GW_045

Global Summary

%DE = 0.17

genes with fdr < 0.2 = 1944 (1018 + / 926 −)

genes with fdr < 0.1 = 1506 (791 + / 715 −)

genes with fdr < 0.05 = 1184 (615 + / 569 −)

genes with fdr < 0.01 = 730 (382 + / 348 −)

genes in genesets = 16332

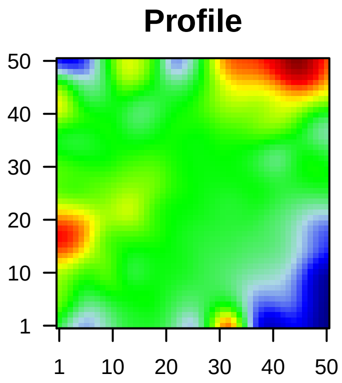
<FC> = 0

<shrinkage−t> = 0

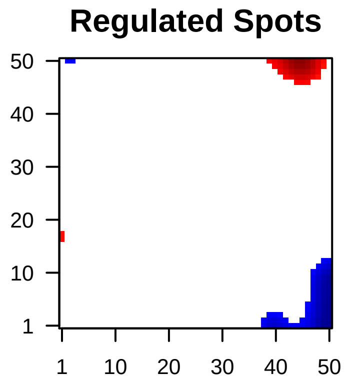
<p−value> = 0.11

<fdr> = 0.83

Profile



Regulated Spots



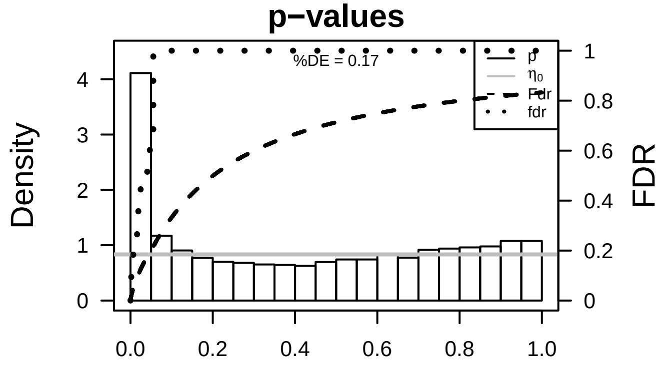
Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	8644	1.76	2e−16	7e−14	1 x 50	aldo−keto reductase family 1, member C3 [Source:HGNC Sy
2	218	2.03	2e−16	7e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
3	339512	1.78	2e−16	7e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
4	793	1.65	2e−16	7e−14	39 x 50	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]
5	4680	−1.84	2e−16	7e−14	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
6	22802	−1.93	2e−16	7e−14	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
7	49860	−1.59	2e−16	7e−14	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
8	57834	2.2	2e−16	7e−14	13 x 50	cytochrome P450, family 4, subfamily F, polypeptide 11 [Sour
9	1843	−2.08	2e−16	7e−14	22 x 50	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3
10	1917	1.61	2e−16	7e−14	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
11	26298	−1.6	2e−16	7e−14	4 x 50	ets homologous factor [Source:HGNC Symbol;Acc:3246]
12	83888	1.96	2e−16	7e−14	50 x 50	fibroblast growth factor binding protein 2 [Source:HGNC Sym
13	2353	−2.08	2e−16	7e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog [Source:
14	2354	−2.6	2e−16	7e−14	22 x 50	FBJ murine osteosarcoma viral oncogene homolog B [Source
15	3169	−1.65	2e−16	7e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
16	2944	1.93	2e−16	7e−14	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
17	283120	−1.83	2e−16	7e−14	25 x 1	H19, imprinted maternally expressed transcript (non−protein
18	3040	2.1	2e−16	7e−14	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
19	3043	2.05	2e−16	7e−14	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
20	51191	1.6	2e−16	7e−14	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	13.55	NULL	142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	13.55	NULL	142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	13.12	NULL	1720	Chr	Chr 1
4	10.28	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
5	9.8	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
6	9.44	NULL	370	BP	mitotic cell cycle
7	9.38	NULL	51	BP	type I interferon signaling pathway
8	8.99	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
9	8.9	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
10	8.68	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
11	8.58	NULL	530	Cancer	Lembcke_Normal vs Adenoma
12	8.35	NULL	109	BP	response to virus
13	8.03	NULL	31	BP	negative regulation of viral genome replication
14	8.01	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
15	7.92	NULL	572	Disease	GUDJ_psoriasis up
16	7.88	NULL	4	MMML CGS	MACIEJ_MMML 47
17	7.22	NULL	957	Chr	Chr 11
18	6.69	NULL	10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
19	6.66	NULL	232	BP	mitosis
20	6.43	NULL	16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
Underexpressed					
1	−11.5	NULL	602	Chr	Chr 10
2	−11.16	NULL	866	Chr	Chr 12
3	−9.82	NULL	918	Chr	Chr 17
4	−9.53	NULL	24	TF Tissue	VAQUERIZAS_Trachea
5	−8.79	NULL	10	GSEA C2	CHASSOT_SKIN_WOUND
6	−8.78	NULL	553	Cancer	Lembcke_Colonic Inflammation
7	−8.48	NULL	16	GSEA C2	UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN
8	−8.33	NULL	16	GSEA C2	AMIT_SERUM_RESPONSE_40_MCF10A
9	−8.2	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
10	−8.07	NULL	15	GSEA C2	AMIT_EGF_RESPONSE_40_HELA
11	−8.01	NULL	386	Chr	Chr 22
12	−7.83	NULL	375	Disease	GUDJ_psoriasis down
13	−7.8	NULL	16	GSEA C2	NAGASHIMA_EGF_SIGNALING_UP
14	−7.54	NULL	16	GSEA C2	AMIT_EGF_RESPONSE_40_MCF10A
15	−7.47	NULL	9	GSEA C2	GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D
16	−7.38	NULL	16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
17	−7.29	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_DN
18	−7.13	NULL	62	TF Tissue	VAQUERIZAS_Lung
19	−7.09	NULL	2659	CC	plasma membrane
20	−6.9	NULL	15	GSEA C2	DIRMEIER_LMP1_RESPONSE_EARLY

