GW_245

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 2106 (1164 + / 942 −)

genes with fdr < 0.1 = 1666 (910 + / 756 −)

genes with fdr < 0.05 = 1442 (792 + / 650 −)

genes with fdr < 0.01 = 1032 (561 + / 471 −)

genes in genesets = 16332

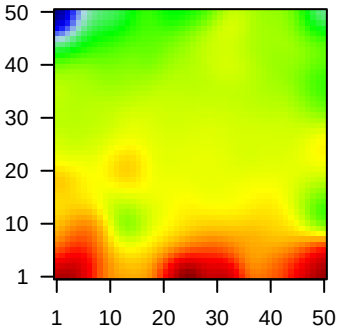
<FC> = 0

<shrinkage−t> = 0

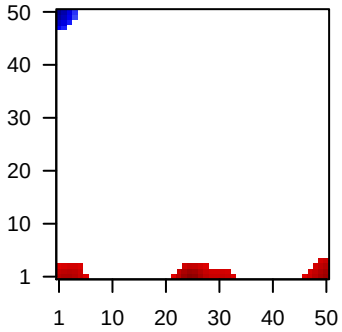
<p−value> = 0.07

<fdr> = 0.85

Profile



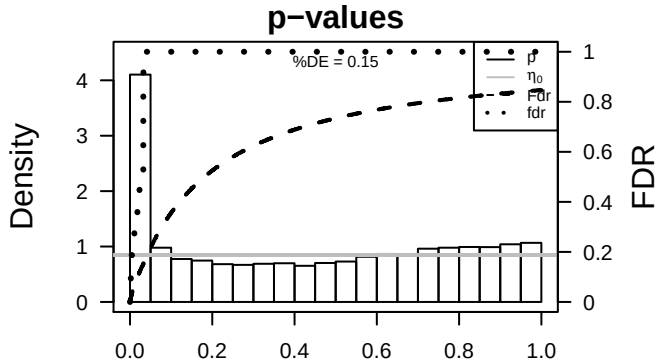
Regulated Spots



Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.7	2e−16	2e−14	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	58	3.08	2e−16	2e−14	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
3	70	3.31	2e−16	2e−14	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
4	72	1.63	2e−16	2e−14	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
5	131	−2.39	2e−16	2e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
6	57016	−2.95	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
7	1109	−1.74	2e−16	2e−14	13 x 50	aldo−keto reductase family 1, member C4 [Source:HGNC Syı
8	216	−1.72	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
9	218	−3.02	2e−16	2e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
10	222	−2.33	2e−16	2e−14	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
11	347	2.5	2e−16	2e−14	50 x 7	apolipoprotein D [Source:HGNC Symbol;Acc:612]
12	633	1.57	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
13	655	−1.82	2e−16	2e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:10
14	11067	1.82	2e−16	2e−14	44 x 1	chromosome 10 open reading frame 10 [Source:HGNC Symt
15	387695	−2.87	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symt
16	388115	1.58	2e−16	2e−14	26 x 2	chromosome 15 open reading frame 52 [Source:HGNC Symt
17	713	1.85	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, B chain [Source
18	714	1.72	2e−16	2e−14	50 x 1	complement component 1, q subcomponent, C chain [Source
19	260436	−1.66	2e−16	2e−14	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
20	375791	−1.64	2e−16	2e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symt

