

# MLH1\_normHNPC vs

## Global Summary

%DE = 0.36  
 # genes with fdr < 0.2 = 1152 ( 607 + / 545 -)  
 # genes with fdr < 0.1 = 451 ( 154 + / 297 -)  
 # genes with fdr < 0.05 = 179 ( 31 + / 148 -)  
 # genes with fdr < 0.01 = 49 ( 3 + / 46 -)  
 # genes in genesets = 18990

<FC> = 0  
 <t-score> = -0.04  
 <p-value> = 0.2  
 <fdr> = 0.65

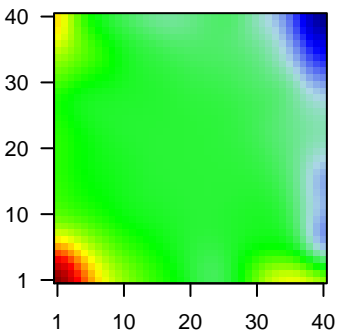
## Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG000000001	-0.03	1e-07	0.001 31 x 25 actin-related protein T3 [Source:HGNC Symbol;Acc:HGNC:2
2	ENSG000000001	-0.02	2e-07	0.001 21 x 8 hydroxylysine kinase [Source:HGNC Symbol;Acc:HGNC:344
3	ENSG000000001	-0.1	3e-07	0.003 36 x 29 aldehyde dehydrogenase 7 family, member A1 [Source:HGNC
4	ENSG000000001	-0.13	6e-07	0.003 36 x 37 angiotensin II receptor-associated protein [Source:HGNC Sy
5	ENSG000000001	-0.13	8e-07	0.005 37 x 35 IQ motif containing GTPase activating protein 3 [Source:HGNC
6	ENSG000000001	-0.07	2e-06	0.005 38 x 36 tumor-associated calcium signal transducer 2 [Source:HGNC
7	ENSG000000001	-0.25	2e-06	0.005 38 x 40 emopamil binding protein-like [Source:HGNC Symbol;Acc:HK
8	ENSG000000002	-0.01	3e-06	0.005 26 x 23 achaete-scute family bHLH transcription factor 5 [Source:HG
9	ENSG000000001	-0.09	3e-06	0.005 37 x 27 aldehyde dehydrogenase 4 family, member A1 [Source:HGNC
10	ENSG000000002	-0.08	3e-06	0.005 37 x 29
11	ENSG000000001	-0.17	3e-06	0.007 30 x 40 glycine cleavage system protein H (aminomethyl carrier) [Sou
12	ENSG000000001	-0.04	4e-06	0.007 25 x 32 meiosis-specific nuclear structural 1 [Source:HGNC Symbol;
13	ENSG000000002	-0.38	6e-06	0.007 40 x 39 centromere protein W [Source:HGNC Symbol;Acc:HGNC:214
14	ENSG000000000	-0.18	6e-06	0.007 38 x 36 aurora kinase A [Source:HGNC Symbol;Acc:HGNC:11393]
15	ENSG000000001	-0.11	6e-06	0.007 37 x 33 kinetochore-localized astrin/SPAG5 binding protein [Source;t
16	ENSG000000001	-0.04	6e-06	0.007 22 x 36 chromosome 3 open reading frame 33 [Source:HGNC Symbc
17	ENSG000000001	-0.07	7e-06	0.008 33 x 32 PARP1 binding protein [Source:HGNC Symbol;Acc:HGNC:26
18	ENSG000000001	-0.08	9e-06	0.008 38 x 23 solute carrier family 29 (equilibrative nucleoside transporter),
19	ENSG000000000	-0.1	9e-06	0.008 35 x 34 origin recognition complex, subunit 1 [Source:HGNC Symbol;
20	ENSG000000001	-0.05	1e-05	0.008 30 x 32 SWI/SNF related, matrix associated, actin dependent regulat

