

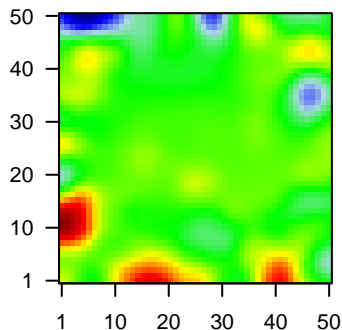
B11_mel

Global Summary

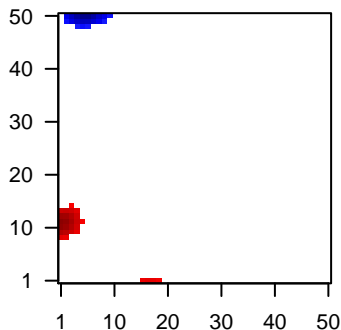
%DE = 0.22
 # genes with fdr < 0.2 = 2865 (1714 + / 1151 -)
 # genes with fdr < 0.1 = 2280 (1395 + / 885 -)
 # genes with fdr < 0.05 = 1953 (1205 + / 748 -)
 # genes with fdr < 0.01 = 1259 (785 + / 474 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0
 <p-value> = 0.07
 <fdr> = 0.78

Profile



Regulated Spots



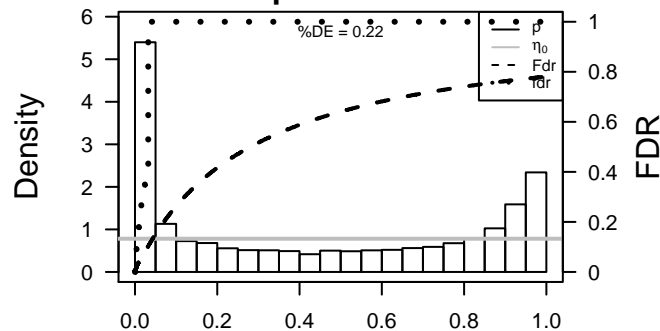
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ADSL	-1.58	2e-16	7e-14	28 x 50 adenylosuccinate lyase [Source:HGNC Symbol;Acc:HGNC:2]
2	ALG3	-1.69	2e-16	7e-14	48 x 50 ALG3, alpha-1,3- mannosyltransferase [Source:HGNC Syml
3	ASPH	-1.13	2e-16	7e-14	35 x 2 aspartate beta-hydroxylase [Source:HGNC Symbol;Acc:HGNC
4	ATIC	-1.73	2e-16	7e-14	44 x 50 5-aminoimidazole-4-carboxamide ribonucleotide formyltrans
5	AVP11	-1.43	2e-16	7e-14	49 x 50 arginine vasopressin-induced 1 [Source:HGNC Symbol;Acc:HG
6	BSCL2	-2.03	2e-16	7e-14	50 x 50 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:HG
7	CADPS	2.03	2e-16	7e-14	25 x 19 Ca++-dependent secretion activator [Source:HGNC Symbol;Acc:HG
8	CALU	-1.58	2e-16	7e-14	45 x 36 calumenin [Source:HGNC Symbol;Acc:HGNC:1458]
9	CCNDBP1	-1.47	2e-16	7e-14	1 x 21 cyclin D-type binding-protein 1 [Source:HGNC Symbol;Acc:HGNC:1
10	CCT4	-1.22	2e-16	7e-14	45 x 38 chaperonin containing TCP1, subunit 4 (delta) [Source:HGNC
11	CKS2	-1.66	2e-16	7e-14	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC Sy
12	COMMD4	-1.59	2e-16	7e-14	11 x 50 COMM domain containing 4 [Source:HGNC Symbol;Acc:HGNC:17
13	EBP	-2.01	2e-16	7e-14	1 x 48 emopamil binding protein (sterol isomerase) [Source:HGNC S
14	ELP2	-1.55	2e-16	7e-14	37 x 50 elongator acetyltransferase complex subunit 2 [Source:HGNC
15	EXOSC8	-1.52	2e-16	7e-14	1 x 50 exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17
16	G6PC3	-1.64	2e-16	7e-14	48 x 49 glucose 6 phosphatase, catalytic, 3 [Source:HGNC Symbol;A
17	GLB1	-1.63	2e-16	7e-14	40 x 50 galactosidase, beta 1 [Source:HGNC Symbol;Acc:HGNC:429
18	HN1	-1.67	2e-16	7e-14	47 x 39 hematological and neurological expressed 1 [Source:HGNC S
19	HSD17B4	-1.63	2e-16	7e-14	11 x 50 hydroxysteroid (17-beta) dehydrogenase 4 [Source:HGNC S
20	MARS	-1.72	2e-16	7e-14	43 x 47 methionyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC

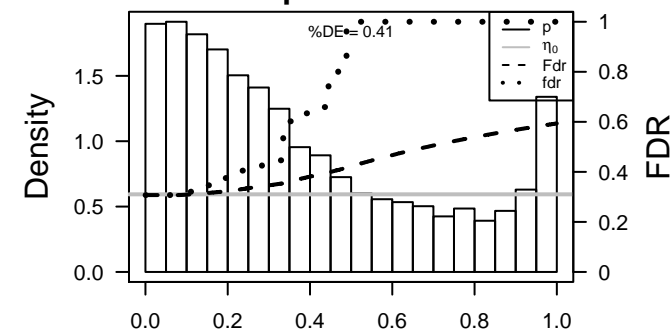
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.01	0.004	1565	BP regulation of transcription, DNA-templated
2	4.78	0.004	5940	Brain Overlap_fetal_midbrain_HetRpts
3	4.54	0.005	1664	BP transcription, DNA-templated
4	4.44	0.005	274	miRNA target-miR-548h
5	4.18	0.006	786	Brain Fetal_EnhG
6	4.09	0.007	12	GSEA C2BIOCARTA_RAB_PATHWAY
7	3.95	0.008	833	GSEA C2DACOSTA_UV_RESPONSE_VIA_ERCC3_DN
8	3.94	0.008	784	GSEA C2BUYAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
9	3.93	0.008	166	miRNA target-miR-548g
10	3.86	0.008	479	miRNA target-miR-16
11	3.81	0.009	289	miRNA target-miR-186
12	3.8	0.009	2037	MF DNA binding
13	3.71	0.010	41	miRNA target-miR-601
14	3.7	0.010	293	miRNA target-miR-548j
15	3.69	0.010	1007	MF poly(A) RNA binding
16	3.66	0.010	75	BP regulation of catalytic activity
17	3.65	0.010	115	miRNA target-miR-515-5p
18	3.64	0.010	2211	LymphoidOPP_Repetitive
19	3.61	0.010	17	BP vesicle docking
20	3.56	0.011	1033	MF nucleic acid binding
<i>Underexpressed</i>				
1	-8.66	5e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
2	-8.49	5e-04	142	Glio WILLSCHER_GBM_Verhaak-CL_up (C
3	-7.36	9e-04	550	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
4	-7.23	9e-04	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
5	-6.78	1e-03	124	GSEA C2ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
6	-6.61	1e-03	155	GSEA C2HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP
7	-6.6	1e-03	145	GSEA C2ZHANG_CYCLING_GENES
8	-6.55	1e-03	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
9	-6.54	8e-01	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
10	-6.33	2e-03	270	GSEA C2BASAKI_YBX1_TARGETS_UP
11	-6.32	2e-03	116	GSEA C2MISSIAGLIA_REGULATED_BY_METHYLATION_DN
12	-6.22	1e-02	15	Cancer RHODES_UNDIFFERENTIATED_CANCER
13	-6.2	2e-03	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
14	-6.12	2e-03	16	GSEA C2KEGG_STEROID_BIOSYNTHESIS
15	-5.96	2e-03	288	GSEA C2WEST_ADRENOCORTECICAL_TUMOR_UP
16	-5.93	2e-03	341	GSEA C2RHEIN_ALL_GLUCCOCORTICOID_THERAPY_DN
17	-5.86	2e-03	81	GSEA C2GRAHAM_NORMAL QUIESCENT_VS_NORMAL_DIVIDING_DN
18	-5.85	2e-03	291	GSEA C2HORIUCHI_WTAP_TARGETS_DN
19	-5.76	2e-03	944	GSEA C2NUYTEN_EZH2_TARGETS_DN
20	-5.76	2e-03	216	GSEA C2MARKER_RB1_ACUTE_LOF_DN

p-values



p-values



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Local Summary

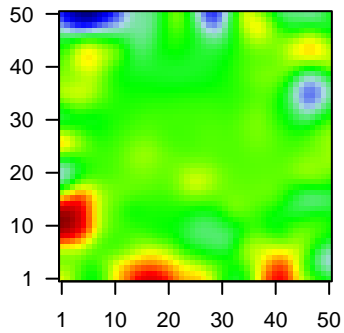
%DE = 0.58
 # metagenes = 4
 # genes = 63
 # genes in genesets = 63