p−values



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.61	NULL	127	H.Tiss	WIRTH_Muscle
2	15.62	NULL	16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
3	14.76	NULL	553	Cancer	Lembcke_Colonic Inflammation
4	14.72	NULL	265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
5	14.72	NULL	265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
6	14.72	NULL	265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
7	14.72	NULL	265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
8	14	NULL	36	BP	muscle filament sliding
9	12.14	NULL	16	H.Tiss	WIRTH_Hippocampus
10	11.72	NULL	51	BP	type I interferon signaling pathway
11	11.61	NULL	312	BP	immune response
12	11.37	NULL	44	MF	structural constituent of muscle
13	11.19	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
14	11.05	NULL	84	BP	muscle contraction
15	10.42	NULL	123	BP	defense response to virus
16	10.35	NULL	190	CC	extracellular matrix
17	10.17	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
18	10.08	NULL	12	CC	myosin filament
19	9.85	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
20	9.62	NULL	10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
Underexpressed					
1	−40.76	NULL	135	H.Tiss	WIRTH_Mucosa
2	−19.02	NULL	21	CC	cornified envelope
3	−17.79	NULL	53	BP	keratinocyte differentiation
4	−17.25	NULL	42	BP	keratinization
5	−15.88	NULL	76	BP	epidermis development
6	−12.55	NULL	8	GSEA C2	LIU_CDX2_TARGETS_DN
7	−12.36	NULL	572	Disease	GUDJ_psoriasis up
8	−11.8	NULL	19	BP	peptide cross−linking
9	−10.87	NULL	15	GSEA C2	AIGNER_ZEB1_TARGETS
10	−10.6	NULL	21	CC	desmosome
11	−9.82	NULL	15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
12	−9.52	NULL	13	H.Tiss	WIRTH_Tonsil
13	−8.83	NULL	186	MF	structural molecule activity
14	−8.26	NULL	82	CC	intermediate filament
15	−7.84	NULL	16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
16	−7.61	NULL	16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
17	−7.61	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
18	−7.57	NULL	10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
19	−7.42	NULL	12	BP	cellular aldehyde metabolic process
20	−7.31	NULL	15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN

GW_245

Local Summary

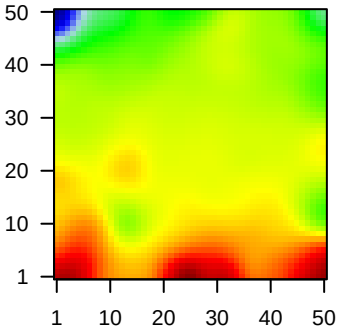
%DE = 0.88
metagenes = 16
genes = 261
genes in genesets = 260

genes with fdr < 0.1 = 209 (203 + / 6 −)
genes with fdr < 0.05 = 202 (196 + / 6 −)
genes with fdr < 0.01 = 155 (152 + / 3 −)

