_STEM_MODULE
- D ■ Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3

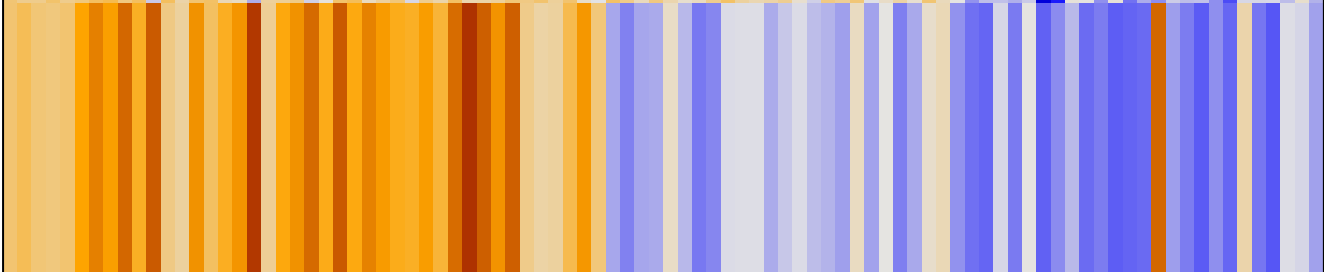


A



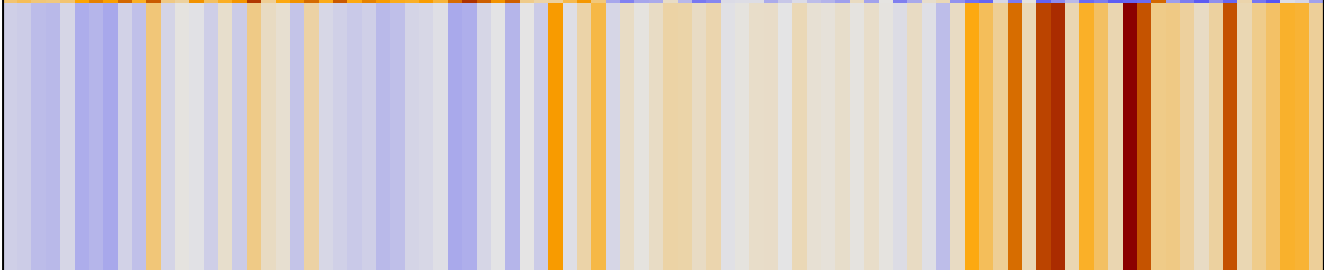
mitochondrion
 HALLMARK_OXIDATIVE_PHOSPHORYLATION
 STEIN_ESRRA_TARGETS_UP

B



cell cycle
 mitotic cell cycle
 WILLSCHER_GBM_Verhaak-CL_up (C)

C

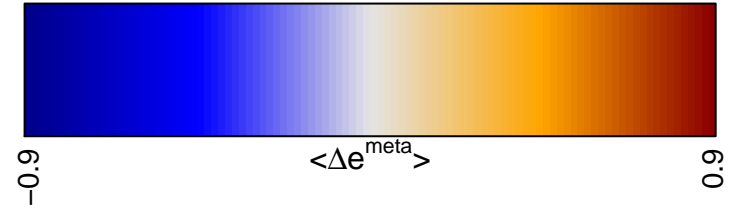
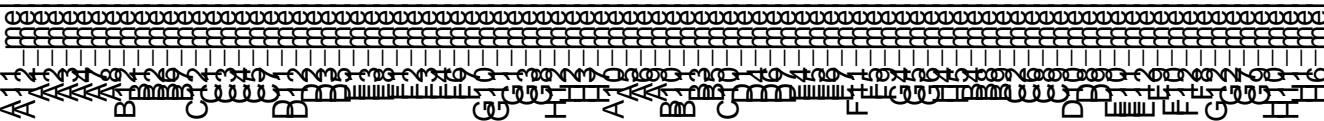


PASINI_SUZ12_TARGETS_DN
 DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
 WONG_ADULT_TISSUE_STEM_MODULE

D



Overlap_fetal_midbrain_HetRpts
 Overlap_fetal_midbrain_ReprPC
 Overlap_fetal_midbrain_K9K27me3





A

mitochondrion
HALLMARK_OXIDATIVE_PHOSPHORYLATION
STEIN_ESRRA_TARGETS_UP

B

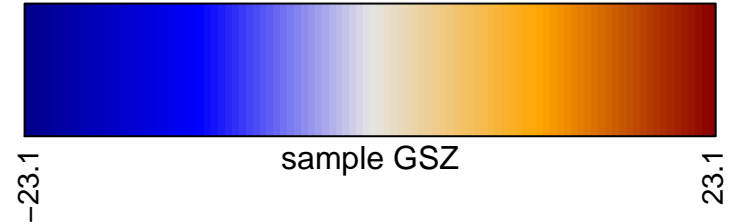
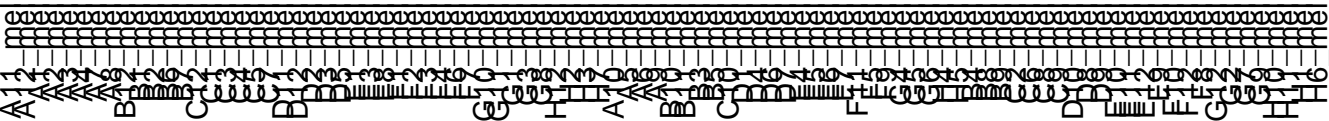
cell cycle
mitotic cell cycle
WILLSCHER_GBM_Verhaak-CL_up (C)

