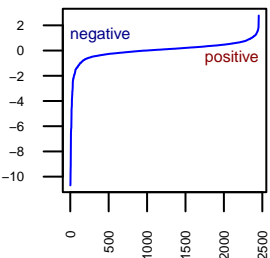


Component # 1 (stability = 0.986)

Metagene (involvement of features)



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)

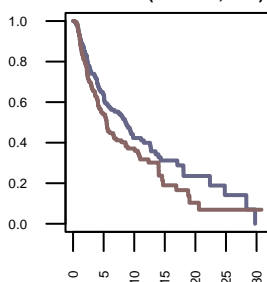
GO:MF pos : 0 terms(FDR<0.1)

94 negative **19 positive**

- MAGEA6
- MAGEA3
- MAGEA12
- CSAG1
- MAGEC1
- MAGEC2
- GABRA3
- CSAG3
- MAGEA10
- PAGE5
- CTAG2
- CSMD1
- MAGEA1
- DSCR8
- FAM133A
- BAGE2
- NAA11
- MAGEA4
- MKRN9P
- MAGEA11
- MAGEB2
- TUBA3C
- ZNF812
- PAGE2
- GABRG2
- ZNF560
- PASD1
- MUC15
- FRG2DP
- MAGEB1
- OVAAL
- SLC30A8
- GABRQ
- KLF14
- VCX3A
- PAGE2B
- RPS4Y1
- GTSF1
- VCX
- AACSP1
- ANGPT1
- SLC5A12
- MAGEB16
- IL13RA2
- ANO3
- CASC9
- GPR158
- HORMAD1
- SLCO1A2
- MYT1L
- HTR2C
- FLJ36000
- KC6
- SSX1
- GAGE2A
- CT55
- FOXR2
- LYPD8
- GAGE1
- DDX3Y
- ZNF300P1
- KDM5D
- MAEL
- POU6F2
- PRDM7
- ZNF280A
- MORC1
- EIF1AY
- ACTBP8
- PSG4
- CDH12
- FSTL5
- SLC44A5
- FAR2P1
- PCSK2
- CDH18
- MIR663AHG
- KLK2
- ZIC1
- HBE1
- MKRN3
- ZFY

- SOX1
- USP43
- DMRT2
- TRIM51CP
- FAM19A5
- GABRA5
- CNNM1
- OLFM1
- KNDC1
- COL2A1
- HUNK
- LONRF3
- TFF3
- B3GAT1
- SH3GL2
- TMEM179
- ADARB2
- AP3B2
- GLB1L2

Cox regression:
logtest pv=4.8e-02
LHR=0.41 (CI = 0.00, 0.81)



- factor
- RNASEQ.CLUSTER_CONSENHIER
 - Retropective.Tissue.Collection
 - Prospective.Tissue.Collection
 - MUTATIONSUBTYPES
 - Days.to.third.new.tumor.event.after.initial.treatment
 - third.prominent.montif
 - Days.to.first.new.tumor.event.after.initial.treatment
 - Cancer.Type.Detailed
 - Oncotree.Code
 - UV.signature

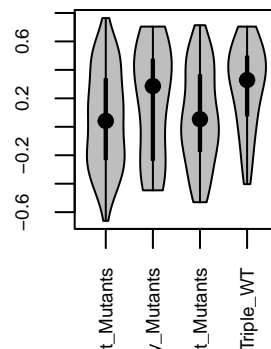
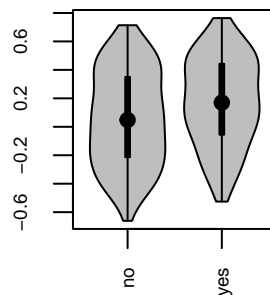
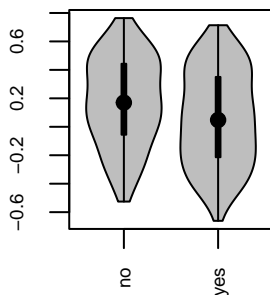
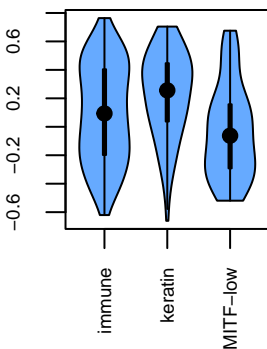
- p.value
- 4.45e-06
 - 1.39e-04
 - 1.39e-04
 - 5.67e-04
 - 1.22e-03
 - 2.49e-03
 - 2.51e-03
 - 3.24e-03
 - 3.24e-03
 - 3.26e-03

RNASEQ.CLUSTER_CONSENHIER
pv=4.4e-06

Retropective.Tissue.Collection
pv=1.4e-04

Prospective.Tissue.Collection
pv=1.4e-04

MUTATIONSUBTYPES
pv=5.7e-04

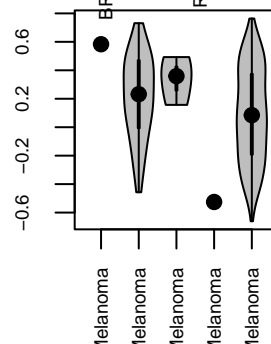
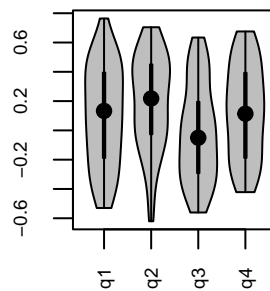
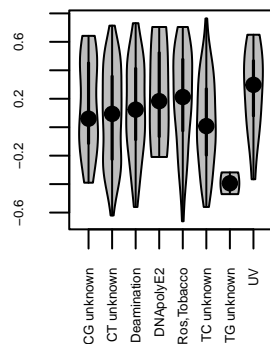
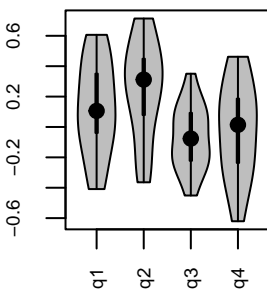


Days.to.third.new.tumor.event.after.initial.tre
pv=1.2e-03

third.prominent.montif
pv=2.5e-03

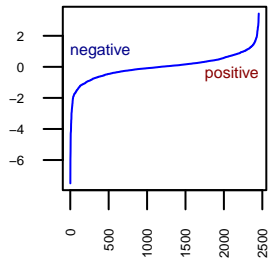
Days.to.first.new.tumor.event.after.initial.tre
pv=2.5e-03

Cancer.Type.Detailed
pv=3.2e-03



Component # 2 (stability = 0.826)

Metagene (involvement of features)



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

Term	FDR
transcription by RNA polymerase II	8.46e-09
negative regulation of cellular macromol...	1.38e-03
positive regulation of transcription, DN...	2.28e-03
negative regulation of neuron differenti...	3.57e-02
anterior/posterior pattern specification	3.80e-02
branching involved in prostate gland mor...	4.44e-02
neuron fate commitment	4.48e-02

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

GO:CC neg : 3 terms(FDR<0.1)

Term	FDR
chromatin	2.77e-10
nucleus	1.67e-03
transcription regulator complex	3.50e-03

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

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

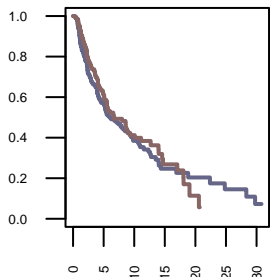
Term	FDR
DNA-binding transcription factor activit...	4.42e-13
cis-regulatory region sequence-specific ...	5.89e-12
RNA polymerase II transcription regulato...	5.89e-12

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

45 negative 28 positive

- | | |
|----------|-----------|
| HOXB13 | KLHL34 |
| HOXC12 | POLC2L |
| HOXC11 | DPP6 |
| HOXC13 | PPP1R3C |
| HOTAIR | PMP2 |
| GATA4 | SH2D4A |
| HOXB9 | COL2A1 |
| TLL6 | TSPYL5 |
| LHX1 | FSTL5 |
| ZNF536 | BMPR1B |
| HOXD13 | TRIM48 |
| HOXC10 | MUC7 |
| PRAC2 | RAMP1 |
| VAX1 | INSC |
| MAGEA4 | MAATS1 |
| IGF2BP1 | TFPI2 |
| LMX1B | COL11A1 |
| PITX2 | CTAG2 |
| HOXB8 | CA8 |
| MAGEA10 | HHATL |
| HOXA13 | MT1A |
| FOXD1 | MEST |
| KLHL13 | SYT6 |
| PAX9 | HSPB6 |
| OLIG2 | COBL |
| NR2E1 | HIST1H2AE |
| PKLR | LY6K |
| RTN4RL1 | DDIT4L |
| PCSK1N | |
| NRN1 | |
| MYO5B | |
| FREM1 | |
| HOXA11 | |
| ADRA2C | |
| DLX1 | |
| KLK6 | |
| CCNO | |
| ELSPBP1 | |
| FEZF1 | |
| VSTM2L | |
| GABRA3 | |
| OLIG1 | |
| PCDHA10 | |
| EFNB3 | |
| IL1RAPL1 | |

Cox regression:
logtest pv=5.4e-01
LHR=-0.19 (CI = -0.78, 0.41)



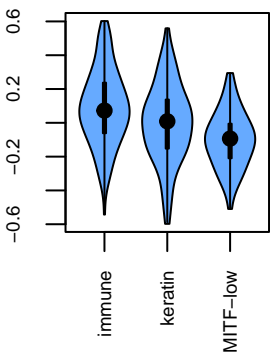
factor

- RNASEQ.CLUSTER_CONSENHIER
- TP53.stopgain
- second.prominent.motif
- Days.to.second.new.tumor.event.after.initial.treatment
- Tumor.tissue.site
- tumor_status_at_last_contact
- ARID2.splice.acceptor
- Tumor.location.site
- UV.signature
- MUTATIONSUBTYPES

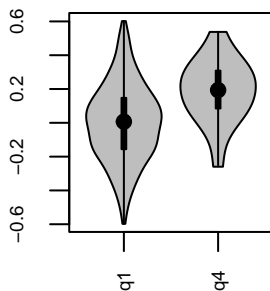
p.value

- 2.29e-08
- 6.01e-04
- 3.92e-03
- 6.33e-03
- 6.59e-03
- 8.23e-03
- 1.66e-02
- 1.81e-02
- 2.62e-02
- 2.68e-02

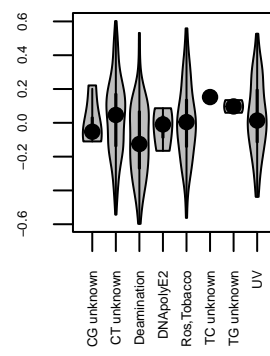
RNASEQ.CLUSTER_CONSENHIER
pv=2.3e-08



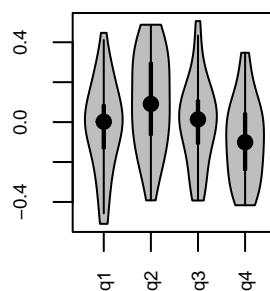
TP53.stopgain
pv=6.0e-04



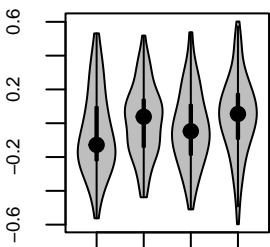
second.prominent.motif
pv=3.9e-03



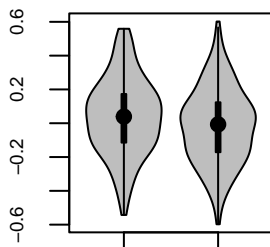
rs.to.second.new.tumor.event.after.initial.t
pv=6.3e-03



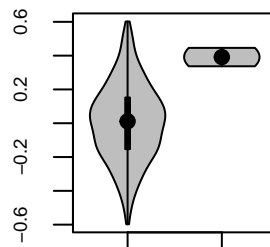
Tumor.tissue.site
pv=6.6e-03



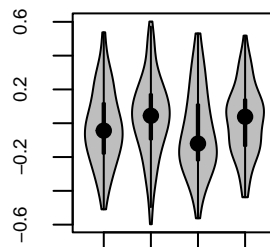
tumor_status_at_last_contact
pv=8.2e-03



ARID2.splice.acceptor
pv=1.7e-02

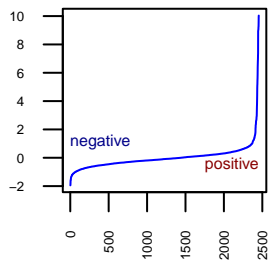


Tumor.location.site
pv=1.8e-02



Component # 3 (stability = 0.987)

Metagene (involvement of features)



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

GO:BP pos : 11 terms(FDR<0.1)

Term	FDR
B cell activation	6.85e-25
B cell receptor signaling pathway	1.05e-23
complement activation, classical pathway	2.12e-16
phagocytosis, engulfment	4.28e-15
phagocytosis, recognition	9.13e-15
Fc receptor mediated stimulatory signali...	1.74e-09
regulation of complement activation	8.01e-09
innate immune response	5.71e-08
defense response to bacterium	2.22e-06
Fc-epsilon receptor signaling pathway	5.42e-04
leukocyte migration	1.38e-02

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

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

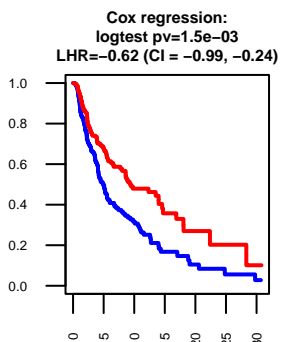
Term	FDR
immunoglobulin complex	8.11e-19
external side of plasma membrane	3.63e-09
blood microparticle	5.72e-07
extracellular exosome	1.60e-03

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

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

Term	FDR
immunoglobulin receptor binding	8.43e-20
antigen binding	1.40e-15

- 4 negative**
- MAGEC2
- MAG
- NPTX1
- PRSS33
- 55 positive**
- ANKRD36BP2
- CD79A
- FCRL5
- IGHA1
- IGHA2
- IGHG1
- IGHG2
- IGHG3
- IGHG4
- IGHGP
- IGHJ2
- IGHJ3
- IGHM
- IGJ
- IGKC
- IGLC2
- IGLC3
- IGLC6
- IGLC7
- IGLL5
- KIAA0125
- MZB1
- PNOC
- POU2AF1
- TNFRSF17
- CD19
- IGHD
- FCRL2
- SCNN1B
- NUGGC
- CR2
- IGHE
- TNFRSF13B
- DPEP1
- BHLHA15
- MS4A1
- FER1L4
- LAX1
- SMPDL3B
- CTAG2
- HSH2D
- PAX5
- ZBP1
- BLK
- FRZB
- FA2H
- CCL19
- PLA2G2D
- TBC1D27
- UGT3A2
- PRSS16
- SSX1
- FCRL1
- MAGEA4
- SLAMF7



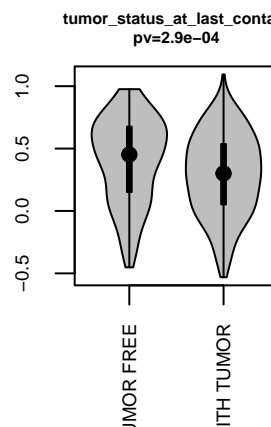
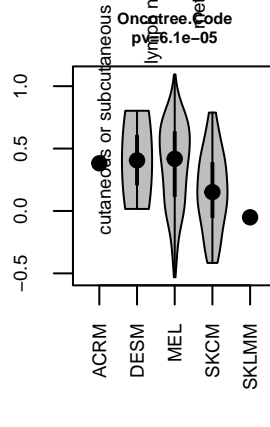
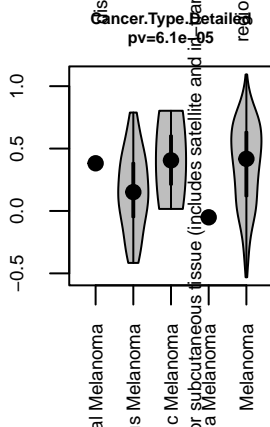
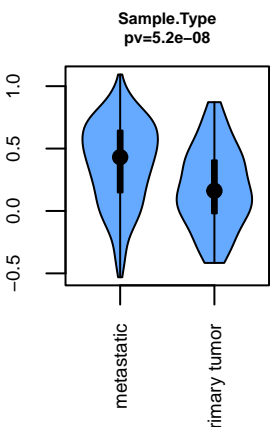
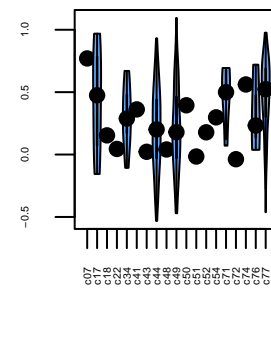
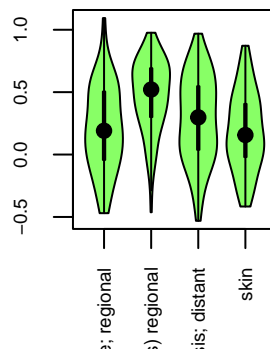
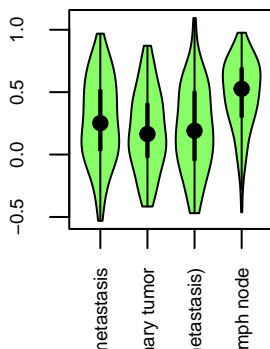
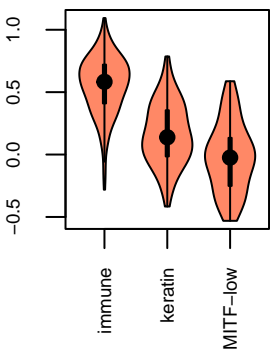
factor	p.value
RNASEQ.CLUSTER_CONSENHIER	1.28e-48
Tumor.tissue.site	5.76e-17
Tumor.location.site	1.29e-16
ICD.10.TopLevel	4.20e-10
Sample.Type	5.18e-08
Cancer.Type.Detailed	6.05e-05
Oncotree.Code	6.05e-05
tumor_status_at_last_contact	2.88e-04
Postoperative.Radio.Therapie	1.36e-03
Adjuvant.Postoperative.Pharmaceutical.Therapy.Administered.Indicator	1.46e-03

RNASEQ.CLUSTER_CONSENHIER
pv=1.3e-48

Tumor.tissue.site
pv=5.8e-17

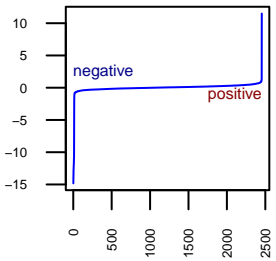
Tumor.location.site
pv=1.3e-16

ICD.10.TopLevel
pv=4.2e-10



Component # 4 (stability = 0.988)

Metagene (involvement of features)



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

Term
cornification

FDR
9.51e-02

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

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

Term
keratin filament

FDR
6.58e-02

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

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

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

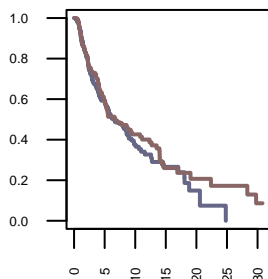
16
negative

DDX3Y
EIF1AY
KDM5D
PRKY
RPS4Y1
TTY15
TXLNGY
USP9Y
UTY
ZFY
NLGN4Y
GYG2P1
DDX43
KRT13
KRT6A
SPRR3

7
positive

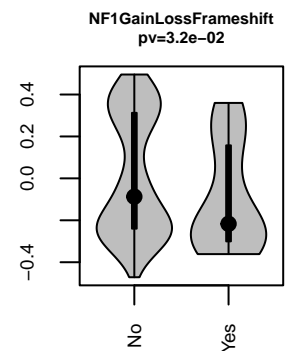
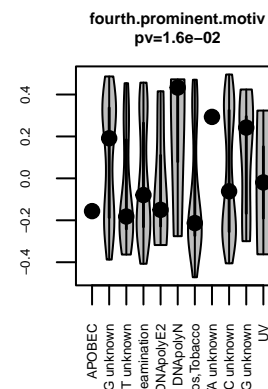
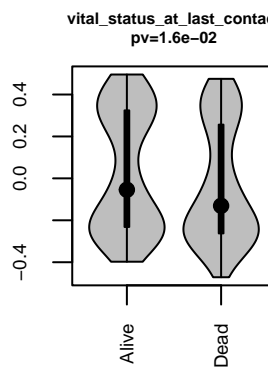
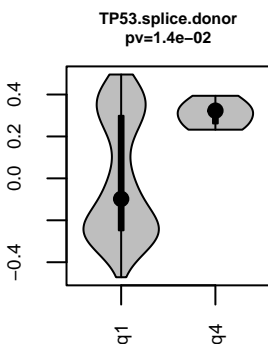
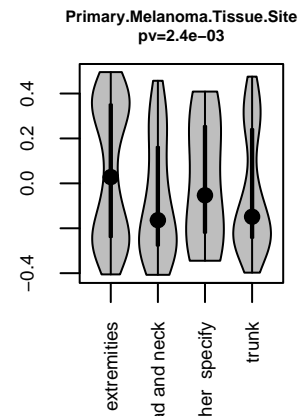
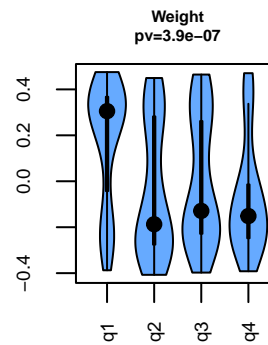
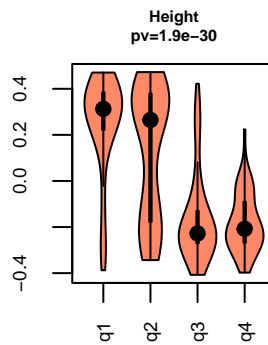
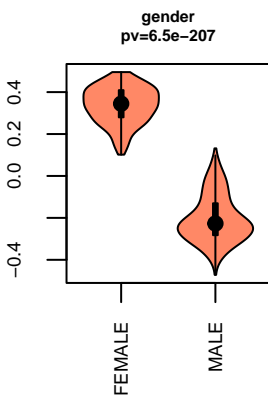
XIST
PAGE2
PPP1R3C
HERC2P3
NLRP2
PCSK2
PDLIM4

Cox regression:
logtest pv=4.9e-02
LHR=-0.47 (CI = -0.95, 0.00)



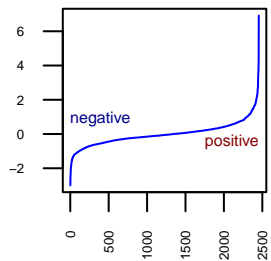
factor
gender
Height
Weight
Primary.Melanoma.Tissue.Site
TP53.splice.donor
vital_status_at_last_contact
fourth.prominent.motiv
NF1GainLossFrameshift
NF1.stopgain
Year.of.last.contact

p.value
6.48e-207
1.89e-30
3.86e-07
2.40e-03
1.39e-02
1.60e-02
1.61e-02
3.22e-02
3.26e-02
3.69e-02



Component # 5 (stability = 0.605)

Metagene (involvement of features)



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 : 1 terms(FDR<0.1)

Term
fibrillar collagen trimer

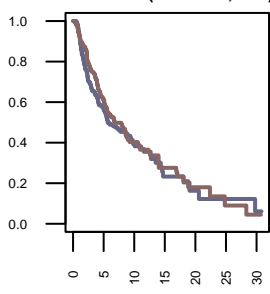
FDR
8.78e-02

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

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

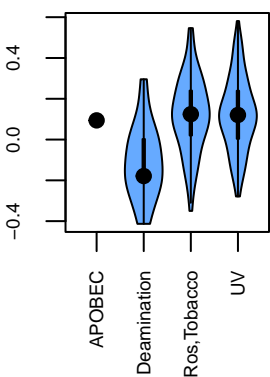
- | | |
|--|--|
| <p>19 negative</p> <ul style="list-style-type: none"> RTN4RL1 HOXB13 KIT ITLN2 ASB11 SLC6A17 KLC3 CCNO SYNPR KLHL13 HTN1 PDE3A FOXO6 VSTM2L CRTAC1 RASL10B TMEM215 PRRT4 LRR4C4B | <p>73 positive</p> <ul style="list-style-type: none"> COL9A1 FRG2DP PMP2 TRIM48 GRIK2 ITIH6 INSC FSTL5 COL19A1 TRIM51CP MUC7 SCRG1 FREM2 HCCAT5 RLBP1 TRIM51 KCNN2 TMEM171 UGT2B7 SLC35F1 MPZ NR0B1 LCE2A SERPINA5 CNDP1 SLITRK6 CA8 SLC5A4 UNC80 NLGN1 DCT PRDM7 S100B CHADL SUSD5 CMTM5 ATP6V0A4 NRG3 RGR APOD SYT6 FOLH1 SOX2 TCN1 UGT8 BMPR1B MMP16 DNAH9 SLAMF9 GABRB3 COL2A1 LRRTM1 RXRG DLGAP1 CST1 SLITRK5 MYPN SERPINA3 ANO3 B3GALT1 BAI3 POU3F2 HAPLN1 SOX8 ENTHD1 NRXN3 ATP10B ENPP2 MRGPRX4 ADAM23 COL11A1 TMEM132D GJB1 |
|--|--|

Cox regression:
logtest pv=1.0e-01
LHR=-0.64 (CI = -1.41, 0.12)

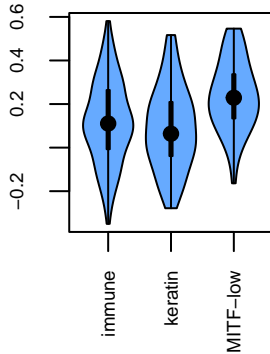


- | factor | p.value |
|---|----------|
| most.prominent.motif | 4.99e-07 |
| RNASEQ.CLUSTER_CONSENHIER | 2.57e-06 |
| UV.signature | 3.33e-05 |
| Primary.Melanoma.Tissue.Site | 6.00e-05 |
| MUTATIONSUBTYPES | 2.74e-04 |
| ICD.10.TopLevel | 5.93e-03 |
| Retropective.Tissue.Collection | 9.19e-03 |
| Prospective.Tissue.Collection | 9.19e-03 |
| Days.to.first.new.tumor.event.after.initial.treatment | 2.26e-02 |
| third.prominent.motif | 2.49e-02 |

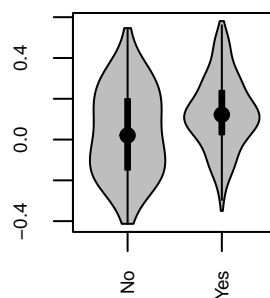
most.prominent.motif
pv=5.0e-07



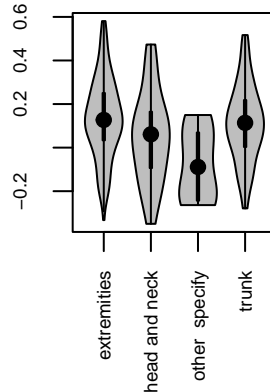
RNASEQ.CLUSTER_CONSENHIER
pv=2.6e-06



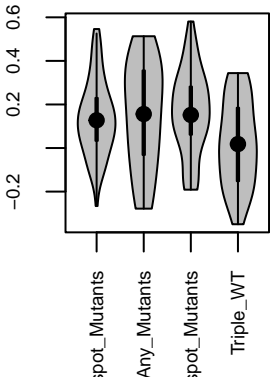
UV.signature
pv=3.3e-05



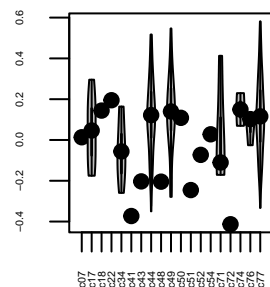
Primary.Melanoma.Tissue.Site
pv=6.0e-05



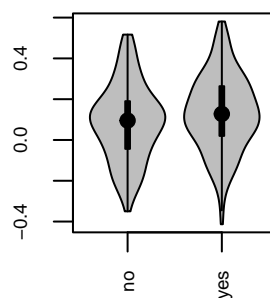
MUTATIONSUBTYPES
pv=2.7e-04



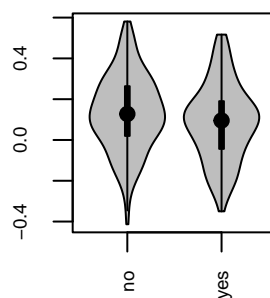
ICD.10.TopLevel
pv=5.9e-03



Retropective.Tissue.Collection
pv=9.2e-03

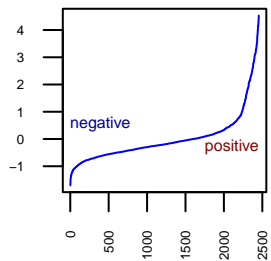


Prospective.Tissue.Collection
pv=9.2e-03



Component # 6 (stability = 0.954)