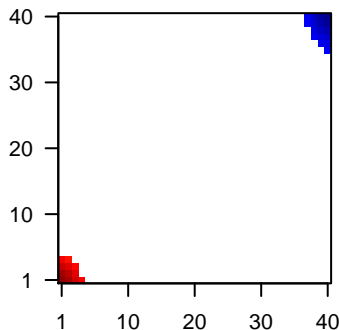
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	24.16	0e+00	844	Colon Cancer_benckke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	20.09	0e+00	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
3	15.75	2e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
4	15.53	2e-05	427	Tissue WIRTH_Immune system
5	15.24	3e-05	368	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_2B
6	14.77	3e-05	263	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
7	14.67	3e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
8	14.23	3e-05	347	LymphomaWIRTH_lymphoma937_spot H
9	14.21	3e-05	3507	CC plasma membrane
10	14.18	4e-05	336	LymphomaLopp_June14_MMML937_tumors+controls_group.overexpression_
11	14.12	4e-05	574	Cancer Lembecke_Colonic Inflammation
12	13.73	4e-05	132	Colon CancerMarrisa_CRC-cluster-b
13	13.29	4e-05	314	LymphomaLopp_June14_MMML937_tumors+controls_group.overexpression_
14	13.21	4e-05	315	LymphomaWIRTH_lymphoma937_spot E
15	12.58	6e-05	507	Colon CancerReTrack_CRC_TCGA_corr_C_normal_UP
16	12.47	6e-05	3109	Colon CancerLiefF_Colon
17	12.26	6e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
18	12.19	6e-05	148	Colon CancerMarrisa_CRC-cluster-a
19	12.17	6e-05	145	LymphomaWIRTH_lymphoma937_spot F
20	12.17	6e-05	145	LymphomaLopp_June14_MMML937_tumors+controls_group.overexpression_
<i>Underexpressed</i>				
1	-28.95	0e+00	550	Cancer Lembecke_Normal vs Adenoma
2	-26.53	0e+00	807	LymphomaLopp_June14_MMML937_tumors+controls_group.overexpression_
3	-26.48	0e+00	811	LymphomaWIRTH_lymphoma937_spot D
4	-21.17	0e+00	830	Colon CancerReTrack_CRC_TCGA_corr_R_normal_DN
5	-19.79	3e-06	713	Colon CancerReTrack_CRC_TCGA_group.over_C_normal_DN
6	-19.37	3e-06	145	Glio WILLSCHER_GBM_Verhaak-CL_up (C)
7	-19.34	3e-06	400	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP
8	-18.39	1e-05	582	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
9	-18.21	1e-05	546	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
10	-17.08	2e-05	316	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
11	-17	2e-05	1298	GSEA C2ODD_NASOPHARYNGEAL_CARINOMA_DN
12	-16.41	2e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
13	-16.35	2e-05	944	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
14	-16.34	2e-05	282	GSEA C2MANALO_HYPOXIA_DN
15	-16.14	2e-05	1441	CC mitochondrion
16	-15.84	2e-05	668	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
17	-15.37	3e-05	10475	Colon CancerLiefF_Colon
18	-15.18	3e-05	775	GSEA C2WEI_MYCN_TARGETS_WITH_E_BOX
19	-14.89	3e-05	248	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
20	-14.68	3e-05	8123	Colon CancerLiefF_Colon

