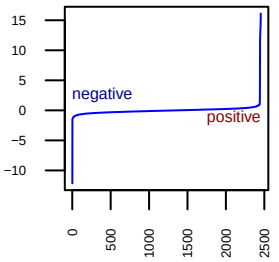
Component # 1 (stability = 0.999)

Metagene
(involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

7 negative	**14 positive**
XIST	DDX3Y
FDCSP	EIF1AY
PPP1R3C	GYG2P1
PAGE2	KDM5D
FRG2DP	NLGN4Y
HCN1	PRKY
PDLIM4	RPS4Y1
	TTTY15
	TXLNGY
	USP9Y
	UTY
	ZFY
	DDX43
	PEX5L

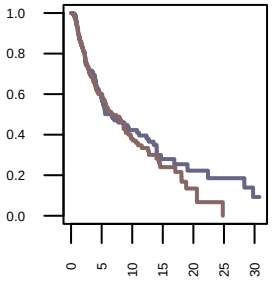
GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 0 terms(FDR<0.1)

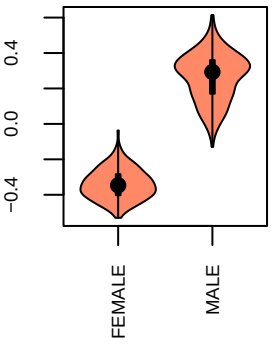
GO:MF pos : 0 terms(FDR<0.1)

Cox regression:
logtest pv=1.9e−01
LHR=0.28 (CI = −0.14, 0.71)

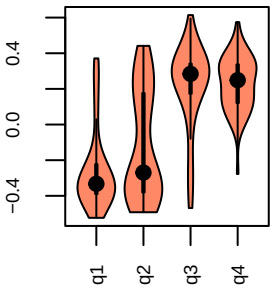


factor	**p.value**
gender	2.01e−203
Height	7.13e−32
Weight	3.83e−08
Year.of.last.contact	7.17e−03
Disease.Free.Status.at.last.contact	7.92e−03
vital_status_at_last_contact	8.81e−03
Sample.country	9.27e−03
Primary.Melanoma.Tissue.Site	9.66e−03
Oncotree.Code	1.09e−02
Cancer.Type.Detailed	1.09e−02

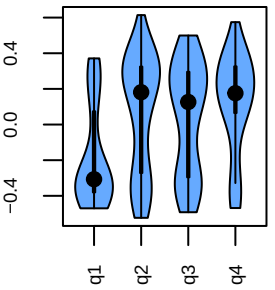
gender
pv=2.0e−203



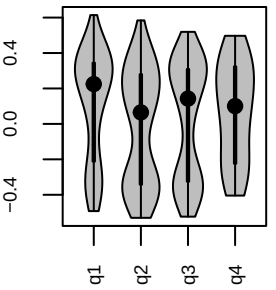
Height
pv=7.1e−32



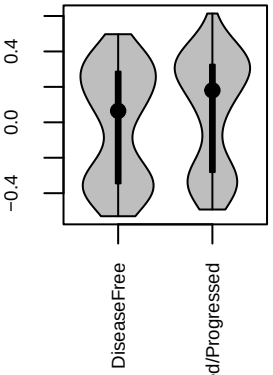
Weight
pv=3.8e−08



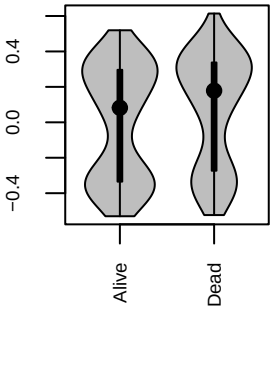
Year.of.last.contact
pv=7.2e−03



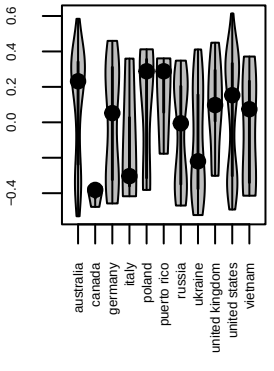
Disease.Free.Status.at.last.contact
pv=7.9e−03



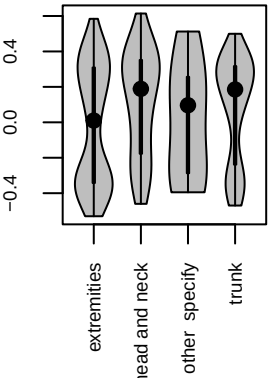
vital_status_at_last_contact
pv=8.8e−03



Sample.country
pv=9.3e−03

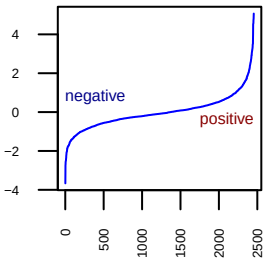


Primary.Melanoma.Tissue.Site
pv=9.7e−03



Component # 2 (stability = 0.927)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 3 terms(FDR<0.1)

Term	FDR
pigment biosynthetic process	2.00e−07
melanocyte differentiation	9.07e−03
melanosome transport	2.10e−02

16 negative	78 positive
EDN3	PMEL
ZNF536	TRPM1
GFRA3	MLANA
NPTX2	TYRP1
HAPLN1	TYR
ST8SIA5	DCT
NEFL	GPR143
GRIA2	TRIM63
KLHDC8A	ABCB5
FAM135B	SLC45A2
PRIMA1	D4S234E
CMTM5	LRRN4CL
GDNF	MCOLN3
GAP43	TUBB4A
KLK6	ASB11
NEFM	CBX3P7
	CDH3
	TEX41
	MLPH
	SLC6A17
	TSPAN10
	GAPDHS
	GMPR
	ABCC2
	SLC24A5
	CDH1
	FAM69C
	IRF4
	CA14
	EPHA5
	ACCSL
	BIRC7
	LDB3
	ESRP1
	CHST9
	CRTAC1
	HPGD
	KIT
	LGI3
	MME
	GYG2
	ST8SIA6
	PRKG2
	KCNJ13
	STK32A
	SFTPC
	CAPN3
	KLHL38
	HRK
	PRDM7
	POU3F3
	PKNOX2
	SULT1C2
	DMKN
	PPARGC1A
	IRX6
	NRG3
	WDR63
	SLC6A15
	SOX6
	GDF15
	PROM1
	QPCT
	VEPH1
	S100A1
	GALNTL6
	IP6K3
	PRAME
	BCHE
	BCAN
	KCNN2
	SLC5A10
	PCDH7
	NMRK2
	RTN4RL1
	IL12RB2
	ALDH3B2
	PRTG

GO:CC neg : 0 terms(FDR<0.1)

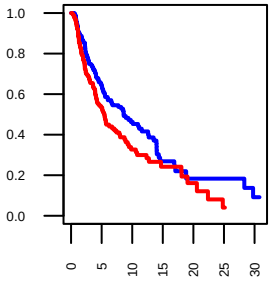
GO:CC pos : 1 terms(FDR<0.1)

Term	FDR
melanosome	4.41e−09

GO:MF neg : 0 terms(FDR<0.1)

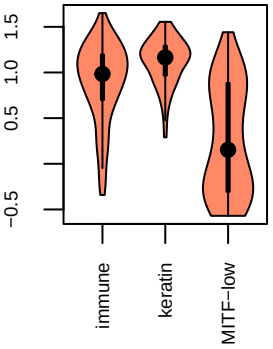
GO:MF pos : 0 terms(FDR<0.1)

Cox regression:
logtest pv=6.6e−03
LHR=0.37 (CI = 0.09, 0.64)

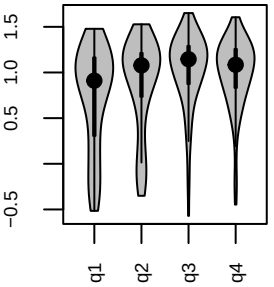


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	2.61e−29
Breslow.Depth	1.24e−04
New.tumor.event.after.initial.treatment	4.78e−04
Cancer.stage.T	7.42e−04
Prospective.Tissue.Collection	8.26e−04
Retropective.Tissue.Collection	8.26e−04
ajcc_pathologic_tumor_stage	1.57e−03
Radiation.therapie	2.97e−03
Did.patient.start.adjuvant.postoperative.radiotherapy.	3.06e−03
initial_pathologic_dx_year	3.08e−03

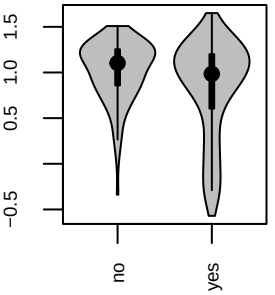
RNASEQ.CLUSTER_CONSENHIER
pv=2.6e−29



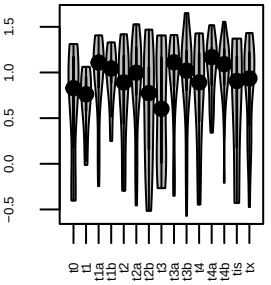
Breslow.Depth
pv=1.2e−04



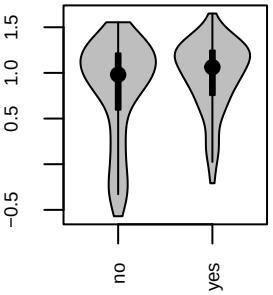
New.tumor.event.after.initial.treatmen
pv=4.8e−04



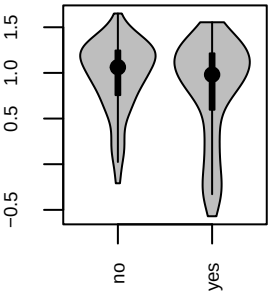
Cancer.stage.T
pv=7.4e−04



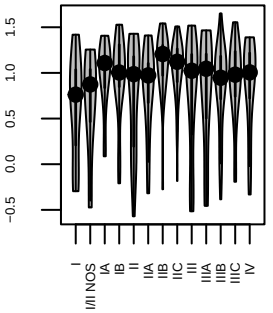
Prospective.Tissue.Collection
pv=8.3e−04



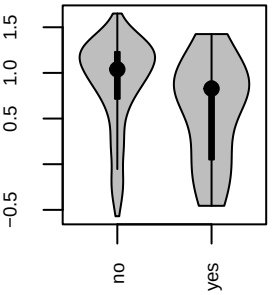
Retropective.Tissue.Collection
pv=8.3e−04



ajcc_pathologic_tumor_stage
pv=1.6e−03

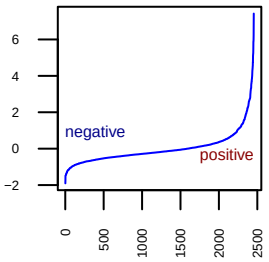


Radiation.therapie
pv=3.0e−03



Component # 3 (stability = 0.968)

Metagene (involvement of features)



2 negative	153 positive
ALB	CALML3
PMP2	CEACAM6
	CRNN
	DSC3
	DSG3
	FGFBP1
	IVL
	KRT13
	KRT14
	KRT16
	KRT4
	KRT5
	KRT6A
	KRT6B
	KRT6C
	LY6D
	PI3
	S100A7
	SERPINB3
	SERPINB5
	SPRR1A
	SPRR1B
	SPRR2A
	SPRR2D
	SPRR2E
	SPRR3
	TRIM29
	CEACAM5
	SERPINB13
	SFN
	KRT17
	TGM3
	MUC21
	KRT78
	A2ML1
	SLPI
	FAM83A
	S100A14
	CLCA4
	DSG1
	BPIFB1
	LCN2
	SPRR2G
	KRT19
	TMPRSS4
	KLK11
	SERPINB4
	TMPRSS11D
	SBSN
	CLCA2
	PKP1
	KLK10
	RAB25
	CALML5
	KLK7
	RHCG
	SPRR2F
	GBP6
	C10orf99
	SCEL
	COL17A1
	MIR205HG
	KRT15
	TMPRSS11E
	KLK13
	FAM83C
	KRTDAP
	S100A8
	KLK12
	SPRR2B
	TACSTD2
	MAL2
	C2orf54
	CXCL17
	AGR2
	GRHL2
	PDZK1IP1
	ANXA8
	SLC6A14
	EVPL
	EHF
	GGT6

GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 8 terms(FDR<0.1)

Term	FDR
keratinocyte differentiation	4.49e−17
intermediate filament organization	6.68e−08
defense response to bacterium	1.97e−07
peptide cross−linking	1.17e−05
antimicrobial humoral response	1.43e−04
negative regulation of endopeptidase act...	4.29e−03
epidermis development	1.50e−02
innate immune response	1.55e−02

GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 8 terms(FDR<0.1)

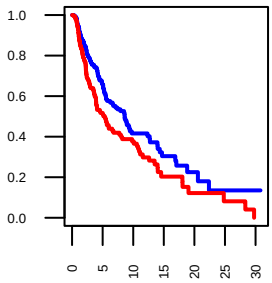
Term	FDR
cornified envelope	7.15e−21
extracellular exosome	4.90e−13
intermediate filament cytoskeleton	1.01e−09
cytosol	3.18e−04
desmosome	2.16e−03
IgG immunoglobulin complex	4.41e−03
immunoglobulin complex, circulating	8.33e−03
extracellular space	8.33e−03

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 5 terms(FDR<0.1)

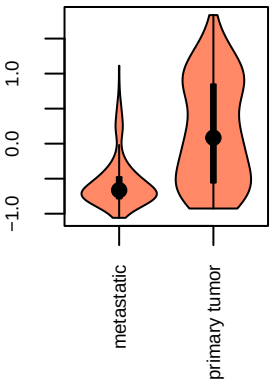
Term	FDR
structural constituent of skin epidermis	1.17e−07
serine−type endopeptidase inhibitor acti...	1.33e−03
serine−type endopeptidase activity	2.40e−03
immunoglobulin receptor binding	9.75e−03
calcium−dependent protein binding	1.72e−02

Cox regression: logtest pv=2.3e−06 LHR=0.66 (CI = 0.41, 0.91)

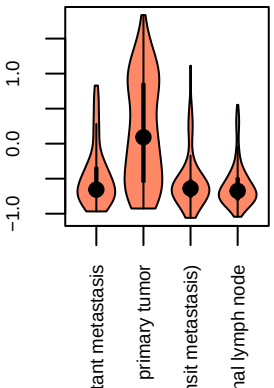


factor	p.value
Sample.Type	1.30e−37
Tumor.tissue.site	6.13e−37
Tumor.location.site	8.93e−37
Cancer.Type.Detailed	2.98e−29
Oncotree.Code	2.98e−29
RNASEQ.CLUSTER_CONSENHIER	1.08e−25
Sample.country	1.02e−22
New.tumor.event.after.initial.treatment	1.13e−18
ICD.10.TopLevel	1.82e−16
Breslow.Depth	1.38e−13

