

MSC1

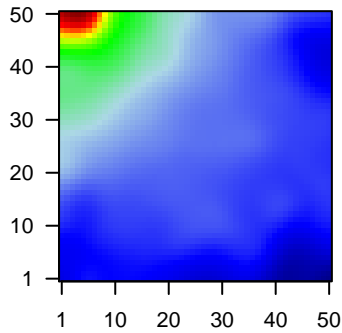
Global Summary

%DE = 0.17
 # genes with $fdr < 0.2$ = 1627 (1034 + / 593 -)
 # genes with $fdr < 0.1$ = 1276 (868 + / 408 -)
 # genes with $fdr < 0.05$ = 1068 (764 + / 304 -)
 # genes with $fdr < 0.01$ = 727 (588 + / 139 -)

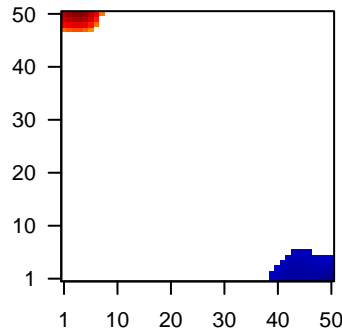
genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.01
 <p-value> = 0.09
 <fdr> = 0.83

Profile



Regulated Spots



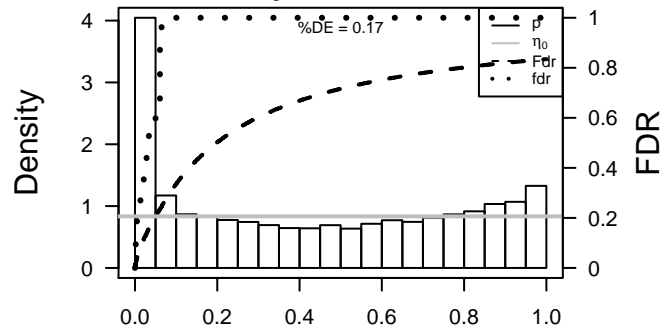
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ACTL6A	0.5	2e-16 2e-14	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ANLN	0.65	2e-16 2e-14	5 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:HGNC:24124]
3	ANP32E	0.28	2e-16 2e-14	8 x 50 acidic (leucine-rich) nuclear phosphoprotein 32 family, memb
4	ANXA1	-0.46	2e-16 2e-14	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
5	APOO	0.42	2e-16 2e-14	2 x 46 apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]
6	ASF1B	1.04	2e-16 2e-14	4 x 50 anti-silencing function 1B histone chaperone [Source:HGNC Symbol;Acc:HGNC:24124]
7	ASPM	0.55	2e-16 2e-14	6 x 50 asp (abnormal spindle) homolog, microcephaly associated (D
8	ATAD2	0.6	2e-16 2e-14	2 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Sym
9	BARD1	0.56	2e-16 2e-14	2 x 50 BRCA1 associated RING domain 1 [Source:HGNC Symbol;A
10	BIRC5	0.85	2e-16 2e-14	6 x 50 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;A
11	BUB1	0.62	2e-16 2e-14	6 x 50 BUB1 mitotic checkpoint serine/threonine kinase [Source:HG
12	BUB1B	0.7	2e-16 2e-14	6 x 50 BUB1 mitotic checkpoint serine/threonine kinase B [Source:H
13	BUB3	0.27	2e-16 2e-14	7 x 48 BUB3 mitotic checkpoint protein [Source:HGNC Symbol;Acc:HGNC:24124]
14	CACYBP	0.17	2e-16 2e-14	8 x 44 calcyclin binding protein [Source:HGNC Symbol;Acc:HGNC:3
15	CAPN3	0.27	2e-16 2e-14	1 x 43 calpain 3, (p94) [Source:HGNC Symbol;Acc:HGNC:1480]
16	CCNB2	0.67	2e-16 2e-14	6 x 50 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
17	CDC45	0.58	2e-16 2e-14	1 x 50 cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1736]
18	CDC6	0.8	2e-16 2e-14	1 x 50 cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
19	CDC45	0.85	2e-16 2e-14	4 x 50 cell division cycle associated 5 [Source:HGNC Symbol;Acc:H
20	CDC47L	0.48	2e-16 2e-14	1 x 50 cell division cycle associated 7-like [Source:HGNC Symbol;A