Metagene (involvement of features)



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

GO:BP pos : 43 terms(FDR<0.1)

Term	FDR
adaptive immune response	3.04e-20
T cell receptor signaling pathway	7.61e-17
positive regulation of T cell activation	1.78e-12
defense response to virus	1.19e-07
immune response	1.37e-07
cytokine-mediated signaling pathway	1.38e-07
T cell selection	2.17e-07
interferon-gamma production	4.28e-07
positive regulation of lymphocyte prolifer...	2.85e-06
regulation of lymphocyte differentiation	3.80e-06
regulation of antigen receptor-mediated ...	7.87e-06
defense response	9.51e-06
positive regulation of innate immune res...	3.44e-05
leukocyte activation	1.90e-04
negative regulation of T cell activation	1.90e-04
regulation of interleukin-2 production	1.90e-04
regulation of interleukin-12 production	2.07e-04
biological process involved in interspec...	5.81e-04
response to tumor necrosis factor	7.51e-04
lymphocyte migration	1.05e-03

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

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

Term	FDR
T cell receptor complex	1.05e-13
external side of plasma membrane	5.25e-11
immunological synapse	6.04e-10

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

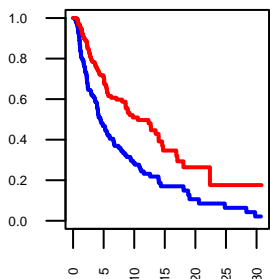
GO:MF pos : 9 terms(FDR<0.1)

Term	FDR
C-C chemokine receptor activity	5.22e-04
C-C chemokine binding	1.10e-03
MHC protein binding	1.40e-02
SH2 domain binding	1.40e-02
CXCR3 chemokine receptor binding	2.29e-02
tumor necrosis factor receptor binding	2.94e-02
pattern recognition receptor activity	5.52e-02
chemokine activity	5.52e-02
G protein-coupled purinergic nucleotide ...	5.80e-02

0 negative 186 positive

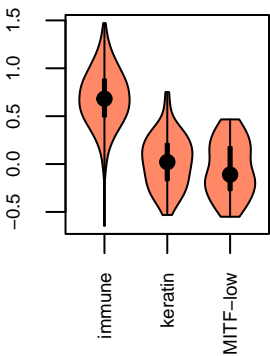
- CD8A
- CD8B
- CXCL10
- CXCL11
- CXCL9
- CXCR2P1
- FASLG
- GBP1P1
- GBP5
- GZMA
- GZMH
- GZMK
- IDO1
- IFNG
- JAKMIP1
- LAG3
- LGALS17A
- NGK7
- PDCD1
- PRF1
- SIRPG
- UBD
- OR211P
- TIGIT
- CCL5
- TRGC2
- CXCL13
- TNFRSF9
- PLA2G2D
- CD2
- GBP4
- GBP1
- CXCR3
- ANKRD22
- CXCR6
- CTSW
- ZBED2
- GZMB
- CCR5
- CD3D
- SH2D1A
- CRTAM
- ETV7
- CD7
- THEMIS
- TBX21
- TRBC2
- FAM26F
- CD3G
- SLA2
- GPR171
- CST7
- KLRD1
- CD3E
- TMEM155
- IKZF3
- UBASH3A
- DTHD1
- TRBV28
- TRAT1
- LCK
- TNIP3
- ZNF683
- TRAC
- ICOS
- SLAMF6
- FCRL3
- SIT1
- ITGAL
- RARRS3
- GPR174
- PYHIN1
- SAMD3
- XIRP1
- TIFAB
- CLEC4E
- TLR8
- CD27
- CCL8
- CD247
- ZNF831
- CD96

Cox regression:
logtest pv=6.3e-08
LHR=-0.79 (CI = -1.08, -0.50)

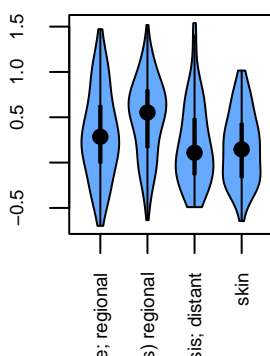


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	2.05e-64
Tumor.location.site	3.72e-10
Tumor.tissue.site	9.64e-10
last_contact_days_to	1.67e-06
Sample.Type	3.18e-06
vital_status_at_last_contact	3.80e-06
ICD.10.TopLevel	6.35e-06
tumor_status_at_last_contact	1.66e-05
Oncotree.Code	1.86e-04
Cancer.Type.Detailed	1.86e-04

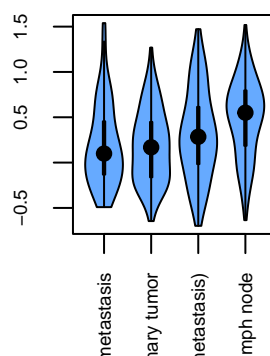
RNASEQ.CLUSTER_CONSENHIER
pv=2.0e-64



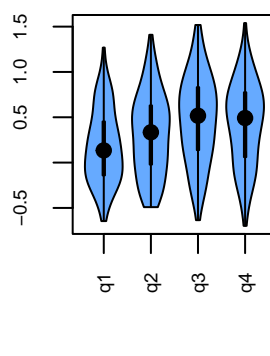
Tumor.location.site
pv=3.7e-10



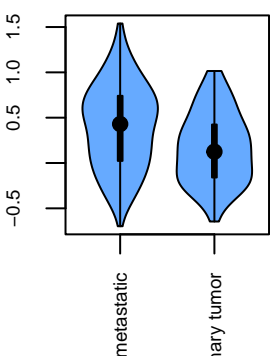
Tumor.tissue.site
pv=9.6e-10



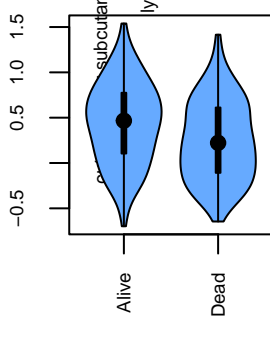
last_contact_days_to
pv=1.7e-06



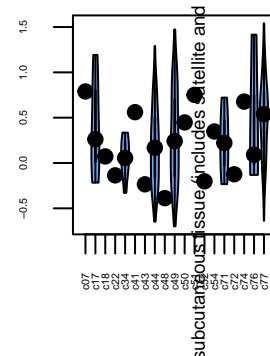
Sample.Type
pv=3.2e-06



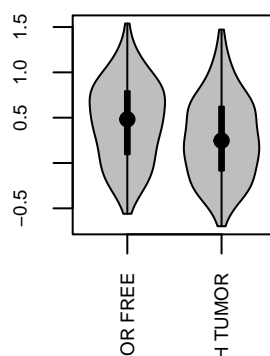
vital_status_at_last_contact
pv=3.8e-06



ICD.10.TopLevel
pv=6.3e-06

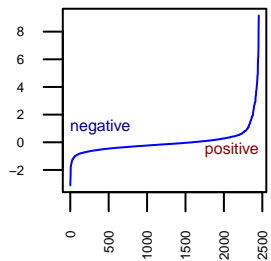


tumor_status_at_last_contact
pv=1.7e-05



Component # 7 (stability = 0.985)

Metagene (involvement of features)



GO:BP neg : 9 terms(FDR<0.1)

Term	FDR
keratinization	1.33e-04
intermembrane lipid transfer	9.83e-03
blood coagulation, fibrin clot formation	9.83e-03
post-translational protein modification	1.40e-02
chylomicron assembly	2.28e-02
chylomicron remodeling	3.57e-02
high-density lipoprotein particle remode...	3.57e-02
positive regulation of substrate adhesio...	3.57e-02
cholesterol metabolic process	4.01e-02

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

Term	FDR
cornification	9.51e-28
peptide cross-linking	2.52e-06
antimicrobial humoral response	7.29e-03
epidermis development	5.71e-02
negative regulation of endopeptidase act...	9.51e-02

GO:CC neg : 11 terms(FDR<0.1)

Term	FDR
endoplasmic reticulum lumen	8.59e-05
blood microparticle	4.15e-04
secretory granule lumen	1.49e-03
chylomicron	1.89e-03
very-low-density lipoprotein particle	1.89e-03
high-density lipoprotein particle	5.41e-03
endocytic vesicle lumen	7.36e-03
extracellular exosome	1.67e-02
low-density lipoprotein particle	2.69e-02
intermediate-density lipoprotein particl...	2.69e-02

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

Term	FDR
cornified envelope	2.58e-16
extracellular space	2.38e-09
intermediate filament cytoskeleton	2.86e-08
cytosol	4.53e-05
desmosome	4.20e-04

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

Term	FDR
cholesterol transfer activity	5.62e-03

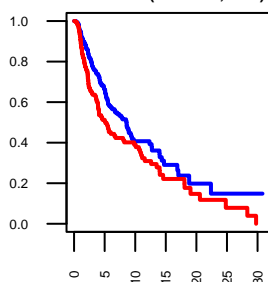
GO:MF pos : 2 terms(FDR<0.1)

Term	FDR
structural molecule activity	1.26e-03
serine-type endopeptidase inhibitor acti...	5.12e-02

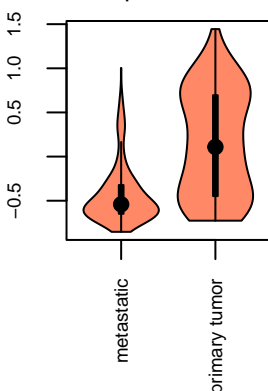
18 negative 132 positive

- ALB
- FGA
- APOB
- FGG
- APOA2
- HP
- GATA4
- PCK1
- ARG1
- DLK1
- APOA1
- LOR
- LCE1B
- COL22A1
- LCE1F
- LCE1A
- LCE1C
- SERPINA12
- A2ML1
- BPIFB1
- CALML3
- CEACAM5
- CEACAM6
- CLCA4
- CRNN
- DSC3
- DSG3
- FAM83A
- FGFBP1
- IVL
- KRT13
- KRT14
- KRT16
- KRT17
- KRT19
- KRT4
- KRT5
- KRT6A
- KRT6B
- KRT6C
- KRT78
- LY6D
- MUC21
- PI3
- PKP1
- S100A14
- S100A7
- SERPINB13
- SERPINB3
- SERPINB5
- SFN
- SPRR1A
- SPRR1B
- SPRR2A
- SPRR2D
- SPRR2E
- SPRR2F
- SPRR3
- TGM3
- TMPRSS11D
- TRIM29
- TMPRSS4
- RHCG
- SERPINB4
- SLPI
- GBP6
- DSG1
- KLK12
- KLK13
- CLCA2
- SPRR2G
- GJB6
- TMPRSS11E
- KRT15
- STATH
- SBSN
- KLK11
- LCN2
- COL17A1
- C10orf99
- KLK10
- SCEL
- RAB25
- FAM83C
- SPRR2B
- EVPL
- TACSTD2
- KLK7
- CXCL17
- MIR205HG
- AGR2
- KRTDAP
- CALML5
- SPINK5
- ZNF750
- ELF3
- TNS4
- PIGR
- PITX1
- ANXA8

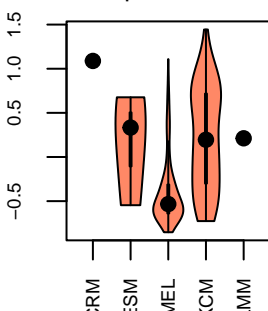
Cox regression:
logtest pv=2.5e-06
LHR=0.79 (CI = 0.48, 1.09)



Sample.Type
pv=1.5e-33



Oncotree.Code
pv=1.1e-26



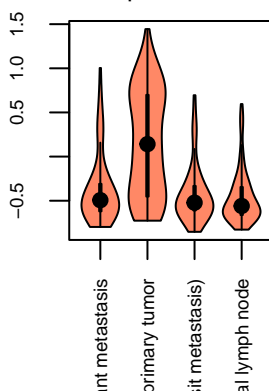
factor

- Sample.Type
- Tumor.tissue.site
- Tumor.location.site
- Cancer.Type.Detailed
- Oncotree.Code
- RNASEQ.CLUSTER_CONSENHIER
- Sample.country
- New.tumor.event.after.initial.treatment
- ICD.10.TopLevel
- Breslow.Depth

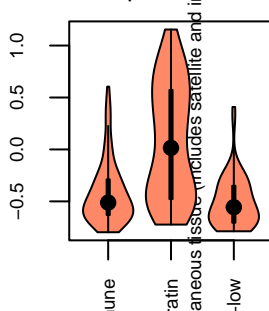
p.value

- 1.49e-33
- 1.73e-32
- 3.14e-32
- 1.15e-26
- 1.15e-26
- 4.44e-24
- 1.45e-20
- 3.08e-17
- 2.25e-15
- 5.60e-13

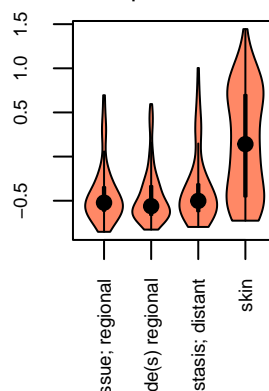
Tumor.tissue.site
pv=1.7e-32



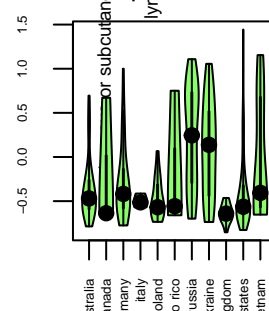
RNASEQ.CLUSTER_CONSENHIER
pv=4.4e-24



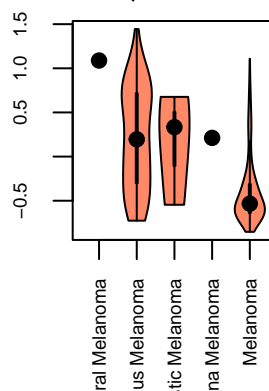
Tumor.location.site
pv=3.1e-32



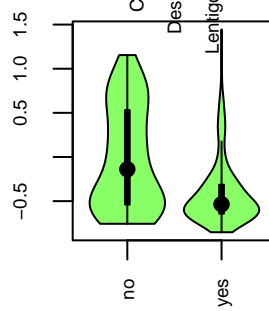
Sample.country
pv=1.4e-20



Cancer.Type.Detailed
pv=1.1e-26

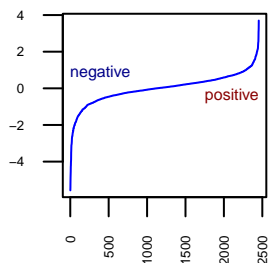


New.tumor.event.after.initial.treatment
pv=3.8e-15



Component # 8 (stability = 0.812)

Metagene (involvement of features)



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)

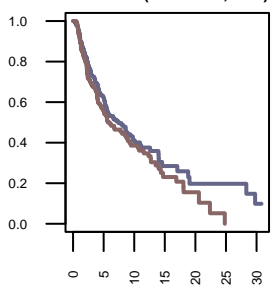
GO:MF neg : 0 terms(FDR<0.1)

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

61 negative **21 positive**

- | | |
|----------|----------|
| TMEM163 | ABCB5 |
| APCDD1 | HTN1 |
| PKHD1 | MEGF10 |
| SP5 | PRSS33 |
| ADCY2 | HHATL |
| GABRG3 | IP6K3 |
| PRSS56 | MRGPRX3 |
| LPPR4 | SEMA3E |
| SLC24A4 | ANKRD30B |
| NOTUM | KCNQ5 |
| GAD1 | CLDN1 |
| EDN3 | CITED1 |
| DNAH9 | COL4A5 |
| SLC7A11 | MTRNR2L1 |
| TFAP2B | TTR |
| BMP7 | MET |
| MNX1 | IL13RA2 |
| TCERG1L | HTN3 |
| GLB1L3 | ITGB8 |
| CTNNA2 | UGT2B7 |
| FAM189A1 | NOX5 |
| TRIM48 | |
| TRIM51CP | |
| HS3ST2 | |
| CDK15 | |
| GPR64 | |
| CYP1A1 | |
| ZIC2 | |
| PART1 | |
| RSP04 | |
| SCUBE2 | |
| DRAXIN | |
| WDR63 | |
| CACNG4 | |
| PPP1R14C | |
| SFRP5 | |
| FREM2 | |
| MCHR1 | |
| VIT | |
| LRP2 | |
| CHIT1 | |
| CST5 | |
| NPPC | |
| GFRA3 | |
| RASEF | |
| TMEM158 | |
| CTTNBP2 | |
| FIBCD1 | |
| NRXN3 | |
| KIT | |
| ISM1 | |
| CSPG5 | |
| DAPL1 | |
| NAT8L | |
| LINGO1 | |
| EPHA4 | |
| SV2C | |
| CCL18 | |
| BEAN1 | |
| KLF14 | |
| HAP1 | |

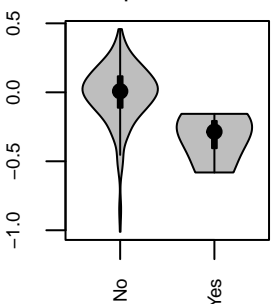
Cox regression:
logtest pv=4.9e-01
LHR=0.22 (CI = -0.42, 0.87)



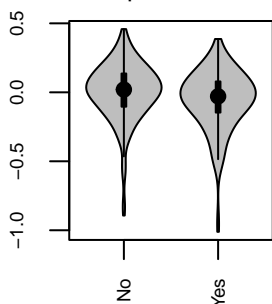
- factor
- KRASQ61.
 - BRAFV600.
 - third.prominent.motif
 - Neoadjuvant.Treatment
 - Distant.Metastasis.Anatomic.Site
 - Primary.Melanoma.Tissue.Site
 - fifth.prominent.motif
 - Primary.Neoplasm.Melanome.Diagnosis
 - Height
 - MUTATIONSUBTYPES

- p.value
- 3.12e-03
 - 3.70e-03
 - 2.42e-02
 - 3.65e-02
 - 3.72e-02
 - 4.25e-02
 - 4.58e-02
 - 5.71e-02
 - 5.96e-02
 - 6.09e-02

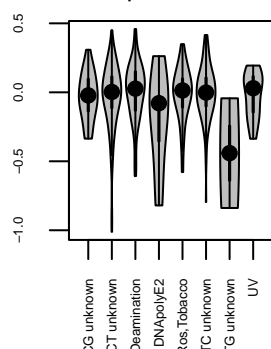
KRASQ61.
pv=3.1e-03



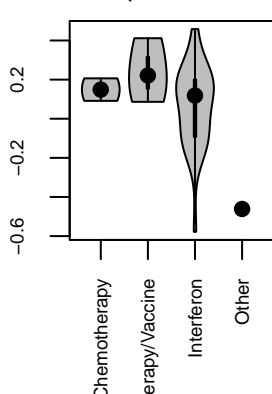
BRAFV600.
pv=3.7e-03



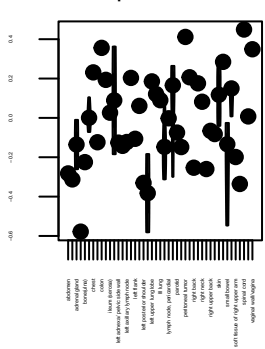
third.prominent.motif
pv=2.4e-02



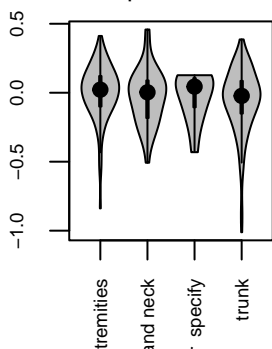
Neoadjuvant.Treatment
pv=3.7e-02



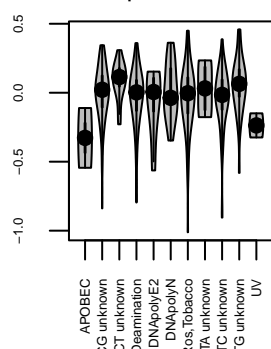
Distant.Metastasis.Anatomic.Site
pv=3.7e-02



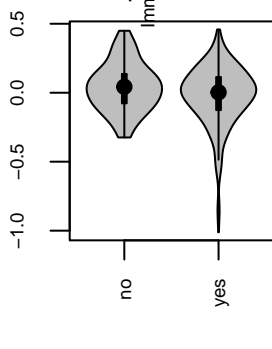
Primary.Melanoma.Tissue.Site
pv=4.3e-02



fifth.prominent.motif
pv=4.6e-02

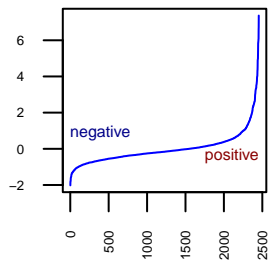


Primary.Neoplasm.Melanome.Diagnosis
pv=5.7e-02



Component # 9 (stability = 0.979)

Metagene (involvement of features)



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

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

Term
extracellular matrix organization

FDR
1.81e-04

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

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

Term
extracellular matrix
extracellular region

FDR
5.34e-13
1.62e-07

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

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

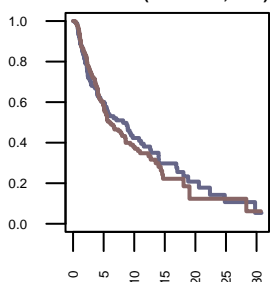
Term
extracellular matrix structural constitu...

FDR
3.81e-08

2 negative 128 positive

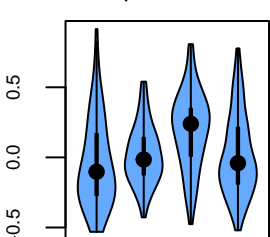
- MT3
- ESPN
- ADIPOQ
- CILP
- COL11A1
- COMP
- CXCL14
- EPYC
- FABP4
- LRRC15
- MFAP5
- MMP13
- OGN
- OMD
- PH16
- PLA2G2A
- SFRP2
- SFRP4
- SPON1
- WISP2
- WNT2
- DPT
- ITGBL1
- PLIN4
- ASPN
- COL10A1
- HTRA3
- TUSC5
- PRG4
- CCL11
- ACKR1
- XPNPEP2
- FNDC1
- PLIN1
- HAS1
- SYNDIG1
- ELN
- FIBIN
- CD300LG
- MMP3
- SELE
- CPA3
- AGTR1
- RBP4
- WT1
- SCARA5
- TPSAB1
- PRND
- FMO1
- ADH1B
- TPSB2
- WBSCR17
- DES
- MFAP4
- ACTC1
- MEG3
- GPD1
- SAA1
- SELP
- PTPRD
- PTGFR
- C3
- GDF10
- KCND2
- MMP7
- CIDEA
- ABI3BP
- STMN2
- PAX1
- SLITRK4
- THBS4
- ST6GAL2
- IBSP
- MXRA5Y
- PENK
- HMCN2
- TWIST2
- CTSG
- LEP
- OSR1
- CES1
- COL8A1
- PCK1
- CPN2

Cox regression:
logtest pv=9.9e-01
LHR=0.00 (CI = -0.44, 0.44)

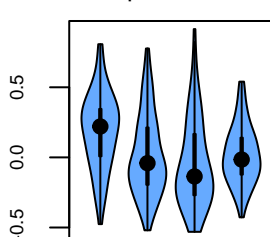


- | factor | p.value |
|-------------------------------------|----------|
| Tumor.tissue.site | 5.77e-07 |
| Tumor.location.site | 6.15e-07 |
| ICD.10.TopLevel | 1.41e-03 |
| RNASEQ.CLUSTER_CONSENHIER | 2.05e-03 |
| Second.new.neoplasm.event.type | 2.91e-02 |
| Prior.Cancer.Diagnosis.Occurrence | 3.21e-02 |
| PTEN.splice.donor | 4.44e-02 |
| Disease.Free.Status.at.last.contact | 5.72e-02 |
| fourth.prominent.motiv | 6.29e-02 |
| CDKN2A.splice.acceptor | 7.19e-02 |

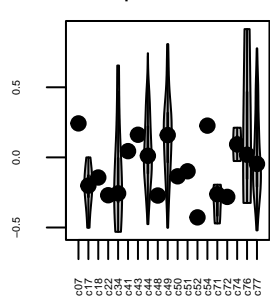
Tumor.tissue.site
pv=5.8e-07



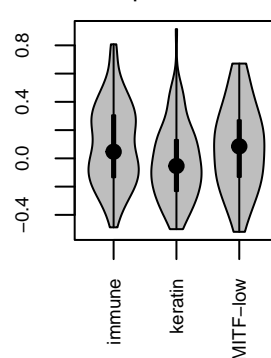
Tumor.location.site
pv=6.1e-07



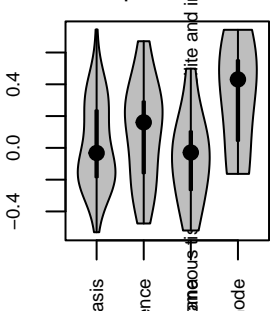
ICD.10.TopLevel
pv=1.4e-03



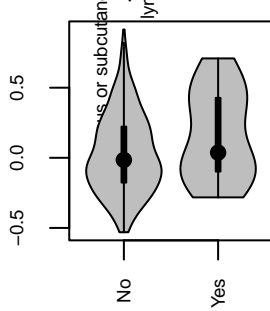
RNASEQ.CLUSTER_CONSENHIER
pv=2.1e-03



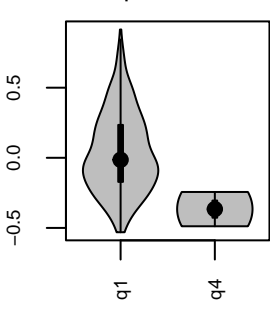
Second.new.neoplasm.event.type
pv=2.9e-02



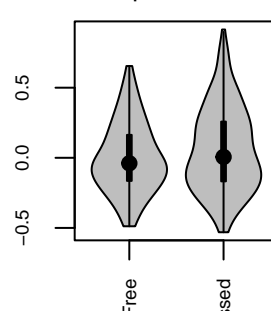
Prior.Cancer.Diagnosis.Occurrence
pv=3.2e-02



PTEN.splice.donor
pv=4.4e-02

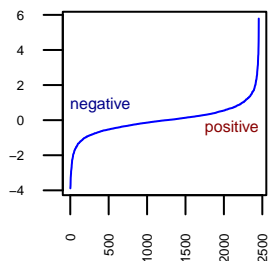


Disease.Free.Status.at.last.contact
pv=5.7e-02



Component # 10 (stability = 0.864)

Metagene (involvement of features)



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

Term
 homophilic cell adhesion via plasma memb...
 calcium-dependent cell-cell adhesion via...