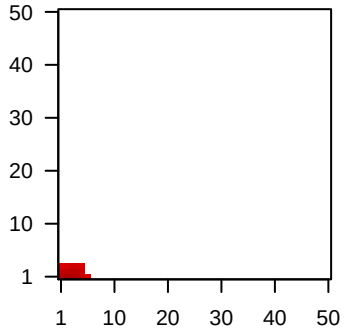
<r> metagenes = 0.97
<r> genes = 0.41

<FC> = 0.68
<shrinkage−t> = 23.79
<p−value> = 0
<fdr> = 0.33

Profile



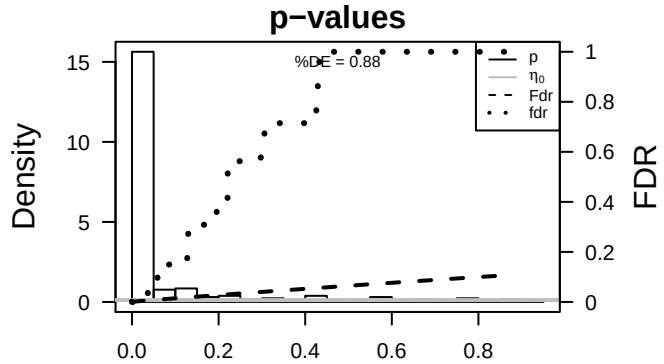
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	72	1.63	2e−16	6e−16	4 x 1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Syml
2	633	1.57	2e−16	6e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
3	3040	1.65	2e−16	6e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
4	3043	1.75	2e−16	6e−16	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
5	4312	1.85	2e−16	6e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
6	4837	1.98	2e−16	6e−16	3 x 1	nicotinamide N−methyltransferase [Source:HGNC Symbol;Ac
7	4973	1.63	2e−16	6e−16	1 x 1	oxidized low density lipoprotein (lectin−like) receptor 1 [Sourc
8	6447	1.96	2e−16	6e−16	1 x 1	secretogranin V (7B2 protein) [Source:HGNC Symbol;Acc:10
9	6696	1.68	2e−16	6e−16	2 x 1	secreted phosphoprotein 1 [Source:HGNC Symbol;Acc:1125
10	6876	1.55	2e−16	6e−16	3 x 1	transgelin [Source:HGNC Symbol;Acc:11553]
11	7057	1.97	2e−16	6e−16	1 x 1	thrombospondin 1 [Source:HGNC Symbol;Acc:11785]
12	7076	2.04	2e−16	6e−16	4 x 1	TIMP metallopeptidase inhibitor 1 [Source:HGNC Symbol;Acc
13	7169	1.52	9e−16	2e−14	3 x 1	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011]
14	5054	1.5	2e−15	1e−13	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
15	4502	1.47	5e−15	3e−13	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]
16	414062	1.45	1e−14	6e−13	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbc
17	5159	1.43	3e−14	3e−12	3 x 1	platelet−derived growth factor receptor, beta polypeptide [Sou
18	2191	1.39	2e−13	3e−12	1 x 1	fibroblast activation protein, alpha [Source:HGNC Symbol;Acc
19	23452	1.38	2e−13	4e−12	3 x 1	angiopoietin−like 2 [Source:HGNC Symbol;Acc:490]
20	23213	1.36	5e−13	4e−12	2 x 1	sulfatase 1 [Source:HGNC Symbol;Acc:20391]

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	32.31	NULL	77 / 250	Lymphoma	LENZ_Stromal signature 1
2	31.43	NULL	67 / 190	CC	extracellular matrix
3	29.22	NULL	14 / 16	MMML Cls	GACIEJ_MMML 1
4	25	NULL	61 / 242	BP	extracellular matrix organization
5	23.66	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
6	23.53	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
7	23.44	NULL	8 / 11	MF	platelet−derived growth factor binding
8	22.45	NULL	12 / 35	Glio	Colman_survival_associated
9	21.97	NULL	31 / 69	BP	extracellular matrix disassembly
10	21.97	NULL	6 / 11	Glio	Phillips MES up vs Prolif & PN
11	21.16	NULL	11 / 19	MF	extracellular matrix binding
12	20.03	NULL	41 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
13	20.03	NULL	41 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
14	20.03	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
15	20.03	NULL	41 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
16	19.97	NULL	8 / 12	miRNA targets	miR−29c
17	19.64	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
18	19.45	NULL	7 / 16	GSEA C2	ZHU_CMV_ALL_DN
19	18.94	NULL	8 / 15	GSEA C2	DASU_IL6_SIGNALING_SCAR_DN
20	18.67	NULL	27 / 64	BP	collagen catabolic process
21	18.33	NULL	2 / 3	GSEA C2	KONDO_HYPOXIA
22	18.15	NULL	6 / 16	GSEA C2	ZHU_CMV_24_HR_DN
23	17.97	NULL	7 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
24	17.52	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
25	17.05	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
26	16.96	NULL	6 / 13	GSEA C2	TSAI_RESPONSE_TO_RADIATION_THERAPY
27	16.87	NULL	2 / 4	MMML Cls	GACIEJ_MMML 23
28	16.76	NULL	19 / 57	MF	extracellular matrix structural constituent
29	16.71	NULL	7 / 16	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC
30	16.57	NULL	7 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
31	16.2	NULL	68 / 553	Cancer	Lembcke_Colonic Inflammation
32	16.16	NULL	20 / 83	CC	basement membrane
33	16.13	NULL	105 / 1182	CC	extracellular region
34	15.84	NULL	7 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
35	15.63	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
36	15.44	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
37	15.3	NULL	80 / 683	CC	extracellular space
38	15.29	NULL	8 / 43	CC	platelet alpha granule lumen
39	15.08	NULL	3 / 7	GSEA C2	DASU_IL6_SIGNALING_DN
40	14.83	NULL	6 / 15	GSEA C2	MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INH

