

Supplementary Table 1: (a) Top driver genes regulating modules enriched in major pathways of cancer.  
 (b) Alterations of the top drivers across all cancer sites

(a)

**Angiogenesis (43 enriched modules)**

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	6	3	3	7	4	4	2	3	2	6	3	43
FSTL1	2	1	0	0	0	0	0	1	1	1	2	8
EMILIN1	0	0	0	1	0	0	0	2	1	1	2	7
BIRC3	2	0	0	3	0	0	0	0	0	0	0	5
SOCS3	2	0	2	0	0	0	0	0	0	0	0	4
CD248	3	0	0	0	0	0	1	0	0	0	0	4
PPP1R3B	0	0	0	4	0	0	0	0	0	0	0	4
NUAK1	0	0	1	0	0	0	0	1	0	1	0	3
SPARCL1	1	0	0	0	0	0	0	2	0	0	0	3
C1S	2	0	0	1	0	0	0	0	0	0	0	3
IL1B	1	0	0	0	1	0	0	0	0	1	0	3
OLFML1	0	1	0	0	0	0	0	0	0	0	2	3
ANGPTL2	0	1	0	0	0	0	0	0	1	0	1	3
CDO1	0	0	1	0	0	0	0	1	0	0	0	2
MSC	2	0	0	0	0	0	0	0	0	0	0	2
MME	0	0	1	0	1	0	0	0	0	0	0	2
SRPX2	0	0	0	2	0	0	0	0	0	0	0	2
CLIP3	2	0	0	0	0	0	0	0	0	0	0	2
WIPF1	2	0	0	0	0	0	0	0	0	0	0	2
VIM	1	0	0	0	1	0	0	0	0	0	0	2
RCN3	2	0	0	0	0	0	0	0	0	0	0	2
PDLIM2	2	0	0	0	0	0	0	0	0	0	0	2
SERPINB1	1	0	0	0	0	0	0	0	0	1	0	2
MCL1	2	0	0	0	0	0	0	0	0	0	0	2
TRIP13	0	1	0	0	0	0	0	0	0	1	0	2
CHEK1	0	0	0	0	0	0	0	1	0	1	0	2
MIDN	1	0	0	0	1	0	0	0	0	0	0	2
ANXA2	0	0	0	2	0	0	0	0	0	0	0	2
DTL	0	0	0	2	0	0	0	0	0	0	0	2
TUBA1C	0	0	0	2	0	0	0	0	0	0	0	2
GPR171	0	1	0	0	0	0	0	0	1	0	0	2
MMP14	0	0	0	1	0	0	0	0	1	0	0	2
INHBA	0	0	0	0	2	0	0	0	0	0	0	2
DDR2	0	0	0	0	0	0	0	1	0	0	1	2
CCLE5	0	1	0	0	0	0	0	0	0	0	1	2
PTPN7	0	1	0	0	0	0	0	0	0	0	1	2
PTPRCAP	0	1	0	0	0	0	0	0	0	0	1	2
RRM2	0	1	0	0	0	0	0	1	0	0	0	2
SNRK	0	0	0	0	0	0	0	2	0	0	0	2
KNTC1	0	1	0	0	0	0	0	1	0	0	0	2
ACTA2	0	0	0	0	0	0	0	0	0	1	1	2
PCOLCE	0	1	0	0	0	0	0	0	0	1	0	2
CTSK	0	1	0	0	0	0	0	0	0	0	1	2
CD247	0	1	0	0	0	0	0	0	0	0	1	2
CD27	0	1	0	0	0	0	1	0	0	0	0	2
GLT25D2	0	0	0	0	0	0	2	0	0	0	0	2

**Hypoxia (44 enriched modules)**

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	4	2	3	8	3	2	2	7	1	10	2	44
BIRC3	2	0	0	3	0	0	0	0	0	0	0	5
SRPX2	0	0	0	4	0	0	0	1	0	0	0	5
PPP1R3B	0	0	0	5	0	0	0	0	0	0	0	5
CD248	2	0	1	0	0	0	1	0	0	0	0	4
CHEK1	0	0	0	0	0	0	0	2	0	2	0	4
IL1B	1	0	0	0	1	0	0	0	0	2	0	4

WIPF1	2	0	0	0	0	0	0	0	0	0	1	3
C1S	2	0	0	1	0	0	0	0	0	0	0	3
MCL1	2	0	0	0	0	0	0	0	0	1	0	3
SOCS3	2	0	1	0	0	0	0	0	0	0	0	3
KNTC1	0	1	0	0	0	0	0	2	0	0	0	3
ACTA2	0	0	0	0	0	0	0	0	0	3	0	3
NUAK1	0	0	1	0	0	0	0	0	0	2	0	3
MME	0	0	1	0	2	0	0	0	0	0	0	3
DTL	0	0	0	2	0	0	0	0	0	1	0	3
FAM83D	0	0	0	0	0	0	0	3	0	0	0	3
NNMT	0	0	0	0	0	0	0	0	0	3	0	3
EV12A	0	0	0	0	0	0	0	0	0	3	0	3
ALPK2	0	0	0	0	0	0	0	0	0	3	0	3
CD274	2	0	0	0	0	0	0	0	0	0	0	2
BATF	0	0	0	2	0	0	0	0	0	0	0	2
FSTL1	1	0	0	0	0	0	0	0	0	1	0	2
SERPINB1	1	0	0	0	0	0	0	0	0	1	0	2
TRIP13	0	1	0	0	0	0	0	0	0	1	0	2
C16orf54	0	1	1	0	0	0	0	0	0	0	0	2
RRM2	0	1	0	0	0	0	0	1	0	0	0	2
GPR171	0	1	0	0	1	0	0	0	0	0	0	2
TRIM22	0	0	1	1	0	0	0	0	0	0	0	2
ATP10A	0	0	1	0	0	0	0	1	0	0	0	2
PTPRC	0	1	0	0	0	0	0	0	0	0	1	2
TGFB3	0	0	1	0	0	0	0	0	0	1	0	2
SLA	0	0	0	1	0	0	0	0	0	0	1	2
ANXA2	0	0	0	2	0	0	0	0	0	0	0	2
RNF149	0	0	0	2	0	0	0	0	0	0	0	2
KIAA0247	0	0	0	1	0	0	0	0	0	1	0	2
TUBA1C	0	0	0	2	0	0	0	0	0	0	0	2
ACTN1	0	0	0	1	0	0	0	1	0	0	0	2
EGLN3	0	0	0	0	0	0	0	2	0	0	0	2
ANGPT2	0	0	0	0	1	0	0	1	0	0	0	2
GLT2SD2	0	0	0	0	0	0	2	0	0	0	0	2
FAP	0	0	0	0	0	0	0	2	0	0	0	2
MYBL2	0	0	0	0	0	0	0	2	0	0	0	2
RHOH	0	0	0	0	0	0	0	0	0	1	1	2
KCNN4	0	0	0	0	0	0	0	2	0	0	0	2
LCP2	0	0	0	0	0	0	0	0	0	1	1	2
RUNX2	0	0	0	0	0	0	0	0	0	2	0	2
PTTG2	0	0	0	0	0	0	0	0	0	2	0	2
GNPMB	0	0	0	0	0	0	0	0	0	2	0	2
RARRES3	0	0	1	0	0	0	1	0	0	0	0	2
ACAP1	0	0	0	1	0	0	0	0	0	0	0	2
CD247	0	0	0	1	0	0	0	0	0	0	0	2
GPR171	0	0	0	1	0	0	0	0	0	0	0	2
AOAH	0	0	0	0	0	0	0	0	0	0	0	2
IL2RG	0	0	0	0	0	0	0	0	0	0	0	2

### Epithelial Mesenchymal Transition (12 enriched modules)

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	1	0	2	1	2	2	0	1	0	3	0	12
TGFB3	0	0	1	0	0	1	0	0	0	1	0	3
NUAK1	0	0	1	0	0	0	0	0	0	2	0	3
CD248	1	0	1	0	0	0	0	0	0	0	0	2
FSTL1	0	0	0	0	0	1	0	0	0	1	0	2
MCL1	1	0	0	0	0	0	0	0	0	1	0	2
SOCS3	1	0	1	0	0	0	0	0	0	0	0	2
MIDN	1	0	0	0	1	0	0	0	0	0	0	2
PPP1R15A	0	0	0	0	0	0	0	1	0	1	0	2
NNMT	0	0	0	0	0	0	0	0	0	2	0	2
EV12A	0	0	0	0	0	0	0	0	0	2	0	2
ACTA2	0	0	0	0	0	0	0	0	0	2	0	2
RUNX2	0	0	0	0	0	0	0	0	0	2	0	2
ALPK2	0	0	0	0	0	0	0	0	0	2	0	2

**Cell cycle (22 enriched modules)**

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	1	2	1	3	1	2	2	3	1	5	1	22
HIST1H2AE	1	1	1	0	0	0	0	1	1	0	1	6
CHEK1	0	0	0	0	0	0	0	2	0	2	0	4
HIST1H3G	1	0	1	0	1	0	0	0	0	0	0	3
KNTC1	0	1	0	0	0	0	0	2	0	0	0	3
HIST1H2BJ	0	1	0	0	0	0	0	1	1	0	0	3
HIST1H3H	0	1	0	0	0	1	0	0	1	0	0	3
DTL	0	0	0	2	0	0	0	0	0	1	0	3
NCAPG2	0	0	0	0	0	1	1	0	0	1	0	3
TPX2	0	0	0	0	0	0	0	0	0	2	0	2
TRIP13	0	1	0	0	0	0	0	0	0	1	0	2
RRM2	0	1	0	0	0	0	0	1	0	0	0	2
ENSA	0	1	0	0	0	0	0	0	1	0	0	2
HIST1H1D	0	1	0	0	0	0	0	0	1	0	0	2
HIST1H3D	0	1	0	0	0	0	0	1	0	0	0	2
HIVEP2	0	0	0	2	0	0	0	0	0	0	0	2
TUBA1C	0	0	0	2	0	0	0	0	0	0	0	2
HINT3	0	0	0	1	0	1	0	0	0	0	0	2
FIG4	0	0	0	0	0	1	0	1	0	0	0	2
MYBL2	0	0	0	0	0	0	0	2	0	0	0	2
EZH2	0	0	0	0	0	0	0	0	0	2	0	2
PTTG2	0	0	0	0	0	0	0	0	0	2	0	2

**Immune response (100 enriched modules)**

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	11	8	8	9	12	7	7	9	9	11	9	100
CCL5	0	2	0	0	2	1	0	2	2	3	2	14
TNFAIP8L2	7	1	0	1	0	0	0	0	0	0	1	10
IL2RB	6	0	0	0	0	0	1	3	0	0	0	10
GPR171	0	2	0	1	4	0	0	0	2	1	0	10
BIRC3	6	0	0	3	0	0	0	0	0	0	0	9
OAS2	1	1	0	1	1	0	1	1	1	1	1	9
TRIM22	0	0	3	1	1	0	0	1	1	2	0	9
TBC1D10C	0	0	0	1	7	1	0	0	0	0	0	9
PPP1R16B	3	1	0	0	0	0	0	2	2	0	0	8
RARRES3	2	0	0	2	1	0	0	1	0	1	1	8
LAPTM5	0	1	0	0	0	2	0	0	0	3	2	8
DOK2	0	1	4	0	0	0	0	0	0	2	1	8
SLA	0	0	3	3	0	0	0	0	0	0	2	8
LCP1	0	0	0	0	4	1	0	3	0	0	0	8
GBP4	0	0	0	0	4	0	0	2	1	1	0	8
LCP2	0	0	0	0	0	0	0	0	1	4	3	8
PREX1	0	0	0	0	7	0	0	0	0	0	0	7
WIPF1	5	0	0	0	0	0	0	0	0	0	1	6
CTSS	1	0	0	0	5	0	0	0	0	0	0	6
PTPN7	0	3	0	0	0	1	0	0	0	0	2	6
GPR65	0	1	0	0	0	1	0	4	0	0	0	6
DAPP1	0	0	1	2	0	2	0	0	0	0	1	6
PLEK	0	0	0	1	0	0	0	0	0	3	2	6
PTPN22	0	0	0	1	0	0	0	1	3	1	0	6
NCF2	0	0	0	0	0	1	0	0	1	3	1	6
RCSD1	0	0	0	0	0	0	0	3	3	0	0	6
CIS	3	0	0	1	1	0	0	0	0	0	0	5
CD274	4	0	0	0	0	0	0	1	0	0	0	5
SOCS3	2	0	2	0	0	0	0	0	0	0	1	5
IL1B	1	0	0	0	1	0	0	0	0	3	0	5
ACAP1	0	4	0	0	0	1	0	0	0	0	0	5
PTPRCAP	0	2	0	0	0	1	0	0	0	1	1	5
SLAMF8	0	2	0	0	0	1	0	0	0	0	2	5

