

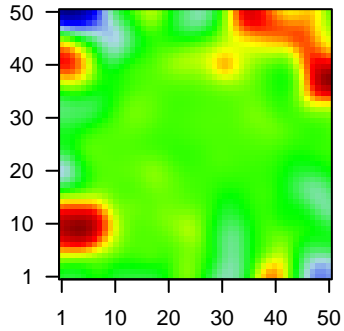
E7_mel

Global Summary

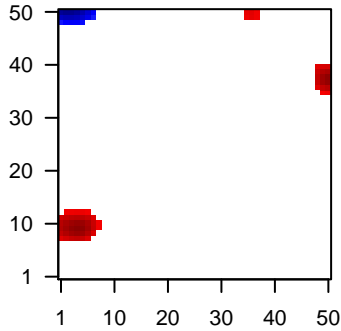
%DE = 0.2
 # genes with fdr < 0.2 = 2497 (1503 + / 994 -)
 # genes with fdr < 0.1 = 1992 (1227 + / 765 -)
 # genes with fdr < 0.05 = 1614 (1017 + / 597 -)
 # genes with fdr < 0.01 = 988 (647 + / 341 -)
 # genes in genesets = 14839

<FC> = 0
 <shrinkage-t> = 0.01
 <p-value> = 0.09
 <fdr> = 0.8

Profile



Regulated Spots



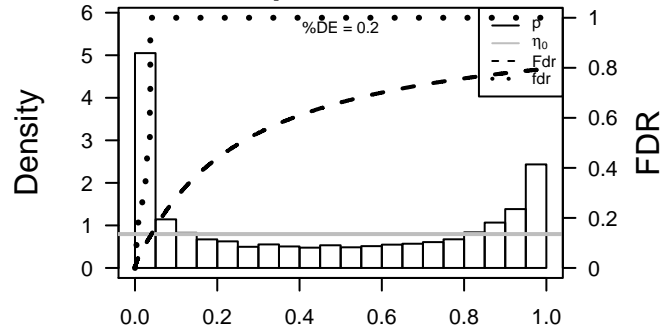
Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ACTL6A	-1.88	2e-16	1e-13	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	BSCL2	-1.12	2e-16	1e-13	50 x 50 Berardinelli-Seip congenital lipodystrophy 2 (seipin) [Source:HGNC Symbol;Acc:HGNC:24124]
3	CTSD	-1.01	2e-16	1e-13	1 x 37 cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]
4	GGH	-2.02	2e-16	1e-13	4 x 47 gamma-glutamyl hydrolase (conjugase, folylpolygamma-glutamate synthase) [Source:HGNC Symbol;Acc:HGNC:24124]
5	GRHPR	-1.34	2e-16	1e-13	26 x 50 glyoxylate reductase/hydroxypyruvate reductase [Source:HGNC Symbol;Acc:HGNC:24124]
6	LGALS1	-1.68	2e-16	1e-13	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:HGNC:24124]
7	LSM8	-1.59	2e-16	1e-13	12 x 44 LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:24124]
8	MARS	-1.72	2e-16	1e-13	43 x 47 methionyl-tRNA synthetase [Source:HGNC Symbol;Acc:HGNC:24124]
9	MRPS23	-1.32	2e-16	1e-13	2 x 26 mitochondrial ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:24124]
10	MSC	-1.62	2e-16	1e-13	32 x 1 myosin, cardiac, 1 [Source:HGNC Symbol;Acc:HGNC:7321]
11	NAA50	-1.68	2e-16	1e-13	28 x 50 N(alpha)-acetyltransferase 50, NatE catalytic subunit [Source:HGNC Symbol;Acc:HGNC:24124]
12	NUPR1	-1.58	2e-16	1e-13	45 x 50 nuclear protein, transcriptional regulator, 1 [Source:HGNC Symbol;Acc:HGNC:24124]
13	OSER1	-1.65	2e-16	1e-13	45 x 6 oxidative stress responsive serine-rich 1 [Source:HGNC Symbol;Acc:HGNC:24124]
14	PLS3	-1.58	2e-16	1e-13	21 x 43 plastin 3 [Source:HGNC Symbol;Acc:HGNC:9091]
15	PMP22	-1.79	2e-16	1e-13	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC:24124]
16	PSMD9	-1.64	2e-16	1e-13	50 x 14 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC Symbol;Acc:HGNC:24124]
17	QPCT	-1.51	2e-16	1e-13	1 x 34 glutaminyl-peptide cyclotransferase [Source:HGNC Symbol;Acc:HGNC:24124]
18	RAD51C	-1.66	2e-16	1e-13	12 x 48 RAD51 paralogs [Source:HGNC Symbol;Acc:HGNC:9820]
19	SAT1	1.04	2e-16	1e-13	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:24124]
20	SF3A3	-1.72	2e-16	1e-13	12 x 50 splicing factor 3a, subunit 3, 60kDa [Source:HGNC Symbol;Acc:HGNC:24124]