GW_245

Local Summary

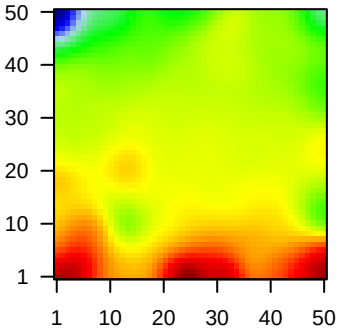
%DE = 0.9
metagenes = 27
genes = 265
genes in genesets = 263

genes with fdr < 0.1 = 226 (224 + / 2 −)
genes with fdr < 0.05 = 215 (213 + / 2 −)
genes with fdr < 0.01 = 196 (194 + / 2 −)

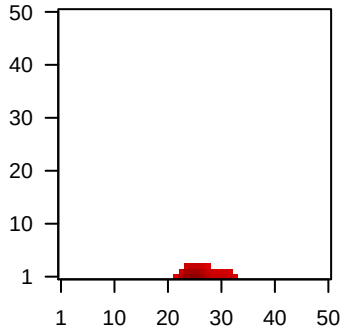
<r> metagenes = 0.72
<r> genes = 0.26

<FC> = 0.94
<shrinkage−t> = 32.88
<p−value> = 0
<fdr> = 0.21

Profile



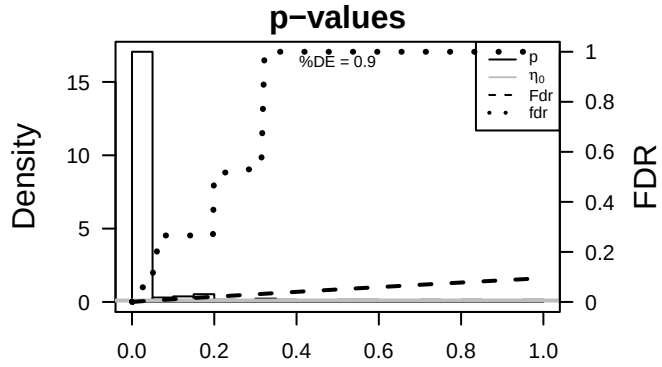
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	58	3.08	2e−16	1e−16	25 x 1	actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12
2	70	3.31	2e−16	1e−16	25 x 1	actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14
3	388115	1.58	2e−16	1e−16	26 x 2	chromosome 15 open reading frame 52 [Source:HGNC Symt
4	834	1.54	2e−16	1e−16	32 x 1	caspase 1, apoptosis−related cysteine peptidase [Source:HG
5	6355	2.3	2e−16	1e−16	32 x 1	chemokine (C−C motif) ligand 8 [Source:HGNC Symbol;Acc:1
6	1114	2.48	2e−16	1e−16	25 x 1	chromogranin B (secretogranin 1) [Source:HGNC Symbol;Acc
7	1158	2.9	2e−16	1e−16	25 x 1	creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]
8	202333	1.83	2e−16	1e−16	25 x 1	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:143
9	1410	1.63	2e−16	1e−16	25 x 1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389]
10	3627	2.44	2e−16	1e−16	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
11	115265	2.26	2e−16	1e−16	25 x 1	DNA−damage−inducible transcript 4−like [Source:HGNC Sym
12	1674	1.66	2e−16	1e−16	25 x 1	desmin [Source:HGNC Symbol;Acc:2770]
13	1917	2	2e−16	1e−16	25 x 1	eukaryotic translation elongation factor 1 alpha 2 [Source:HG
14	2318	2.72	2e−16	1e−16	25 x 1	filamin C, gamma [Source:HGNC Symbol;Acc:3756]
15	2633	1.64	2e−16	1e−16	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGI
16	115362	1.76	2e−16	1e−16	32 x 1	guanylate binding protein 5 [Source:HGNC Symbol;Acc:1989
17	10561	1.54	2e−16	1e−16	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
18	10964	1.86	2e−16	1e−16	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
19	3433	2.01	2e−16	1e−16	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [Sc
20	8519	1.73	2e−16	1e−16	32 x 1	interferon induced transmembrane protein 1 [Source:HGNC S