NCKAP1L	0	0	2	0	0	3	0	0	0	0	0	5
CD6	0	0	0	1	4	0	0	0	0	0	0	5
PTPRC	0	1	0	0	0	0	0	3	0	0	1	5
FPR2	0	0	4	0	0	0	1	0	0	0	0	5
PPP1R3B	0	0	0	4	0	0	1	0	0	0	0	5
SLCO2B1	0	0	0	0	0	1	0	0	0	3	1	5
ITK	0	0	0	0	0	0	1	0	4	0	0	5
CD5	0	0	0	0	0	0	0	2	2	1	0	5
RHOH	0	0	0	0	0	0	0	1	0	3	1	5

#### Apoptosis (50 enriched modules)

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	3	3	3	11	4	5	1	3	3	9	5	50
OAS2	1	1	0	1	2	0	0	1	1	1	1	9
TRIM22	0	0	1	1	2	0	0	0	1	1	0	6
BIRC3	2	0	0	3	0	0	0	0	0	0	0	5
RARRES3	0	0	0	2	0	0	0	1	0	1	0	4
PARP9	2	0	0	0	0	0	0	0	1	0	1	4
IL1B	1	0	0	0	1	0	0	0	0	2	0	4
CCL5	0	1	0	0	0	0	0	0	1	1	1	4
PSMB8	0	1	0	2	0	0	0	0	0	1	0	4
BST2	0	0	1	2	0	0	0	1	0	0	0	4
SRPX2	0	0	0	3	0	1	0	0	0	0	0	4
CD274	3	0	0	0	0	0	0	0	0	0	0	3
IRF7	1	0	0	1	1	0	0	0	0	0	0	3
SP100	0	0	0	0	1	0	0	1	1	0	0	3
BATF2	0	1	0	0	0	0	0	0	1	1	0	3
ETV7	0	1	0	0	1	0	0	0	0	0	1	3
MX2	0	1	0	0	1	0	0	0	0	1	0	3
OAS1	0	1	0	0	0	0	0	0	0	1	1	3
PPP1R3B	0	0	0	3	0	0	0	0	0	0	0	3
IFI35	0	0	0	1	0	0	0	0	0	1	1	3
EPST11	0	0	0	0	2	0	0	0	0	0	1	3
XAF1	0	0	0	0	0	0	0	0	1	1	1	3

#### Metastases (85 enriched modules)

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	11	7	6	7	9	6	2	7	10	14	6	85
FSTL1	2	1	0	0	0	1	0	1	2	3	2	12
EMILIN1	0	0	0	1	0	0	0	1	1	1	3	7
GJB5	1	0	1	0	0	0	0	1	2	0	1	6
CD248	3	0	1	0	0	0	1	0	0	0	0	5
KRT16	2	2	0	0	0	0	0	0	0	1	0	5
OAS2	1	1	0	1	0	0	0	0	0	1	1	5
IL1RN	1	0	0	0	0	0	0	0	4	0	0	5
NUAK1	0	0	1	0	0	0	0	1	0	3	0	5
SDR9C7	0	0	0	0	5	0	0	0	0	0	0	5
BIRC3	2	0	0	2	0	0	0	0	0	0	0	4
IL1B	1	0	0	0	1	0	0	0	0	2	0	4
S100A14	1	0	0	0	0	0	0	0	2	0	1	4
OLFML1	0	1	0	0	0	0	0	0	0	1	2	4
TRIM29	0	1	0	0	0	0	0	0	1	2	0	4
NCCRP1	0	1	0	0	3	0	0	0	0	0	0	4
A2ML1	0	1	0	0	0	0	0	0	2	0	1	4
ACTA2	0	0	0	0	0	0	0	0	0	3	1	4
TGFB3	0	0	1	0	0	1	0	0	0	2	0	4
NNMT	0	0	0	0	0	0	0	0	0	4	0	4
RUNX2	0	0	0	0	0	0	0	0	0	4	0	4
CLIP3	2	0	0	0	0	0	0	0	0	0	1	3
KRT5	1	0	0	0	0	0	0	0	2	0	0	3
TMEM40	1	0	0	0	0	0	0	0	1	1	0	3
MCL1	2	0	0	0	0	0	0	0	0	1	0	3

SOCS3	2	0	1	0	0	0	0	0	0	0	0	3
GNAI5	0	0	0	0	0	0	0	1	2	0	0	3
CHEK1	0	0	0	0	0	0	0	1	0	2	0	3
S100A16	1	0	0	0	0	0	0	2	0	0	0	3
PCOLCE	0	1	0	0	0	0	0	0	0	2	0	3
ANGPTL2	0	1	0	0	0	0	0	0	1	0	1	3
KCNJ11	0	1	0	0	0	1	0	1	0	0	0	3
DDR2	0	0	0	0	0	0	0	0	1	1	1	3
OAS1	0	1	0	0	0	0	0	0	0	1	1	3
PSMB8	0	1	0	1	0	0	0	0	0	1	0	3
SFN	0	0	1	0	0	1	0	0	0	0	1	3
S100A9	0	0	0	0	0	0	0	0	3	0	0	3
SRPX2	0	0	0	1	0	1	0	1	0	0	0	3
PPP1R3B	0	0	0	3	0	0	0	0	0	0	0	3
DTL	0	0	0	2	0	0	0	0	0	1	0	3
TMEM173	0	0	0	1	0	0	1	0	0	1	0	3
MMP14	0	0	0	1	0	0	0	0	2	0	0	3
IFI35	0	0	0	1	0	0	0	0	0	1	1	3
GJB2	0	0	0	0	3	0	0	0	0	0	0	3
DSG1	0	0	0	0	3	0	0	0	0	0	0	3
GPC6	0	0	0	0	2	0	0	0	0	0	1	3
KRT19	0	0	0	0	0	1	0	0	0	0	2	3
PRKCDBP	0	0	0	0	0	0	0	0	0	2	1	3
FAP	0	0	0	0	0	0	0	3	0	0	0	3
TNFSF4	0	0	0	0	0	0	0	2	1	0	0	3
CLCA2	0	0	0	0	0	0	0	0	3	0	0	3
STMN1	0	0	0	0	0	0	0	0	0	3	0	3
ALPK2	0	0	0	0	0	0	0	0	0	3	0	3

#### Integrin (one enriched module)

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	0	0	0	1	0	0	0	0	0	0	0	1
SVIL	0	0	0	1	0	0	0	0	0	0	0	1
COL5A2	0	0	0	1	0	0	0	0	0	0	0	1
ISLR	0	0	0	1	0	0	0	0	0	0	0	1
TMEM173	0	0	0	1	0	0	0	0	0	0	0	1
CTHRC1	0	0	0	1	0	0	0	0	0	0	0	1
PDLIM1	0	0	0	1	0	0	0	0	0	0	0	1

#### Epidermal Growth Factor Receptor (34 enriched modules)

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
Number of enriched modules	2	5	0	7	1	2	1	3	2	9	2	34
OAS2	1	1	0	1	1	0	0	0	1	1	0	6
HIST1H2AE	1	1	0	0	0	0	0	1	1	0	1	5
CHEK1	0	0	0	0	0	0	0	2	0	2	0	4
KNTC1	0	2	0	0	0	0	0	2	0	0	0	4
BIRC3	1	0	0	2	0	0	0	0	0	0	0	3
RARRES3	0	0	0	1	0	0	0	0	0	2	0	3
TRIP13	0	2	0	0	0	0	0	0	0	1	0	3
IRF7	1	0	0	1	1	0	0	0	0	0	0	3
HIST1H2BJ	0	1	0	0	0	0	0	1	1	0	0	3
HIST1H3H	0	1	0	0	0	1	0	0	1	0	0	3
TRIM22	0	0	0	0	1	0	0	0	1	1	0	3
BATF2	0	1	0	0	0	0	0	0	1	1	0	3
MX2	0	1	0	0	1	0	0	0	0	1	0	3
PSMB8	0	1	0	1	0	0	0	0	0	1	0	3
PPP1R3B	0	0	0	3	0	0	0	0	0	0	0	3
DTL	0	0	0	2	0	0	0	0	0	1	0	3
NCAPG2	0	0	0	0	0	1	1	0	0	1	0	3
NNMT	0	0	0	0	0	0	0	0	0	3	0	3
SP110	1	0	0	0	1	0	0	0	0	0	0	2
PARP9	1	0	0	0	0	0	0	0	1	0	0	2

TPX2	0	0	0	0	0	0	0	0	0	2	0	2
SP100	0	0	0	0	1	0	0	0	1	0	0	2
CDT1	0	2	0	0	0	0	0	0	0	0	0	2
FANCA	0	2	0	0	0	0	0	0	0	0	0	2
CCL5	0	0	0	0	0	0	0	0	1	1	0	2
CDC7	0	2	0	0	0	0	0	0	0	0	0	2
RRM2	0	1	0	0	0	0	0	1	0	0	0	2
SP140	0	1	0	0	0	1	0	0	0	0	0	2
ENSA	0	1	0	0	0	0	0	0	1	0	0	2
HIST1H1D	0	1	0	0	0	0	0	0	1	0	0	2
HIST1H3D	0	1	0	0	0	0	0	1	0	0	0	2
PSRC1	0	1	0	0	0	0	1	0	0	0	0	2
OAS1	0	1	0	0	0	0	0	0	0	1	0	2
SRPX2	0	0	0	2	0	0	0	0	0	0	0	2
ANXA2	0	0	0	2	0	0	0	0	0	0	0	2
HIVEP2	0	0	0	2	0	0	0	0	0	0	0	2
KIAA0247	0	0	0	0	0	0	0	0	0	2	0	2
TUBA1C	0	0	0	2	0	0	0	0	0	0	0	2
HINT3	0	0	0	1	0	1	0	0	0	0	0	2
IFI35	0	0	0	1	0	0	0	0	0	1	0	2
TMEM71	0	0	0	0	0	0	0	0	0	2	0	2
CH13L1	0	0	0	1	0	0	0	0	0	1	0	2
XAF1	0	0	0	0	0	0	0	0	1	1	0	2
FIG4	0	0	0	0	0	1	0	1	0	0	0	2
MYBL2	0	0	0	0	0	0	0	2	0	0	0	2
STMN1	0	0	0	0	0	0	0	0	0	2	0	2
TMEM140	0	0	0	0	0	0	0	0	0	2	0	2
EZH2	0	0	0	0	0	0	0	0	0	2	0	2
PTTG2	0	0	0	0	0	0	0	0	0	2	0	2

(b)

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC
CHEK1	Amplified		Amplified					Amplified		Amplified	
FSTL1	Hypo-methylated	Hyper-methylated				Hyper-methylated		Hyper-methylated	Hyper-methylated	Hypo and hyper-methylated	Hypo and hyper-methylated
TGFB3			Hyper-methylated			Hyper-methylated				Hyper-methylated	
NUAK1			Hyper-methylated		Hypo-methylated			Hypo and hyper-methylated	Hypo and hyper-methylated	Hypo-methylated	Hypo and hyper-methylated
CCL5		Hyper-methylated			Hyper-methylated	Hyper-methylated		Hyper-methylated	Hyper-methylated	Hyper-methylated	Hyper-methylated

Supplementary Table 2: Driver genes ranked according to the number of regulated modules across all cancers