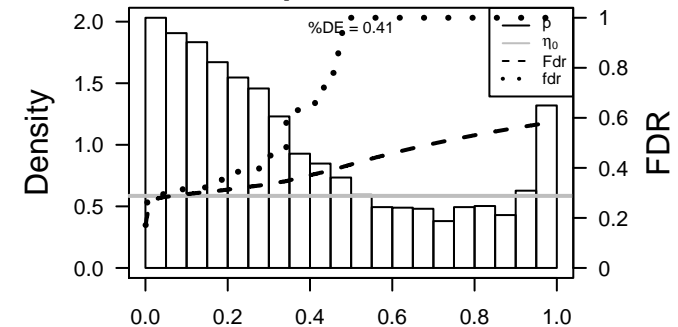
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	5.15	0.003	209	GSEA C2LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
2	3.96	0.008	18	GSEA C2BIOCARTA_RAC1_PATHWAY
3	3.77	0.009	13	BP snRNA processing
4	3.76	0.009	11	MF cAMP response element binding
5	3.53	0.011	114	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
6	3.49	0.012	151	Chr Chr 21
7	3.45	0.012	63	CC mitochondrial intermembrane space
8	3.4	0.012	13	CC integrator complex
9	3.32	0.013	135	BP cellular metabolic process
10	3.3	0.014	61	BP regulation of translation
11	3.29	0.014	13	Lymphonoma BENTINK_mBL UP
12	3.28	0.014	7209	Lymphonoma OPP_Weak_promoter
13	3.2	0.015	34	BP retrograde vesicle-mediated transport, Golgi to ER
14	3.19	0.015	37	MF coenzyme binding
15	3.19	0.015	13	BP COPII coating of Golgi vesicle
16	3.15	0.016	1468	CC mitochondrion
17	3.11	0.016	18	BP melanocyte differentiation
18	3.1	0.017	39	GSEA C2CHANDRAN_METASTASIS_TOP50_DN
19	3.08	0.017	16	CC eukaryotic translation initiation factor 3 complex
20	3.02	0.018	4	Glio WILLSCHEER_GBM_Verhaak-PN (mut&wt)_UP (L)
<i>Underexpressed</i>				
1	-10.72	2e-04	305	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
2	-10.69	2e-04	550	GSEA C2BOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
3	-10.6	2e-04	139	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
4	-10.21	2e-04	197	HM HALLMARK_E2F_TARGETS
5	-9.87	3e-04	142	Glio WILLSCHEER_GBM_Verhaak-CL_up (C)
6	-9.8	3e-04	96	GSEA C2CROONQUIST_IL6_DEPRIVATION_DN
7	-9.17	4e-04	72	GSEA C2CROONQUIST_NRAS_SIGNALING_DN
8	-9.01	4e-04	242	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
9	-8.98	4e-04	145	GSEA C2CHANG_CYCLING_GENES
10	-8.87	4e-04	54	GSEA C2KANG_DOXORUBICIN_RESISTANCE_UP
11	-8.53	4e-02	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
12	-8.39	5e-04	99	GSEA C2BURTON_ADIPOGENESIS_3
13	-8.09	6e-04	308	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_3_UP
14	-8.05	6e-04	270	GSEA C2BASAKI_YBX1_TARGETS_UP
15	-8.03	6e-04	89	GSEA C2MORI_IMMATURE_B_LYMPHOCYTE_DN
16	-7.88	7e-04	50	GSEA C2SHIDA_E2F_TARGETS
17	-7.63	8e-04	616	GSEA C2BENPORATH_CYCLING_GENES
18	-7.62	8e-04	267	GSEA C2ZHANG_TLX_TARGETS_60HR_DN
19	-7.49	8e-04	436	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
20	-7.45	8e-04	58	GSEA C2SONG_TARGETS_OF_IE86_CMV_PROTEIN