C

PASINI_SUZ12_TARGETS_DN
DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
WONG_ADULT_TISSUE_STEM_MODULE

D

Overlap_fetal_midbrain_HetRpts
Overlap_fetal_midbrain_ReprPC
Overlap_fetal_midbrain_K9K27me3



Group Overexpression Spot

Spot Summary: A

metagenes = 24
genes = 353

<r> metagenes = 0.96
<r> genes = 0.15
beta: r2= 3.26 / log p= -Inf

samples with spot = 7 (7.6 %)
MSC1 : 3 (7.1 %)
MSC2 : 4 (16 %)

Spot Genelist

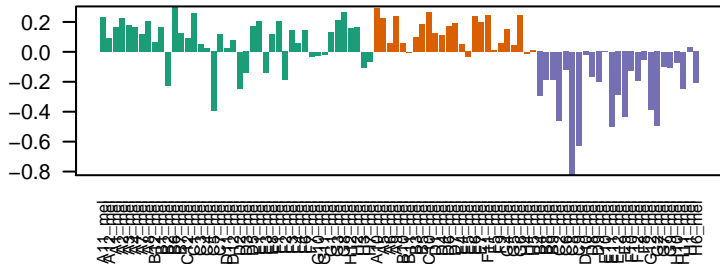
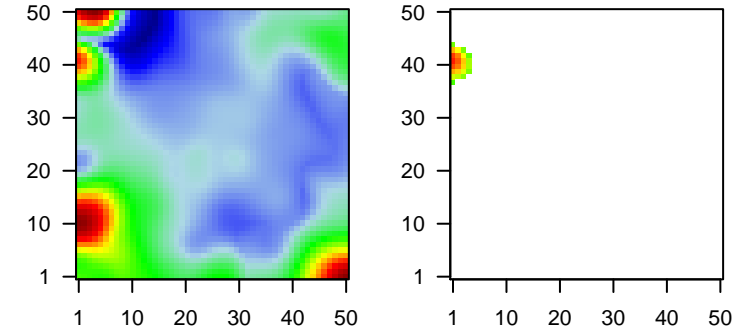
Rank	ID	max e	r	min e	Description
1	ZNF577	1.94	-0.21	0.27	ZNF577 zinc finger protein 577 [Source:HGNC Symbol;Acc:HGNC:28]
2	BCS1L	1.71	-0.91	0.27	BCS1L BC1 (ubiquinol-cytochrome c reductase) synthesis-like [Sou
3	GAPDHS	1.71	-1.17	0.59	GAPDHSglyceraldehyde-3-phosphate dehydrogenase, spermatogeni
4	ST6GALNAC3	1.69	-0.39	0.32	ST6GALNAC3(alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-
5	TRMT1	1.65	-0.71	0.36	TRMT1 tRNA methyltransferase 1 homolog (S. cerevisiae) [Source:HG
6	NMRK2	1.63	-1.2	0.71	NMRK2 nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:HG
7	NT5DC1	1.63	-0.93	0.28	NT5DC1 5'-nucleotidase domain containing 1 [Source:HGNC Symbol;
8	SEPSECS	1.63	-0.31	0.32	SEPSECSep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA syr
9	WIPF3	1.62	-0.29	0.33	WIPF3 WAS/WASL interacting protein family, member 3 [Source:HG
10	ANO2	1.61	-0.48	0.34	ANO2 anoctamin 2, calcium activated chloride channel [Source:HG
11	CAPG	1.58	-0.72	0.39	CAPG capping protein (actin filament), gelsolin-like [Source:HGNC :
12	NPAS2	1.58	-0.27	0.28	NPAS2 neuronal PAS domain protein 2 [Source:HGNC Symbol;Acc:HG
13	MAPK10	1.57	-0.69	0.44	MAPK10 mitogen-activated protein kinase 10 [Source:HGNC Symbol;
14	SNAP29	1.56	-0.44	0.3	SNAP29 synaptosomal-associated protein, 29kDa [Source:HGNC Syr
15	C1orf21	1.56	-0.91	0.34	C1orf21 chromosome 1 open reading frame 21 [Source:HGNC Symbc
16	LINS	1.55	-0.78	0.26	LINS lines homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:
17	ISY1	1.53	-0.64	0.24	ISY1 ISY1 splicing factor homolog (S. cerevisiae) [Source:HGNC S
18	SNX8	1.52	-0.75	0.39	SNX8 sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
19	TOE1	1.52	-0.48	0.26	TOE1 target of EGR1, member 1 (nuclear) [Source:HGNC Symbol;
20	FAM193B	1.52	-0.7	0.27	FAM193Bfamily with sequence similarity 193, member B [Source:HGNC