 # genes with $fdr < 0.1$ = 22 (21 + / 1 -)
 # genes with $fdr < 0.05$ = 18 (18 + / 0 -)
 # genes with $fdr < 0.01$ = 15 (15 + / 0 -)

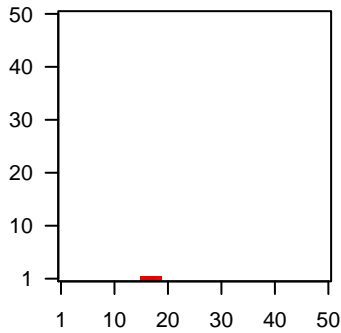
$\langle r \rangle$ metagenes = 0.95
 $\langle r \rangle$ genes = 0.13

 $\langle FC \rangle$ = 0.36
 $\langle \text{shrinkage-t} \rangle$ = 5.59
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.61

Profile



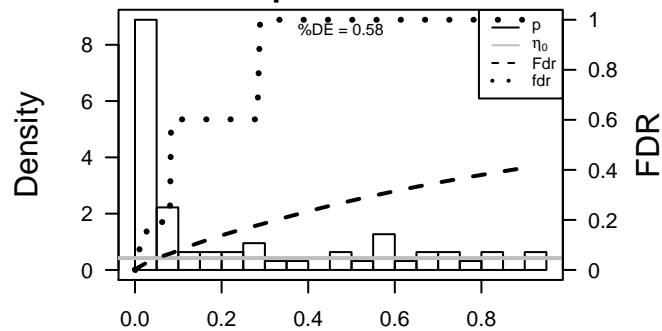
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	NFIX	1.34	8e-09	2e-07	18 x 1 nuclear factor I/X (CCAAT-binding transcription factor) [Sourc
2	PPP2R4	1.33	1e-08	1e-06	17 x 1 protein phosphatase 2A activator, regulatory subunit 4 [Sourc
3	KIAA0586	1.26	6e-08	1e-06	18 x 1 KIAA0586 [Source:HGNC Symbol;Acc:HGNC:19960]
4	SARS2	1.24	1e-07	2e-06	17 x 1 seryl-tRNA synthetase 2, mitochondrial [Source:HGNC Synt
5	PRMT9	1.22	2e-07	4e-06	18 x 1 protein arginine methyltransferase 9 [Source:HGNC Symbol;/
6	BTBD9	1.19	3e-07	1e-05	17 x 1 BTB (POZ) domain containing 9 [Source:HGNC Symbol;Acc:!
7	AP1G1	1.14	8e-07	2e-04	19 x 1 adaptor-related protein complex 1, gamma 1 subunit [Source
8	BCAR1	1.04	8e-06	3e-04	16 x 1 breast cancer anti-estrogen resistance 1 [Source:HGNC Syrr
9	KCTD20	0.98	2e-05	4e-04	16 x 1 potassium channel tetramerization domain containing 20 [So
10	PHF14	0.95	4e-05	5e-04	16 x 1 PHD finger protein 14 [Source:HGNC Symbol;Acc:HGNC:22z
11	IL13RA1	0.92	8e-05	5e-04	17 x 1 interleukin 13 receptor, alpha 1 [Source:HGNC Symbol;Acc:H
12	CDK12	0.92	9e-05	5e-04	17 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:HG
13	FXR1	0.79	1e-04	2e-03	18 x 1 fragile X mental retardation, autosomal homolog 1 [Source:H
14	AREL1	0.88	2e-04	9e-03	19 x 1 apoptosis resistant E3 ubiquitin protein ligase 1 [Source:HG
15	HERC2	0.79	7e-04	9e-03	19 x 1 HECT and RLD domain containing E3 ubiquitin protein ligase
16	YAE1D1	0.78	8e-04	1e-02	19 x 1 Yae1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC
17	ATXN2L	0.74	2e-03	1e-02	16 x 1 ataxin 2-like [Source:HGNC Symbol;Acc:HGNC:31326]
18	ATF6B	0.73	2e-03	4e-02	16 x 1 activating transcription factor 6 beta [Source:HGNC Symbol;/
19	DIP2B	0.69	3e-03	5e-02	19 x 1 DIP2 disco-interacting protein 2 homolog B (Drosophila) [So
20	ZHX1	0.6	1e-02	5e-02	19 x 1 zinc fingers and homeoboxes 1 [Source:HGNC Symbol;Acc:!