FDR
 2.28e-03
 1.19e-02

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)

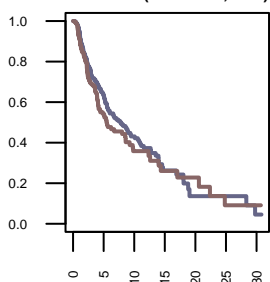
GO:MF pos : 0 terms(FDR<0.1)

36 negative **43 positive**

- PCDHB5
- PCDHB2
- PCDHB16
- PCDHB8
- MCHR1
- MAT1A
- CMTM5
- ABCA8
- MAGEC2
- ITGA10
- CTTNBP2
- PTCHD4
- PCDHA11
- LRRTM4
- ASB4
- EDA2R
- PCDHB11
- FGF2
- PCDHB3
- IGF2BP1
- PCDHA10
- CHRNA6
- SLC22A17
- SEMA3E
- PCDHA3
- FAM133A
- PPP1R3C
- CES3
- SPEF2
- HOGA1
- C16orf89
- CMBL
- GRIP1
- AGMO
- MAB21L1
- HHATL

- NEFH
- SOX2
- KCNS1
- RFPL1S
- OPRD1
- MAP7D2
- SMC1B
- TTC39A
- TDRD9
- SULT4A1
- TKTL1
- RNF212
- SOX1
- FAM178B
- DPP10
- NEURL1
- ISL1
- CTAG2
- POMC
- TCAM1P
- INA
- LPAR3
- MAPK15
- DLX6
- GCK
- HORMAD1
- NELL1
- CACNA1B
- DDX25
- EYA1
- MAGEA4
- DCAF12L1
- DLL3
- HRASLS
- TMEM171
- LY6K
- TDRD12
- PNLDC1
- BMP8B
- GBX2
- GJA3
- NEFM
- CST2

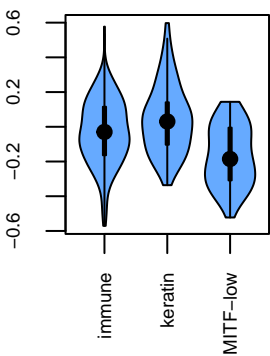
Cox regression:
 logtest pv=1.2e-01
 LHR=0.53 (CI = -0.13, 1.19)



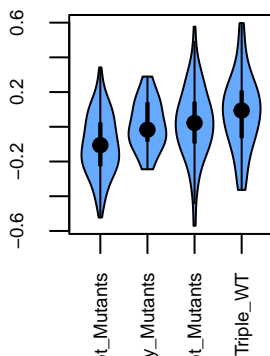
factor
 RNASEQ.CLUSTER_CONSENHIER
 MUTATIONSUBTYPES
 BRAFV600.
 UV.signature
 initial_pathologic_dx_year
 last_contact_days_to
 Clark.Level
 fourth.prominent.motiv
 tumor_status_at_last_contact
 most.prominent.motiv

p.value
 1.82e-10
 6.08e-10
 3.34e-06
 4.16e-05
 4.05e-04
 1.11e-03
 1.52e-03
 2.16e-03
 2.43e-03
 5.13e-03

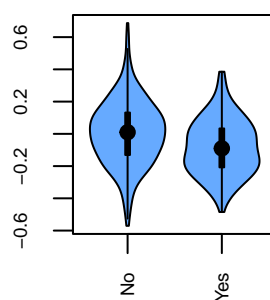
RNASEQ.CLUSTER_CONSENHIER
 pv=1.8e-10



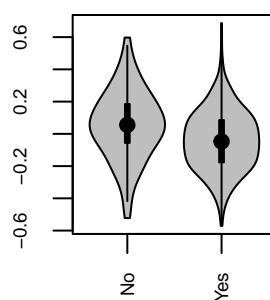
MUTATIONSUBTYPES
 pv=6.1e-10



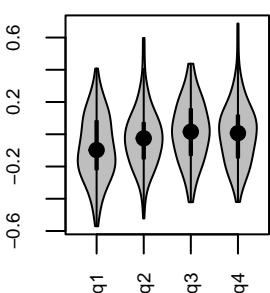
BRAFV600.
 pv=3.3e-06



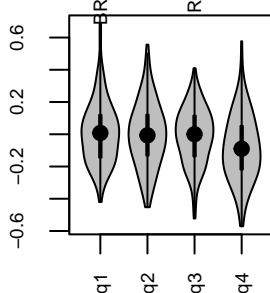
UV.signature
 pv=4.2e-05



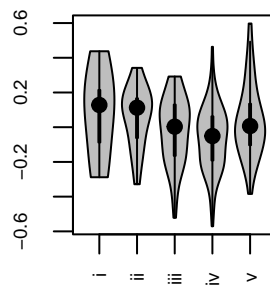
initial_pathologic_dx_year
 pv=4.0e-04



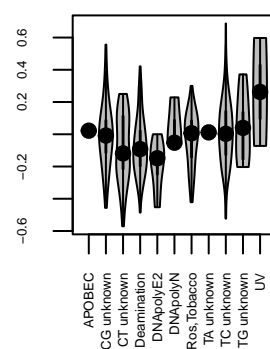
last_contact_days_to
 pv=1.1e-03



Clark.Level
 pv=1.5e-03

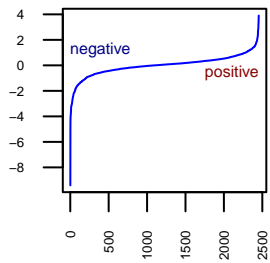


fourth.prominent.motiv
 pv=2.2e-03



Component # 11 (stability = 0.847)

Metagene (involvement of features)



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

Term
pigment biosynthetic process

FDR
1.14e-05

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

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

Term
melanosome

FDR
2.19e-07

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

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

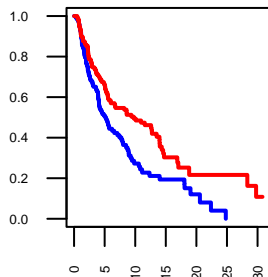
GO:MF pos : 0 terms(FDR<0.1)

81
negative

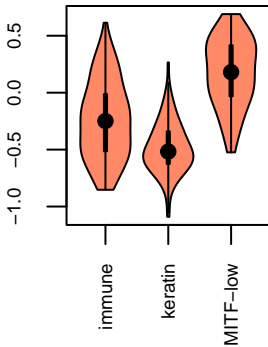
31
positive

- | | |
|----------|----------|
| TYRP1 | OLIG2 |
| TRPM1 | SFRP1 |
| PMEL | ANO4 |
| OCA2 | ITIH6 |
| VEPH1 | OLIG1 |
| ABCB5 | ITGA10 |
| CHST9 | HAPLN1 |
| SLC45A2 | ALDH1A3 |
| MLIP | TFAP2C |
| FAM69C | LOXL4 |
| OR7A5 | MMP16 |
| TSPAN10 | GDNF |
| IP6K3 | NELL1 |
| TRIM63 | ITGB3 |
| SYNPR | DMRTA1 |
| PKLR | SALL1 |
| KCNJ13 | PHKA1 |
| DCT | FAM19A5 |
| CDH3 | CA6 |
| PRDM7 | NPTX2 |
| KCNN2 | PPP1R9A |
| QPCT | RNF175 |
| CTNNA2 | LOXL3 |
| SLC5A10 | GAPDHP14 |
| OR7C1 | SERPINA3 |
| BCAN | TRPM8 |
| SLC24A4 | CNTNAP3 |
| ROBO2 | BAALC |
| MLANA | TSPAN7 |
| EPHA5 | SHISA2 |
| FSTL4 | PLCB4 |
| NOV | |
| GPR143 | |
| CDK15 | |
| SLC24A5 | |
| CFAP61 | |
| KCNU1 | |
| ASPA | |
| NTNG1 | |
| FSTL5 | |
| CDH1 | |
| TYR | |
| MME | |
| MDGA2 | |
| CA14 | |
| SULT1C2 | |
| WISP2 | |
| GPM6A | |
| GABRG3 | |
| SLC7A4 | |
| SLC16A6 | |
| TUBB4A | |
| APCDD1 | |
| PCSK9 | |
| C15orf59 | |
| GMPR | |
| MET | |
| GALNTL6 | |
| LRRTM1 | |
| MLPH | |
| SP5 | |
| AQP4 | |
| RPH3A | |
| ABCC2 | |
| PRRT4 | |
| PNLIPRP3 | |
| PKHD1 | |
| PAEP | |
| ADAM23 | |
| PDE3A | |
| ACCSL | |
| AFF3 | |
| CA8 | |
| SLC38A8 | |
| TMPRSS13 | |
| ITIH3 | |
| LPPR4 | |
| PART1 | |
| CTSK | |
| PRSS56 | |
| RAB3C | |

Cox regression:
logtest pv=1.2e-05
LHR=-0.83 (CI = -1.21, -0.45)



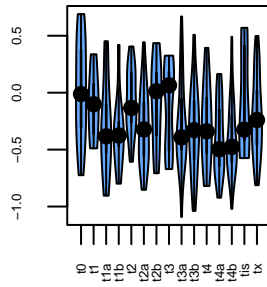
RNASEQ.CLUSTER_CONSENHIER
pv=2.4e-31



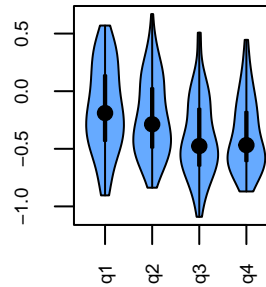
- factor
- RNASEQ.CLUSTER_CONSENHIER
 - Cancer.stage.T
 - Breslow.Depth
 - ajcc_pathologic_tumor_stage
 - initial_pathologic_dx_year
 - MUTATIONSUBTYPES
 - birth_days_to_initial_diagnosis
 - age_at_initial_pathologic_diagnosis
 - last_contact_days_to
 - Sample.Type

- p.value
- 2.41e-31
 - 1.59e-07
 - 3.72e-07
 - 4.89e-07
 - 2.85e-06
 - 7.04e-06
 - 1.37e-05
 - 1.47e-05
 - 1.63e-05
 - 1.80e-05

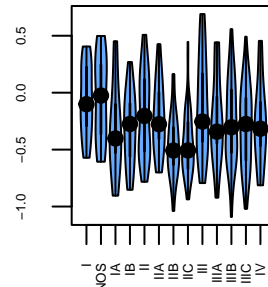
Cancer.stage.T
pv=1.6e-07



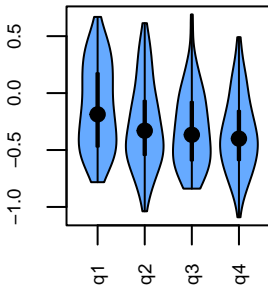
Breslow.Depth
pv=3.7e-07



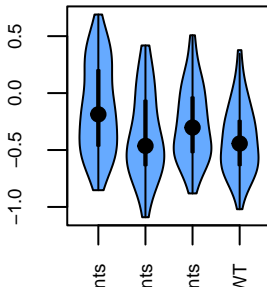
ajcc_pathologic_tumor_stage
pv=4.9e-07



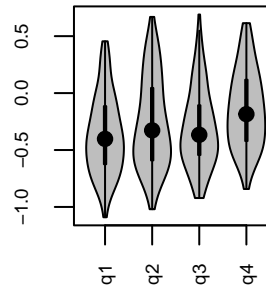
initial_pathologic_dx_year
pv=2.8e-06



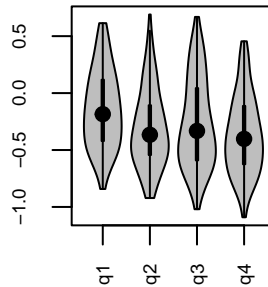
MUTATIONSUBTYPES
pv=7.0e-06



birth_days_to_initial_diagnosis
pv=1.4e-05

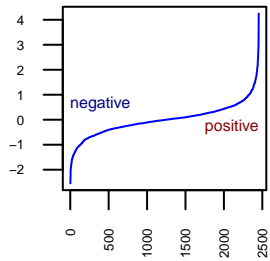


age_at_initial_pathologic_diagnosis
pv=1.5e-05



Metagene

(involvement of features)



Component # 12 (stability = 0.480)

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)

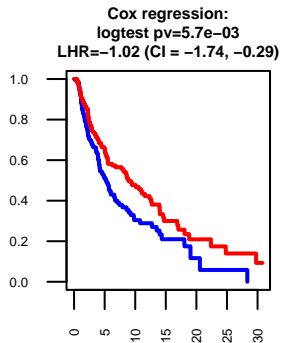
GO:MF neg : 0 terms(FDR<0.1)

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

22
negative

44
positive

- SH3GL2
- BMPR1B
- NR2E1
- IRX2
- D4S234E
- C5orf38
- FCRLA
- MMP8
- FRG2DP
- SPTBN2
- ENTHD1
- IL12RB2
- SLC6A17
- ABCB5
- ST8SIA6
- ADCY1
- ACTL8
- CPNE7
- PAX9
- IL1RAPL1
- FOXF2
- SLC6A15
- EYA1
- FABP7
- SOSTDC1
- CLDN1
- PMP2
- MEGF10
- COL20A1
- CNTN6
- MUC7
- PLCH1
- CHL1
- CNDP1
- PEX5L
- MYBPC1
- HTN1
- NTNG1
- ZNF536
- CHST9
- C1QTNF3
- MLIP
- GRIK3
- LIN28A
- MOXD1
- SCRG1
- UG0898H09
- SLC5A4
- BMP7
- COL22A1
- KCNJ10
- SYNPR
- MET
- RAB3C
- POPDC3
- GJB2
- OR7A5
- FREM1
- OR7C1
- SLC18A1
- SCN1A
- GABRP
- HS3ST5
- SERPINA5
- PSAT1
- LIMCH1



- factor
- RNASEQ.CLUSTER_CONSENHIER
 - MUTATIONSUBTYPES
 - Breslow.Depth
 - birth_days_to_initial_diagnosis
 - age_at_initial_pathologic_diagnosis
 - Tumor.location.site
 - Sample.Type
 - Tumor.tissue.site
 - UV.signature
 - Clark.Level

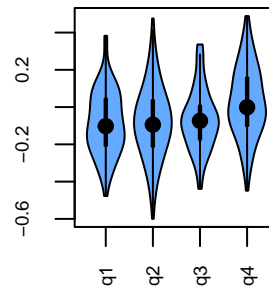
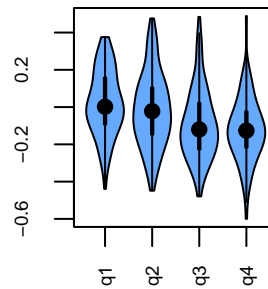
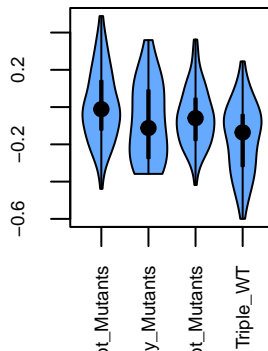
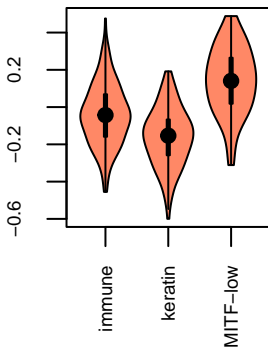
- p.value
- 5.19e-24
 - 2.11e-07
 - 2.20e-07
 - 1.75e-06
 - 1.75e-06
 - 2.14e-05
 - 2.38e-05
 - 3.89e-05
 - 7.62e-05
 - 1.43e-04

RNASEQ.CLUSTER_CONSENHIER
pv=5.2e-24

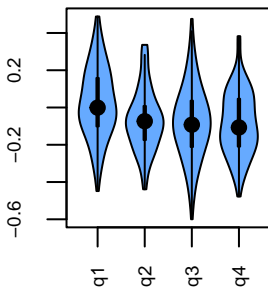
MUTATIONSUBTYPES
pv=2.1e-07

Breslow.Depth
pv=2.2e-07

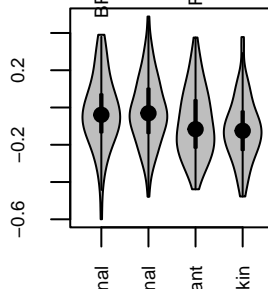
birth_days_to_initial_diagnosis
pv=1.8e-06



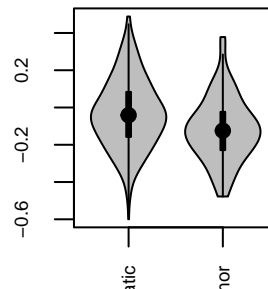
age_at_initial_pathologic_diagnosis
pv=1.8e-06



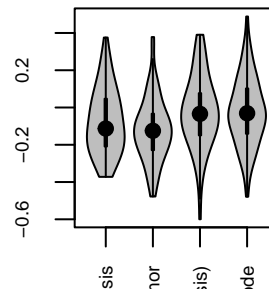
Tumor.location.site
pv=2.1e-05



Sample.Type
pv=2.4e-05

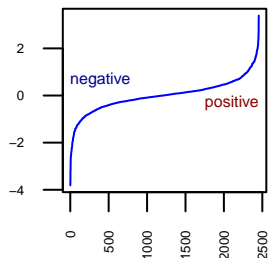


Tumor.tissue.site
pv=3.9e-05



Component # 13 (stability = 0.603)

Metagene (involvement of features)



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

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

Term
positive regulation of synapse assembly

FDR
3.04e-03

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

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

Term
glutamatergic synapse

FDR
9.25e-02

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

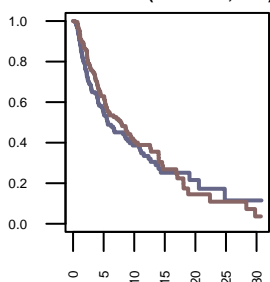
GO:MF pos : 0 terms(FDR<0.1)

51 negative 45 positive

- FLJ16779
- NMRK2
- MAPK4
- NKAIN4
- CST1
- CFAP61
- DNAH9
- CLDN14
- TF
- BIRC7
- PPARGC1A
- MYH14
- CNDP1
- PRKG2
- ADCY2
- AGT
- LG13
- PAEP
- TTC39A
- TMEM163
- KLK6
- PLEKHA6
- RAMP1
- SCUBE1
- CHST9
- HHATL
- CST2
- BAI1
- ATP6V0D2
- CAPG
- SCML4
- SLC38A8
- TAF7L
- COL20A1
- GBX2
- HES2
- ARHGAP8
- SCUBE2
- MUC7
- SULT1C2
- GADL1
- WFDC1
- PDE11A
- C2orf70
- GATA4
- PLCB4
- NRAP
- NALCN
- DNER
- SHANK1
- PRSS56

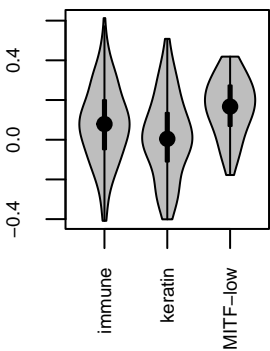
- SOX2
- DKK1
- MRGPRX3
- IL1RAPL1
- PAPL
- ALDH3B2
- SH3GL2
- NR2E1
- CDH2
- TYRP1
- SHISA2
- GNG4
- PNMA2
- PROX1
- EFNB3
- FLRT3
- GFRA3
- KCNG1
- ITGB8
- FREM2
- POU3F2
- BDNF
- SYT14
- FOXF2
- GJA3
- SLITRK2
- LPAR3
- AK5
- HORMAD1
- GABRA2
- PTPRZ1
- MLIP
- SP8
- SEPT3
- UGT8
- MYRIP
- SLC35F1
- IRX2
- NLGN1
- KIAA1045
- TMEM59L
- DNAH2
- CYSLTR2
- PHGDH
- ABCA8

Cox regression:
logtest pv=6.5e-02
LHR=-0.63 (CI = -1.30, 0.04)

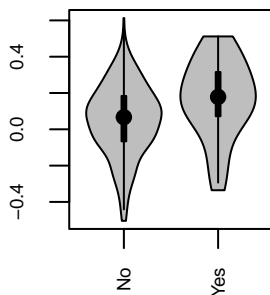


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	1.59e-05
NF1GainLossFrameshift	4.31e-04
Year.of.Birth	9.37e-04
initial_pathologic_dx_year	1.17e-03
birth_days_to_initial_diagnosis	1.73e-03
MUTATIONSUBTYPES	2.54e-03
age_at_initial_pathologic_diagnosis	2.69e-03
ajcc_pathologic_tumor_stage	4.07e-03
Cancer.stage.N	4.52e-03
NF1.stopgain	4.60e-03

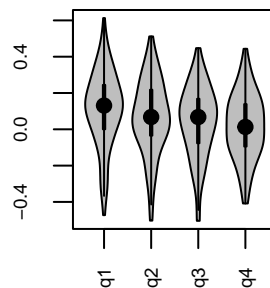
RNASEQ.CLUSTER_CONSENHIER
pv=1.6e-05



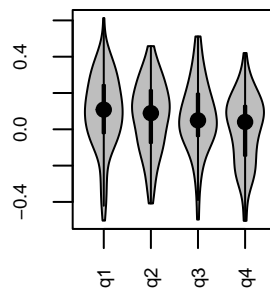
NF1GainLossFrameshift
pv=4.3e-04



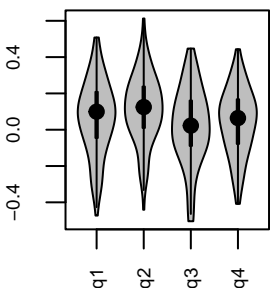
Year.of.Birth
pv=9.4e-04



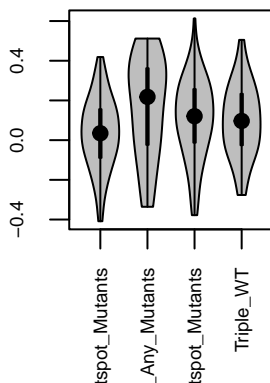
initial_pathologic_dx_year
pv=1.2e-03



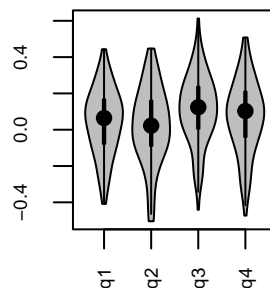
birth_days_to_initial_diagnosis
pv=1.7e-03



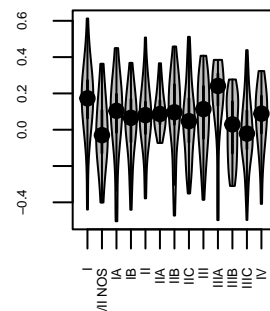
MUTATIONSUBTYPES
pv=2.5e-03



age_at_initial_pathologic_diagnosis
pv=2.7e-03

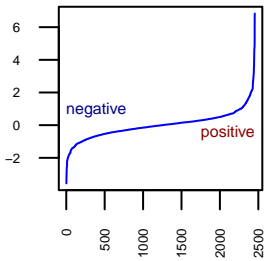


ajcc_pathologic_tumor_stage
pv=4.1e-03



Component # 14 (stability = 0.820)

Metagene (involvement of features)



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

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

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

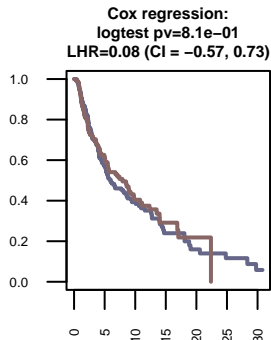
GO:CC pos : 0 terms(FDR<0.1)

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

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

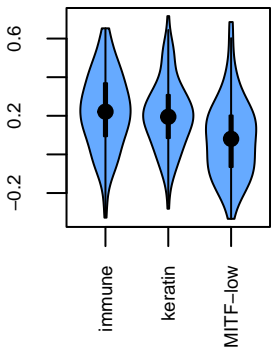
18 negative **50 positive**

- PI15
- EDN3
- RASEF
- SLC7A11
- NELL1
- DNAJC12
- SEC14L4
- PNLIPRP3
- COL19A1
- SLC30A10
- NPTX2
- ITIH5
- MYCNUT
- CYP1A1
- TINCR
- GDF15
- ABCA8
- MYCNOS
- CMTM5
- MPZ
- SFRP5
- BEX1
- FXYD3
- MAL
- PKLR
- MMP8
- COL20A1
- RDH8
- ACSBG1
- ANGPTL7
- CHRN2
- KCNJ10
- BCAN
- SLC28A3
- LG14
- CDH1
- TTYH1
- KIAA1045
- CHAD
- SEMA3B
- MAGEL2
- KRT27
- WNK4
- LIN28A
- L1CAM
- PCSK2
- C2orf70
- ATP1A2
- CDH15
- MDF1
- DCT
- OLIG1
- ITIH6
- UCN2
- GABRP
- INSC
- PMEL
- RASGRF1
- WFDC2
- MYH7
- PLEKHA6
- KCNA2
- KRT80
- CADM3
- CST5
- STRA6
- PKNOX2
- NGFR

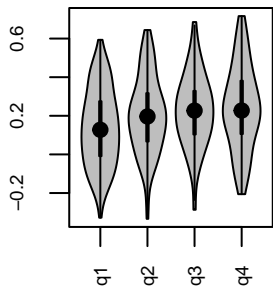


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	6.73e-06
initial_pathologic_dx_year	7.01e-04
tumor_status_at_last_contact	1.67e-03
fourth.prominent.motiv	1.96e-03
Prospective.Tissue.Collection	2.02e-03
Retropective.Tissue.Collection	2.02e-03
New.tumor.event.after.initial.treatment	7.66e-03
ajcc_pathologic_tumor_stage	7.67e-03
Disease.Free.Status.at.last.contact	9.18e-03
vital_status_at_last_contact	1.03e-02

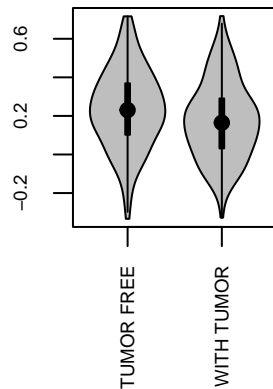
RNASEQ.CLUSTER_CONSENHIER
pv=6.7e-06



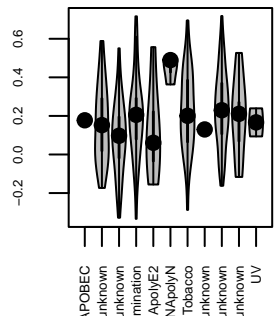
initial_pathologic_dx_year
pv=7.0e-04



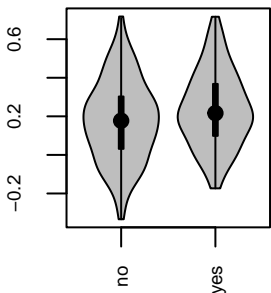
tumor_status_at_last_contact
pv=1.7e-03



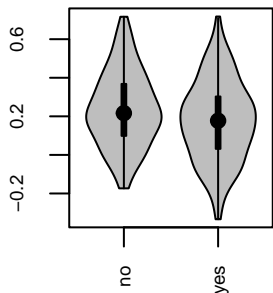
fourth.prominent.motiv
pv=2.0e-03



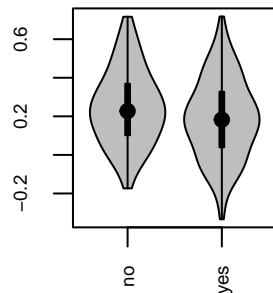
Prospective.Tissue.Collection
pv=2.0e-03



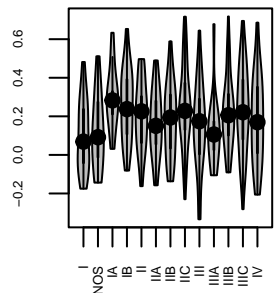
Retropective.Tissue.Collection
pv=2.0e-03



New.tumor.event.after.initial.treatment
pv=7.7e-03

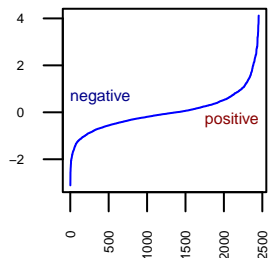


ajcc_pathologic_tumor_stage
pv=7.7e-03



Component # 15 (stability = 0.808)

Metagene (involvement of features)



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 : 3 terms(FDR<0.1)

Term
 intrinsic component of presynaptic activ...
 catenin complex
 glutamatergic synapse

FDR
 5.15e-03
 4.39e-02
 5.72e-02

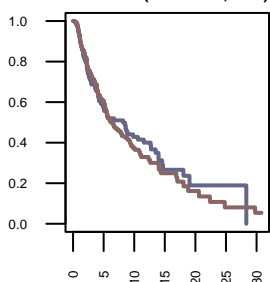
GO:MF neg : 0 terms(FDR<0.1)

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

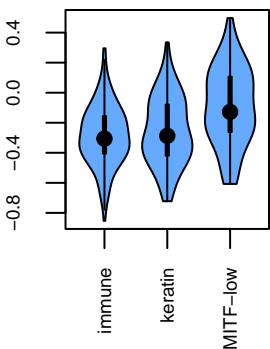
13 negative **81 positive**

- PRIMA1
- BMP7
- PSCA
- TFF3
- COL22A1
- IGFL4
- PKD1L2
- PI15
- ALDH3B2
- SEC14L4
- CNDP1
- LINGO1
- SYT6
- CHST9
- PCDH10
- PCLO
- HNF4G
- GLRB
- ERBB4
- ISL1
- CDH7
- LMO3
- FOXP2
- DPP10
- MUC7
- BTC
- WDR17
- EPHA5
- PKIA
- SLITRK5
- DSG2
- CXXC4
- ANO5
- GALNT13
- PITX2
- RORB
- CXorf57
- IRS4
- HCN1
- CCSER1
- CLGN
- MUM1L1
- EPHA6
- ESRRG
- EYA4
- FEZF1
- CNTN3
- BAI3
- GABRA2
- RPS6KA6
- ONECUT2
- LRFN5
- STXBPSL
- ZNF711
- POU4F1
- XK
- TEX15
- PRSS12
- VWDE
- ROBO2
- BMPR1B
- GALNTL6
- NAP1L3
- NRG3
- KCNQ5
- GPC5
- SH3GL2
- MGST1
- CACNA2D1
- PCOLCE2
- NDST3
- SPOCK3
- FAM184A
- COL9A1
- PRKAA2
- GRID2
- LINGO2
- LRAT
- OGDHL
- FSTL5
- PVRL3
- COL4A5
- SLCO5A1
- IL13RA2
- CBLN2
- DTNA
- CADM2
- MLIP
- ADAMTS3
- ILDR2
- PRKG2
- AQP4
- SYT1
- HRASLS

Cox regression:
 logtest pv=2.9e-01
 LHR=0.31 (CI = -0.26, 0.88)



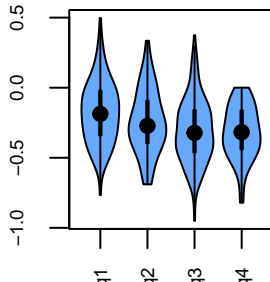
RNASEQ.CLUSTER_CONSENHIER
 pv=9.8e-08



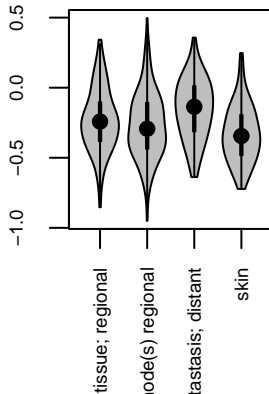
factor
 RNASEQ.CLUSTER_CONSENHIER
 Year.of.last.contact
 Tumor.location.site
 Tumor.tissue.site
 Sample.country
 initial_pathologic_dx_year
 Prospective.Tissue.Collection
 Retropective.Tissue.Collection
 Sample.Type
 tumor_status_at_last_contact

p.value
 9.78e-08
 2.56e-06
 1.15e-05
 1.91e-05
 7.77e-05
 8.30e-05
 1.82e-04
 1.82e-04
 2.89e-04
 5.24e-04

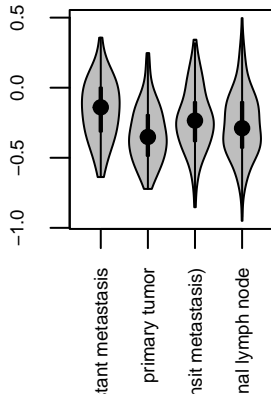
Year.of.last.contact
 pv=2.6e-06



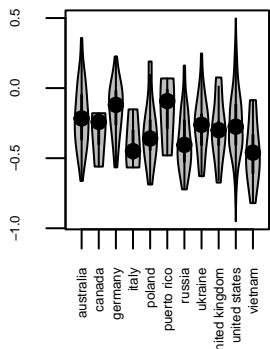
Tumor.location.site
 pv=1.1e-05



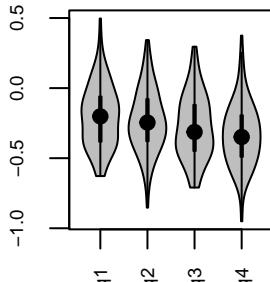
Tumor.tissue.site
 pv=1.9e-05



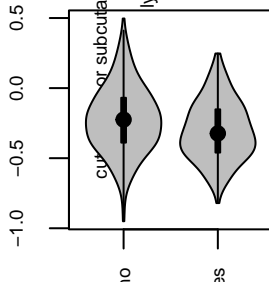
Sample.country
 pv=7.8e-05



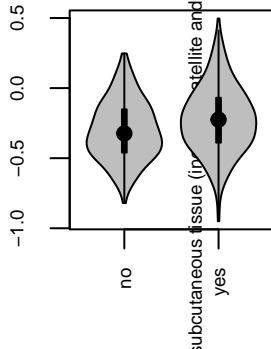
initial_pathologic_dx_year
 pv=8.3e-05



Prospective.Tissue.Collection
 pv=1.8e-04

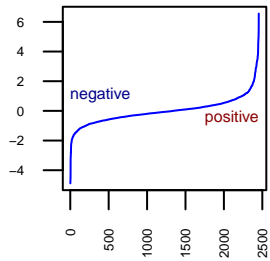


Retropective.Tissue.Collection
 pv=1.8e-04



Component # 16 (stability = 0.956)

Metagene (involvement of features)



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 : 1 terms(FDR<0.1)

Term
integrator complex

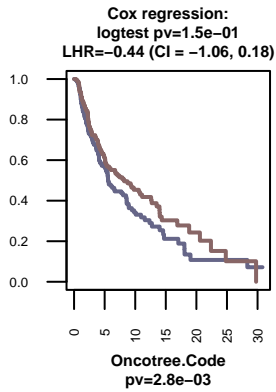
FDR
2.96e-02

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

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

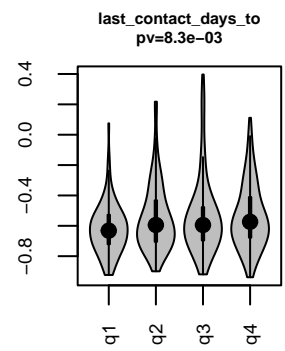
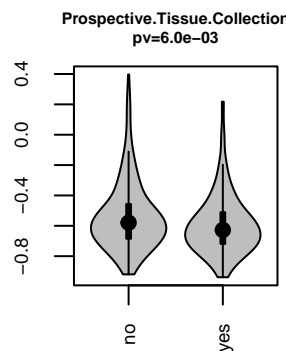
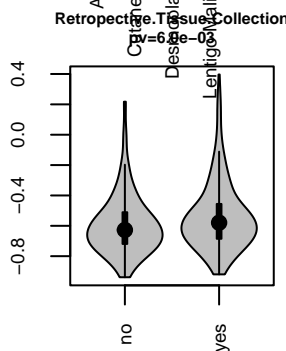
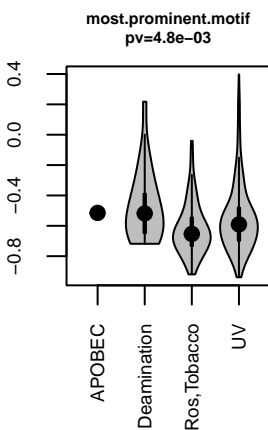
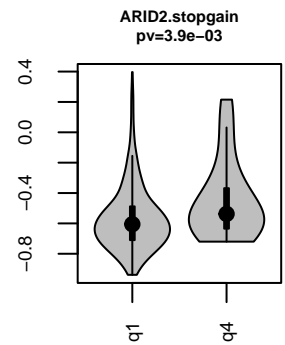
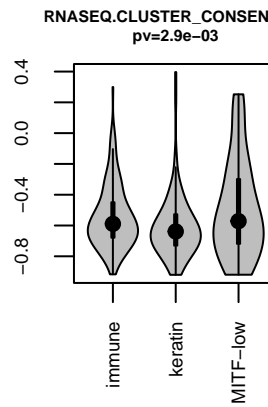
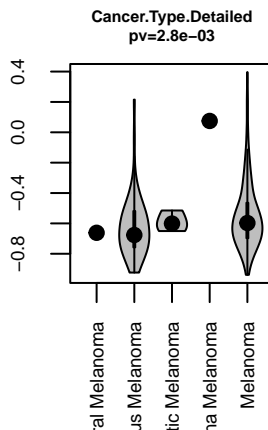
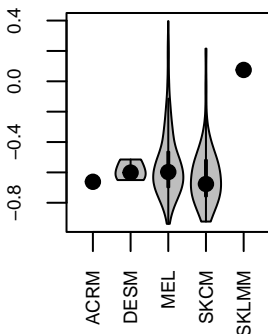
15 negative 63 positive

- MAGEA6
- MAGEA3
- MAGEA12
- CSAG1
- ZIC1
- DLK1
- GABRA3
- CRTAC1
- ZIC4
- BAALC
- BCHE
- MAGEC2
- DNASE2B
- LRRTM4
- BMP7
- CT55
- MAGEA4
- PAGE1
- SAGE1
- MAGEB2
- PASD1
- CT45A10
- CTCF
- MAEL
- CT45A1
- FAR2P1
- POU6F2
- CLEC2L
- VCX
- MAGEA11
- MAGEB1
- MAGEA10
- PAGE5
- AACSP1
- ACTL8
- GALNT8
- GAGE1
- VCX3A
- NLRP4
- NAA11
- WDR72
- PNMA5
- TUBA3C
- TFF2
- GAGE2A
- STK31
- CTAG2
- FOXR2
- GTSF1
- BAGE2
- SLC6A10P
- CASC9
- PRSS21
- SLC30A8
- XAGE3
- MYT1L
- LIN28B
- MUC15
- PAGE2B
- CCNYL2
- NLRP11
- ACTBP8
- PAGE2
- USP43
- PRSS50
- CNR1
- MAGEB16
- SSX1
- XAGE2B
- LY6K
- COL2A1
- GABRB3
- PROM1
- HBE1
- PKHD1
- RSP04
- GABRG3
- MAGEB17



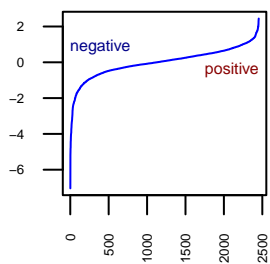
- factor
- Oncotree.Code
 - Cancer.Type.Detailed
 - RNASEQ.CLUSTER_CONSENHIER
 - ARID2.stopgain
 - most.prominent.motif
 - Retropective.Tissue.Collection
 - Prospective.Tissue.Collection
 - last_contact_days_to
 - ARID2.splice.donor
 - Cancer.stage.T

- p.value
- 2.83e-03
 - 2.83e-03
 - 2.91e-03
 - 3.85e-03
 - 4.82e-03
 - 5.97e-03
 - 5.97e-03
 - 8.35e-03
 - 8.57e-03
 - 1.72e-02



Component # 17 (stability = 0.900)

Metagene (involvement of features)



48 negative **3 positive**

- CXCL5
- MMP1
- CSF3
- FDCSP
- MMP3
- SERPIN2
- CXCL1
- IL1B
- CXCL8
- CXCL6
- CCL20
- IL11
- TREM1
- PTPRN
- MMP10
- EREG
- PI3
- PTGS2
- MMP12
- ANGPTL4
- S100A8
- SLAMF9
- AREG
- AQP9
- SAA1
- VEGF
- IL1A
- LRP2
- S100A12
- S100A9
- TFPI2
- CALB2
- MT1H
- HAS1
- RNF182
- CA12
- DKK1
- TMEM158
- NRG1
- CCL18
- CCL13
- KCNK3
- LBP
- GLDC
- CHI3L1
- MARCO
- MMP8
- MCHR1

GO:BP neg : 15 terms(FDR<0.1)

Term	FDR
cytokine-mediated signaling pathway	1.43e-06
neutrophil chemotaxis	1.28e-05
response to lipopolysaccharide	3.17e-05
neutrophil mediated immunity	1.43e-04
acute inflammatory response	1.43e-04
antimicrobial humoral response	1.58e-04
regulation of interleukin-6 production	3.45e-03
positive regulation of intracellular sig...	3.45e-03
collagen catabolic process	4.01e-03
cellular response to interleukin-1	7.61e-03
positive regulation of angiogenesis	1.73e-02
positive regulation of nitric oxide bios...	3.65e-02
positive regulation of DNA-binding trans...	5.41e-02
inflammatory response	8.15e-02
response to fungus	9.51e-02

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

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

Term	FDR
extracellular space	6.30e-07
secretory granule lumen	1.05e-05
tertiary granule lumen	7.00e-04
extracellular matrix	1.76e-02

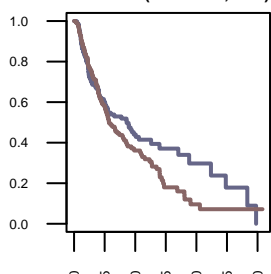
GO:CC pos : 0 terms(FDR<0.1)

GO:MF neg : 4 terms(FDR<0.1)

Term	FDR
cytokine activity	1.20e-06
growth factor receptor binding	7.36e-02
growth factor activity	7.36e-02
CXCR chemokine receptor binding	8.53e-02

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

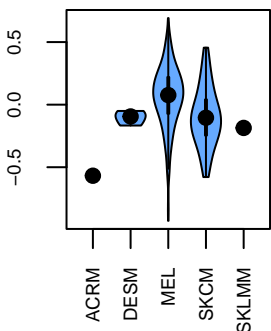
Cox regression:
logtest pv=4.4e-01
LHR=0.21 (CI = -0.33, 0.75)



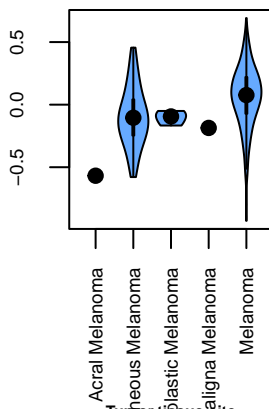
- factor
- Oncotree.Code
- Cancer.Type.Detailed
- Sample.Type
- BRAFV600.
- Tumor.location.site
- Tumor.tissue.site
- UV.signature
- most.prominent.motif
- Sample.country
- TP53.stopgain

- p.value
- 3.87e-06
- 3.87e-06
- 5.83e-06
- 1.80e-05
- 4.05e-05
- 7.04e-05
- 1.50e-04
- 1.73e-04
- 4.15e-04
- 5.24e-04

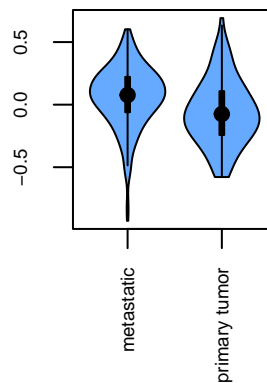
Oncotree.Code
pv=3.9e-06



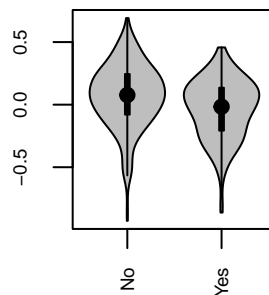
Cancer.Type.Detailed
pv=3.9e-06



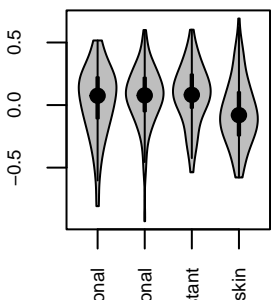
Sample.Type
pv=5.8e-06



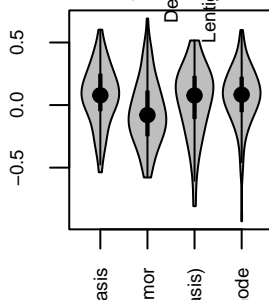
BRAFV600.
pv=1.8e-05



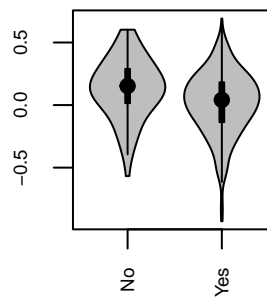
Tumor.location.site
pv=4.0e-05



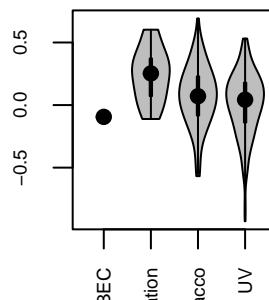
Tumor.tissue.site
pv=7.8e-05



UV.signature
pv=1.5e-04

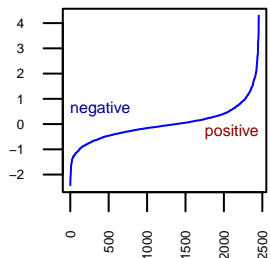


most.prominent.motif
pv=1.7e-04



Component # 18 (stability = 0.607)

Metagene (involvement of features)



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

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

Term
pigment biosynthetic process

FDR
3.42e-04

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

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

Term
melanosome

FDR
6.87e-06

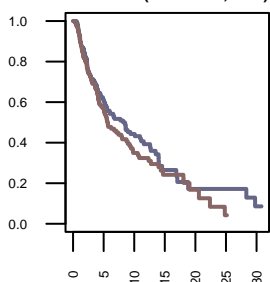
GO:MF neg : 0 terms(FDR<0.1)

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

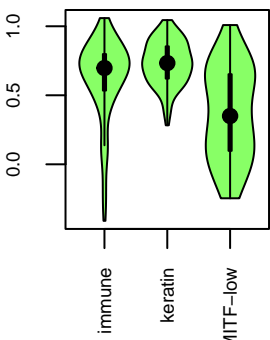
10 negative 78 positive

- ZNF536
- PMP2
- NDP
- KANK4
- KCNG1
- FGF5
- NRXN1
- IGF2BP1
- KLHDC8A
- DKK1
- NELL1
- TYR
- DCT
- HRK
- MLANA
- TRIM51
- PRSS33
- GAPDHS
- D4S234E
- PMEL
- PRKG2
- GPR143
- CBX3P7
- SHISA2
- SLC24A5
- TRIM63
- SLC6A17
- MCOLN3
- PRDM7
- SFRP1
- VEGF
- ABCB5
- FRG2DP
- BIRC7
- CDH3
- GJB1
- NAT8L
- LDB3
- LRRN4CL
- OLIG1
- IL12RB2
- S100A1
- DMKN
- IRX6
- TUBB4A
- GDF15
- SLC45A2
- TRPM1
- CDH1
- RLBP1
- PROM1
- PLA1A
- RAB17
- ADCY1
- CPN1
- DNASE2B
- SLC6A15
- CAPN3
- CEACAM1
- APOD
- ABCC2
- IRF4
- EWSAT1
- HCG20
- STK32A
- MRGPRX4
- CNTNAP3
- ITIH6
- CNNM1
- SALL1
- ALDH3B2
- CHRNA6
- DLL3
- ST8SIA6
- GYG2
- CNTNAP3B
- FLJ16779
- NRG3
- ROPN1
- NKAIN4
- FXYD3
- ESRP1
- OLIG2
- CA14
- FZD9
- ENTHD1
- CKMT1B
- FCRLA

Cox regression:
logtest pv=4.6e-01
LHR=0.17 (CI = -0.29, 0.62)



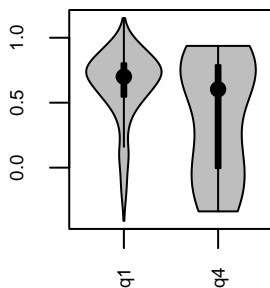
RNASEQ.CLUSTER_CONSENHIER
pv=9.2e-15



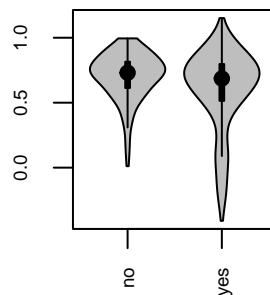
- factor
- RNASEQ.CLUSTER_CONSENHIER
 - TP53.stopgain
 - New.tumor.event.after.initial.treatment
 - ICD.O.3.Histologie
 - most.prominent.motif
 - Breslow.Depth
 - Cancer.stage.T
 - Retropective.Tissue.Collection
 - Prospective.Tissue.Collection
 - Radiation.therapie

- p.value
- 9.22e-15
 - 4.26e-04
 - 7.10e-04
 - 3.47e-03
 - 4.39e-03
 - 5.22e-03
 - 1.43e-02
 - 1.58e-02
 - 1.58e-02
 - 1.99e-02

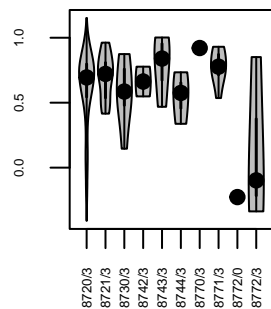
TP53.stopgain
pv=4.3e-04



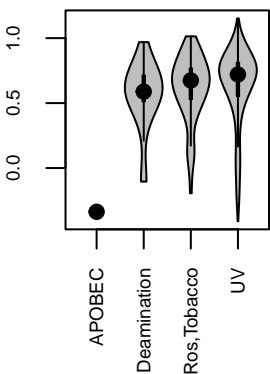
New.tumor.event.after.initial.treatment
pv=7.1e-04



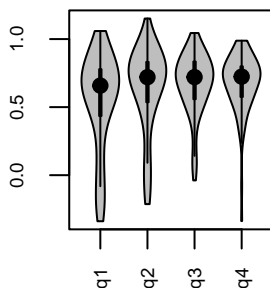
ICD.O.3.Histologie
pv=3.5e-03



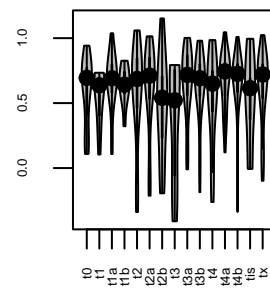
most.prominent.motif
pv=4.4e-03



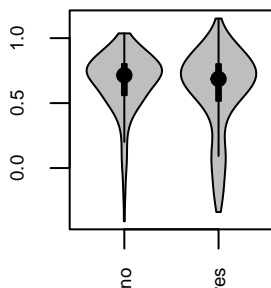
Breslow.Depth
pv=5.2e-03



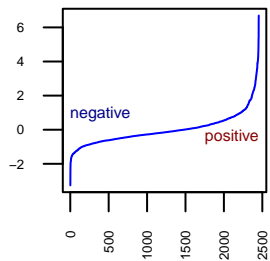
Cancer.stage.T
pv=1.4e-02



Retropective.Tissue.Collection
pv=1.6e-02



Metagene
(involvement of features)



Component # 19 (stability = 0.963)

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

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

Term	FDR
B cell activation	2.76e-06
B cell receptor signaling pathway	2.90e-03
immunoglobulin production	2.73e-02
lymph node development	7.99e-02
regulation of dendritic cell apoptotic p...	7.99e-02

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

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

Term	FDR
cell surface	5.53e-06
intrinsic component of plasma membrane	3.63e-04

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

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

Term	FDR
lipopeptide binding	1.75e-02
immunoglobulin binding	4.21e-02
endogenous lipid antigen binding	8.03e-02
exogenous lipid antigen binding	8.03e-02

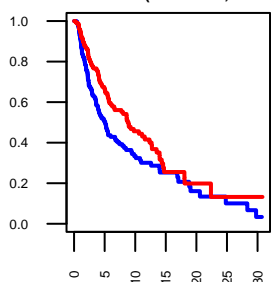
3 negative **95 positive**

COL11A1
MMP13
HAPLN1

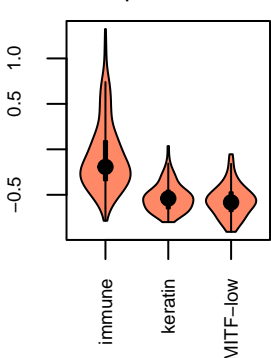
CCL21
CR2
FCAMR
FCER2
TCL1A
PAX5
FDCSP
MS4A1
CNR2
IGHD
FAM129C
FCRL1
IGHE
VPREB3
SERPINA9
NPHS1
CXCR5
CCL19
SHISA3
CLEC4M
BLK
ART4
TREM2
BANK1
C7
CLEC17A
AICDA
DNASE1L3
SPIB
ADH1B
NPY1R
XKR4
CD19
SLC22A3
NTS
CD22
HTR3A
TBC1D27
CAPN6
CCR7
TNFRSF13B
STAP1
CD24
TLR10
LILRA4
TNFSF11

PLD5
CD1C
FCRL2
GPR64
P2RX5
LTB
MMRN1
GYTL1B
NOG
PLAC8
BCL11A
CD40LG
RGS13
CXCL14
EXOC3L4
NPY5R
PTPRT
CLU
VIPR1
LBP
ACKR1
HP
SELL
NLRP4
BEND4
RIC3
CNTNAP2
HMCN2
PKP2
SELP
CD1E
LAMC2
CD79B
GAPT
TIMD4
PLCX3D

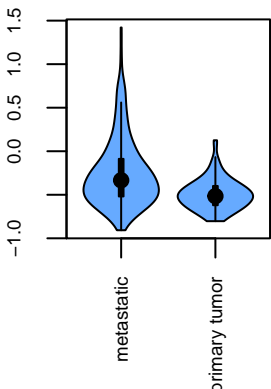
Cox regression:
logtest pv=8.3e-03
LHR=-0.53 (CI = -0.94, -0.12)



RNASEQ.CLUSTER_CONSENHIER
pv=1.0e-35



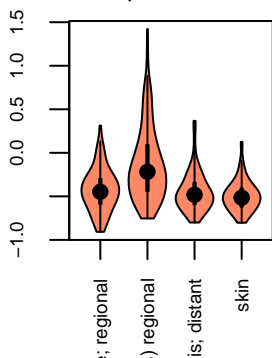
Sample.Type
pv=1.2e-09



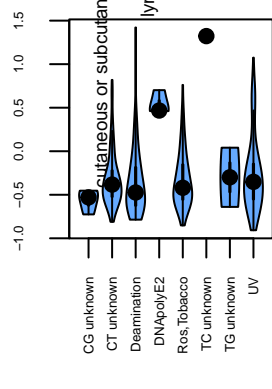
factor
RNASEQ.CLUSTER_CONSENHIER
Tumor.location.site
Tumor.tissue.site
ICD.10.TopLevel
Sample.Type
second.prominent.motif
Oncotree.Code
Cancer.Type.Detailed
Normal.control.type
ajcc_pathologic_tumor_stage

p.value
1.04e-35
3.07e-23
3.63e-23
3.39e-15
1.18e-09
8.12e-07
3.72e-05
3.72e-05
7.27e-05
9.31e-05

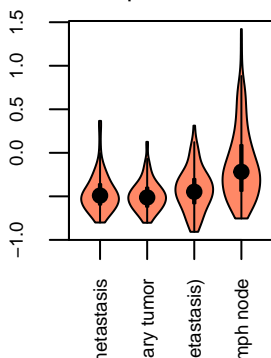
Tumor.location.site
pv=3.1e-23



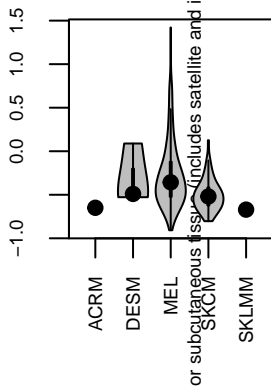
second.prominent.motif
pv=8.1e-07



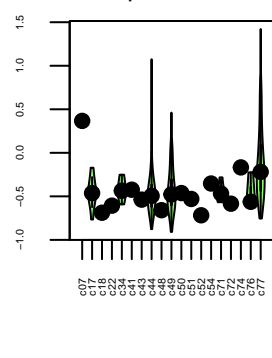
Tumor.tissue.site
pv=3.6e-23



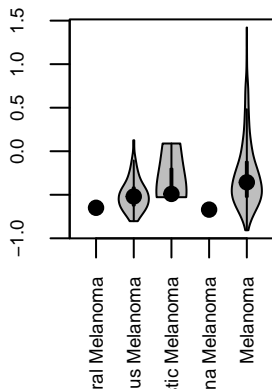
Oncotree.Code
pv=3.7e-05



ICD.10.TopLevel
pv=3.4e-15

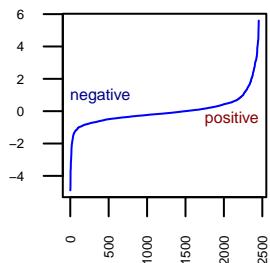


Cancer.Type.Detailed
pv=3.7e-05



Component # 20 (stability = 0.981)