Geneset Overrepresentation

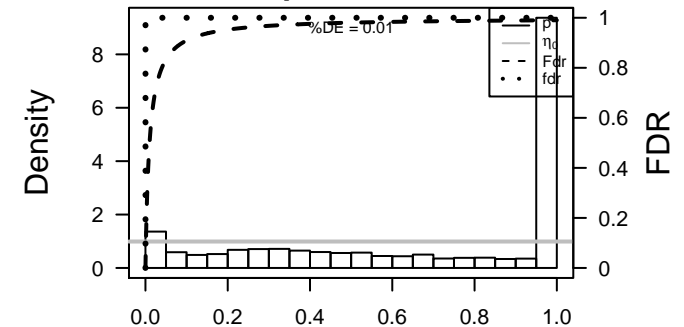
Rank	p-value	#in/all	Geneset
1	3e-18	91 / 1468	CC mitochondrion
2	6e-18	32 / 198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	1e-16	41 / 368	GSE/ STEIN_ESRRA_TARGETS_UP
4	7e-15	242 / 7203	Colon TssF_Colon
5	1e-14	45 / 500	GSE/ STEIN_ESRRA_TARGETS
6	1e-14	40 / 401	CC mitochondrial inner membrane
7	4e-13	38 / 405	GSE/ MOOTHA_HUMAN_MITODB_6_2002
8	3e-12	52 / 756	GSE/ WEI_MYCN_TARGETS_WITH_E_BOX
9	7e-12	256 / 8205	CC cytoplasm
10	2e-11	35 / 398	GSE/ MOOTHA_PGC
11	3e-11	36 / 421	GSE/ MOOTHA_MITOCHONDRIA
12	3e-11	281 / 9482	Colon TssA_Colon
13	4e-10	82 / 1730	BP small molecule metabolic process
14	9e-10	29 / 325	GSE/ PENG_GLUTAMINE_DEPRIVATION_DN
15	2e-09	24 / 233	GSE/ PENG_RAPAMYCIN_RESPONSE_DN
16	2e-09	60 / 1126	GSE/ BLALOCK_ALZHEIMERS_DISEASE_DN
17	3e-09	35 / 478	GSE/ STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
18	5e-09	52 / 925	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
19	1e-08	34 / 475	GSE/ ONKEN_UVEAL_MELANOMA_DN
20	2e-08	263 / 9013	Brain Overlap_fetal_midbrain_K9K27me3
21	2e-08	36 / 541	BP oxidation-reduction process
22	4e-08	27 / 338	GSE/ DAIRKEE_TERT_TARGETS_UP
23	4e-08	19 / 177	GSE/ YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17
24	1e-07	25 / 312	GSE/ WONG_EMBRYONIC_STEM_CELL_CORE
25	1e-07	260 / 9027	Color Tx_Colon
26	2e-07	11 / 63	Glio Stuehler_Proteins_up_in_STS
27	5e-07	9 / 42	Lymph CARO_OxPhos_in_DLBCL_UP
28	5e-07	87 / 2193	CC extracellular exosome
29	7e-07	6 / 15	GSE/ MOOTHA_TCA
30	8e-07	10 / 57	HM HALLMARK_MYC_TARGETS_V2
31	9e-07	9 / 45	MF NAD binding
32	1e-06	43 / 831	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
33	2e-06	9 / 48	GSE/ REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
34	2e-06	6 / 17	BP mitochondrial respiratory chain complex I assembly
35	2e-06	25 / 363	GSE/ RUTELLA_RESPONSE_TO_HGF_UP
36	2e-06	24 / 340	GSE/ RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP
37	2e-06	61 / 1400	TF ICGC_Myc_targets
38	2e-06	276 / 9988	CC organelle
39	2e-06	17 / 188	HM HALLMARK_ADIPOGENESIS
40	3e-06	37 / 685	GSE/ KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_UP

Overview Map

Spot



p-values



Group Overexpression Spot

Spot Summary: B

metagenes = 27
genes = 406

<r> metagenes = 0.92
<r> genes = 0.27
beta: r2= 8.57 / log p= -Inf

samples with spot = 28 (30.4 %)
MSC1 : 27 (64.3 %)
MSC3 : 1 (4 %)