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of regulated modules
FSTL1	4	6	0	0	0	1	0	5	3	8	4	31
IFFO1	8	2	10	0	0	0	0	2	4	0	3	29
MLPH	0	14	6	0	1	0	0	0	4	0	3	28
SPARCL1	8	0	0	0	4	2	0	10	2	0	0	26
CLIP3	12	0	0	0	0	0	0	3	0	2	7	24
MFAP4	0	10	0	0	0	0	0	0	8	2	4	24
BEND5	5	0	0	0	9	0	0	5	3	0	0	22
NUAK1	0	0	6	0	1	0	0	4	1	5	4	21
CAPS	4	0	1	2	2	2	0	3	2	2	3	21
PPP1R16B	8	4	0	0	0	0	0	3	4	0	2	21
OLFML1	0	6	0	1	0	4	0	0	0	4	6	21
SLA	0	0	7	11	0	0	0	0	0	0	2	20
DDR2	0	3	0	0	4	3	0	2	2	2	4	20
CDO1	1	1	7	0	2	0	0	6	0	2	0	19
C1S	8	2	0	4	1	4	0	0	0	0	0	19
EFEMP2	0	4	0	3	0	0	3	4	3	0	2	19
EMILIN1	0	0	0	1	0	0	0	6	5	2	5	19
OSMR	8	0	9	0	0	0	0	0	0	0	0	17
SULT1C4	6	0	0	0	0	1	1	0	5	4	0	17
RARRES3	2	1	0	3	1	0	0	1	0	7	2	17
CCL5	0	3	0	0	2	1	0	3	3	3	2	17
TBC1D10C	0	0	0	1	11	1	2	0	0	2	0	17
SMO	0	1	6	0	0	0	0	1	1	6	1	16
TRIM22	0	1	4	2	2	0	0	2	1	3	1	16
GPX2	3	2	1	0	4	0	0	1	4	0	1	16
IGF1	13	0	0	0	0	0	0	2	0	0	1	16
RIN1	2	0	0	4	0	2	2	0	4	0	2	16
BCL2	0	5	0	0	9	0	0	0	2	0	0	16
ACTA2	0	2	0	0	0	0	0	0	3	7	4	16
ATP10A	0	1	9	0	0	0	2	3	0	0	0	15
TGFB3	0	0	9	0	0	4	0	0	0	2	0	15
DOCK2	0	1	8	0	0	0	0	0	6	0	0	15
METTL7A	0	0	7	0	3	0	0	5	0	0	0	15
LTBP3	0	0	5	0	3	0	6	0	0	0	1	15
CHST10	2	0	4	0	3	2	0	1	3	0	0	15
DAPP1	0	0	3	3	0	2	2	2	1	1	1	15
HSPB6	0	6	2	0	0	0	0	0	6	0	1	15
OLFM1	10	1	2	0	0	0	0	2	0	0	0	15
SRPX2	0	0	1	7	0	5	0	2	0	0	0	15
WIPF1	10	1	0	0	0	0	0	0	0	0	4	15
VIM	6	3	0	0	5	0	1	0	0	0	0	15
IL2RB	6	0	0	0	0	0	5	4	0	0	0	15
RECK	6	0	0	0	5	0	0	0	4	0	0	15
MYEF2	5	0	0	0	1	0	2	0	7	0	0	15
SELENBP1	0	0	0	0	0	0	2	7	4	0	2	15
LDOC1	0	0	12	0	0	0	2	0	0	0	0	14
GYPC	0	1	10	0	0	0	0	0	0	0	3	14
GBP4	0	0	0	0	6	0	3	2	2	1	0	14
SPATA18	0	0	0	0	0	0	0	6	0	4	4	14
CHST3	2	7	4	0	0	0	0	0	0	0	0	13
CD248	6	0	4	0	0	0	3	0	0	0	0	13
KIAA1324	0	0	3	0	0	0	0	0	2	3	5	13
PREX1	0	1	0	0	12	0	0	0	0	0	0	13
PKIA	0	1	0	0	2	1	2	0	0	5	2	13
CTSZ	0	0	0	3	0	2	8	0	0	0	0	13
DOK2	0	1	7	0	0	0	0	0	0	3	1	12
SOCS3	2	0	6	0	0	0	0	0	0	0	4	12
TUBGCP6	1	0	4	2	0	0	0	2	2	1	0	12
SFN	0	0	4	0	0	1	0	0	0	4	3	12
PKLR	0	0	2	0	0	4	6	0	0	0	0	12
BIRC3	7	0	0	5	0	0	0	0	0	0	0	12
TNFAIP8L2	7	1	0	3	0	0	0	0	0	0	1	12
SV2A	1	0	0	0	2	0	0	6	0	0	3	12
BCL11A	0	7	0	4	0	0	0	0	1	0	0	12
SLC44A4	0	4	0	0	1	1	0	1	4	0	1	12
PTPRCAP	0	2	0	0	0	1	6	0	0	2	1	12
CYFIP2	0	0	0	5	0	0	0	0	7	0	0	12
TMEM173	0	0	0	2	0	1	1	2	2	4	0	12
FLRT2	0	0	8	0	3	0	0	0	0	0	0	11
TRIB2	0	0	7	4	0	0	0	0	0	0	0	11
PNMA1	5	0	4	2	0	0	0	0	0	0	0	11
GJB5	5	0	2	0	0	0	0	1	2	0	1	11
BCAS1	8	3	0	0	0	0	0	0	0	0	0	11
OAS2	1	1	0	1	2	0	2	1	1	1	1	11
CRISPLD1	1	0	0	0	2	0	0	0	1	5	2	11
CSTA	1	0	0	9	0	0	0	0	1	0	0	11
PCOLCE	0	7	0	0	0	0	0	0	0	4	0	11
VTCN1	0	3	0	0	0	0	0	0	1	5	2	11
GPR171	0	2	0	2	4	0	0	0	2	1	0	11
ATP8A2	0	0	0	7	0	0	0	0	2	2	0	11
TLR8	0	0	0	7	0	0	4	0	0	0	0	11
PLEK	0	0	0	5	0	0	0	0	0	4	2	11

CCDC89	0	0	0	2	0	1	0	3	1	1	3	11
PTPRM	0	0	0	0	10	0	0	0	0	0	1	11
LCP1	0	0	0	0	6	1	0	3	1	0	0	11
MSI1	0	0	0	0	5	0	0	0	6	0	0	11
SERPINF1	0	0	0	0	3	5	0	3	0	0	0	11
CMTM3	0	0	7	0	0	1	0	0	1	0	1	10
NCKAP1L	0	1	6	0	0	3	0	0	0	0	0	10
LRRC2	0	0	3	0	0	2	0	0	0	0	5	10
CTTNBP2	0	4	1	0	2	0	0	0	3	0	0	10
DIXDC1	7	3	0	0	0	0	0	0	0	0	0	10
DSE	6	0	0	0	0	0	0	0	4	0	0	10
C14orf132	4	0	0	0	0	6	0	0	0	0	0	10
CTSS	2	0	0	0	8	0	0	0	0	0	0	10
TRIM29	0	4	0	0	0	0	0	0	1	5	0	10
ARAP3	0	2	0	0	0	8	0	0	0	0	0	10
TAGLN	0	2	0	0	0	5	0	0	0	1	2	10
ELOVL4	0	1	0	0	0	0	0	2	0	0	7	10
WNK2	0	1	0	0	8	0	0	0	1	0	0	10
BASP1	0	0	0	6	1	0	2	0	0	0	1	10
KIAA0247	0	0	0	3	0	0	0	1	0	6	0	10
TCF4	0	0	0	0	6	0	0	0	0	0	4	10
ADD2	0	0	0	0	1	0	0	0	8	0	1	10
ATRNL1	0	0	0	0	0	4	0	0	6	0	0	10
RCSD1	0	0	0	0	0	1	0	3	6	0	0	10



Supplementary Table 3: prediction AMARETTO results given CNV data only, MET data only or both CNV and MET data

	Rsquare			MSE			Rsquare increase with MET	MSE decrease with MET
	CNV	MET	CNV and MET	CNV	MET	CNV and MET		
BLCA	0.63491905	0.75918536	0.747088771	0.129120599	0.085754521	0.089623734	11%	4%
BRCA	0.55196631	0.68744417	0.707869718	0.134388745	0.0974036	0.089678172	16%	4%
COADREAD	0.560722577	0.686874503	0.706325299	0.13707469	0.097421053	0.092378388	15%	4%
GBM	0.625180223	0.711656734	0.717314742	0.140220484	0.113400472	0.11207482	9%	3%
HNSC	0.631380908	0.744118759	0.743615174	0.140991015	0.099974654	0.098737876	11%	4%
KIRC	0.651631817	0.734516833	0.712217622	0.123120399	0.095397403	0.101818509	6%	2%
LAML	0.611068775	0.757019741	0.738212603	0.150347928	0.091011585	0.101038635	13%	5%
LUAD	0.602504957	0.682858619	0.696236704	0.131973988	0.0995979	0.095490869	9%	4%
LUSC	0.65723949	0.716856013	0.71251301	0.111968514	0.101453676	0.092118849	6%	2%
OV	0.562328171	0.64142021	0.667417273	0.114725012	0.096584823	0.088217345	11%	3%
UCEC	0.5214479	0.685517255	0.665556488	0.148878157	0.101523068	0.107419615	14%	4%

Supplementary Table 4: Description of the pancancer AMARETTO communities

	BLCA	BRCA	COADREAD	GBM	HNSC	KIRC	LAML	LUAD	LUSC	OV	UCEC	Total number of modules
Community 1	9	9	7	4	8	10	0	8	9	1	9	74
Community 2	6	4	8	9	8	7	9	5	7	5	5	73
Community 3	9	7	9	5	7	5	1	4	5	7	5	64
Community 4	9	5	3	0	10	3	0	6	9	5	5	55
Community 5	3	5	7	3	6	3	0	8	9	1	6	51
Community 6	4	8	5	3	3	8	2	4	4	2	5	48
Community 7	4	7	5	1	6	3	5	6	4	2	2	45
Community 8	2	3	1	4	2	3	1	3	1	3	5	28
Community 9	2	2	2	0	3	2	0	9	4	0	3	27
Community 10	2	0	2	2	2	1	1	1	3	2	2	20
Community 11	2	1	2	1	2	1	1	1	2	1	2	16
Community 12	1	2	1	1	2	0	1	2	2	1	2	15
Community 13	2	1	1	0	3	0	0	2	3	1	2	15
Community 14	2	1	1	2	3	0	1	1	1	2	1	15
Community 15	3	2	0	0	2	0	0	3	1	1	1	13
Community 16	1	1	2	0	2	1	1	1	1	1	1	12
Community 17	1	1	1	1	1	1	1	1	1	1	1	11
Community 18	2	0	0	2	0	1	1	1	0	3	0	10
Community 19	1	1	0	0	3	1	0	0	1	1	1	9
Community 20	0	1	0	2	1	0	1	1	1	1	1	9

Supplementary Table 5: top driver genes and enrichment results of the smoking community

## Regulators

	M11_BLCA	M65_BLCA	M15_BRCA	M46_COADREAD	M27_HNSC	M41_HNSC	M57_HNSC	M10_LUAD	M72_LUAD	M64_LUSC	M99_LUSC	M71_LUSC	M72_OV	M60_UCEC	M97_UCEC	# regulated modules
GPX2	1	1	0	0	1	0	1	1	0	1	1	0	0	0	1	8
ABCB6	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	3
SLC7A11	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	3
CYP4F3	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	3
GPC1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
CBR1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2
NQO1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
ZNF323	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
UBXN10	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	2
AKR1B1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	2
ME1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	2
RIT1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	2
SLC47A2	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	2
UCHL1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	2
GSR	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	2
ABCC2	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	2
KIAA1324	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2
SPATA18	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2
CAPS	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2
AKR1B10	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2
ABHD4	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2
CYP4F11	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2
SOST	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2

## Gene enrichment

Gene set	M11_BLCA	M65_BLCA	M15_BRCA	M46_COADREAD	M27_HNSC	M41_HNSC	M57_HNSC	M10_LUAD	M72_LUAD	M64_LUSC	M99_LUSC	M71_LUSC	M72_OV	M60_UCEC	M97_UCEC	# significant enrichments	Averaged p-value	
NFE2L2.V2	2.95E-14	0.1205776	1	1	8.51E-12	1	1	1.05E-18	1	4.43E-02	8.39E-27	2.88E-07	1	1	4.25E-07	7	1.44E-02	
17115125-SuppTable2	1.50E-14	1	1	1	4.25E-14	1	1	4.00E-20	1	1.97E-05	3.44E-16	1	1	1	2.50E-09	6	3.29E-06	
17115125-SuppTable4	5.39E-09	1	1	1	1.35E-06	1	1	3.54E-11	1	2.86E-06	1	1	1	1	8.15E-03	5	8.45E-07	
19334046-TableS3a	8.54E-09	1	1	1	2.00E-06	1	1	5.71E-13	1	1	1	2.42E-05	1	1	4.06E-10	5	5.24E-06	
OXIDOREDUCTASE_ACTIVITY	1.88E-05	1	1	1	3.63E-05	1	1	3.66E-08	1	1	7.69E-07	1	1	1	9.32E-07	5	1.14E-05	
17115125-SuppTable6	7.25E-07	1	1	1	1	1	1	3.36E-09	1	2.68E-06	1	1	1	1	2.36E-10	4	8.51E-07	
ONDER_CDH1_TARGETS_1_UP	1.07E-05	1	1	1	1.86E-05	1	1	3.24E-04	1	1	2.32E-04	1	1	1	1	1	4	1.46E-04
HALLMARK_XENOBIOTIC_METABOLISM	9.09E-05	1	1	1	2.80E-06	1	1	2.68E-03	1	1	2.86E-08	1	1	1	1	1	4	6.95E-04
16491124-SuppTable1	1	1	1	7.57E-04	1	1	1	1	1	1	1	1	1.05E-04	1.67E-05	1	1	3	2.93E-04
19204204-SupplementaryTable2	1	1	0.132088818	0.828638008	7.09E-06	2.22E-03	1	1	1	1	1	1	1	1	3.19E-04	1	3	6.49E-02
DOANE_BREAST_CANCER_ESR1_UP	1	1	1	7.18E-04	1	1	1	1	1	1	1	1	9.96E-05	1.57E-05	1	1	3	2.78E-04
KAN_RESPONSE_TO_ARSENIC_TRIOXIDE	4.87E-06	1	1	1	8.48E-06	1	1	1.49E-04	1	1	1	1	1	1	1	1	3	5.41E-05
WOOD_EBV_EBNA1_TARGETS_UP	2.47E-06	1	1	1	1	1	1	7.61E-05	1	1	8.45E-07	1	1	1	1	1	3	2.65E-05
19306456-TableS2b	1	1	1.33E-02	3.02E-04	1	1	1	1	1	1	1	1	1	1	1	1	2	6.82E-03
16115903-TableS1	1	1	1	1.28E-02	1	1	1	1	1	1	1	1	1.33E-03	1	1	1	2	7.07E-03
17115125-SuppTable3	8.99E-11	1	1	1	1	1	1	1.48E-14	1	1	1	1	1	1	1	1	2	4.50E-11
19489030-SuppTable4	1.55E-05	1	1	1	1	1	1	1	1	1	2.62E-11	1	1	1	1	1	2	7.76E-06
18662380-S3-ESR1	1	1	1	1.14E-04	1	1	1	1	1	1	1	1	2.58E-02	1	1	1	2	1.86E-02
17603561-STable1	1	1	1	1.72E-02	1	1	1	1	1	1	1	1	7.53E-05	1	1	1	2	8.65E-03
16912175-SuppTable3b	1	1	1	2.01E-04	1	1	1	1	1	1	1	1	1	4.18E-02	1	1	2	2.10E-02
19204204-SupplementaryTable6	1	1	4.21E-02	1	2.00E-02	1	1	1	1	1	1	1	1	1	1	1	2	3.11E-02
19204204-SupplementaryTable3	1	1	4.01E-02	1	1.95E-02	1	1	1	1	1	1	1	1	1	1	1	2	3.02E-02
LIU_PROSTATE_CANCER_DN	1	1	5.86E-03	1	1	1.53E-02	1	1	1	1	1	1	1	1	1	1	2	1.06E-02
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	1	1	1	2.88E-03	1	1	1	1	1	1	1	1	1	2.49E-03	1	1	2	2.69E-03
RUTELLA_RESPONSE_TO_HGF_UP	1	1	1	1	1.21E-02	1	1	0.1845591	1	1	8.48E-03	1	1	1	1	1	2	2.26E-02
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP	1	1	1	1	1.05E-02	1	1	0.1610243	1	1	7.22E-03	1	1	1	1	1	2	1.96E-02
CARBOXYLIC_ACID_METABOLIC_PROCESS	1	1	1	1	1	1	1	1.35E-03	1	1	5.37E-07	1	1	1	1	1	2	6.75E-04
ORGANIC_ACID_METABOLIC_PROCESS	1	1	1	1	1	1	1	1.44E-03	1	1	5.90E-07	1	1	1	1	1	2	7.21E-04