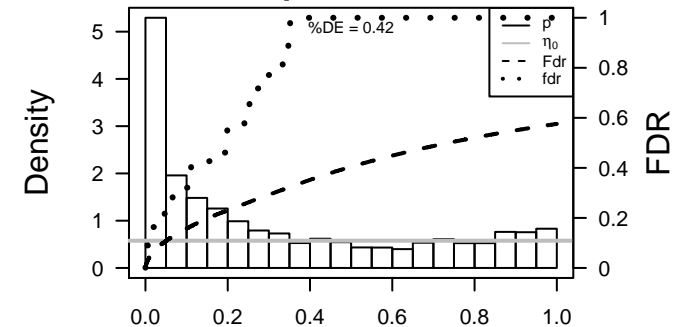
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	45.51	0e+00	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
2	44.7	0e+00	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
3	43.85	0e+00	550	GSEA C2GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	42.64	0e+00	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
5	41.5	0e+00	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
6	41.37	0e+00	197	HM HALLMARK_E2F_TARGETS
7	38.44	0e+00	1192	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
8	37.63	0e+00	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
9	37.5	0e+00	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
10	37.22	0e+00	145	GSEA C2ZHANG_CYCLING_GENES
11	37.16	8e-05	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	35.8	0e+00	99	GSEA C2BURTON_ADIPOGENESIS_3
13	35.76	0e+00	96	GSEA C2ROONQUIST_IL6_DEPRIVATION_DN
14	35.68	0e+00	327	GSEA C2BLUM_RESPONSE_TO_SALIRASIB_DN
15	35.61	0e+00	700	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
16	35.44	0e+00	110	GSEA C2WHITEFORD_PEDIATRIC_CANCER_MARKERS
17	35.31	0e+00	390	GSEA C2PUJANA_BRCA2_PCC_NETWORK
18	35.3	0e+00	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
19	34.82	0e+00	50	GSEA C2SHIDA_E2F_TARGETS
20	34.59	0e+00	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
<i>Underexpressed</i>				
1	-10.7	7e-05	3396	LymphomaOPP_Repressed
2	-9.45	2e-04	472	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
3	-9.31	2e-04	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
4	-8.64	2e-04	2188	LymphomaOPP_Poised_promoter
5	-8.46	3e-04	594	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
6	-7.8	4e-04	2159	Colon CancerPC_Colon
7	-7.79	4e-04	2185	Brain Fetal_TssA
8	-7.45	4e-04	749	GSEA C2CUI_TCF21_TARGETS_2_DN
9	-7.43	4e-04	930	GSEA C2NUYTEN_EZH2_TARGETS_UP
10	-7.31	5e-04	3088	CC plasma membrane
11	-7.3	5e-04	730	GSEA C2RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED
12	-7.29	5e-04	784	GSEA C2BUYAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
13	-7.27	5e-04	1949	Brain Fetal_TssF
14	-6.69	7e-04	616	GSEA C2NABA_MATRISOME
15	-6.67	7e-04	1907	Brain Fetal_TxTrans
16	-6.65	7e-04	286	GSEA C2PASINI_SUZ12_TARGETS_DN
17	-6.42	8e-04	2142	Colon CancerPC_Colon
18	-6.35	8e-04	622	GSEA C2LEE_BMP2_TARGETS_UP
19	-6.31	8e-04	396	GSEA C2JOHNSTONE_PARVB_TARGETS_3_UP
20	-6.31	8e-04	426	GSEA C2ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF

p-values



p-values



MSC1

Local Summary

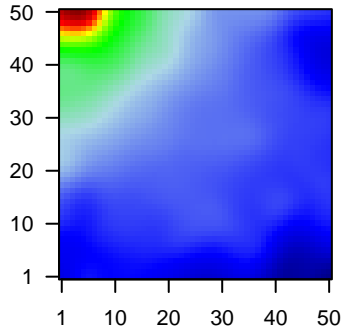
%DE = 1
 # metagenes = 28
 # genes = 413
 # genes in genesets = 412