p-values



B11_mel

Local Summary

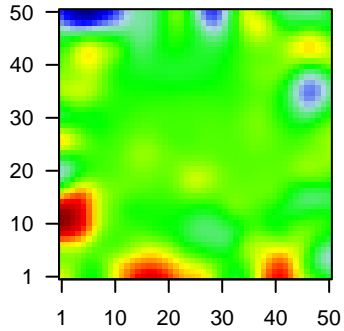
%DE = 0.72
 # metagenes = 24
 # genes = 289
 # genes in genesets = 288

 # genes with $fdr < 0.1$ = 142 (117 + / 25 -)
 # genes with $fdr < 0.05$ = 123 (102 + / 21 -)
 # genes with $fdr < 0.01$ = 83 (70 + / 13 -)

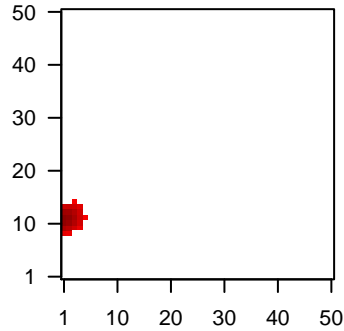
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.12

 $\langle FC \rangle$ = 0.26
 $\langle \text{shrinkage-t} \rangle$ = 4.27
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.55

Profile



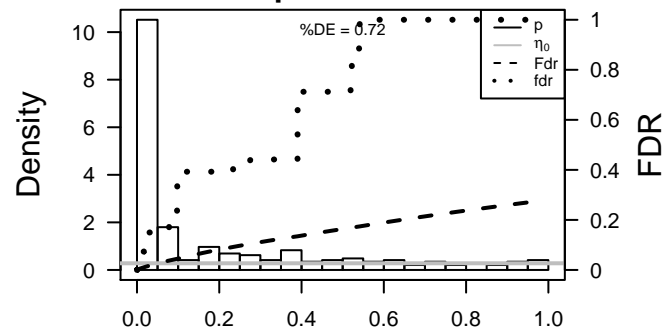
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	VAV3	1.65	2e-12	8e-11	1 x 14 vav 3 guanine nucleotide exchange factor [Source:HGNC Syr
2	SAT1	0.66	2e-12	4e-08	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC
3	RAPGEF6	1.46	4e-10	2e-07	1 x 10 Rap guanine nucleotide exchange factor (GEF) 6 [Source:HG
4	LIN52	1.39	2e-09	2e-07	1 x 13 lin-52 DREAM MuvB core complex component [Source:HGN
5	C18orf21	1.36	5e-09	4e-07	4 x 12 chromosome 18 open reading frame 21 [Source:HGNC Symt
6	SGK1	0.55	1e-08	4e-07	1 x 13 serum/glucocorticoid regulated kinase 1 [Source:HGNC Syml
7	OBFC1	1.31	2e-08	4e-07	4 x 13 oligonucleotide/oligosaccharide-binding fold containing 1 [So
8	ZNF559	1.31	2e-08	5e-07	3 x 15 zinc finger protein 559 [Source:HGNC Symbol;Acc:HGNC:28
9	GAS8	1.3	3e-08	5e-07	1 x 10 growth arrest-specific 8 [Source:HGNC Symbol;Acc:HGNC:4
10	BBS5	1.29	4e-08	5e-07	1 x 11 Bardet-Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC
11	ZNF44	1.28	4e-08	2e-06	3 x 12 zinc finger protein 44 [Source:HGNC Symbol;Acc:HGNC:131
12	NR6A1	1.26	7e-08	2e-06	4 x 13 nuclear receptor subfamily 6, group A, member 1 [Source:HG
13	ADIPOR2	1.25	9e-08	3e-06	1 x 10 adiponectin receptor 2 [Source:HGNC Symbol;Acc:HGNC:24
14	ARAP1	1.23	1e-07	4e-06	1 x 11 ArfGAP with RhoGAP domain, ankyrin repeat and PH domain
15	SCIN	1.22	2e-07	4e-06	1 x 12 scinderin [Source:HGNC Symbol;Acc:HGNC:21695]
16	SOS1	1.21	2e-07	6e-06	4 x 12 son of sevenless homolog 1 (Drosophila) [Source:HGNC Syrr
17	SUOX	1.2	3e-07	1e-05	1 x 12 sulfite oxidase [Source:HGNC Symbol;Acc:HGNC:11460]
18	RCHY1	1.08	8e-07	1e-05	2 x 13 ring finger and CHY zinc finger domain containing 1, E3 ubiq
19	RGS12	1.15	8e-07	1e-05	1 x 9 regulator of G-protein signaling 12 [Source:HGNC Symbol;A
20	MKS1	1.15	9e-07	1e-05	3 x 13 Meckel syndrome, type 1 [Source:HGNC Symbol;Acc:HGNC:

p-values



B11_mel

Local Summary

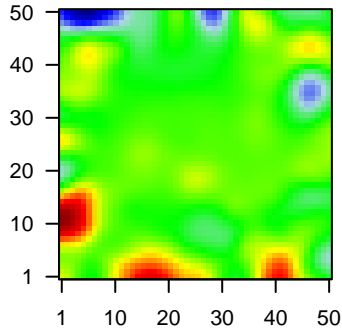
%DE = 0.85
 # metagenes = 20
 # genes = 269
 # genes in genesets = 269

 # genes with $fdr < 0.1$ = 168 (31 + / 137 -)
 # genes with $fdr < 0.05$ = 138 (28 + / 110 -)
 # genes with $fdr < 0.01$ = 96 (23 + / 73 -)

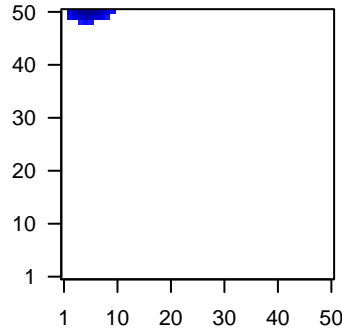
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.33

 $\langle FC \rangle$ = -0.32
 $\langle \text{shrinkage-t} \rangle$ = -5.06
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.53

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	CKS2	-1.66	2e-16	9e-15	5 x 50 CDC28 protein kinase regulatory subunit 2 [Source:HGNC S]
2	CDKN3	-1.32	2e-14	2e-12	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;A
3	TMEM106C	-0.92	8e-14	5e-10	5 x 48 transmembrane protein 106C [Source:HGNC Symbol;Acc:HG
4	RFC5	-1.39	1e-11	5e-10	2 x 50 replication factor C (activator 1) 5, 36.5kDa [Source:HGNC S]
5	TUBB4B	-1.21	3e-11	2e-09	7 x 50 tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:HGNC
6	MAD2L1	-1.35	8e-11	3e-08	5 x 50 MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC S]
7	MIS18A	-1.3	9e-10	3e-08	3 x 49 MIS18 kinetochore protein A [Source:HGNC Symbol;Acc:HGI
8	HMGB2	-1.28	2e-09	3e-08	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:
9	TUBA1B	-0.57	2e-09	2e-07	6 x 48 tubulin, alpha 1b [Source:HGNC Symbol;Acc:HGNC:18809]
10	POLH	1.36	6e-09	4e-07	8 x 49 polymerase (DNA directed), eta [Source:HGNC Symbol;Acc:t
11	FAIM	1.32	2e-08	5e-07	4 x 48 Fas apoptotic inhibitory molecule [Source:HGNC Symbol;Acc
12	KIAA0101	-1.18	3e-08	5e-07	3 x 50 KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
13	RRM1	-1.02	4e-08	5e-06	2 x 50 ribonucleotide reductase M1 [Source:HGNC Symbol;Acc:HGI
14	HSD17B11	-1.07	2e-07	5e-06	8 x 50 hydroxysteroid (17-beta) dehydrogenase 11 [Source:HGNC t
15	MPHOSPH9	-1.17	3e-07	9e-06	7 x 49 M-phase phosphoprotein 9 [Source:HGNC Symbol;Acc:HGNC
16	AURKA	1.17	5e-07	1e-05	8 x 50 aurora kinase A [Source:HGNC Symbol;Acc:HGNC:11393]
17	ZWINT	-1.13	8e-07	2e-05	5 x 50 ZW10 interacting kinetochore protein [Source:HGNC Symbol;
18	KANSL2	-1.11	2e-06	2e-05	9 x 50 KAT8 regulatory NSL complex subunit 2 [Source:HGNC Syml
19	NCAPG2	1.1	2e-06	2e-05	6 x 48 non-SMC condensin II complex, subunit G2 [Source:HGNC t
20	NEDD1	1.08	3e-06	2e-05	8 x 49 neural precursor cell expressed, developmentally down-regul

p-values