p-values



p-values



E7_mel

Local Summary

%DE = 0.72
 # metagenes = 41
 # genes = 377
 # genes in genesets = 375

 # genes with $fdr < 0.1$ = 190 (157 + / 33 -)
 # genes with $fdr < 0.05$ = 160 (140 + / 20 -)
 # genes with $fdr < 0.01$ = 95 (88 + / 7 -)

<r> metagenes = 0.86

<r> genes = 0.1

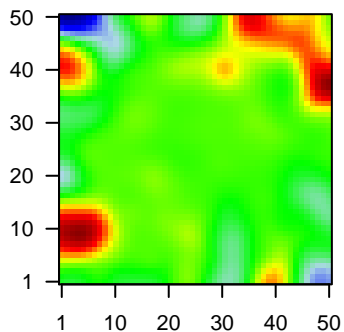
<FC> = 0.31

<shrinkage-t> = 5.1

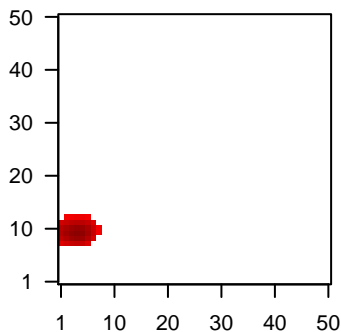
<p-value> = 0.01

<fdr> = 0.57

Profile



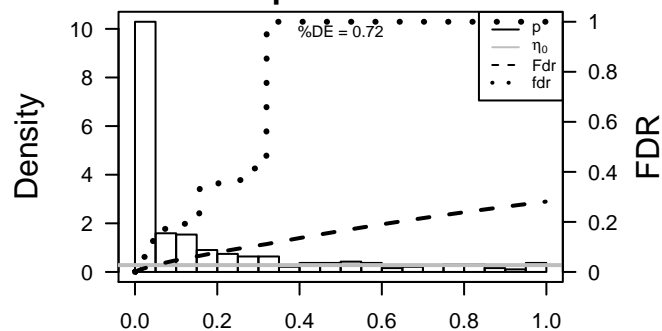
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	SAT1	1.04	2e-16	2e-14	1 x 11 spermidine/spermine N1-acetyltransferase 1 [Source:HGNC
2	EGLN3	1.89	1e-14	1e-08	2 x 12 egl-9 family hypoxia-inducible factor 3 [Source:HGNC Symb
3	LYRM9	1.58	1e-10	7e-08	1 x 12 LYR motif containing 9 [Source:HGNC Symbol;Acc:HGNC:27
4	MCF2	1.5	9e-10	7e-08	5 x 10 MCF.2 cell line derived transforming sequence [Source:HGNC
5	AADAT	1.49	1e-09	7e-08	8 x 10 aminoadipate aminotransferase [Source:HGNC Symbol;Acc:t
6	NPM3	1.47	2e-09	7e-08	4 x 10 nucleophosmin/nucleoplasmin 3 [Source:HGNC Symbol;Acc:
7	PRKAR2B	1.46	3e-09	1e-07	6 x 9 protein kinase, cAMP-dependent, regulatory, type II, beta [Sc
8	PLA2G4B	1.45	4e-09	2e-07	3 x 9 phospholipase A2, group IVB (cytosolic) [Source:HGNC Syml
9	SEMA3A	1.43	5e-09	2e-07	7 x 12 sema domain, immunoglobulin domain (Ig), short basic doma
10	ZNF18	1.41	1e-08	2e-07	2 x 8 zinc finger protein 18 [Source:HGNC Symbol;Acc:HGNC:129
11	TIGD7	1.4	1e-08	2e-07	8 x 10 tigger transposable element derived 7 [Source:HGNC Symbo
12	CEACAM1	-1.27	1e-08	2e-07	1 x 10 carcinoembryonic antigen-related cell adhesion molecule 1 (I
13	SLC9A1	1.39	1e-08	6e-07	3 x 10 solute carrier family 9, subfamily A (NHE1, cation proton anti
14	MMP8	1.37	2e-08	6e-07	5 x 12 matrix metalloproteinase 8 [Source:HGNC Symbol;Acc:HGNC
15	PLA1A	1.37	3e-08	9e-07	1 x 10 phospholipase A1 member A [Source:HGNC Symbol;Acc:HG
16	RUNX2	1.35	4e-08	9e-07	6 x 13 runt-related transcription factor 2 [Source:HGNC Symbol;Acc
17	STAT6	1.34	5e-08	9e-07	3 x 13 signal transducer and activator of transcription 6, interleukin-
18	ERMARD	1.33	5e-08	9e-07	6 x 8 ER membrane-associated RNA degradation [Source:HGNC
19	TSPAN4	1.33	6e-08	5e-06	6 x 13 tetraspanin 4 [Source:HGNC Symbol;Acc:HGNC:11859]
20	TDRD3	1.29	1e-07	5e-06	7 x 9 tudor domain containing 3 [Source:HGNC Symbol;Acc:HGNC