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	41.28	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_F
2	41.21	NULL	60 / 127	H.Tiss	WIRTH_Muscle
3	35.67	NULL	23 / 36	BP	muscle filament sliding
4	34.6	NULL	11 / 16	H.Tiss	WIRTH_Hippocampus
5	30.2	NULL	23 / 44	MF	structural constituent of muscle
6	29.82	NULL	29 / 51	BP	type I interferon signaling pathway
7	29.77	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
8	29.27	NULL	10 / 12	CC	myosin filament
9	26.57	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
10	24.28	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
11	23.99	NULL	8 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
12	23.67	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
13	23.12	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
14	22.06	NULL	23 / 84	BP	muscle contraction
15	21.01	NULL	11 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
16	20.85	NULL	8 / 14	CC	contractile fiber
17	20.13	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
18	19.8	NULL	8 / 16	CC	M band
19	19.72	NULL	31 / 123	BP	defense response to virus
20	19.32	NULL	27 / 109	BP	response to virus
21	19.21	NULL	6 / 12	BP	skeletal muscle contraction
22	17.97	NULL	13 / 31	BP	negative regulation of viral genome replication
23	17.93	NULL	5 / 11	BP	cardiac muscle tissue morphogenesis
24	17.86	NULL	21 / 88	CC	Z disc
25	17.7	NULL	9 / 20	CC	I band
26	17.04	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
27	17.03	NULL	7 / 12	MF	titin binding
28	16.94	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
29	16.33	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
30	16.2	NULL	12 / 37	CC	sarcomere
31	16.14	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
32	16.05	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
33	16.05	NULL	5 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
34	15.8	NULL	8 / 13	CC	muscle myosin complex
35	15.77	NULL	34 / 204	BP	cytokine−mediated signaling pathway
36	15.58	NULL	17 / 34	CC	myofibril
37	15.27	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
38	15.07	NULL	6 / 6	Lymphoma	DAVE_MHCCII BL DN
39	13.91	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
40	13.86	NULL	3 / 4	MMML C5	GOCIEJ_MMML 47

GW_245

Local Summary

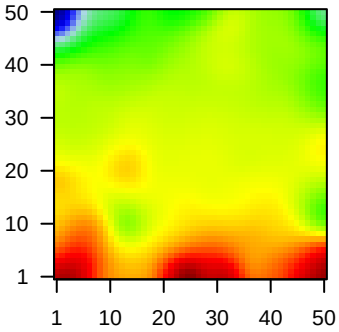
%DE = 0.81
metagenes = 14
genes = 257
genes in genesets = 255

genes with fdr < 0.1 = 185 (179 + / 6 −)
genes with fdr < 0.05 = 166 (162 + / 4 −)
genes with fdr < 0.01 = 151 (147 + / 4 −)