Spot Genelist

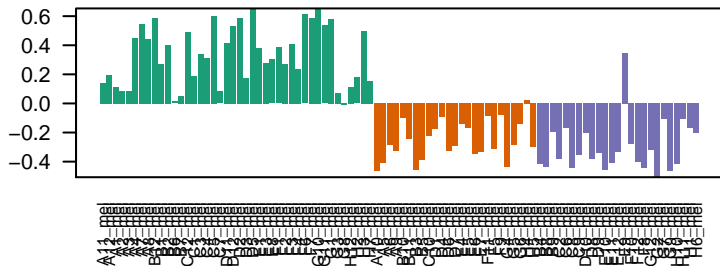
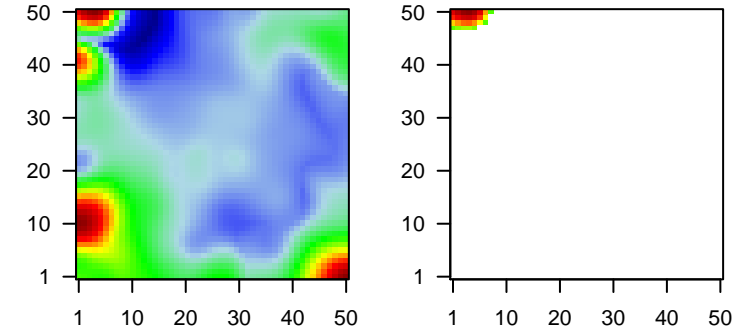
Rank	ID	max e	r	min e	Description
					Symbol
1	CEP97	2.41	-1.21	0.26	CEP97 centrosomal protein 97kDa [Source:HGNC Symbol;Acc:HGNC:10000]
2	UBE2C	2.22	-1.05	0.87	UBE2C ubiquitin-conjugating enzyme E2C [Source:HGNC Symbol;Acc:HGNC:10000]
3	NUF2	2.2	-0.57	0.84	NUF2 NUF2, NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:HGNC:10000]
4	CDK1	2.16	-1.11	0.84	CDK1 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
5	CCNB1	2.14	-1.08	0.66	CCNB1 cyclin B1 [Source:HGNC Symbol;Acc:HGNC:1579]
6	NEK2	2.14	-0.38	0.68	NEK2 NIMA-related kinase 2 [Source:HGNC Symbol;Acc:HGNC:7700]
7	SMCO4	2.1	-0.21	0.34	SMCO4 single-pass membrane protein with coiled-coil domains 4 [Source:HGNC Symbol;Acc:HGNC:10000]
8	PLK1	2.09	-0.46	0.65	PLK1 polo-like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]
9	AURKB	2.03	-0.61	0.79	AURKB aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]
10	CKAP2L	2.01	-0.57	0.84	CKAP2L cytoskeleton associated protein 2-like [Source:HGNC Symbol;Acc:HGNC:10000]
11	CDC20	2	-0.67	0.71	CDC20 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1720]
12	KIF20A	1.98	-0.39	0.74	KIF20A kinesin family member 20A [Source:HGNC Symbol;Acc:HGNC:10000]
13	NDC80	1.96	-0.62	0.87	NDC80 NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:HGNC:10000]
14	DLGAP5	1.93	-0.47	0.78	DLGAP5 discs, large (Drosophila) homolog-associated protein 5 [Source:HGNC Symbol;Acc:HGNC:10000]
15	PRR11	1.93	-0.5	0.75	PRR11 proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]
16	RRM2	1.92	-0.76	0.86	RRM2 ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGNC:10000]
17	SGOL1	1.91	-0.72	0.75	SGOL1 shugoshin-like 1 (S. pombe) [Source:HGNC Symbol;Acc:HGNC:10000]
18	HIST1H4E	1.9	-0.46	0.45	HIST1H4E histone cluster 1, H4e [Source:HGNC Symbol;Acc:HGNC:4730]
19	CDCA3	1.88	-0.49	0.83	CDCA3 cell division cycle associated 3 [Source:HGNC Symbol;Acc:HGNC:10000]
20	PBK	1.85	-0.67	0.8	PBK PDZ binding kinase [Source:HGNC Symbol;Acc:HGNC:1828]

Geneset Overrepresentation

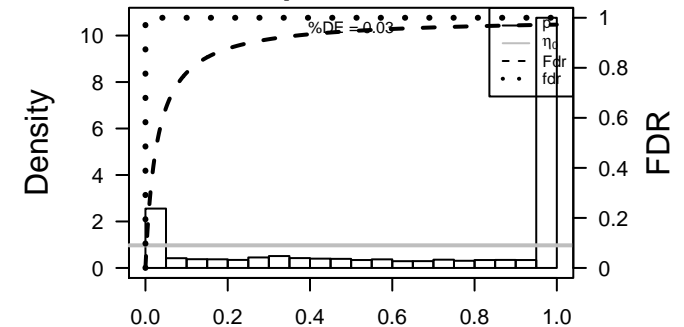
Rank	p-value	#in/all	Geneset
1	1e-99	213 / 1110	BP cell cycle
2	1e-99	131 / 412	BP mitotic cell cycle
3	1e-99	123 / 142	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
4	1e-99	110 / 197	HM HALLMARK_E2F_TARGETS
5	1e-99	12 / 16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
6	1e-99	256 / 1192	GSE/ KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
7	1e-99	222 / 1251	GSE/ DODD_NASOPHARYNGEAL_CARCINOMA_DN
8	1e-99	137 / 505	GSE/ BERENJENO_TRANSFORMED_BY_RHOA_UP
9	1e-99	102 / 139	GSE/ ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
10	1e-99	127 / 390	GSE/ PUJANA_BRCA2_PCC_NETWORK
11	1e-99	188 / 944	GSE/ NUYTEN_EZH2_TARGETS_DN
12	1e-99	163 / 616	GSE/ BENPORATH_CYCLING_GENES
13	1e-99	197 / 700	GSE/ MARSON_BOUND_BY_E2F4_UNSTIMULATED
14	1e-99	121 / 327	GSE/ BLUM_RESPONSE_TO_SALIRASIB_DN
15	1e-99	95 / 145	GSE/ CHANG_CYCLING_GENES
16	1e-99	145 / 436	GSE/ SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
17	1e-99	125 / 267	GSE/ ZHANG_TLX_TARGETS_60HR_DN
18	1e-99	143 / 242	GSE/ KOBAYASHI_EGFR_SIGNALING_24HR_DN
19	1e-99	175 / 305	GSE/ DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
20	1e-99	232 / 550	GSE/ GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
21	2e-94	87 / 162	GSE/ GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP
22	5e-94	72 / 96	GSE/ CROONQUIST_IL6_DEPRIVATION_DN
23	2e-91	84 / 155	GSE/ HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
24	3e-90	77 / 124	GSE/ ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
25	2e-89	115 / 388	GSE/ REACTOME_CELL_CYCLE
26	5e-89	125 / 489	Cancer Lembcke_Normal vs Adenoma
27	2e-87	68 / 93	GSE/ KONG_E2F3_TARGETS
28	7e-87	99 / 270	GSE/ BASAKI_YBX1_TARGETS_UP
29	7e-87	72 / 110	GSE/ WHITEFORD_PEDIATRIC_CANCER_MARKERS
30	2e-86	111 / 373	GSE/ VECCHI_GASTRIC_CANCER_EARLY_UP
31	7e-86	101 / 291	GSE/ HORIUCHI_WTAP_TARGETS_DN
32	1e-85	102 / 301	GSE/ REACTOME_CELL_CYCLE_MITOTIC
33	1e-84	124 / 517	GSE/ FEVR_CTNNB1_TARGETS_DN
34	2e-84	102 / 308	GSE/ LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
35	3e-84	68 / 99	GSE/ BURTON_ADIPOGENESIS_3
36	4e-84	141 / 724	GSE/ PUJANA_CHEK2_PCC_NETWORK
37	6e-84	63 / 81	GSE/ GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
38	8e-83	86 / 198	GSE/ FUJII_YBX1_TARGETS_DN
39	3e-82	67 / 99	GSE/ LEE_EARLY_T_LYMPHOCYTE_UP
40	4e-82	130 / 609	GSE/ RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP

Overview Map

Spot



p-values



Group Overexpression Spot

Spot Summary: C

metagenes = 53
genes = 624

<r> metagenes = 0.9
<r> genes = 0.14
beta: r2= 3.41 / log p= -Inf

samples with spot = 11 (12 %)
MSC1 : 1 (2.4 %)
MSC3 : 10 (40 %)

Spot Genelist

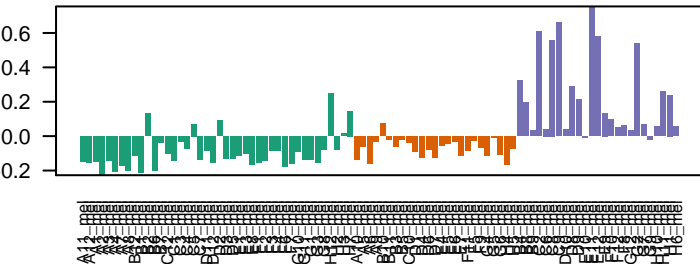
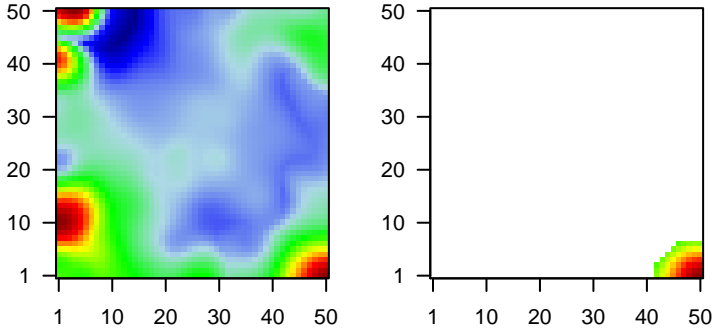
Rank	ID	max e	r	min e	Description
					Symbol
1	LUM	3.07	-0.63	0.39	LUM lumican [Source:HGNC Symbol;Acc:HGNC:6724]
2	DKK1	2.85	-0.31	0.63	DKK1 dickkopf WNT signaling pathway inhibitor 1 [Source:HGNC S
3	IL24	2.78	-0.11	0.59	IL24 interleukin 24 [Source:HGNC Symbol;Acc:HGNC:11346]
4	HBEGF	2.46	-0.25	0.53	HBEGF heparin-binding EGF-like growth factor [Source:HGNC Synt
5	ANXA1	2.44	-0.5	0.78	ANXA1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
6	FADS3	2.35	-0.24	0.56	FADS3 fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:35
7	PTPRZ1	2.31	-0.37	0.7	PTPRZ1 protein tyrosine phosphatase, receptor-type, Z polypeptide 1
8	NAV3	2.3	-0.23	0.73	NAV3 neuron navigator 3 [Source:HGNC Symbol;Acc:HGNC:15998]
9	RGS4	2.3	-0.3	0.4	RGS4 regulator of G-protein signaling 4 [Source:HGNC Symbol;Acc
10	A2M	2.29	-0.9	0.52	A2M alpha-2-macroglobulin [Source:HGNC Symbol;Acc:HGNC:7
11	RGS2	2.26	-0.52	0.33	RGS2 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
12	KCNJ2	2.26	-0.25	0.68	KCNJ2 potassium channel, inwardly rectifying subfamily J, member 2
13	HIST1H3D	2.25	-0.35	0.37	HIST1H3Dhistone cluster 1, H3d [Source:HGNC Symbol;Acc:HGNC:47
14	FN1	2.23	-1.04	0.4	FN1 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
15	SERPINI1	2.21	-0.56	0.39	SERPINIserpin peptidase inhibitor, clade I (neuroserpin), member 1 [S
16	LMCD1	2.2	-0.68	0.32	LMCD1 LIM and cysteine-rich domains 1 [Source:HGNC Symbol;Acc
17	VTN	2.14	-0.36	0.67	VTN vitronectin [Source:HGNC Symbol;Acc:HGNC:12724]
18	SLC40A1	2.11	-0.56	0.38	SLC40A1solute carrier family 40 (iron-regulated transporter), member
19	ARRDC3	2.09	-0.76	0.5	ARRDC3arrestin domain containing 3 [Source:HGNC Symbol;Acc:HGI
20	CAV1	2.08	-0.76	0.44	CAV1 caveolin 1, caveolae protein, 22kDa [Source:HGNC Symbol;A