p-values



E7_mel

Local Summary

%DE = 0.73
 # metagenes = 17
 # genes = 179
 # genes in genesets = 178

 # genes with $fdr < 0.1$ = 93 (77 + / 16 -)
 # genes with $fdr < 0.05$ = 79 (65 + / 14 -)
 # genes with $fdr < 0.01$ = 57 (48 + / 9 -)

<r> metagenes = 0.93

<r> genes = 0.09

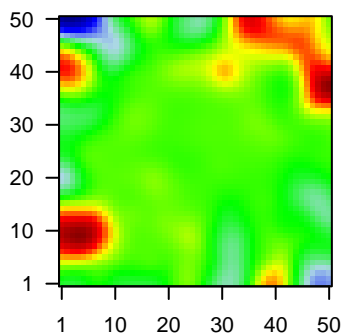
<FC> = 0.31

<shrinkage-t> = 5.15

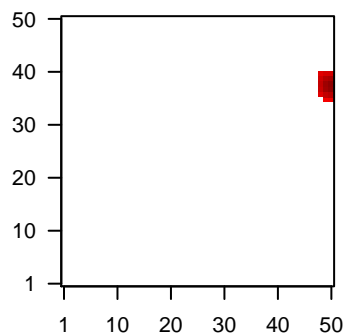
<p-value> = 0.01

<fdr> = 0.53

Profile



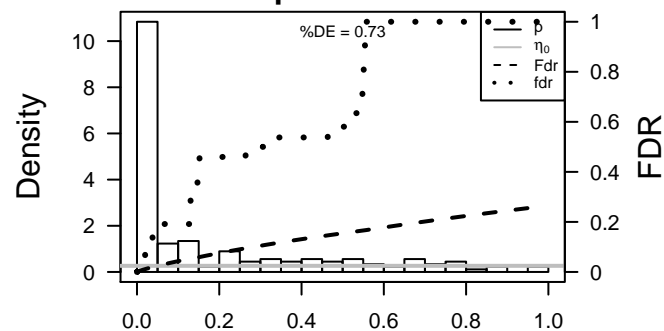
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	GLS2	1.59	1e-10	2e-08	48 x 38 glutaminase 2 (liver, mitochondrial) [Source:HGNC Symbol;A
2	MYOM1	1.51	8e-10	2e-08	50 x 37 myosin 1 [Source:HGNC Symbol;Acc:HGNC:7613]
3	SEC61A2	1.5	1e-09	2e-08	48 x 37 Sec61 alpha 2 subunit (S. cerevisiae) [Source:HGNC Symbol
4	NOSIP	-1.34	1e-09	2e-08	50 x 35 nitric oxide synthase interacting protein [Source:HGNC Symb
5	ZNF35	1.48	2e-09	8e-08	50 x 37 zinc finger protein 35 [Source:HGNC Symbol;Acc:HGNC:130
6	NRIP3	1.45	3e-09	4e-07	50 x 38 nuclear receptor interacting protein 3 [Source:HGNC Symbol;
7	RNF139	1.37	2e-08	4e-07	50 x 37 ring finger protein 139 [Source:HGNC Symbol;Acc:HGNC:171
8	PRKAB2	1.37	2e-08	4e-06	50 x 38 protein kinase, AMP-activated, beta 2 non-catalytic subunit [
9	TAMM41	1.29	1e-07	4e-06	49 x 38 TAM41, mitochondrial translocator assembly and maintenanc