 # genes with $fdr < 0.1$ = 411 (411 + / 0 -)
 # genes with $fdr < 0.05$ = 411 (411 + / 0 -)
 # genes with $fdr < 0.01$ = 409 (409 + / 0 -)

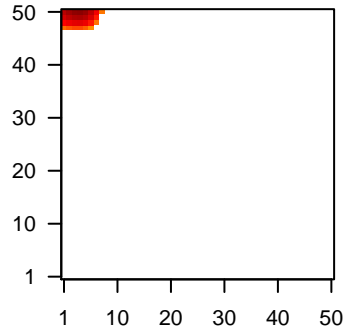
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.92

 $\langle FC \rangle$ = 0.41
 $\langle \text{shrinkage-t} \rangle$ = 4.08
 $\langle p\text{-value} \rangle$ = 0
 $\langle fdr \rangle$ = 0.02

Profile



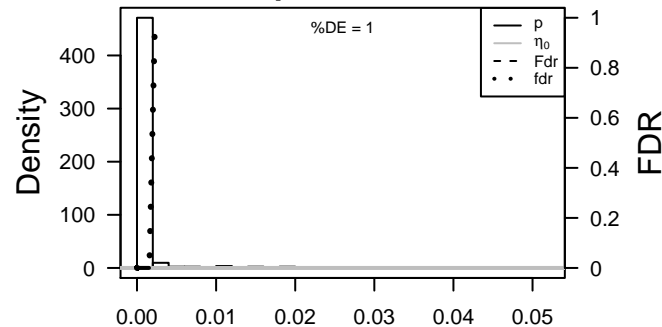
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	0.5	2e-16	2e-18	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	ANLN	0.65	2e-16	2e-18	5 x 50 anillin, actin binding protein [Source:HGNC Symbol;Acc:HGNC:24124]
3	ANP32E	0.28	2e-16	2e-18	8 x 50 acidic (leucine-rich) nuclear phosphoprotein 32 family, member 3 [Source:HGNC Symbol;Acc:HGNC:24124]
4	ASF1B	1.04	2e-16	2e-18	4 x 50 anti-silencing function 1B histone chaperone [Source:HGNC Symbol;Acc:HGNC:24124]
5	ASPM	0.55	2e-16	2e-18	6 x 50 asp (abnormal spindle) homolog, microcephaly associated [Source:HGNC Symbol;Acc:HGNC:24124]
6	ATAD2	0.6	2e-16	2e-18	2 x 50 ATPase family, AAA domain containing 2 [Source:HGNC Symbol;Acc:HGNC:24124]
7	BARD1	0.56	2e-16	2e-18	2 x 50 BRCA1 associated RING domain 1 [Source:HGNC Symbol;Acc:HGNC:24124]
8	BIRC5	0.65	2e-16	2e-18	6 x 50 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;Acc:HGNC:24124]
9	BUB1	0.62	2e-16	2e-18	6 x 50 BUB1 mitotic checkpoint serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:24124]
10	BUB1B	0.7	2e-16	2e-18	6 x 50 BUB1 mitotic checkpoint serine/threonine kinase B [Source:HGNC Symbol;Acc:HGNC:24124]
11	BUB3	0.27	2e-16	2e-18	7 x 48 BUB3 mitotic checkpoint protein [Source:HGNC Symbol;Acc:HGNC:24124]
12	CCNB2	0.67	2e-16	2e-18	6 x 50 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
13	CDC45	0.58	2e-16	2e-18	1 x 50 cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1736]
14	CDC6	0.8	2e-16	2e-18	1 x 50 cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]
15	CDC45	0.65	2e-16	2e-18	4 x 50 cell division cycle associated 5 [Source:HGNC Symbol;Acc:HGNC:1744]
16	CDC47L	0.48	2e-16	2e-18	1 x 50 cell division cycle associated 7-like [Source:HGNC Symbol;Acc:HGNC:1744]
17	CDK1	1.01	2e-16	2e-18	5 x 50 cyclin-dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:1744]
18	CDKN3	0.75	2e-16	2e-18	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:1744]
19	CENPF	0.64	2e-16	2e-18	6 x 50 centromere protein F, 350/400kDa [Source:HGNC Symbol;Acc:HGNC:1744]
20	CENPK	0.72	2e-16	2e-18	3 x 50 centromere protein K [Source:HGNC Symbol;Acc:HGNC:294]

p-values



MSC1

Local Summary

%DE = 0.77
 # metagenes = 58
 # genes = 648
 # genes in genesets = 648

 # genes with $fdr < 0.1$ = 427 (3 + / 424 -)
 # genes with $fdr < 0.05$ = 326 (1 + / 325 -)
 # genes with $fdr < 0.01$ = 205 (0 + / 205 -)