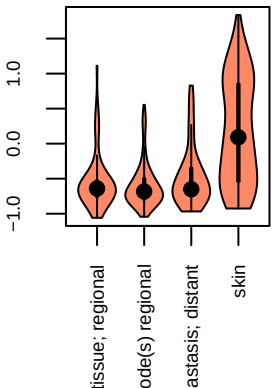
Sample.Type pv=1.3e−37



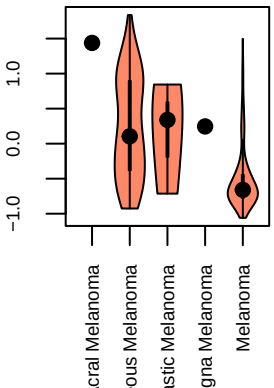
Tumor.tissue.site pv=6.1e−37



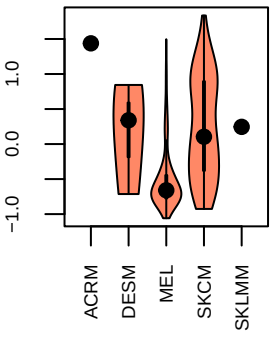
Tumor.location.site pv=8.9e−37



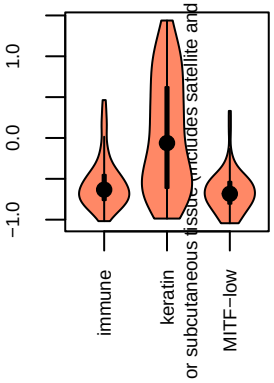
Cancer.Type.Detailed pv=3.0e−29



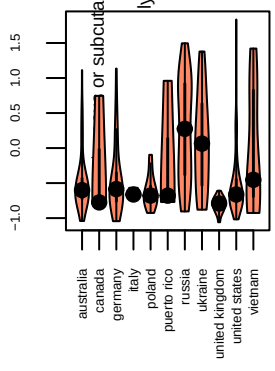
Oncotree.Code pv=3.0e−29



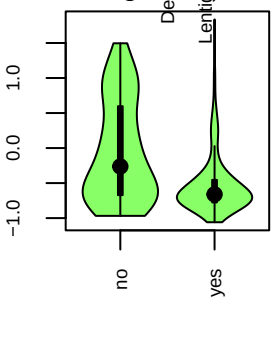
RNASEQ.CLUSTER_CONSENHIER pv=1.1e−25



Sample.country pv=1.0e−22

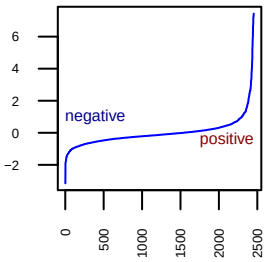


New.tumor.event.after.initial.treatmen pv=1.8e−16



Component # 4 (stability = 0.985)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 1 terms(FDR<0.1)

Term	FDR
negative regulation of transcription by ...	6.49e−02

16 negative	125 positive
SOX1	AACSP1
FAM19A5	BAGE2
BAI1	CSAG1
KNDC1	CSAG3
KIF1A	CSMD1
ADARB2	CT55
TMEM179	CTAG2
CRTAC1	DSCR8
DMRT2	FAM133A
OLFM1	GABRA3
HUNK	GABRG2
BCHE	GAGE1
GPR27	MAGEA1
SOX8	MAGEA10
FIBCD1	MAGEA11
P2RY12	MAGEA12
	MAGEA3
	MAGEA4
	MAGEA6
	MAGEB1
	MAGEB2
	MAGEC1
	MAGEC2
	MKRN9P
	MUC15
	NAA11
	PAGE1
	PAGE2
	PAGE5
	PASD1
	TUBA3C
	ZNF812
	SLC30A8
	VCX
	VCX3A
	GAGE2A
	ZNF560
	GTSF1
	POU6F2
	NLRP11
	FAR2P1
	MAGEB16
	MAT1A
	OVAAL
	MORC1
	MYT1L
	CASC9
	MAEL
	PAGE2B
	ACTBP8
	NLRP4
	FLJ36000
	SLC5A12
	FRG2DP
	SSX1
	CLEC2L
	FOXR2
	SLCO1A2
	SAGE1
	XAGE3
	ASB4
	KLK2
	CTCFL
	CT45A10
	PAEP
	KLF14
	WDR72
	HBE1
	STK31
	KC6
	HTR2C
	CDH12
	IL13RA2
	CDH18
	ANGPT1
	PNMA5
	C5orf17
	GPR158
	LIN28B
	GCSAML
	TSPEAR
	CT45A1

GO:CC neg : 0 terms(FDR<0.1)

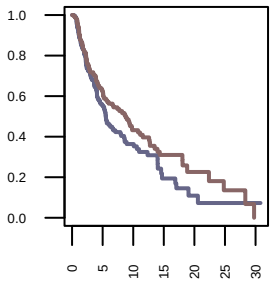
GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 1 terms(FDR<0.1)

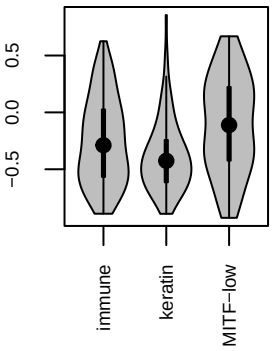
Term	FDR
histone deacetylase binding	1.25e−03

Cox regression:
logtest pv=6.5e−02
LHR=−0.34 (CI = −0.71, 0.03)

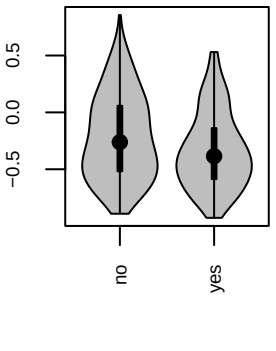


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	4.45e−05
Prospective.Tissue.Collection	3.83e−04
Retropective.Tissue.Collection	3.83e−04
MUTATIONSUBTYPES	1.11e−03
Days.to.third.new.tumor.event.after.initial.treatment	2.83e−03
Days.to.first.new.tumor.event.after.initial.treatment	2.86e−03
third.prominent.montif	4.99e−03
Cancer.Type.Detailed	5.13e−03
Oncotree.Code	5.13e−03
last_contact_days_to	5.49e−03

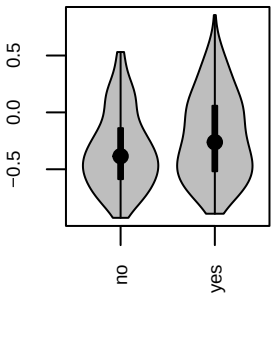
RNASEQ.CLUSTER_CONSENHIER
pv=4.4e−05



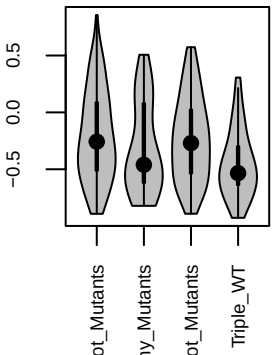
Prospective.Tissue.Collection
pv=3.8e−04



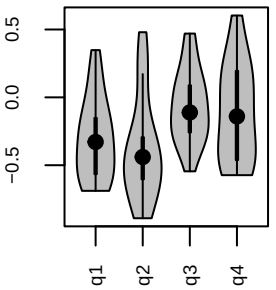
Retropective.Tissue.Collection
pv=3.8e−04



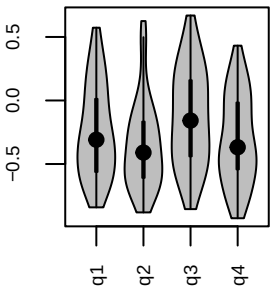
MUTATIONSUBTYPES
pv=1.1e−03



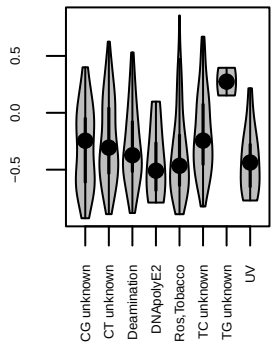
ays.to.third.new.tumor.event.after.initial.trea
pv=2.8e−03



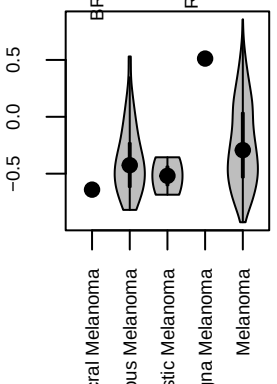
ays.to.first.new.tumor.event.after.initial.trea
pv=2.9e−03



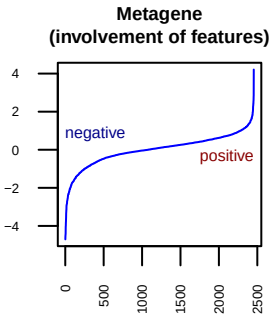
third.prominent.montif
pv=5.0e−03



Cancer.Type.Detailed
pv=5.1e−03



Component # 5 (stability = 0.829)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

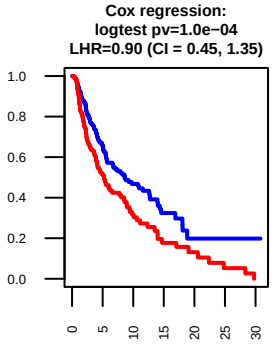
65 negative	10 positive
ITIH6	TYRP1
OLIG1	IP6K3
NELL1	FOXD1
CPN1	PITX2
SFRP1	DKK1
OLIG2	FGF5
ITGA10	NOV
RLBP1	KCNG1
GJB1	ASPA
TRIM51CP	CXCL5
TRIM51	
SHISA2	
LOXL4	
CNTNAP3	
CNTNAP3B	
MUC7	
APOD	
MRGPRX4	
EWSAT1	
PRSS33	
EYA1	
CA6	
EDN3	
CHL1	
WNK4	
FREM2	
ALDH1A3	
EYA4	
MIA	
SOX8	
COL9A1	
RAB17	
FAM84B	
SLC24A5	
RXRG	
ROPN1	
PRKG2	
HAPLN1	
TSPAN7	
S100B	
SERPINA5	
MMP16	
VGF	
FAM19A5	
GABRR1	
GPR37	
S100A1	
MPPED2	
ID4	
SERPINA3	
TESC	
MPZ	
C1QTNF3	
HRK	
UNC80	
CDH19	
CHRM3	
NRG3	
PLCB4	
PPP1R9A	
TYR	
RIPK4	
DNASE2B	
GAPDHS	
NAT8L	

GO:CC neg : 0 terms(FDR<0.1)

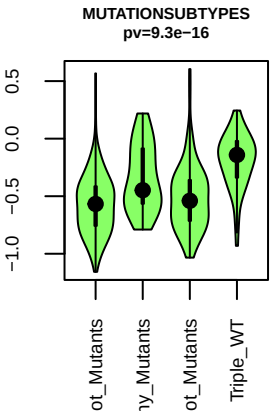
GO:CC pos : 0 terms(FDR<0.1)

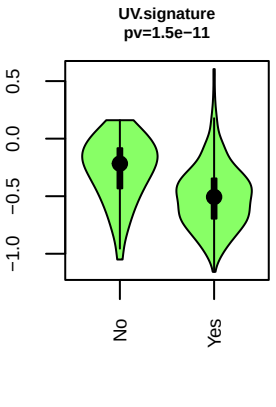
GO:MF neg : 0 terms(FDR<0.1)

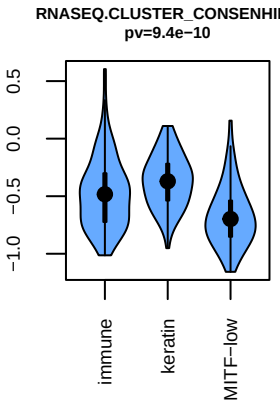
GO:MF pos : 0 terms(FDR<0.1)

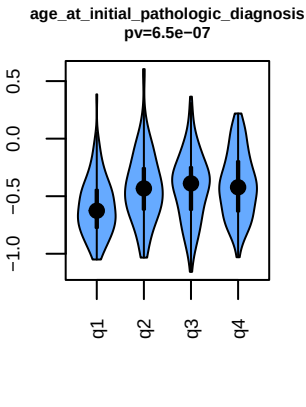


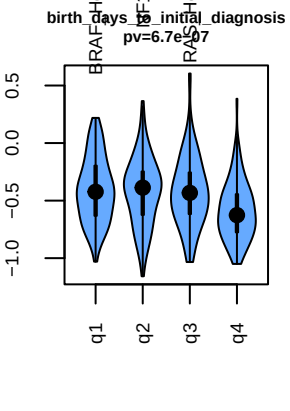
factor	p.value
MUTATIONSUBTYPES	9.34e−16
UV.signature	1.54e−11
RNASEQ.CLUSTER_CONSENHIER	9.38e−10
age_at_initial_pathologic_diagnosis	6.46e−07
birth_days_to_initial_diagnosis	6.70e−07
BRAFV600.	4.11e−06
Year.of.Birth	5.23e−06
third.prominent.montif	8.46e−06
most.prominent.motif	1.12e−05
age.at.last.contact	7.78e−05

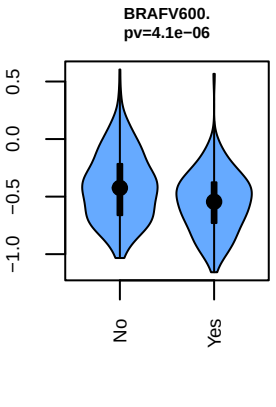


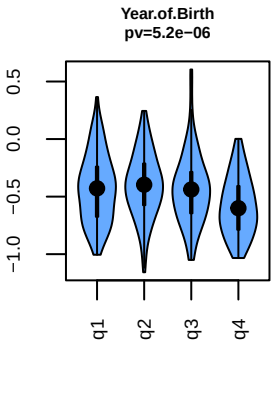


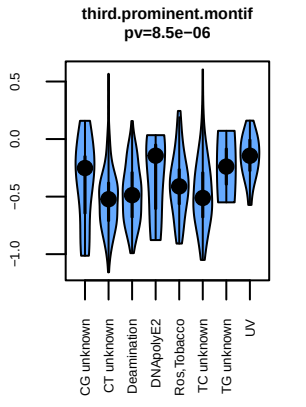






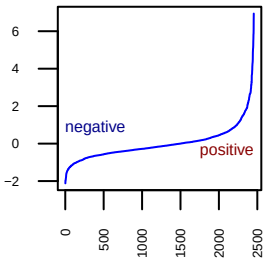






Component # 6 (stability = 0.983)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 1 terms(FDR<0.1)

Term	FDR
extracellular matrix organization	5.82e−05

GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 2 terms(FDR<0.1)

Term	FDR
extracellular matrix	3.92e−12
extracellular region	6.86e−06

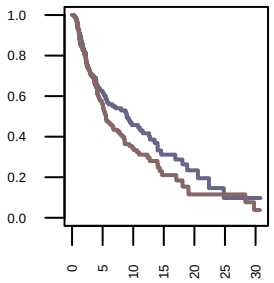
GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 1 terms(FDR<0.1)

Term	FDR
extracellular matrix structural constitu...	3.28e−08

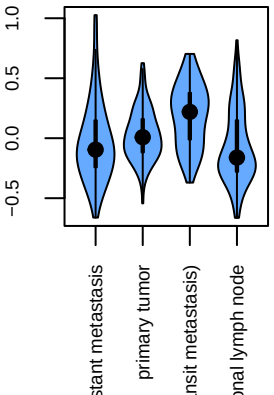
6 negative	127 positive
MMP12	CILP
SHISA3	COL10A1
FDCSP	COL11A1
CR2	COMP
LRP2	EPYC
KCNG1	ITGBL1
	LRRC15
	MFAP5
	MMP13
	OGN
	OMD
	PI16
	PLA2G2A
	SFRP2
	SFRP4
	WISP2
	WNT2
	ADIPOQ
	ASPN
	CXCL14
	SPON1
	HTRA3
	DPT
	FNDC1
	CCL11
	FIBIN
	FABP4
	XPNPEP2
	ELN
	WBSCR17
	PRG4
	WT1
	AGTR1
	FMO1
	SYNDIG1
	MXRA5Y
	KCND2
	PTPRD
	PRND
	CPA3
	TPSAB1
	MMP3
	COL8A1
	TPSB2
	ACKR1
	STMN2
	ST6GAL2
	NRK
	RBP4
	SCARA5
	TUSC5
	CD300LG
	MFAP4
	MEG3
	HAS1
	PLIN4
	THBS4
	GDF10
	PAX1
	SELE
	PLIN1
	F2RL2
	C3
	CTSG
	IBSP
	ACTC1
	MMP7
	POSTN
	SLITRK4
	PTGFR
	PTN
	PENK
	IL20RA
	MEOX2
	TWIST2
	ABI3BP
	MMP2
	CES1
	DIO2
	FGF10
	ISM1
	KLK4