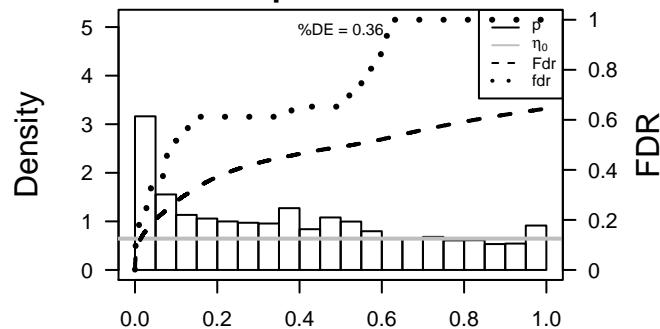
Profile



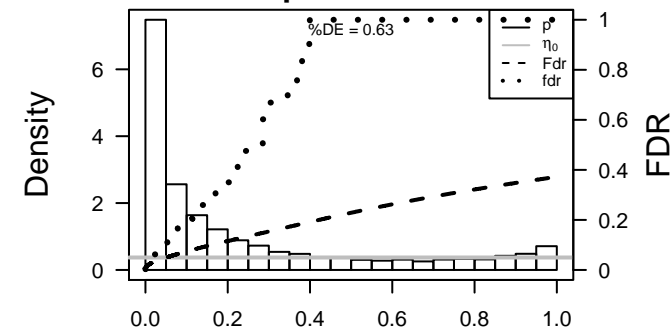
Regulated Spots



p-values



p-values



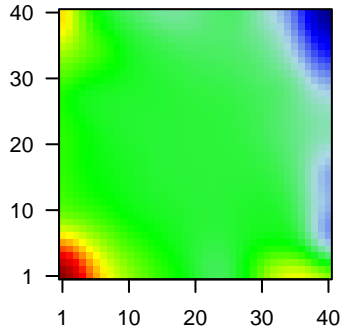
# MLH1\_normHNPC vs

## Local Summary

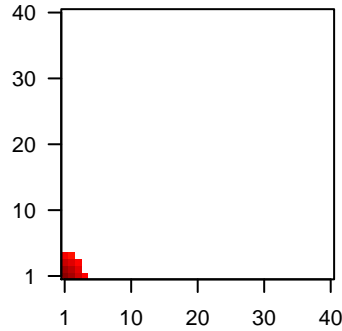
%DE = 0.97  
 # metagenes = 12  
 # genes = 256  
 # genes in genesets = 251  
  
 # genes with  $fdr < 0.1$  = 245 ( 245 + / 0 -)  
 # genes with  $fdr < 0.05$  = 236 ( 236 + / 0 -)  
 # genes with  $fdr < 0.01$  = 210 ( 210 + / 0 -)

<r> metagenes = 1  
 <r> genes = 0.88  
  
 <FC> = 0.36  
 <t-score> = 3.76  
 <p-value> = 0.01  
 <fdr> = 0.24

Profile



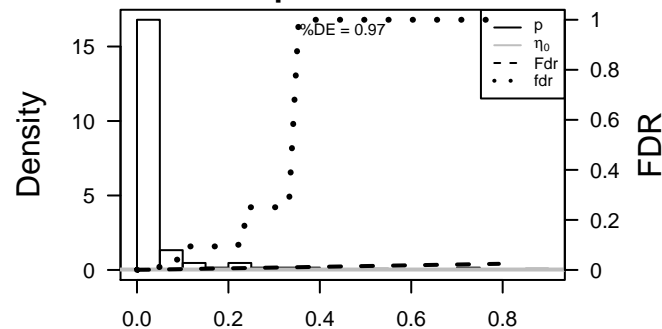
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000002	0.41	7e-05	4e-04	3 x 1 Spi-B transcription factor (Spi-1/PU.1 related) [Source:HGNC]
2	ENSG000001	0.44	1e-04	4e-04	1 x 1 interleukin 2 receptor, gamma [Source:HGNC Symbol;Acc:HGNC:1271]
3	ENSG000001	0.27	2e-04	4e-04	4 x 1 pleckstrin homology domain containing, family F (with FYVE c
4	ENSG000001	0.41	3e-04	4e-04	1 x 4 nuclear factor of kappa light polypeptide gene enhancer in B-
5	ENSG000001	0.72	3e-04	4e-04	1 x 1 pre-B lymphocyte 3 [Source:HGNC Symbol;Acc:HGNC:1271]
6	ENSG000001	0.68	3e-04	5e-04	1 x 1 B-cell translocation gene 1, anti-proliferative [Source:HGNC]
7	ENSG000001	0.82	5e-04	5e-04	1 x 1 CD79a molecule, immunoglobulin-associated alpha [Source:
8	ENSG000001	1.42	6e-04	5e-04	1 x 1 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc:
9	ENSG000001	1.15	7e-04	5e-04	1 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;A
10	ENSG000001	1.03	7e-04	5e-04	1 x 1 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
11	ENSG000001	0.37	7e-04	5e-04	3 x 1 family with sequence similarity 102, member A [Source:HGNC]
12	ENSG000001	0.31	7e-04	8e-04	2 x 1 lymphocyte antigen 86 [Source:HGNC Symbol;Acc:HGNC:16
13	ENSG000000	0.56	1e-03	8e-04	1 x 1 CD79b molecule, immunoglobulin-associated beta [Source:H
14	ENSG000002	0.61	1e-03	8e-04	1 x 1 major histocompatibility complex, class II, DP beta 1 [Source:
15	ENSG000001	1.16	2e-03	8e-04	1 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc
16	ENSG000001	0.36	2e-03	8e-04	1 x 1 Fc receptor-like A [Source:HGNC Symbol;Acc:HGNC:18504]
17	ENSG000001	0.54	2e-03	8e-04	1 x 1 clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
18	ENSG000001	1.23	2e-03	8e-04	1 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc
19	ENSG000001	0.41	2e-03	8e-04	1 x 4 tumor necrosis factor, alpha-induced protein 3 [Source:HGNC]
20	ENSG000001	0.76	2e-03	8e-04	1 x 1 lysosomal protein transmembrane 5 [Source:HGNC Symbol;A

p-values



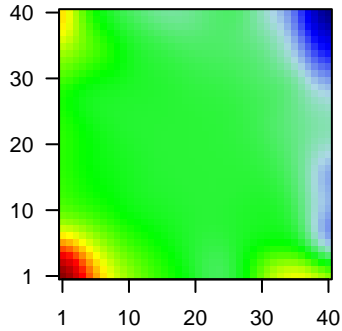
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## Local Summary