p−values



GW_045

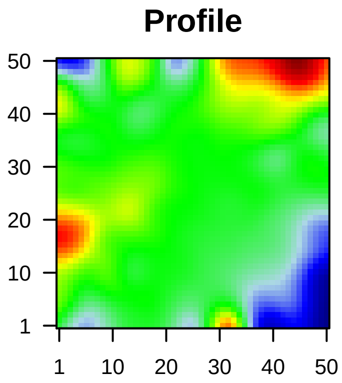
Local Summary

%DE = 0.7
metagenes = 2
genes = 33
genes in genesets = 33

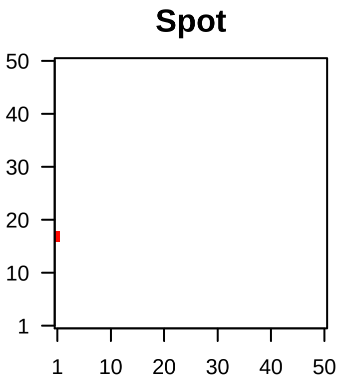
genes with fdr < 0.1 = 18 (17 + / 1 −)
genes with fdr < 0.05 = 18 (17 + / 1 −)
genes with fdr < 0.01 = 11 (10 + / 1 −)

<r> metagenes = 1
<r> genes = 0.37

<FC> = 0.37
<shrinkage−t> = 13.09
<p−value> = 0.01
<fdr> = 0.48



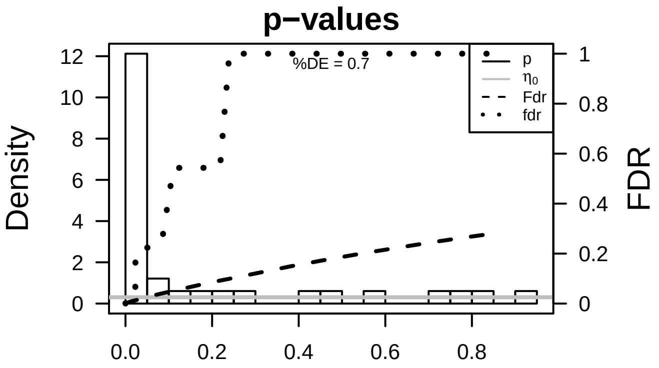
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	283869	1.06	3e−08	2e−04	1 x 17	neuropeptide W [Source:HGNC Symbol;Acc:30509]
2	57761	0.79	4e−05	2e−04	1 x 17	tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:16228]
3	63875	0.77	6e−05	2e−04	1 x 18	mitochondrial ribosomal protein L17 [Source:HGNC Symbol;
4	5425	0.75	8e−05	2e−04	1 x 17	polymerase (DNA directed), delta 2, accessory subunit [Sour
5	54606	0.75	9e−05	1e−03	1 x 17	DEAD (Asp−Glu−Ala−Asp) box helicase 56 [Source:HGNC S
6	84262	0.68	4e−04	1e−03	1 x 18	proteasome (prosome, macropain) assembly chaperone 3 [S
7	10436	0.67	5e−04	1e−03	1 x 17	Ribosomal RNA small subunit methyltransferase NEP1 [Sour
8	1152	0.66	5e−04	5e−03	1 x 17	creatine kinase, brain [Source:HGNC Symbol;Acc:1991]
9	64960	0.62	1e−03	6e−03	1 x 18	mitochondrial ribosomal protein S15 [Source:HGNC Symbol;
10	10419	0.59	2e−03	6e−03	1 x 17	protein arginine methyltransferase 5 [Source:HGNC Symbol;
11	51629	−0.58	2e−03	6e−03	1 x 18	solute carrier family 25, member 39 [Source:HGNC Symbol;A
12	2184	0.57	3e−03	1e−02	1 x 18	fumarylacetoacetate hydrolase (fumarylacetoacetase) [Sourc
13	79102	0.55	4e−03	2e−02	1 x 18	ring finger protein 26 [Source:HGNC Symbol;Acc:14646]
14	51400	0.52	6e−03	3e−02	1 x 18	protein phosphatase methylesterase 1 [Source:HGNC Symbo
15	741	0.48	1e−02	3e−02	1 x 17	zinc finger, HIT−type containing 2 [Source:HGNC Symbol;Ac
16	2932	0.47	1e−02	4e−02	1 x 17	glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc
17	6182	0.45	2e−02	4e−02	1 x 18	mitochondrial ribosomal protein L12 [Source:HGNC Symbol;
18	55210	0.43	2e−02	4e−02	1 x 18	ATPase family, AAA domain containing 3A [Source:HGNC Sy
19	142678	0.43	2e−02	2e−01	1 x 17	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symb
20	92856	0.38	5e−02	2e−01	1 x 18	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)