10	P2RX7	1.28	2e-07	9e-06	50 x 38 purinergic receptor P2X, ligand gated ion channel, 7 [Source:
11	ZFC3H1	1.21	8e-07	9e-06	50 x 39 zinc finger, C3H1-type containing [Source:HGNC Symbol;Ao
12	HPS5	-1.17	9e-07	9e-06	49 x 40 Hermansky-Pudlak syndrome 5 [Source:HGNC Symbol;Acc:
13	WDR59	1.2	9e-07	9e-06	48 x 39 WD repeat domain 59 [Source:HGNC Symbol;Acc:HGNC:25:
14	ZNF75A	1.2	1e-06	9e-06	50 x 38 zinc finger protein 75a [Source:HGNC Symbol;Acc:HGNC:13
15	KPNA5	1.19	1e-06	2e-05	50 x 38 karyopherin alpha 5 (importin alpha 6) [Source:HGNC Symbc
16	ETHE1	1.16	2e-06	2e-05	50 x 38 ethylmalonic encephalopathy 1 [Source:HGNC Symbol;Acc:H
17	FEZ2	1.16	2e-06	2e-05	49 x 40 fasciculation and elongation protein zeta 2 (zygin II) [Source:t
18	MGEA5	1.01	3e-06	2e-05	50 x 40 meningioma expressed antigen 5 (hyaluronidase) [Source:HC
19	OBSL1	1.14	3e-06	2e-05	50 x 35 obscurin-like 1 [Source:HGNC Symbol;Acc:HGNC:29092]
20	HACL1	1.14	3e-06	2e-05	50 x 39 2-hydroxyacyl-CoA lyase 1 [Source:HGNC Symbol;Acc:HGN

p-values



E7_mel

Local Summary

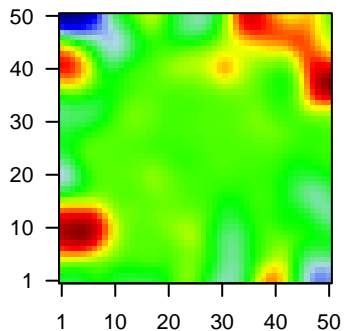
%DE = 0.84
 # metagenes = 6
 # genes = 81
 # genes in genesets = 81

 # genes with $fdr < 0.1$ = 55 (43 + / 12 -)
 # genes with $fdr < 0.05$ = 48 (38 + / 10 -)
 # genes with $fdr < 0.01$ = 37 (28 + / 9 -)