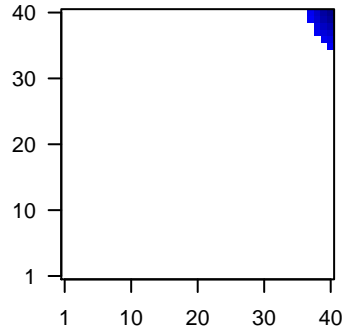
%DE = 0.96  
 # metagenes = 17  
 # genes = 393  
 # genes in genesets = 387  
  
 # genes with  $fdr < 0.1$  = 379 ( 4 + / 375 -)  
 # genes with  $fdr < 0.05$  = 359 ( 4 + / 355 -)  
 # genes with  $fdr < 0.01$  = 71 ( 0 + / 71 -)

$\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.86  
 $\langle FC \rangle$  = -0.28  
 $\langle t\text{-score} \rangle$  = -3.96  
 $\langle p\text{-value} \rangle$  = 0.06  
 $\langle fdr \rangle$  = 0.47

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.25	2e-06	3e-05	38 x 40 emopamil binding protein-like [Source:HGNC Symbol;Acc:HK
2	ENSG0000002	-0.38	6e-06	3e-05	40 x 39 centromere protein W [Source:HGNC Symbol;Acc:HGNC:214
3	ENSG0000001	-0.19	1e-05	3e-05	38 x 38 translocase of outer mitochondrial membrane 40 homolog (ye
4	ENSG0000001	-0.19	1e-05	3e-05	38 x 38 transmembrane protein 97 [Source:HGNC Symbol;Acc:HGNC
5	ENSG0000001	-0.33	1e-05	3e-05	40 x 38 dCTP pyrophosphatase 1 [Source:HGNC Symbol;Acc:HGNC
6	ENSG0000001	-0.34	1e-05	3e-05	40 x 40 transmembrane emp24 protein transport domain containing 3
7	ENSG0000001	-0.28	1e-05	3e-05	39 x 39 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
8	ENSG0000002	-0.38	2e-05	1e-04	40 x 40 NME/NM23 nucleoside diphosphate kinase 1 [Source:HGNC
9	ENSG0000001	-0.29	3e-05	1e-04	39 x 38 stomatin (EPB72)-like 2 [Source:HGNC Symbol;Acc:HGNC:1
10	ENSG0000001	-0.33	5e-05	1e-04	40 x 39 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172
11	ENSG0000001	-0.39	6e-05	1e-04	39 x 40 heat shock 10kDa protein 1 [Source:HGNC Symbol;Acc:HGNC
12	ENSG0000001	-0.21	6e-05	1e-04	39 x 39 ribophorin I [Source:HGNC Symbol;Acc:HGNC:10381]
13	ENSG0000000	-0.21	6e-05	2e-04	40 x 39 solute carrier family 25, member 39 [Source:HGNC Symbol;A
14	ENSG0000001	-0.35	7e-05	3e-04	40 x 39 prohibitin [Source:HGNC Symbol;Acc:HGNC:8912]
15	ENSG0000001	-0.81	9e-05	3e-04	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source
16	ENSG0000000	-0.31	1e-04	3e-04	38 x 39 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:H
17	ENSG0000001	-0.52	1e-04	3e-04	40 x 40 malectin [Source:HGNC Symbol;Acc:HGNC:28973]
18	ENSG0000001	-0.18	2e-04	3e-04	38 x 37 basic leucine zipper and W2 domains 2 [Source:HGNC Synt
19	ENSG0000001	-0.28	2e-04	3e-04	37 x 40 solute carrier family 35 (adenosine 3'-phospho 5'-phospho
20	ENSG0000001	-0.85	2e-04	4e-04	40 x 40 prostate cancer susceptibility candidate 1 [Source:HGNC Syr

p-values