Geneset Overrepresentation

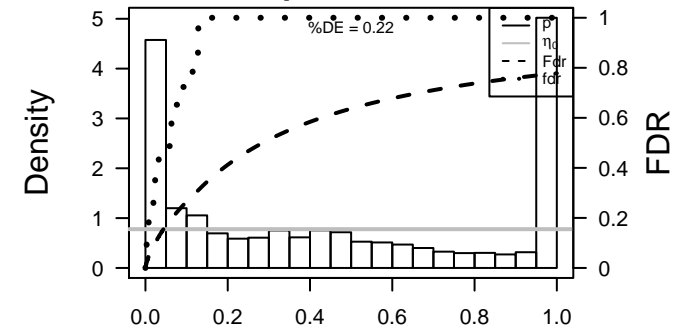
Rank	p-value	#in/all	Geneset
1	9e-32	67 / 286	GSE# PASINI_SUZ12_TARGETS_DN
2	2e-30	84 / 472	GSE# DUTERTRE_ESTRADIOL_RESPONSE_24HR_DN
3	2e-28	92 / 594	GSE# WONG_ADULT_TISSUE_STEM_MODULE
4	3e-28	104 / 749	GSE# CUI_TCF21_TARGETS_2_DN
5	9e-25	72 / 425	GSE# CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN
6	1e-23	59 / 302	GSE# KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
7	4e-23	49 / 212	Lymp# LENZ_Stromal signature 1
8	3e-22	100 / 833	GSE# DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
9	1e-20	104 / 930	GSE# NUYTEN_EZH2_TARGETS_UP
10	4e-20	91 / 761	GSE# KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3
11	1e-19	40 / 168	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
12	7e-19	60 / 385	GSE# REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
13	5e-18	60 / 401	GSE# CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
14	4e-17	87 / 784	GSE# BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
15	5e-17	43 / 227	GSE# DAVICIONI_TARGETS_OF_PAX_FOXP01_FUSIONS_UP
16	1e-16	50 / 308	CC focal adhesion
17	1e-16	36 / 163	GSE# PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
18	1e-16	65 / 494	GSE# CHICAS_RB1_TARGETS_CONFLUENT
19	3e-16	58 / 410	GSE# LIM_MAMMARY_STEM_CELL_UP
20	4e-16	47 / 283	GSE# SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
21	2e-15	31 / 131	Color Marisa_CRC-cluster-a
22	5e-15	42 / 245	GSE# WANG_SMARCE1_TARGETS_UP
23	9e-15	34 / 166	GSE# RODWELL_AGING_KIDNEY_NO_BLOOD_UP
24	1e-14	55 / 406	GSE# BAELDE_DIABETIC_NEPHROPATHY_DN
25	2e-14	40 / 234	GSE# LU_AGING_BRAIN_UP
26	6e-14	30 / 137	HM HALLMARK_UV_RESPONSE_DN
27	1e-13	36 / 200	GSE# ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF
28	3e-13	41 / 263	Color Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
29	5e-13	26 / 111	GSE# ZHU_CMV_ALL_DN
30	5e-13	57 / 473	GSE# DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN
31	6e-13	30 / 149	GSE# PHONG_TNF_RESPONSE_VIA_P38_PARTIAL
32	9e-13	36 / 215	GSE# BILD_HRAS_ONCOGENIC_SIGNATURE
33	1e-12	30 / 153	GSE# WU_CELL_MIGRATION
34	1e-12	3 / 14	Canc# LIU_PROSTATE_CANCER_DN
35	1e-12	31 / 164	GSE# TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP
36	2e-12	56 / 475	GSE# ONKEN_UVEAL_MELANOMA_DN
37	3e-12	36 / 222	GSE# UDAYAKUMAR_MED1_TARGETS_DN
38	3e-12	70 / 683	GSE# KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP
39	3e-12	73 / 730	GSE# RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN
40	4e-12	22 / 85	GSE# BURTON_ADIPOGENESIS_9

Overview Map

Spot



p-values



Rank	p-value	#in/all	Geneset
1	0.0000	77	aging_genes_meth_UP
2	0.0000	100	aging_genes_meth_DOWN
3	0.0000	100	TESCHENDORFF_age_hypermethylated

Rank	p-value	#in/all	Geneset
1	0.0000	141	EMBOCKE_Colonic_Inflammation
2	0.0000	234	pancan_F103_geneset_nanostring
3	0.0000	298	pancan_F103_geneset_nanostring

Rank	p-value	#in/all	Geneset
1	0.0000	111	pancan_RAS_geneset_nanostring
2	0.0000	111	pancan_Wnt_geneset_nanostring
3	0.0000	111	pancan_Txmi3kd_geneset_nanostring

Rank	p-value	#in/all	Geneset
1	0.0000	120	pancan_COU60n_geneset_nanostring
2	0.0000	120	pancan_COU60n_geneset_nanostring
3	0.0000	120	pancan_COU60n_geneset_nanostring

Rank	p-value	#in/all	Geneset
1	0.0000	253	marisa_CRC_cluster-a
2	0.0000	1290	marisa_CRC_TCGA_corr_J_msi-h_UP_mss_DN
3	0.0000	1290	marisa_CRC_cluster-b

Rank	p-value	#in/all	Geneset
1	0.0000	120	DIOPTERIN_2_TARGETS_DN
2	0.0000	120	DIOPTERIN_2_TARGETS_DN
3	0.0000	120	DIOPTERIN_2_TARGETS_DN

Rank	p-value	#in/all	Geneset
1	0.0000	120	DIOPTERIN_2_TARGETS_DN
2	0.0000	120	DIOPTERIN_2_TARGETS_DN
3	0.0000	120	DIOPTERIN_2_TARGETS_DN