Supplementary Table 6: (a) Signatures used for validation of GPX2 and correlation results  
 (b) Correlation results of GPX2 expression with smoking clinical data

(a)

**Signatures**

Oxidative gene signature	Xenobiotic metabolism gene signature
ANGPTL7	NCEH1
APOA4	GSTM4
APT X	ACSM2B
ATOX1	AOC1
CCL5	GSTM3
CYGB	MGST2
DGKK	DPEP1
DHCR24	AIP
DUSP1	AS3MT
ERCC1	RORC
ERCC2	UGT1A8
ERCC3	UGT1A10
ERCC6	UGT1A7
ERCC8	GSTO1
GCLC	GGT2
GCLM	UGT2B28
GLRX2	CES1
GPX3	PON3
GSS	GRIN1
IPCEF1	NAT2
MPO	MGST1
MSRA	GSTM2
NDUFA12	ACSM1
NDUFA6	FMO3
NDUFB4	SULT1A2
NDUFS2	SULT1A1
NDUFS8	CYP1A1
NUDT1	PTGS1
OXS R1	UGT2B4
PDLIM1	FMO2
PNKP	ACY3
PRDX2	SULT1B1
PRDX5	EPHX2
PRDX6	ACY1
PRNP	MGST3

RNF7  
S100A7  
SCARA3  
SELS  
SEPP1  
SGK2  
SOD1  
SOD2  
SRXN1  
STK25  
TXNRD2

CYP3A7  
GSTA4  
FMO1  
GSTM1  
CYP2W1  
CYP2C9  
NAT1  
STAR  
SULT1A3  
UGT1A9  
GSTP1  
AKR7A3  
GGT1  
CYP2F1  
AKR1C1  
UGT2B11  
CYP46A1  
CMBL  
UGT1A6  
AADAC  
ALDH3A1  
AOC2  
CYP2A13  
CYP1B1  
AKR7A2  
UGT1A4  
UGT1A1  
GSTO2  
AOC3  
CYP3A4  
CYP2D7  
CYP2E1  
CYP1A2  
AHR  
UGT2B15  
UGT1A5  
UGT1A3  
HNF4A  
RORA  
BPHL  
CYP2C19

CYP2C18  
 CES2  
 POR  
 ACSL1  
 NR1I2  
 CYP2J2  
 CYP2B6  
 GLYAT  
 NQO1  
 CYP2D6  
 CYP2C8  
 AKR7L  
 LPO  
 EPHX1  
 CYP3A5  
 CYP26A1  
 CYP26B1  
 S100A12  
 CRYZ

## Correlations

	Oxidative signature		Xenobiotic signature	
	Correlation	p-value	Correlation	p-value
BLCA	-0.007815478	8.75E-01	<b>0.5368829</b>	<b>1.29E-32</b>
BRCA	<b>0.175857826</b>	<b>4.83E-07</b>	<b>0.2936691</b>	<b>3.50E-22</b>
COADREAD	<b>0.12825616</b>	<b>3.37E-03</b>	<b>0.1633479</b>	<b>1.38E-05</b>
HNSC	<b>0.24393133</b>	<b>1.16E-06</b>	<b>0.6525858</b>	<b>2.05E-64</b>
LUAD	<b>0.422645132</b>	<b>1.98E-20</b>	<b>0.6229901</b>	<b>1.85E-55</b>
LUSC	<b>0.257088866</b>	<b>2.10E-09</b>	<b>0.5053464</b>	<b>2.85E-34</b>
OV	0.040147626	3.51E-01	<b>0.2494615</b>	<b>4.05E-09</b>
UCEC	<b>0.240126434</b>	<b>6.20E-08</b>	<b>0.3462708</b>	<b>1.10E-17</b>

(b)

	Smoking profile		Number of smoked years			Pack years		
	p-value	Percentage of NAs	Correlation	p-value	Percentage of NAs	Correlation	p-value	Percentage of NAs
BLCA	<b>0.05</b>	8%	NA	NA	100%	0.11257321	0.259951146	43%
HNSC	<b>1.50E-08</b>	8%	<b>0.25042771</b>	<b>0.01112927</b>	63%	<b>0.21146548</b>	<b>0.003001313</b>	47%
LUAD	0.26	9%	0.08253822	0.2845951	62%	-0.00863001	0.879323118	36%
LUSC	0.21	18%	0.03909737	0.59127115	68%	-0.03396215	0.528338745	29%

Supplementary Table 7: Experimental validation of the modules and their target genes regulated by GPX2 as a causative driver of the pancancer smoking community.

SUMMARY

Cancer	Module	consensus (A549/CGS001_A549_96H.GPX2.1)	shRNA2 (A549/KDC007_A549_96H.TRCN0000046238.666)	shRNA1 (A549/KDC007_A549_96H.TRCN0000046239.666)	Size # genes in module	Size # genes measured in LINC	Size Leading Edge	Size Leading Edge shRNA2 (A549/KDC007_A549_96H.TRCN0000046238.666)	Size Leading Edge shRNA1 (A549/KDC007_A549_96H.TRCN0000046239.666)
LUAD	10	P-value<0.0001 & FDR<0.0001	P-value<0.0001 & FDR<0.0001	P-value=0.0039 & FDR=0.0040	39	15	11	11	10
LUSC	64	P-value=0.3194 & FDR=0.3176	P-value=0.0919 & FDR=0.1311	P-value=0.3152 & FDR=0.2990	29	11		6	
	99	P-value<0.0001 & FDR<0.0001	P-value<0.0001 & FDR<0.0001	P-value<0.0001 & FDR<0.0001	41	25	19	17	20
BLCA	11	P-value<0.0001 & FDR=0.0051	P-value<0.0001 & FDR=0.0059	P-value<0.0001 & FDR=0.0010	23	14	9	10	10
	65	P-value=0.1846 & FDR=0.3592	P-value=0.2718 & FDR=0.2760	P-value=0.0809 & FDR=0.1511	30	6			5
HNSC	27	P-value=0.1176 & FDR=0.1307	P-value=0.1582 & FDR=0.1784	P-value=0.0325 & FDR=0.0374	28	18	14	9	12
	57	P-value=0.6747 & FDR=0.6836	P-value=0.7072 & FDR=0.7117	P-value=0.7390 & FDR=0.7393	31	6			
UCEC	97	P-value=0.0062 & FDR=0.0054	P-value=0.0104 & FDR=0.0095	P-value=0.0042 & FDR=0.0044	16	9	8	7	8
LUAD	10	NES=-2.4871	NES=-2.549	NES=-2.085	39	15	11	11	10
LUSC	64	NES=-1.1048	NES=-1.4226	NES=-1.1213	29	11		6	
	99	NES=-2.4916	NES=-2.2605	NES=-2.6911	41	25	19	17	20
BLCA	11	NES=-2.0557	NES=-2.0557	NES=-2.2099	23	14	9	10	10
	65	NES=-1.2769	NES=1.1567	NES=1.4928	30	6			5
HNSC	27	NES=-1.3909	NES=-1.3095	NES=-1.6539	28	18	14	9	12
	57	NES=0.8261	NES=-0.8042	NES=0.7859	31	6			
UCEC	97	NES=-1.9858	NES=-1.947	NES=-1.9961	16	9	8	7	8
z-score	GPX2	-0.5892	-0.7039	-0.775					

Experimental validation results on the gene level. Table shows the detailed GSEA enrichment results for the target genes of GPX2 in each of the three perturbation experiments upon GPX2 knockdown in the lung adenocarcinoma A549 cell line derived from LINC (columns: consensus, shRNA1, shRNA2) in each of the 8 modules regulated by GPX2 in the 5 cancer sites (rows: modules organized by the 5 sites in the following order: LUAD, LUSC, BLCA, HNSC, UCEC). For each of the 8 modules in the 5 cancer sites, we enlisted the predicted target genes of modules regulated by GPX2 as an activator of its targets. The z-score for each GPX2 knockdown experiment and each target gene is shown. Target genes repressed and induced by GPX2 knockdown experiments are represented in blue and red, respectively, and those that were identified as 'leading edge' genes driving the GSEA enrichment scores are highlighted in bold. The leading edge columns indicate whether the target gene is part of the leading edge gene set, and a value of NA is shown if the enrichment is not significant (FDR>0.25). Genes are sorted from highest negative z-score to highest positive z-score in the consensus signature. The rightmost column indicates whether genes are part of the LINC landmark or bing rowspaces in yellow, and visualized in grey if not a member of these rowspaces.

DETAILED

Cancer	Module	P-value & FDR consensus (A549/CGS001_A549_96H.GPX2.1)	P-value & FDR shRNA2 (A549/KDC007_A549_96H.TRCN0000046238.666)	P-value & FDR shRNA1 (A549/KDC007_A549_96H.TRCN0000046239.666)	Gene	z-scores consensus (A549/CGS001_A549_96H.GPX2.1)	z-scores shRNA2 (A549/KDC007_A549_96H.TRCN0000046238.666)	z-scores shRNA1 (A549/KDC007_A549_96H.TRCN0000046239.666)	Leading Edge consensus (A549/CGS001_A549_96H.GPX2.1)	Leading Edge shRNA2 (A549/KDC007_A549_96H.TRCN0000046238.666)	Leading Edge shRNA1 (A549/KDC007_A549_96H.TRCN0000046239.666)	Measured in LINC
LUAD	10	P-value<0.0001 & FDR<0.0001	P-value<0.0001 & FDR<0.0001	P-value=0.0039 & FDR=0.0040	NQO1	-3.9077	-5.05	-4.1151	yes	yes	yes	yes
					AKR1C2	-1.5429	-1.397	-1.9425	yes	yes	yes	yes
					AKR1C1	-1.4129	-1.2672	-1.7733	yes	yes	yes	yes
					PIR	-1.1001	-1.5504	-1.2525	yes	yes	yes	yes
					AKR1C3	-1.0573	-1.5112	-0.8801	yes	yes	yes	yes
					ALDH3A1	-0.8894	-0.6218	-1.5314	yes	yes	yes	yes
					SLC7A11	-0.765	-0.7579	-0.9556	yes	yes	yes	yes
					GULP1	-0.7022	0.4383	-1.6805	yes	no	yes	yes
					TPD52L1	-0.5999	-0.8206	-0.288	yes	yes	no	yes
					AKR1B10	-0.5828	-1.0199	-0.5283	yes	yes	no	yes
					SLC27A2	-0.5489	-0.6873	-0.3873	yes	yes	no	yes
					CES1	-0.3253	0.527	-1.0298	no	no	yes	yes
					HGD	-0.1697	-0.9737	0.3265	no	yes	no	yes
					CYP4F3	-0.1391	0.5664	-0.7957	no	no	yes	yes
					CBR3	0.0549	-0.0434	0.0346	no	no	no	yes
					ALOX12P2	NA	NA	NA	NA	NA	NA	no
					ATAT1	NA	NA	NA	NA	NA	NA	no
					BTBD11	NA	NA	NA	NA	NA	NA	no