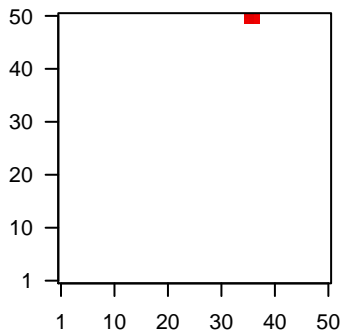
<r> metagenes = 0.97
 <r> genes = 0.1

<FC> = 0.33
 <shrinkage-t> = 5.44
 <p-value> = 0
 <fdr> = 0.45

Profile



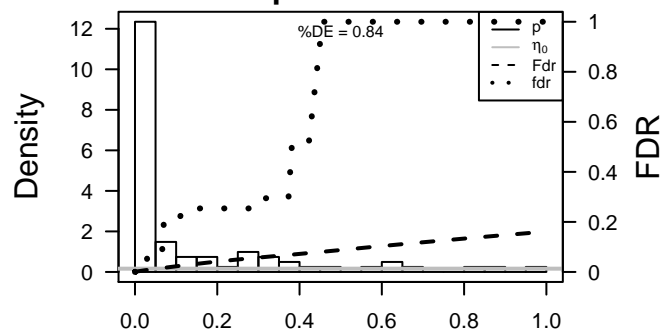
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	LPCAT3	1.53	4e-10	5e-09	35 x 50 lysophosphatidylcholine acyltransferase 3 [Source:HGNC Syr
2	LOH12CR1	1.51	7e-10	1e-07	36 x 50 loss of heterozygosity, 12, chromosomal region 1 [Source:HG
3	ING5	1.39	1e-08	1e-07	35 x 50 inhibitor of growth family, member 5 [Source:HGNC Symbol;A
4	TRAM1L1	1.37	2e-08	6e-07	36 x 50 translocation associated membrane protein 1-like 1 [Source:l
5	CDK10	1.33	6e-08	4e-06	37 x 49 cyclin-dependent kinase 10 [Source:HGNC Symbol;Acc:HG
6	TTC4	1.24	4e-07	4e-06	35 x 49 tetratricopeptide repeat domain 4 [Source:HGNC Symbol;Acc
7	PIGN	1.19	6e-07	8e-06	36 x 50 phosphatidylinositol glycan anchor biosynthesis, class N [Sou
8	KDM4A	1.19	1e-06	2e-05	36 x 50 lysine (K)-specific demethylase 4A [Source:HGNC Symbol;A
9	LRRC42	1.15	3e-06	8e-05	35 x 50 leucine rich repeat containing 42 [Source:HGNC Symbol;Acc
10	IKBKAP	1.05	2e-05	8e-05	35 x 50 inhibitor of kappa light polypeptide gene enhancer in B-cells,
11	MECR	1.04	2e-05	8e-05	37 x 50 mitochondrial trans-2-enoyl-CoA reductase [Source:HGNC
12	EDEM2	1.03	2e-05	8e-05	37 x 50 ER degradation enhancer, mannosidase alpha-like 2 [Source
13	SNUPN	1.03	3e-05	2e-04	35 x 50 snurportin 1 [Source:HGNC Symbol;Acc:HGNC:14245]
14	TMEM126B	0.99	4e-05	2e-04	35 x 50 transmembrane protein 126B [Source:HGNC Symbol;Acc:HG
15	KDM3A	-0.98	6e-05	2e-04	35 x 50 lysine (K)-specific demethylase 3A [Source:HGNC Symbol;A
16	TRIM37	-0.94	8e-05	9e-04	37 x 50 tripartite motif containing 37 [Source:HGNC Symbol;Acc:HG
17	DCTD	-0.88	3e-04	9e-04	37 x 50 dCMP deaminase [Source:HGNC Symbol;Acc:HGNC:2710]
18	RAB11A	-0.54	4e-04	9e-04	36 x 50 RAB11A, member RAS oncogene family [Source:HGNC Sym
19	TRAPPC11	0.86	4e-04	9e-04	36 x 50 trafficking protein particle complex 11 [Source:HGNC Symbol
20	NAT10	0.86	5e-04	9e-04	35 x 50 N-acetyltransferase 10 (GCN5-related) [Source:HGNC Symt

p-values



E7_mel

Local Summary

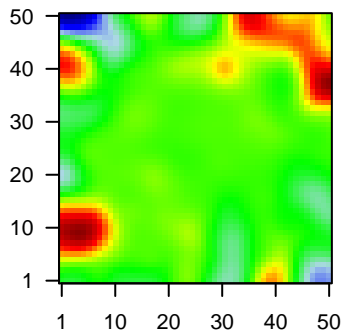
%DE = 0.78
 # metagenes = 19
 # genes = 318
 # genes in genesets = 317