Rank	p-value	#in/all	Geneset
1	0.0000	120	DIOPTERIN_2_TARGETS_DN

Rank	p-value	#in/all	Geneset
1	0.0000	3068	signal transduction
2	0.0000	2710	cell junction organization
3	0.0000	2110	anatomical structure development

Rank	p-value	#in/all	Geneset
1	0.0000	293	cytoskeleton organization
2	0.0000	293	extracellular matrix organization
3	0.0000	293	cell cycle arrest

Rank	p-value	#in/all	Geneset
1	0.0000	566	locomotion
2	0.0000	566	cell differentiation
3	0.0000	566	negative regulation of transcription from RNA polymerase II promoter

Rank	p-value	#in/all	Geneset
1	0.0000	566	hipo signaling
2	0.0000	566	dendrite morphogenesis
3	0.0000	566	regulation of cell proliferation

Rank	p-value	#in/all	Geneset
1	0.0000	566	axonal outgrowth
2	0.0000	566	plasma membrane organization
3	0.0000	566	cell-cell junction assembly

Rank	p-value	#in/all	Geneset
1	0.0000	566	positive regulation of apoptotic process
2	0.0000	566	cell migration
3	0.0000	566	negative regulation of cell proliferation

Rank	p-value	#in/all	Geneset
1	0.0000	293	actin cytoskeleton
2	0.0000	293	cell surface
3	0.0000	293	extracellular exosome

Rank	p-value	#in/all	Geneset
1	0.0000	293	extracellular exosome

Rank	p-value	#in/all	Geneset
1	0.0000	293	proteaceous extracellular matrix
2	0.0000	293	cytoskeleton
3	0.0000	293	plasma membrane

Rank	p-value	#in/all	Geneset
1	0.0000	32	cell-cell junction
2	0.0000	32	extracellular region
3	0.0000	32	Z disc

Rank	p-value	#in/all	Geneset
1	0.0000	32	basement membrane
2	0.0000	32	extracellular matrix
3	0.0000	32	postsynaptic density

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission
2	0.0000	32	synaptic transmission
3	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	32	synaptic transmission

Rank	p-value	#in/all	Geneset
1	0.0000	1013	overlap_fetal_midbrain_ReprPC
2	0.0000	930	overlap_fetal_midbrain_HetRpts
3	0.0000	930	overlap_fetal_midbrain_ReprCwK

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp
2	0.0000	930	overlap_fetal_midbrain_Lssp
3	0.0000	930	overlap_fetal_midbrain_Lssp

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp
2	0.0000	930	overlap_fetal_midbrain_Lssp
3	0.0000	930	overlap_fetal_midbrain_Lssp

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp
2	0.0000	930	overlap_fetal_midbrain_Lssp
3	0.0000	930	overlap_fetal_midbrain_Lssp

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp
2	0.0000	930	overlap_fetal_midbrain_Lssp
3	0.0000	930	overlap_fetal_midbrain_Lssp

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp
2	0.0000	930	overlap_fetal_midbrain_Lssp
3	0.0000	930	overlap_fetal_midbrain_Lssp

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp
2	0.0000	930	overlap_fetal_midbrain_Lssp
3	0.0000	930	overlap_fetal_midbrain_Lssp

Rank	p-value	#in/all	Geneset
1	0.0000	930	overlap_fetal_midbrain_Lssp

Group Overexpression Spot

Spot Summary: D

metagenes = 154
genes = 1247

<r> metagenes = 0.56

beta: r2= 1.29 / log p= -Inf

samples with spot = 2 (2.2 %)
MSC2 : 2 (8 %)