					CA8	NA	NA	NA	NA	NA	NA	no
					CES1P1	NA	NA	NA	NA	NA	NA	no
					CKMT1A	NA	NA	NA	NA	NA	NA	no
					CKMT1B	NA	NA	NA	NA	NA	NA	no
					CYP4F11	NA	NA	NA	NA	NA	NA	no
					FAM110C	NA	NA	NA	NA	NA	NA	no
					GNAL	NA	NA	NA	NA	NA	NA	no
					GRM1	NA	NA	NA	NA	NA	NA	no
					HOGA1	NA	NA	NA	NA	NA	NA	no
					JAKMIP3	NA	NA	NA	NA	NA	NA	no
					LINC01554	NA	NA	NA	NA	NA	NA	no
					NRG4	NA	NA	NA	NA	NA	NA	no
					OSGIN1	NA	NA	NA	NA	NA	NA	no
					PCDHA13	NA	NA	NA	NA	NA	NA	no
					PPP2R2C	NA	NA	NA	NA	NA	NA	no
					RASAL1	NA	NA	NA	NA	NA	NA	no
					SLC44A5	NA	NA	NA	NA	NA	NA	no
					SLC9A2	NA	NA	NA	NA	NA	NA	no
					TAT	NA	NA	NA	NA	NA	NA	no
					UGT1A6	NA	NA	NA	NA	NA	NA	no
					WIPF3	NA	NA	NA	NA	NA	NA	no
LUSC	64	P-value=0.3194 & FDR=0.3176	P-value=0.0919 & FDR=0.1311	P-value=0.3152 & FDR=0.2990	AKR1C2	-1.5429	-1.397	-1.9425	NA	yes	NA	yes
					ALDH3A1	-0.8894	-0.6218	-1.5314	NA	yes	NA	yes
					IGFBP3	-0.7059	0.0352	-1.239	NA	no	NA	yes
					NMB	-0.7045	-0.5993	-0.9201	NA	yes	NA	yes
					AKR1B10	-0.5828	-1.0199	-0.5283	NA	yes	NA	yes
					GABRE	-0.3885	-0.646	-0.4588	NA	yes	NA	yes
					DNASE1L3	-0.2633	0.4008	-0.7632	NA	no	NA	yes
					CCNA1	0.6155	0.1569	1.1229	NA	no	NA	yes
					FLG	0.8481	1.0695	0.7032	NA	no	NA	yes
					GSTM1	0.8944	0.8134	0.9605	NA	no	NA	yes
					FGFR1	1.1187	-0.8718	2.2158	NA	yes	NA	yes
					ADH7	NA	NA	NA	NA	NA	NA	no
					ANKRD2	NA	NA	NA	NA	NA	NA	no
					AQP10	NA	NA	NA	NA	NA	NA	no
					ARTN	NA	NA	NA	NA	NA	NA	no
					BTBD11	NA	NA	NA	NA	NA	NA	no
					CAGE1	NA	NA	NA	NA	NA	NA	no
					CHP2	NA	NA	NA	NA	NA	NA	no
					CLDN8	NA	NA	NA	NA	NA	NA	no
					CREG2	NA	NA	NA	NA	NA	NA	no
					FAM110C	NA	NA	NA	NA	NA	NA	no
					GPNMB	NA	NA	NA	NA	NA	NA	no
					LEXM	NA	NA	NA	NA	NA	NA	no
					LOC285629	NA	NA	NA	NA	NA	NA	no
					NRG4	NA	NA	NA	NA	NA	NA	no
					PHEX	NA	NA	NA	NA	NA	NA	no
					RNF217-AS1	NA	NA	NA	NA	NA	NA	no
					SLC47A2	NA	NA	NA	NA	NA	NA	no
					UGT1A6	NA	NA	NA	NA	NA	NA	no
	99	P-value<0.0001 & FDR<0.0001	P-value<0.0001 & FDR<0.0001	P-value<0.0001 & FDR<0.0001	NQO1	-3.9077	-5.05	-4.1151	yes	yes	yes	yes
					TXNRD1	-3.5245	-5.0027	-3.5326	yes	yes	yes	yes
					AKR1C1	-1.4129	-1.2672	-1.7733	yes	yes	yes	yes
					G6PD	-1.2406	-1.3019	-1.7672	yes	yes	yes	yes
					TRIM16	-1.1942	-0.8852	-1.726	yes	yes	yes	yes
					AKR1C3	-1.0573	-1.5112	-0.8801	yes	yes	yes	yes
					GCLM	-1.0461	-1.0761	-1.133	yes	yes	yes	yes
					PHGDH	-0.9391	-1.2214	-1.1398	yes	yes	yes	yes
					UBL4A	-0.8477	-1.1137	-0.894	yes	yes	yes	yes
					PGD	-0.7854	-0.5597	-1.4009	yes	yes	yes	yes
					ME1	-0.7668	-1.6032	-0.7622	yes	yes	yes	yes
					SLC7A11	-0.765	-0.7579	-0.9556	yes	yes	yes	yes
					GSR	-0.6728	0.1165	-1.0326	yes	no	yes	yes
					TIMP4	-0.5654	-1.2904	-0.5245	yes	yes	yes	yes
					CBR1	-0.5507	-0.3507	-0.7467	yes	yes	yes	yes
					GCLC	-0.4777	-0.3749	-0.6569	yes	yes	yes	yes
					LPCAT1	-0.4186	-0.5052	-0.7413	yes	yes	yes	yes
					ABCC3	-0.3173	-0.7101	-0.3496	yes	yes	no	yes



				ABCC2	-0.3033	0.1059	-0.9073	yes	no	yes	yes
				CYP4F3	-0.1391	0.5664	-0.7957	no	no	yes	yes
				SLC7A5	0	0	0	no	no	no	yes
				CBR3	0.0549	-0.0434	0.0346	no	no	no	yes
				EGF	0.2223	0.592	0.0753	no	no	no	yes
				TNFSF9	0.5654	2.1874	-0.4707	no	no	yes	yes
				STC2	1.0092	1.7661	0.6807	no	no	no	yes
				ABCA4	NA	NA	NA	NA	NA	NA	no
				CDRT1	NA	NA	NA	NA	NA	NA	no
				CYP4F11	NA	NA	NA	NA	NA	NA	no
				FBXW10	NA	NA	NA	NA	NA	NA	no
				GCSH	NA	NA	NA	NA	NA	NA	no
				GPAT3	NA	NA	NA	NA	NA	NA	no
				HHIPL2	NA	NA	NA	NA	NA	NA	no
				NKX2-8	NA	NA	NA	NA	NA	NA	no
				OSGIN1	NA	NA	NA	NA	NA	NA	no
				PANX2	NA	NA	NA	NA	NA	NA	no
				PCDHB16	NA	NA	NA	NA	NA	NA	no
				PPP2R2C	NA	NA	NA	NA	NA	NA	no
				PTGR1	NA	NA	NA	NA	NA	NA	no
				SRXN1	NA	NA	NA	NA	NA	NA	no
				TRIM16L	NA	NA	NA	NA	NA	NA	no
				VSIG10L	NA	NA	NA	NA	NA	NA	no
BLCA	11	P-value<0.0001 & FDR=0.0051	P-value<0.0001 & FDR=0.0059	P-value<0.0001 & FDR=0.0010	NQO1	-3.9077	-5.05	-4.1151	yes	yes	yes
					AKR1C2	-1.5429	-1.397	-1.9425	yes	yes	yes
					AKR1C1	-1.4129	-1.2672	-1.7733	yes	yes	yes
					PIR	-1.1001	-1.5504	-1.2525	yes	yes	yes
					AKR1C3	-1.0573	-1.5112	-0.8801	yes	yes	yes
					ALDH3A1	-0.8894	-0.6218	-1.5314	yes	yes	yes
					SLC7A11	-0.765	-0.7579	-0.9556	yes	yes	yes
					PART1	-0.6328	-0.4605	-0.8708	yes	yes	yes
					AKR1B10	-0.5828	-1.0199	-0.5283	yes	yes	no
					ABCC2	-0.3033	0.1059	-0.9073	no	no	yes
					GALNT14	-0.2911	-1.556	0.006	no	yes	no
					CYP4F3	-0.1391	0.5664	-0.7957	no	no	yes
					HKDC1	0.2159	0.3039	0.0716	no	no	no
					ACKR3	0.7931	0.7037	1.0838	no	no	yes
					ABCA13	NA	NA	NA	NA	NA	no
					ABCA4	NA	NA	NA	NA	NA	no
					ARTN	NA	NA	NA	NA	NA	no
					CYP4F11	NA	NA	NA	NA	NA	no
					FBXW10	NA	NA	NA	NA	NA	no
					PANX2	NA	NA	NA	NA	NA	no
					PTGR1	NA	NA	NA	NA	NA	no
					VSIG10L	NA	NA	NA	NA	NA	no
					WNT5A	NA	NA	NA	NA	NA	no
	65	P-value=0.1846 & FDR=0.3592	P-value=0.2718 & FDR=0.2760	P-value=0.0809 & FDR=0.1511	FLRT3	-0.4733	-0.0908	-0.7503	NA	NA	no
					GPRC5C	0.0896	-0.0065	0.4883	NA	NA	yes
					GSTT1	0.1928	-0.1707	0.618	NA	NA	yes
					MAOA	0.243	0.301	0.5727	NA	NA	yes
					MECOM	0.4886	0.7462	0.2961	NA	NA	yes
					GSTM3	1.5561	1.0332	2.554	NA	NA	yes
					ABO	NA	NA	NA	NA	NA	no
					ADRB1	NA	NA	NA	NA	NA	no
					BMP7	NA	NA	NA	NA	NA	no
					BTG2	NA	NA	NA	NA	NA	no
					CEL	NA	NA	NA	NA	NA	no
					COLCA1	NA	NA	NA	NA	NA	no
					CYP4X1	NA	NA	NA	NA	NA	no
					FSTL4	NA	NA	NA	NA	NA	no
					GSTM4	NA	NA	NA	NA	NA	no
					HS6ST2	NA	NA	NA	NA	NA	no
					MAPK10	NA	NA	NA	NA	NA	no
					MPPED2	NA	NA	NA	NA	NA	no
					MRAP2	NA	NA	NA	NA	NA	no
					NPAS1	NA	NA	NA	NA	NA	no
					NRG4	NA	NA	NA	NA	NA	no
					PADI3	NA	NA	NA	NA	NA	no