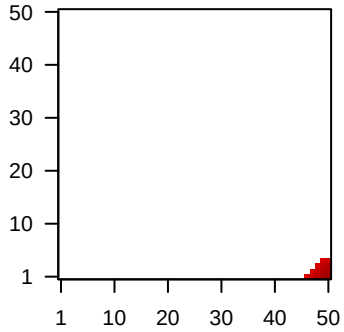
<r> metagenes = 0.99
<r> genes = 0.59

<FC> = 0.63
<shrinkage−t> = 22.05
<p−value> = 0
<fdr> = 0.34

Profile



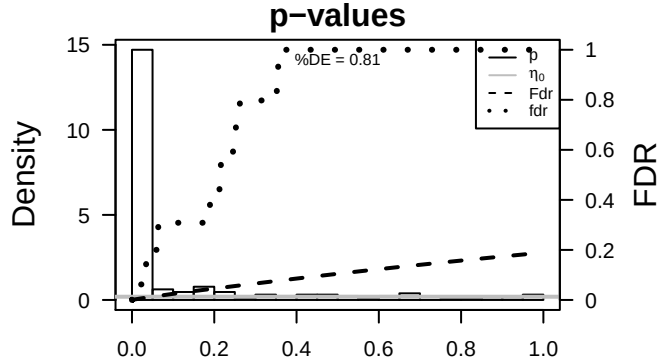
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	713	1.85	2e−16	1e−15	50 x 1	complement component 1, q subcomponent, B chain [Source
2	714	1.72	2e−16	1e−15	50 x 1	complement component 1, q subcomponent, C chain [Source
3	260436	−1.66	2e−16	1e−15	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symbc
4	6347	2.18	2e−16	1e−15	50 x 4	chemokine (C−C motif) ligand 2 [Source:HGNC Symbol;Acc:1
5	1116	1.67	2e−16	1e−15	50 x 4	chitinase 3−like 1 (cartilage glycoprotein−39) [Source:HGNC
6	4283	1.73	2e−16	1e−15	49 x 1	chemokine (C−X−C motif) ligand 9 [Source:HGNC Symbol;Ac
7	2207	1.81	2e−16	1e−15	50 x 1	Fc fragment of IgE, high affinity I, receptor for; gamma polype
8	115361	1.68	2e−16	1e−15	48 x 1	guanylate binding protein 4 [Source:HGNC Symbol;Acc:2048
9	3126	1.99	2e−16	1e−15	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
10	3620	1.63	2e−16	1e−15	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:1
11	7305	1.7	2e−16	1e−15	50 x 1	TYRO protein tyrosine kinase binding protein [Source:HGNC
12	64231	1.51	1e−15	3e−14	50 x 1	membrane−spanning 4−domains, subfamily A, member 6A [S
13	2359	1.5	2e−15	9e−14	50 x 3	formyl peptide receptor 3 [Source:HGNC Symbol;Acc:3828]
14	55303	1.47	6e−15	9e−14	50 x 1	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:
15	10437	1.47	7e−15	9e−14	46 x 1	interferon, gamma−inducible protein 30 [Source:HGNC Symb
16	929	1.46	7e−15	2e−13	50 x 3	CD14 molecule [Source:HGNC Symbol;Acc:1628]
17	3001	1.45	1e−14	6e−13	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
18	3113	1.43	2e−14	6e−13	50 x 1	major histocompatibility complex, class II, DP alpha 1 [Source
19	9332	1.43	4e−14	1e−12	50 x 4	CD163 molecule [Source:HGNC Symbol;Acc:1631]
20	7941	1.41	8e−14	1e−12	50 x 3	phospholipase A2, group VII (platelet−activating factor acetyll

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	25.28	NULL	12 / 15	CC	MHC class II protein complex
2	23.46	NULL	88 / 417	H.Tiss	WIRTH_Immune system
3	20.73	NULL	40 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
4	20.73	NULL	40 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
5	20.73	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
6	20.73	NULL	40 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
7	19.2	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEMEN
8	18.64	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
9	17.87	NULL	6 / 15	Glio	Donson−chemokines/cytokines−associated with LTS in HGA
10	17.78	NULL	90 / 553	Cancer	Lembcke_Colonic Inflammation
11	16.85	NULL	51 / 312	BP	immune response
12	16.45	NULL	15 / 47	BP	antigen processing and presentation
13	16.4	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
14	15.91	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
15	15.54	NULL	4 / 8	GSEA C2	NIELSEN_SYNOVIAL_SARCOMA_DN
16	14.36	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
17	14.23	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
18	13.95	NULL	17 / 74	BP	regulation of immune response
19	13.87	NULL	2 / 7	GSEA C2	BIOCARTA_COMP_PATHWAY
20	13.61	NULL	5 / 12	BP	immunoglobulin mediated immune response
21	13.6	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
22	12.85	NULL	2 / 8	GSEA C2	BIOCARTA_CLASSIC_PATHWAY
23	12.85	NULL	2 / 8	GSEA C2	REACTOME_COMPLEMENT_CASCADE
24	12.85	NULL	2 / 8	GSEA C2	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT
25	12.68	NULL	6 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
26	12.57	NULL	3 / 16	GSEA C2	KAAB_FAILED_HEART_VENTRICLE_DN
27	12.19	NULL	3 / 11	GSEA C2	WILENSKY_RESPONSE_TO_DARAPLADIB
28	12.11	NULL	7 / 21	CC	clathrin−coated endocytic vesicle membrane
29	12.04	NULL	5 / 13	GSEA C2	HAHTOLA_CTCL_PATHOGENESIS
30	12.04	NULL	3 / 11	GSEA C2	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY
31	11.97	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
32	11.95	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
33	11.85	NULL	4 / 8	Lymphoma	MASCQUE_ABC UP
34	11.7	NULL	4 / 21	BP	cellular response to interferon−gamma
35	11.7	NULL	13 / 87	BP	antigen processing and presentation of exogenous peptide antigen
36	11.68	NULL	3 / 13	GSEA C2	CAVARD_LIVER_CANCER_MALIGNANT_VS_BENIGN
37	11.61	NULL	4 / 11	GSEA C2	APPEL_IMATINIB_RESPONSE
38	11.54	NULL	14 / 60	BP	T cell costimulation
39	11.53	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
40	11.5	NULL	7 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane

GW_245

Local Summary

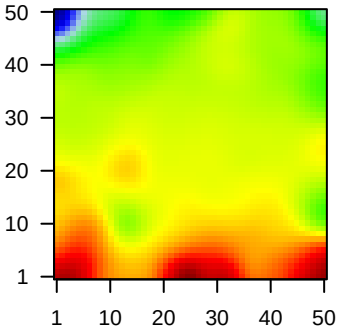
%DE = 0.98
metagenes = 13
genes = 192
genes in genesets = 187

genes with fdr < 0.1 = 187 (6 + / 181 −)
genes with fdr < 0.05 = 187 (6 + / 181 −)
genes with fdr < 0.01 = 170 (3 + / 167 −)

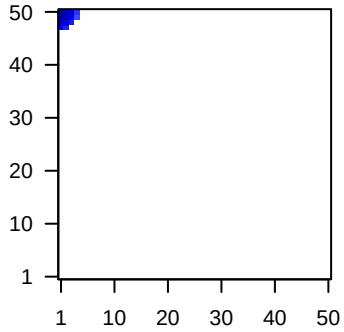
<r> metagenes = 0.98
<r> genes = 0.48

<FC> = −1.5
<shrinkage−t> = −53.27
<p−value> = 0
<fdr> = 0.09

Profile



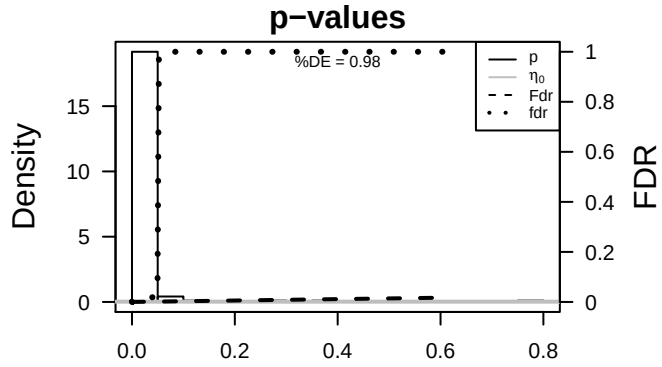
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	144568	−1.7	2e−16	1e−17	1 x 50	alpha−2−macroglobulin−like 1 [Source:HGNC Symbol;Acc:23
2	131	−2.39	2e−16	1e−17	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3	57016	−2.95	2e−16	1e−17	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
4	218	−3.02	2e−16	1e−17	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGNC
5	222	−2.33	2e−16	1e−17	1 x 49	aldehyde dehydrogenase 3 family, member B2 [Source:HGNC
6	387695	−2.87	2e−16	1e−17	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symbo
7	375791	−1.64	2e−16	1e−17	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Symbo
8	810	−3.24	2e−16	1e−17	1 x 50	calmodulin−like 3 [Source:HGNC Symbol;Acc:1452]
9	51806	−2.34	2e−16	1e−17	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
10	84290	−1.77	2e−16	1e−17	1 x 50	calpain, small subunit 2 [Source:HGNC Symbol;Acc:16371]
11	100133941	−1.81	2e−16	1e−17	3 x 50	CD24 molecule [Source:HGNC Symbol;Acc:1645]
12	1048	−1.59	2e−16	1e−17	2 x 50	carcinoembryonic antigen−related cell adhesion molecule 5 [S
13	4680	−2.86	2e−16	1e−17	1 x 50	carcinoembryonic antigen−related cell adhesion molecule 6 (
14	22802	−2.5	2e−16	1e−17	1 x 50	chloride channel accessory 4 [Source:HGNC Symbol;Acc:20
15	9022	−1.69	2e−16	1e−17	1 x 50	chloride intracellular channel 3 [Source:HGNC Symbol;Acc:2(
16	84518	−3	2e−16	1e−17	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
17	1382	−2.04	2e−16	1e−17	1 x 48	cellular retinoic acid binding protein 2 [Source:HGNC Symbol
18	54544	−1.65	2e−16	1e−17	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:29875
19	49860	−2.59	2e−16	1e−17	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
20	1475	−2.34	2e−16	1e−17	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]