p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	28.31	NULL	1 / 3	TF	MYC_DNA replication UP
2	17.02	NULL	2 / 14	GSEA C2	REACTOME_PI3K_AKT_SIGNALLING
3	15.73	NULL	2 / 16	GSEA C2	REACTOME_SIGNALLING_BY_NGF
4	15.73	NULL	2 / 16	GSEA C2	REACTOME_TRKA_SIGNALLING_FROM_THE_PLASMA_MEMB
5	14.19	NULL	2 / 13	BP	ribosomal small subunit biogenesis
6	13.86	NULL	1 / 9	GSEA C2	MARZEC_IL2_SIGNALING_UP
7	12.98	NULL	1 / 10	GSEA C2	NOJIMA_SFRP2_TARGETS_UP
8	12.98	NULL	1 / 10	GSEA C2	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN
9	12.38	NULL	1 / 10	GSEA C2	REACTOME_GLOBAL_GENOMIC_NER
10	12.38	NULL	1 / 10	GSEA C2	REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE_FROM
11	12.24	NULL	1 / 11	BP	positive regulation of ubiquitin−protein ligase activity
12	11.92	NULL	1 / 11	miRNA target−starBase	hsa−miR−604
13	11.67	NULL	1 / 11	GSEA C2	KEGG_NUCLEOTIDE_EXCISION_REPAIR
14	11.67	NULL	1 / 11	GSEA C2	REACTOME_TRANSCRIPTION_COUPLED_NER
15	11.62	NULL	1 / 9	GSEA C2	GOUYER_TUMOR_INVASIVENESS
16	11.61	NULL	1 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
17	11.25	NULL	1 / 21	BP	feeding behavior
18	11.07	NULL	1 / 12	GSEA C2	REACTOME_NUCLEOTIDE_EXCISION_REPAIR
19	11.06	NULL	1 / 13	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_DN
20	11.06	NULL	1 / 13	GSEA C2	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN
21	10.88	NULL	1 / 10	BP	creatine metabolic process
22	10.58	NULL	1 / 14	GSEA C2	REACTOME_CD28_CO_STIMULATION
23	10.58	NULL	1 / 14	GSEA C2	REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING
24	10.58	NULL	1 / 14	GSEA C2	REACTOME_IRS_RELATED_EVENTS
25	10.55	NULL	1 / 13	GSEA C2	SCHUHMACHER_MYC_TARGETS_UP
26	10.49	NULL	1 / 13	GSEA C2	FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP
27	10.19	NULL	2 / 34	BP	positive regulation of protein binding
28	10.15	NULL	1 / 15	GSEA C2	PRAMOONJAGO_SOX4_TARGETS_UP
29	10.15	NULL	1 / 15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
30	10.15	NULL	1 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_UP
31	10.09	NULL	1 / 14	GSEA C2	DITTMER_PTHLH_TARGETS_DN
32	10.09	NULL	1 / 14	GSEA C2	MISSIAGLIA_REGULATED_BY_METHYLATION_DN
33	10.09	NULL	1 / 14	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_UP
34	10.09	NULL	1 / 14	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_DN
35	10.09	NULL	1 / 14	GSEA C2	REACTOME_POLYMERASE_SWITCHING
36	10.09	NULL	1 / 14	GSEA C2	REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE
37	10.03	NULL	1 / 14	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_UP
38	9.86	NULL	2 / 24	BP	telomere maintenance via recombination
39	9.77	NULL	1 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_E
40	9.77	NULL	1 / 16	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHRO

GW_045

Local Summary

%DE = 0.67

metagenes = 39

genes = 513

genes in genesets = 510

genes with fdr < 0.1 = 216 (211 + / 5 −)

genes with fdr < 0.05 = 214 (209 + / 5 −)

genes with fdr < 0.01 = 152 (149 + / 3 −)

<r> metagenes = 0.87

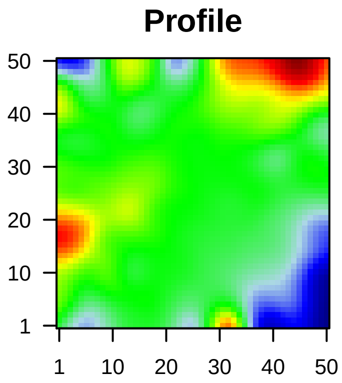
<r> genes = 0.32

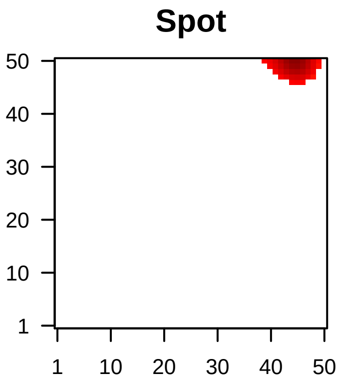
<FC> = 0.37

<shrinkage−t> = 13.05

<p−value> = 0.01

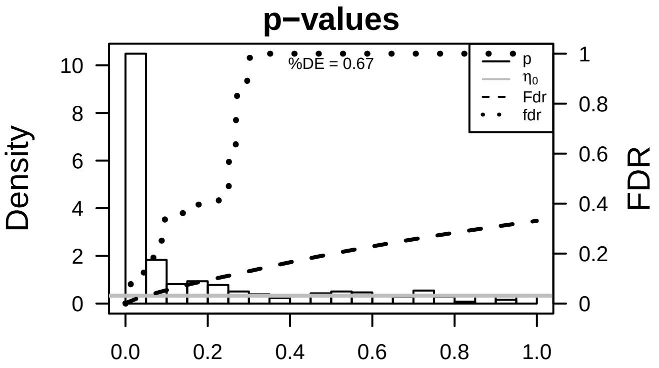
<fdr> = 0.54





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	793	1.65	2e−16	4e−14	39 x 50	calbindin 1, 28kDa [Source:HGNC Symbol;Acc:1434]
2	55832	1.28	2e−11	2e−09	47 x 50	cullin−associated and neddylation−dissociated 1 [Source:HG
3	3304	−1.16	3e−11	2e−09	49 x 49	heat shock 70kDa protein 1A [Source:HGNC Symbol;Acc:523
4	10576	1.26	4e−11	7e−09	41 x 50	chaperonin containing TCP1, subunit 2 (beta) [Source:HGNC
5	8089	1.24	8e−11	7e−09	46 x 50	YEATS domain containing 4 [Source:HGNC Symbol;Acc:248
6	139728	1.23	1e−10	2e−08	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
7	9355	1.2	3e−10	2e−08	47 x 47	LIM homeobox 2 [Source:HGNC Symbol;Acc:6594]
8	9076	−1.19	4e−10	1e−07	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
9	5984	1.16	1e−09	1e−07	46 x 50	replication factor C (activator 1) 4, 37kDa [Source:HGNC Sy
10	57122	1.15	2e−09	5e−07	45 x 49	nucleoporin 107kDa [Source:HGNC Symbol;Acc:29914]
11	116832	1.12	4e−09	3e−06	46 x 50	ribosomal protein L39−like [Source:HGNC Symbol;Acc:1709
12	55839	1.05	4e−08	3e−06	44 x 50	centromere protein N [Source:HGNC Symbol;Acc:30873]
13	81831	1.05	4e−08	3e−06	42 x 50	neuropilin (NRP) and tolloid (TLL)−like 2 [Source:HGNC Sym
14	9833	1.03	6e−08	3e−06	44 x 50	maternal embryonic leucine zipper kinase [Source:HGNC Sy
15	8833	1.03	7e−08	7e−06	45 x 50	guanine monphosphate synthase [Source:HGNC Symbol;Ac
16	54913	0.99	2e−07	7e−06	48 x 47	ribonuclease P/MRP 25kDa subunit [Source:HGNC Symbol;
17	898	0.99	2e−07	7e−06	42 x 47	cyclin E1 [Source:HGNC Symbol;Acc:1589]
18	7027	0.98	2e−07	7e−06	43 x 50	transcription factor Dp−1 [Source:HGNC Symbol;Acc:11749]
19	3428	0.98	3e−07	7e−06	45 x 50	interferon, gamma−inducible protein 16 [Source:HGNC Symb
20	123811	0.98	3e−07	1e−05	48 x 50	FGFR1OP N−terminal like [Source:HGNC Symbol;Acc:2643