					PCP4L1	NA	NA	NA	NA	NA	NA	no					
					RASSF6	NA	NA	NA	NA	NA	NA	no					
					RGS6	NA	NA	NA	NA	NA	NA	no					
					SLC52A1	NA	NA	NA	NA	NA	NA	no					
					UGT1A6	NA	NA	NA	NA	NA	NA	no					
					UGT1A9	NA	NA	NA	NA	NA	NA	no					
					WBSCR27	NA	NA	NA	NA	NA	NA	no					
					ZNF703	NA	NA	NA	NA	NA	NA	no					
HNSC	27	P-value=0.1176 & FDR=0.1307	P-value=0.1582 & FDR=0.1784	P-value=0.0325 & FDR=0.0374	NQO1	-3.9077	-5.05	-4.1151	yes	yes	yes	yes					
					AKR1C2	-1.5429	-1.397	-1.9425	yes	yes	yes	yes					
					AKR1C1	-1.4129	-1.2672	-1.7733	yes	yes	yes	yes					
					AKR1C3	-1.0573	-1.5112	-0.8801	yes	yes	yes	yes					
					ME1	-0.7668	-1.6032	-0.7622	yes	yes	yes	yes					
					SLC7A11	-0.765	-0.7579	-0.9556	yes	yes	yes	yes					
					AKR1B10	-0.5828	-1.0199	-0.5283	yes	yes	yes	yes					
					LPCAT1	-0.4186	-0.5052	-0.7413	yes	yes	yes	yes					
					METAP2	-0.4097	0.1892	-0.6109	yes	no	yes	yes					
					CES1	-0.3253	0.527	-1.0298	yes	no	yes	yes					
					ABCC2	-0.3033	0.1059	-0.9073	yes	no	yes	yes					
					CYP4F3	-0.1391	0.5664	-0.7957	yes	no	yes	yes					
					GSTA4	-0.0927	-0.5167	0.1488	yes	yes	no	yes					
					TSPAN7	-0.079	0.202	-0.3327	yes	no	no	yes					
					RAP1GAP	0.365	-0.1657	0.3302	no	no	no	yes					
					GSTM1	0.8944	0.8134	0.9605	no	no	no	yes					
					GSTM2	0.9471	0.731	1.0905	no	no	no	yes					
					GSTM3	1.5561	1.0332	2.554	no	no	no	yes					
					SEPT5	NA	NA	NA	NA	NA	NA	no					
					CHODL	NA	NA	NA	NA	NA	NA	no					
					CYP4F11	NA	NA	NA	NA	NA	NA	no					
					GPAT3	NA	NA	NA	NA	NA	NA	no					
					GSTM4	NA	NA	NA	NA	NA	NA	no					
					HHIPL2	NA	NA	NA	NA	NA	NA	no					
					MAP2	NA	NA	NA	NA	NA	NA	no					
					OSGIN1	NA	NA	NA	NA	NA	NA	no					
					PCDHB16	NA	NA	NA	NA	NA	NA	no					
					SOST	NA	NA	NA	NA	NA	NA	no					
					HNSC	57	P-value=0.6747 & FDR=0.6836	P-value=0.7072 & FDR=0.7117	P-value=0.7390 & FDR=0.7393	NMB	-0.7045	-0.5993	-0.9201	NA	NA	NA	yes
										ABCC3	-0.3173	-0.7101	-0.3496	NA	NA	NA	yes
										MATN2	-0.1975	0.5157	-0.663	NA	NA	NA	yes
PFN2	0.3866	0.3465	0.4914	NA						NA	NA	yes					
ACKR3	0.7931	0.7037	1.0838	NA						NA	NA	yes					
GLI2	0.8461	-0.4884	1.9946	NA						NA	NA	yes					
ADSSL1	NA	NA	NA	NA						NA	NA	no					
ARTN	NA	NA	NA	NA						NA	NA	no					
B4GALNT1	NA	NA	NA	NA						NA	NA	no					
CCL26	NA	NA	NA	NA						NA	NA	no					
CHP2	NA	NA	NA	NA						NA	NA	no					
CREG2	NA	NA	NA	NA						NA	NA	no					
DGKG	NA	NA	NA	NA						NA	NA	no					
FER1L6	NA	NA	NA	NA						NA	NA	no					
GPNMB	NA	NA	NA	NA						NA	NA	no					
HOGA1	NA	NA	NA	NA						NA	NA	no					
LMO1	NA	NA	NA	NA						NA	NA	no					
NANOS1	NA	NA	NA	NA						NA	NA	no					
NAP1L2	NA	NA	NA	NA						NA	NA	no					
NDRG4	NA	NA	NA	NA						NA	NA	no					
NDUFA4L2	NA	NA	NA	NA						NA	NA	no					
NGEF	NA	NA	NA	NA						NA	NA	no					
NKX2-8	NA	NA	NA	NA						NA	NA	no					
NOS1	NA	NA	NA	NA						NA	NA	no					
NRG4	NA	NA	NA	NA						NA	NA	no					
PANX2	NA	NA	NA	NA						NA	NA	no					
PHEX	NA	NA	NA	NA						NA	NA	no					
SLC13A5	NA	NA	NA	NA						NA	NA	no					
SLC22A18AS	NA	NA	NA	NA						NA	NA	no					
STK31	NA	NA	NA	NA						NA	NA	no					
WNT9A	NA	NA	NA	NA						NA	NA	no					
UCEC	97	P-value=0.0062 &	P-value=0.0104 &	P-value=0.0042 &	NQO1	-3.9077	-5.05	-4.1151	yes	yes	yes	yes					



Supplementary Table 8: Top drivers and enrichment results of the immune response community

## Regulators

	M30_BLCA	M58_BLCA	M35_BRCA	M90_COADREAD	M14_GBM	M48_GBM	M17_HNSC	M40_HNSC	M83_HNSC	M84_LAML	M60_LUAD	M85_LUSC	M97_OV	M68_OV	M62_UCEC	# regulated modules
OAS2	1	0	1	0	0	1	0	1	1	1	1	1	0	1	1	10
TRIM22	0	0	0	1	1	0	0	1	1	0	0	1	1	0	0	6
SP110	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	4
SP100	0	1	0	0	0	0	0	0	1	0	1	1	0	0	0	4
PSMB8	0	0	1	0	1	1	0	0	0	0	1	0	1	0	0	4
BST2	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	4
RARRRES3	0	0	0	0	1	1	0	0	0	0	1	0	1	0	0	4
EPS11	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	4
IRF7	1	0	0	0	0	1	0	1	1	0	0	0	0	0	0	4
PARP9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3
BATF2	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0	3
EIV7	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	3
MX2	0	0	1	0	0	0	0	0	1	0	0	0	0	1	0	3
OAS1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	3
IFI35	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	3
XAF1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	3
HCP5	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	2
ISG20	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	2
AIM2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	2
TRIM21	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	2
NMI	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	2
GBP4	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	2
SLC15A3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	2
IFI6	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	2
HLA-F	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	2
CCL5	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	2
TMEM140	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	2

## Gene enrichment

Gene set	M30_BLCA	M58_BLCA	M35_BRCA	M90_COADREAD	M14_GBM	M48_GBM	M17_HNSC	M40_HNSC	M83_HNSC	M84_LAML	M60_LUAD	M85_LUSC	M97_OV	M68_OV	M62_UCEC	# significant enrichments	Averaged p-value
17823660-TableS1b	7.82E-15	3.42E-09	6.68E-19	3.38E-18	5.63E-08	8.86E-19	1	1.15E-05	3.01E-16	1.53E-03	3.85E-09	4.05E-14	3.21E-02	2.18E-26	6.43E-18	14	2.40E-03
18245496-SuppTable2	8.52E-17	6.78E-08	4.33E-20	2.08E-14	1.10E-13	1.01E-18	1	1.21E-04	4.77E-09	4.31E-08	9.17E-15	1.72E-15	2.11E-18	2.71E-19	14	8.67E-06	
12747878-Table2	2.36E-23	1.93E-06	4.34E-24	4.29E-25	1.34E-22	3.50E-28	1	6.54E-10	4.07E-25	2.61E-05	5.06E-14	1.20E-22	3.37E-12	7.61E-29	3.40E-27	14	2.00E-06
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	6.89E-20	3.64E-03	3.48E-19	4.21E-23	2.36E-07	1.65E-30	1	2.83E-04	4.94E-22	2.21E-05	1.03E-07	3.40E-10	2.28E-05	4.46E-35	5.46E-22	14	2.83E-04
BROWNE_INTERFERON_RESPONSE_GENES	2.20E-26	6.52E-16	1.16E-25	2.76E-31	9.21E-27	4.00E-29	1	5.66E-11	5.62E-28	9.21E-10	1.67E-14	1.38E-21	4.68E-21	2.31E-39	1.41E-31	14	6.98E-11
WALLACE_PROSTATE_CANCER_RACE_UP	5.94E-19	4.68E-11	9.45E-25	2.06E-16	6.22E-16	5.00E-21	1	9.33E-06	5.68E-23	2.26E-12	3.11E-09	1.72E-16	2.08E-16	4.00E-21	6.95E-22	14	6.67E-07
GSE10325_CD4_TCELL_VS_L1UPUS_CD4_TCELL_DN	4.77E-31	2.16E-07	3.07E-26	2.99E-23	1.44E-22	1.54E-41	1	6.63E-09	1.04E-33	1.20E-04	1.70E-15	8.35E-24	7.41E-11	7.65E-51	1.09E-31	14	8.60E-06
GSE13484_UNSTIM_VS_YF17D_VACCINE_STIM_PBMC_DN	1.46E-33	1.15E-05	2.35E-28	3.32E-30	1.59E-24	2.73E-47	1	9.84E-11	1.60E-36	1.20E-04	5.25E-13	8.35E-24	1.26E-17	9.02E-61	5.71E-34	14	9.41E-06
GSE13485_CTRL_VS_DAY3_YF17D_VACCINE_PBMC_DN	2.30E-44	5.13E-04	3.13E-37	1.22E-32	2.24E-13	2.49E-50	1	1.41E-14	1.85E-39	3.14E-12	3.96E-18	1.64E-29	7.88E-05	5.71E-66	1.49E-43	14	4.23E-05
GSE13485_CTRL_VS_DAY7_YF17D_VACCINE_PBMC_DN	2.74E-47	4.64E-11	8.99E-47	2.52E-40	1.61E-26	1.63E-53	1	1.95E-13	1.53E-42	3.14E-12	3.96E-18	1.64E-29	7.13E-16	9.65E-80	1.23E-48	14	3.54E-12
GSE13485_DAY1_VS_DAY7_YF17D_VACCINE_PBMC_DN	2.30E-44	5.13E-04	5.97E-35	1.22E-32	1.44E-22	2.49E-50	1	1.59E-18	1.60E-36	3.24E-10	3.96E-18	1.40E-26	9.73E-08	5.71E-66	4.35E-41	14	3.66E-05
GSE14000_UNSTIM_VS_4H_LPS_DC_TRANSLATED_RNA_DN	1.34E-28	2.16E-07	5.97E-35	4.77E-21	2.14E-08	3.80E-36	1	9.84E-11	5.36E-31	2.56E-14	3.96E-18	3.69E-21	7.13E-16	1.68E-41	1.88E-29	14	1.70E-08
GSE14000_UNSTIM_VS_4H_LPS_DC_DN	3.24E-26	2.16E-07	5.97E-35	4.77E-21	2.24E-13	1.46E-33	1	9.84E-11	2.23E-28	3.14E-12	1.70E-15	8.35E-24	3.69E-14	7.65E-51	5.71E-34	14	1.54E-08
GSE1432_CTRL_VS_IFNG_24H_MICROGLIA_DN	3.29E-15	5.48E-15	2.68E-16	8.30E-13	7.24E-35	1.97E-19	1	1.41E-14	3.11E-12	1.20E-04	2.83E-06	1.92E-07	5.93E-27	1.44E-22	5.54E-17	14	8.80E-06
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_6H_DN	3.81E-36	5.13E-04	3.07E-26	3.89E-35	1.20E-20	1.54E-41	1	1.19E-18	5.36E-31	1.78E-16	5.25E-13	3.69E-21	1.74E-12	9.89E-56	1.09E-31	14	3.66E-05
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_8H_DN	1.46E-33	3.43E-09	1.64E-30	3.89E-35	1.27E-30	8.38E-39	1	5.95E-23	5.36E-31	2.56E-14	5.25E-13	3.69E-21	1.26E-17	2.87E-53	5.71E-34	14	2.45E-10
GSE18791_UNSTIM_VS_NEWCASTLE_VIRUS_DC_6H_DN	3.81E-36	1.15E-05	1.04E-32	1.07E-37	1.49E-28	1.54E-41	1	5.95E-23	5.36E-31	2.56E-14	5.25E-13	3.69E-21	7.13E-16	9.89E-56	2.69E-36	14	8.23E-07
GSE18791_UNSTIM_VS_NEWCASTLE_VIRUS_DC_10H_DN	1.46E-33	2.16E-07	3.07E-26	1.22E-32	1.59E-24	3.80E-36	1	5.95E-23	2.23E-28	2.81E-08	5.25E-13	3.69E-21	7.13E-16	1.87E-48	1.88E-29	14	1.74E-08
GSE22886_CTRL_VS_LPS_24H_DC_DN	1.46E-33	4.64E-11	1.64E-30	4.77E-21	1.59E-24	8.38E-39	1	3.83E-07	1.04E-33	1.20E-04	1.70E-15	1.40E-26	2.99E-21	1.87E-48	2.69E-36	14	8.61E-06
GSE6269_FLU_VS_STREP_PNEUMO_INF_PBMC_UP	4.15E-25	1.88E-04	2.07E-34	1.82E-24	3.55E-16	9.07E-38	1	9.92E-08	1.12E-29	7.22E-09	1.12E-13	1.58E-19	9.66E-12	5.43E-39	5.49E-31	14	1.35E-05
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.46E-33	4.82E-17	1.04E-32	7.89E-28	7.24E-35	3.80E-36	1	1.41E-14	5.36E-31	2.81E-08	5.25E-13	8.35E-24	2.99E-21	9.89E-56	2.69E-36	14	2.01E-09
17823660-TableS1a	8.89E-15	6.76E-03	1.32E-13	3.44E-16	3.67E-05	1.02E-16	1	1.01E-02	3.42E-16	1.62E-03	4.16E-09	4.52E-14	1	1.96E-24	2.76E-14	13	1.43E-03
18698033-tableS1-STAT1	3.12E-19	5.83E-06	2.81E-23	3.26E-14	1.21E-13	3.60E-24	1	9.33E-06	1.64E-20	1	3.06E-08	1.28E-14	2.05E-07	5.35E-22	3.26E-17	13	4.67E-07
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	1.27E-13	9.23E-05	1.89E-14	1.38E-09	2.74E-13	6.23E-24	1	1	3.80E-19	1.64E-05	1.72E-05	1.93E-08	2.52E-12	7.81E-24	9.75E-21	13	9.68E-06
GSE10325_BCCELL_VS_L1UPUS_BCCELL_DN	6.81E-24	1	2.35E-28	8.22E-17	3.24E-26	1	1.88E-05	2.23E-28	1.20E-04	3.96E-18	3.69E-21	2.84E-09	9.97E-33	5.19E-23	13	1.07E-05	
GSE10325_MYELOID_VS_L1UPUS_MYELOID_DN	6.81E-24	1	3.83E-20	6.69E-19	2.24E-13	1.46E-33	1	7.73E-04	2.23E-28	1.20E-04	5.25E-13	3.38E-16	9.73E-08	4.81E-37	6.04E-19	13	6.87E-05
GSE13485_DAY1_VS_DAY7_YF17D_VACCINE_PBMC_DN	2.02E-44	1	2.76E-37	9.54E-38	5.83E-17	2.17E-50	1	1.29E-16	1.66E-39	3.10E-10	3.75E-18	1.30E-26	7.59E-05	5.85E-77	3.81E-41	13	5.84E-06
GSE13485_PRE_VS_POST_YF17D_VACCINATION_PBMC_DN	2.74E-47	1	3.13E-37	2.52E-40	3.95E-15	1.63E-53	1	1.38E-16	1.85E-39	2.81E-08	3.96E-18	1.64E-29	7.13E-08	4.32E-74	4.54E-46	13	9.64E-09
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_4H_DN	1.46E-33	1	1.04E-32	1.22E-32	1.15E-11	3.80E-36	1	6.63E-09	1.04E-33	2.81E-08	1.70E-15	3.69E-21	1.82E-03	9.89E-56	1.88E-29	13	1.40E-04
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_10H_DN	6.81E-24	2.16E-07	3.83E-20	2.99E-23	1.44E-22	6.80E-24	1	1.41E-14	5.15E-21	1.20E-04	1	7.22E-14	7.13E-16	9.97E-33	5.19E-23	13	9.26E-06
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_16H_DN	6.81E-24	1	3.83E-20	8.22E-17	5.25E-10	6.80E-24	1	7.73E-04	5.15E-21	2.03E-06	2.12E-08	3.69E-21	2.96E-06	1.60E-26	5.19E-23	13	5.99E-05
GSE18791_UNSTIM_VS_NEWCASTLE_VIRUS_DC_18H_DN	6.81E-24	1	3.83E-20	4.77E-21	2.14E-08	1.34E-28	1	1.26E-12	1.04E-18	3.14E-12	2.12E-08	1.24E-11	2.96E-06	9.97E-33	5.19E-23	13	2.31E-07
GSE2706_UNSTIM_VS_8H_R848_DC_DN	1.98E-19	1	1.22E-12	8.84E-15	2.43E-05	1.97E-19	1	3.83E-07	1.76E-16	2.03E-06	2.83E-06	1.24E-11	3.61E-02	1.27E-30	4.54E-15	13	2.78E-03
GSE34205_RSV_VS_FLU_INF_INFANT_PBMC_DN	8.80E-06	5.13E-04	3.37E-18	1.47E-05	2.43E-05	3.08E-11	1	7.73E-04	3.21E-10	1.20E-04	1	1.70E-05	1.82E-03	6.25E-17	2.15E-11	13	2.53E-04
HALLMARK_INTERFERON_ALPHA_RESPONSE	1.25E-34	6.07E-10	3.59E-30	1.68E-23	4.32E-38	1.25E-34	1	8.67E-12	2.35E-28	1	3.25E-13	1.50E-22	8.74E-21	2.79E-56	3.40E-36	13	4.74E-11
16479007-Table3	1.24E-17	1	6.11E-18	6.87E-20	9.54E-15	8.78E-26	1	1.22E-18	1	2.21E-08	4.99E-10	7.60E-12	2.69E-16	2.14E-29	5.73E-21	12	1.89E-09
18691624-Table1	5.39E-23	9.70E-08	1.78E-25	2.74E-17	2.44E-10	5.30E-44	1	1	3.10E-30	1	4.99E-10	7.60E-12	8.75E-08	6.50E-46	7.35E-29	12	1.54E-08
16818636-TableS2	4.98E-38	1	1.17E-27	6.10E-32	1.12E-03	2.10E-49	1	1.22E-03	1.01E-38	3.47E-06	1.06E-12	2.53E-23	1	1.69E-59	1.73E-35	12	1.95E-04
17823660-TableS2	3.15E-09	5.57E-06	2.98E-11	1.9													

HECKER_IFNB1_TARGETS	1.18E-49	1	7.83E-38	4.92E-34	8.85E-10	1.17E-49	1	9.13E-10	3.27E-37	6.53E-11	8.07E-22	1.07E-31	1	7.73E-71	3.68E-47	12	1.55E-10
GSE13485_DAY7_VS_DAY21_YF17D_VACCINE_PBMC_UP	3.24E-26	1	3.07E-26	2.99E-23	6.62E-04	1.46E-33	1	7.73E-04	7.60E-26	2.03E-06	5.25E-13	1.26E-18	1	9.89E-56	4.11E-25	12	1.20E-04
GSE14000_UNSTIM_VS_16H_LPS_DC_TRANSLATED_RNA_DN	3.43E-13	1	1.22E-12	6.76E-11	1.54E-02	1.97E-19	1	1	1.04E-18	2.81E-08	2.83E-06	1.92E-07	7.88E-05	1.44E-22	3.31E-13	12	1.29E-03
GSE1432_CTRL_VS_IFNG_6H_MICROGLIA_DN	1.58E-07	4.64E-11	6.96E-11	2.87E-07	1.49E-28	3.42E-13	1	9.84E-11	2.78E-08	1.20E-04	1	1	5.93E-27	6.25E-17	6.12E-08	12	1.01E-05
GSE17974_IL4_AND_ANTI_IL12_VS_UNTREATED_24H_ACT_CD4_TCELL_DN	4.77E-31	1	3.83E-20	4.77E-21	1.54E-02	4.76E-31	1	7.73E-04	2.23E-28	2.03E-06	1.21E-10	1.26E-18	1	2.96E-39	2.93E-27	12	1.34E-03
GSE24634_IL4_VS_CTRL_TREATED_NAIVE_CD4_TCELL_DAYS_DN	3.43E-13	2.16E-07	2.68E-16	8.22E-17	1.15E-11	2.73E-17	1	1	5.15E-21	1.20E-04	1	1.72E-09	9.73E-08	9.05E-19	4.54E-15	12	1.00E-05
GSE2706_UNSTIM_VS_2H_LPS_AND_R848_DC_DN	3.29E-15	1	6.96E-11	6.76E-11	6.62E-04	3.08E-11	1	1.88E-05	3.21E-10	1	2.12E-08	1.24E-11	2.96E-06	2.23E-13	4.54E-15	12	5.70E-05
GSE34205_HEALTHY_VS_FLU_INF_INFANT_PBMC_DN	6.81E-24	1	2.35E-28	6.69E-19	6.62E-04	1.34E-28	1	7.77E-04	2.23E-28	1.20E-04	1.21E-10	1.26E-18	1	4.81E-37	5.19E-23	12	1.30E-04
15735721-SuppTable1b	2.84E-26	1	2.07E-20	1.55E-16	1.79E-06	2.50E-39	1	1	3.14E-28	1	8.37E-12	8.24E-18	5.89E-06	1.32E-50	2.51E-23	11	6.98E-07
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	7.11E-19	1	3.26E-21	5.00E-16	2.34E-09	1.44E-29	1	1	1.62E-25	1	2.66E-09	1.44E-13	6.18E-07	3.23E-32	7.35E-27	11	5.66E-08
DER_IFN_ALPHA_RESPONSE_UP	1.07E-15	1	4.99E-18	3.43E-20	3.10E-19	1.26E-20	1	1	2.89E-19	1	6.56E-09	4.90E-13	3.22E-16	4.17E-26	1.33E-18	11	5.97E-10
DER_IFN_BETA_RESPONSE_UP	1.67E-16	1	2.99E-16	9.22E-21	2.68E-17	3.04E-21	1	1	4.05E-20	1	4.74E-08	7.06E-12	1.90E-14	6.99E-26	5.23E-19	11	4.31E-09
SANA_TNF_SIGNALING_UP	7.19E-13	1	4.11E-07	7.92E-15	2.70E-12	1.22E-10	1	3.87E-06	2.11E-11	1	1	8.15E-08	4.00E-06	1.54E-18	5.83E-18	11	7.61E-07
HELLER_SILENCED_BY_METHYLATION_UP	1.56E-11	3.89E-03	3.30E-06	1.58E-04	1	2.56E-15	1	1	1.17E-12	1	2.23E-05	2.73E-08	2.85E-06	1.15E-14	1.31E-06	11	3.71E-04
MOSERLE_IFNA_RESPONSE	1.58E-45	1	7.10E-29	1.07E-34	1	5.02E-42	1	6.21E-14	1.22E-33	4.37E-15	2.54E-14	1.49E-22	1	1.51E-42	8.54E-39	11	8.35E-15
GSE1432_1H_VS_6H_IFNG_MICROGLIA_DN	1.58E-07	1.15E-05	5.98E-06	2.87E-07	1.20E-20	1.58E-07	1	6.63E-09	1.19E-04	1	1	1	2.02E-19	5.21E-10	9.85E-05	11	2.14E-05
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_12H_DN	1.98E-19	1	1.22E-12	8.30E-13	6.29E-17	1.97E-19	1	9.84E-11	3.11E-12	1	1	1.72E-09	7.41E-11	1.60E-26	5.54E-17	11	1.73E-10
GSE2706_R848_VS_R848_AND_LPS_2H_STIM_DC_DN	3.09E-11	1.15E-05	3.50E-09	2.87E-07	1.54E-02	3.28E-15	1	1	2.55E-14	1	1	1.92E-07	1.82E-03	3.92E-15	6.12E-08	11	1.56E-03
GSE3982_CTRL_VS_LPS_48H_DC_DN	3.43E-13	5.13E-04	1.91E-14	4.76E-09	1	1.24E-21	1	1	1.76E-16	2.03E-06	1.21E-10	1.24E-11	1	9.05E-19	4.54E-15	11	4.68E-05
15735721-Table3	1.40E-18	1	5.45E-16	1.13E-13	1	6.68E-26	1	1	7.42E-20	1	2.47E-10	1.05E-11	9.21E-04	2.62E-32	1.46E-16	10	9.21E-05
19014521-TableS6b	8.92E-05	1.12E-04	2.68E-10	4.69E-10	3.10E-11	2.03E-08	1	1	3.34E-07	1	1	1	1.70E-10	7.76E-08	1.25E-12	10	2.02E-05
16818636-TableS3	1.16E-21	1	1.29E-17	2.23E-13	1	7.84E-33	1	1	3.76E-26	3.40E-06	1.54E-08	2.76E-13	1	2.25E-28	2.65E-20	10	3.42E-07
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP	4.41E-28	1	5.45E-24	3.24E-18	1	2.92E-41	1	1	5.54E-33	3.70E-07	1.69E-11	2.20E-17	1	1.49E-37	4.34E-27	10	3.70E-08
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP	4.27E-19	1	1.26E-10	1.70E-14	9.54E-04	5.56E-17	1	1	2.11E-18	1	3.91E-06	1.24E-13	1	4.87E-26	3.89E-11	10	9.58E-05
SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP	6.59E-26	1	4.19E-18	8.65E-23	1	2.24E-31	1	1	1.68E-27	2.66E-07	1.56E-11	1.06E-15	1	4.89E-31	1.93E-23	10	2.66E-08
RADAEVA_RESPONSE_TO_IFNA1_UP	5.82E-20	1	1.26E-17	1.42E-19	4.05E-10	3.18E-28	1	1	6.32E-24	1	1.71E-15	2.46E-14	1	6.59E-29	3.83E-18	10	4.05E-11
JISON_SICKLE_CELL_DISEASE_UP	9.67E-10	1	1.29E-09	1.93E-09	3.34E-04	9.65E-10	1	1	1.25E-08	1	1	9.36E-06	3.60E-05	1.73E-10	7.07E-12	10	3.80E-05
LTE2_UP_V1_DN	8.41E-22	1	2.52E-20	5.24E-11	1.33E-02	2.88E-31	1	1	1.46E-23	1	1.77E-08	9.22E-19	1	2.46E-37	3.89E-21	10	1.33E-03
GSE1432_1H_VS_24H_IFNG_MICROGLIA_DN	4.08E-04	5.42E-13	1.98E-04	1.47E-05	1.61E-26	4.08E-04	1	9.84E-11	1	1	1	1	4.07E-23	7.65E-07	3.09E-03	10	4.12E-04
GSE18791_CTRL_VS_NEWCASTLE_VIRUS_DC_14H_DN	3.43E-13	1	6.96E-11	8.30E-13	2.43E-05	3.28E-15	1	1	2.55E-14	1	1	1.72E-09	1.82E-03	9.05E-19	3.31E-13	10	1.85E-04
GSE24634_IL4_VS_CTRL_TREATED_NAIVE_CD4_TCELL_DAY3_DN	1	3.43E-09	1.98E-04	1.47E-05	9.11E-19	1.58E-07	1	6.63E-09	1.19E-04	1	1	1	3.69E-14	5.21E-10	3.09E-03	10	3.42E-04
GSE2706_2H_VS_8H_R848_STIM_DC_DN	3.43E-13	1	5.98E-06	6.76E-11	7.71E-07	1.58E-07	1	7.77E-04	2.78E-08	1	1	1.92E-07	1	1.19E-20	1.22E-09	10	7.80E-05
GSE6269_HEALTHY_VS_FLU_INF_PBMC_DN	1.39E-18	1	3.64E-28	4.18E-18	1	5.53E-33	1	1	4.22E-30	3.16E-05	1.73E-16	2.72E-17	1	4.33E-35	1.01E-24	10	3.16E-06