 # genes with $fdr < 0.1$ = 179 (23 + / 156 -)
 # genes with $fdr < 0.05$ = 159 (20 + / 139 -)
 # genes with $fdr < 0.01$ = 88 (13 + / 75 -)

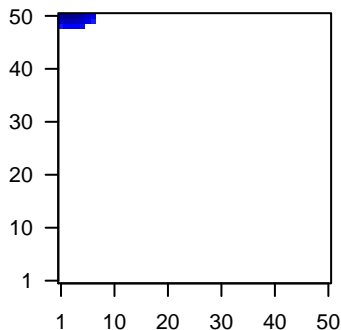
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.31

 $\langle FC \rangle$ = -0.38
 $\langle \text{shrinkage-t} \rangle$ = -6.17
 $\langle p\text{-value} \rangle$ = 0.01
 $\langle fdr \rangle$ = 0.53

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ACTL6A	-1.88	2e-16	8e-15	4 x 50 actin-like 6A [Source:HGNC Symbol;Acc:HGNC:24124]
2	STMN1	-0.86	2e-16	8e-15	5 x 50 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
3	TK1	-1.55	4e-15	2e-13	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC:10000]
4	PCNA	-1.43	6e-15	3e-09	2 x 50 proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:HGNC:10000]
5	NUP54	-1.41	4e-11	6e-09	1 x 50 nucleoporin 54kDa [Source:HGNC Symbol;Acc:HGNC:17359]
6	ZNF143	1.57	2e-10	6e-09	5 x 50 zinc finger protein 143 [Source:HGNC Symbol;Acc:HGNC:12000]
7	TYMS	-1.37	2e-10	6e-09	3 x 50 thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12000]
8	RANBP1	-1.36	3e-10	8e-08	1 x 48 RAN binding protein 1 [Source:HGNC Symbol;Acc:HGNC:98000]
9	FEN1	-1.34	1e-09	2e-07	1 x 50 flap structure-specific endonuclease 1 [Source:HGNC Symbol;Acc:HGNC:10000]
10	MCM4	-1.13	6e-09	2e-07	1 x 50 minichromosome maintenance complex component 4 [Source:HGNC Symbol;Acc:HGNC:10000]
11	EXOSC9	-1.29	8e-09	2e-07	1 x 50 exosome component 9 [Source:HGNC Symbol;Acc:HGNC:91000]
12	HMGB2	-1.28	1e-08	6e-07	5 x 50 high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:10000]
13	BIRC5	-1.24	2e-08	6e-07	6 x 50 baculoviral IAP repeat containing 5 [Source:HGNC Symbol;Acc:HGNC:10000]
14	HAUS1	-1.04	3e-08	1e-06	1 x 50 HAUS augmin-like complex, subunit 1 [Source:HGNC Symbol;Acc:HGNC:10000]
15	EMP2	-1.22	5e-08	1e-06	2 x 50 epithelial membrane protein 2 [Source:HGNC Symbol;Acc:HGNC:10000]
16	HELLS	-1.23	8e-08	1e-06	1 x 50 helicase, lymphoid-specific [Source:HGNC Symbol;Acc:HGNC:10000]
17	KIAA0101	-1.2	9e-08	6e-06	3 x 50 KIAA0101 [Source:HGNC Symbol;Acc:HGNC:28961]
18	TRIP13	-1.2	2e-07	6e-06	5 x 50 thyroid hormone receptor interactor 13 [Source:HGNC Symbol;Acc:HGNC:10000]
19	SMCHD1	-1.14	3e-07	6e-06	1 x 48 structural maintenance of chromosomes flexible hinge domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000]
20	LRR1	-1.19	4e-07	2e-05	4 x 49 leucine rich repeat protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]

p-values