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	38.5	NULL	91 / 142	Glio	willscher_GBM_Verhaak−CL_expression_C_up
2	38.5	NULL	91 / 142	Glio	willscher_GBM_Verhaak−PNmut_expression_C_down
3	23.7	NULL	109 / 370	BP	mitotic cell cycle
4	23.54	NULL	13 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_2
5	22.5	NULL	12 / 13	GSEA C2	CROONQUIST_IL6_DEPRIVATION_DN
6	22.3	NULL	8 / 10	GSEA C2	MONTERO_THYROID_CANCER_POOR_SURVIVAL_UP
7	21.23	NULL	16 / 16	GSEA C2	EGUCHI_CELL_CYCLE_RB1_TARGETS
8	20.84	NULL	10 / 14	GSEA C2	ZHAN_MULTIPLE_MYELOMA_PR_UP
9	19.56	NULL	11 / 16	GSEA C2	KANG_DOXORUBICIN_RESISTANCE_UP
10	19.4	NULL	10 / 15	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_UP
11	19.03	NULL	10 / 14	GSEA C2	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
12	18.05	NULL	105 / 530	Cancer	Lembcke_Normal vs Adenoma
13	18.01	NULL	14 / 15	GSEA C2	FINETTI_BREAST_CANCER_KINOME_RED
14	18.01	NULL	15 / 16	GSEA C2	FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
15	17.46	NULL	8 / 11	GSEA C2	KALMA_E2F1_TARGETS
16	16.98	NULL	43 / 149	BP	DNA replication
17	16.7	NULL	10 / 16	GSEA C2	GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN
18	16.55	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
19	16.54	NULL	11 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
20	15.61	NULL	17 / 30	BP	DNA strand elongation involved in DNA replication
21	15.49	NULL	8 / 15	GSEA C2	KAUFFMANN_DNA_REPLICATION_GENES
22	15.1	NULL	9 / 16	GSEA C2	PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP
23	15.08	NULL	11 / 16	GSEA C2	CROONQUIST_NRAS_SIGNALING_DN
24	15.02	NULL	9 / 16	GSEA C2	FRASOR_RESPONSE_TO_SERM_OR_FULVESTRANT_DN
25	14.85	NULL	119 / 949	CC	nucleoplasm
26	14.71	NULL	24 / 57	Glio	developing astrocytes
27	14.56	NULL	12 / 14	MMML CGS	MACIEJ_MMML 4
28	14.5	NULL	39 / 148	BP	G1/S transition of mitotic cell cycle
29	14.37	NULL	9 / 15	GSEA C2	WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
30	14.31	NULL	7 / 13	GSEA C2	PUJANA_XPRSS_INT_NETWORK
31	14.17	NULL	8 / 13	GSEA C2	WINNEPENNINCKX_MELANOMA_METASTASIS_UP
32	14.13	NULL	7 / 13	GSEA C2	VECCHI_GASTRIC_CANCER_EARLY_UP
33	14.07	NULL	9 / 15	GSEA C2	SMID_BREAST_CANCER_LUMINAL_A_DN
34	13.96	NULL	8 / 14	GSEA C2	AMUNDSON_GAMMA_RADIATION_RESPONSE
35	13.95	NULL	9 / 15	GSEA C2	LY_AGING_MIDDLE_DN
36	13.94	NULL	8 / 14	GSEA C2	PUJANA_BRCA_CENTERED_NETWORK
37	13.82	NULL	69 / 572	Disease	GUDJ_psoriasis up
38	13.76	NULL	8 / 15	GSEA C2	CHANG_CYCLING_GENES
39	13.74	NULL	7 / 13	GSEA C2	REN_BOUND_BY_E2F
40	13.74	NULL	8 / 16	GSEA C2	CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP

GW_045

Local Summary

%DE = 0.76

metagenes = 71

genes = 972

genes in genesets = 941

genes with fdr < 0.1 = 497 (22 + / 475 −)

genes with fdr < 0.05 = 375 (19 + / 356 −)

genes with fdr < 0.01 = 226 (12 + / 214 −)

<r> metagenes = 0.72

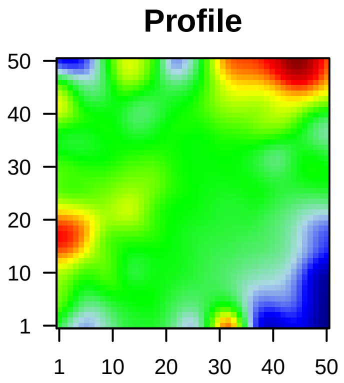
<r> genes = 0.27

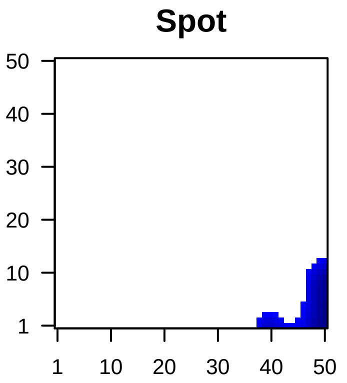
<FC> = −0.36

<shrinkage−t> = −12.48

<p−value> = 0.01

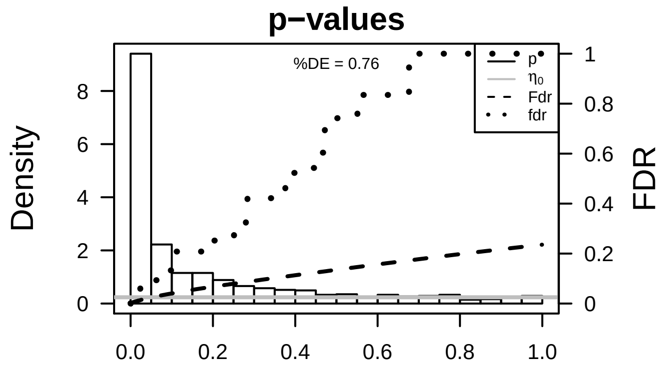
<fdr> = 0.6





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3169	−1.65	2e−16	3e−14	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
2	6192	−2.3	2e−16	3e−14	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc:
3	4283	−1.55	4e−16	1e−12	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
4	894	−1.49	6e−15	1e−11	50 x 4	cyclin D2 [Source:HGNC Symbol;Acc:1583]
5	23643	1.44	5e−14	2e−11	50 x 3	lymphocyte antigen 96 [Source:HGNC Symbol;Acc:17156]
6	3488	−1.41	1e−13	6e−10	50 x 7	insulin−like growth factor binding protein 5 [Source:HGNC Sy
7	6578	−1.32	4e−12	6e−10	50 x 4	solute carrier organic anion transporter family, member 2A1 [S
8	140032	−1.31	6e−12	3e−09	49 x 10	ribosomal protein S4, Y−linked 2 [Source:HGNC Symbol;Acc:
9	6451	−1.27	3e−11	3e−09	50 x 5	SH3 domain binding glutamic acid−rich protein like [Source:H
10	84952	−1.27	3e−11	1e−08	50 x 10	cingulin−like 1 [Source:HGNC Symbol;Acc:25931]
11	1675	−1.24	8e−11	2e−08	50 x 9	complement factor D (adipsin) [Source:HGNC Symbol;Acc:27
12	10365	−1.21	2e−10	2e−08	50 x 3	Kruppel−like factor 2 [Source:HGNC Symbol;Acc:6347]
13	51303	−1.21	2e−10	6e−08	49 x 3	FK506 binding protein 11, 19 kDa [Source:HGNC Symbol;Ac
14	57523	−1.18	5e−10	6e−08	50 x 12	NYN domain and retroviral integrase containing [Source:HGN
15	115361	−1.17	8e−10	6e−08	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
16	5996	−1.16	1e−09	6e−08	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
17	28996	−1.15	1e−09	6e−08	40 x 1	homeodomain interacting protein kinase 2 [Source:HGNC Sy
18	1847	−1.15	2e−09	6e−08	47 x 7	dual specificity phosphatase 5 [Source:HGNC Symbol;Acc:30
19	65108	−1.15	2e−09	2e−07	44 x 1	MARCKS−like 1 [Source:HGNC Symbol;Acc:7142]
20	9086	−1.14	3e−09	4e−07	48 x 9	eukaryotic translation initiation factor 1A, Y−linked [Source:H



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−15.37	NULL	14 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−14.65	NULL	151 / 553	Cancer	Lembcke_Colonic Inflammation
3	−14.54	NULL	14 / 15	CC	MHC class II protein complex
4	−14.3	NULL	3 / 7	MMML CGS	MACIEJ_MMML 5
5	−13.74	NULL	85 / 312	BP	immune response
6	−13.72	NULL	120 / 417	H.Tiss	WIRTH_Immune system
7	−13.71	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
8	−13.28	NULL	3 / 8	GSEA C2	RUNNE_GENDER_EFFECT_UP
9	−11.94	NULL	7 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
10	−11.16	NULL	9 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
11	−9.42	NULL	4 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
12	−8.9	NULL	20 / 47	BP	antigen processing and presentation
13	−8.58	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
14	−8.56	NULL	5 / 16	GSEA C2	KORKOLA_TERATOMA_UP
15	−8.39	NULL	5 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
16	−8.35	NULL	4 / 20	Lymphoma	ROSOLOWSKI_red UP
17	−8.28	NULL	4 / 8	Lymphoma	MASCQUE_ABC UP
18	−8.17	NULL	2 / 7	GSEA C2	LEE_NAIVE_T_LYMPHOCYTE
19	−8.13	NULL	6 / 15	GSEA C2	ROSS_LEUKEMIA_WITH_MLL_FUSIONS
20	−7.95	NULL	42 / 162	CC	external side of plasma membrane
21	−7.94	NULL	5 / 7	GSEA C2	LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN
22	−7.9	NULL	5 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
23	−7.82	NULL	13 / 43	MF	chemokine activity
24	−7.81	NULL	3 / 5	GSEA C2	NAKAMURA_ALVEOLAR_EPITHELIUM
25	−7.75	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
26	−7.63	NULL	9 / 16	Lymphoma	WRIGHT_ABC UP
27	−7.6	NULL	3 / 13	GSEA C2	KANG_IMMORTALIZED_BY_TERT_UP
28	−7.5	NULL	4 / 34	Chr	Chr Y
29	−7.41	NULL	6 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
30	−7.36	NULL	23 / 60	BP	T cell costimulation
31	−7.36	NULL	4 / 13	GSEA C2	NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN
32	−7.34	NULL	2 / 9	GSEA C2	REACTOME_REGULATION_OF_BETA_CELL_DEVELOPMENT
33	−7.24	NULL	4 / 11	GSEA C2	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN
34	−7.2	NULL	71 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
35	−7.2	NULL	71 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
36	−7.2	NULL	71 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
37	−7.2	NULL	71 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
38	−7.1	NULL	5 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
39	−6.83	NULL	7 / 12	GSEA C2	BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_
40	−6.82	NULL	5 / 12	BP	dendritic cell chemotaxis

GW_045

Local Summary

%DE = 0.85

metagenes = 2

genes = 24

genes in genesets = 23

genes with fdr < 0.1 = 19 (2 + / 17 −)

genes with fdr < 0.05 = 19 (2 + / 17 −)

genes with fdr < 0.01 = 17 (1 + / 16 −)

<r> metagenes = 1

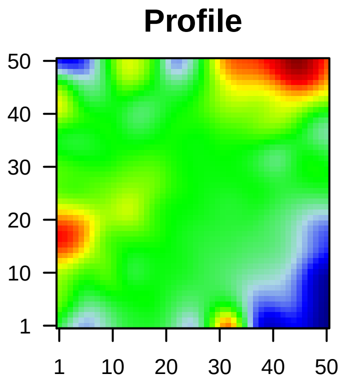
<r> genes = 0.53

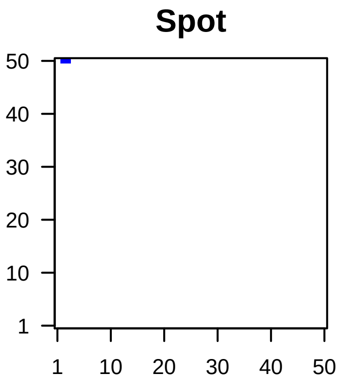
<FC> = −0.62

<shrinkage−t> = −21.89

<p−value> = 0

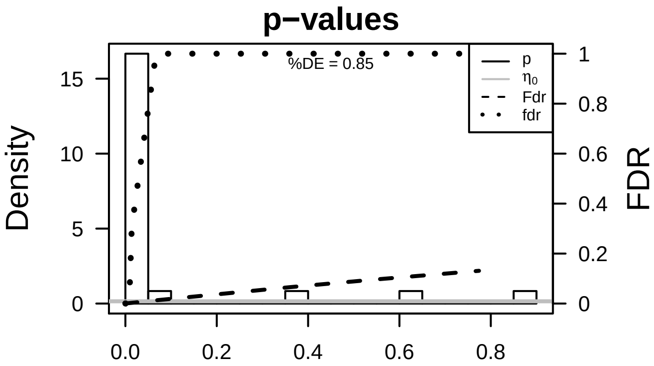
<fdr> = 0.2





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	1048	−1.36	9e−13	1e−09	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
2	5307	−1.13	4e−10	1e−09	3 x 50	paired−like homeodomain 1 [Source:HGNC Symbol;Acc:9004
3	5507	−1.17	8e−10	1e−09	3 x 50	protein phosphatase 1, regulatory subunit 3C [Source:HGNC
4	100133941	−1.16	1e−09	2e−08	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
5	79852	−1.11	6e−09	4e−08	3 x 50	epoxide hydrolase 3 [Source:HGNC Symbol;Acc:23760]
6	388610	−1.08	2e−08	1e−06	3 x 50	TMF1−regulated nuclear protein 1 [Source:HGNC Symbol;Ac
7	131177	−0.97	3e−07	3e−06	3 x 50	family with sequence similarity 3, member D [Source:HGNC S
8	2012	−0.85	1e−06	3e−05	3 x 50	epithelial membrane protein 1 [Source:HGNC Symbol;Acc:33
9	124976	−0.82	2e−05	3e−05	2 x 50	spinster homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:
10	51228	−0.75	2e−05	3e−05	2 x 50	glycolipid transfer protein [Source:HGNC Symbol;Acc:24867]
11	6947	−0.8	3e−05	4e−05	2 x 50	transcobalamin I (vitamin B12 binding protein, R binder family
12	2525	−0.77	5e−05	4e−05	3 x 50	fucosyltransferase 3 (galactoside 3(4)−L−fucosyltransferase,
13	339967	−0.77	5e−05	1e−04	2 x 50	transmembrane protease, serine 11A [Source:HGNC Symbol
14	57111	0.75	9e−05	4e−04	2 x 50	RAB25, member RAS oncogene family [Source:HGNC Symb
15	394263	−0.71	2e−04	9e−04	3 x 50	
16	84525	−0.66	5e−04	9e−04	2 x 50	HOP homeobox [Source:HGNC Symbol;Acc:24961]
17	6337	−0.65	7e−04	7e−03	3 x 50	sodium channel, non−voltage−gated 1 alpha subunit [Source:
18	92196	0.57	3e−03	2e−02	3 x 50	death associated protein−like 1 [Source:HGNC Symbol;Acc:2
19	10205	−0.49	1e−02	2e−02	3 x 50	myelin protein zero−like 2 [Source:HGNC Symbol;Acc:3496]
20	2941	−0.46	2e−02	3e−01	3 x 50	glutathione S−transferase alpha 4 [Source:HGNC Symbol;Ac



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−33.57	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
2	−23.29	NULL	1 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
3	−22.71	NULL	3 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
4	−21.02	NULL	1 / 8	TF Tissue	VAQUERIZAS_Tongue
5	−18.79	NULL	1 / 4	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN
6	−16.34	NULL	1 / 13	H.Tiss	WIRTH_Tonsil
7	−15.04	NULL	1 / 11	GSEA C2	BENPORATH_ES_2
8	−14.67	NULL	1 / 9	GSEA C2	WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_UP
9	−14.3	NULL	1 / 13	MF	RNA polymerase II transcription factor binding transcription factor a
10	−14.3	NULL	1 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
11	−14.08	NULL	1 / 5	GSEA C2	ZEMBUTSU_SENSITIVITY_TO_DOXORUBICIN
12	−13.18	NULL	1 / 11	GSEA C2	ROME_INSULIN_TARGETS_IN_MUSCLE_DN
13	−12.91	NULL	1 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
14	−12.9	NULL	1 / 13	CC	nuclear euchromatin
15	−12.66	NULL	1 / 15	BP	glycogen biosynthetic process
16	−12.66	NULL	1 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
17	−12.26	NULL	1 / 9	Cancer	WANG_ER_DN
18	−12.1	NULL	1 / 16	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP
19	−11.25	NULL	1 / 10	MF	fucosyltransferase activity
20	−10.97	NULL	1 / 19	TF Tissue	VAQUERIZAS_Pituitary
21	−10.45	NULL	1 / 14	GSEA C2	ROVERSI_GLIOMA_LOH_REGIONS
22	−10.45	NULL	1 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_NORMAL_DN
23	−10.45	NULL	1 / 14	GSEA C2	SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN
24	−9.94	NULL	1 / 15	GSEA C2	KORKOLA_TERATOMA
25	−9.94	NULL	1 / 15	GSEA C2	ALONSO_METASTASIS_NEURAL_UP
26	−9.78	NULL	1 / 13	BP	lymph node development
27	−9.75	NULL	8 / 135	H.Tiss	WIRTH_Mucosa
28	−9.74	NULL	1 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN
29	−9.5	NULL	1 / 16	MMML CGS	MACIEJ_MMML 1
30	−9.5	NULL	1 / 16	GSEA C2	KORKOLA_TERATOMA_UP
31	−9.5	NULL	1 / 16	GSEA C2	GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_
32	−9.5	NULL	1 / 16	GSEA C2	GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP
33	−9.5	NULL	1 / 16	GSEA C2	ALONSO_METASTASIS_EMT_UP
34	−9.5	NULL	1 / 16	GSEA C2	GENTILE_UV_RESPONSE_CLUSTER_D8
35	−9.4	NULL	1 / 24	miRNA target starBase	hsa−miR−220b
36	−9.2	NULL	1 / 13	BP	oligosaccharide biosynthetic process
37	−9.2	NULL	1 / 13	GSEA C2	WAGNER_APO2_SENSITIVITY
38	−9.2	NULL	1 / 13	GSEA C2	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_N
39	−9.15	NULL	1 / 25	BP	pituitary gland development
40	−8.93	NULL	1 / 26	BP	embryonic hindlimb morphogenesis