Supplementary Table 9: Correlation results between OAS2 expression and PDL1, PDL2 expression

	PDL1		PDL2	
	Correlation	p-value	Correlation	p-value
BLCA	<b>0.37986076</b>	<b>1.33E-07</b>	<b>0.47881211</b>	<b>9.23E-12</b>
BRCA	<b>0.50650067</b>	<b>2.64E-65</b>	<b>0.50711491</b>	<b>1.75E-65</b>
COADREAD	<b>0.60207578</b>	<b>2.25E-59</b>	<b>0.57225802</b>	<b>1.55E-52</b>
GBM	<b>0.2443322</b>	<b>3.03E-08</b>	<b>0.44456103</b>	<b>1.10E-25</b>
HNSC	<b>0.46167336</b>	<b>5.53E-21</b>	<b>0.58763591</b>	<b>8.03E-36</b>
LAML	<b>0.35092034</b>	<b>2.21E-06</b>	<b>0.47037297</b>	<b>6.58E-11</b>
LUAD	<b>0.46354703</b>	<b>2.02E-27</b>	<b>0.50251799</b>	<b>1.19E-32</b>
LUSC	<b>0.3021614</b>	<b>8.38E-12</b>	<b>0.41479729</b>	<b>8.47E-22</b>
OV	<b>0.48596421</b>	<b>2.07E-33</b>	<b>0.42196289</b>	<b>9.07E-25</b>
UCEC	<b>0.46365178</b>	<b>1.93E-28</b>	<b>0.39655769</b>	<b>1.40E-20</b>

Supplementary Table 10: Top drivers and enrichment results of the cell community

**Regulators**

	M31_BLCA	M13_BRCA	M26_COADREAD	M33_GBM	M80_HNSC	M87_KIRC	M93_LAML	M51_LUAD	M84_LUSC	M39_OV	M10_UCEC
HIST1H2AE	1	1	1	0	0	0	0	1	1	0	1
HIST1H3G	1	0	1	0	1	0	0	0	0	0	0
HIST1H2BJ	0	1	0	0	0	0	0	1	1	0	0
HIST1H3H	0	1	0	0	0	1	0	0	1	0	0
ENSA	0	1	0	0	0	0	0	0	1	0	0
HIST1H1D	0	1	0	0	0	0	0	0	1	0	0
HIST1H3D	0	1	0	0	0	0	0	1	0	0	0
FIG4	0	0	0	0	0	1	0	1	0	0	0

**Gene enrichment**

Gene sets	M31_BLCA	M13_BRCA	M26_COADREAD	M33_GBM	M80_HNSC	M87_KIRC	M93_LAML	M51_LUAD	M84_LUSC	M39_OV	M10_UCEC	# significant enrichments	Averaged p-value
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	6.76E-33	8.12E-54	1.04E-26	1.74E-21	5.51E-16	3.78E-25	3.75E-34	4.18E-32	5.28E-29	1.19E-46	8.83E-30	11	2.40E-03
REACTOME_MEIOSIS	2.24E-31	6.04E-41	6.53E-25	1.53E-17	9.61E-17	8.63E-15	7.11E-23	2.90E-27	7.01E-19	1.20E-33	4.46E-31	11	8.67E-06
REACTOME_CELL_CYCLE	1.44E-11	3.09E-20	5.32E-09	2.84E-11	3.91E-05	4.03E-04	1.27E-09	1.32E-10	6.74E-07	3.30E-20	5.31E-13	11	2.00E-06
REACTOME_RNA_POL_I_TRANSCRIPTION	2.29E-33	1.23E-43	1.67E-26	2.47E-16	8.02E-18	7.23E-16	1.36E-24	5.50E-29	3.27E-20	3.46E-36	6.19E-33	11	2.83E-04
REACTOME_TRANSCRIPTION	4.83E-27	3.72E-35	1.99E-21	1.72E-12	2.30E-14	2.05E-12	4.01E-19	1.69E-23	5.87E-16	3.58E-28	5.02E-27	11	6.98E-11
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_	5.31E-31	1.92E-40	1.30E-24	6.62E-15	1.54E-16	1.38E-14	1.50E-22	6.13E-27	1.25E-18	3.60E-33	9.96E-31	11	6.67E-07
REACTOME_CHROMOSOME_MAINTENANCE	1.37E-17	1.08E-29	6.65E-14	2.73E-17	2.21E-08	2.36E-07	1.31E-15	4.54E-16	3.10E-11	8.62E-31	4.87E-19	11	8.60E-06
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCL	7.39E-21	5.96E-35	1.52E-16	7.44E-18	4.14E-10	4.45E-09	7.15E-19	5.07E-19	1.45E-13	9.59E-37	2.61E-22	11	9.41E-06
REACTOME_RNA_POL_I_PROMOTER_OPENING	3.56E-36	1.76E-47	9.93E-29	5.29E-18	2.57E-19	2.32E-17	5.24E-27	2.10E-31	4.58E-22	8.20E-40	1.51E-35	11	4.23E-05
REACTOME_MEIOTIC_RECOMBINATION	1.25E-33	5.45E-44	1.04E-26	4.82E-19	5.81E-18	5.23E-16	8.08E-25	3.27E-29	2.19E-20	1.60E-36	3.53E-33	11	3.54E-12
REACTOME_MEIOTIC_SYNOPSIS	3.53E-20	7.61E-34	5.36E-16	3.04E-17	9.39E-10	1.01E-08	3.41E-18	2.07E-18	4.40E-13	1.74E-35	1.25E-21	11	3.66E-05
REACTOME_AMYLOIDS	6.71E-34	2.33E-44	6.30E-27	1.19E-16	4.15E-18	3.74E-16	4.72E-25	1.91E-29	1.45E-20	7.17E-37	1.97E-33	11	1.70E-08
REACTOME_PACKAGING_OF_TELOMERE_ENDS	2.26E-22	1.85E-37	9.31E-18	3.23E-19	6.79E-11	7.32E-10	2.19E-20	1.50E-22	1.24E-14	1.29E-39	7.95E-24	11	1.54E-08
REACTOME_TELOMERE_MAINTENANCE	4.85E-20	1.28E-33	6.93E-16	9.69E-20	1.11E-09	1.19E-08	4.68E-18	2.77E-18	5.51E-13	3.13E-35	1.72E-21	11	8.80E-06
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	1.74E-06	1.27E-22	2.99E-07	4.11E-10	9.84E-07	1.00E-07	1.49E-12	4.99E-09	4.99E-09	1.20E-15	1.23E-13	11	3.66E-05
18172295-SuppTable3	3.38E-08	1.99E-11	1.36E-05	1.13E-04	1	6.19E-10	2.74E-08	6.48E-13	6.48E-13	9.33E-11	1.36E-05	10	2.45E-10
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	2.54E-09	5.06E-14	4.04E-05	9.58E-06	1	2.35E-11	3.42E-09	3.28E-14	3.67E-12	2.27E-11	1.20E-08	10	8.23E-07
18798265-tableS2	3.91E-10	8.35E-15	1.23E-06	1	1	2.87E-09	4.50E-05	8.50E-11	1.40E-08	6.44E-11	4.74E-11	9	1.74E-08
HELLER_HDAC_TARGETS_UP	1.73E-05	8.91E-11	3.00E-06	1	1	1.06E-08	6.22E-06	7.68E-12	8.18E-10	2.29E-10	1.81E-04	9	8.61E-06
18172295-SuppTable2	2.83E-04	8.81E-10	1	1	1	3.12E-07	6.79E-05	1.79E-10	1.79E-10	1.33E-09	1	8	1.35E-05
15489886-TableS1a	1.47E-03	2.99E-10	1	1	1	1.44E-04	4.59E-04	2.21E-09	1.05E-05	7.83E-07	3.49E-04	8	2.01E-09
GEORGANTAS_HSC_MARKERS	1.61E-12	1.03E-15	1	1	1	8.49E-09	1.66E-13	8.20E-16	1.17E-10	9.07E-12	4.11E-16	8	1.43E-03
EGFR_UPV1_DN	4.12E-05	3.41E-11	1	9.69E-09	1	3.93E-06	1	1.56E-07	1.43E-05	9.14E-15	9.61E-06	8	4.67E-07
MEK_UPV1_DN	4.25E-05	2.71E-09	1	5.81E-05	1	4.05E-06	1	1.48E-05	1.48E-05	4.00E-11	9.91E-06	8	9.68E-06
STK33_SKM_UP	7.86E-06	2.56E-11	1	1	1	4.57E-07	5.51E-08	2.45E-12	2.93E-10	8.69E-08	9.22E-05	8	1.07E-05
HADDAD_B_LYMPHOCYTE_PROGENITOR	4.81E-04	1.06E-07	1	1.46E-05	1	1	1.26E-04	3.74E-08	1.69E-04	3.52E-09	1	7	6.87E-05
16109776-TableS1	5.12E-03	4.99E-02	1	1	1	1	4.05E-02	1.82E-03	1.82E-03	1	1	5	5.84E-06
18757322-TableS3	1	1.16E-05	1	1	1	1	1	4.72E-08	1.11E-04	5.83E-03	1	4	9.64E-09
19429869-TableS1	1	2.43E-05	1	1.45E-06	1	1	1	6.01E-04	1	1.00E-06	1	4	1.40E-04
15459216-TableA2e	1	6.43E-22	1	1	1	1	7.57E-14	6.01E-13	1	2.66E-17	1	4	9.26E-06
DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP	1	7.85E-04	1	2.55E-03	1	1	1.51E-02	1	1	2.83E-05	1	4	5.99E-05
GSE13411_PLASMA_CELL_VS_MEMORY_BCELL_UP	1	1.15E-05	1	6.76E-05	1	1	1.60E-07	1	1	1.25E-07	1	4	2.31E-07
GSE29618_MONOCYTE_VS_MDC_DN	1	1.15E-05	1	1.24E-08	1	1	4.14E-04	1	1	1.25E-07	1	4	2.78E-03
18362358-Table10	1	9.58E-04	1	8.78E-05	1	1	1	1	1	3.66E-05	1	3	2.53E-04
18487511-TableS1	1	5.47E-06	1	2.62E-11	1	1	1	1	1	1.23E-12	1	3	4.74E-11
17823660-TableS2	1	1.49E-04	1	1	1	1	1	2.36E-03	1	4.51E-02	1	3	1.89E-09
GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN	1	5.55E-03	1	5.23E-04	1	1	1	1	1	5.40E-03	1	3	1.54E-08
DAZARD_RESPONSE_TO_UV_NHEK_UP	1	1	1	2.21E-04	1	1	1.34E-03	1	1	6.63E-04	1	3	1.95E-04
ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	1	1.70E-15	1	1	1	1	2.44E-07	1	1	8.24E-08	1	3	2.50E-05
GSE29618_MONOCYTE_VS_MDC_DAY7_FLU_VACCINE_DN	1	1.15E-05	1	6.76E-05	1	1	1	1	1	1.25E-07	1	3	9.27E-08
GSE29618_LAIV_VS_TIV_FLU_VACCINE_DAY7_PDC_DN	1	1.15E-05	1	6.76E-05	1	1	1	1	1	1.25E-07	1	3	7.77E-04
19181379-Table2	1	3.84E-10	1	1	1	1	1	1	1	1.05E-11	1	2	1.13E-03
16434974-Table1	1	1	1	5.06E-06	1	1	1	1	1	8.45E-06	1	2	4.00E-03
16909110-Table1	1	2.04E-06	1	1	1	1	1	6.54E-08	1	1	1	2	2.21E-09
OLSSON_E2F3_TARGETS_DN	1	9.69E-08	1	1	1	1	1	3.08E-09	1	1	1	2	1.55E-10
KOBAYASHI_EGFR_SIGNALING_24HR_UP	1	8.47E-06	1	1	1	1	1	1	1	2.02E-08	1	2	1.20E-04
GSE12845_IJD_POS_VS_NEG_BLOOD_BCELL_UP	1	1.15E-05	1	1	1	1	1	1	1	1.25E-07	1	2	1.29E-03
GSE12845_IJD_POS_BLOOD_VS_NAIVE_TONSIL_BCELL_UP	1	1.15E-05	1	1	1	1	1	1	1	1.69E-04	1	2	1.01E-05
GSE22886_CTRL_VS_LPS_24H_DC_DN	1	1.15E-05	1	1	1	1	1	1	1	4.96E-06	1	2	1.34E-03