p−values



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−67.63	NULL	77 / 135	H.Tiss	WIRTH_Mucosa
2	−39.09	NULL	16 / 21	CC	cornified envelope
3	−36.42	NULL	19 / 42	BP	keratinization
4	−33.21	NULL	21 / 53	BP	keratinocyte differentiation
5	−28.9	NULL	9 / 19	BP	peptide cross−linking
6	−26.47	NULL	82 / 572	Disease	GUDJ_psoriasis up
7	−24.79	NULL	20 / 76	BP	epidermis development
8	−18.97	NULL	7 / 15	GSEA C2	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCE
9	−15.72	NULL	3 / 11	GSEA C2	MURAKAMI_UV_RESPONSE_6HR_DN
10	−15.61	NULL	6 / 16	GSEA C2	CROMER_TUMORIGENESIS_DN
11	−14.93	NULL	5 / 10	MF	RAGE receptor binding
12	−14.86	NULL	3 / 10	GSEA C2	MURAKAMI_UV_RESPONSE_1HR_UP
13	−14.16	NULL	6 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
14	−14.06	NULL	1 / 6	GSEA C2	SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN
15	−13.45	NULL	18 / 186	MF	structural molecule activity
16	−13.38	NULL	3 / 12	BP	cellular aldehyde metabolic process
17	−13.29	NULL	6 / 16	GSEA C2	WANG_BARRETTS_ESOPHAGUS_DN
18	−13.22	NULL	2 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
19	−12.8	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
20	−12.51	NULL	3 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
21	−12.39	NULL	5 / 21	CC	desmosome
22	−11.64	NULL	6 / 13	BP	negative regulation of peptidase activity
23	−11.52	NULL	6 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
24	−11.12	NULL	8 / 44	CC	keratin filament
25	−10.39	NULL	3 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
26	−10.05	NULL	4 / 13	H.Tiss	WIRTH_Tonsil
27	−9.85	NULL	4 / 10	GSEA C2	SMID_BREAST_CANCER_ERBB2_UP
28	−9.36	NULL	3 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
29	−9.21	NULL	10 / 82	CC	intermediate filament
30	−9.16	NULL	4 / 15	GSEA C2	LEE_LIVER_CANCER_MYC_E2F1_UP
31	−8.77	NULL	6 / 51	MF	protein binding, bridging
32	−8.76	NULL	3 / 10	GSEA C2	KEGG_LINOLEIC_ACID_METABOLISM
33	−8.57	NULL	2 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_LIVER_UP
34	−8.26	NULL	7 / 38	BP	epithelial cell differentiation
35	−8.24	NULL	2 / 12	GSEA C2	REACTOME_GAP_JUNCTION_ASSEMBLY
36	−8.06	NULL	3 / 14	BP	defense response to fungus
37	−7.89	NULL	3 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
38	−7.85	NULL	2 / 13	GSEA C2	REACTOME_GAP_JUNCTION_TRAFFICKING
39	−7.74	NULL	2 / 14	GSEA C2	KEGG_PHENYLALANINE_METABOLISM
40	−7.53	NULL	3 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP