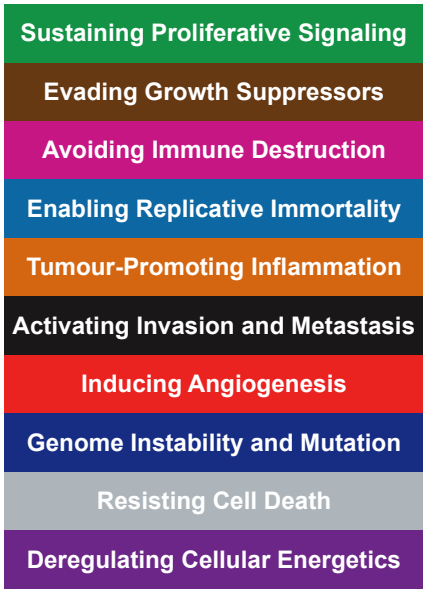
Pathway-based dissection of the genomic heterogeneity of cancer hallmarks' acquisition with SLAPenrich

Francesco Iorio, Luz Garcia-Alonso, Jonathan S. Brammeld, Inĩgo Martincorena, David R. Wille, Ultan McDermott, and Julio Saez-Rodriguez

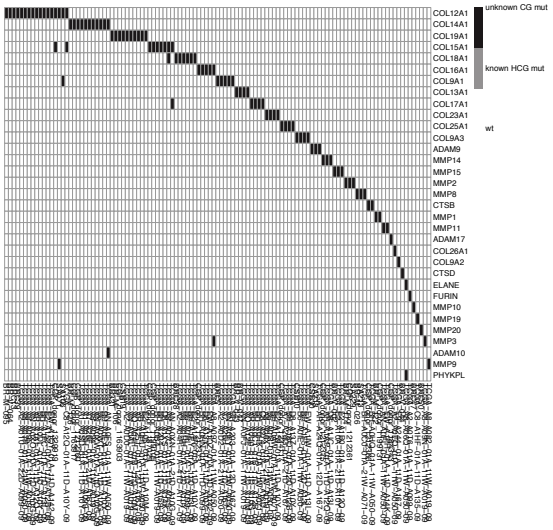
Supplementary Results

Color legend:

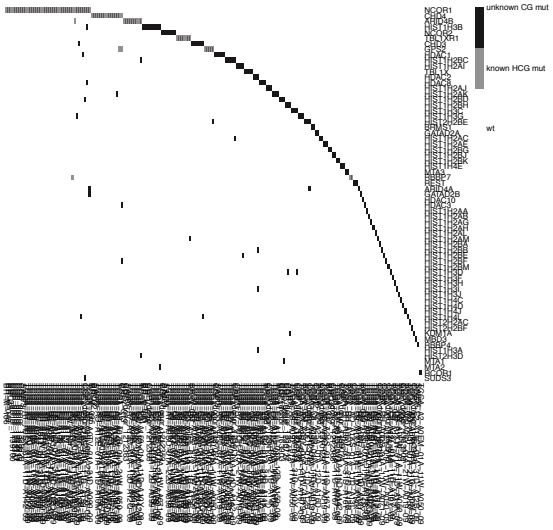


BRCA

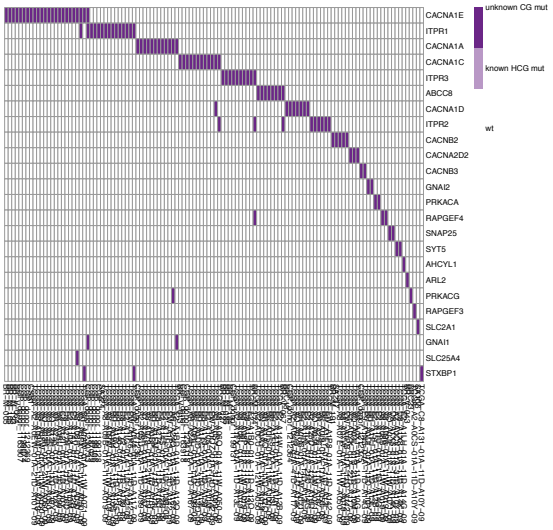
Collagen Degradation
FDR = 1.1%, FDR nod = 2.2%



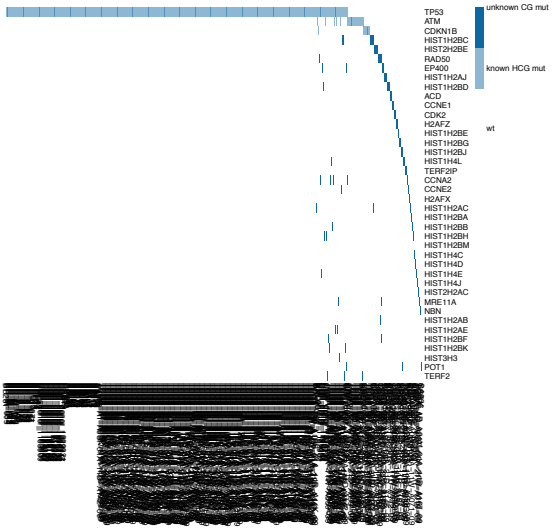
HDACs Deacetylate Histones
FDR = 1.6e−10%, FDR nod = 0.066%



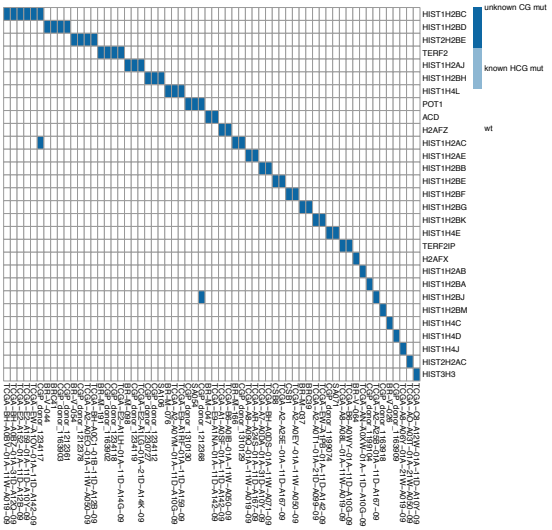
Regulation Of Insulin Secretion
FDR = 0.57%, FDR nod = 1.2%



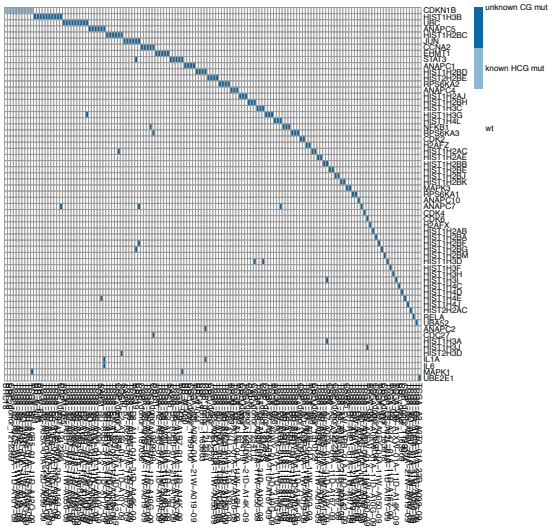
DNA Damage/Telomere Stress Induced Senescence
FDR = 7e−12%, FDR nod = 0.0024%

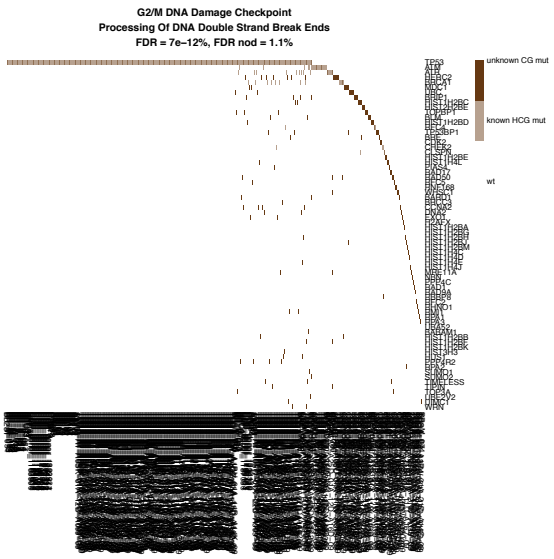


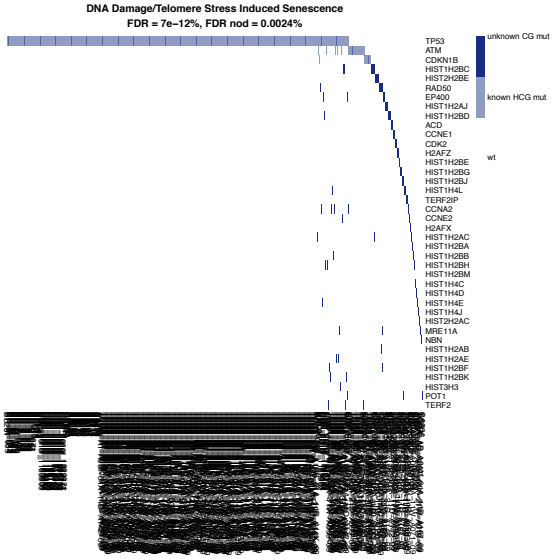
Packaging Of Telomere Ends
FDR = 1.3e−10%, FDR nod = 1.2e−09%

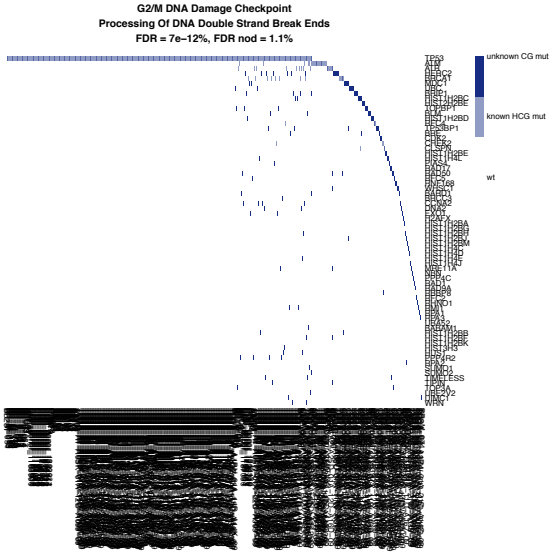


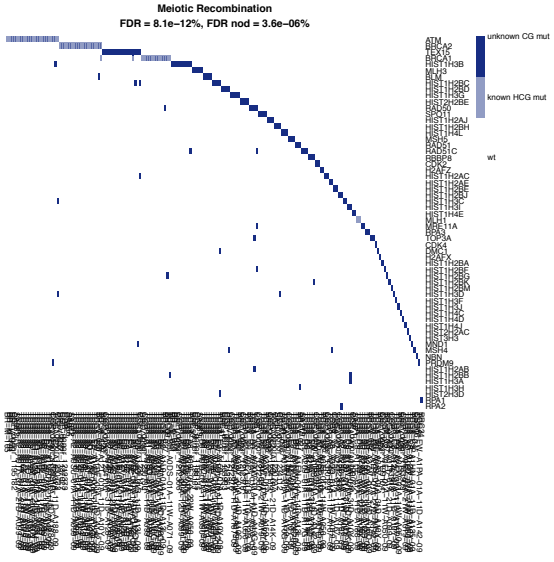
Senescence Associated Secretory Phenotype (SASP)
FDR = 0.00031%, FDR nod = 0.016%

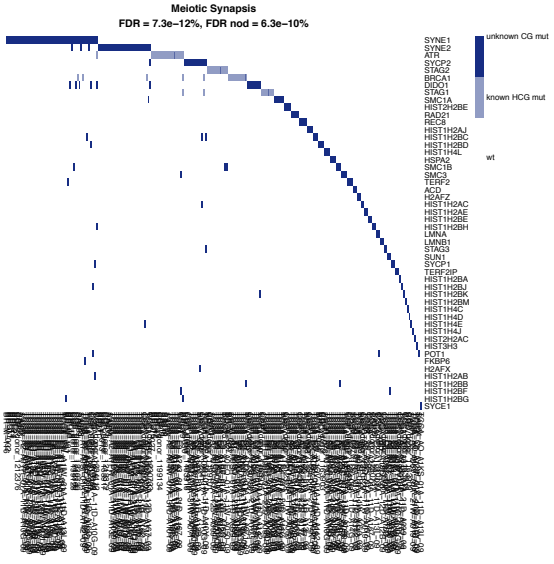


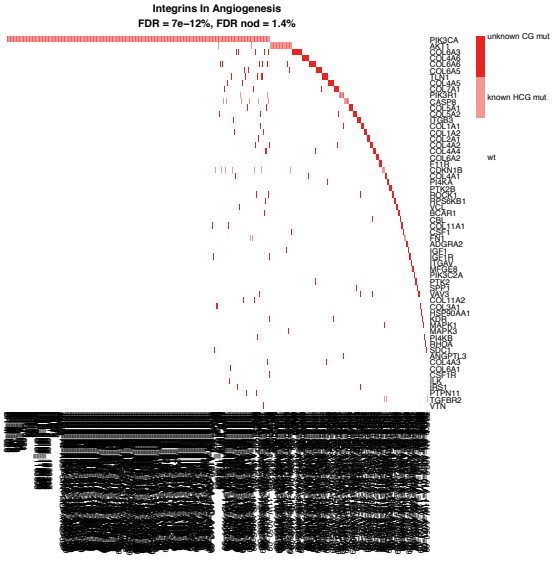

G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 7e−12%, FDR nod = 1.1%
unknown CG mut
known HCG mut
wt

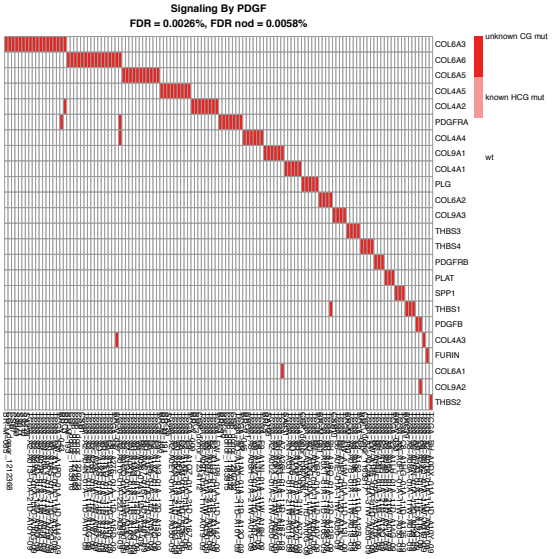

DNA Damage/Telomere Stress Induced Senescence
FDR = 7e−12%, FDR nod = 0.0024%
unknown CG mut
known HCG mut
wt

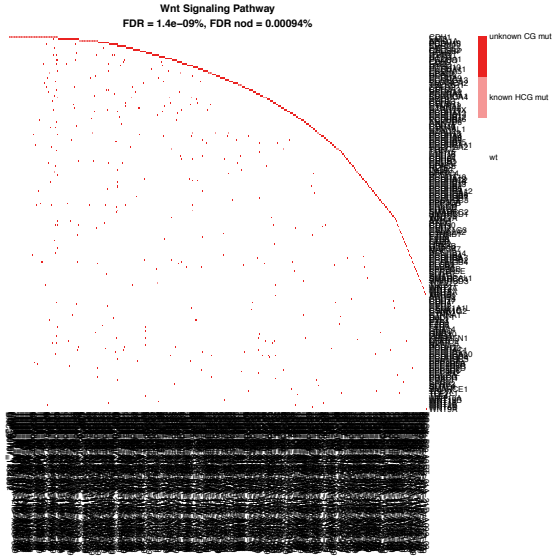

G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 7e−12%, FDR nod = 1.1%
unknown CG mut
known HCG mut
wt

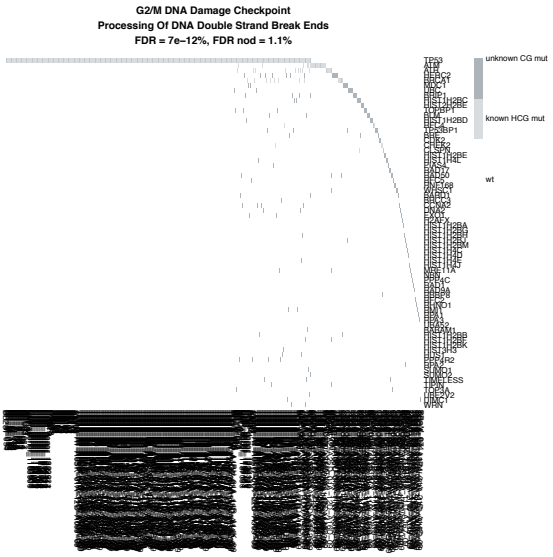

Meiotic Recombination
FDR = 8.1e−12%, FDR nod = 3.6e−06%
unknown CG mut
known HCG mut
wt

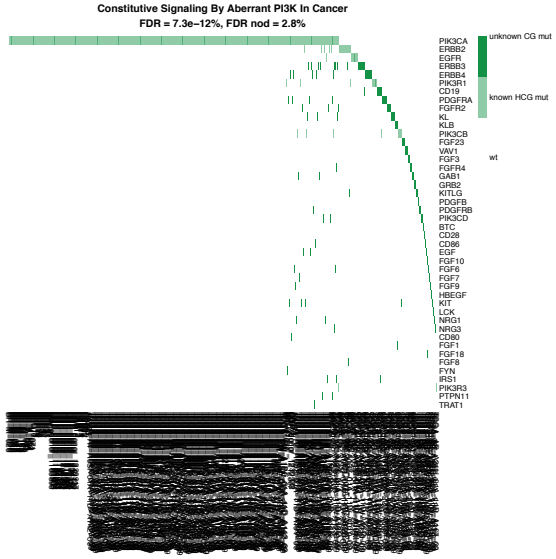

Meiotic Synapsis
FDR = 7.3e−12%, FDR nod = 6.3e−10%
unknown CG mut
known HCG mut
wt

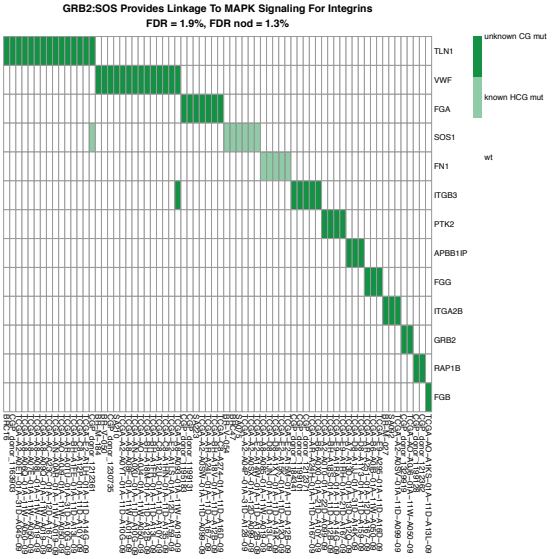

Integrins In Angiogenesis
FDR = 7e−12%, FDR nod = 1.4%
unknown CG mut
known HCG mut
wt

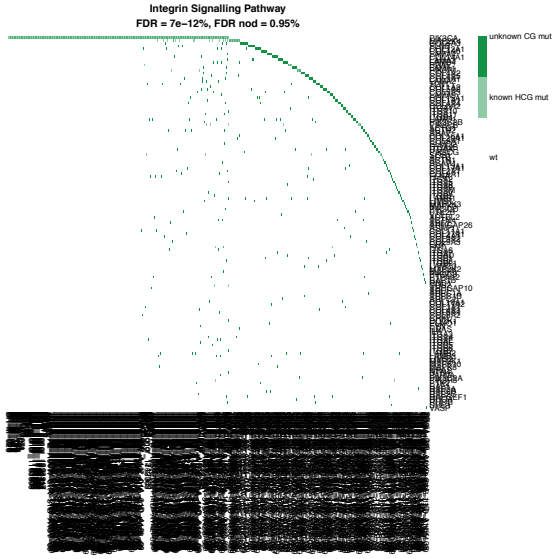

Signaling By PDGF
FDR = 0.0026%, FDR nod = 0.0058%
COL6A3
COL6A6
COL6A5
COL4A5
COL4A2
PDGFRA
COL4A4
COL9A1
COL4A1
PLG
COL6A2
COL9A3
THBS3
THBS4
PDGFRB
PLAT
SPP1
THBS1
PDGFB
COL4A3
FURIN
COL6A1
COL9A2
THBS2
unknown CG mut
known HCG mut
wt


Wnt Signaling Pathway
FDR = 1.4e−09%, FDR nod = 0.00094%
unknown CG mut
known HCG mut
wt

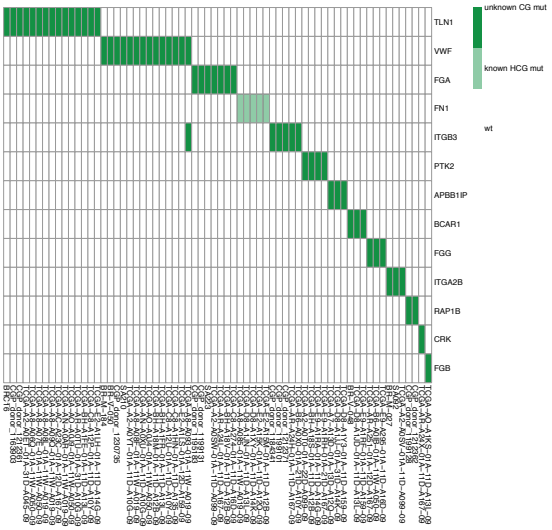

G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 7e−12%, FDR nod = 1.1%
unknown CG mut
known HCG mut
wt


Constitutive Signaling By Aberrant PI3K In Cancer
FDR = 7.3e−12%, FDR nod = 2.8%
PIK3CA
ERBB2
EGFR
ERBB3
ERBB4
PIK3R1
CD19
PDGFRA
FGFR2
KL
KLB
PIK3CB
FGF23
VAV1
FGF3
FGFR4
GAB1
GRB2
KITLG
PDGFB
PDGFRB
PIK3CD
BTC
CD28
CD86
EGF
FGF10
FGF6
FGF7
FGF9
HBEGF
KIT
LCK
NRG1
NRG3
CD80
FGF1
FGF18
FGF8
FYN
IRS1
PIK3R3
PTPN11
TRAT1
unknown CG mut
known HCG mut
wt

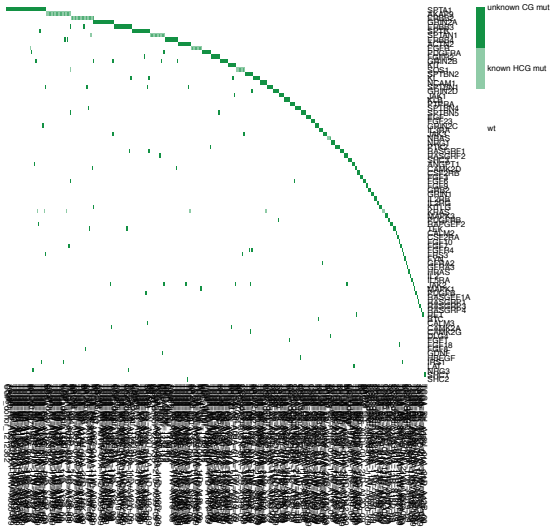

GRB2:SOS Provides Linkage To MAPK Signaling For Integrins
FDR = 1.9%, FDR nod = 1.3%
TLN1
VWF
FGA
SOS1
FN1
ITGB3
PTK2
APBB1IP
FGG
ITGA2B
GRB2
RAP1B
FGB
unknown CG mut
known HCG mut
wt


Integrin Signalling Pathway
FDR = 7e−12%, FDR nod = 0.95%
unknown CG mut
known HCG mut
wt

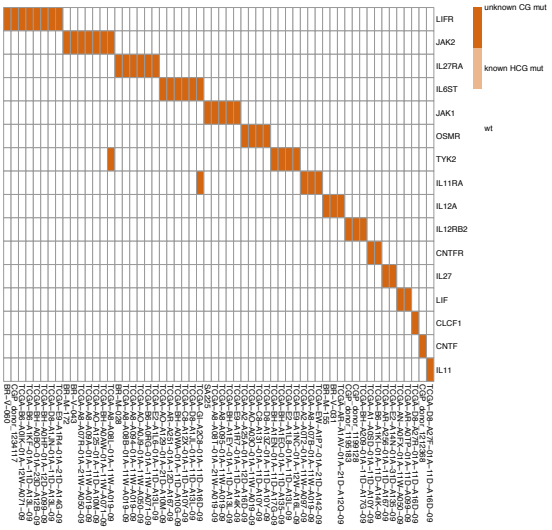
P130Cas Linkage To MAPK Signaling For Integrins
FDR = 5.5%, FDR nod = 3.3%



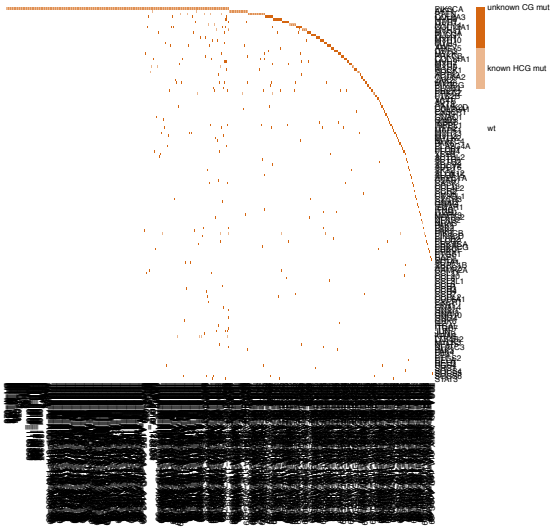
RAF/MAP Kinase Cascade
FDR = 0.07%, FDR nod = 3%



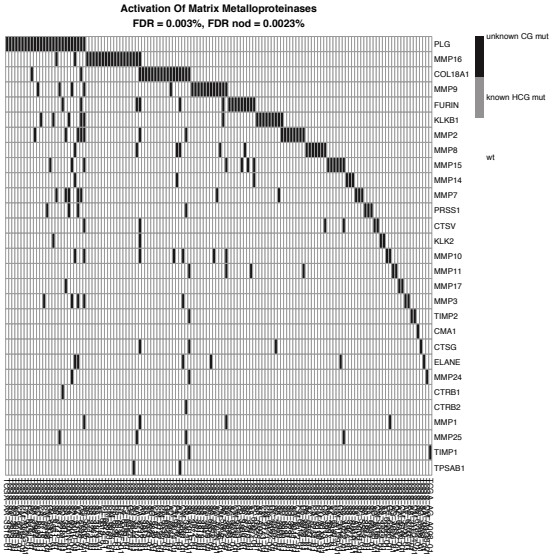
IL 6 Type Cytokine Receptor Ligand Interactions
FDR = 0.16%, FDR nod = 0.6%

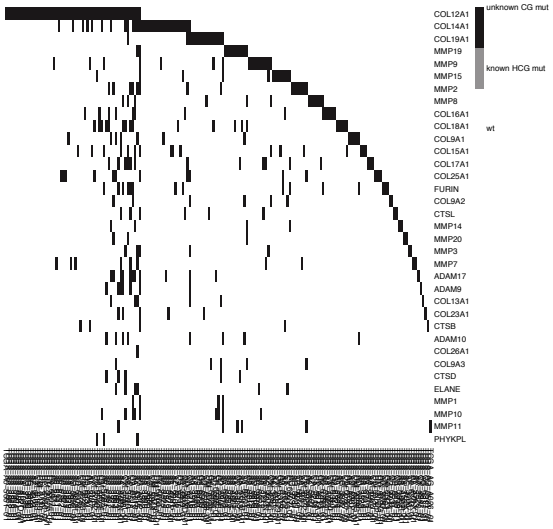


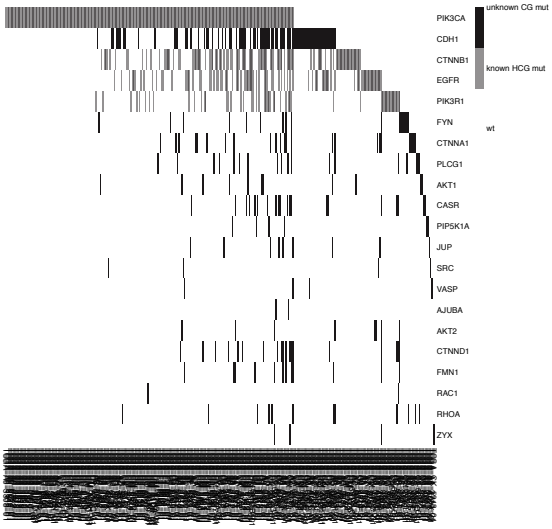
Inflammation Mediated By Chemokine And Cytokine Signaling Pathway
FDR = 7e−12%, FDR nod = 0.036%

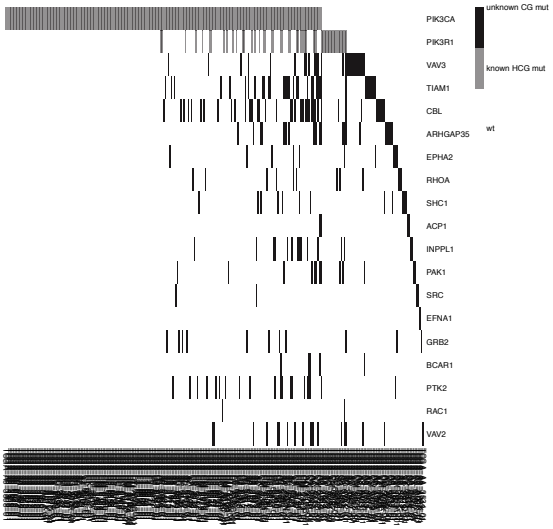


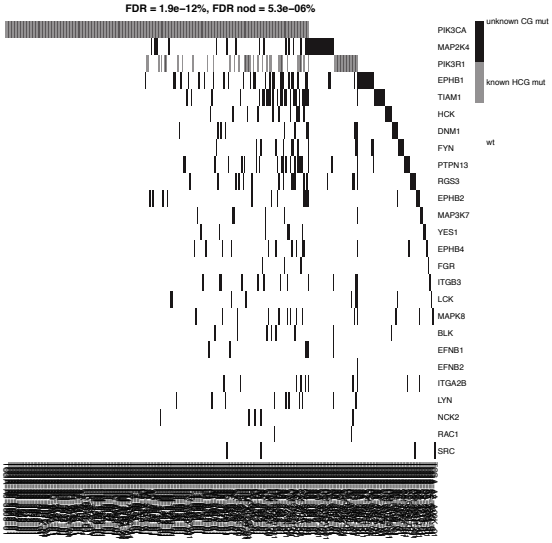
COREAD

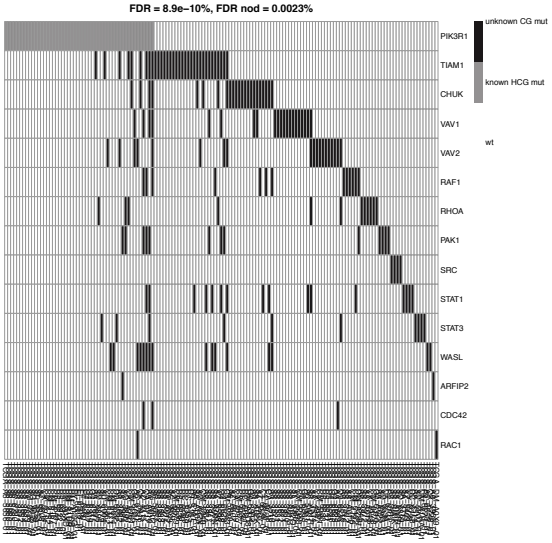

Activation Of Matrix Metalloproteinases
FDR = 0.003%, FDR nod = 0.0023%
PLG
MMP16
COL18A1
MMP9
FURIN
KLKB1
MMP2
MMP8
MMP15
MMP14
MMP7
PRSS1
CTSV
KLK2
MMP10
MMP11
MMP17
MMP3
TIMP2
CMA1
CTSG
ELANE
MMP24
CTRB1
CTRB2
MMP1
MMP25
TIMP1
TPSAB1
unknown CG mut
known HCG mut
wt

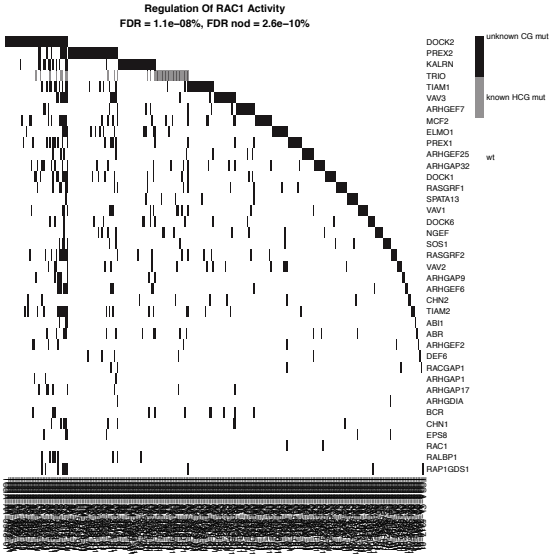

Collagen Degradation
FDR = 0.054%, FDR nod = 0.028%
COL12A1
COL14A1
COL19A1
MMP19
MMP9
MMP15
MMP2
MMP8
COL16A1
COL18A1
COL9A1
COL15A1
COL17A1
COL25A1
FURIN
COL9A2
CTSL
MMP14
MMP20
MMP3
MMP7
ADAM17
ADAM9
COL13A1
COL23A1
CTSB
ADAM10
COL26A1
COL9A3
CTSD
ELANE
MMP1
MMP10
MMP11
PHYKPL
unknown CG mut
known HCG mut
wt

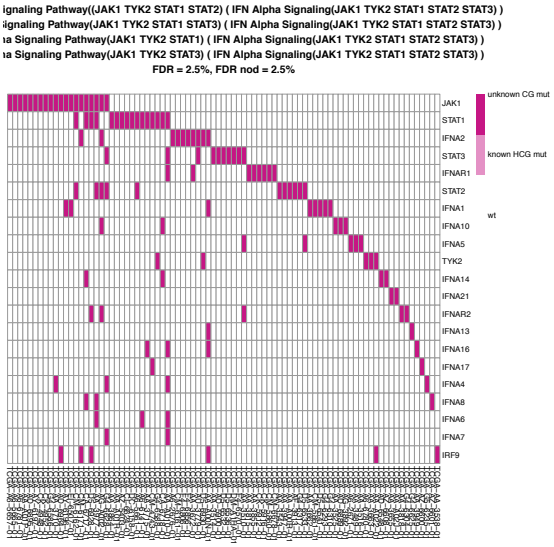

E Cadherin Signaling In Keratinocytes
FDR = 1.9e−12%, FDR nod = 2e−04%
PIK3CA
CDH1
CTNNB1
EGFR
PIK3R1
FYN
CTNNA1
PLCG1
AKT1
CASR
PIP5K1A
JUP
SRC
VASP
AJUBA
AKT2
CTNND1
FMN1
RAC1
RHOA
ZYX
unknown CG mut
known HCG mut
wt

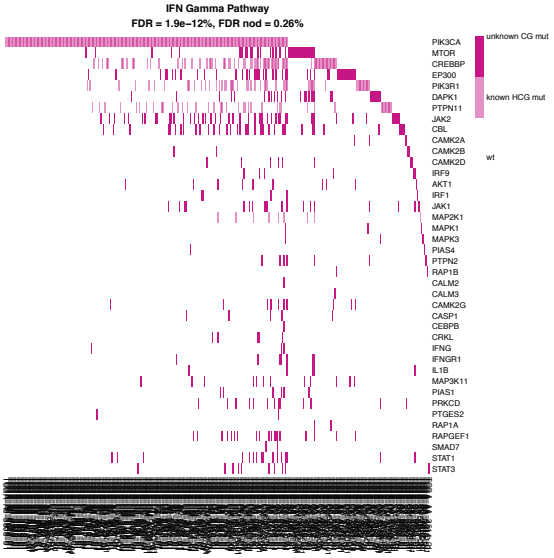

EPHA2 Forward Signaling
FDR = 1.9e−12%, FDR nod = 5.3e−06%
PIK3CA
PIK3R1
VAV3
TIAM1
CBL
ARHGAP35
EPHA2
RHOA
SHC1
ACP1
INPPL1
PAK1
SRC
EFNA1
GRB2
BCAR1
PTK2
RAC1
VAV2
unknown CG mut
known HCG mut
wt

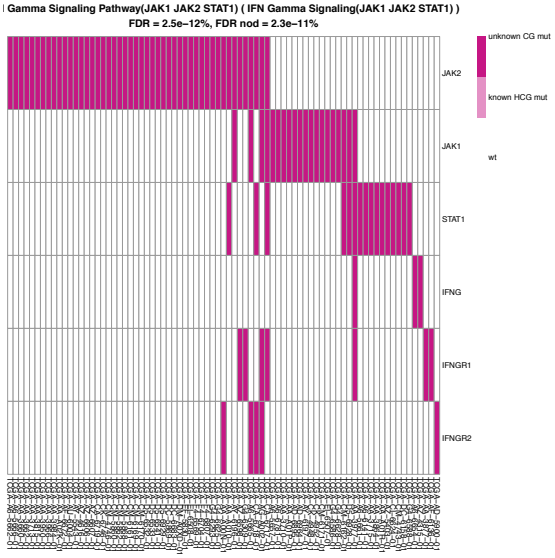

Ephrin B Reverse Signaling
FDR = 1.9e−12%, FDR nod = 5.3e−06%
PIK3CA
MAP2K4
PIK3R1
EPHB1
TIAM1
HCK
DNM1
FYN
PTPN13
RGS3
EPHB2
MAP3K7
YES1
EPHB4
FGR
ITGB3
LCK
MAPK8
BLK
EFNB1
EFNB2
ITGA2B
LYN
NCK2
RAC1
SRC
unknown CG mut
known HCG mut
wt

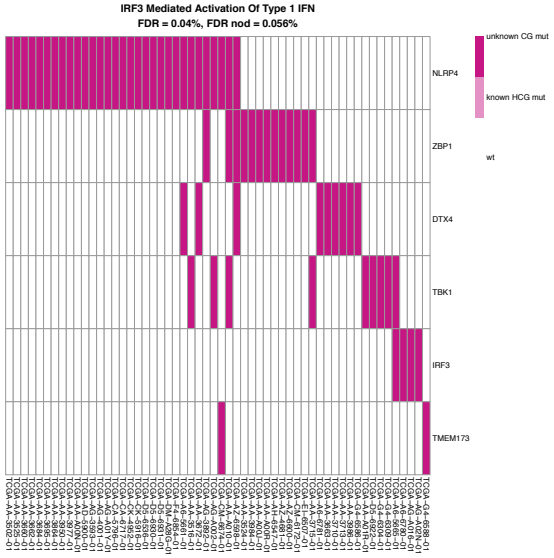

PDGF Pathway
FDR = 8.9e−10%, FDR nod = 0.0023%
PIK3R1
TIAM1
CHUK
VAV1
VAV2
RAF1
RHOA
PAK1
SRC
STAT1
STAT3
WASL
ARFIP2
CDC42
RAC1
unknown CG mut
known HCG mut
wt

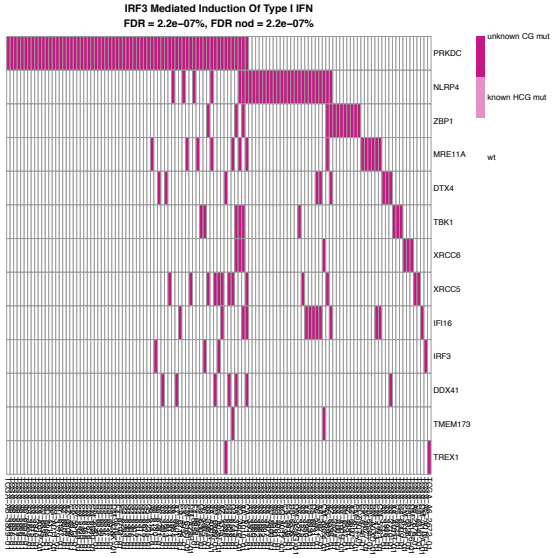

Regulation Of RAC1 Activity
FDR = 1.1e−08%, FDR nod = 2.6e−10%
DOCK2
PREX2
KALRN
TRIO
TIAM1
VAV3
ARHGEF7
MCF2
ELMO1
PREX1
ARHGEF25
ARHGAP32
DOCK1
RASGRF1
SPATA13
VAV1
DOCK6
NGEF
SOS1
RASGRF2
VAV2
ARHGAP9
ARHGEF6
CHN2
TIAM2
ABI1
ABR
ARHGEF2
DEF6
RACGAP1
ARHGAP1
ARHGAP17
ARHGDIA
BCR
CHN1
EPS8
RAC1
RALBP1
RAP1GDS1
unknown CG mut
known HCG mut
wt


ignaling Pathway((JAK1 TYK2 STAT1 STAT2) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
ignaling Pathway(JAK1 TYK2 STAT1 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
a Signaling Pathway(JAK1 TYK2 STAT1) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
a Signaling Pathway(JAK1 TYK2 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
FDR = 2.5%, FDR nod = 2.5%
JAK1
STAT1
IFNA2
STAT3
IFNAR1
STAT2
IFNA1
IFNA10
IFNA5
TYK2
IFNA14
IFNA21
IFNAR2
IFNA13
IFNA16
IFNA17
IFNA4
IFNA8
IFNA6
IFNA7
IRF9
unknown CG mut
known HCG mut
wt

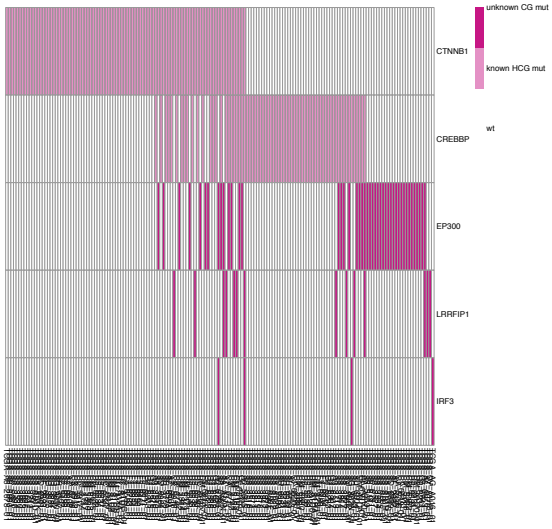

IFN Gamma Pathway
FDR = 1.9e−12%, FDR nod = 0.26%
PIK3CA
MTOR
CREBBP
EP300
PIK3R1
DAPK1
PTPN11
JAK2
CBL
CAMK2A
CAMK2B
CAMK2D
IRF9
AKT1
IRF1
JAK1
MAP2K1
MAPK1
MAPK3
PIAS4
PTPN2
RAP1B
CALM2
CALM3
CAMK2G
CASP1
CEBPB
CRKL
IFNG
IFNGR1
IL1B
MAP3K11
PIAS1
PRKCD
PTGES2
RAP1A
RAPGEF1
SMAD7
STAT1
STAT3
unknown CG mut
known HCG mut
wt


Gamma Signaling Pathway(JAK1 JAK2 STAT1) (IFN Gamma Signaling(JAK1 JAK2 STAT1))
FDR = 2.5e−12%, FDR nod = 2.3e−11%
JAK2
JAK1
STAT1
IFNG
IFNGR1
IFNGR2
unknown CG mut
known HCG mut
wt

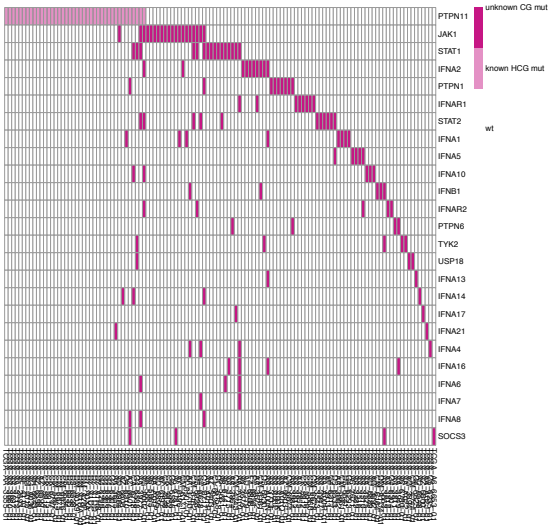

IRF3 Mediated Activation Of Type 1 IFN
FDR = 0.04%, FDR nod = 0.056%
NLRP4
ZBP1
DTX4
TBK1
IRF3
TMEM173
unknown CG mut
known HCG mut
wt


IRF3 Mediated Induction Of Type I IFN
FDR = 2.2e−07%, FDR nod = 2.2e−07%
PRKDC
NLRP4
ZBP1
MRE11A
DTX4
TBK1
XRCC6
XRCC5
IFI16
IRF3
DDX41
TMEM173
TREX1
unknown CG mut
known HCG mut
wt

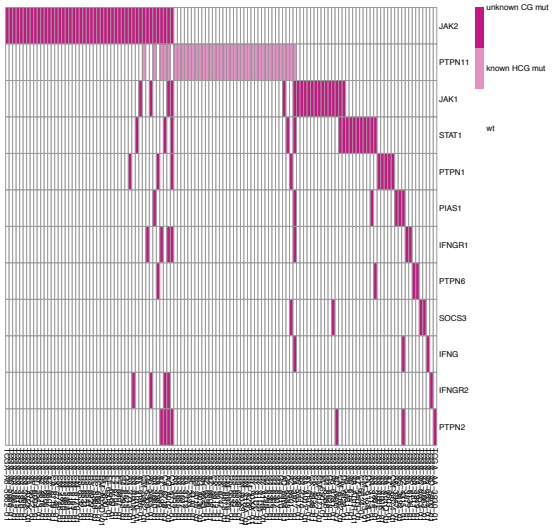
LRR FLII Interacting Protein 1 (LRRFIP1) Activates Type I IFN Production
FDR = 1.9e−12%, FDR nod = 0.021%



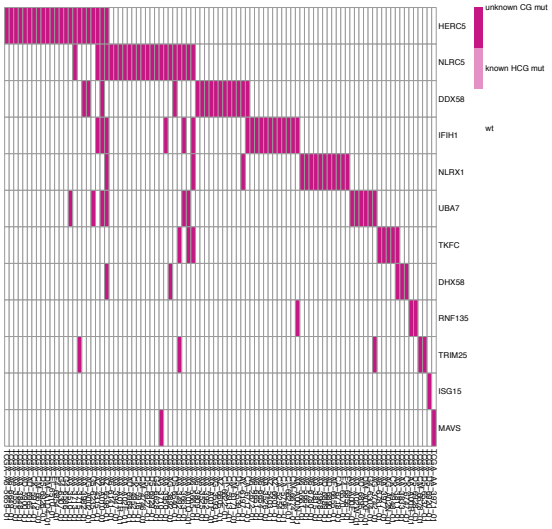
Regulation Of IFNA Signaling
FDR = 1.9e−07%, FDR nod = 0.54%



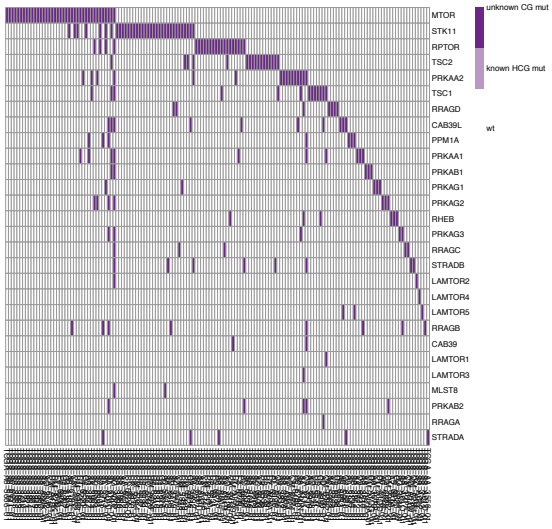
Regulation Of IFNG Signaling
FDR = 1.5e−11%, FDR nod = 0.0025%



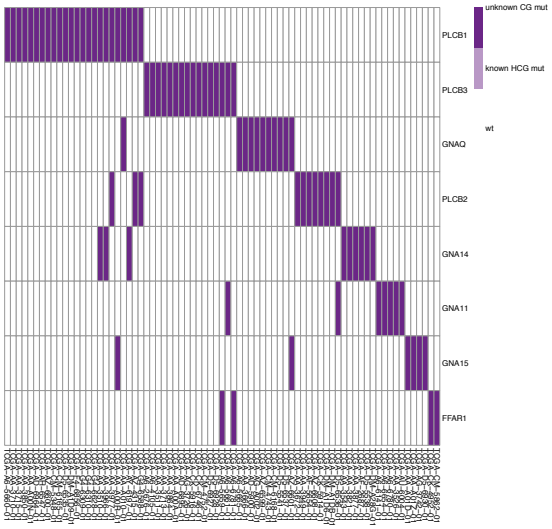
RIG I/MDA5 Mediated Induction Of IFN Alpha/beta Pathways
FDR = 0.8%, FDR nod = 0.78%



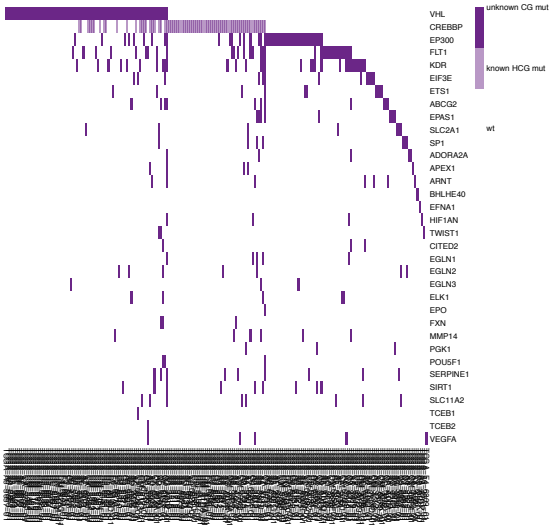
Energy Dependent Regulation Of MTOR By LKB1 AMPK
FDR = 4.4%, FDR nod = 3.2%



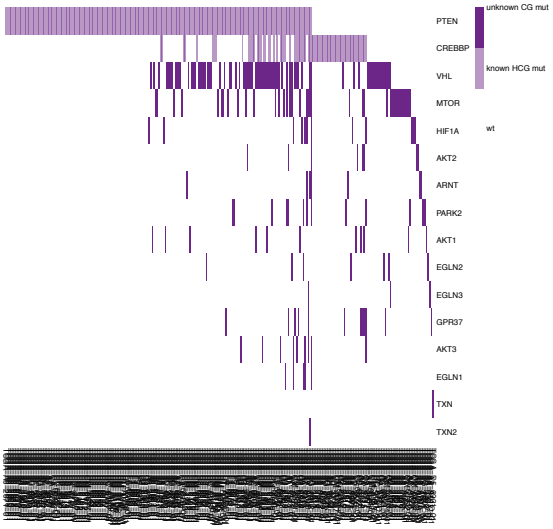
Fatty Acids Bound To GPR40 (FFAR1) Regulate Insulin Secretion
FDR = 0.56%, FDR nod = 0.64%



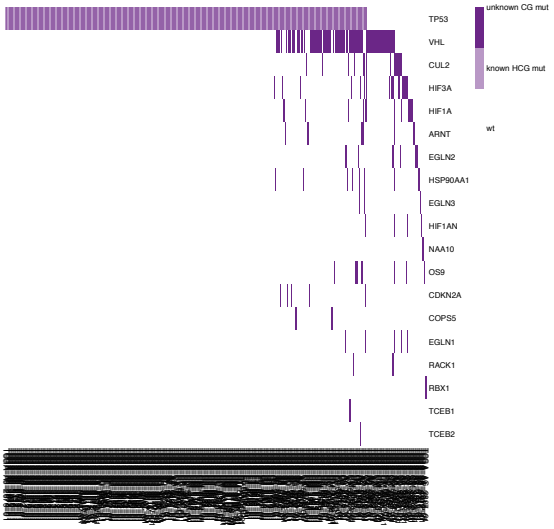
HIF 2 Alpha Transcription Factor Network
FDR = 2e−04%, FDR nod = 0.2%



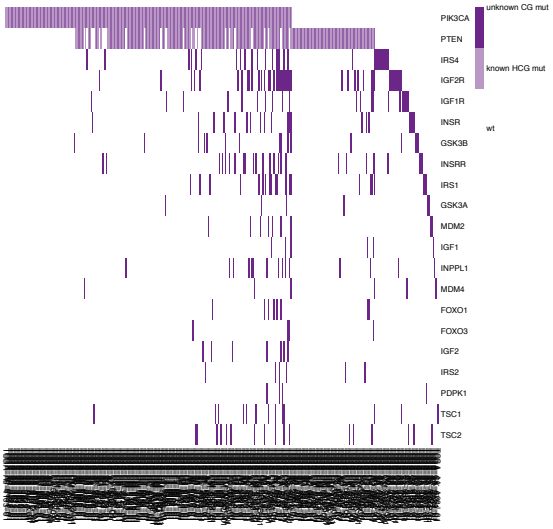
Hypoxia Response Via HIF Activation
FDR = 1.9e−12%, FDR nod = 3.7e−09%



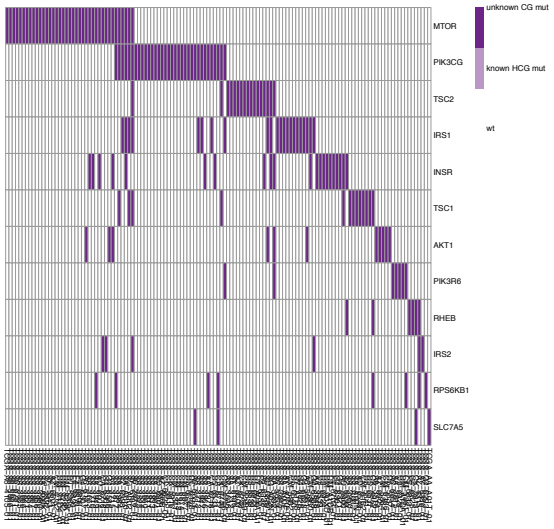
Hypoxic And Oxygen Homeostasis Regulation Of HIF 1 Alpha
FDR = 1.9e−12%, FDR nod = 0.018%



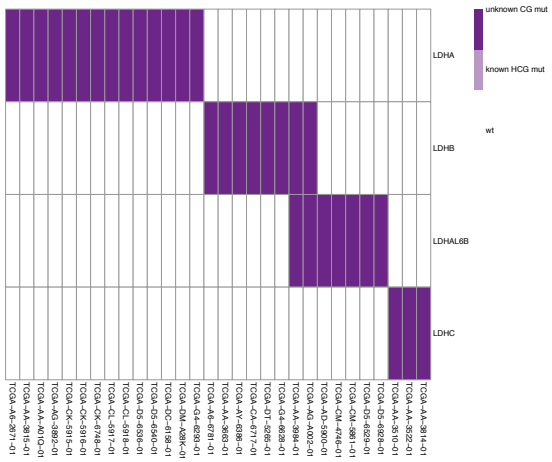
Insulin/IGF Pathway Protein Kinase B Signaling Cascade
FDR = 1.9e−12%, FDR nod = 0.18%



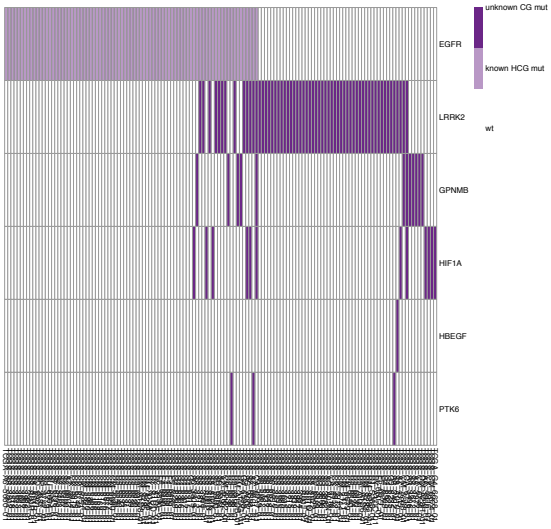
Leucine Stimulation On Insulin Signaling
FDR = 0.003%, FDR nod = 0.0024%



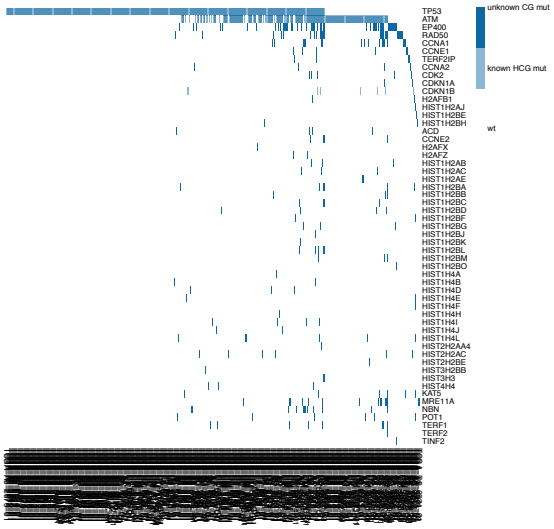
NAD+ + (S) Lactic Acid = NADH + Pyruvic Acid (Glycolysis And Gluconeogenesis)
NAD+ + (S) Lactic Acid = NADH + Pyruvic Acid (Pyruvate Metabolism)
NAD+ + 2 Hydroxy Butanoic Acid = NADH + 2 Oxo Butanoic Acid (Propanoate Metabolism)
Mercapto Lactic Acid = NADH + 3 Mercapto Pyruvic Acid (Methionine And Cysteine Metabolism)
FDR = 0.65%, FDR nod = 0.97%



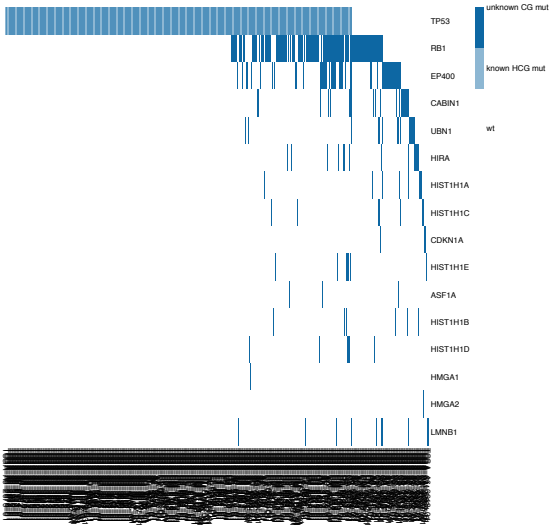
PTK6 Promotes HIF1A Stabilization
FDR = 2e−12%, FDR nod = 2.6e−08%



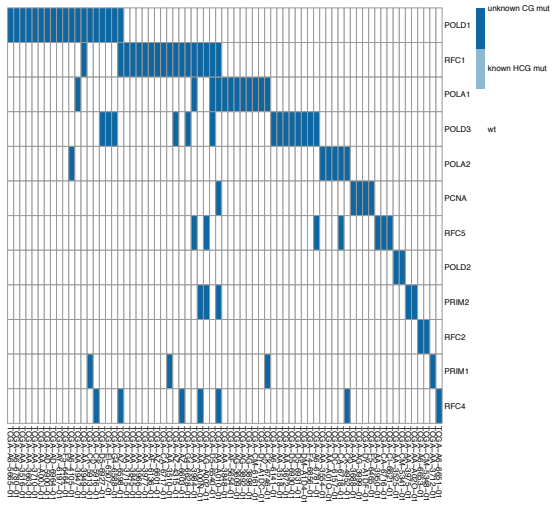
DNA Damage/Telomere Stress Induced Senescence
FDR = 1.9e−12%, FDR nod = 0.14%



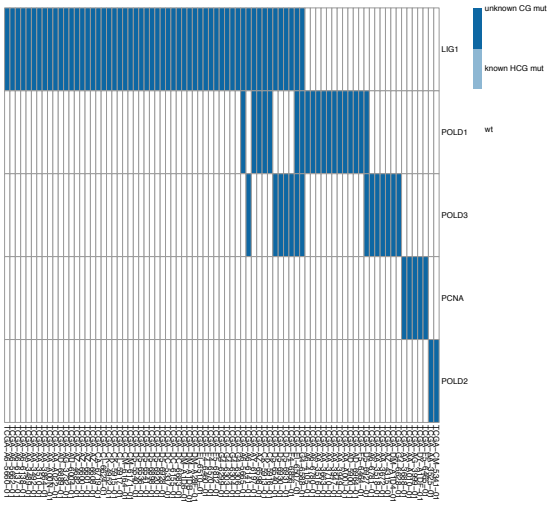
Formation Of Senescence Associated Heterochromatin Foci (SAHF)
FDR = 1.9e−12%, FDR nod = 2.3e−11%



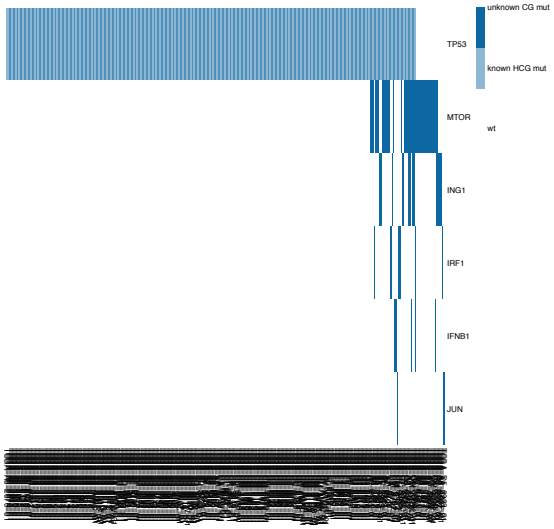
Polymerase Switching
Polymerase Switching On The C Strand Of The Telomere
FDR = 4.4%, FDR nod = 4.6%



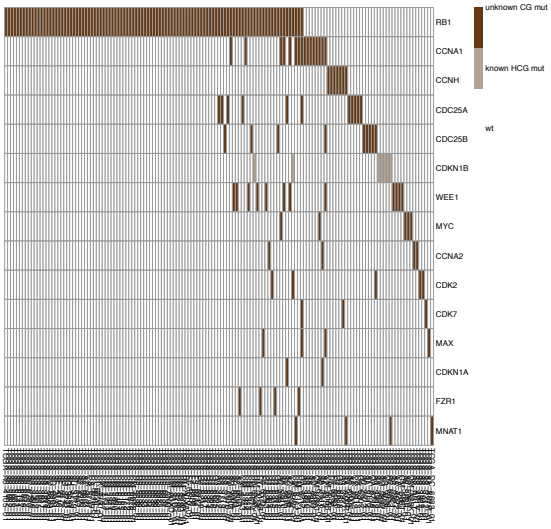
Processive Synthesis On The C Strand Of The Telomere
Telomere C Strand (Lagging Strand) Synthesis
FDR = 1.9e−12%, FDR nod = 2.3e−11%



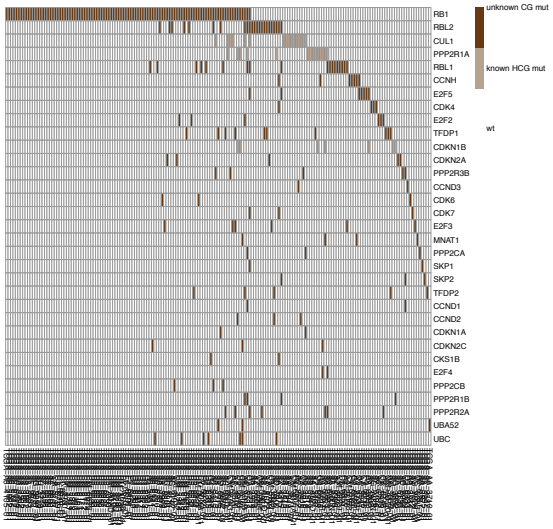
Senescence And Autophagy In Cancer
FDR = 1.9e−12%, FDR nod = 0.72%



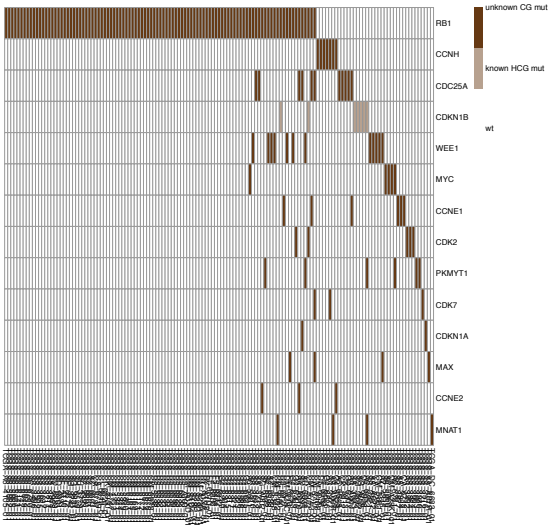
Cyclin A:Cdk2 Associated Events At S Phase Entry
FDR = 1.9e−12%, FDR nod = 2.3e−11%



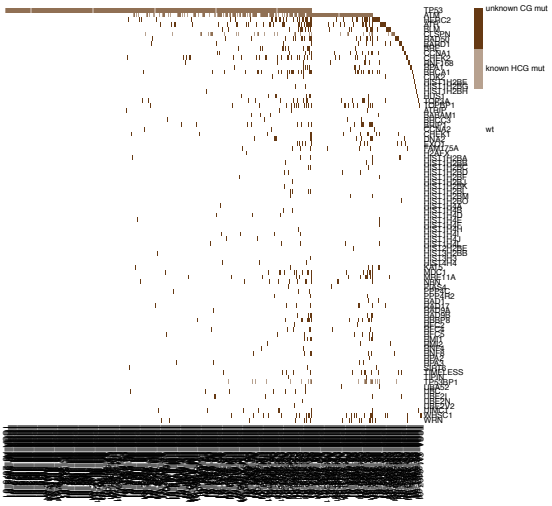
Cyclin D Associated Events In G1
FDR = 0.79%, FDR nod = 1.9%



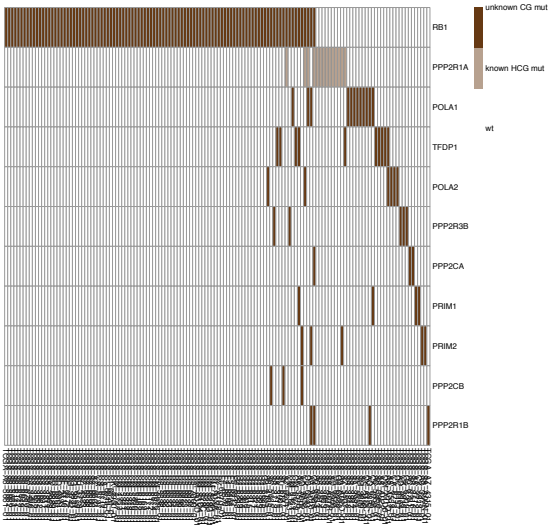
Cyclin E Associated Events During G1/S Transition
FDR = 1.9e−12%, FDR nod = 2.3e−11%



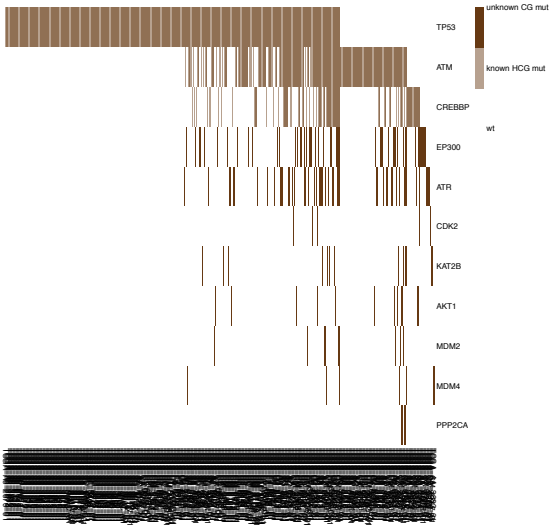
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 1.9e−12%, FDR nod = 4.6%

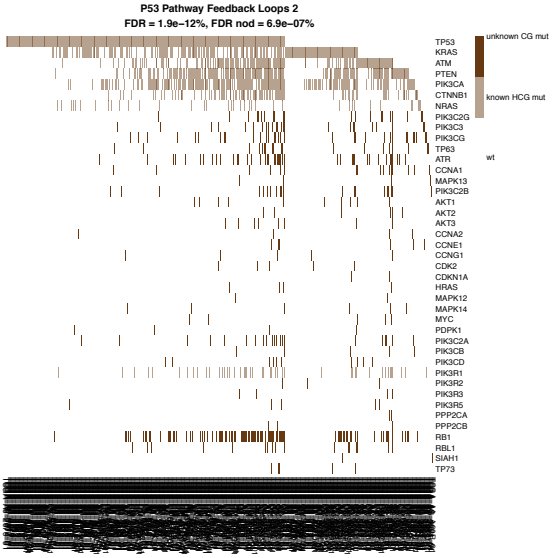


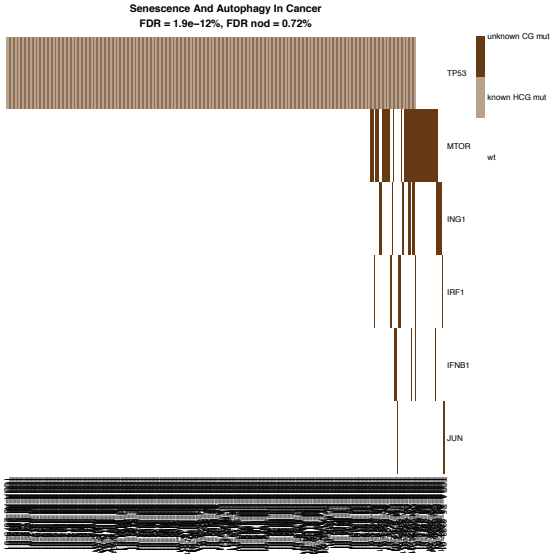
Inhibition Of Replication Initiation Of Damaged DNA By RB1/E2F1
FDR = 2e−12%, FDR nod = 2.3e−11%

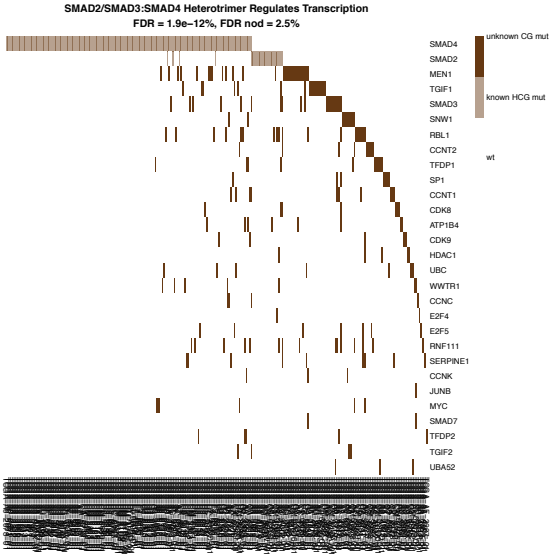


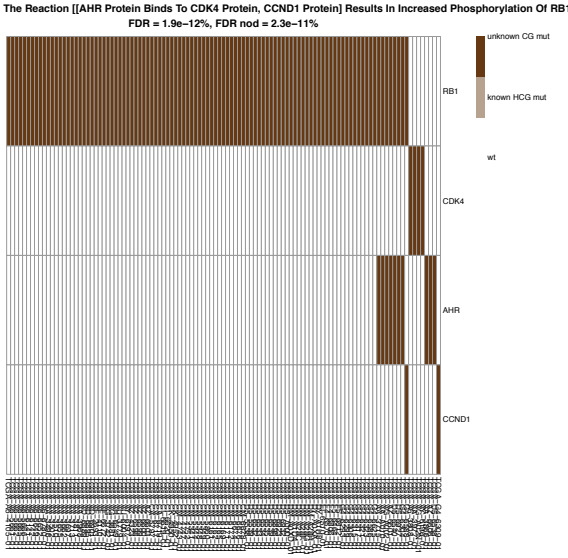
P53 Pathway
FDR = 1.9e−12%, FDR nod = 0.0042%

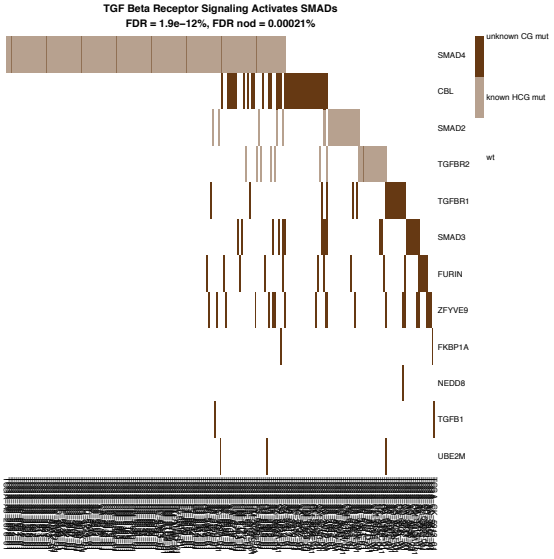


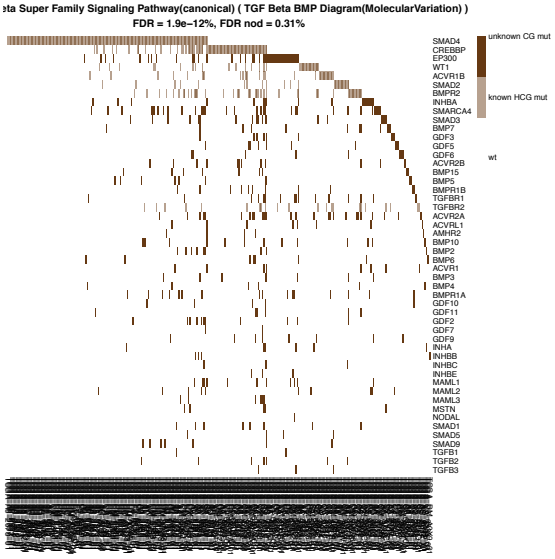

P53 Pathway Feedback Loops 2
FDR = 1.9e−12%, FDR nod = 6.9e−07%
TP53
KRAS
ATM
PTEN
PIK3CA
CTNNB1
NRAS
PIK3C2G
PIK3C3
PIK3CG
TP63
ATR
CCNA1
MAPK13
PIK3C2B
AKT1
AKT2
AKT3
CCNA2
CCNE1
CCNG1
CDK2
CDKN1A
HRAS
MAPK12
MAPK14
MYC
PDPK1
PIK3C2A
PIK3CB
PIK3CD
PIK3R1
PIK3R2
PIK3R3
PIK3R5
PPP2CA
PPP2CB
RB1
RBL1
SIAH1
TP73
unknown CG mut
known HCG mut
wt


Senescence And Autophagy In Cancer
FDR = 1.9e−12%, FDR nod = 0.72%
TP53
MTOR
ING1
IRF1
IFNB1
JUN
unknown CG mut
known HCG mut
wt

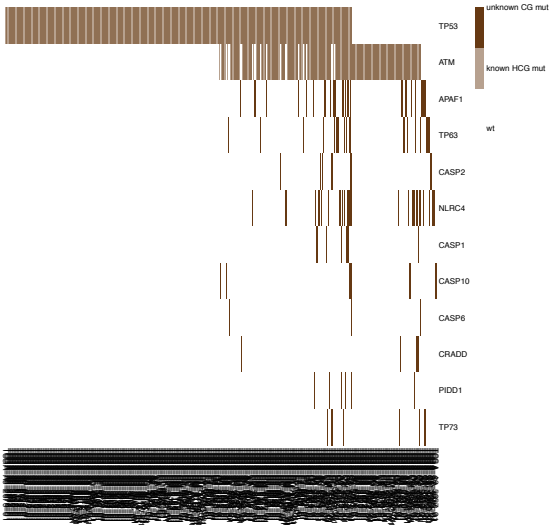

SMAD2/SMAD3:SMAD4 Heterotrimer Regulates Transcription
FDR = 1.9e−12%, FDR nod = 2.5%
SMAD4
SMAD2
MEN1
TGIF1
SMAD3
SNW1
RBL1
CCNT2
TFDP1
SP1
CCNT1
CDK8
ATP1B4
CDK9
HDAC1
UBC
WWTR1
CCNC
E2F4
E2F5
RNF111
SERPINE1
CCNK
JUNB
MYC
SMAD7
TFDP2
TGIF2
UBA52
unknown CG mut
known HCG mut
wt


The Reaction [[AHR Protein Binds To CDK4 Protein, CCND1 Protein] Results In Increased Phosphorylation Of RB1
FDR = 1.9e−12%, FDR nod = 2.3e−11%
RB1
CDK4
AHR
CCND1
unknown CG mut
known HCG mut
wt

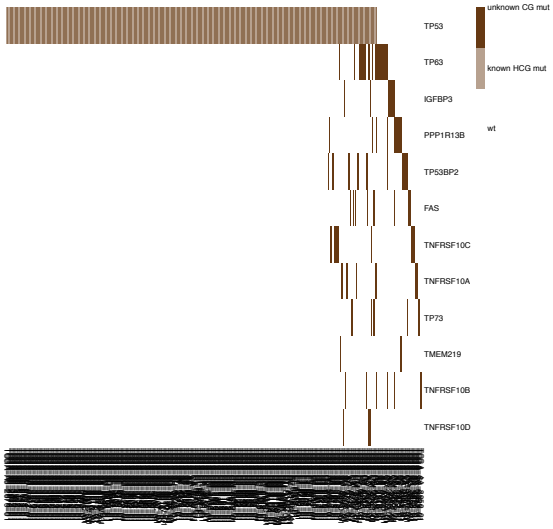

TGF Beta Receptor Signaling Activates SMADs
FDR = 1.9e−12%, FDR nod = 0.00021%
SMAD4
CBL
SMAD2
TGFBR2
TGFBR1
SMAD3
FURIN
ZFYVE9
FKBP1A
NEDD8
TGFB1
UBE2M
unknown CG mut
known HCG mut
wt


ta Super Family Signaling Pathway(canonical) (TGF Beta BMP Diagram(MolecularVariation))
FDR = 1.9e−12%, FDR nod = 0.31%
SMAD4
CREBBP
EP300
WT1
ACVR1B
SMAD2
BMPR2
INHBA
SMARCA4
SMAD3
BMP7
GDF3
GDF5
GDF6
ACVR2B
BMP15
BMP5
BMPR1B
TGFBR1
TGFBR2
ACVR2A
ACVRL1
AMHR2
BMP10
BMP2
BMP6
ACVR1
BMP3
BMP4
BMPR1A
GDF10
GDF11
GDF2
GDF7
GDF9
INHA
INHBB
INHBC
INHBE
MAML1
MAML2
MAML3
MSTN
NODAL
SMAD1
SMAD5
SMAD9
TGFB1
TGFB2
TGFB3
unknown CG mut
known HCG mut
wt

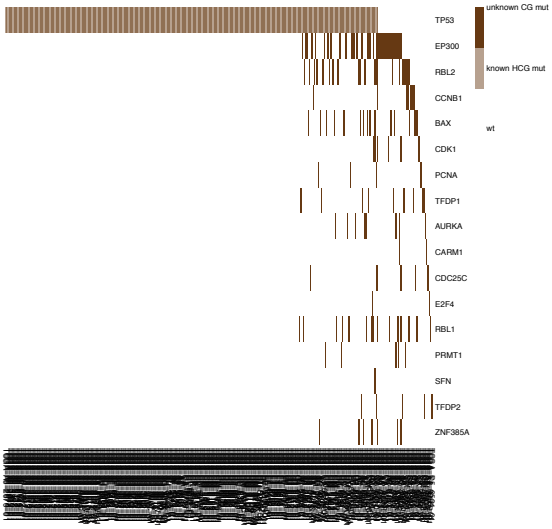
TP53 Regulates Transcription Of Caspase Activators And Caspases
FDR = 1.9e−12%, FDR nod = 1.1%



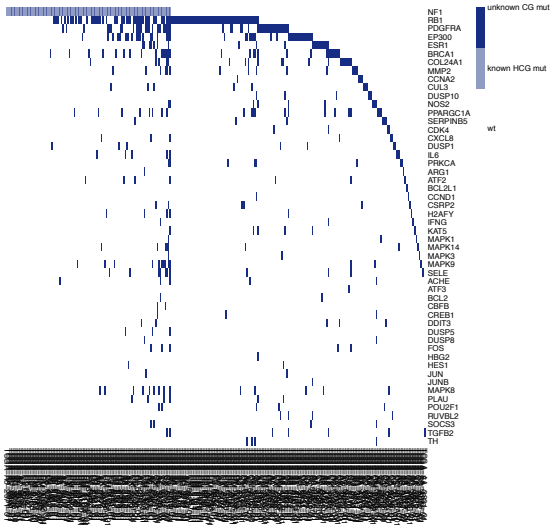
TP53 Regulates Transcription Of Death Receptors And Ligands
FDR = 1.9e−12%, FDR nod = 3.6%



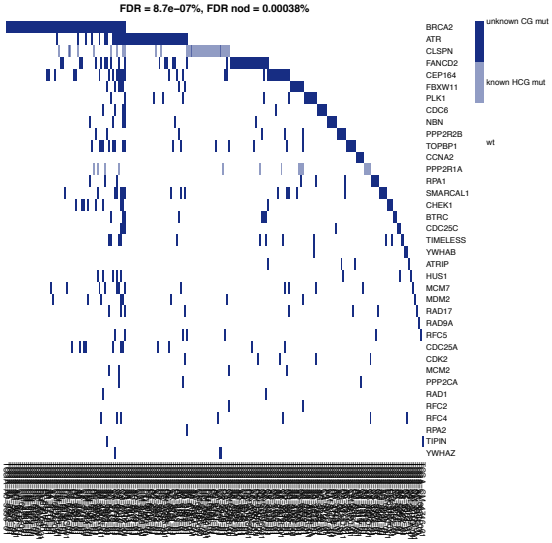
TP53 Regulates Transcription Of Genes Involved In G2 Cell Cycle Arrest
FDR = 1.9e−12%, FDR nod = 0.011%



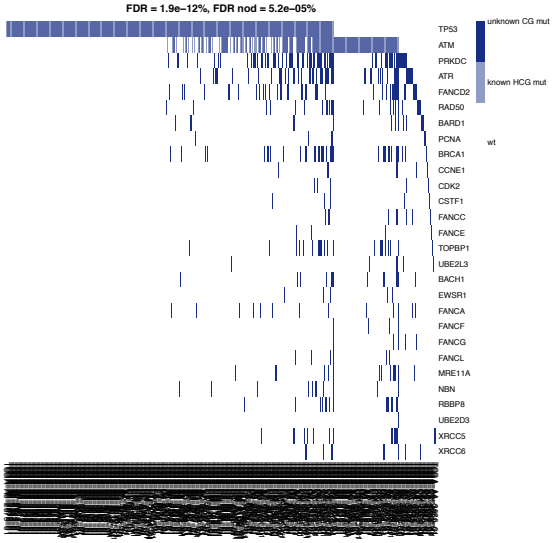
ATF 2 Transcription Factor Network
FDR = 7e−08%, FDR nod = 0.00047%



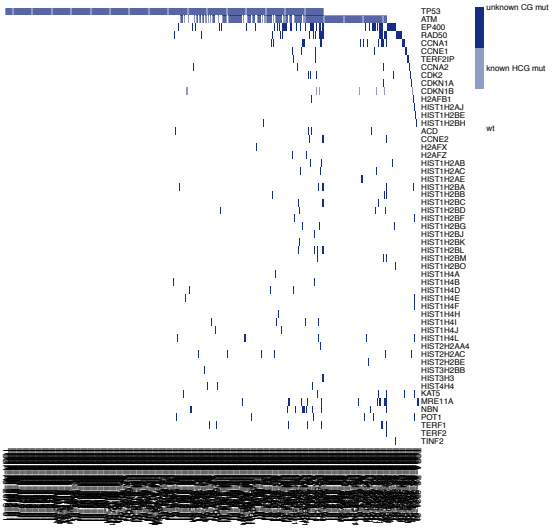
ATR Signaling Pathway
FDR = 8.7e−07%, FDR nod = 0.00038%



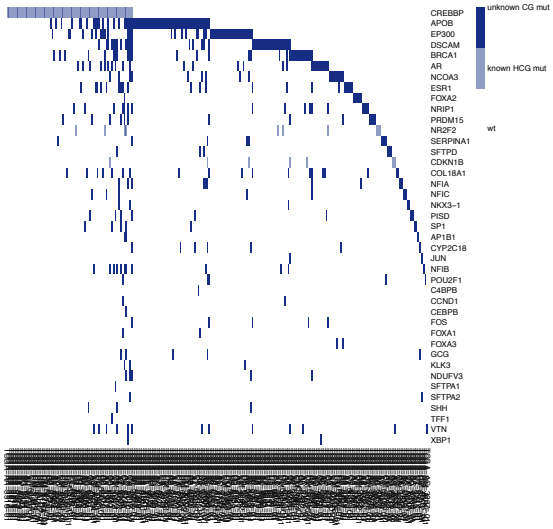
BARD1 Signaling Events
FDR = 1.9e−12%, FDR nod = 5.2e−05%



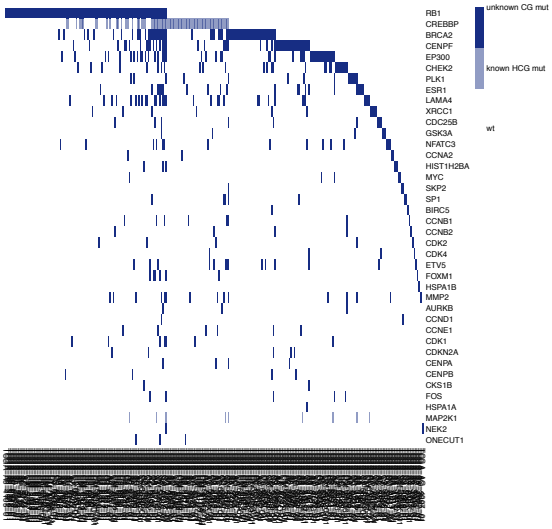
DNA Damage/Telomere Stress Induced Senescence
FDR = 1.9e−12%, FDR nod = 0.14%



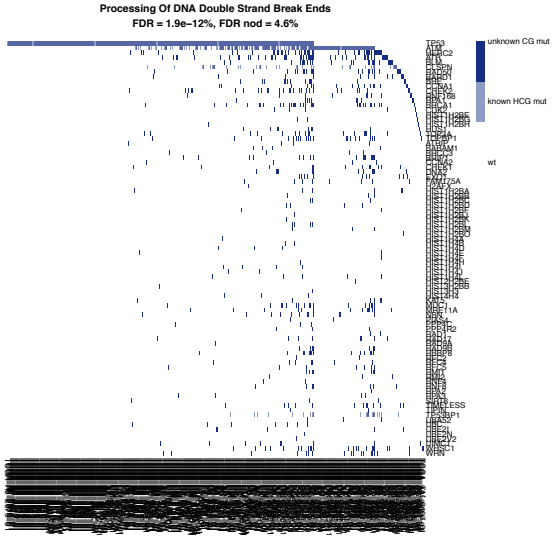
FOXA1 Transcription Factor Network
FDR = 2.3e−06%, FDR nod = 0.015%



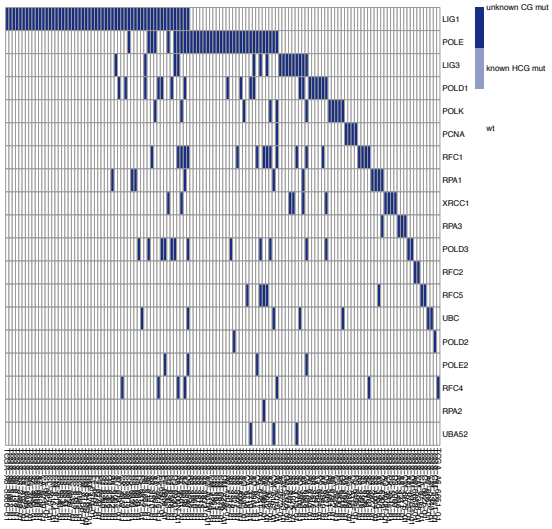
FOXM1 Transcription Factor Network
FDR = 1.9e−12%, FDR nod = 2.3e−11%



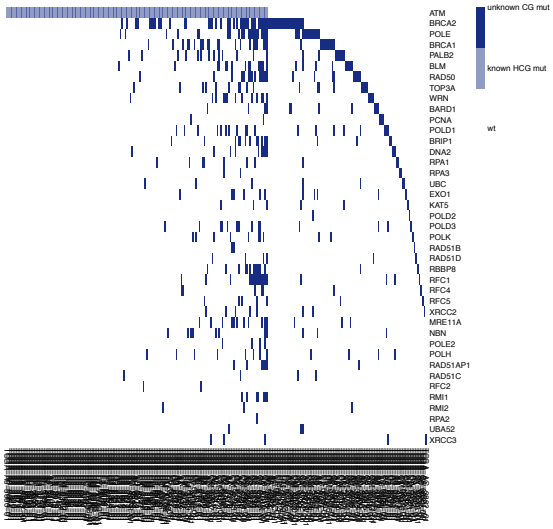
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 1.9e−12%, FDR nod = 4.6%

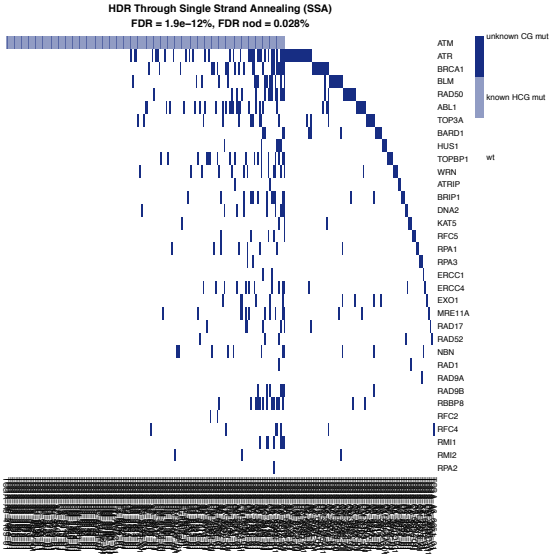


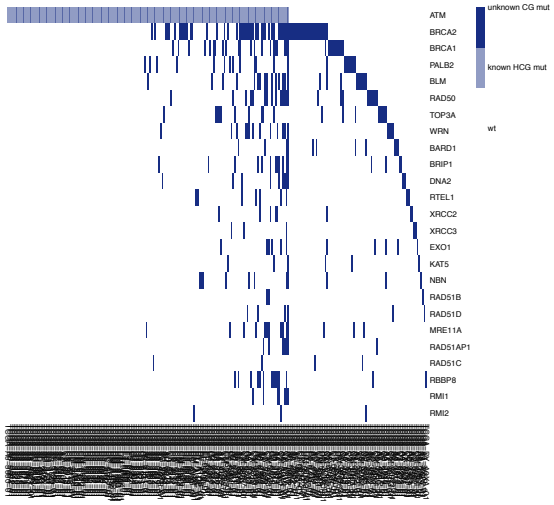
Gap Filling DNA Repair Synthesis And Ligation In GG NER
FDR = 0.002%, FDR nod = 0.0016%

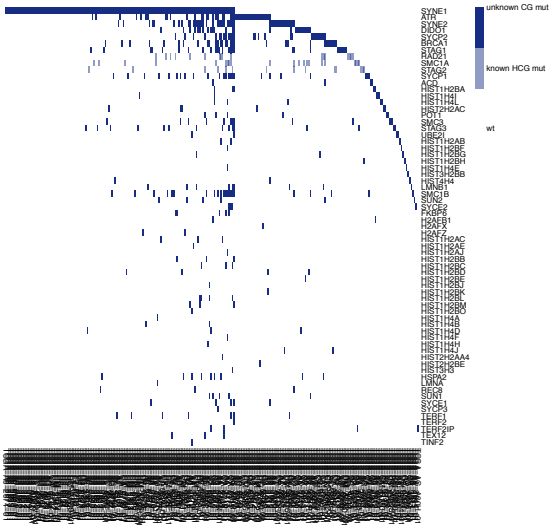


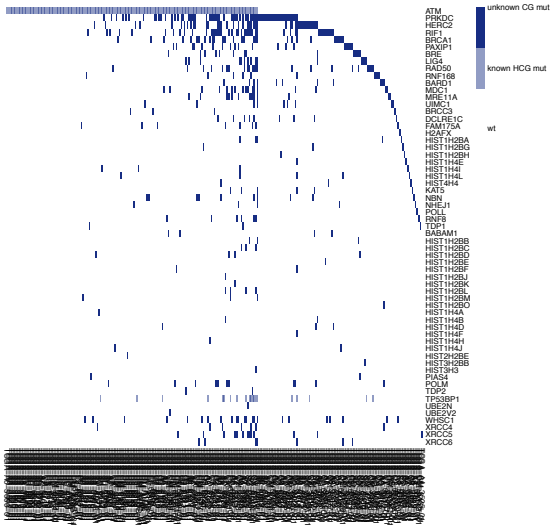
HDR Through Homologous Recombination (HRR)
FDR = 2.3e−12%, FDR nod = 0.51%

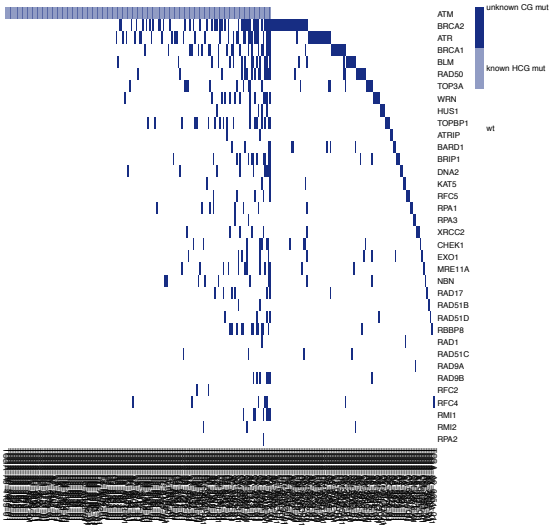


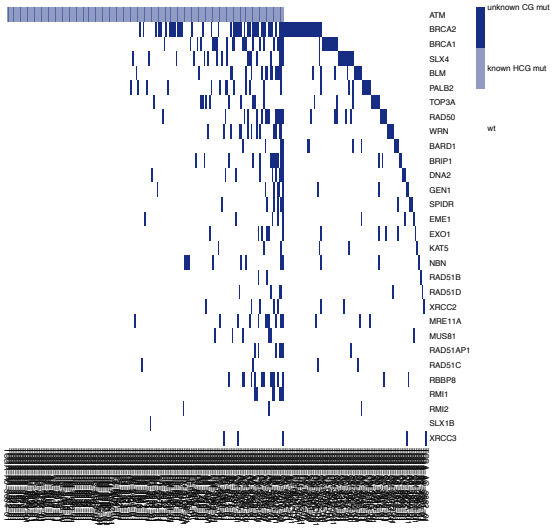

HDR Through Single Strand Annealing (SSA)
FDR = 1.9e−12%, FDR nod = 0.028%
unknown CG mut
known HCG mut
wt
ATM
ATR
BRCA1
BLM
RAD50
ABL1
TOP3A
BARD1
HUS1
TOPBP1
WRN
ATRIP
BRIP1
DNA2
KAT5
RFC5
RPA1
RPA3
ERCC1
ERCC4
EXO1
MRE11A
RAD17
RAD52
NBN
RAD1
RAD9A
RAD9B
RBBP8
RFC2
RFC4
RMI1
RMI2
RPA2


Homologous DNA Pairing And Strand Exchange
esolution Of D Loop Structures Through Synthesis Dependent Strand Annealing (SDSA)
FDR = 1.9e−12%, FDR nod = 0.014%
unknown CG mut
known HCG mut
wt
ATM
BRCA2
BRCA1
PALB2
BLM
RAD50
TOP3A
WRN
BARD1
BRIP1
DNA2
RTEL1
XRCC2
XRCC3
EXO1
KAT5
NBN
RAD51B
RAD51D
MRE11A
RAD51AP1
RAD51C
RBBP8
RMI1
RMI2

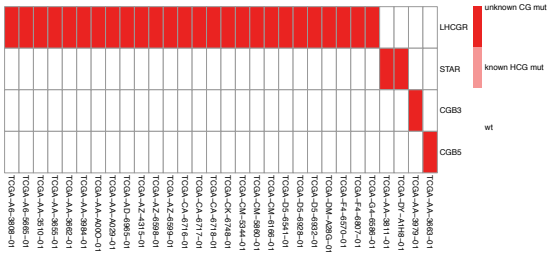

Meiotic Synapsis
FDR = 7.1e−09%, FDR nod = 2.6e−10%
unknown CG mut
known HCG mut
wt
SYNE1
ATR
SYNE2
DCLRE1C
BRCA1
SYCE1
RAD21
SMC1A
STAG2
SYCP1
ACD
HIST1H2BA
HIST1H4I
HIST1H4L
HIST2H2AC
POT1
SMC3
STAG3
HIST1H2AB
HIST1H2BF
HIST1H2BG
HIST1H2BH
HIST1H4E
HIST1H2BB
HIST1H4H
LMNB1
SMC1B
SUN2
SYCE2
FAM9B
H2AFB1
H2AFZ
H2AFX
HIST1H2AC
HIST1H2AE
HIST1H2AJ
HIST1H2BB
HIST1H2BC
HIST1H2BD
HIST1H2BE
HIST1H2BJ
HIST1H2BK
HIST1H2BL
HIST1H2BM
HIST1H2BO
HIST1H1A
HIST1H4B
HIST1H1D
HIST1H1E
HIST1H1T
HIST2H2AA4
HIST2H2BE
HIST1H1B
HSPA2
LMNA
REC8
SUN1
SYCE1
SYCP3
TERF1
TERF2
TERF2IP
TINF2


Nonhomologous End Joining (NHEJ)
FDR = 1.5e−07%, FDR nod = 1.3%
unknown CG mut
known HCG mut
wt
ATM
PRKDC
HERC2
RIF1
BRCA1
PAXIP1
BRE
LIG4
RAD50
RNF168
BARD1
MDC1
MRE11A
UIMC1
BRCC3
DCLRE1C
FAM175A
H2AFX
HIST1H2BA
HIST1H2BG
HIST1H2BH
HIST1H4E
HIST1H4I
HIST1H4L
HIST2H4
KAT5
NBN
NHEJ1
POLL
RNF8
TDP1
BABAM1
HIST1H2BB
HIST1H2BC
HIST1H2BD
HIST1H2BE
HIST1H2BF
HIST1H2BJ
HIST1H2BK
HIST1H2BL
HIST1H2BM
HIST1H2BO
HIST1H4A
HIST1H4B
HIST1H4D
HIST1H4F
HIST1H4H
HIST1H4J
HIST2H2BE
HIST3H2BB
HIST3H3
PIAS4
POLM
TDP2
TP53BP1
UBE2N
UBE2V2
WHSC1
XRCC4
XRCC5
XRCC6

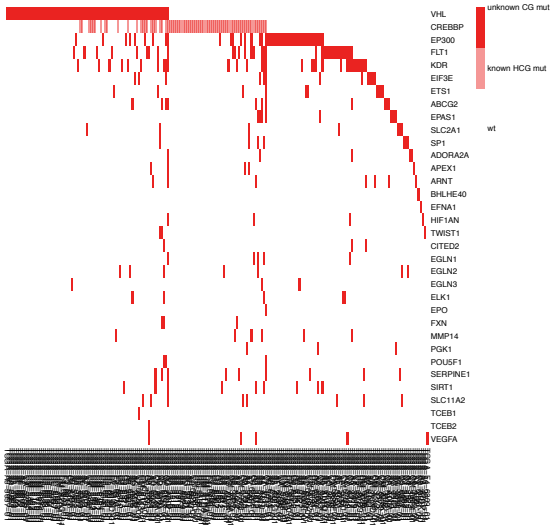

Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange
FDR = 2e−12%, FDR nod = 0.0018%
unknown CG mut
known HCG mut
wt
ATM
BRCA2
ATR
BRCA1
BLM
RAD50
TOP3A
WRN
HUS1
TOPBP1
ATRIP
BARD1
BRIP1
DNA2
KAT5
RFC5
RPA1
RPA3
XRCC2
CHEK1
EXO1
MRE11A
NBN
RAD17
RAD51B
RAD51D
RBBP8
RAD1
RAD51C
RAD9A
RAD9B
RFC2
RFC4
RMI1
RMI2
RPA2


Resolution Of D Loop Structures Through Holliday Junction Intermediates
FDR = 1.9e−12%, FDR nod = 0.29%
unknown CG mut
known HCG mut
wt
ATM
BRCA2
BRCA1
SLX4
BLM
PALB2
TOP3A
RAD50
WRN
BARD1
BRIP1
DNA2
GEN1
SPIDR
EME1
EXO1
KAT5
NBN
RAD51B
RAD51D
XRCC2
MRE11A
MUS81
RAD51AP1
RAD51C
RBBP8
RMI1
RMI2
SLX1B
XRCC3

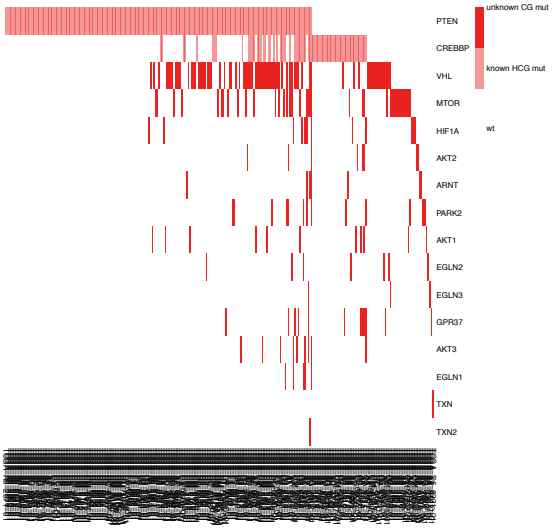
[CGB Protein Results In Increased Activity Of LHCGR Protein]
de Results In Decreased Activity Of PTGS2 Protein] Inhibits The Reaction [CGB Protein Results In Increased Chen
(3, 2 F)quinazoline 1,3 Diamine Binds To F2R Protein] Promotes The Reaction [CGB Protein Results In Increased
ne Inhibits The Reaction [CGB Protein Results In Increased Chemical Synthesis Of Androgens]
ıtrazine Inhibits The Reaction [CGB Protein Results In Increased Secretion Of Cyclic AMP]
forsin Promotes The Reaction [CGB Protein Results In Increased Abundance Of Cyclic AMP]
Reaction [[Gonadotropins, Equine Co Treated With CGB Protein] Results In Increased Abundance Of Progesteron
hibits The Reaction [[CGB Protein Co Treated With Colforsin] Results In Increased Abundance Of Cyclic AMP]
Protein Promotes The Reaction [CGB Protein Results In Increased Abundance Of Progesterone]
ole Metabolite Inhibits The Reaction [CGB Protein Results In Increased Abundance Of Testosterone]
se Chloride Inhibits The Reaction [CGB Protein Results In Increased Expression Of STAR Protein]
terone Promotes The Reaction [CGB Protein Results In Increased Expression Of VEGFA MRNA]
one Enanthate Inhibits The Reaction [CGB Protein Results In Increased Abundance Of Androgens]
FDR = 0.0063%, FDR nod = 0.012%



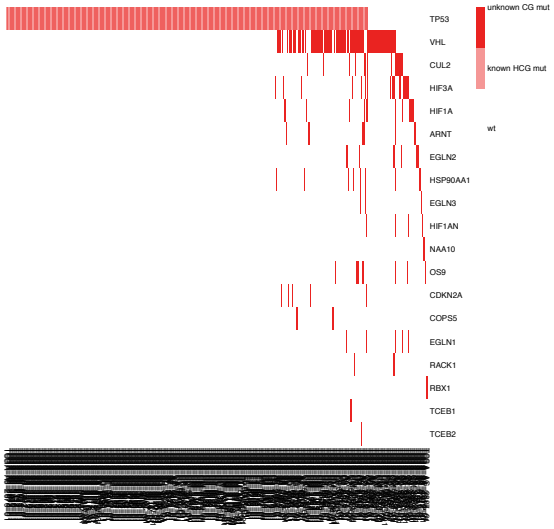
HIF 2 Alpha Transcription Network
FDR = 2e−04%, FDR nod = 0.2%



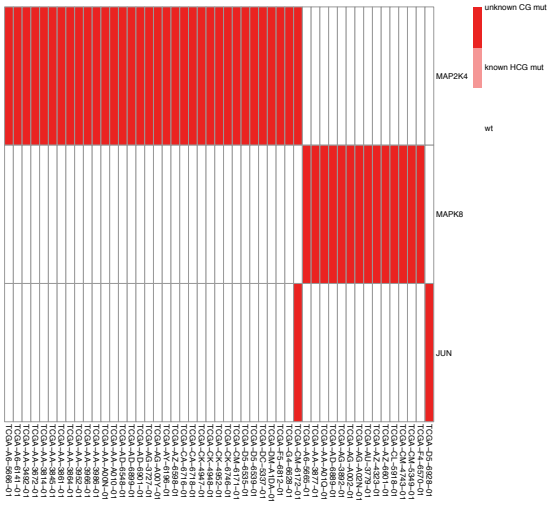
Hypoxia Response Via HIF Activation
FDR = 1.9e−12%, FDR nod = 3.7e−09%



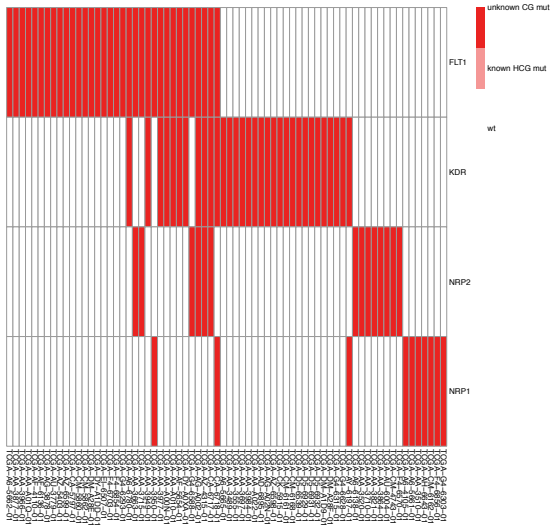
Hypoxic And Oxygen Homeostasis Regulation Of HIF 1 Alpha
FDR = 1.9e−12%, FDR nod = 0.018%



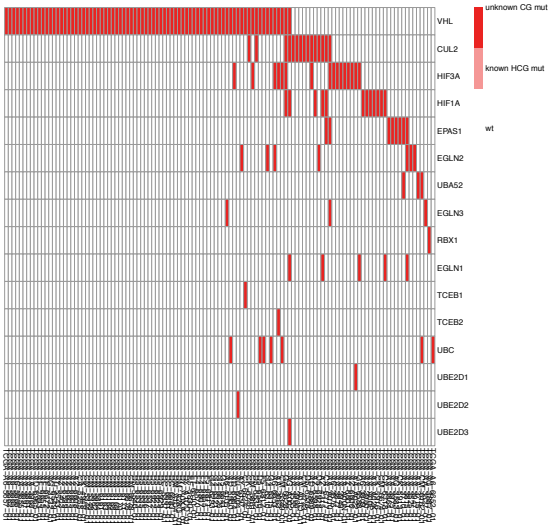
JNK Cascade (EGF Signaling Pathway Diagram)
JNK Cascade (PDGF Signaling Pathway)
FDR = 0.00054%, FDR nod = 0.0011%



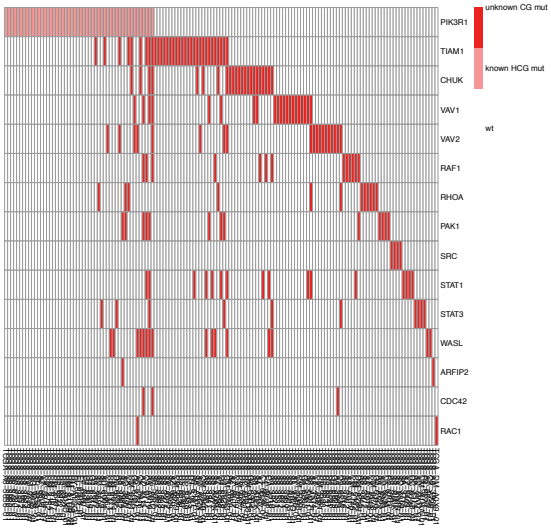
Neurophilin Interactions With VEGF And VEGFR
FDR = 0.68%, FDR nod = 0.78%



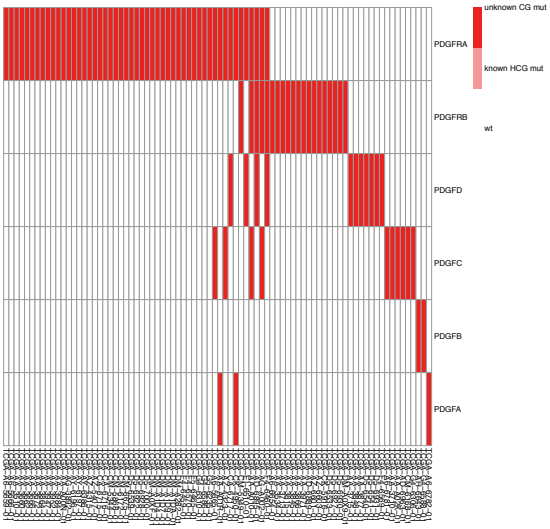
Oxygen Dependent Proline Hydroxylation Of Hypoxia Inducible Factor Alpha
FDR = 0.01%, FDR nod = 0.0092%



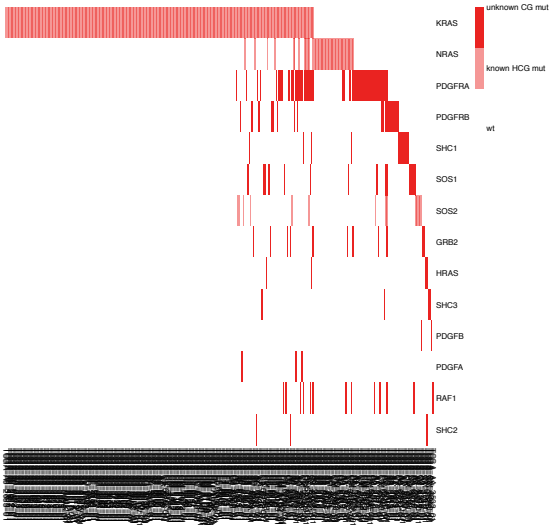
PDGF Pathway
FDR = 8.9e−10%, FDR nod = 0.0023%



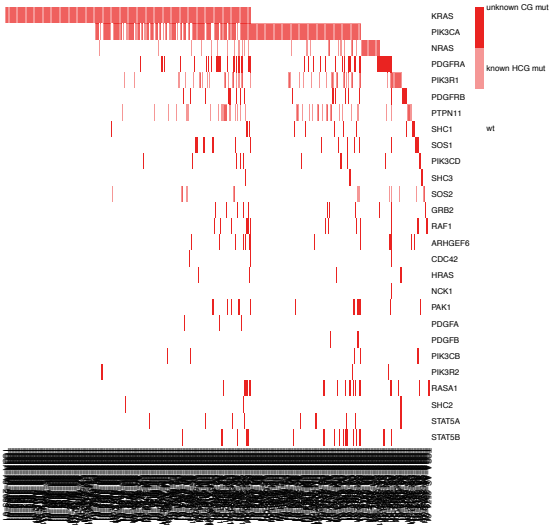
PDGF Receptor Signaling Network
FDR = 7e−08%, FDR nod = 1.2e−07%



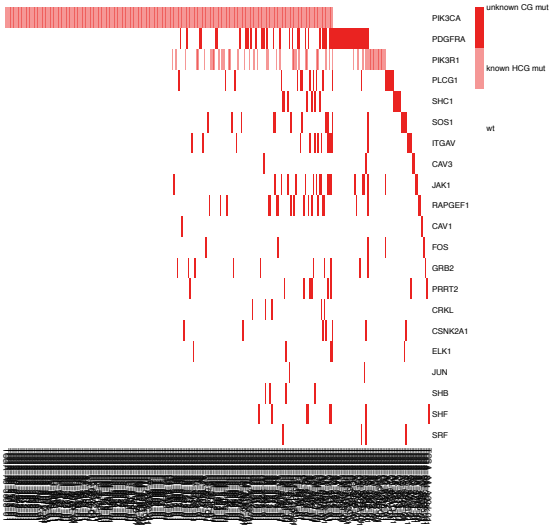
PDGF Signaling Pathway (PDGF Signaling Pathway)
FDR = 1.9e−12%, FDR nod = 0.00016%



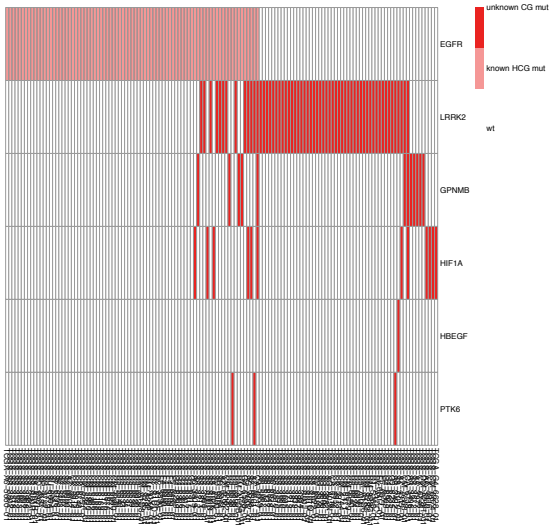
PDGF Signaling Pathway (Mammal) (PDGF Signaling Pathway)
FDR = 1.9e−12%, FDR nod = 0.16%



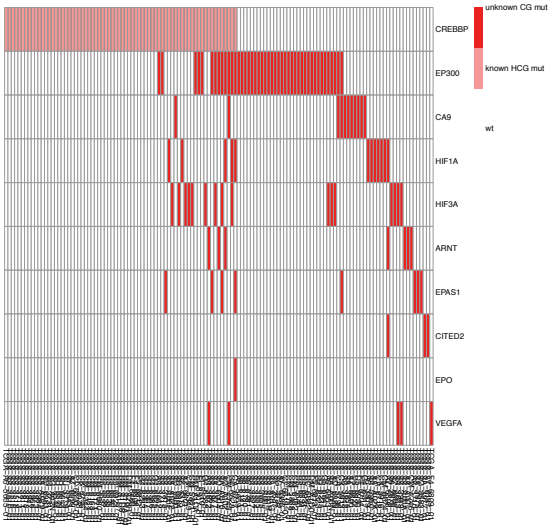
PDGFR Alpha Signaling Pathway
FDR = 1.9e−12%, FDR nod = 0.0023%



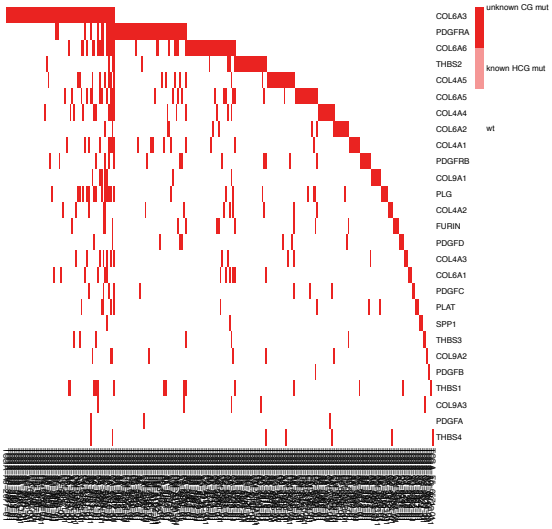
PTK6 Promotes HIF1A Stabilization
FDR = 2e−12%, FDR nod = 2.6e−08%



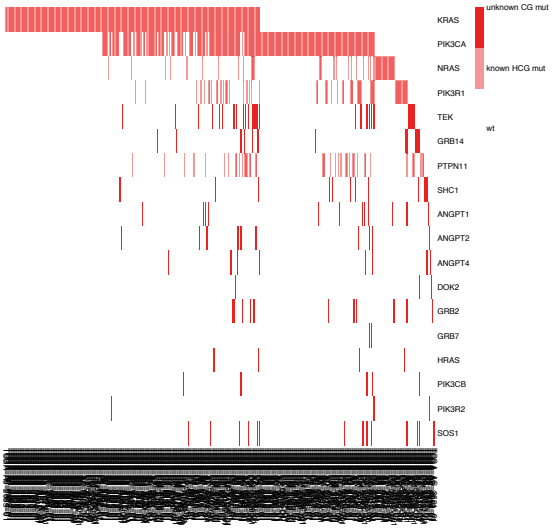
Regulation Of Gene Expression By Hypoxia Inducible Factor
FDR = 4.9e−09%, FDR nod = 1.8%



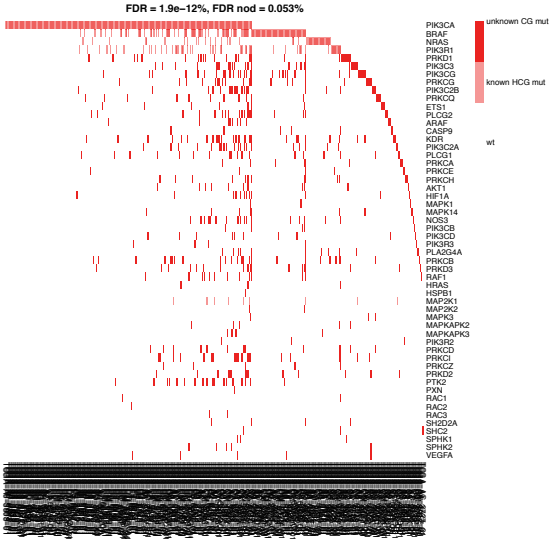
Signaling By PDGF
FDR = 1.9e−12%, FDR nod = 2.3e−11%



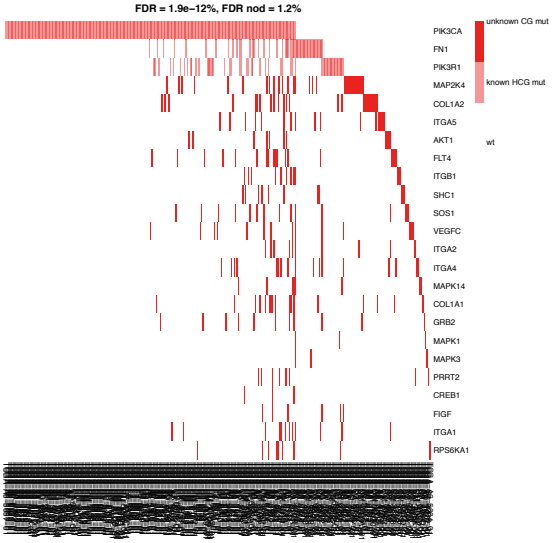
Tie2 Signaling
FDR = 1.9e−12%, FDR nod = 0.074%



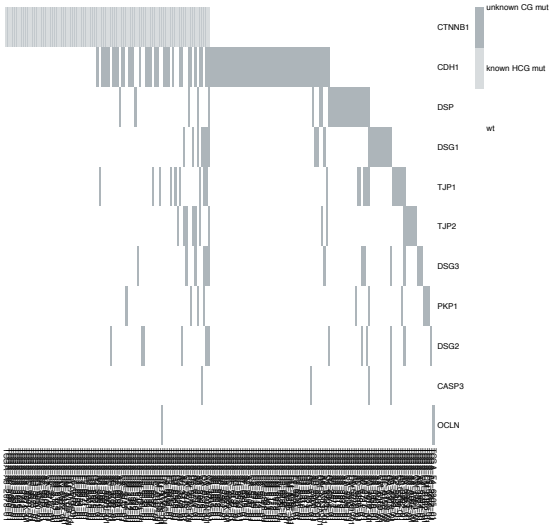
VEGF Signaling Pathway
FDR = 1.9e−12%, FDR nod = 0.053%



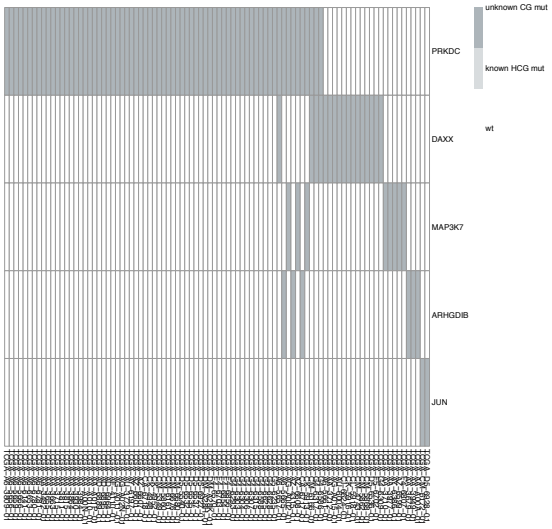
VEGFR3 Signaling In Lymphatic Endothelium
FDR = 1.9e−12%, FDR nod = 1.2%



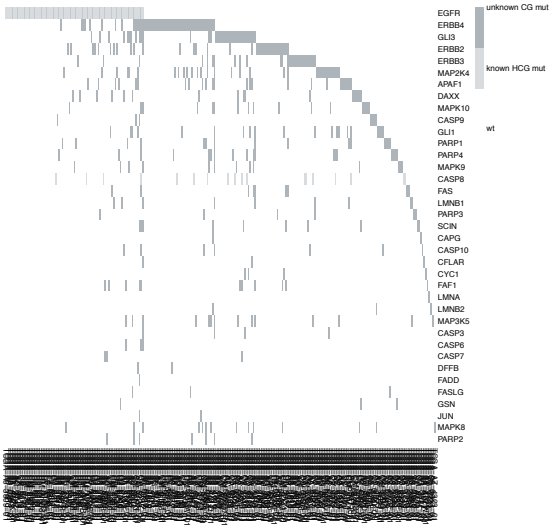
Apoptotic Cleavage Of Cell Adhesion Proteins
FDR = 1.9e−12%, FDR nod = 2.3e−11%



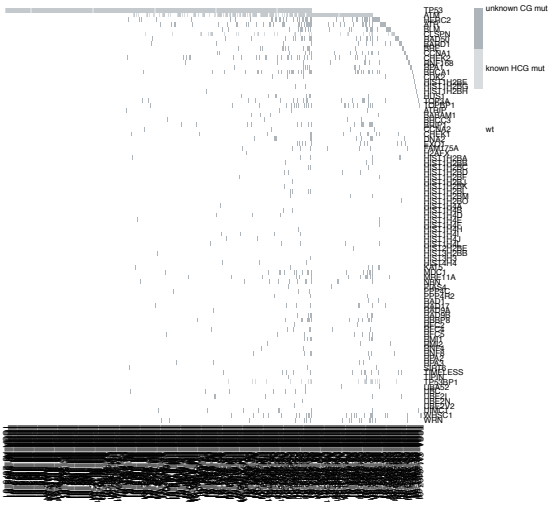
FAS Pathway And Stress Induction Of HSP Regulation
FDR = 4e−06%, FDR nod = 5.5e−06%



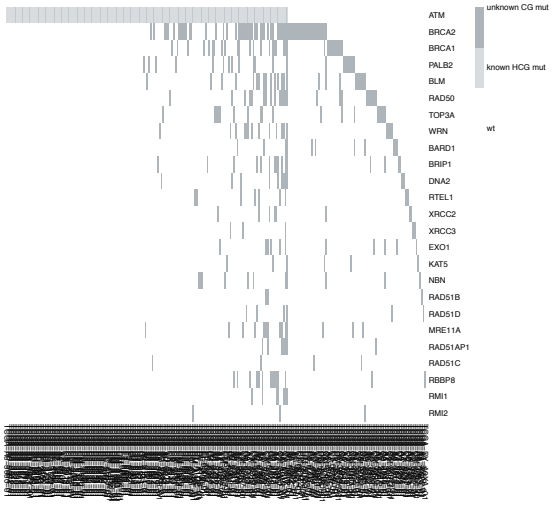
FAS Signaling Pathway
FDR = 2.4e−12%, FDR nod = 3.7e−06%



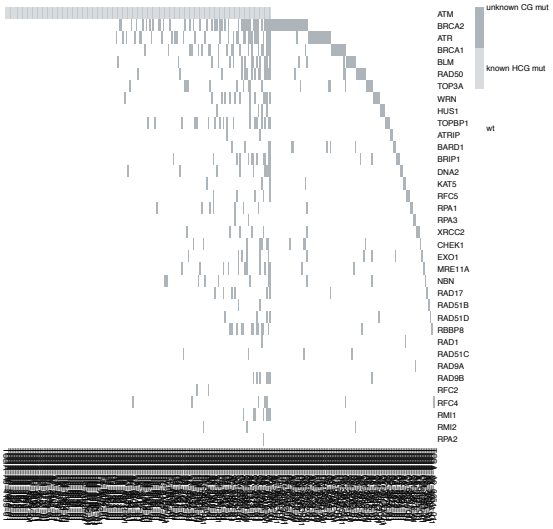
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 1.9e−12%, FDR nod = 4.6%

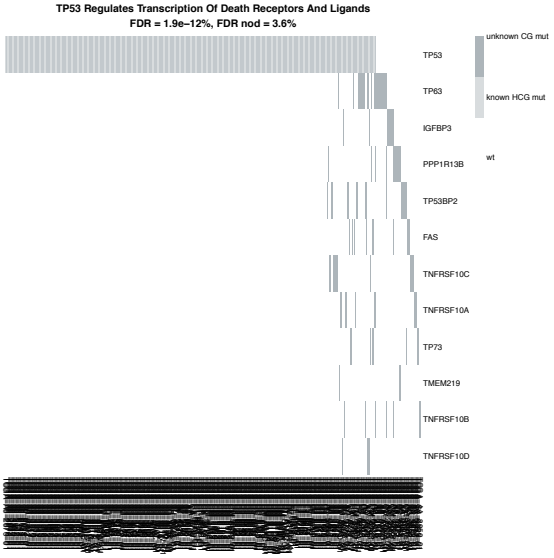


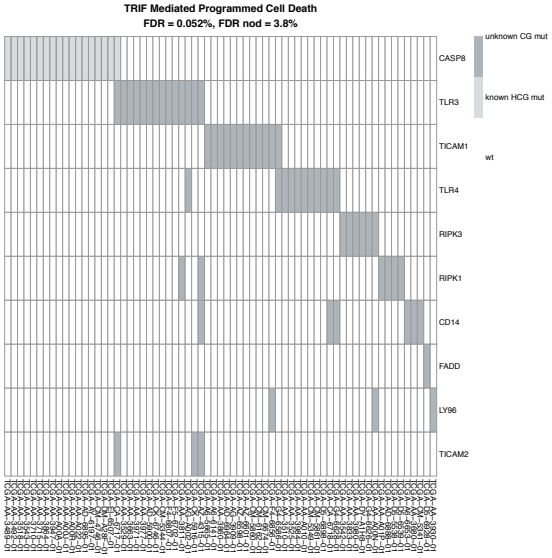
Homologous DNA Pairing And Strand Exchange
esolution Of D Loop Structures Through Synthesis Dependent Strand Annealing (SDSA)
FDR = 1.9e−12%, FDR nod = 0.014%

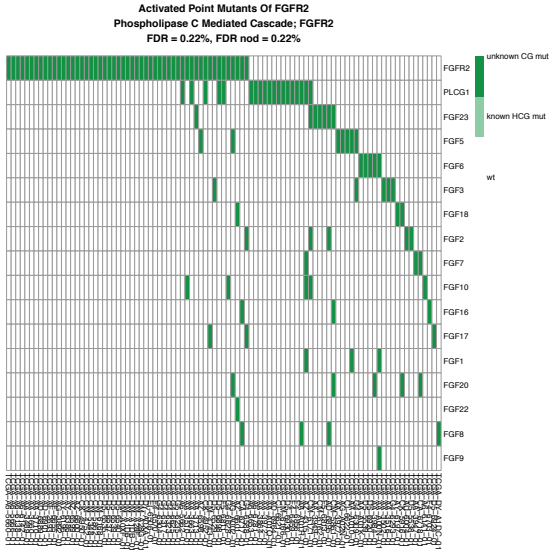


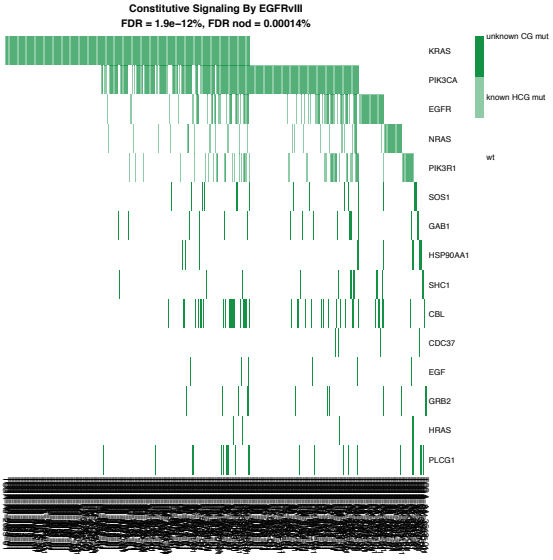
Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange
FDR = 2e−12%, FDR nod = 0.0018%

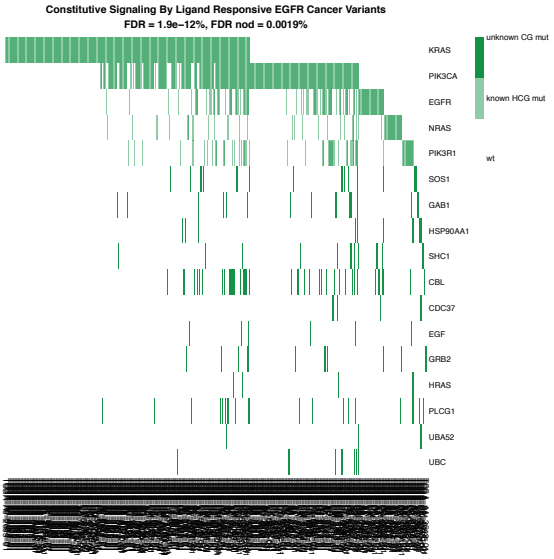


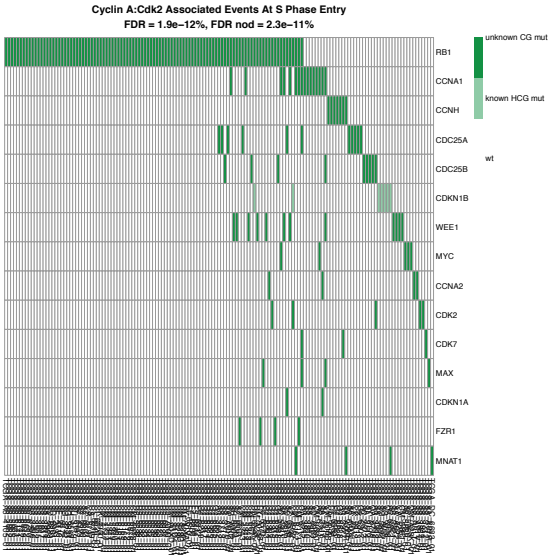

TP53 Regulates Transcription Of Death Receptors And Ligands
FDR = 1.9e−12%, FDR nod = 3.6%
TP53
TP63
IGFBP3
PPP1R13B
TP53BP2
FAS
TNFRSF10C
TNFRSF10A
TP73
TMEM219
TNFRSF10B
TNFRSF10D
unknown CG mut
known HCG mut
wt


TRIF Mediated Programmed Cell Death
FDR = 0.052%, FDR nod = 3.8%
CASP8
TLR3
TICAM1
TLR4
RIPK3
RIPK1
CD14
FADD
LY96
TICAM2
unknown CG mut
known HCG mut
wt

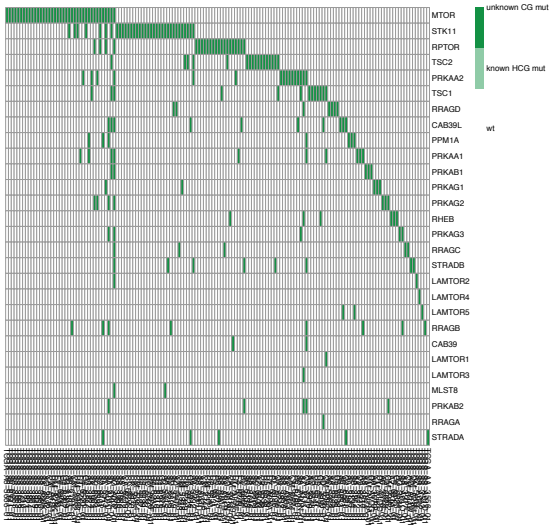

Activated Point Mutants Of FGFR2
Phospholipase C Mediated Cascade; FGFR2
FDR = 0.22%, FDR nod = 0.22%
FGFR2
PLCG1
FGF23
FGF5
FGF6
FGF3
FGF18
FGF2
FGF7
FGF10
FGF16
FGF17
FGF1
FGF20
FGF22
FGF8
FGF9
unknown CG mut
known HCG mut
wt


Constitutive Signaling By EGFRvIII
FDR = 1.9e−12%, FDR nod = 0.00014%
KRAS
PIK3CA
EGFR
NRAS
PIK3R1
SOS1
GAB1
HSP90AA1
SHC1
CBL
CDC37
EGF
GRB2
HRAS
PLCG1
unknown CG mut
known HCG mut
wt

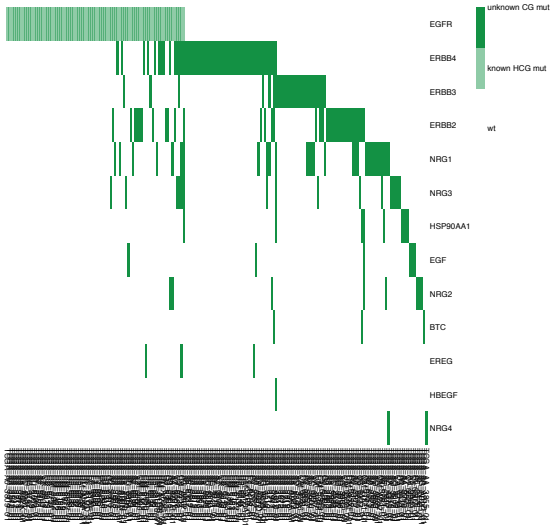

Constitutive Signaling By Ligand Responsive EGFR Cancer Variants
FDR = 1.9e−12%, FDR nod = 0.0019%
KRAS
PIK3CA
EGFR
NRAS
PIK3R1
SOS1
GAB1
HSP90AA1
SHC1
CBL
CDC37
EGF
GRB2
HRAS
PLCG1
UBA52
UBC
unknown CG mut
known HCG mut
wt


Cyclin A:Cdk2 Associated Events At S Phase Entry
FDR = 1.9e−12%, FDR nod = 2.3e−11%
RB1
CCNA1
CCNH
CDC25A
CDC25B
CDKN1B
WEE1
MYC
CCNA2
CDK2
CDK7
MAX
CDKN1A
FZR1
MNAT1
unknown CG mut
known HCG mut
wt

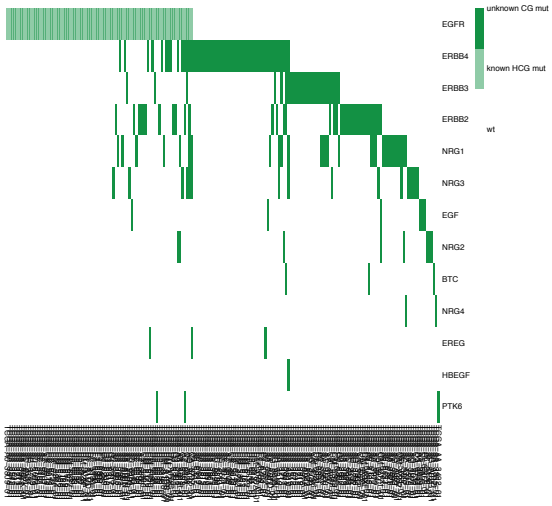
Energy Dependent Regulation Of MTOR By LKB1 AMPK
FDR = 4.4%, FDR nod = 3.2%



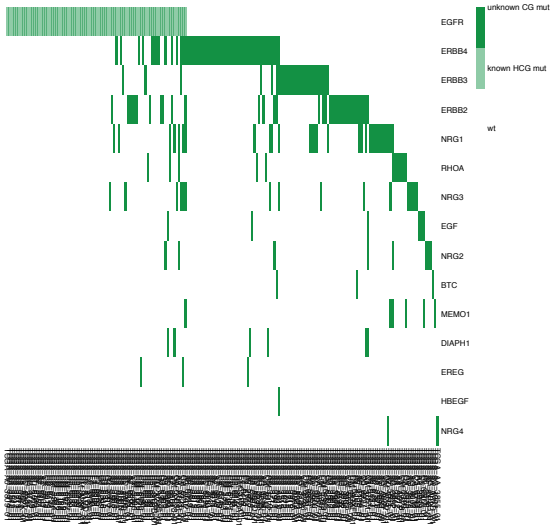
ErbB Receptor Signaling Network
FDR = 2e−12%, FDR nod = 2.3e−11%