<r> metagenes = 0.96

<r> genes = 0.76

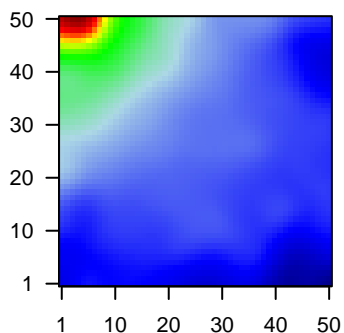
<FC> = -0.13

<shrinkage-t> = -1.29

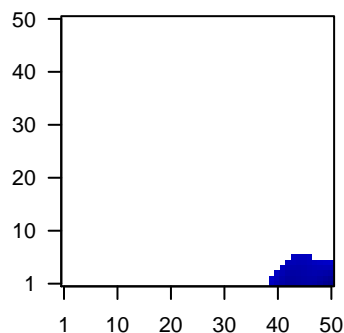
<p-value> = 0.01

<fdr> = 0.52

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANXA1	-0.46	2e-16	3e-14	50 x 1 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
2	ANXA2	-0.16	2e-11	1e-08	50 x 3 annexin A2 [Source:HGNC Symbol;Acc:HGNC:537]
3	DLGAP4	-0.37	2e-10	1e-08	50 x 1 discs, large (Drosophila) homolog-associated protein 4 [Sou
4	MARCKS	-0.22	3e-10	1e-08	46 x 1 myristoylated alanine-rich protein kinase C substrate [Source
5	CTNNA1	-0.13	3e-10	5e-08	46 x 4 catenin (cadherin-associated protein), alpha 1, 102kDa [Sou
6	EDIL3	-0.4	7e-10	5e-08	50 x 1 EGF-like repeats and discoidin I-like domains 3 [Source:HGI
7	CRYAB	-0.51	1e-09	2e-07	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
8	PLK2	-0.44	2e-09	2e-07	50 x 1 polo-like kinase 2 [Source:HGNC Symbol;Acc:HGNC:19699]
9	USP53	-0.29	4e-09	1e-06	48 x 1 ubiquitin specific peptidase 53 [Source:HGNC Symbol;Acc:H
10	PRICKLE2	-0.3	1e-08	2e-06	44 x 3 prickle homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:H
11	MYOF	-0.33	3e-08	2e-06	50 x 1 myoferlin [Source:HGNC Symbol;Acc:HGNC:3656]
12	C15orf52	-0.27	4e-08	2e-06	47 x 1 chromosome 15 open reading frame 52 [Source:HGNC Synt
13	SOX4	-0.23	5e-08	2e-06	41 x 1 SRY (sex determining region Y)-box 4 [Source:HGNC Symb
14	TMEM45A	-0.33	6e-08	2e-06	50 x 1 transmembrane protein 45A [Source:HGNC Symbol;Acc:HGNC
15	CALD1	-0.25	7e-08	2e-06	50 x 1 caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
16	SAMD4A	-0.26	7e-08	3e-06	49 x 1 sterile alpha motif domain containing 4A [Source:HGNC Sym
17	KRTAP7-1	-0.33	1e-07	9e-06	50 x 1 keratin associated protein 7-1 (gene/pseudogene) [Source:H
18	AMMECR1	-0.28	2e-07	9e-06	42 x 1 Alport syndrome, mental retardation, midface hypoplasia and
19	MATN2	-0.31	2e-07	9e-06	50 x 1 matrilin 2 [Source:HGNC Symbol;Acc:HGNC:6908]
20	CYTH3	-0.28	3e-07	9e-06	46 x 5 cytohesin 3 [Source:HGNC Symbol;Acc:HGNC:9504]

p-values