Cox regression:
logtest pv=8.7e−02
LHR=0.35 (CI = −0.05, 0.75)

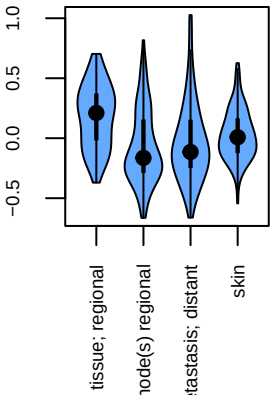


factor	p.value
Tumor.tissue.site	4.75e−10
Tumor.location.site	5.99e−10
ICD.10.TopLevel	4.56e−06
tumor_status_at_last_contact	7.03e−04
RNASEQ.CLUSTER_CONSENHIER	1.88e−03
vital_status_at_last_contact	4.14e−03
ajcc_pathologic_tumor_stage	1.23e−02
Disease.Free.Status.at.last.contact	1.58e−02
Cancer.stage.T	1.84e−02
Normal.control.type	1.95e−02

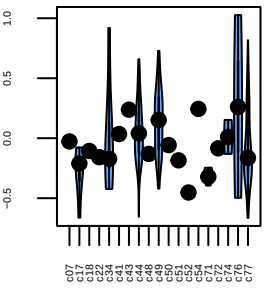
Tumor.tissue.site
pv=4.7e−10



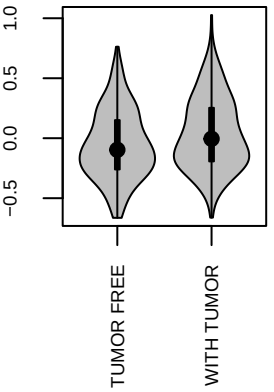
Tumor.location.site
pv=6.0e−10



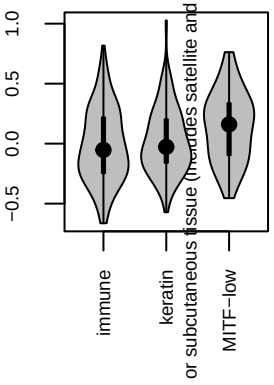
ICD.10.TopLevel
pv=4.6e−06



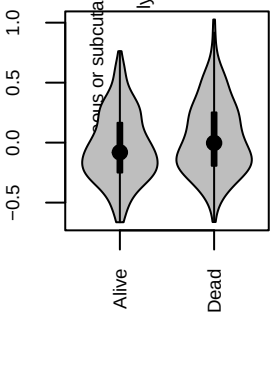
tumor_status_at_last_contact
pv=7.0e−04



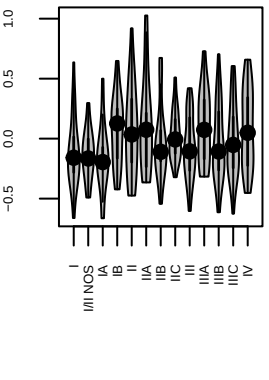
RNASEQ.CLUSTER_CONSENHIER
pv=1.9e−03



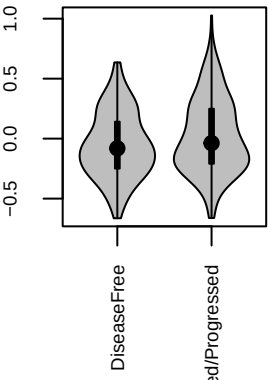
vital_status_at_last_contact
pv=4.1e−03



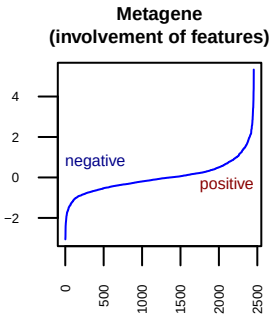
ajcc_pathologic_tumor_stage
pv=1.2e−02



Disease.Free.Status.at.last.contact
pv=1.6e−02



Component # 7 (stability = 0.790)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

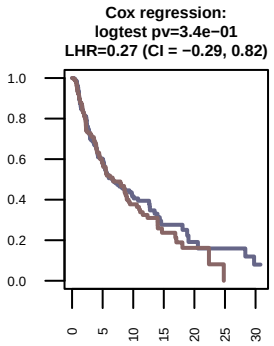
GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 0 terms(FDR<0.1)

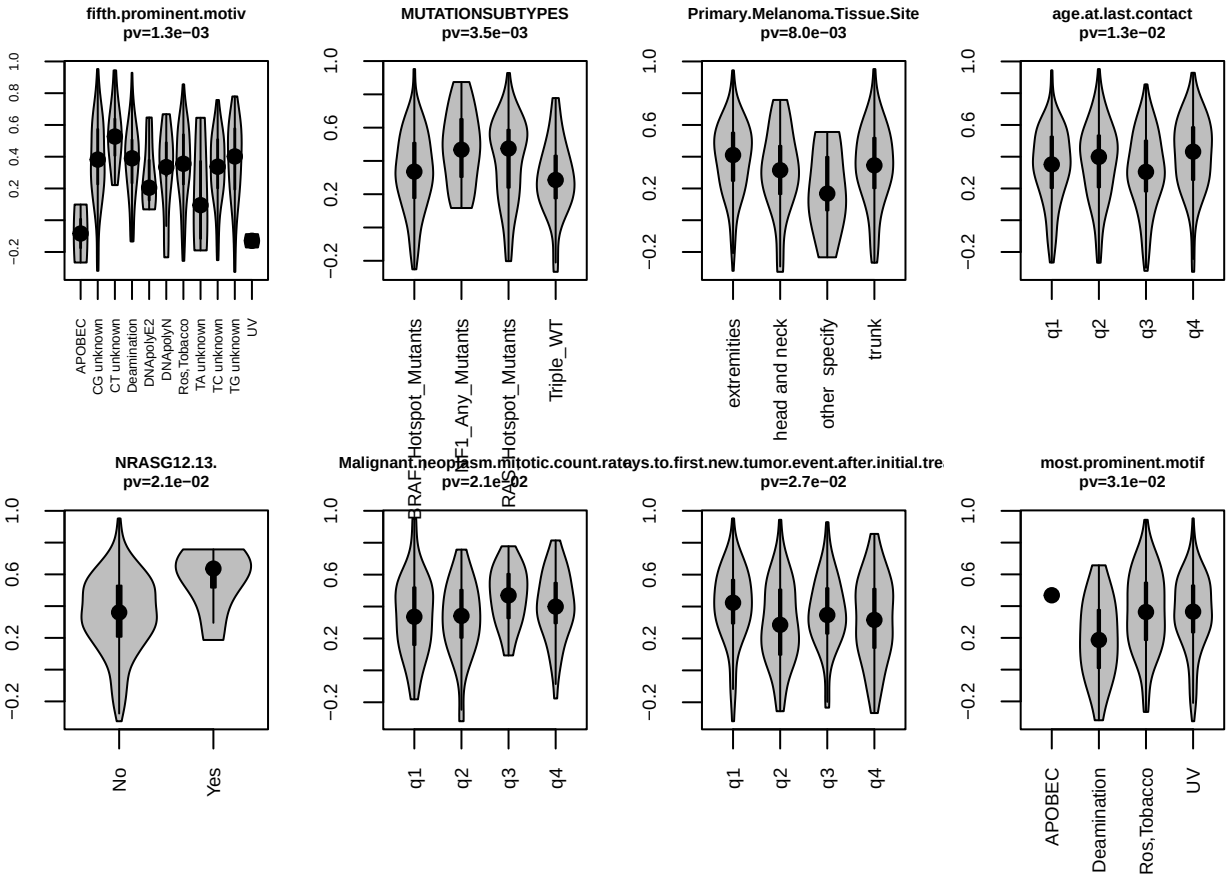
GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 0 terms(FDR<0.1)

15 negative	77 positive
TMEM163	PMP2
PRKG2	FRG2DP
RTN4RL1	FABP7
ZIC2	INSC
ASB11	CMTM5
SLC6A17	TYRP1
EDN3	ZNF536
OGDHL	MPZ
SNED1	TCN1
ANO4	MLIP
CYP24A1	SLC5A4
HAP1	DCT
MT1M	GRIK2
IFNLR1	CLDN1
MNX1	UGT8
	ABCB5
	PRDM7
	CNDP1
	MEGF10
	COL19A1
	HCCAT5
	NLGN1
	RDH8
	MDGA2
	UGT2B7
	BCAN
	LRAT
	SOX2
	ATP6V0A4
	KCNJ13
	ANGPTL7
	CA8
	SLC35F1
	KCNN2
	GRIK3
	ADAM23
	VEPH1
	GPR126
	LRRTM2
	MRGPRX3
	TTR
	FLRT3
	PMEL
	RGR
	POU3F2
	ATP10B
	SERPINA5
	PLP1
	SEMA3B
	TMEM171
	FREM2
	IGSF11
	PTPRZ1
	FSTL5
	POPDC3
	SLC7A4
	SOSTDC1
	CA14
	ITGB8
	B3GALT2
	SLITRK2
	UG0898H09
	ENTHD1
	ASPA
	MOXD1
	NOV
	SLITRK6
	DLGAP1
	S100B
	APOD
	SLAMF9
	PKLR
	MUC7
	FCRLA
	WISP2
	SORCS1
	KCNJ10

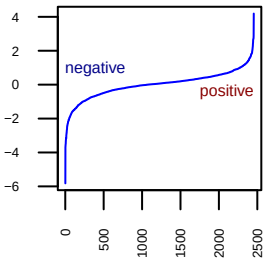


factor	p.value
fifth.prominent.motiv	1.30e−03
MUTATIONSUBTYPES	3.52e−03
Primary.Melanoma.Tissue.Site	7.97e−03
age.at.last.contact	1.34e−02
NRASG12.13.	2.08e−02
Malignant.neoplasm.mitotic.count.rate	2.10e−02
Days.to.first.new.tumor.event.after.initial.treatment	2.70e−02
most.prominent.motif	3.08e−02
second.prominent.motif	3.86e−02
New.tumor.event.after.initial.treatment	5.02e−02



Component # 8 (stability = 0.805)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

66 negative	22 positive
PAEP	ASB11
SLC38A8	CHRM1
VGF	ANGPTL7
ATP6V0D2	SCRG1
MAPK4	SOX9
RDH8	HHATL
DNER	POU3F3
UCN2	LRP2
CLDN14	CRTAC1
CFAP61	BANCR
CTCFL	NELL1
OCA2	LRRTM4
SLC5A4	SOX2
SLC7A4	KCNIP1
CA8	GRIK3
ROBO2	PCDH7
SLAMF9	B4GALNT4
SLC16A6	KCNJ13
FAM163A	UG0898H09
VEPH1	COL24A1
EPHA4	MAP2
ENTHD1	HPSE2
PCSK9	
PNLIPRP3	
NMRK2	
PRDM7	
RIPK4	
HES2	
POU3F1	
SPACA3	
MCF2	
OR2C3	
DLGAP1	
GADL1	
MMP8	
FSTL5	
FAM132B	
LAMA1	
EYA4	
LONRF2	
CXADR	
RFPL2	
KLK6	
ADCY2	
ONECUT2	
PMEL	
CNDP1	
NALCN	
CHGB	
CYP1A1	
L1CAM	
PCLO	
SYT5	
CDH7	
CPSF1P1	
TMEM56	
NECAB2	
POPDC3	
TMEM246	
GABRA5	
TM4SF19	
LUZP4	
MCTP2	
OGDHL	
TCN1	
PTPRU	

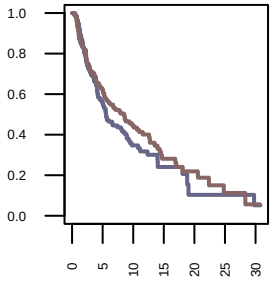
GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 0 terms(FDR<0.1)

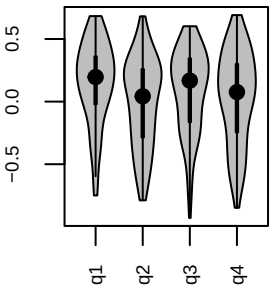
GO:MF pos : 0 terms(FDR<0.1)

Cox regression:
logtest pv=3.3e−02
LHR=−0.44 (CI = −0.83, −0.04)

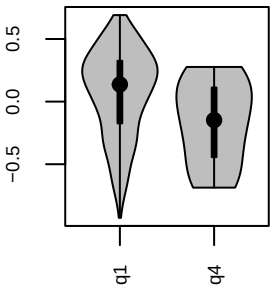


factor	p.value
initial_pathologic_dx_year	1.53e−03
TP53.stopgain	4.84e−03
Days.to.third.new.tumor.event.after.initial.treatment	7.34e−03
RNASEQ.CLUSTER_CONSENHIER	9.48e−03
Days.to.first.new.tumor.event.after.initial.treatment	2.27e−02
ARID2.splice.acceptor	2.85e−02
ajcc_pathologic_tumor_stage	4.49e−02
fifth.prominent.motiv	8.26e−02
days_to_death_after_initial_diagnosis	8.51e−02
CDKN2A.splice.acceptor	1.00e−01

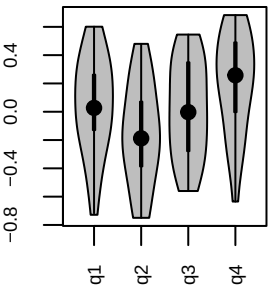
initial_pathologic_dx_year
pv=1.5e−03



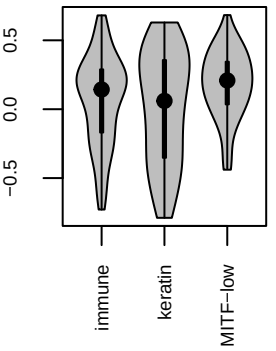
TP53.stopgain
pv=4.8e−03



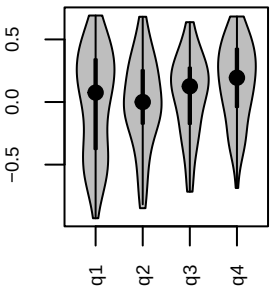
ays.to.third.new.tumor.event.after.initial.tre
pv=7.3e−03



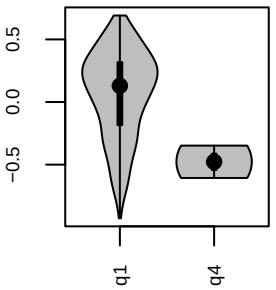
RNASEQ.CLUSTER_CONSENHIER
pv=9.5e−03



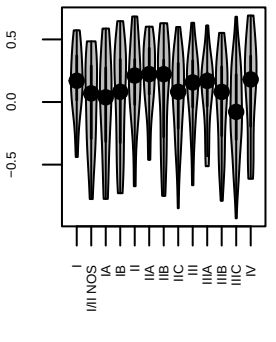
ays.to.first.new.tumor.event.after.initial.tre
pv=2.3e−02



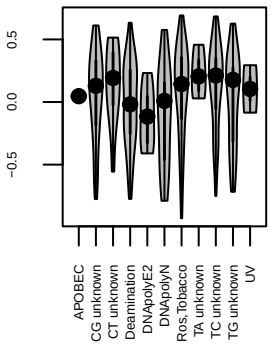
ARID2.splice.acceptor
pv=2.9e−02



ajcc_pathologic_tumor_stage
pv=4.5e−02

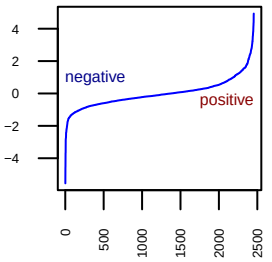


fifth.prominent.motiv
pv=8.3e−02



Component # 9 (stability = 0.945)

Metagene (involvement of features)



19 negative

KRT4
KRT13
BPIFB1
SPRR3
MUC21
CRNN
STATH
KRT19
PIGR
IGHG1
IGHG3
IGKC
IGHG4
DMBT1
IL13RA2
IGLC3
IGLL5
IGHGP
IGLC2

77 positive

LOR
KRT1
CASP14
FLG2
LCE1C
KRT2
KPRP
LCE1B
LCE2B
LCE1A
DSC1
LCE1F
LCE2C
C1orf68
PSAPL1
LCE6A
HAL
LCE2D
WFDC12
CALML5
ARG1
LCE3E
CDSN
WFDC5
KRTDAP
PLA2G4D
ACER1
LY6G6C
LCE1D
KLK5
LGALS7
ASPRV1
BPIFC
LCE3D
CARD18
KRT77
AADACL2
UNC93A
MUCL1
IGFL1
PLA2G2F
LGALS7B
S100A7A
KLK9
SERPINA12
SPTSSB
SERPINB12
PGLYRP4
GLB1L3
SDR9C7
IRX4
ALOX12B
SPRR4
CYP4F22
SLURP1
DSG1
CHP2
KLK8
CIDEA
SLC15A1
ALOXE3
CAPNS2
TCERG1L
FAM25A
KRT75
KLK7
POU2F3
GJB6
PGLYRP3
ABCA12
PLA2G4F
S100A7
PLA2G3
TP53AIP1
CST6
SLC6A11
IRX2

GO:BP neg : 7 terms(FDR<0.1)

Term	FDR
phagocytosis, engulfment	4.25e−12
phagocytosis, recognition	4.25e−12
complement activation, classical pathway	2.39e−10
positive regulation of B cell activation	2.86e−10
B cell receptor signaling pathway	3.82e−09
defense response to bacterium	1.05e−07
innate immune response	1.23e−04

GO:BP pos : 4 terms(FDR<0.1)

Term	FDR
skin development	3.34e−17
regulation of water loss via skin	1.10e−03
epidermis development	3.18e−02
ceramide metabolic process	5.97e−02

GO:CC neg : 6 terms(FDR<0.1)

Term	FDR
immunoglobulin complex, circulating	9.60e−11
IgG immunoglobulin complex	4.07e−10
blood microparticle	3.92e−08
extracellular exosome	4.16e−06
external side of plasma membrane	1.92e−05
secretory IgA immunoglobulin complex	7.51e−02

GO:CC pos : 4 terms(FDR<0.1)

Term	FDR
cornified envelope	2.35e−08
keratin filament	2.25e−02
cytosol	3.92e−02
epidermal lamellar body	8.82e−02

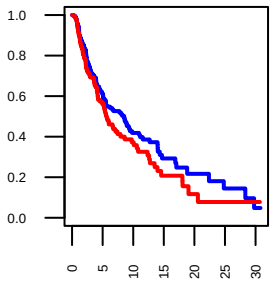
GO:MF neg : 2 terms(FDR<0.1)

Term	FDR
immunoglobulin receptor binding	2.46e−13
antigen binding	2.87e−10

GO:MF pos : 1 terms(FDR<0.1)

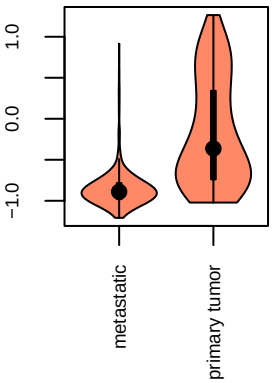
Term	FDR
calcium−dependent phospholipase A2 activ...	3.28e−02

Cox regression: logtest pv=1.5e−04 LHR=0.64 (CI = 0.34, 0.94)

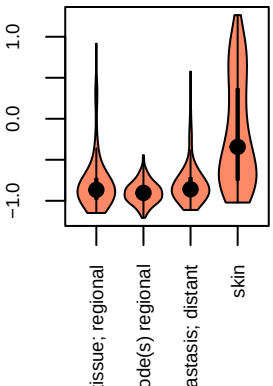


factor	p.value
Sample.Type	1.34e−49
Tumor.location.site	1.10e−48
Tumor.tissue.site	3.14e−48
Oncotree.Code	5.55e−34
Cancer.Type.Detailed	5.55e−34
Sample.country	1.92e−31
RNASEQ.CLUSTER_CONSENHIER	3.24e−27
New.tumor.event.after.initial.treatment	7.61e−20
ICD.10.TopLevel	1.56e−17
initial_pathologic_dx_year	8.61e−15

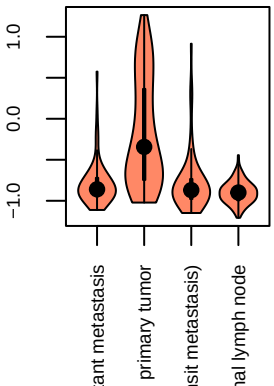
Sample.Type pv=1.3e−49



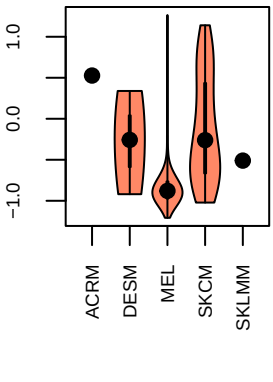
Tumor.location.site pv=1.1e−48



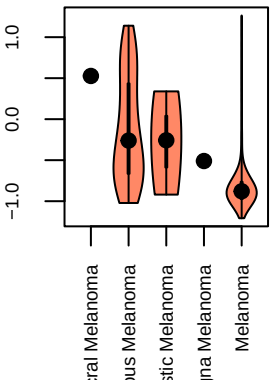
Tumor.tissue.site pv=3.1e−48



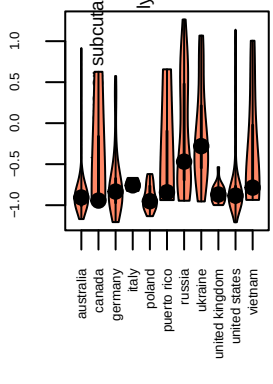
Oncotree.Code pv=5.6e−34



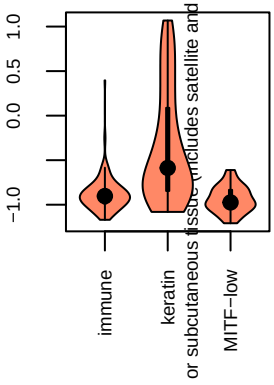
Cancer.Type.Detailed pv=5.6e−34



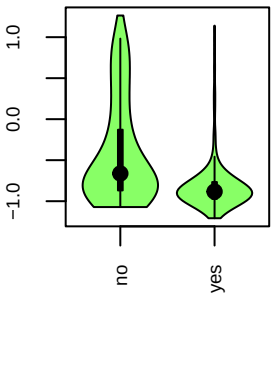
Sample.country pv=1.9e−31



RNASEQ.CLUSTER_CONSENHIER pv=3.2e−27

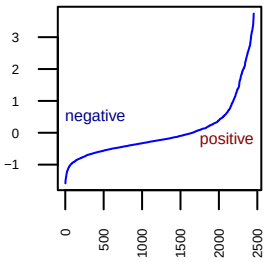


New.tumor.event.after.initial.treatmen pv=7.6e−20



Component # 10 (stability = 0.927)

Metagene (involvement of features)



0 negative	234 positive
	CXCL9
	IFNG
	IGHG1
	IGKC
	PLA2G2D
	CD8A
	GBP5
	CXCL13
	IGHG3
	LAG3
	CXCL10
	IDO1
	CD8B
	NKG7
	PDCD1
	CXCR2P1
	UBD
	IGHGP
	OR2I1P
	IGLC2
	FASLG
	IGLC3
	MZB1
	IGHM
	IGJ
	GZMH
	GZMK
	IGLL5
	CXCL11
	GZMA
	JAKMIP1
	LGALS17A
	SIRPG
	PRF1
	TIGIT
	CCL5
	IGHG2
	ZBED2
	ANKRD22
	TRGC2
	GBP1P1
	SH2D1A
	CD2
	CXCR6
	CXCR3
	TNFRSF9
	IKZF3
	GPR171
	THEMIS
	CD3D
	GZMB
	KLRD1
	SLAMF6
	TRAT1
	GBP4
	CCR5
	TRBC2
	CD3G
	IGHG4
	CD3E
	FCRL3
	FAM26F
	TRBV28
	CRTAM
	CD7
	GBP1
	TNIP3
	SLA2
	ADAMDEC1
	TBX21
	UBASH3A
	ZBP1
	TRAC
	CTSW
	FCRL5
	LCK
	CD38
	CD27
	P2RY10
	LAX1
	DTHD1
	TLR8

GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 42 terms(FDR<0.1)

Term	FDR
immune response−regulating cell surface ...	4.77e−28
adaptive immune response	4.77e−28
innate immune response	9.86e−24
positive regulation of lymphocyte activa...	5.97e−23
B cell activation	1.15e−20
T cell activation	4.14e−12
phagocytosis, engulfment	3.54e−11
response to virus	9.19e−11
humoral immune response mediated by circ...	4.56e−10
positive regulation of cytokine producti...	2.48e−09
response to bacterium	5.38e−09
immune response	2.47e−08
inflammatory response	3.52e−08
lymphocyte mediated immunity	1.84e−07
phagocytosis, recognition	2.48e−07
cytokine−mediated signaling pathway	2.62e−07
positive regulation of defense response	1.24e−06
T cell selection	1.43e−06
lymphocyte differentiation	2.11e−06
positive regulation of response to exter...	2.62e−06

GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 8 terms(FDR<0.1)

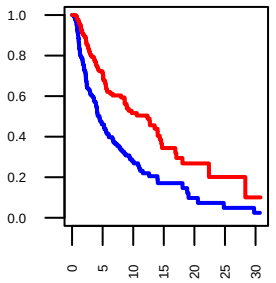
Term	FDR
external side of plasma membrane	9.80e−29
T cell receptor complex	2.16e−12
immunoglobulin complex	9.15e−09
immunological synapse	8.57e−08
cytolytic granule	3.53e−03
blood microparticle	8.98e−03
membrane raft	1.68e−02
tertiary granule membrane	3.43e−02

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 13 terms(FDR<0.1)

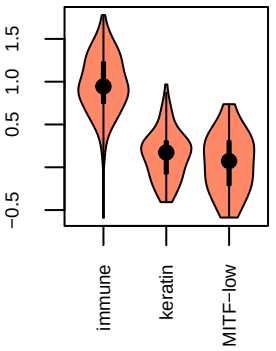
Term	FDR
antigen binding	5.13e−14
immunoglobulin receptor binding	8.42e−11
C−C chemokine receptor activity	1.23e−03
C−C chemokine binding	3.75e−03
tumor necrosis factor receptor binding	5.75e−03
chemokine activity	7.53e−03
CCR chemokine receptor binding	2.51e−02
MHC protein binding	2.51e−02
purinergic nucleotide receptor activity	2.51e−02
MHC protein complex binding	3.17e−02

Cox regression:
logtest pv=2.2e−07
LHR=−0.63 (CI = −0.87, −0.39)

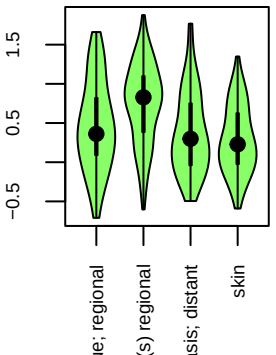


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	3.57e−72
Tumor.location.site	1.59e−14
Tumor.tissue.site	4.92e−14
Sample.Type	8.45e−09
ICD.10.TopLevel	1.26e−08
last_contact_days_to	5.13e−07
Oncotree.Code	6.41e−06
Cancer.Type.Detailed	6.41e−06
vital_status_at_last_contact	2.24e−05
tumor_status_at_last_contact	3.04e−05

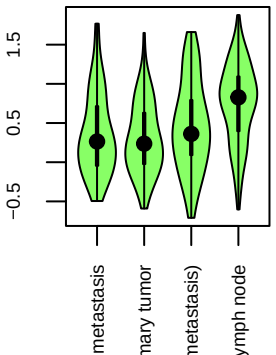
RNASEQ.CLUSTER_CONSENHIER
pv=3.6e−72



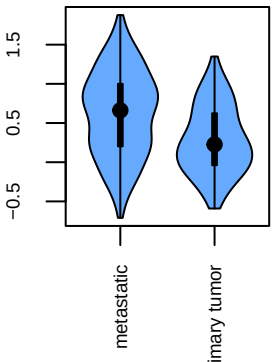
Tumor.location.site
pv=1.6e−14



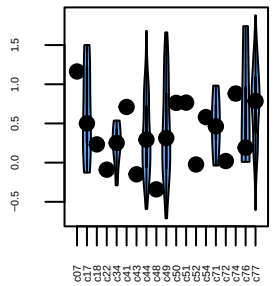
Tumor.tissue.site
pv=4.9e−14



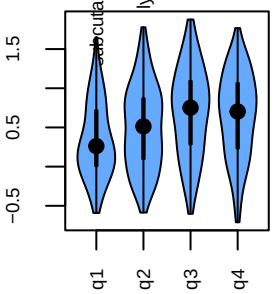
Sample.Type
pv=8.4e−09



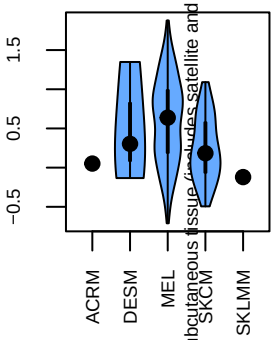
ICD.10.TopLevel
pv=1.3e−08



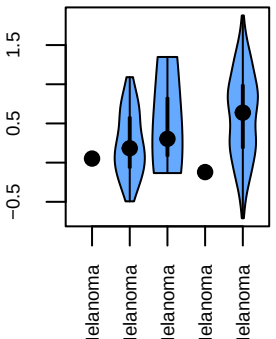
last_contact_days_to
pv=5.1e−07



Oncotree.Code
pv=6.4e−06

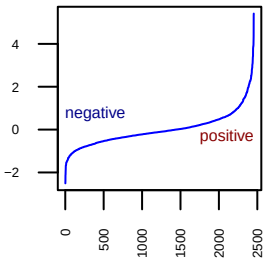


Cancer.Type.Detailed
pv=6.4e−06



Component # 11 (stability = 0.959)

Metagene (involvement of features)



4 negative	90 positive
MMP13	CCL21
COL11A1	CR2
SALL1	ADH1B
COL22A1	FCER2
	PAX5
	C7
	CCL19
	IGHD
	MS4A1
	FCAMR
	IGHE
	NPY1R
	TCL1A
	SHISA3
	BLK
	CNR2
	CD19
	VPREB3
	CAPN6
	FCRL1
	CXCR5
	FAM129C
	BANK1
	ART4
	DNASE1L3
	IGHA1
	CD79A
	SERPINA9
	NPHS1
	TNFRSF13B
	CLU
	CLEC17A
	CXCL14
	IGHA2
	PI16
	KIAA0125
	HP
	ACKR1
	SPIB
	CLEC4M
	MMRN1
	LTF
	SELP
	PTPRT
	VIPR1
	FCRL2
	IGHM
	SLC22A3
	XKR4
	FABP4
	TBC1D27
	CHRDL1
	HMCN2
	FCRL5
	AICDA
	CD24
	FDCSP
	MFAP4
	NTS
	POU2AF1
	TSPAN8
	HTR3A
	TREML2
	IGLC7
	LBP
	IGLL5
	TLR10
	PLCXD3
	NPY5R
	CD1C
	PLD5
	CCR7
	ELN
	CP
	IGHG2
	IGHG4
	KLHL14
	GYLTL1B
	PNOC
	LTB
	STAP1
	MEOX1

GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 10 terms(FDR<0.1)

Term	FDR
B cell activation	1.62e−18
B cell receptor signaling pathway	2.77e−17
humoral immune response mediated by circ...	1.37e−13
phagocytosis, engulfment	2.08e−11
phagocytosis, recognition	3.05e−10
positive regulation of lymphocyte activa...	3.34e−09
response to bacterium	9.00e−07
innate immune response	8.95e−05
regulation of dendritic cell apoptotic p...	4.88e−02
immune response	5.15e−02

GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 4 terms(FDR<0.1)

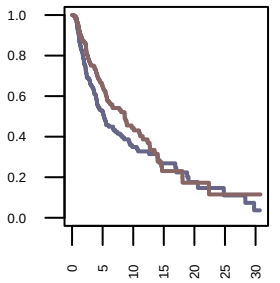
Term	FDR
immunoglobulin complex	2.06e−12
cell surface	5.39e−11
blood microparticle	4.25e−07
integral component of plasma membrane	7.11e−02

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 6 terms(FDR<0.1)

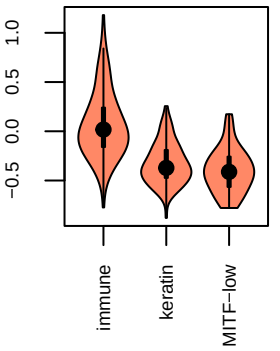
Term	FDR
immunoglobulin receptor binding	2.87e−13
antigen binding	7.29e−12
lipopeptide binding	6.30e−03
immunoglobulin binding	2.26e−02
endogenous lipid antigen binding	5.82e−02
exogenous lipid antigen binding	5.82e−02

Cox regression:
logtest pv=2.2e−02
LHR=−0.47 (CI = −0.89, −0.06)

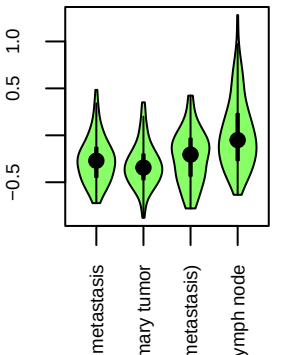


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	4.08e−32
Tumor.tissue.site	3.24e−20
Tumor.location.site	9.26e−20
ICD.10.TopLevel	8.76e−13
Sample.Type	1.94e−09
second.prominent.motif	1.72e−05
Oncotree.Code	4.88e−05
Cancer.Type.Detailed	4.88e−05
Breslow.Depth	9.16e−05
New.tumor.event.after.initial.treatment	4.62e−04

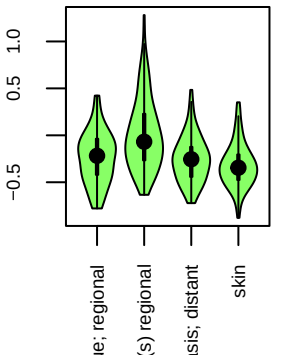
RNASEQ.CLUSTER_CONSENHIER pv=4.1e−32



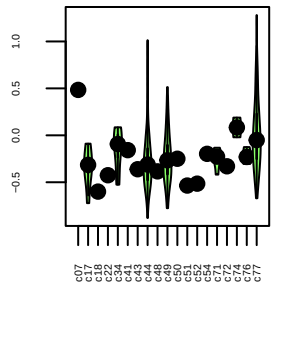
Tumor.tissue.site pv=3.2e−20



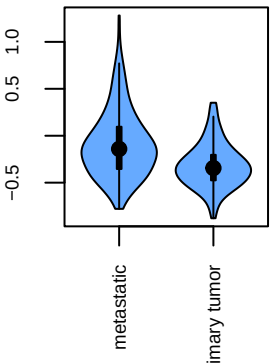
Tumor.location.site pv=9.3e−20



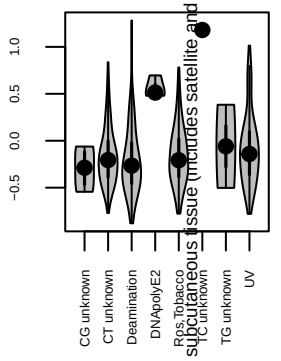
ICD.10.TopLevel pv=8.8e−13



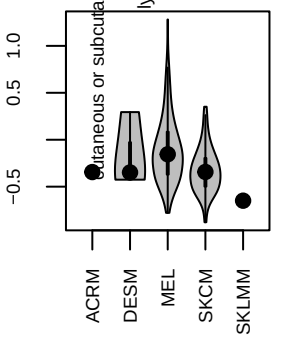
Sample.Type pv=1.9e−09



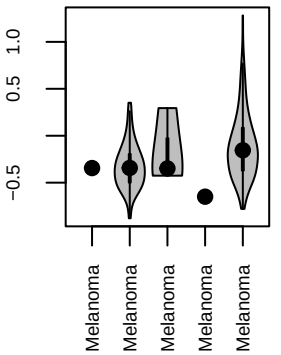
second.prominent.motif pv=1.7e−05



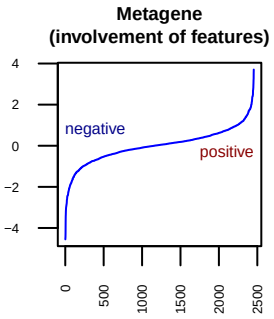
Oncotree.Code pv=4.9e−05



Cancer.Type.Detailed pv=4.9e−05



Component # 12 (stability = 0.837)



47 negative	23 positive
HOXB13	OCA2
RTN4RL1	FRG2DP
TTLL6	COL2A1
LRRTM4	GRIK2
EYA1	BMPR1B
OLFM3	IRS4
FREM1	SUSD5
PKLR	MAL
CADPS	SLC6A15
CMTM5	LPAR3
PRAC2	TRIM48
VSTM2L	TOX3
BHLHE22	XAGE2B
ETNPPL	OPRD1
KLHL13	ABCC2
LRRTM1	SEPT3
ZNF536	DNAJC6
HOXD13	IL12RB2
FXYD3	DPP10
GATA4	RAMP1
CDH1	PSG4
HOXA13	PRUNE2
KCNJ10	SOX2
CRB1	
HCCAT5	
KLHL14	
TMEM246	
GJB2	
FABP7	
LPPR5	
PMP2	
RAB3C	
RIMS2	
MYO5B	
NELL1	
HOXB9	
KCNG3	
LHX1	
ASB4	
CHST9	
TEKT5	
HOXC10	
PRIMA1	
RDH12	
LGALS12	
HTR2B	
COL25A1	

GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 1 terms(FDR<0.1)

Term	FDR
positive regulation of extrinsic apoptot...	7.35e−02

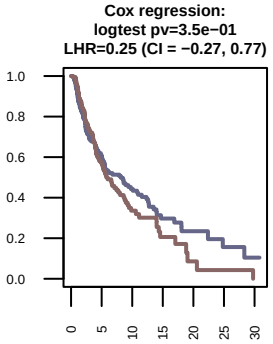
GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 1 terms(FDR<0.1)

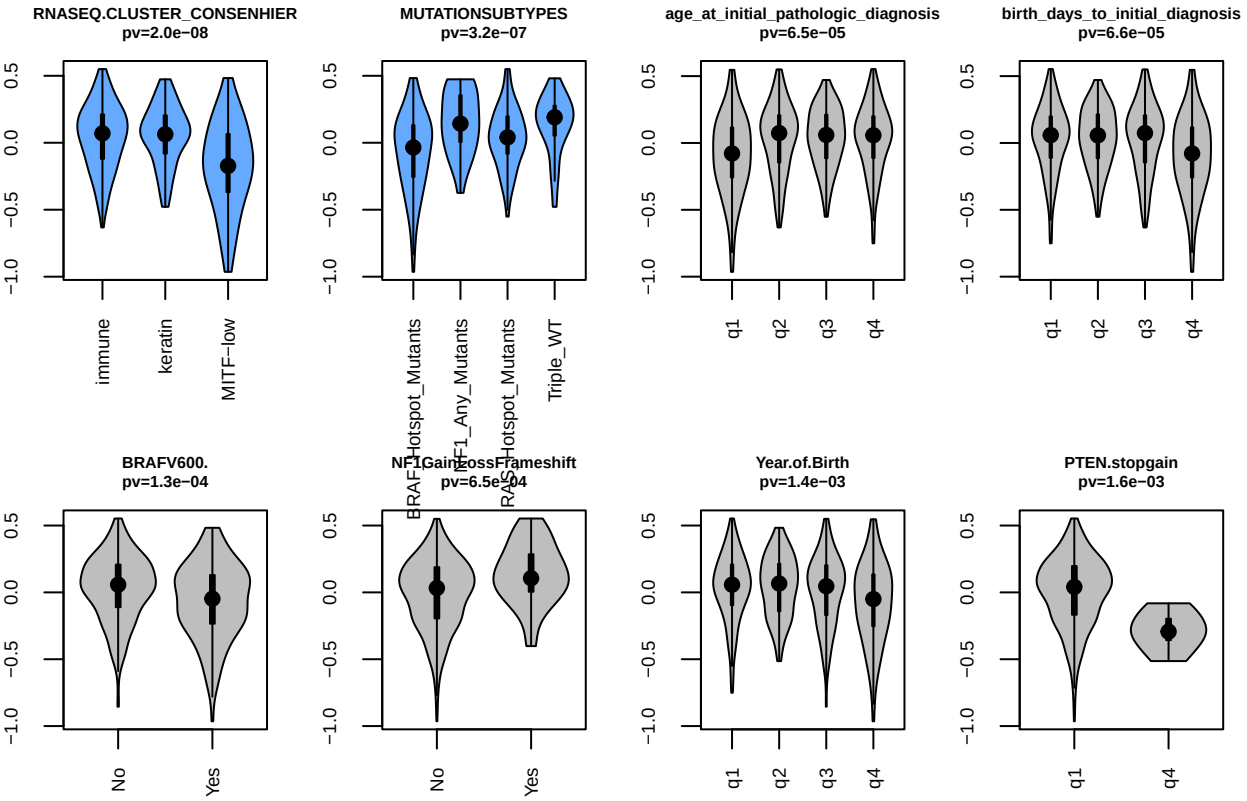
Term	FDR
collagen type XI trimer	6.27e−03

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 0 terms(FDR<0.1)

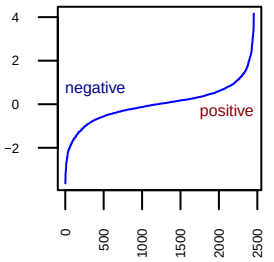


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	1.98e−08
MUTATIONSUBTYPES	3.18e−07
age_at_initial_pathologic_diagnosis	6.55e−05
birth_days_to_initial_diagnosis	6.58e−05
BRAFV600.	1.26e−04
NF1GainLossFrameshift	6.52e−04
Year.of.Birth	1.44e−03
PTEN.stopgain	1.61e−03
NF1.stopgain	1.82e−03
TP53.stopgain	2.28e−03



Component # 13 (stability = 0.954)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

40 negative	49 positive
SH2D4A	TNNT1
ANXA3	LHX1
LOXL4	BRSK2
PQLC2L	CDK5R2
ETNPPL	ZIC2
MT1A	HCN2
COL2A1	VAX1
PPP1R3C	FAM155B
CMBL	HOXC13
KLHL34	TMEM59L
PRSS21	EEF1A2
HCAR1	C1QL4
RAMP1	PHF21B
TSPYL5	NPTXR
ABHD12B	FOXD1
DDIT4L	DPYSL5
GFRA3	VGF
LY6K	SYT3
GJB6	LMX1B
MARC1	LRRC4B
PAPL	GAD1
HRASLS5	APLP1
ARHGEF35	PCSK1N
LRP2	PAX9
TFPI2	KCNN1
CNDP1	GNAO1
SEC14L4	HOXC10
MEST	ZFR2
RHOD	OLIG2
ARHGEF5	KCNQ2
SLC9A7P1	L1CAM
PON3	FSD1
TMEM215	SULT4A1
CNTN1	IGF2BP1
MT1M	ADRA2C
COL11A1	TMEM151A
DSG2	FOXF2
ESRRG	OLFM1
DNALI1	POU3F2
MT1L	B4GALNT4
	RASGEF1C
	MNX1
	JPH3
	PCSK2
	ZNF536
	EFNB3
	SP8
	HOXC12
	HOXC11

GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 2 terms(FDR<0.1)

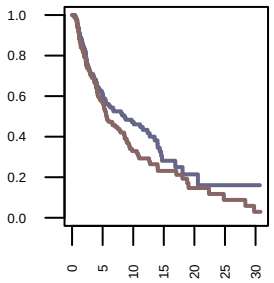
Term	FDR
chromatin	1.57e−04
transcription regulator complex	9.80e−02

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 3 terms(FDR<0.1)

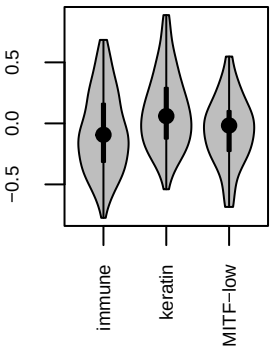
Term	FDR
DNA−binding transcription factor activit...	2.87e−05
RNA polymerase II transcription regulato...	1.98e−04
cis−regulatory region sequence−specific ...	1.98e−04

Cox regression:
logtest pv=2.1e−01
LHR=0.27 (CI = −0.15, 0.69)

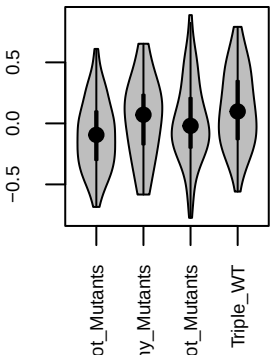


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	5.27e−05
MUTATIONSUBTYPES	1.74e−04
age_at_initial_pathologic_diagnosis	4.00e−04
birth_days_to_initial_diagnosis	4.03e−04
Year.of.Birth	4.48e−04
age.at.last.contact	6.35e−04
BRAFV600.	3.68e−03
new_tumor_event_type	4.32e−03
KRASQ61.	4.61e−03
tumor_status_at_last_contact	7.89e−03

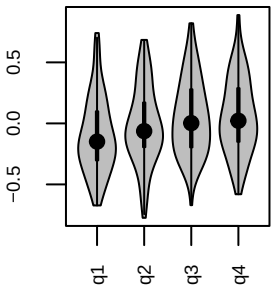
RNASEQ.CLUSTER_CONSENHIER
pv=5.3e−05



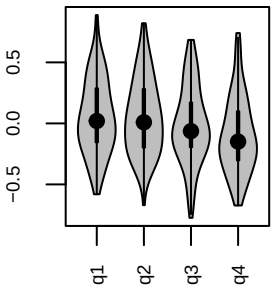
MUTATIONSUBTYPES
pv=1.7e−04



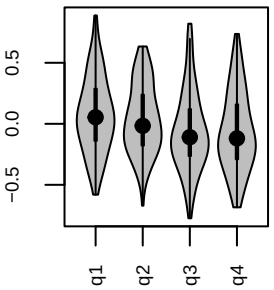
age_at_initial_pathologic_diagnosis
pv=4.0e−04