Spot Genelist

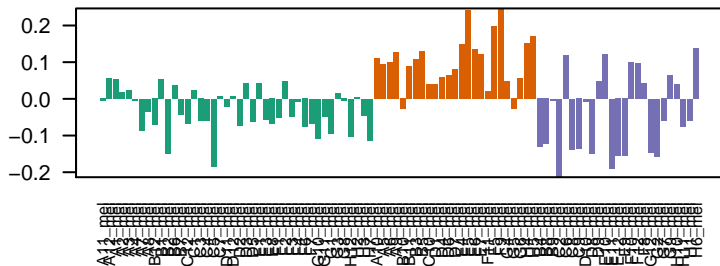
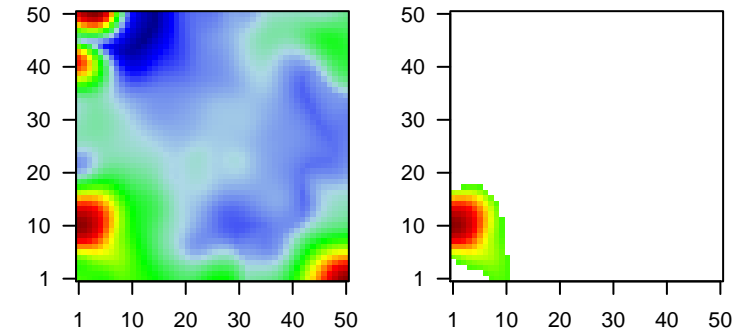
Rank	ID	max e	r	min e	Description
					Symbol
1	PDCD11	2.19	-0.54	0.24	PDCD11 programmed cell death 11 [Source:HGNC Symbol;Acc:HGNC
2	MAGEA1	2.11	-0.1	0.48	MAGEA1 melanoma antigen family A1 [Source:HGNC Symbol;Acc:HGNC
3	FZD3	2.09	-0.27	0.28	FZD3 frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4
4	SLC25A14	2.08	-0.21	0.26	SLC25A14 solute carrier family 25 (mitochondrial carrier, brain), member
5	POPDC2	2.06	-0.33	0.46	POPDC2 popeye domain containing 2 [Source:HGNC Symbol;Acc:HGNC
6	METAP1D	2.04	-0.33	0.31	METAP1D methionyl aminopeptidase type 1D (mitochondrial) [Source:HGNC
7	ADARB1	2.04	-0.86	0.37	ADARB1 adenosine deaminase, RNA-specific, B1 [Source:HGNC Syn
8	RNF40	1.97	-0.54	0.27	RNF40 ring finger protein 40, E3 ubiquitin protein ligase [Source:HGNC
9	IFI44	1.95	-0.25	0.34	IFI44 interferon-induced protein 44 [Source:HGNC Symbol;Acc:HGNC
10	SLC24A1	1.94	-0.09	0.54	SLC24A1 solute carrier family 24 (sodium/potassium/calcium exchange
11	GPR183	1.92	-0.15	0.49	GPR183 G protein-coupled receptor 183 [Source:HGNC Symbol;Acc:HGNC
12	HDAC11	1.91	-0.17	0.36	HDAC11 histone deacetylase 11 [Source:HGNC Symbol;Acc:HGNC:11
13	LPHN1	1.9	-0.17	0.32	LPHN1 leucine-rich repeat protein 1 [Source:HGNC Symbol;Acc:HGNC
14	EGLN3	1.89	-0.41	0.36	EGLN3 egl-9 family hypoxia-inducible factor 3 [Source:HGNC Symb
15	PORCN	1.88	-0.18	0.38	PORCN porcupine homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC
16	KCNQ5	1.87	-0.46	0.35	KCNQ5 potassium channel, voltage gated KQT-like subfamily Q, member
17	TKTL1	1.87	-0.19	0.27	TKTL1 transketolase-like 1 [Source:HGNC Symbol;Acc:HGNC:1183
18	CFAP61	1.86	-0.52	0.45	CFAP61 cilia and flagella associated protein 61 [Source:HGNC Symb
19	LYRM9	1.85	-0.31	0.28	LYRM9 LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
20	RHPN2	1.85	-0.17	0.36	RHPN2 rhophilin, Rho GTPase binding protein 2 [Source:HGNC Sym

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-15	627 / 5940	Brain Overlap_fetal_midbrain_HetRpts
2	1e-14	900 / 9330	Brain Overlap_fetal_midbrain_ReprPC
3	1e-11	860 / 9013	Brain Overlap_fetal_midbrain_K9K27me3
4	2e-11	861 / 9027	Colon Tx_Colon
5	1e-10	855 / 9020	Brain Overlap_fetal_midbrain_ReprPCWk
6	2e-10	895 / 9528	Brain Overlap_fetal_midbrain_Quies
7	4e-10	817 / 8580	Colon TxWk_Colon
8	6e-10	888 / 9482	Colon TssA_Colon
9	4e-08	669 / 6929	Lymp HOPP_Txn_elongation
10	5e-08	145 / 1128	Lymp SPANG_BCR_DN
11	2e-07	786 / 8415	Colon Quies3_Colon
12	1e-06	713 / 7592	Lymp HOPP_Active_promoter
13	2e-06	508 / 5184	Lymp HOPP_Txn_transition
14	5e-06	9 / 18	BP melanocyte differentiation
15	1e-05	382 / 3812	Colon TssD1_Colon
16	1e-05	9 / 20	BP semaphorin-plexin signaling pathway
17	2e-05	113 / 925	GSE/ KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
18	2e-05	456 / 4689	TF ICGC_Taf1_targets
19	3e-05	455 / 4682	TF ICGC_Pol24_targets
20	3e-05	400 / 4054	TF ICGC_Egr1_targets
21	3e-05	54 / 367	GSE/ MONNIER_POSTRADIATION_TUMOR_ESCAPE_UP
22	3e-05	160 / 1418	TF ICGC_Ets1_targets
23	4e-05	227 / 2136	TF ICGC_GabpPcr2_targets
24	5e-05	4 / 4	GSE/ KERLEY_RESPONSE_TO_CISPLATIN_DN
25	5e-05	555 / 5880	Colon TssD2_Colon
26	1e-04	153 / 1383	TF ICGC_Six5_targets
27	1e-04	518 / 5495	TF ICGC_Yy1_targets
28	2e-04	8 / 21	GSE/ BIOCARTA_IL6_PATHWAY
29	2e-04	9 / 27	GSE/ SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_DN
30	2e-04	19 / 94	CC melanosome
31	2e-04	423 / 4414	TF ICGC_Bclaf101388_targets
32	3e-04	273 / 2714	TF ICGC_Irf4_targets
33	3e-04	465 / 4909	TF ICGC_Stat5_targets
34	3e-04	503 / 5355	TF ICGC_Pol2_targets
35	3e-04	196 / 1872	TF ICGC_Mef2_targets
36	3e-04	491 / 5219	TF ICGC_Tcf3_targets
37	3e-04	6 / 13	GSE/ REACTOME_OTHER_SEMAPHORIN_INTERACTIONS
38	4e-04	658 / 7203	Colon TssF_Colon
39	4e-04	304 / 3081	Brain Mid_Frontal_Lobe_ZNF
40	4e-04	412 / 4314	TF ICGC_Ebfc137065_targets

Overview Map

Spot



p-values