Metagene (involvement of features)



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

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

Term	FDR
keratinocyte differentiation	9.51e-28
peptide cross-linking	2.33e-04
negative regulation of endopeptidase act...	1.30e-02
establishment of skin barrier	1.52e-02
antimicrobial humoral response	2.09e-02
epidermis development	2.22e-02
defense response to bacterium	3.12e-02

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

Term
extracellular exosome

FDR
4.77e-04

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

Term	FDR
cornified envelope	1.24e-12
cytosol	9.54e-05
keratin filament	3.18e-04
epidermal lamellar body	8.35e-03
extracellular region	3.63e-02
gap junction	7.63e-02

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

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

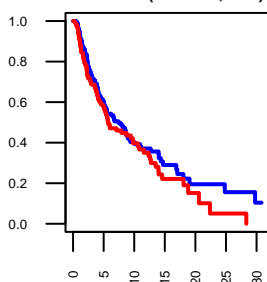
Term	FDR
serine-type endopeptidase inhibitor acti...	1.28e-03
structural constituent of skin epidermis	1.81e-03
calcium-dependent phospholipase A2 activ...	6.42e-02
phospholipase A2 activity (consuming 1,2...	6.42e-02
phospholipase A2 activity consuming 1,2-...	6.42e-02

33 negative 153 positive

- KRT4
- KRT19
- BPIFB1
- KRT13
- PIGR
- SLC34A2
- MUC21
- SFTPB
- STATH
- CEACAM6
- DMBT1
- WFDC2
- KRT7
- FOLR1
- AGR2
- SFTPA2
- CXCL17
- MUC5B
- ELF3
- PPP1R1B
- CLDN3
- GSTA1
- KRT8
- EPCAM
- MS4A8
- CTSE
- TMPRSS2
- SPRR3
- SFTPA1
- NTS
- FIBCD1
- LTF
- CRNN

- C1orf68
- CASP14
- CDSN
- DSC1
- FLG2
- KPRP
- KRT1
- KRT2
- LCE1A
- LCE1B
- LCE1C
- LCE1F
- LCE2B
- LCE2C
- LCE2D
- LCE3D
- LCE3E
- LCE6A
- LOR
- PSAPL1
- WFDC12
- S100A7A
- SPRR2G
- WFDC5
- HAL
- KLK9
- SERPINB12
- BPIFC
- SERPINA12
- IGFL1
- KRTDAP
- LY6G6C
- SLURP1
- PLA2G4D
- ACER1
- LCE1D
- FLG
- S100A7
- ARG1
- KLK5
- IL36RN
- CALML5
- LCE3A
- AADACL2
- CARD18
- PLA2G2F
- UNC93A
- FAM25A
- DSG1
- SDR9C7
- LGALS7
- KLK8
- CRCT1
- CYP4F22
- ALOX12B
- SPRR4
- PGLYRP4
- ALOXE3
- LCE2A
- ASPRV1
- SBSN
- GSDMA
- PAPL
- C10orf99
- KLK7
- KRT6C
- SLC15A1
- SERPINB7
- ABCA12
- PGLYRP3
- ELMOD1
- RPTN
- SPRR2B
- KRT9
- IL36G
- SPRR2E
- RNASE7
- CHP2
- FAM83C
- PLA2G4E
- LGALS7B
- CIDEA

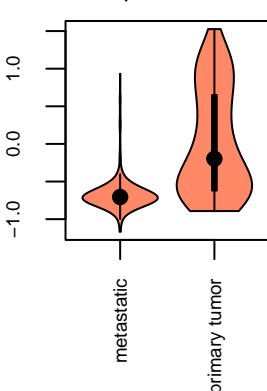
Cox regression:
logtest pv=1.2e-04
LHR=0.65 (CI = 0.35, 0.94)



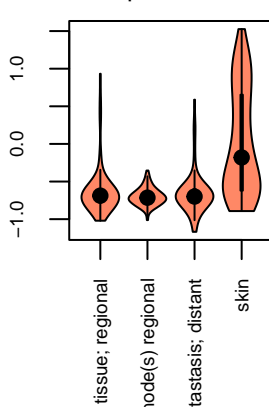
- factor
- Sample.Type
- Tumor.location.site
- Tumor.tissue.site
- Oncotree.Code
- Cancer.Type.Detailed
- Sample.country
- RNASEQ.CLUSTER_CONSENHIER
- New.tumor.event.after.initial.treatment
- ICD.10.TopLevel
- Breslow.Depth

- p.value
- 1.62e-48
- 9.77e-47
- 1.48e-46
- 1.01e-34
- 1.01e-34
- 8.45e-30
- 3.24e-24
- 3.96e-21
- 7.64e-18
- 1.51e-13

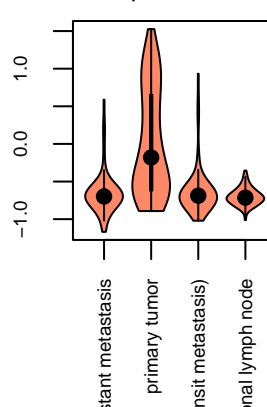
Sample.Type
pv=1.6e-48



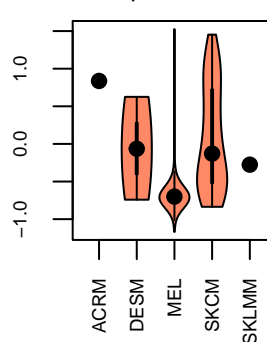
Tumor.location.site
pv=9.8e-47



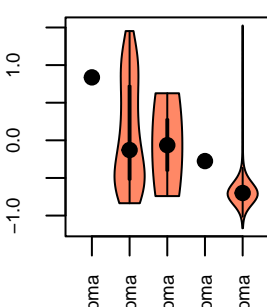
Tumor.tissue.site
pv=1.5e-46



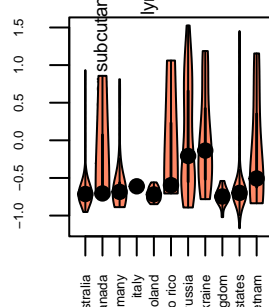
Oncotree.Code
pv=1.0e-34



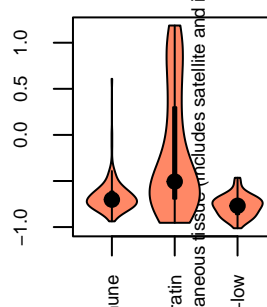
Cancer.Type.Detailed
pv=1.0e-34



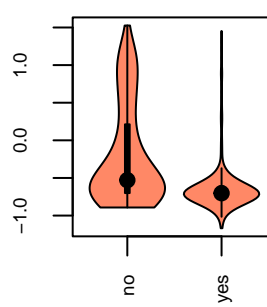
Sample.country
pv=8.5e-30



RNASEQ.CLUSTER_CONSENHIER
pv=3.2e-24

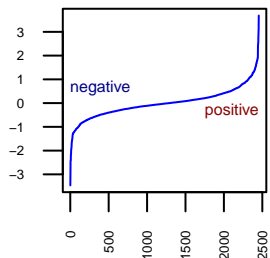


New.tumor.event.after.initial.treatment
pv=4.0e-21



Component # 21 (stability = 0.480)

Metagene (involvement of features)



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)

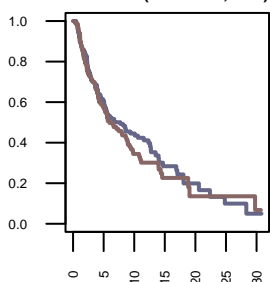
GO:MF neg : 0 terms(FDR<0.1)

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

25 negative **47 positive**

- LRRTM1
- HHATL
- INSC
- PRIMA1
- LRRTM4
- PMP2
- ASPA
- IP6K3
- OLFM3
- RIMS2
- UG0898H09
- ZNF536
- SCN7A
- TRPV3
- CHST9
- CRB1
- SSX1
- UGT2B7
- SSX5
- BHLHE22
- TMEM171
- JPH1
- FLRT1
- TIMP4
- NPY6R
- OLIG1
- OCA2
- VEGF
- PAEP
- CPN1
- SHISA2
- EYA4
- OLIG2
- SFRP1
- SLC16A6
- DMRT2
- FZD9
- MFI2
- HCG20
- ROPN1
- SLC5A4
- MRGPRX4
- IRS4
- RAB17
- MGAT5B
- SLC24A5
- SLC6A15
- CTTNBP2
- LAMA1
- DLL3
- RIPK4
- ITGA10
- DNER
- KLF14
- NAT16
- NR4A3
- ITLN2
- CNTNAP3
- IL12RB2
- CEACAM1
- TOX3
- CTLA4
- MAL
- CA6
- IGF2BP3
- CHRM3
- CA14
- GJB1
- CXCL1
- ARX
- KCNK2
- PCSK1

Cox regression:
logtest pv=3.7e-01
LHR=0.36 (CI = -0.43, 1.14)



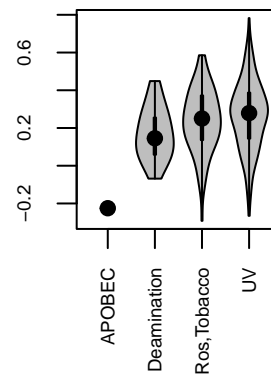
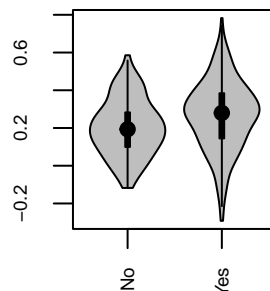
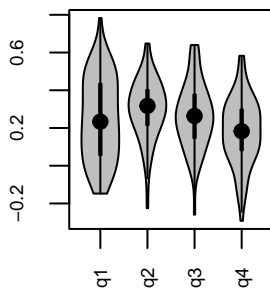
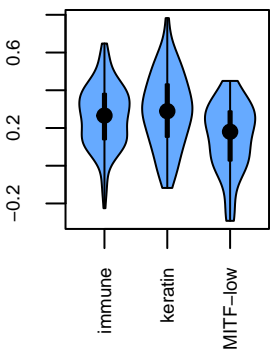
- factor
- RNASEQ.CLUSTER_CONSENHIER
 - Days.to.first.new.tumor.event.after.initial.treatment
 - UV.signature
 - most.prominent.motif
 - fifth.prominent.motiv
 - KRASQ61.
 - Sample.country
 - third.prominent.montif
 - New.tumor.event.after.initial.treatment
 - ICD.O.3.Histologie

- p.value
- 4.24e-06
 - 1.89e-03
 - 3.22e-03
 - 3.35e-03
 - 4.44e-03
 - 9.66e-03
 - 2.66e-02
 - 3.11e-02
 - 4.33e-02
 - 5.37e-02

RNASEQ.CLUSTER_CONSENHIER Days.to.first.new.tumor.event.after.initial.tre.
pv=4.2e-06 pv=1.9e-03

UV.signature
pv=3.2e-03

most.prominent.motif
pv=3.3e-03

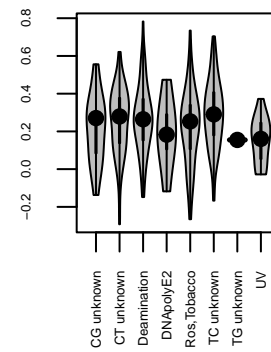
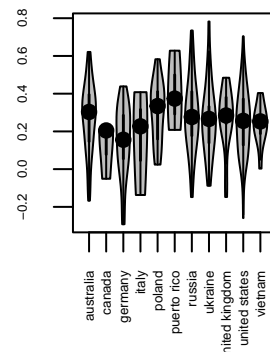
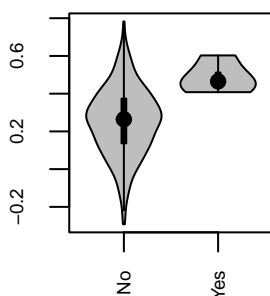
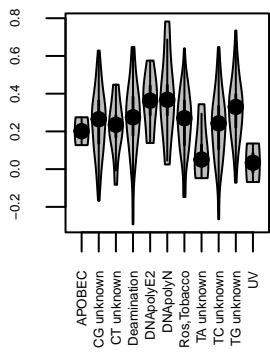


fifth.prominent.motiv
pv=4.4e-03

KRASQ61.
pv=9.7e-03

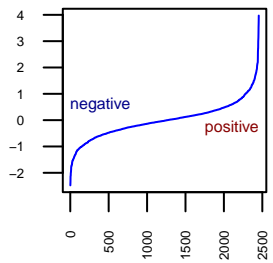
Sample.country
pv=2.7e-02

third.prominent.montif
pv=3.1e-02



Component # 22 (stability = 0.572)

Metagene (involvement of features)



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)

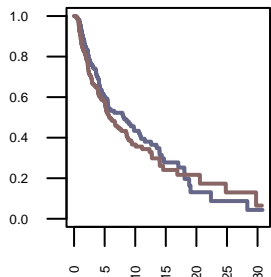
GO:MF neg : 0 terms(FDR<0.1)

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

9 negative **30 positive**

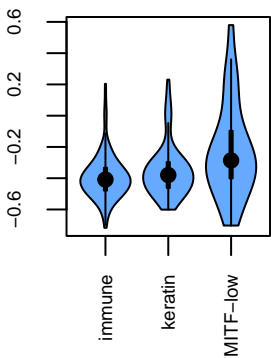
- | | |
|---------|-----------|
| BTC | TRIM71 |
| MF12 | IGDCC3 |
| IL13RA2 | LIN28A |
| S100A1 | MSI1 |
| CDH15 | LIN28B |
| GATA4 | CRABP1 |
| FCRLA | COL20A1 |
| HHATL | GABRR1 |
| TMEM171 | CNTFR |
| | MYCN |
| | DLK1 |
| | SOSTDC1 |
| | FBN3 |
| | SULT1C4 |
| | CACNG4 |
| | C1orf106 |
| | CAMKV |
| | SOX11 |
| | MYCNOS |
| | EMILIN3 |
| | DPYSL5 |
| | TOX3 |
| | DLX2 |
| | CYP26A1 |
| | SCN1A |
| | MDF1 |
| | PIANP |
| | IGSF9 |
| | SPATA31C2 |
| | CHAD |

Cox regression:
logtest pv=8.5e-02
LHR=0.56 (CI = -0.06, 1.19)

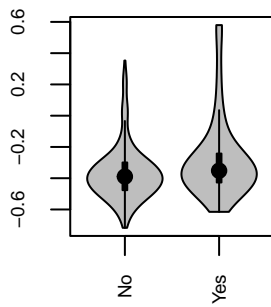


- | factor | p.value |
|---|----------|
| RNASEQ.CLUSTER_CONSENHIER | 6.35e-08 |
| NRASQ61. | 3.72e-05 |
| Sample.Type | 3.39e-04 |
| UV.signature | 4.34e-04 |
| Breslow.Depth | 5.42e-04 |
| Tumor.location.site | 5.96e-04 |
| ICD.10.TopLevel | 5.98e-04 |
| Tumor.tissue.site | 6.82e-04 |
| New.tumor.event.after.initial.treatment | 2.45e-03 |
| new_tumor_event_site_other | 3.12e-03 |

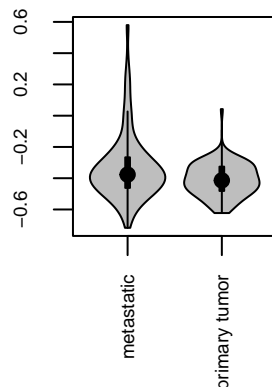
RNASEQ.CLUSTER_CONSENHIER
pv=6.3e-08



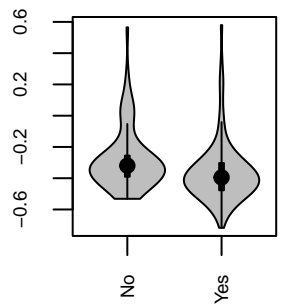
NRASQ61.
pv=3.7e-05



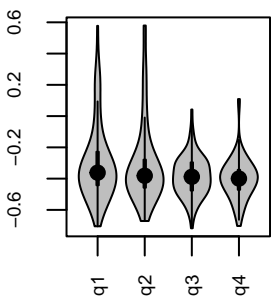
Sample.Type
pv=3.4e-04



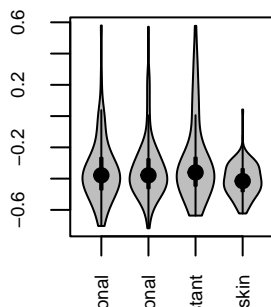
UV.signature
pv=4.3e-04



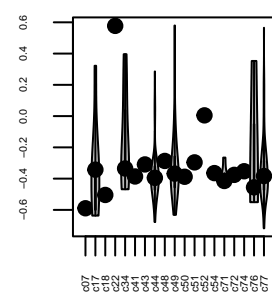
Breslow.Depth
pv=5.4e-04



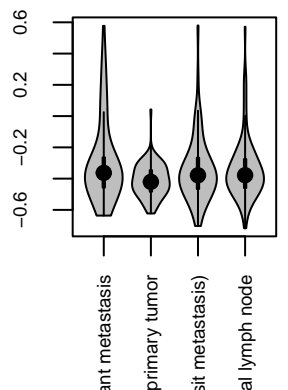
Tumor.location.site
pv=6.0e-04



ICD.10.TopLevel
pv=6.0e-04

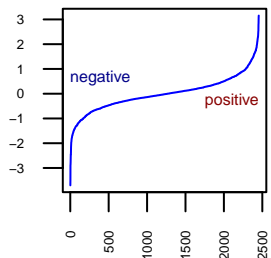


Tumor.tissue.site
pv=6.8e-04



Component # 23 (stability = 0.582)

Metagene (involvement of features)



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

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

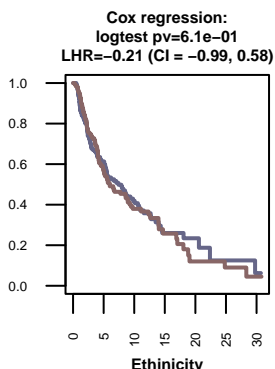
GO:CC neg : 0 terms(FDR<0.1)

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

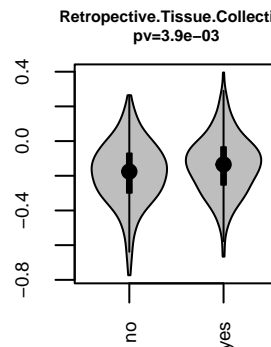
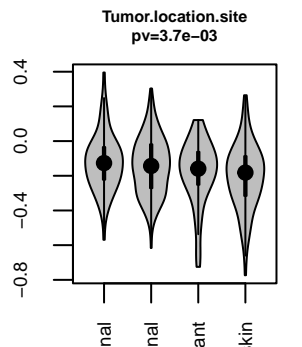
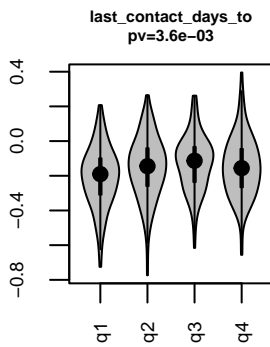
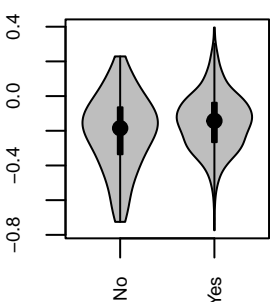
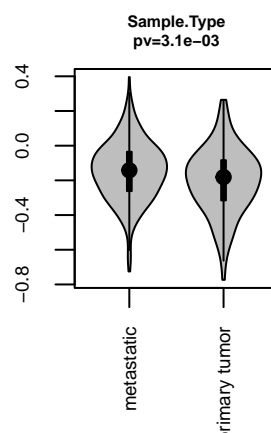
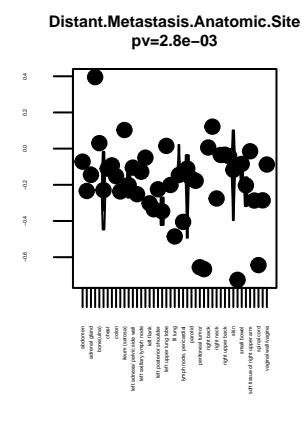
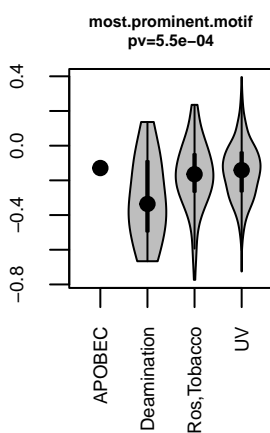
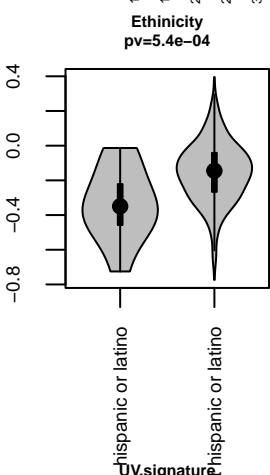
GO:MF neg : 0 terms(FDR<0.1)

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

- | | |
|--|--|
| <p>17 negative</p> <ul style="list-style-type: none"> CHRM1 LG13 EPS8L2 CHADL MAL SFTPC FAM69C HSPB7 EXTL1 LRRN4CL OCA2 ITIH6 ABCC11 XYLT1 COL11A2 LY6K COL9A1 | <p>35 positive</p> <ul style="list-style-type: none"> CTCF PNLIPRP3 TCN1 ALDH3B2 HTN1 SYT6 MORC1 CNDP1 ASB4 PHGDH BAAT DYDC2 RASEF RDH8 ITGA7 PTPRR RASGRF1 GRM1 SPACA3 PCSK9 TMEM255A SHISA2 HTN3 HPCAL4 CDH1 LUZP4 OGDHL LONRF2 FOXO6 PAPL ABC5 RIMS2 ZNF365 UCN2 PYY2 |
|--|--|



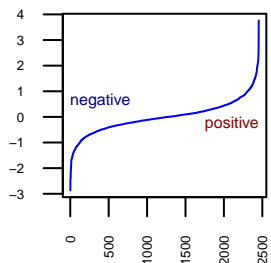
factor	p.value
Ethnicity	5.40e-04
most.prominent.motif	5.45e-04
Distant.Metastasis.Anatomic.Site	2.82e-03
Sample.Type	3.15e-03
UV.signature	3.45e-03
last_contact_days_to	3.56e-03
Tumor.location.site	3.71e-03
Retropective.Tissue.Collection	3.86e-03
Prospective.Tissue.Collection	3.86e-03
MUTATIONSUBTYPES	7.58e-03



Component # 24 (stability = 0.527)

Metagene

(involvement of features)



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

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

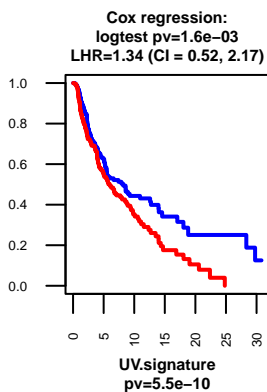
GO:CC neg : 0 terms(FDR<0.1)

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

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

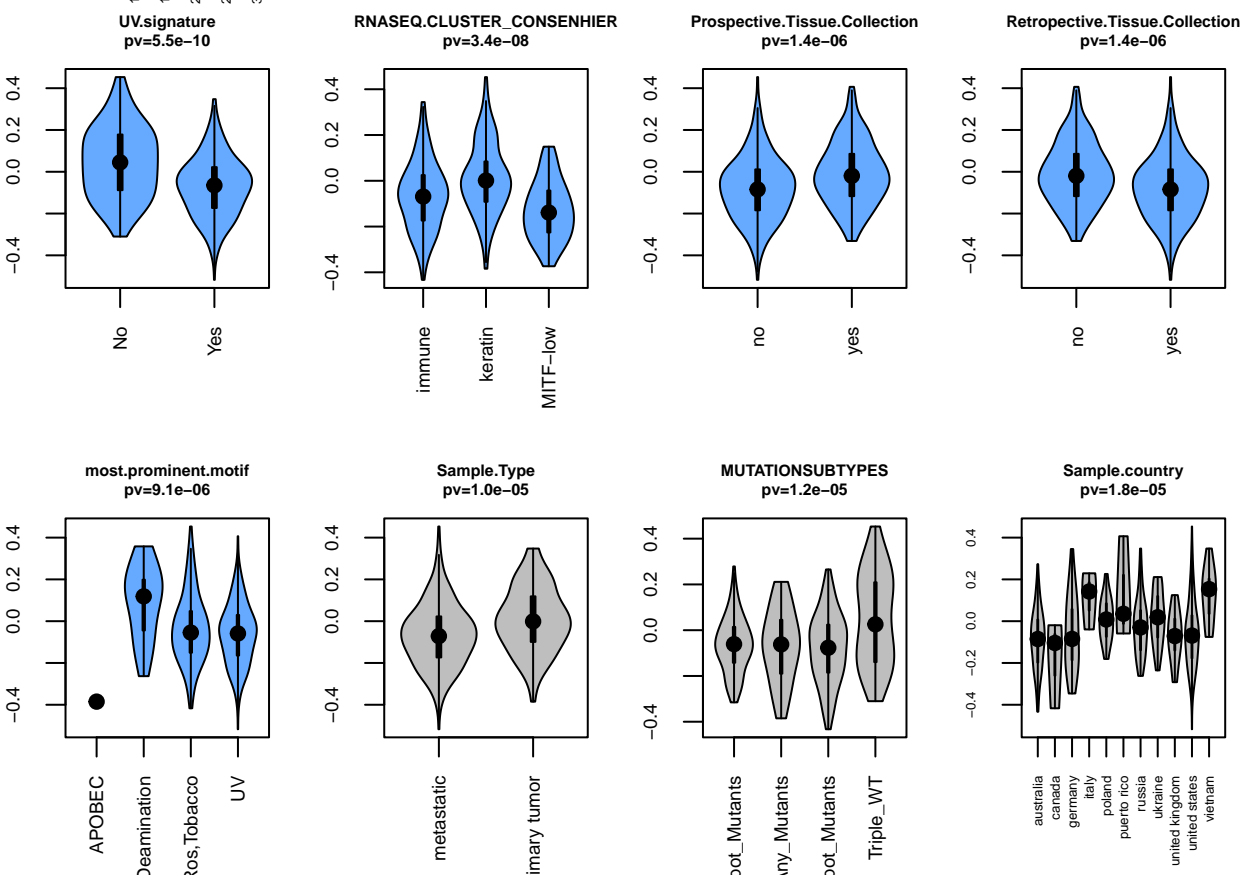
GO:MF pos : 0 terms(FDR<0.1)

- | | |
|---|--|
| <p>19 negative</p> <ul style="list-style-type: none"> TNNT1 BRSK2 CADPS PMP2 PRDM7 CDK5R2 SYT5 RGS11 NELL1 TDRD9 VEPH1 SLITRK5 SEZ6L2 TMEM59L FSD1 FAM163A ALK TMEM151A WDR17 | <p>40 positive</p> <ul style="list-style-type: none"> LRP2 BANCR SCIN ASB11 CHRM1 IRS4 PRKG2 HPGD LRRC52 TMEM215 AGT IL12RB2 OR7C1 CST2 PDE11A AMER2 OR7A5 CDK15 FZD9 RXRG DAPL1 TFAP2B COL2A1 KIT IL1RAPL1 LPAR3 FRG2DP ADAMTS16 COL11A2 RYR2 OLIG1 SEMA3E TYRP1 CCDC129 C1orf95 PITX2 MOG WIPF3 NR0B1 PRRT4 |
|---|--|



- factor**
- UV.signature
 - RNASEQ.CLUSTER_CONSENHIER
 - Prospective.Tissue.Collection
 - Retropective.Tissue.Collection
 - most.prominent.motif
 - Sample.Type
 - MUTATIONSUBTYPES
 - Sample.country
 - New.tumor.event.after.initial.treatment
 - Tumor.location.site

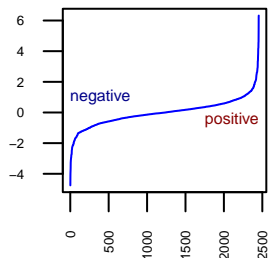
- p.value**
- 5.51e-10
 - 3.36e-08
 - 1.36e-06
 - 1.36e-06
 - 9.10e-06
 - 1.05e-05
 - 1.24e-05
 - 1.76e-05
 - 3.17e-05
 - 3.18e-05



Component # 25 (stability = 0.940)

Metagene

(involvement of features)



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

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

Term	FDR
gluconeogenesis	3.52e-02
acute-phase response	6.02e-02
cellular oxidant detoxification	6.02e-02

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

Term
synaptic vesicle membrane

FDR
2.48e-02

GO:CC pos : 7 terms(FDR<0.1)

Term	FDR
endocytic vesicle lumen	2.67e-06
lipid droplet	2.51e-03
high-density lipoprotein particle	2.51e-03
haptoglobin-hemoglobin complex	1.05e-02
blood microparticle	1.91e-02
cytosol	3.34e-02
extracellular exosome	5.45e-02

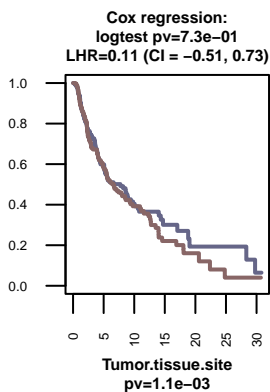
GO:MF neg : 0 terms(FDR<0.1)

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

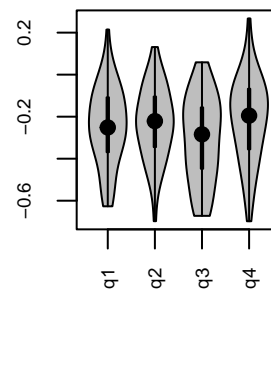
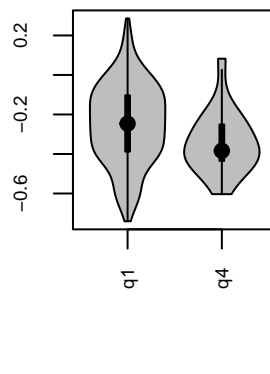
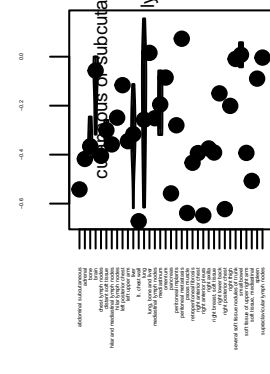
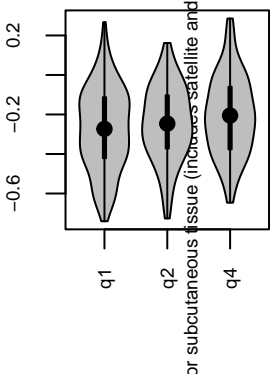
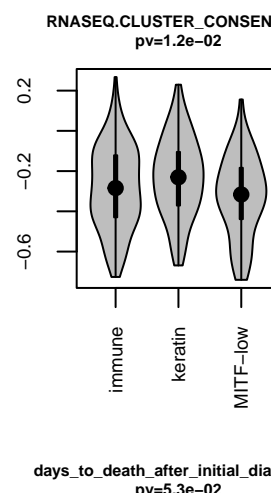
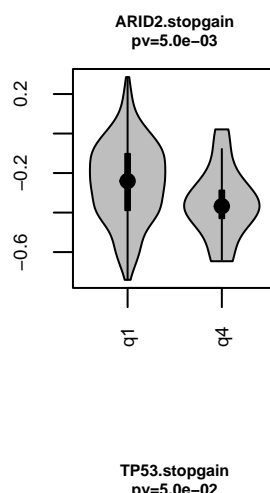
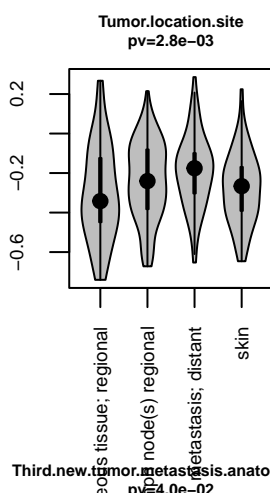
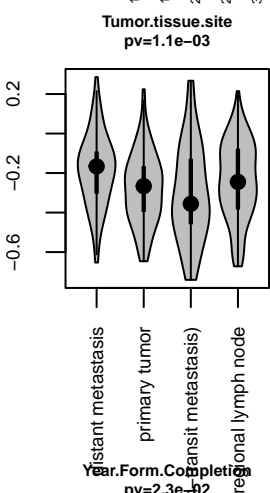
Term	FDR
antioxidant activity	2.41e-02

23 negative 33 positive

- | | |
|----------|----------|
| COL10A1 | ADH1B |
| LRRC15 | ADIPOQ |
| EPYC | PLIN4 |
| COL11A1 | TUSC5 |
| MMP13 | FABP4 |
| WNT2 | PLIN1 |
| OPRD1 | CIDEA |
| INHBA | PI16 |
| ITGBL1 | PLA2G2A |
| SYNDIG1 | HP |
| PPAPDC1A | CD300LG |
| ST6GAL2 | RBP4 |
| OLR1 | SAA1 |
| IL13RA2 | GPD1 |
| FNDC1 | LBP |
| RPH3A | LIN28B |
| CST2 | LIN28A |
| PSG4 | PCK1 |
| FIBIN | HBA2 |
| TENM3 | LEP |
| HS3ST5 | FAM178B |
| COMP | FLJ36000 |
| CST1 | AKR1C2 |
| | HBB |
| | LGALS12 |
| | HIF3A |
| | MGST1 |
| | SLC7A10 |
| | CHRD1 |
| | PRG4 |
| | SCARA5 |
| | ALB |
| | NGEF |



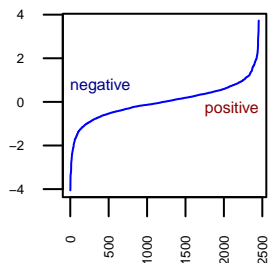
factor	p.value
Tumor.tissue.site	1.11e-03
Tumor.location.site	2.78e-03
ARID2.stopgain	5.03e-03
RNASEQ.CLUSTER_CONSENHIER	1.18e-02
Year.Form.Completion	2.34e-02
Third.new.tumor.metastasis.anatomic.site	3.98e-02
TP53.stopgain	4.98e-02
days_to_death_after_initial_diagnosis	5.35e-02
age.at.death	6.91e-02
Second.new.tumor.metastasis.anatomic.site	6.92e-02



Component # 26 (stability = 0.684)

Metagene

(involvement of features)



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

Term	FDR
homophilic cell adhesion via plasma memb...	3.80e-03
calcium-dependent cell-cell adhesion via...	4.14e-03
neurofilament bundle assembly	3.17e-02

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

Term	FDR
post-translational protein modification	1.33e-03
intermembrane lipid transfer	3.66e-02
chylomicron assembly	9.51e-02

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

Term	FDR
neurofilament	2.77e-03

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

Term	FDR
endoplasmic reticulum lumen	2.00e-03
blood microparticle	1.74e-02
very-low-density lipoprotein particle	1.74e-02
chylomicron	1.74e-02
high-density lipoprotein particle	4.77e-02

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

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

Term	FDR
cholesterol transfer activity	1.45e-02

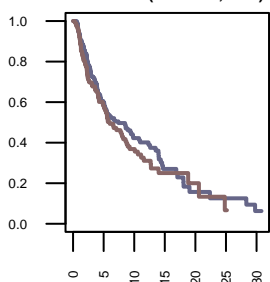
27 negative

PCDHB6
NEFL
PCDHB5
NUDT10
PCDHA11
SFRP1
TRIM58
PCDHA3
PCDHB2
NEFM
PCDHB8
PCDHB3
PCDHB11
NTNG1
MAGEA4
NPTX2
PRIMA1
RNF212
PCDHA10
NUDT11
BEX1
NEFH
SYT6
NELL1
RFPPL1S
KCNS1
GSG1L

15 positive

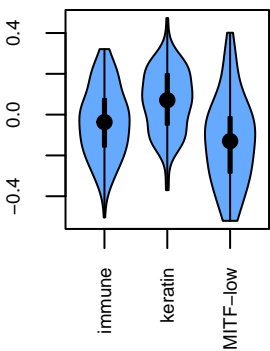
MAGEB1
ALB
ASB11
APOA2
CDKN2A
FGA
MAGEB2
CPN1
CDH15
APOB
SOSTDC1
NECAB2
OVAAL
TEX15
APOA1

Cox regression:
logtest pv=2.0e-02
LHR=0.84 (CI = 0.13, 1.55)

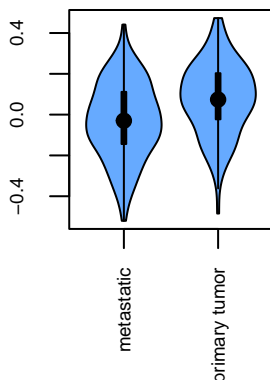


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	1.65e-10
Sample.Type	2.97e-07
initial_pathologic_dx_year	2.98e-06
Breslow.Depth	9.35e-06
Tumor.location.site	1.04e-05
Tumor.tissue.site	1.24e-05
New.tumor.event.after.initial.treatment	3.80e-05
last_contact_days_to	9.03e-05
Sample.country	1.08e-04
Retropective.Tissue.Collection	2.20e-04

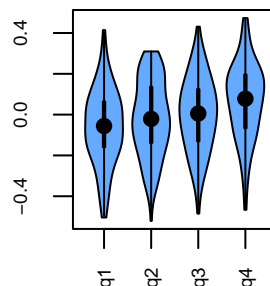
RNASEQ.CLUSTER_CONSENHIER
pv=1.6e-10



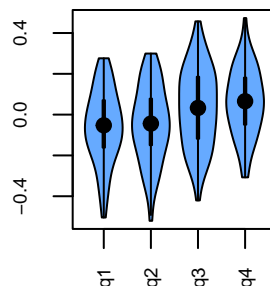
Sample.Type
pv=3.0e-07



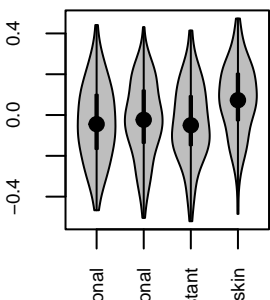
initial_pathologic_dx_year
pv=3.0e-06



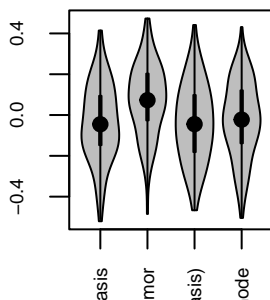
Breslow.Depth
pv=9.4e-06



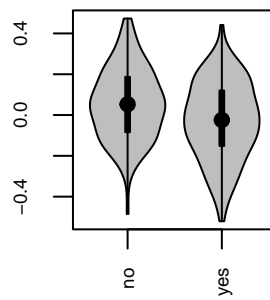
Tumor.location.site
pv=1.0e-05



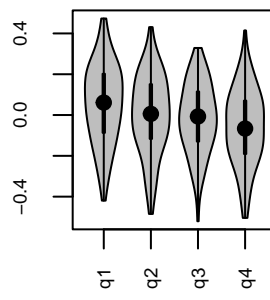
Tumor.tissue.site
pv=1.2e-05



New.tumor.event.after.initial.treatment
pv=3.8e-05

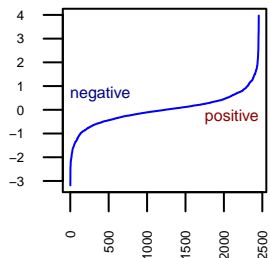


last_contact_days_to
pv=9.0e-05



Component # 27 (stability = 0.549)

Metagene (involvement of features)



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

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

Term
anterior/posterior pattern specification

FDR
2.66e-03

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
RNA polymerase II cis-regulatory region ...

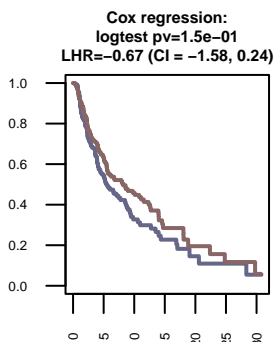
FDR
9.83e-02

27 negative

ZNF667
ZNF415
COL20A1
PSG4
ZNF471
MNX1
PNMA2
BANCR
CKMT1B
SCRG1
SOX1
SCG3
KIF1A
AK5
ZNF229
SLITRK1
LRRC4B
CHRM1
POU3F3
ZNF883
DISC1FP1
ZNF560
SLC35F1
CADM3
CKMT1A
FIBCD1
OLIG2

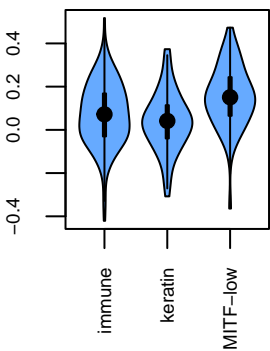
29 positive

BAAT
IL13RA2
RND2
MYL10
GATA4
FAM178B
ASB4
ZNF280A
HOXA10
HOXD13
ZDHHHC8P1
GDF15
HOXA7
CPSF1P1
MAGEA4
LOXL4
FKSG51
SNHG18
UGT2B7
HOXC12
HOXA4
KLHL13
PRAME
C2orf70
PSCA
SFRP5
FGFBP2
MAMDC2
PYY2

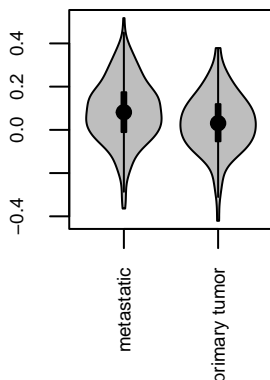


factor	p.value
RNASEQ.CLUSTER_CONSENHIER	7.22e-06
Sample.Type	1.06e-03
Primary.Melanoma.Tissue.Site	1.86e-03
Tumor.location.site	5.23e-03
Tumor.tissue.site	6.84e-03
Retropective.Tissue.Collection	7.12e-03
Prospective.Tissue.Collection	7.12e-03
Drug.name	7.16e-03
Third.new.tumor.metastasis.anatomic.site	1.69e-02
Days.to.second.new.tumor.event.after.initial.treatment	2.25e-02

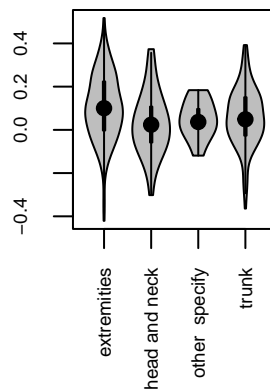
RNASEQ.CLUSTER_CONSENHIER
pv=7.2e-06



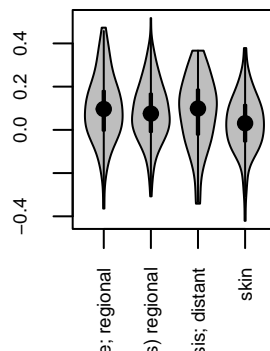
Sample.Type
pv=1.1e-03



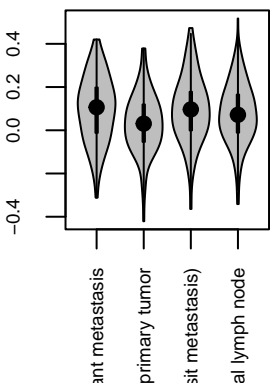
Primary.Melanoma.Tissue.Site
pv=1.9e-03



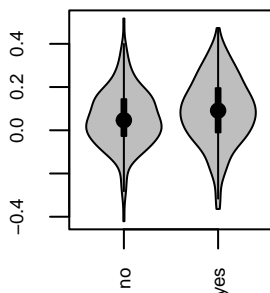
Tumor.location.site
pv=5.2e-03



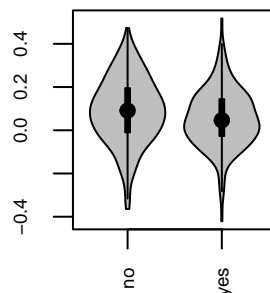
Tumor.tissue.site
pv=6.8e-03



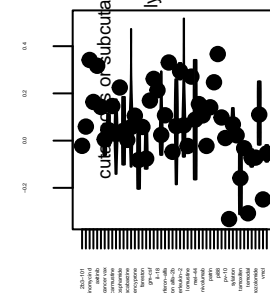
Retropective.Tissue.Collection
pv=7.1e-03



Prospective.Tissue.Collection
pv=7.1e-03

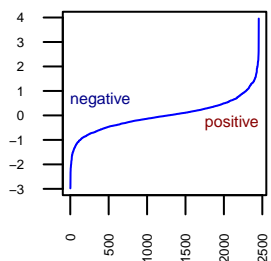


Drug.name
pv=7.2e-03



Component # 28 (stability = 0.539)

Metagene (involvement of features)



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)

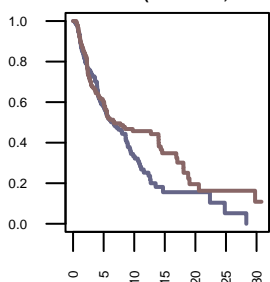
GO:MF neg : 0 terms(FDR<0.1)

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

12 negative **25 positive**

- LCE2A
- MMP8
- PCSK2
- NCAM1
- CCDC129
- ADCY2
- CA8
- DCX
- AMPH
- PRKG2
- SPOCK1
- KCNK2
- MAG
- EDN3
- GAL3ST1
- BAI1
- TESC
- COL9A3
- EWSAT1
- SEMA3B
- LCN2
- LONRF2
- DCSTAMP
- RASAL1
- KLHDC8A
- FAM131B
- HHATL
- SOX8
- RIMS2
- CDH19
- ENTPD2
- MRGPRX4
- NRTN
- ASIC4
- CD22
- ARC
- TNN1

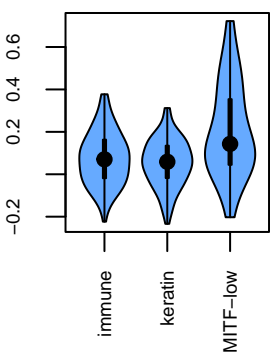
Cox regression:
logtest pv=1.4e-02
LHR=-1.12 (CI = -2.03, -0.20)



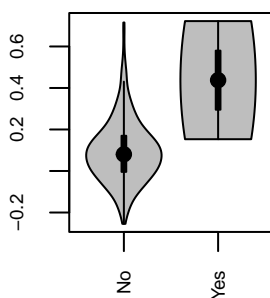
- factor
- RNASEQ.CLUSTER_CONSENHIER
 - HRASQ61.
 - Cancer.stage.N
 - BRAFV600.
 - Primary.Neoplasm.Melanome.Diagnosis
 - ARID2.stopgain
 - age_at_initial_pathologic_diagnosis
 - birth_days_to_initial_diagnosis
 - NF1GainLossFrameshift
 - Year.of.Birth

- p.value
- 1.29e-10
 - 1.24e-03
 - 1.81e-03
 - 3.87e-03
 - 4.24e-03
 - 4.89e-03
 - 5.48e-03
 - 5.77e-03
 - 9.36e-03
 - 1.05e-02

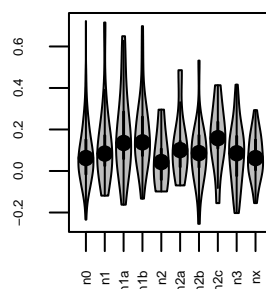
RNASEQ.CLUSTER_CONSENHIER
pv=1.3e-10



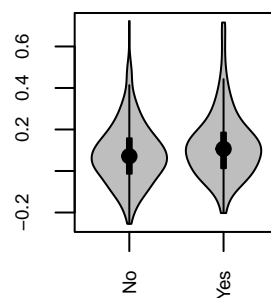
HRASQ61.
pv=1.2e-03



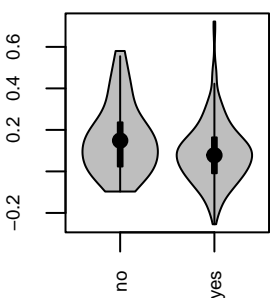
Cancer.stage.N
pv=1.8e-03



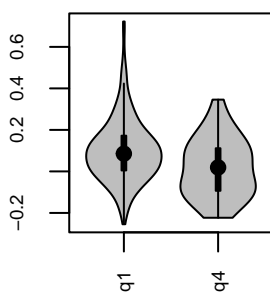
BRAFV600.
pv=3.9e-03



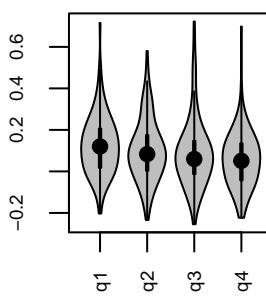
Primary.Neoplasm.Melanome.Diagnosis
pv=4.2e-03



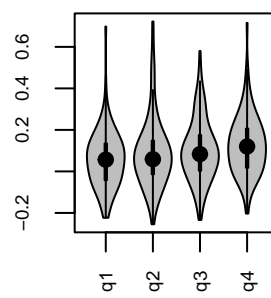
ARID2.stopgain
pv=4.9e-03



age_at_initial_pathologic_diagnosis
pv=5.5e-03



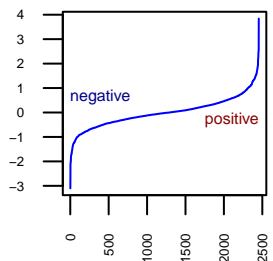
birth_days_to_initial_diagnosis
pv=5.8e-03



Component # 29 (stability = 0.455)

Metagene

(involvement of features)



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

Term
homophilic cell adhesion via plasma memb...
calcium-dependent cell-cell adhesion via...

FDR
2.28e-08
2.00e-03

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

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

Term
integral component of plasma membrane

FDR
6.01e-02

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

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

Term
calcium ion binding

FDR
4.01e-03

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

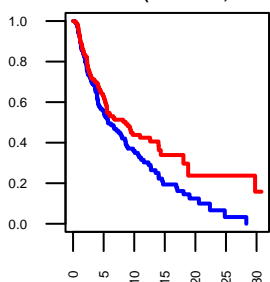
8 negative

MEGF10
PCDHB5
CAP2
MME
PCDHB2
PCDHB8
PCDHA10
FRG2DP

16 positive

EDN3
FAM135B
LCN2
PRSS33
TRIM67
CST1
BMP7
DCSTAMP
ITIH5
RIMS2
TFF2
CHGB
DNASE2B
COL19A1
LHX1
FAM19A3

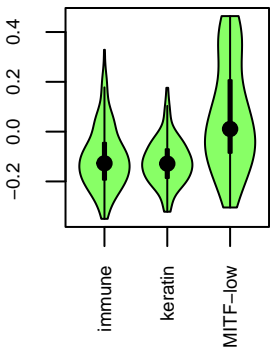
Cox regression:
logtest pv=8.0e-04
LHR=-1.54 (CI = -2.48, -0.61)



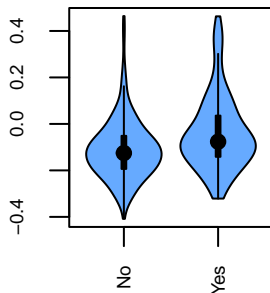
factor
RNASEQ.CLUSTER_CONSENHIER
BRAFV600.
MUTATIONSUBTYPES
ajcc_pathologic_tumor_stage
NF1GainLossFrameshift
Neoadjuvant.Treatment
NRASQ61.
NF1.stopgain
ARID2.splice.donor
Cancer.stage.T

p.value
3.87e-16
2.34e-07
2.41e-07
6.44e-05
3.71e-04
4.40e-04
6.02e-04
7.31e-04
1.21e-03
1.64e-03

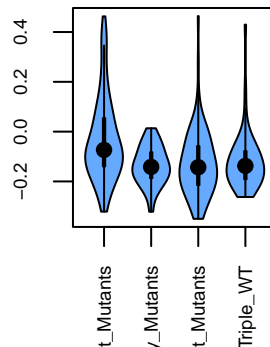
RNASEQ.CLUSTER_CONSENHIER
pv=3.9e-16



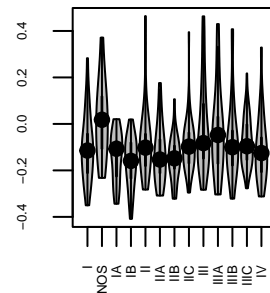
BRAFV600.
pv=2.3e-07



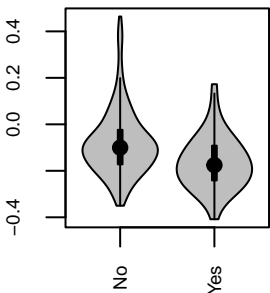
MUTATIONSUBTYPES
pv=2.4e-07



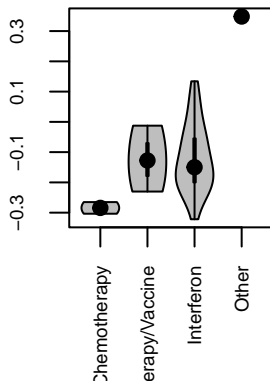
ajcc_pathologic_tumor_stage
pv=6.4e-05



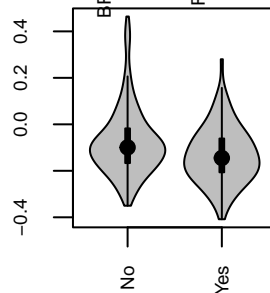
NF1GainLossFrameshift
pv=3.7e-04



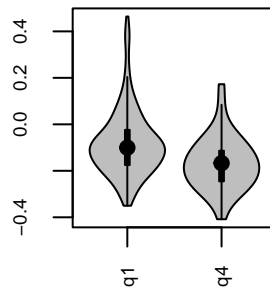
Neoadjuvant.Treatment
pv=4.4e-04



BRAF_Hotspot_Mutants
pv=6.0e-04



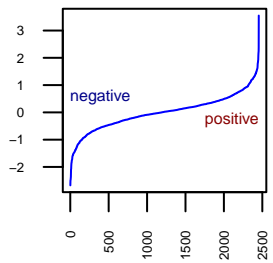
NF1.stopgain
pv=7.3e-04



Component # 30 (stability = 0.481)

Metagene

(involvement of features)



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)

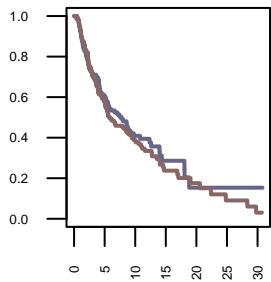
GO:MF pos : 0 terms(FDR<0.1)

12
negative

7
positive

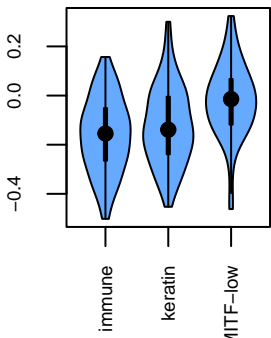
- | | |
|---------|----------|
| CA8 | TMEM132D |
| ILDR2 | POU3F3 |
| KLHL30 | CYSLTR2 |
| MUC7 | SLITRK2 |
| PLCB4 | C5orf38 |
| CST2 | IRX2 |
| ALDH3B2 | TCERG1L |
| CYP2J2 | |
| KLC3 | |
| NPPC | |
| CST5 | |
| MYOZ2 | |

Cox regression:
logtest pv=6.5e-01
LHR=0.18 (CI = -0.61, 0.98)

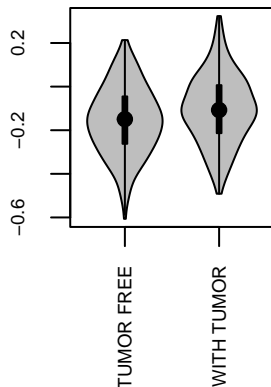


- | factor | p.value |
|-------------------------------------|----------|
| RNASEQ.CLUSTER_CONSENHIER | 1.62e-08 |
| tumor_status_at_last_contact | 3.47e-04 |
| Year.of.last.contact | 1.45e-03 |
| initial_pathologic_dx_year | 2.59e-03 |
| UV.signature | 1.04e-02 |
| Disease.Free.Status.at.last.contact | 1.92e-02 |
| vital_status_at_last_contact | 2.04e-02 |
| fifth.prominent.motiv | 2.43e-02 |
| KRASG12.13. | 2.76e-02 |
| Cancer.stage.T | 3.13e-02 |

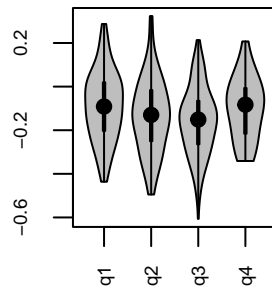
RNASEQ.CLUSTER_CONSENHIER
pv=1.6e-08



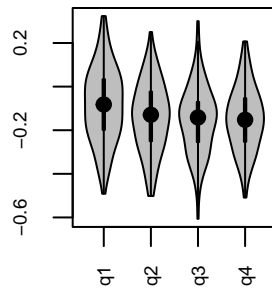
tumor_status_at_last_contact
pv=3.5e-04



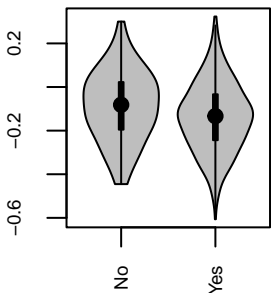
Year.of.last.contact
pv=1.4e-03



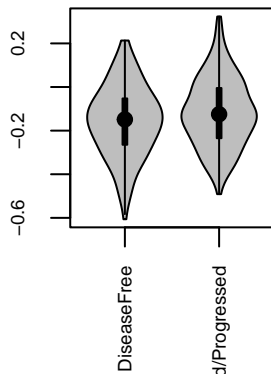
initial_pathologic_dx_year
pv=2.6e-03



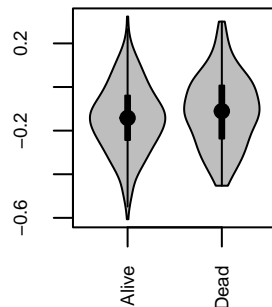
UV.signature
pv=1.0e-02



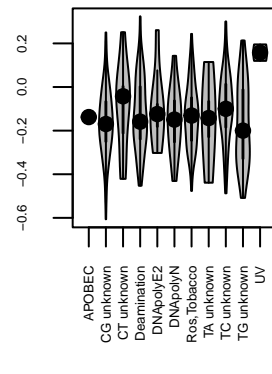
Disease.Free.Status.at.last.contact
pv=1.9e-02



vital_status_at_last_contact
pv=2.0e-02

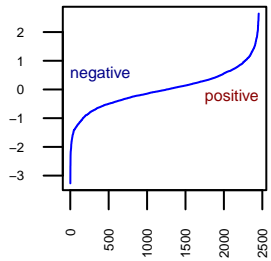


fifth.prominent.motiv
pv=2.4e-02



Component # 31 (stability = 0.516)

Metagene (involvement of features)



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)

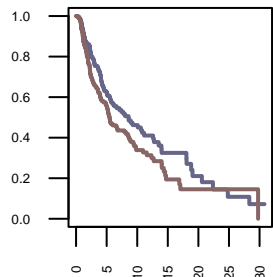
GO:MF neg : 0 terms(FDR<0.1)

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

4 negative **11 positive**

- NELL1
- MYPN
- RPH3A
- CHRNA1
- NR0B1
- TF
- CDH1
- SEMA3D
- PTPRZ1
- GJA3
- NPTX1
- LRP2
- MTRNR2L1
- GPR126
- TMEM151B

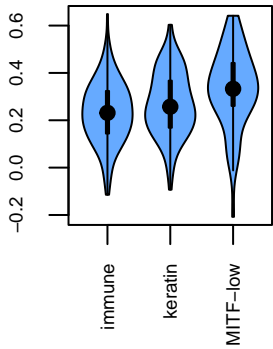
Cox regression:
logtest pv=1.0e-01
LHR=0.72 (CI = -0.15, 1.58)



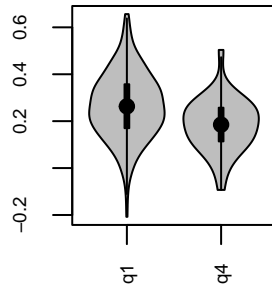
- factor
- RNASEQ.CLUSTER_CONSENHIER
 - NF1.stopgain
 - fifth.prominent.motiv
 - UV.signature
 - second.prominent.motiv
 - NF1GainLossFrameshift
 - fourth.prominent.motiv
 - ARID2.stopgain
 - third.prominent.motiv
 - BRAFV600.

- p.value
- 7.06e-06
 - 1.34e-03
 - 5.92e-03
 - 8.65e-03
 - 1.13e-02
 - 1.15e-02
 - 1.80e-02
 - 2.11e-02
 - 2.42e-02
 - 2.44e-02

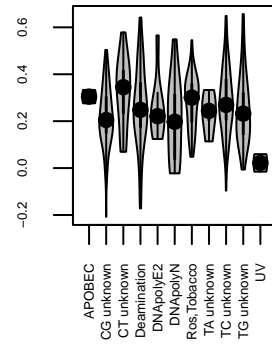
RNASEQ.CLUSTER_CONSENHIER
pv=7.1e-06



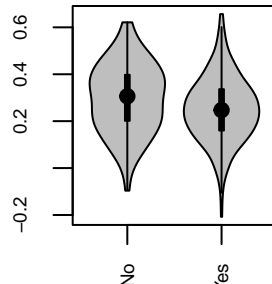
NF1.stopgain
pv=1.3e-03



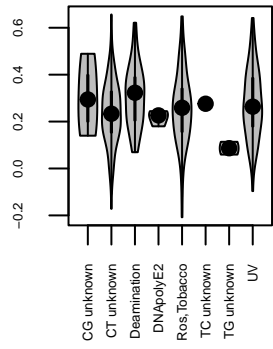
fifth.prominent.motiv
pv=5.9e-03



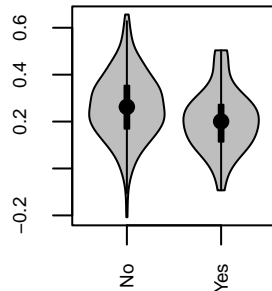
UV.signature
pv=8.6e-03



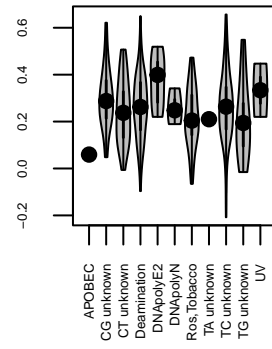
second.prominent.motiv
pv=1.1e-02



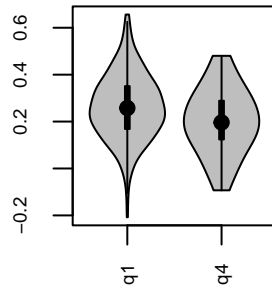
NF1GainLossFrameshift
pv=1.1e-02



fourth.prominent.motiv
pv=1.8e-02

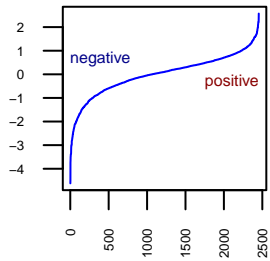


ARID2.stopgain
pv=2.1e-02



Component # 32 (stability = 0.942)

Metagene (involvement of features)



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

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

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

Term	FDR
extracellular exosome	5.34e-07
apicolateral plasma membrane	4.77e-04
clathrin-coated endocytic vesicle	5.49e-02
intermediate filament	5.49e-02

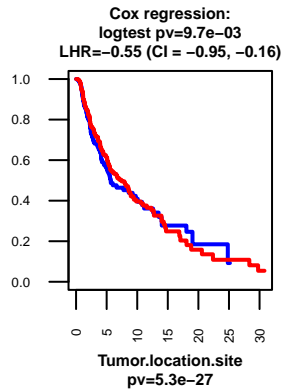
GO:CC pos : 0 terms(FDR<0.1)

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

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

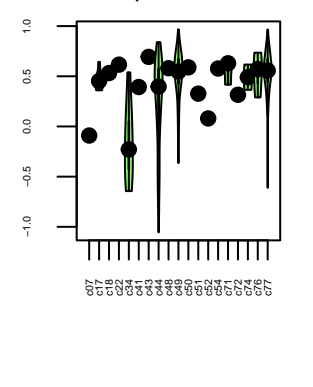
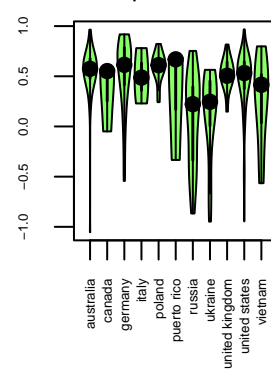
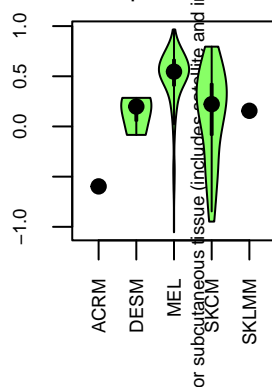
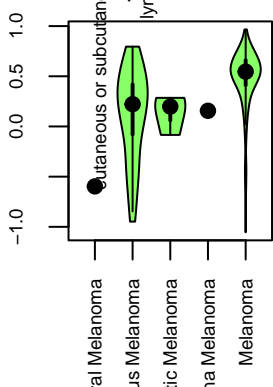
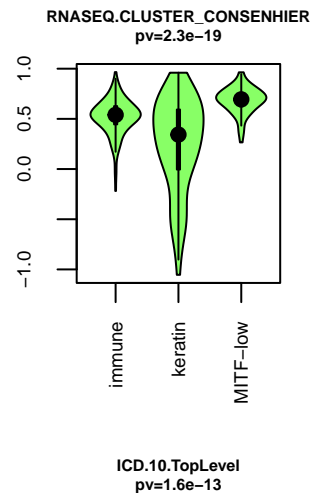
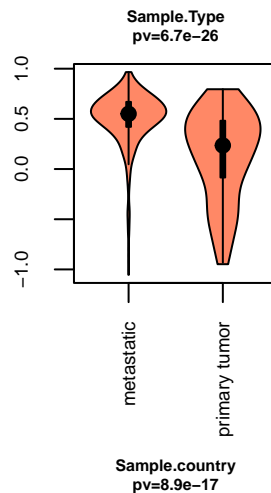
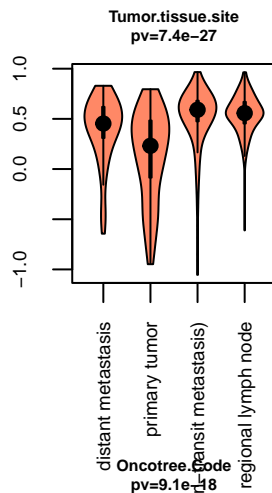
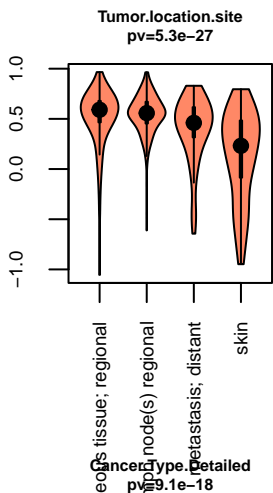
33 negative 0 positive

- SLC34A2
- KRT19
- SFTPB
- KRT7
- SFTPA1
- SFTPA2
- AP1M2
- CST6
- FOLR1
- PRSS8
- WFDC2
- CYP4B1
- ELF3
- AGR2
- GRHL2
- SCNN1A
- EPCAM
- MUC15
- PDZK1IP1
- PIGR
- CLDN4
- SFTPD
- CCDC64B
- GRB7
- KDF1
- MMP7
- CEACAM6
- RAB25
- GGT6
- MAL2
- MUCL1
- DMKN
- SCNN1B



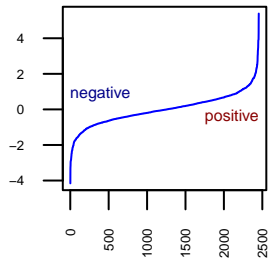
- factor
- Tumor.location.site
 - Tumor.tissue.site
 - Sample.Type
 - RNASEQ.CLUSTER_CONSENHIER
 - Cancer.Type.Detailed
 - Oncotree.Code
 - Sample.country
 - ICD.10.TopLevel
 - Prospective.Tissue.Collection
 - Retropective.Tissue.Collection

- p.value
- 5.35e-27
 - 7.42e-27
 - 6.71e-26
 - 2.27e-19
 - 9.14e-18
 - 9.14e-18
 - 8.94e-17
 - 1.57e-13
 - 5.51e-11
 - 5.51e-11



Component # 33 (stability = 0.942)

Metagene (involvement of features)



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

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

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

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

Term
intermediate filament

FDR
4.96e-02

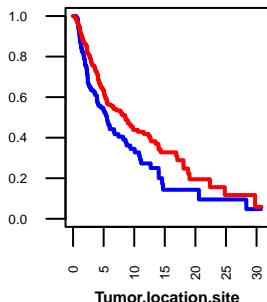
GO:MF neg : 0 terms(FDR<0.1)

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

11 negative 16 positive

- KRT14
- KRT5
- RSPO4
- VEG
- KRT6B
- KRT17
- IRX2
- SCRG1
- CXCL14
- F2RL2
- STMN2
- KRT4
- KRT13
- CRNN
- C7
- CHIT1
- MARCO
- SPRR3
- SLAMF9
- MMP12
- HAMP
- DNAJC5B
- MUC21
- WT1
- TREM1
- OLR1
- SV2B

Cox regression:
logtest pv=4.4e-04
LHR=-1.37 (CI = -2.12, -0.62)



- factor
- Tumor.location.site
 - Sample.Type
 - Tumor.tissue.site
 - Sample.country
 - Cancer.Type.Detailed
 - Oncotree.Code
 - initial_pathologic_dx_year
 - New.tumor.event.after.initial.treatment
 - RNASEQ.CLUSTER_CONSENHIER
 - last_contact_days_to

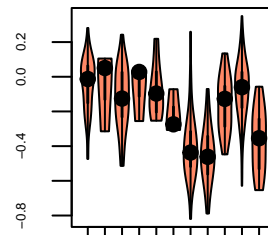
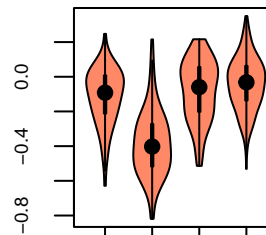
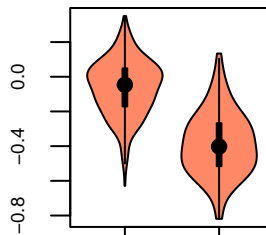
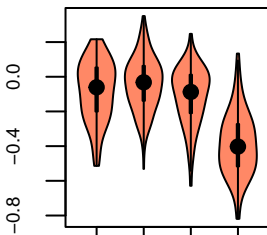
- p.value
- 8.76e-54
 - 3.48e-53
 - 3.22e-52
 - 5.40e-44
 - 1.56e-33
 - 1.56e-33
 - 3.71e-25
 - 2.64e-24
 - 8.34e-23
 - 1.79e-17

Tumor.location.site
pv=8.8e-54

Sample.Type
pv=3.5e-53

Tumor.tissue.site
pv=3.2e-52

Sample.country
pv=5.4e-44

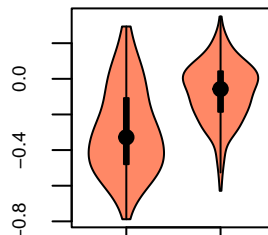
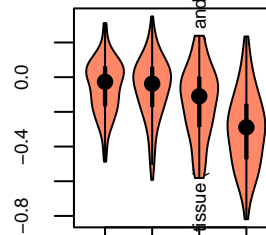
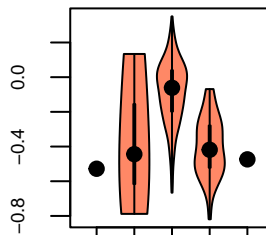
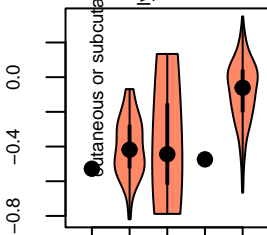


Cancer.Type.Detailed
pv=1.6e-33

Oncotree.Code
pv=1.6e-33

initial_pathologic_dx_year
pv=3.7e-25

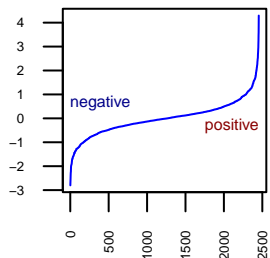
New.tumor.event.after.initial.treatment
pv=2.6e-24



Component # 34 (stability = 0.677)

Metagene

(involvement of features)



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 : 3 terms(FDR<0.1)

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

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

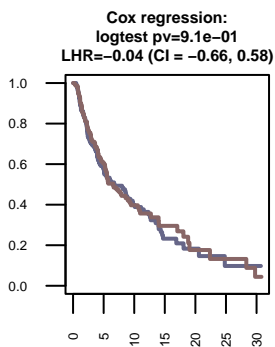
20 negative **38 positive**

- HPGD
- GFRA3
- ANXA3
- RXRG
- COL2A1
- TMEM215
- HOXB13
- CST2
- DNAH2
- PDE11A
- CNTN3
- CYP2J2
- ARHGEF5
- SYTL5
- TFAP2B
- LRP2
- FRG2DP
- SOSTDC1
- MAB21L1
- SLC9A7P1

- TNNT1
- CDK5R2
- TMEM151A
- EEF1A2
- BRSK2
- SULT4A1
- VGF
- C1QL4
- HCN2
- FAM155B
- APLP1
- PHF21B
- KCNN1
- L1CAM
- LHFPL4
- ATP1A3
- BEX1
- SYT3
- NPTXR
- RTBDN
- TMEM59L
- KCNQ2
- CADPS
- UNC13A
- SEZ6L2
- NAT16
- NPTX2
- SYT5
- MAPK8IP2
- SNAP25
- FSD1
- GNAO1
- GABRB3
- VSTM2L
- SCN8A
- WDR17
- ZFR2
- SCG3

Term
 axon
 somatodendritic compartment
 synapse

FDR
 3.91e-02
 8.27e-02
 8.27e-02



factor
 ARID2.stopgain
 RNASEQ.CLUSTER_CONSENHIER
 MUTATIONSUBTYPES
 age_at_initial_pathologic_diagnosis
 birth_days_to_initial_diagnosis
 most.prominent.motif
 BRAFV600.
 Third.new.tumor.metastasis.anatomic.site
 age.at.last.contact
 NRASQ61.

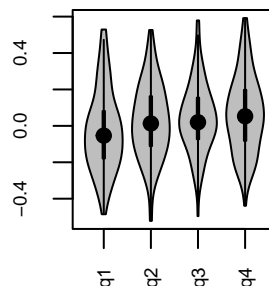
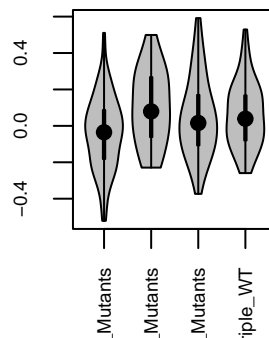
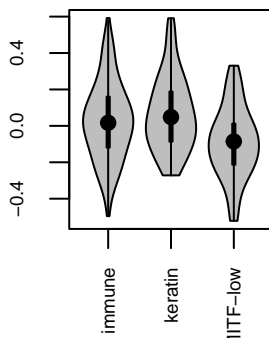
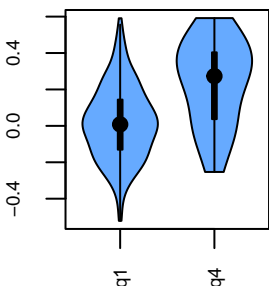
p.value
 4.96e-08
 2.49e-05
 2.50e-04
 7.49e-03
 7.64e-03
 8.01e-03
 8.85e-03
 1.29e-02
 1.89e-02
 1.89e-02

ARID2.stopgain
 pv=5.0e-08

RNASEQ.CLUSTER_CONSENHIER
 pv=2.5e-05

MUTATIONSUBTYPES
 pv=2.5e-04

age_at_initial_pathologic_diagnosis
 pv=7.5e-03

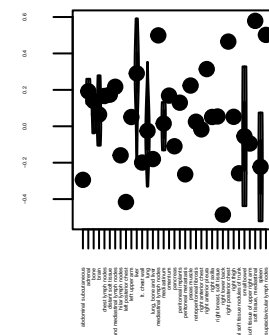
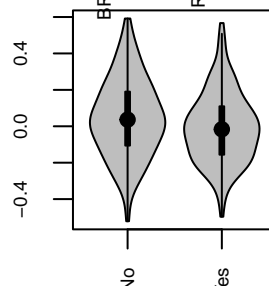
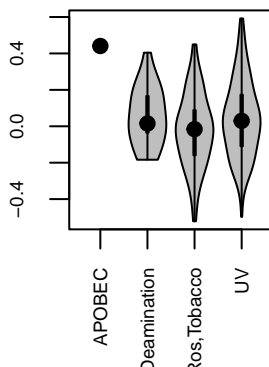
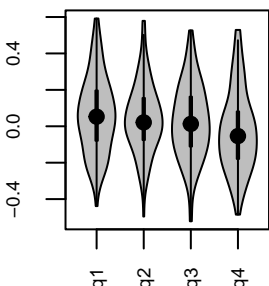


birth_days_to_initial_diagnosis
 pv=7.6e-03

most.prominent.motif
 pv=8.0e-03

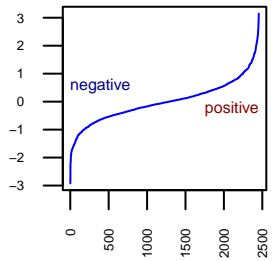
BRAFV600
 pv=8.8e-03

Third.new.tumor.metastasis.anatomic.s
 pv=1.3e-02



Component # 35 (stability = 0.555)

Metagene (involvement of features)



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)

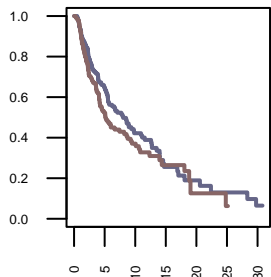
GO:MF neg : 0 terms(FDR<0.1)

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

2 negative **12 positive**

- CDH19
- TMEM178B
- VEPH1
- NTNG1
- SERPINB7
- LCE2A
- MTRNR2L1
- NTSR1
- FAM180A
- MMP1
- TUNAR
- WNT7B
- CORO2B
- SLC14A1

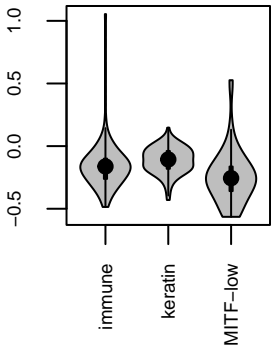
Cox regression:
logtest pv=6.5e-02
LHR=0.74 (CI = -0.02, 1.49)



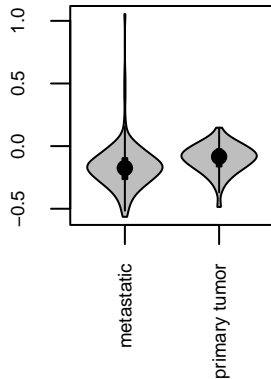
- factor
- RNASEQ.CLUSTER_CONSENHIER
- Sample.Type
- Drug.name
- Tumor.tissue.site
- Tumor.location.site
- New.tumor.event.after.initial.treatment
- Days.to.third.new.tumor.event.after.initial.treatment
- initial_pathologic_dx_year
- Year.of.Birth
- Days.to.second.new.tumor.event.after.initial.treatment

- p.value
- 3.84e-05
- 2.64e-04
- 2.83e-04
- 7.11e-04
- 1.10e-03
- 3.10e-03
- 5.62e-03
- 6.96e-03
- 6.99e-03
- 7.81e-03

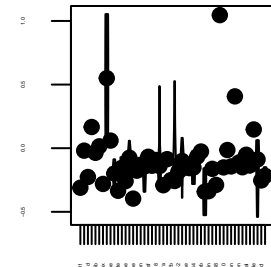
RNASEQ.CLUSTER_CONSENHIER
pv=3.8e-05



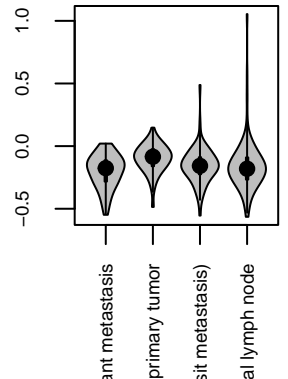
Sample.Type
pv=2.6e-04



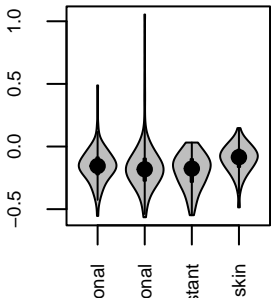
Drug.name
pv=2.8e-04



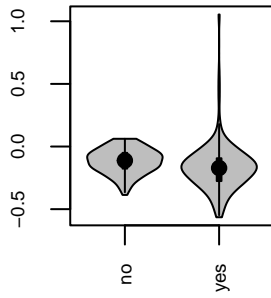
Tumor.tissue.site
pv=7.1e-04



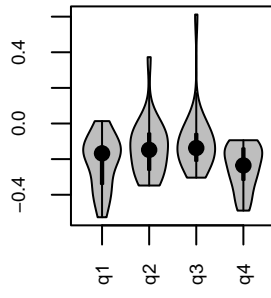
Tumor.location.site
pv=1.1e-03



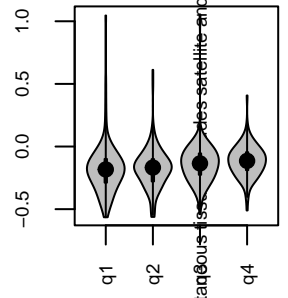
New.tumor.event.after.initial.treatment
pv=3.1e-03



Days.to.third.new.tumor.event.after.initial.treatment
pv=5.6e-03

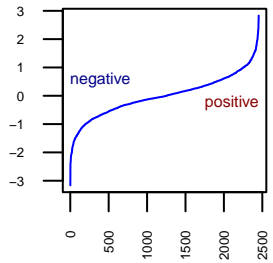


initial_pathologic_dx_year
pv=7.0e-03



Component # 36 (stability = 0.588)

Metagene (involvement of features)



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)

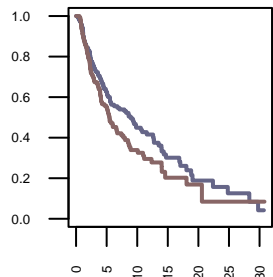
GO:MF neg : 0 terms(FDR<0.1)

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

- 1 negative**
- 4 positive**
- COL20A1
- HS6ST2
- RIMS4
- DSG2
- CKMT1B

Term
creatine kinase activity
FDR
9.23e-02

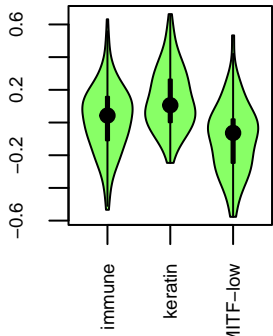
Cox regression:
logtest pv=5.2e-02
LHR=0.63 (CI = -0.01, 1.27)



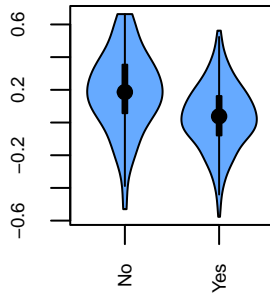
- factor**
- RNASEQ.CLUSTER_CONSENHIER
- UV.signature
- Tumor.tissue.site
- Tumor.location.site
- most.prominent.motif
- Retropective.Tissue.Collection
- Prospective.Tissue.Collection
- initial_pathologic_dx_year
- MUTATIONSUBTYPES
- ajcc_pathologic_tumor_stage

- p.value**
- 1.28e-11
- 1.29e-09
- 2.67e-08
- 8.82e-08
- 5.86e-07
- 7.46e-07
- 7.46e-07
- 3.91e-05
- 1.03e-04
- 1.29e-04

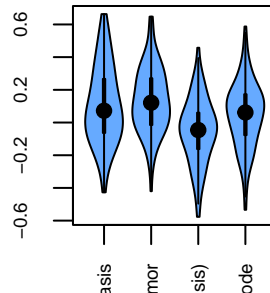
RNASEQ.CLUSTER_CONSENHIER
pv=1.3e-11



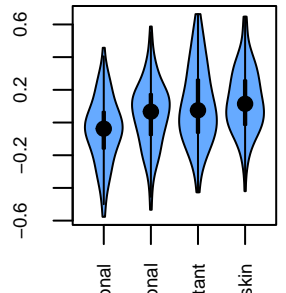
UV.signature
pv=1.3e-09



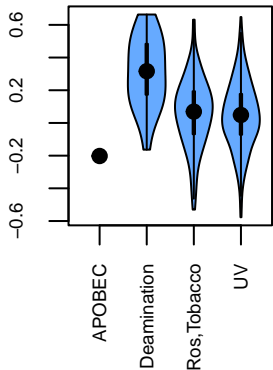
Tumor.tissue.site
pv=2.7e-08



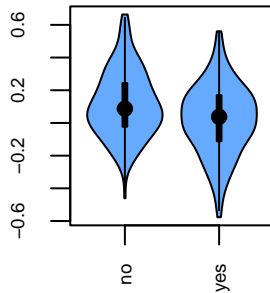
Tumor.location.site
pv=8.8e-08



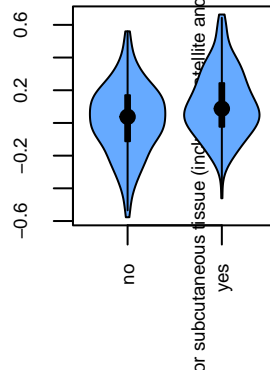
most.prominent.motif
pv=5.9e-07



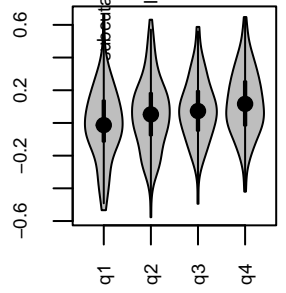
Retropective.Tissue.Collection
pv=7.5e-07



Prospective.Tissue.Collection
pv=7.5e-07

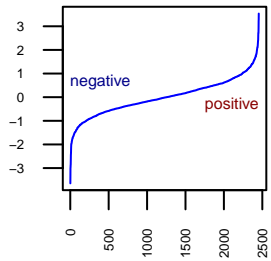


initial_pathologic_dx_year
pv=3.9e-05



Component # 37 (stability = 0.676)

Metagene (involvement of features)



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

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

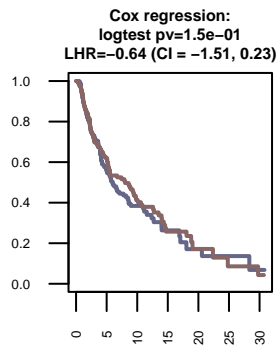
GO:CC neg : 0 terms(FDR<0.1)

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

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

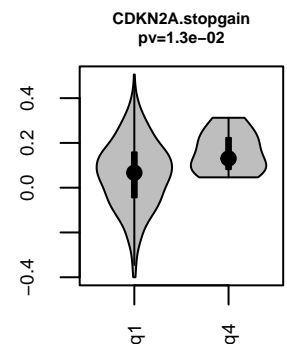
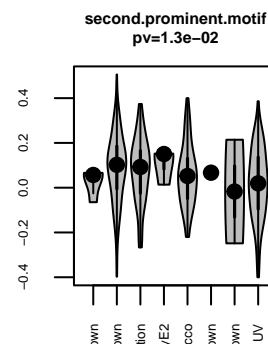
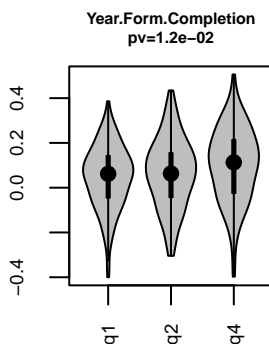
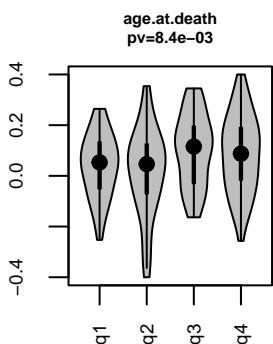
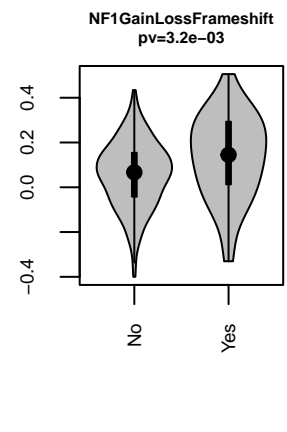
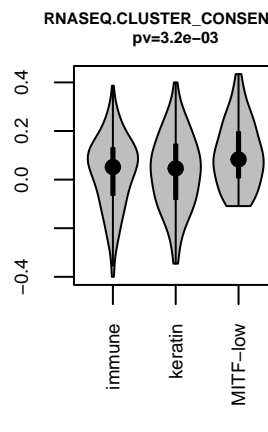
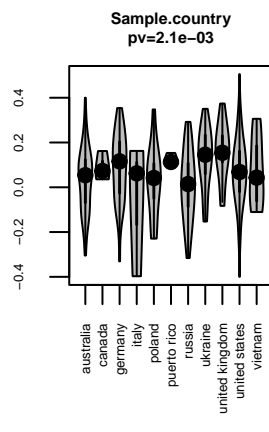
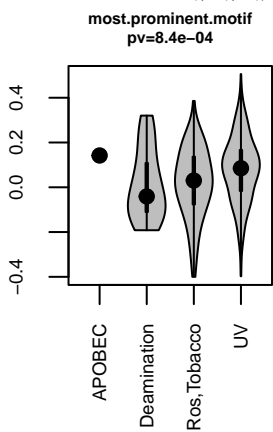
GO:MF pos : 0 terms(FDR<0.1)

- | | |
|----------------------|----------------------|
| 6
negative | 7
positive |
| NELL1 | ALB |
| TYRP1 | DPY19L2 |
| CHRNA6 | TF |
| HS3ST2 | FER1L4 |
| TRIM58 | COL11A2 |
| CHIT1 | FLJ16779 |
| | MIAT |



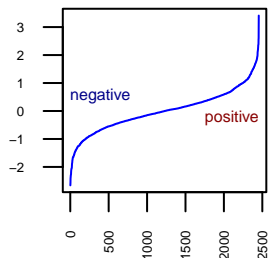
- factor
- most.prominent.motif
 - Sample.country
 - RNASEQ.CLUSTER_CONSENHIER
 - NF1GainLossFrameshift
 - age.at.death
 - Year.Form.Completion
 - second.prominent.motif
 - CDKN2A.stopgain
 - Year.of.last.contact
 - NRASQ61.

- p.value
- 8.41e-04
 - 2.05e-03
 - 3.16e-03
 - 3.23e-03
 - 8.38e-03
 - 1.18e-02
 - 1.25e-02
 - 1.30e-02
 - 1.36e-02
 - 1.70e-02



Component # 38 (stability = 0.668)

Metagene (involvement of features)



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

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

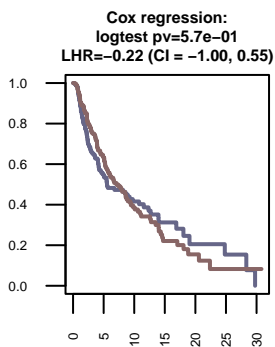
GO:CC neg : 0 terms(FDR<0.1)

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

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

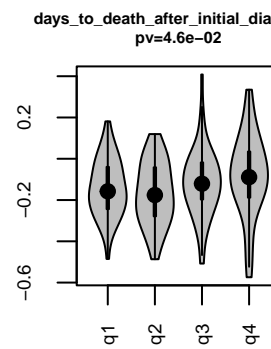
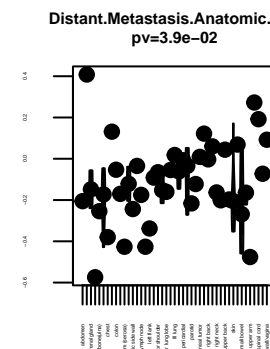
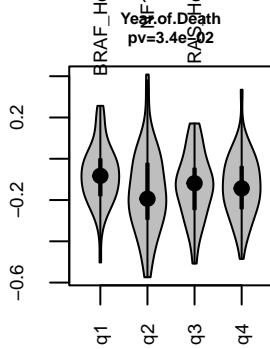
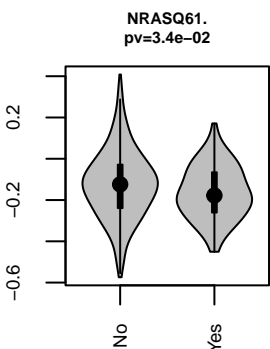
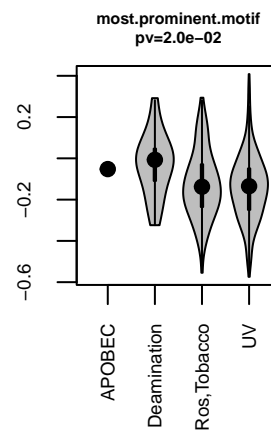
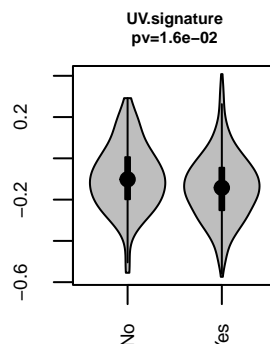
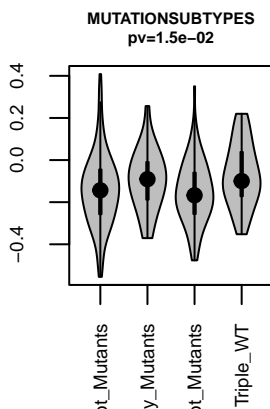
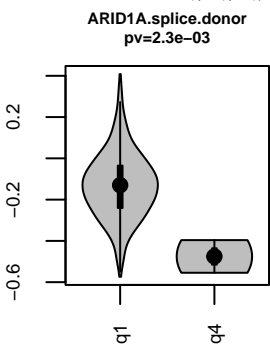
GO:MF pos : 0 terms(FDR<0.1)

0 negative
2 positive
DPP6
LRAT



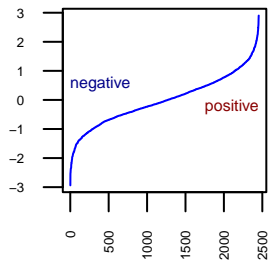
- factor
- ARID1A.splice.donor
 - MUTATIONSUBTYPES
 - UV.signature
 - most.prominent.motif
 - NRASQ61.
 - Year.of.Death
 - Distant.Metastasis.Anatomic.Site
 - days_to_death_after_initial_diagnosis
 - Neoadjuvant.Treatment
 - TP53.stopgain

- p.value
- 2.30e-03
 - 1.47e-02
 - 1.63e-02
 - 2.01e-02
 - 3.39e-02
 - 3.40e-02
 - 3.90e-02
 - 4.60e-02
 - 6.24e-02
 - 7.54e-02



Component # 39 (stability = 0.747)

Metagene (involvement of features)



0 negative 0 positive

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

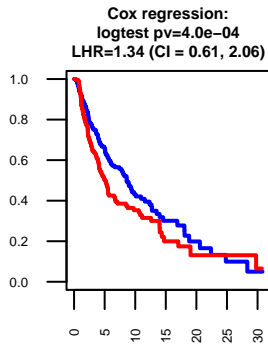
GO:BP pos : 0 terms(FDR<0.1)

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

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

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

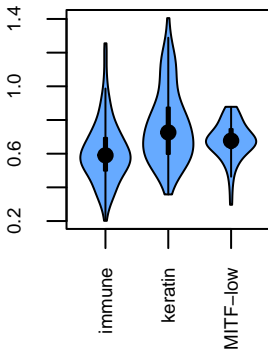
GO:MF pos : 0 terms(FDR<0.1)



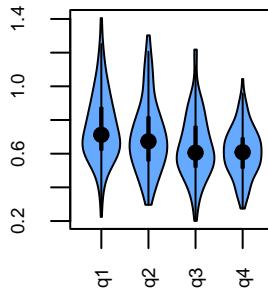
factor
RNASEQ.CLUSTER_CONSENHIER
last_contact_days_to
Sample.Type
Tumor.tissue.site
Tumor.location.site
initial_pathologic_dx_year
Cancer.Type.Detailed
Oncotree.Code
Sample.country
Year.Form.Completion

p.value
2.43e-09
3.23e-08
4.31e-08
9.04e-08
3.88e-07
1.39e-06
3.61e-05
3.61e-05
4.01e-05
1.89e-04

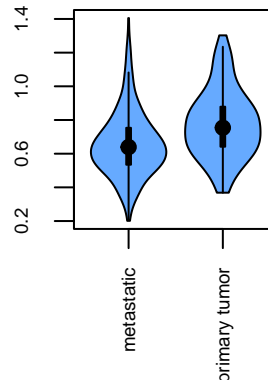
RNASEQ.CLUSTER_CONSENHIER
pv=2.4e-09



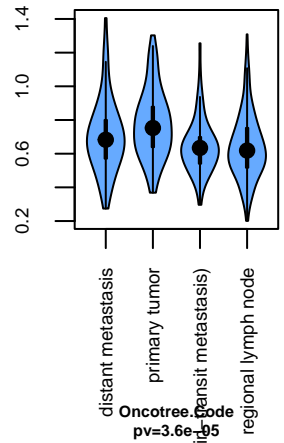
last_contact_days_to
pv=3.2e-08



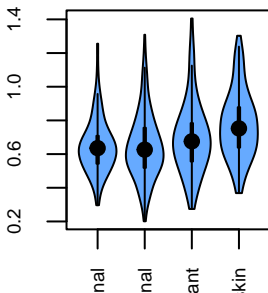
Sample.Type
pv=4.3e-08



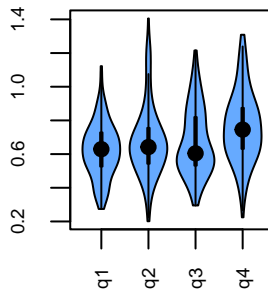
Tumor.tissue.site
pv=9.0e-08



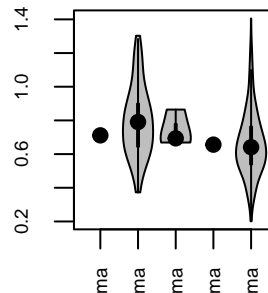
Tumor.location.site
pv=3.9e-07



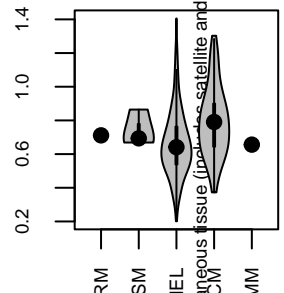
initial_pathologic_dx_year
pv=1.4e-06



Cancer.Type.Detailed
pv=3.6e-05

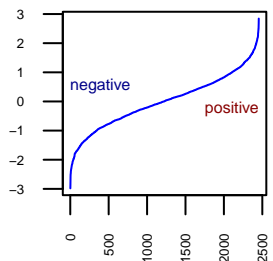


Oncotree.Code
pv=3.6e-05



Component # 40 (stability = 0.846)

Metagene (involvement of features)



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

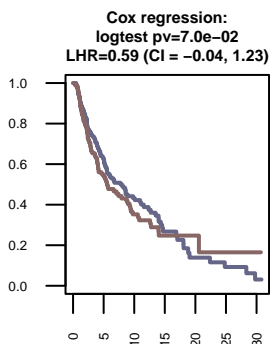
GO:BP pos : 0 terms(FDR<0.1)

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
- RNASEQ.CLUSTER_CONSENHIER
 - Year.Form.Completion
 - initial_pathologic_dx_year
 - Tumor.tissue.site
 - Tumor.location.site
 - last_contact_days_to
 - Sample.country
 - most.prominent.motif
 - Sample.Type
 - second.prominent.motif

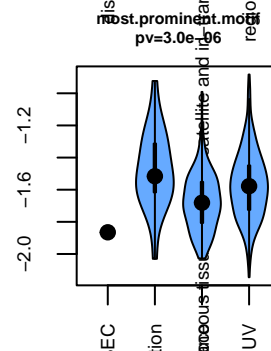
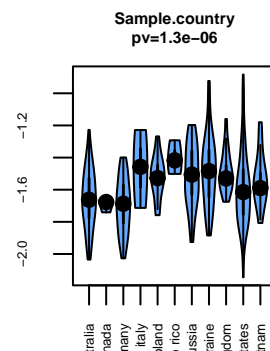
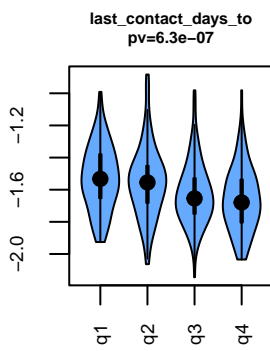
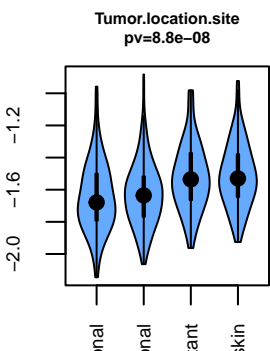
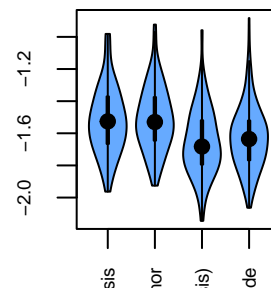
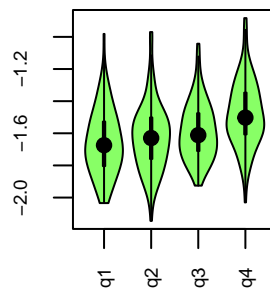
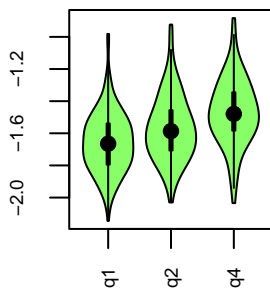
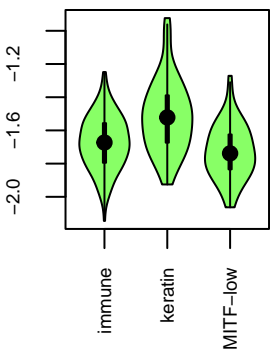
- p.value
- 5.43e-14
 - 9.24e-14
 - 9.14e-11
 - 2.19e-08
 - 8.76e-08
 - 6.33e-07
 - 1.28e-06
 - 2.98e-06
 - 3.66e-06
 - 8.02e-06

RNASEQ.CLUSTER_CONSENHIER
pv=5.4e-14

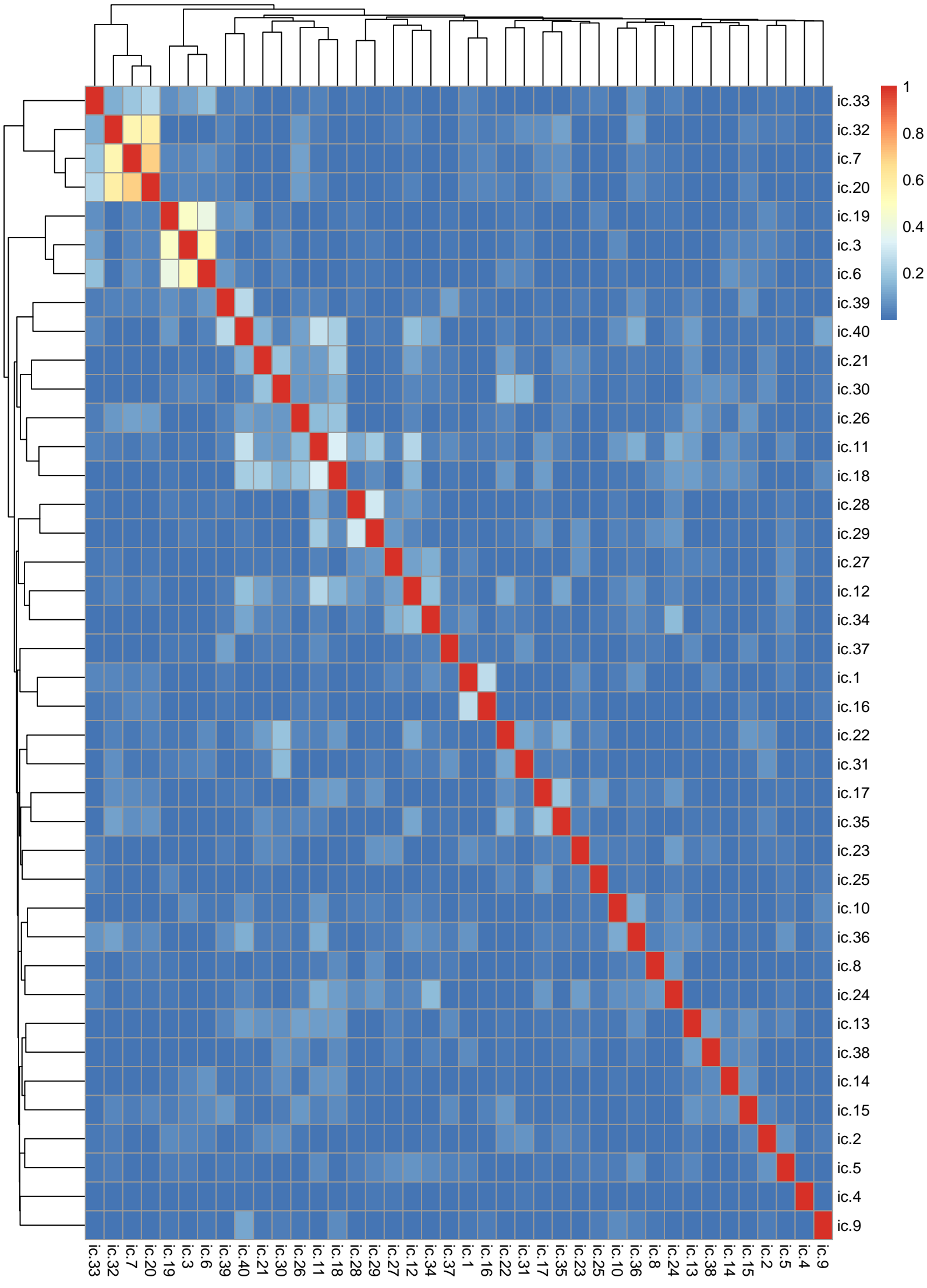
Year.Form.Completion
pv=9.2e-14

initial_pathologic_dx_year
pv=9.1e-11

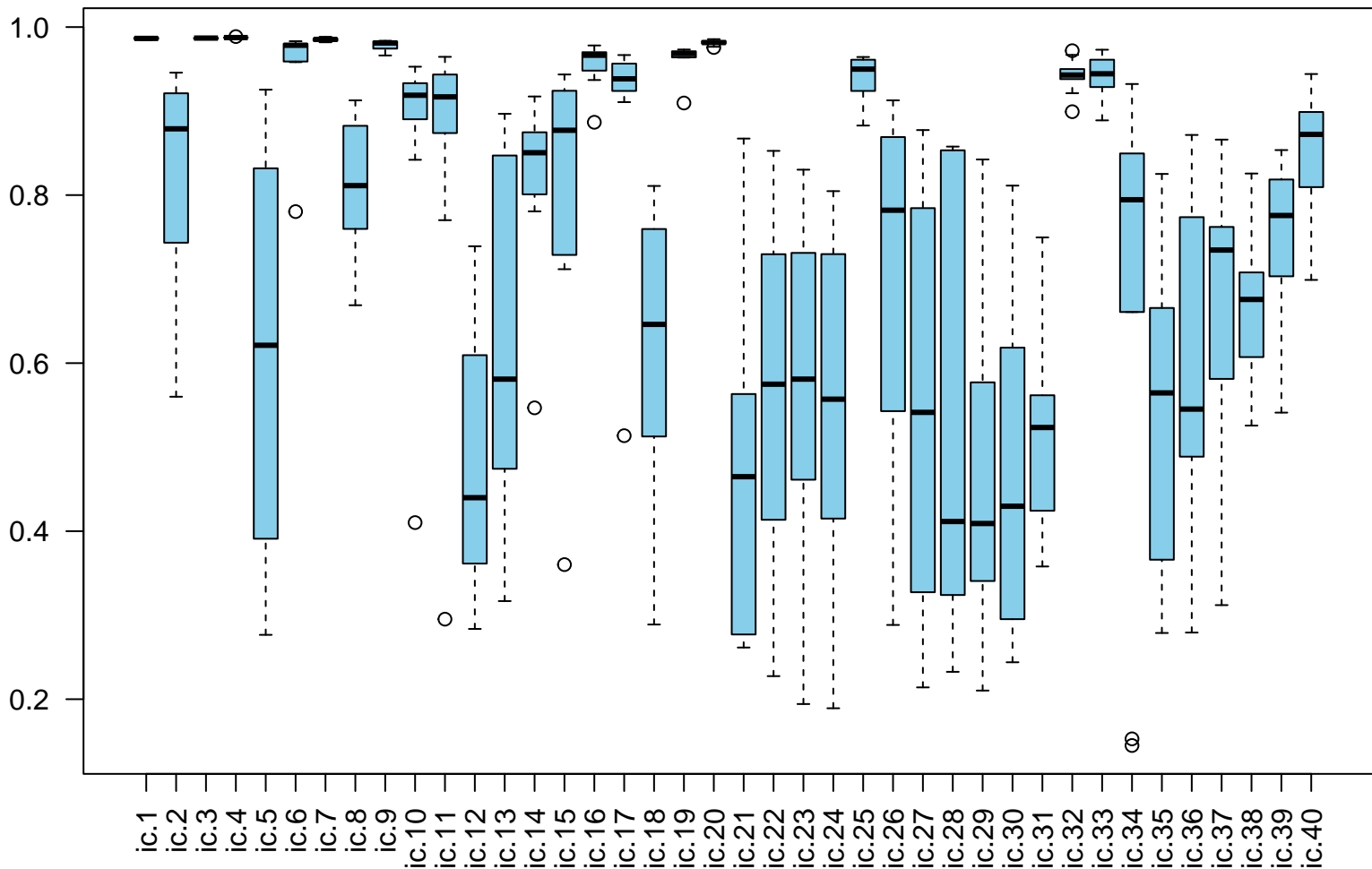
Tumor.tissue.site
pv=2.2e-08



R2 of M-matrix



Stability (10 runs)



Distribution of mean R2 among rows of M-matrix