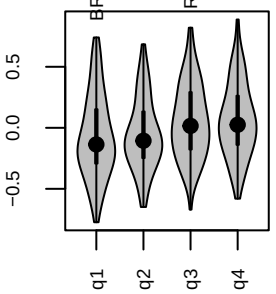
birth_days_to_initial_diagnosis
pv=4.0e−04



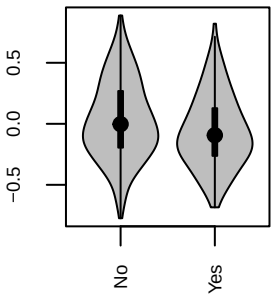
Year.of.Birth
pv=4.5e−04



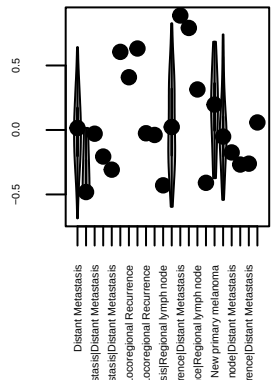
age.at.last.contact
pv=6.4e−04



BRAFV600.
pv=3.7e−03

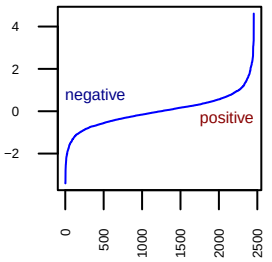


new_tumor_event_type
pv=4.3e−03



Component # 14 (stability = 0.752)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

12 negative	27 positive
HTN1	MMP8
MRGPRX3	FXYD3
SOSTDC1	UCN2
EYA1	ADCY2
PI15	KRT27
MLIP	SCUBE2
ABCA8	ACSBG1
RBM20	MPZ
DSP	CMTM5
MET	HRH2
DSG2	ST8SIA2
POU3F3	ANO4
	CHRNA1
	SFRP5
	BRSK2
	TEKT5
	TMEM163
	PLEKHA6
	C2orf70
	NPPC
	L1CAM
	NGFR
	SLC28A3
	AMPH
	CAMK2A
	FXYD7
	COL20A1

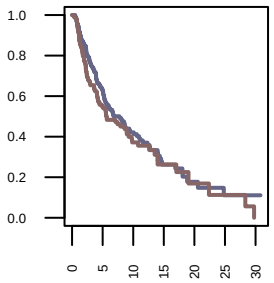
GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 0 terms(FDR<0.1)

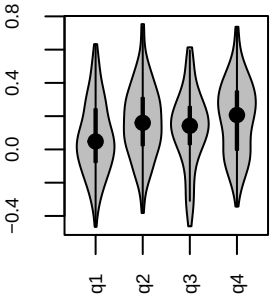
GO:MF pos : 0 terms(FDR<0.1)

Cox regression:
logtest pv=4.1e−01
LHR=0.25 (CI = −0.35, 0.85)

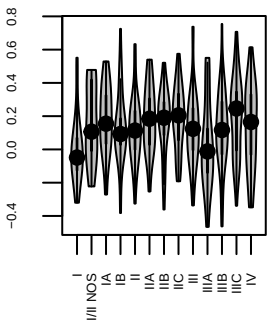


factor	p.value
initial_pathologic_dx_year	1.59e−04
ajcc_pathologic_tumor_stage	7.12e−03
ICD.10.TopLevel	9.91e−03
ARID2.stopgain	1.07e−02
most.prominent.motif	1.15e−02
Postoperative.Radio.Therapie	1.22e−02
Adjuvant.Postoperative.Pharmaceutical.Therapy.Administered.Indicator	1.33e−02
Sample.Type	1.94e−02
Cancer.Type.Detailed	2.21e−02
Oncotree.Code	2.21e−02

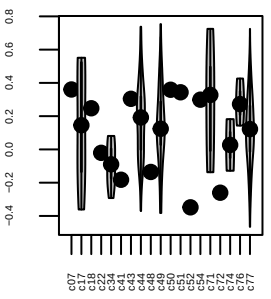
initial_pathologic_dx_year
pv=1.6e−04



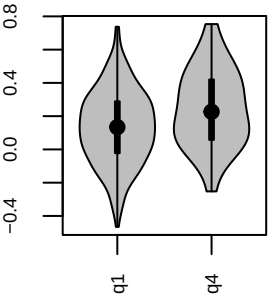
ajcc_pathologic_tumor_stage
pv=7.1e−03



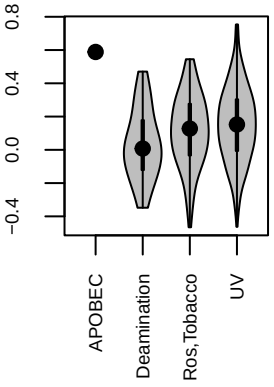
ICD.10.TopLevel
pv=9.9e−03



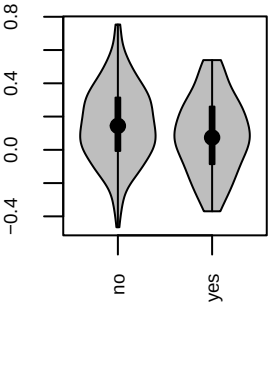
ARID2.stopgain
pv=1.1e−02



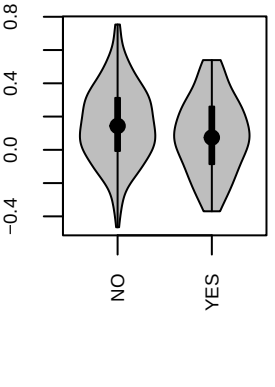
most.prominent.motif
pv=1.2e−02



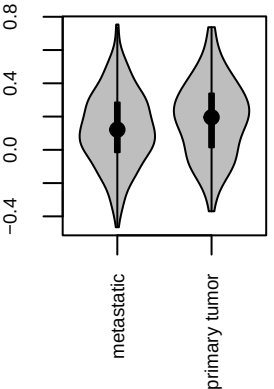
Postoperative.Radio.Therapie
pv=1.2e−02



stoperative.Pharmaceutical.Therapy.Admi
pv=1.3e−02

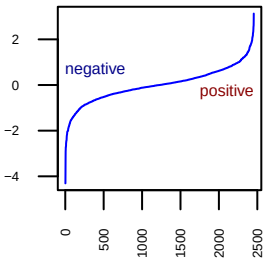


Sample.Type
pv=1.9e−02



Component # 15 (stability = 0.776)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

18 negative	11 positive
LIN28A	RASEF
LIN28B	TCN1
TRIM71	CCNO
COL20A1	ITGB8
IGDCC3	NRCAM
INSC	ST8SIA6
FAM178B	FDCSP
HIF3A	TRPM8
RCOR2	PPP1R14C
COL2A1	FABP7
ATP2B3	MAOB
NEFH	
MDFI	
CAMKV	
CTCFL	
MSI1	
COL11A2	
NKAIN4	

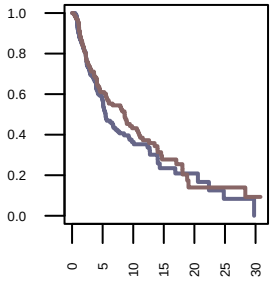
GO:CC neg : 0 terms(FDR<0.1)

GO:CC pos : 0 terms(FDR<0.1)

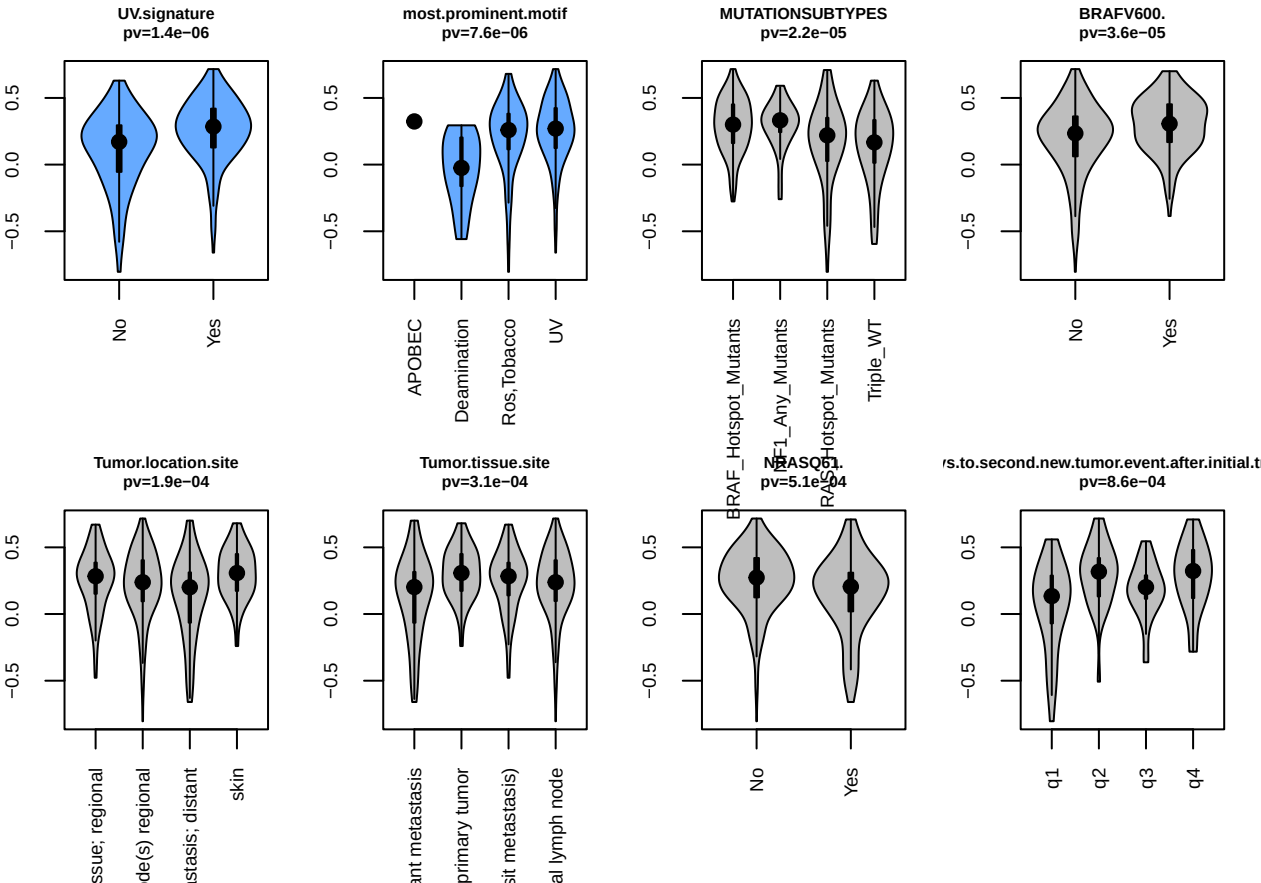
GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 0 terms(FDR<0.1)

Cox regression:
logtest pv=1.5e−02
LHR=−0.61 (CI = −1.09, −0.13)

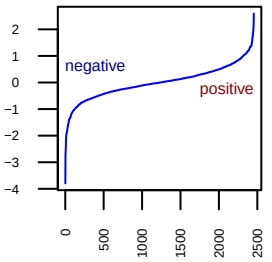


factor	p.value
UV.signature	1.44e−06
most.prominent.motif	7.64e−06
MUTATIONSUBTYPES	2.17e−05
BRAFV600.	3.64e−05
Tumor.location.site	1.93e−04
Tumor.tissue.site	3.14e−04
NRASQ61.	5.12e−04
Days.to.second.new.tumor.event.after.initial.treatment	8.65e−04
Sample.Type	1.27e−03
fourth.prominent.motiv	4.31e−03



Component # 16 (stability = 0.686)

Metagene (involvement of features)



GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

17 negative	**9 positive**
HHATL	SHISA2
UGT2B7	CRABP1
DNAH9	LINGO2
MAT1A	DKK1
CRYAB	NDST3
AGT	CBLN2
HOGA1	TMEFF2
TF	COL20A1
TRPM8	CNTN4
CAMK2A	
COBL	
CHI3L2	
ENTHD1	
IP6K3	
MAG	
PPARGC1A	
CDH15	

GO:CC neg : 0 terms(FDR<0.1)

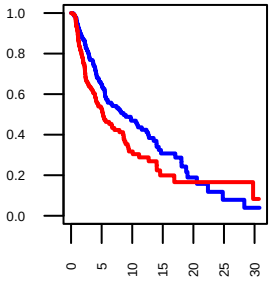
GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 1 terms(FDR<0.1)

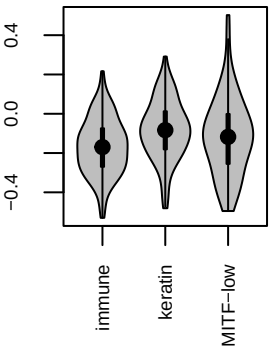
Term	**FDR**
miRNA binding	4.11e−03

Cox regression:
logtest pv=3.1e−03
LHR=1.19 (CI = 0.41, 1.97)

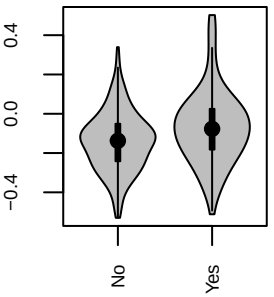


factor	**p.value**
RNASEQ.CLUSTER_CONSENHIER	9.84e−05
NRASQ61.	1.06e−04
Primary.Neoplasm.Melanome.Diagnosis	2.42e−03
ICD.10.TopLevel	3.61e−03
birth_days_to_initial_diagnosis	3.62e−03
age_at_initial_pathologic_diagnosis	3.92e−03
ARID1A.splice.donor	4.60e−03
Oncotree.Code	9.61e−03
Cancer.Type.Detailed	9.61e−03
MUTATIONSUBTYPES	1.39e−02

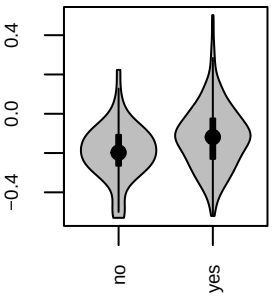
RNASEQ.CLUSTER_CONSENHIER
pv=9.8e−05



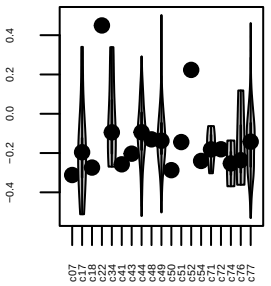
NRASQ61.
pv=1.1e−04



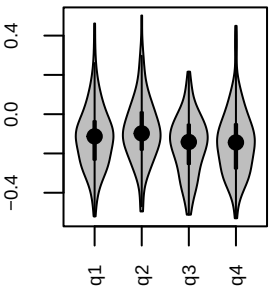
Primary.Neoplasm.Melanome.Diagnosi
pv=2.4e−03



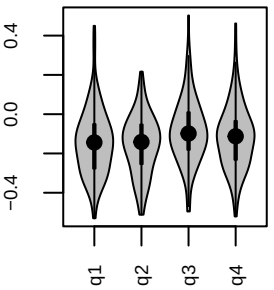
ICD.10.TopLevel
pv=3.6e−03



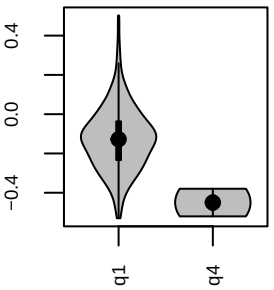
birth_days_to_initial_diagnosis
pv=3.6e−03



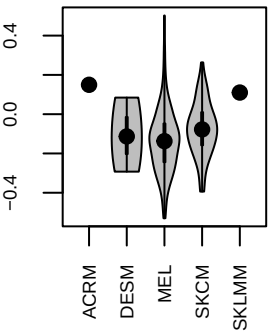
age_at_initial_pathologic_diagnosis
pv=3.9e−03



ARID1A.splice.donor
pv=4.6e−03

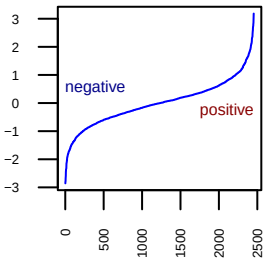


Oncotree.Code
pv=9.6e−03



Component # 17 (stability = 0.816)

Metagene (involvement of features)



5 negative

DMRTA1
HMGA2
MME
WDR17
HHATL

12 positive

ARX
PKHD1
OCA2
GABRG3
BMP7
HOXB13
LRP2
GFRA3
KIT
OR7C1
SOX1
CDK15

GO:BP neg : 0 terms(FDR<0.1)

GO:BP pos : 0 terms(FDR<0.1)

GO:CC neg : 0 terms(FDR<0.1)

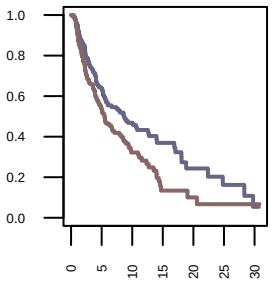
GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 0 terms(FDR<0.1)

GO:MF pos : 1 terms(FDR<0.1)

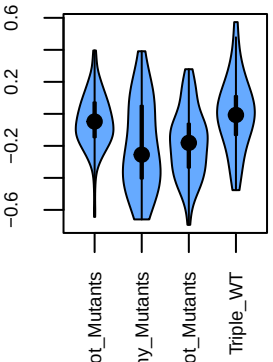
Term	FDR
olfactory receptor activity	3.28e−02

Cox regression: logtest pv=3.9e−02 LHR=0.66 (CI = 0.03, 1.29)

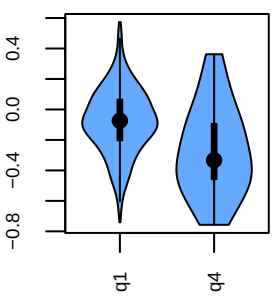


factor	p.value
MUTATIONSUBTYPES	6.46e−09
ARID2.stopgain	5.47e−06
NRASQ61.	8.28e−06
Prospective.Tissue.Collection	1.03e−05
Retropective.Tissue.Collection	1.03e−05
UV.signature	1.97e−05
TP53.stopgain	4.59e−05
Sample.country	1.41e−04
RNASEQ.CLUSTER_CONSENHIER	2.23e−04
last_contact_days_to	5.99e−04

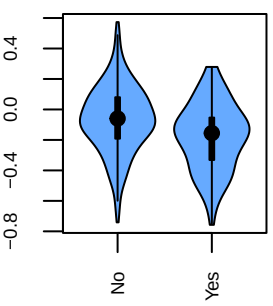
MUTATIONSUBTYPES pv=6.5e−09



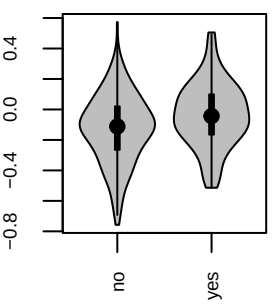
ARID2.stopgain pv=5.5e−06



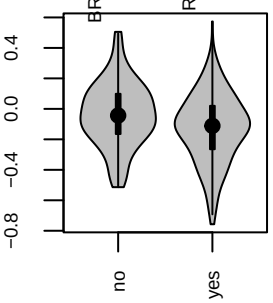
NRASQ61. pv=8.3e−06



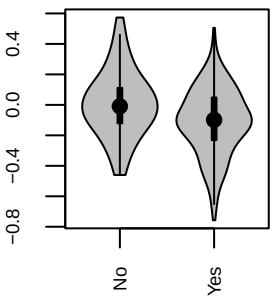
Prospective.Tissue.Collection pv=1.0e−05



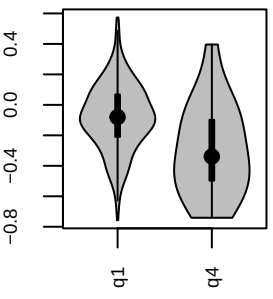
Retropective.Tissue.Collection pv=1.0e−05



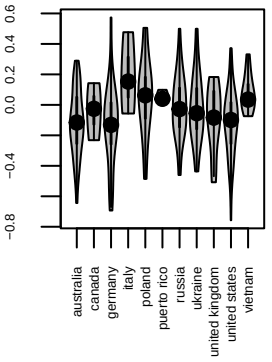
UV.signature pv=2.0e−05



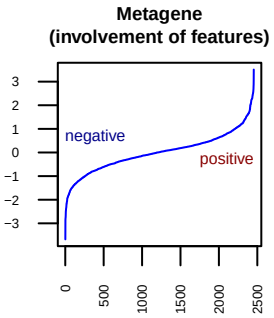
TP53.stopgain pv=4.6e−05



Sample.country pv=1.4e−04



Component # 18 (stability = 0.822)



5 negative	4 positive
ILDR2	CXCL5
BEX1	MMP1
ENPP5	SERPINB2
RIMS4	TRIM48
MAGEA4	

GO:BP neg : 0 terms(FDR<0.1)

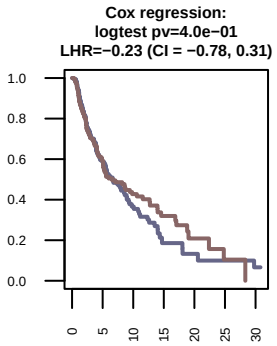
GO:BP pos : 0 terms(FDR<0.1)

GO:CC neg : 0 terms(FDR<0.1)

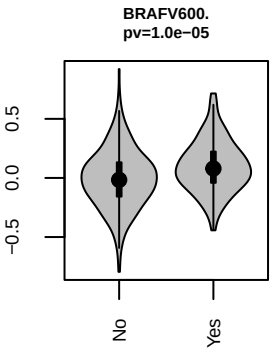
GO:CC pos : 0 terms(FDR<0.1)

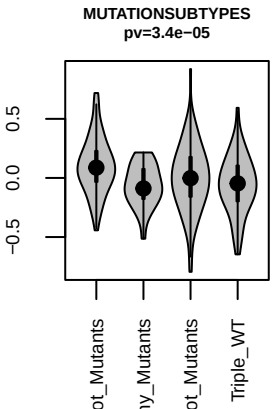
GO:MF neg : 0 terms(FDR<0.1)

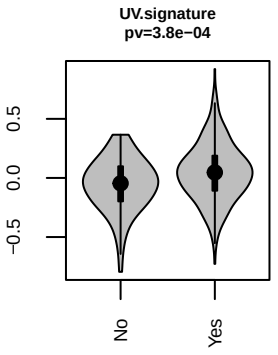
GO:MF pos : 0 terms(FDR<0.1)

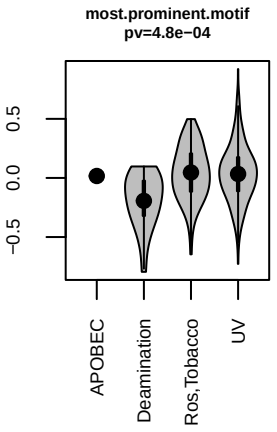


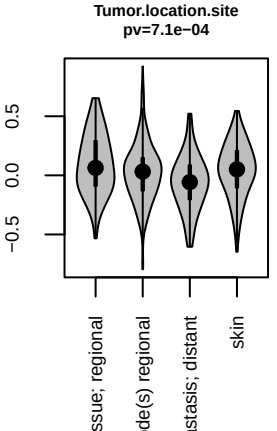
factor	p.value
BRAFV600.	1.04e−05
MUTATIONSUBTYPES	3.39e−05
UV.signature	3.85e−04
most.prominent.motif	4.82e−04
Tumor.location.site	7.07e−04
Tumor.tissue.site	1.80e−03
NRASG12.13.	1.29e−02
Primary.Melanoma.Tissue.Site	2.96e−02
TP53.stopgain	3.31e−02
BMI	3.51e−02

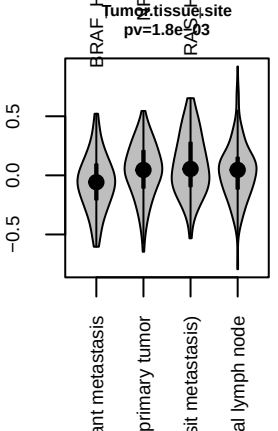


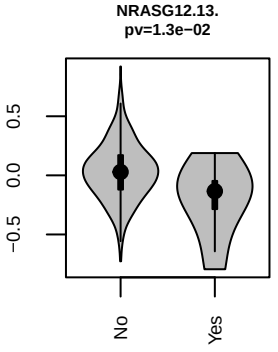


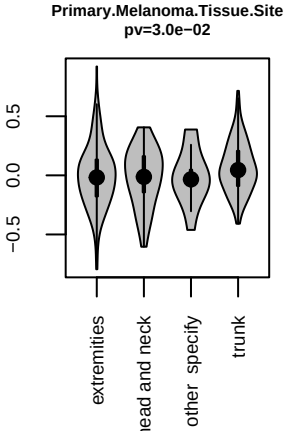




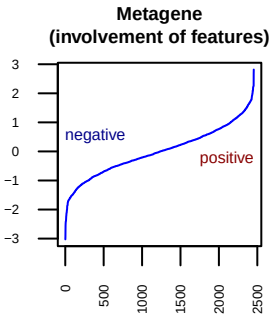








Component # 19 (stability = 0.864)



0
negative

0
positive

GO:BP neg : 0 terms(FDR<0.1)

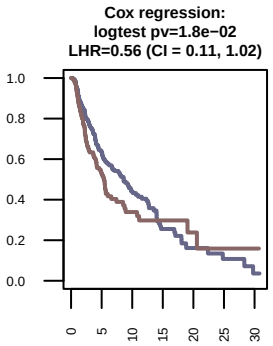
GO:BP pos : 0 terms(FDR<0.1)

GO:CC neg : 0 terms(FDR<0.1)

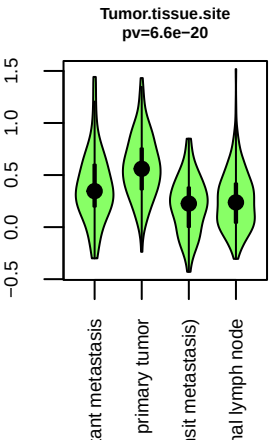
GO:CC pos : 0 terms(FDR<0.1)

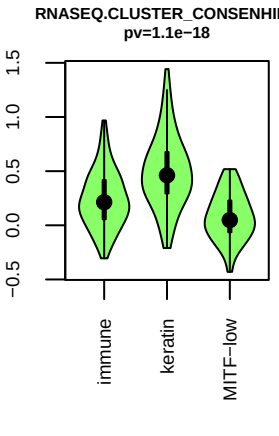
GO:MF neg : 0 terms(FDR<0.1)

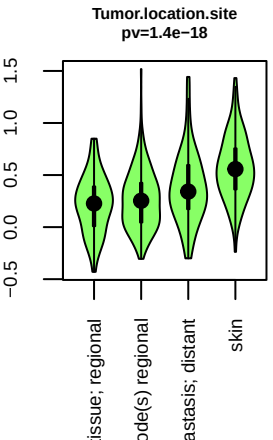
GO:MF pos : 0 terms(FDR<0.1)

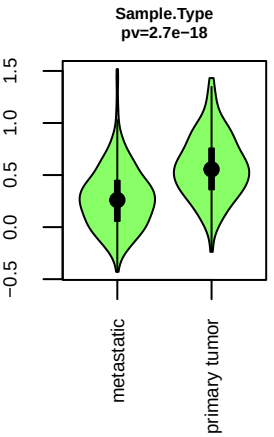


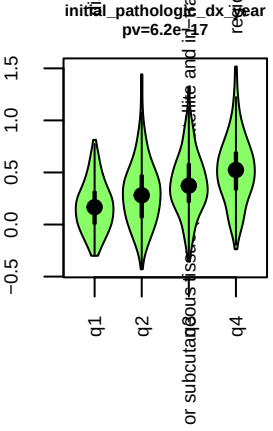
factor	p.value
Tumor.tissue.site	6.58e−20
RNASEQ.CLUSTER_CONSENHIER	1.14e−18
Tumor.location.site	1.38e−18
Sample.Type	2.68e−18
initial_pathologic_dx_year	6.19e−17
Sample.country	1.96e−16
Retropective.Tissue.Collection	2.28e−12
Prospective.Tissue.Collection	2.28e−12
last_contact_days_to	4.38e−11
Cancer.Type.Detailed	1.91e−10

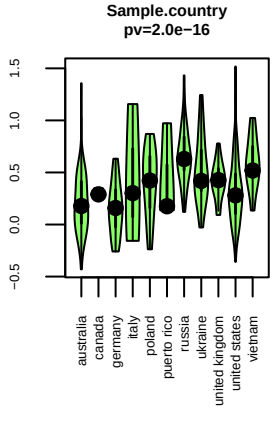


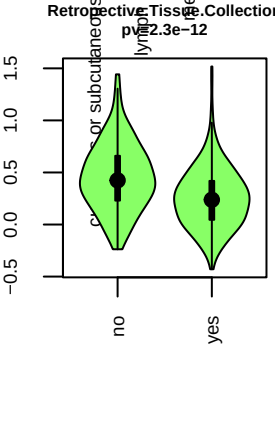


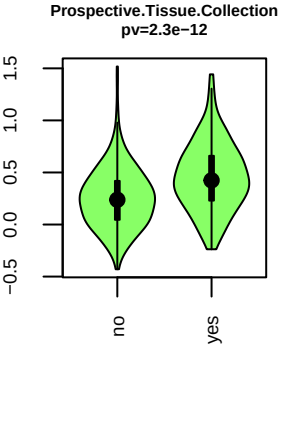




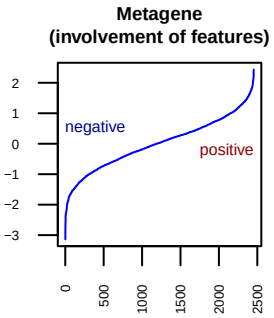








Component # 20 (stability = 0.903)



0
negative

0
positive

GO:BP neg : 0 terms(FDR<0.1)

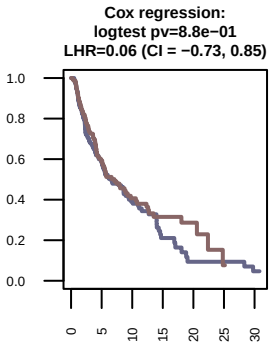
GO:BP pos : 0 terms(FDR<0.1)

GO:CC neg : 0 terms(FDR<0.1)

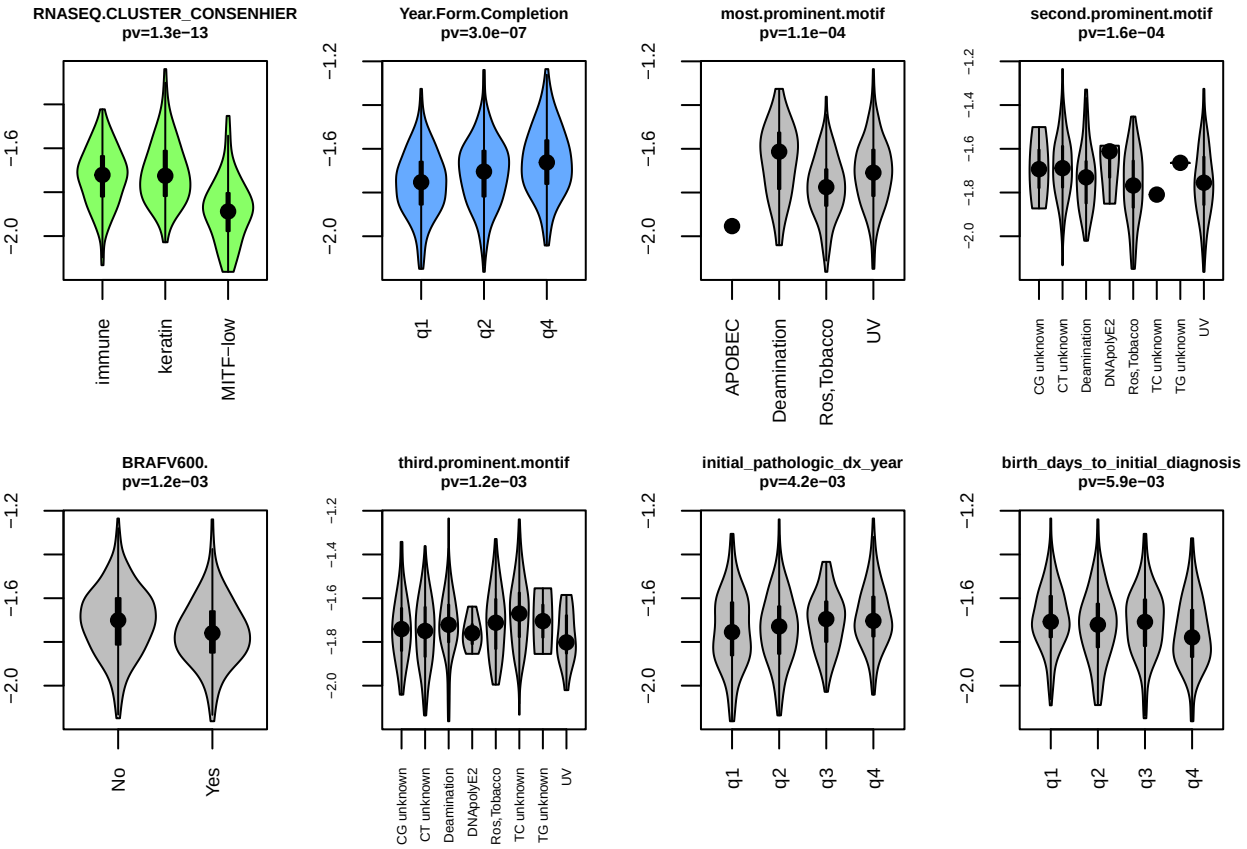
GO:CC pos : 0 terms(FDR<0.1)

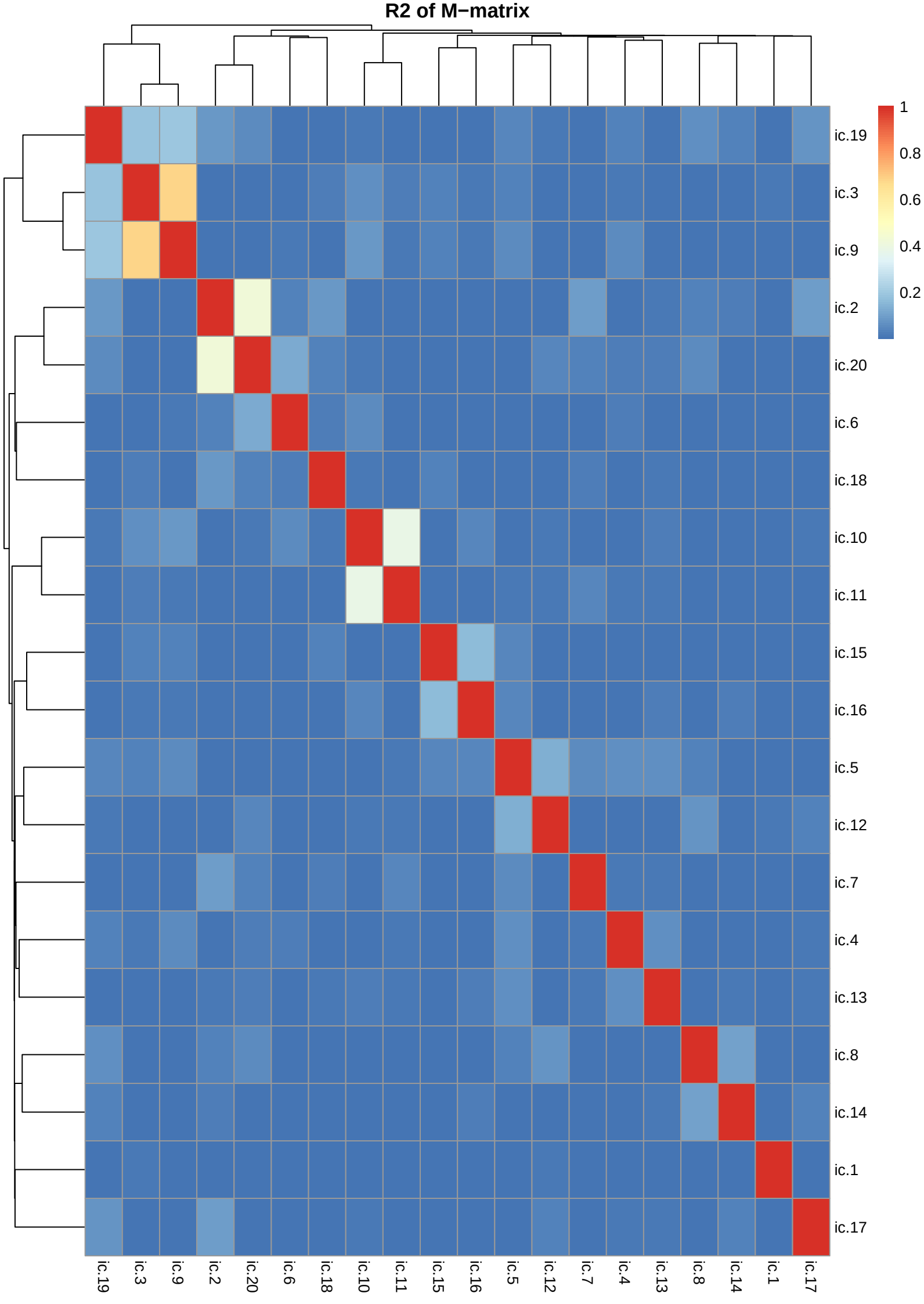
GO:MF neg : 0 terms(FDR<0.1)

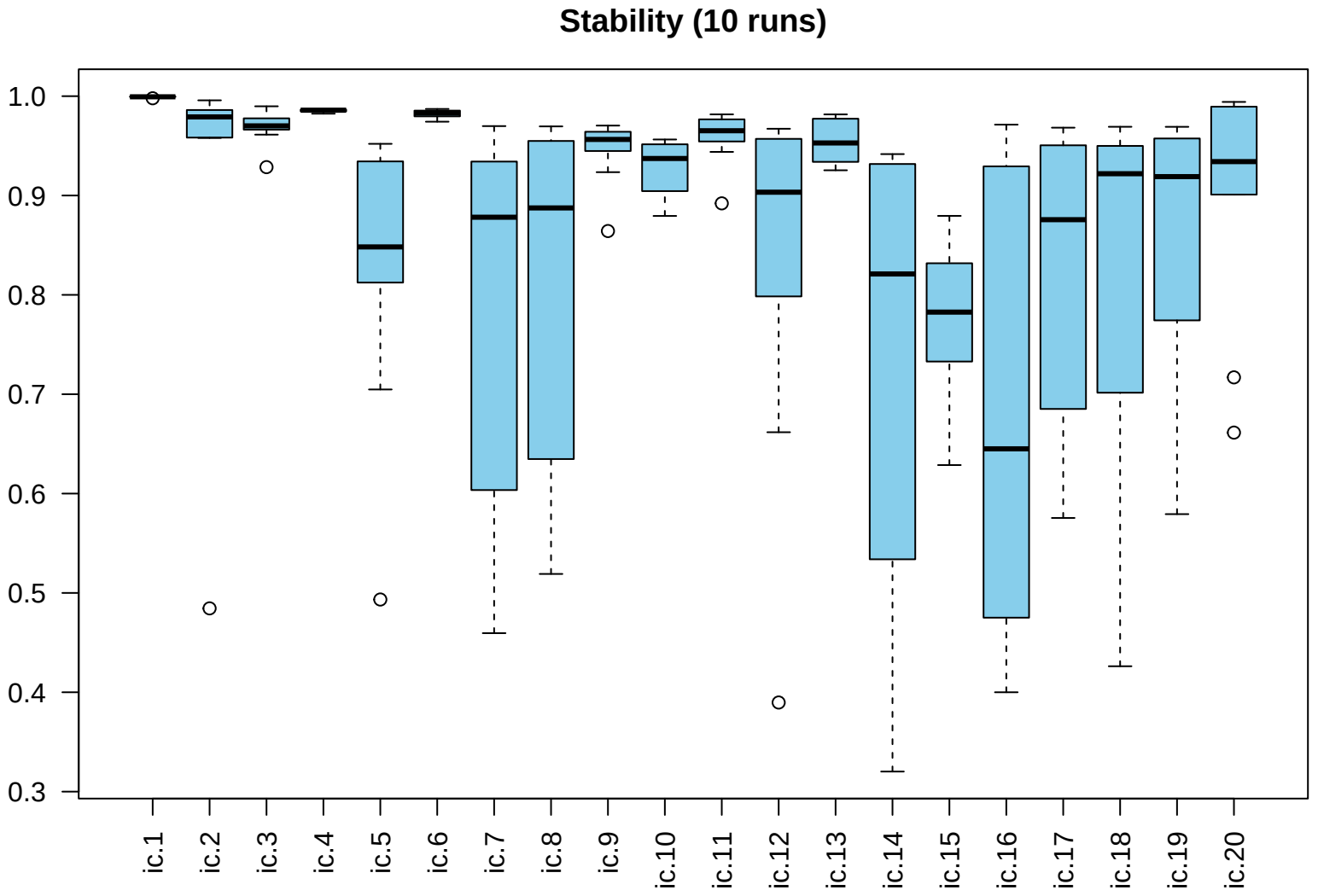
GO:MF pos : 0 terms(FDR<0.1)

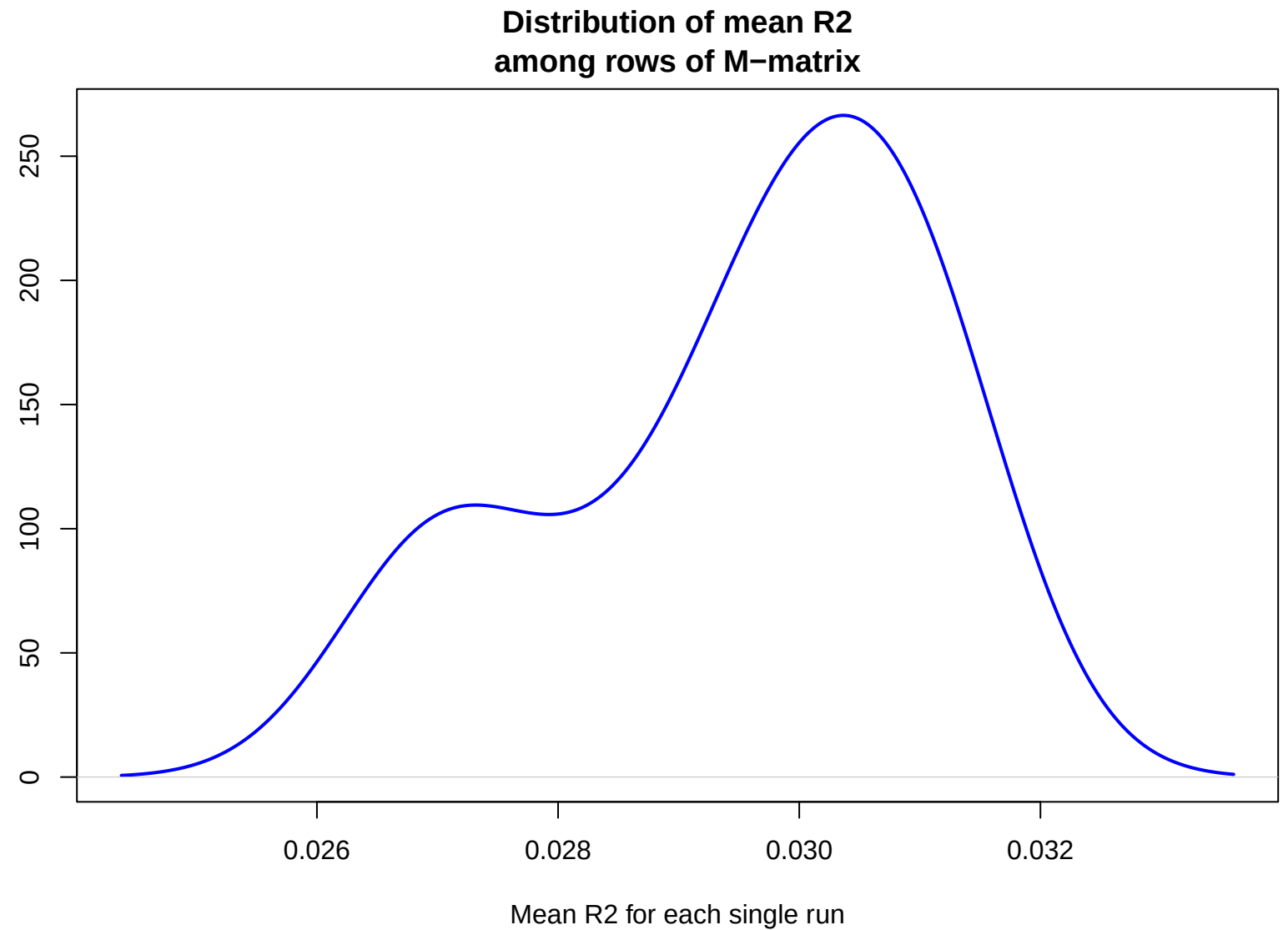


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	1.26e−13
Year.Form.Completion	3.01e−07
most.prominent.motif	1.07e−04
second.prominent.motif	1.62e−04
BRAFV600.	1.16e−03
third.prominent.montif	1.17e−03
initial_pathologic_dx_year	4.15e−03
birth_days_to_initial_diagnosis	5.90e−03
age_at_initial_pathologic_diagnosis	7.10e−03
fifth.prominent.motiv	1.17e−02




R2 of M−matrix
1
0.8
0.6
0.4
0.2
ic.19
ic.3
ic.9
ic.2
ic.20
ic.6
ic.18
ic.10
ic.11
ic.15
ic.16
ic.5
ic.12
ic.7
ic.4
ic.13
ic.8
ic.14
ic.1
ic.17


Stability (10 runs)
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
ic.1
ic.2
ic.3
ic.4
ic.5
ic.6
ic.7
ic.8
ic.9
ic.10
ic.11
ic.12
ic.13
ic.14
ic.15
ic.16
ic.17
ic.18
ic.19
ic.20


Distribution of mean R2
among rows of M−matrix
250
200
150
100
50
0
0.026
0.028
0.030
0.032
Mean R2 for each single run