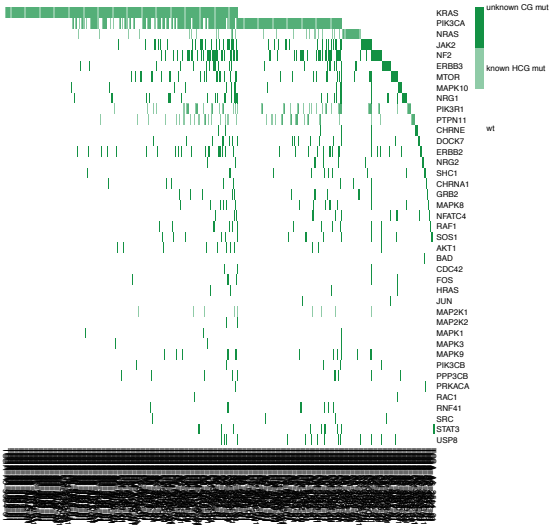
ERBB2 Activates PTK6 Signaling
Signaling By ERBB4
FDR = 1.9e−12%, FDR nod = 2.3e−11%



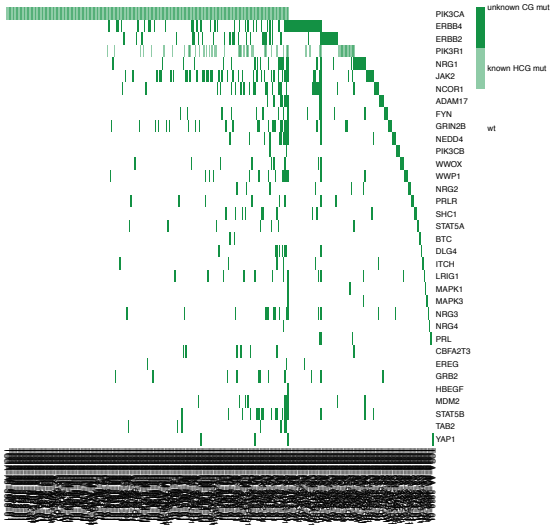
ERBB2 Regulates Cell Motility
FDR = 1.9e−12%, FDR nod = 5.5e−11%



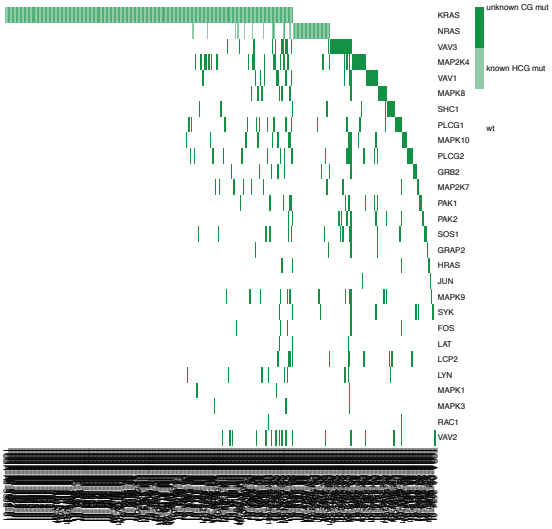
ErbB2/ErbB3 Signaling Events
FDR = 1.9e−12%, FDR nod = 1.1e−09%



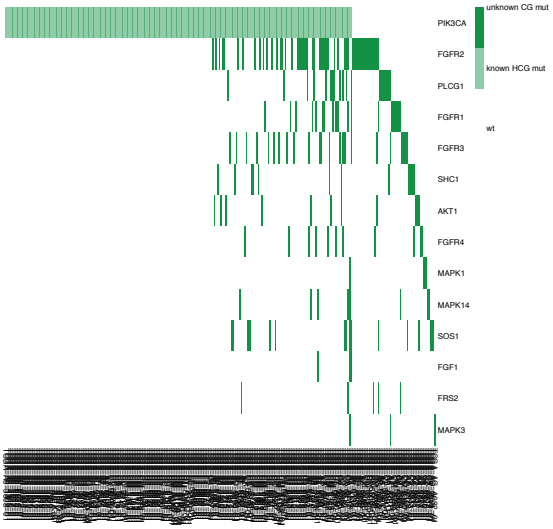
ErbB4 Signaling Events
FDR = 1.9e−12%, FDR nod = 3.6e−06%



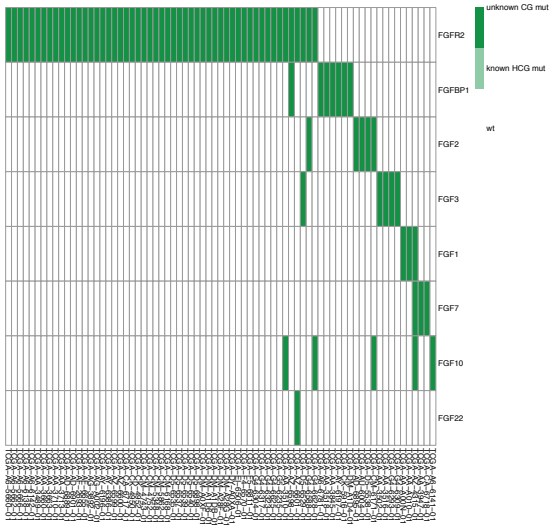
FCERI Mediated MAPK Activation
FDR = 1.9e−12%, FDR nod = 0.049%



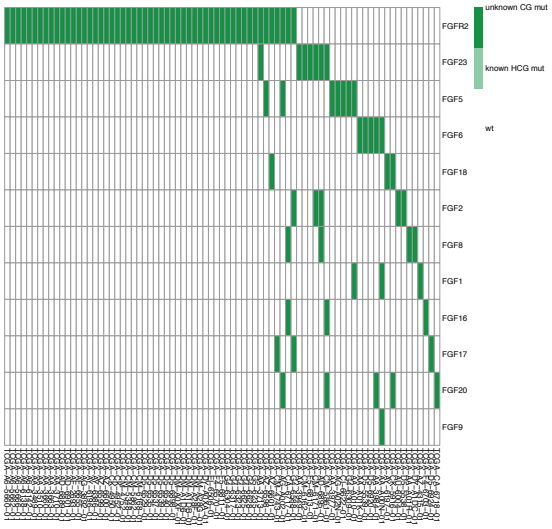
FGF Signaling Pathway
FDR = 1.9e−12%, FDR nod = 0.00054%



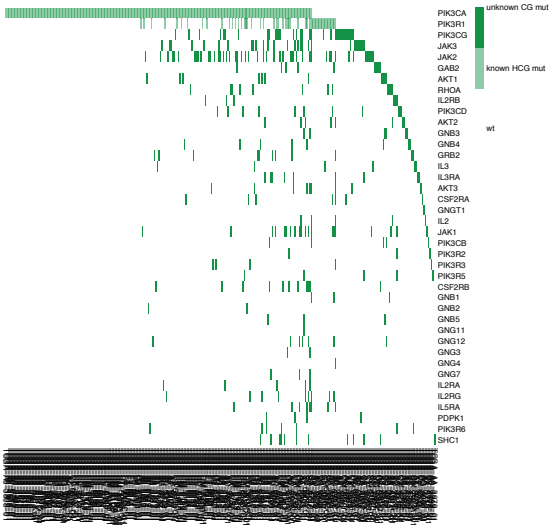
FGFR2b Ligand Binding And Activation
FDR = 9.7e−05%, FDR nod = 0.00016%



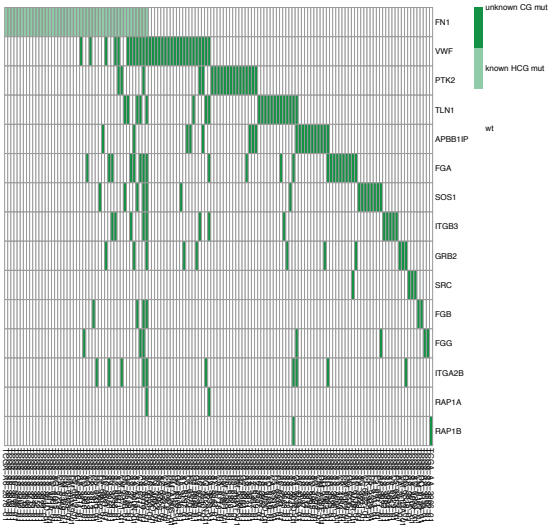
FGFR2c Ligand Binding And Activation
FDR = 0.0063%, FDR nod = 0.0079%

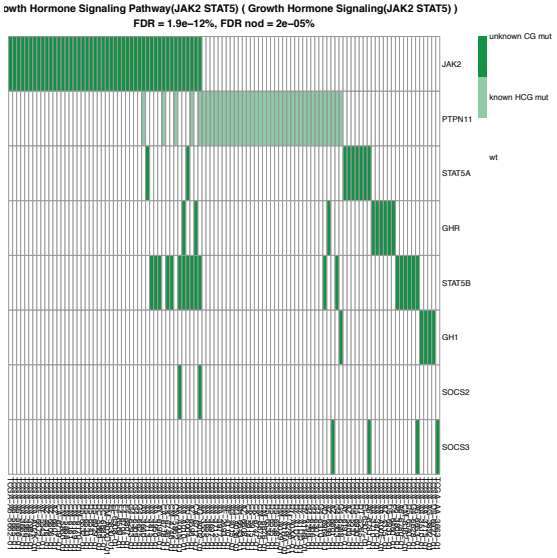


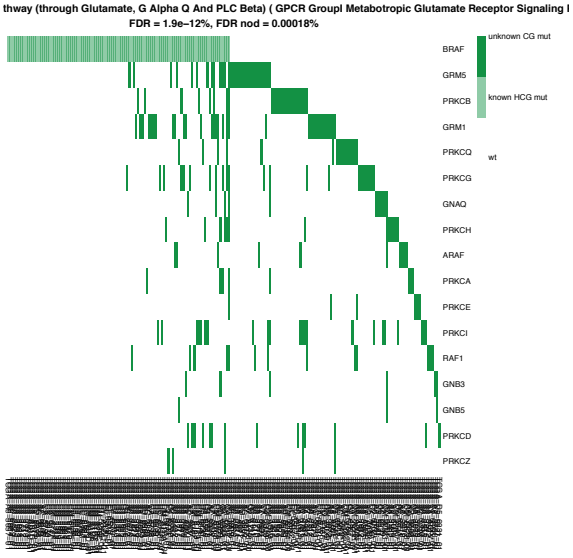
G Beta:gamma Signalling Through PI3Kgamma
FDR = 1.9e−12%, FDR nod = 0.45%

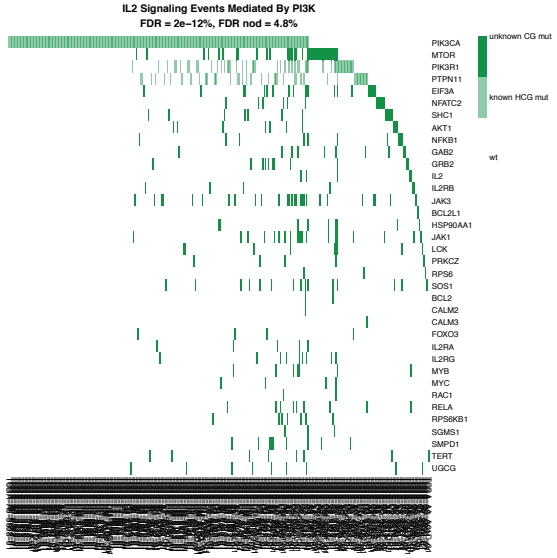


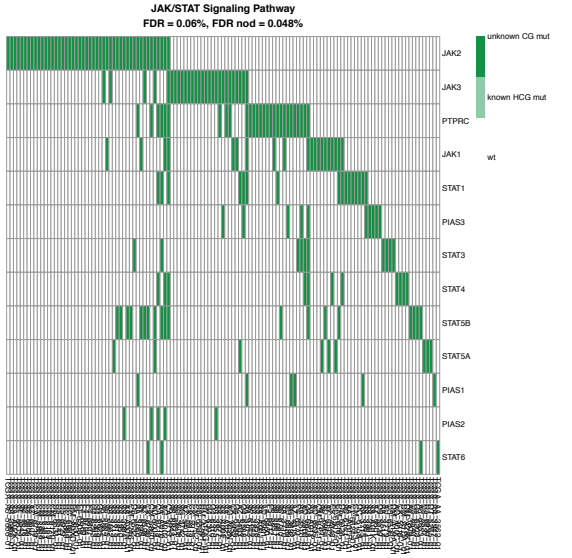
GRB2:SOS Provides Linkage To MAPK Signaling For Integrins
FDR = 0.064%, FDR nod = 4.4%

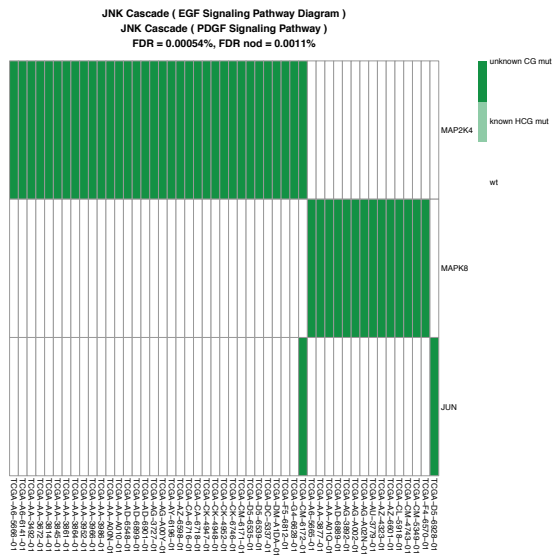


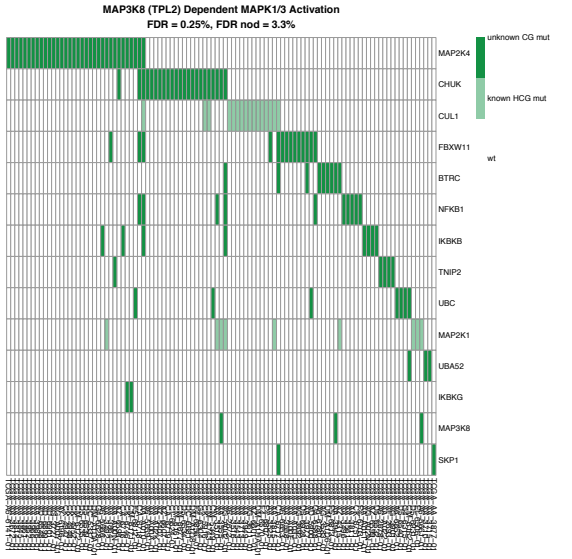

owth Hormone Signaling Pathway(JAK2 STAT5) (Growth Hormone Signaling(JAK2 STAT5))
FDR = 1.9e−12%, FDR nod = 2e−05%
JAK2
PTPN11
STAT5A
GHR
STAT5B
GH1
SOCS2
SOCS3
unknown CG mut
known HCG mut
wt

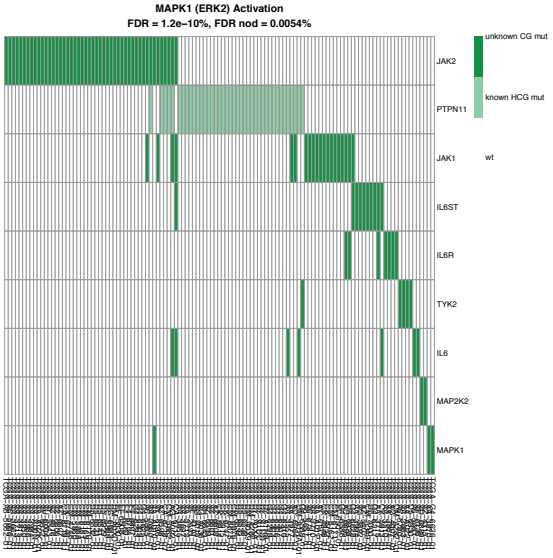

thway (through Glutamate, G Alpha Q And PLC Beta) (GPCR Groupl Metabotropic Glutamate Receptor Signaling I
FDR = 1.9e−12%, FDR nod = 0.00018%
BRAF
GRM5
PRKCB
GRM1
PRKCQ
PRKCG
GNAQ
PRKCH
ARAF
PRKCA
PRKCE
PRKCI
RAF1
GNB3
GNB5
PRKCD
PRKCZ
unknown CG mut
known HCG mut
wt

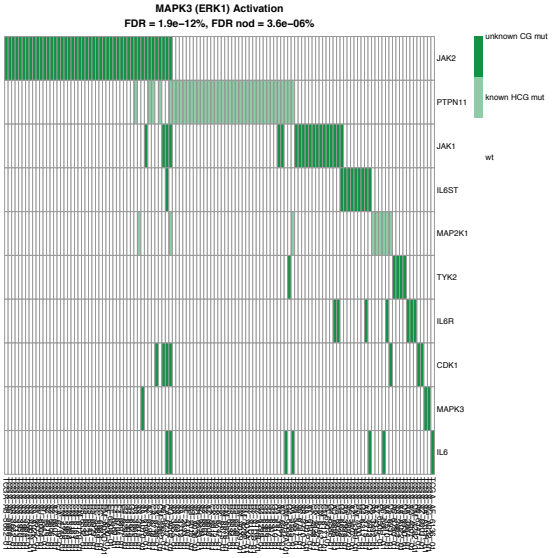

IL2 Signaling Events Mediated By PI3K
FDR = 2e−12%, FDR nod = 4.8%
PIK3CA
MTOR
PIK3R1
PTPN11
EIF3A
NFATC2
SHC1
AKT1
NFKB1
GAB2
GRB2
IL2
IL2RB
JAK3
BCL2L1
HSP90AA1
JAK1
LCK
PRKCZ
RPS6
SOS1
BCL2
CALM2
CALM3
FOXO3
IL2RA
IL2RG
MYB
MYC
RAC1
RELA
RPS6KB1
SGMS1
SMPD1
TERT
UGCG
unknown CG mut
known HCG mut
wt

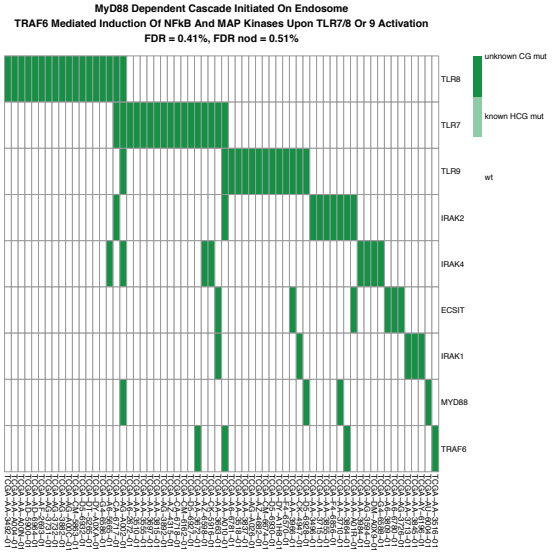

JAK/STAT Signaling Pathway
FDR = 0.06%, FDR nod = 0.048%
JAK2
JAK3
PTPRC
JAK1
STAT1
PIAS3
STAT3
STAT4
STAT5B
STAT5A
PIAS1
PIAS2
STAT6
unknown CG mut
known HCG mut
wt

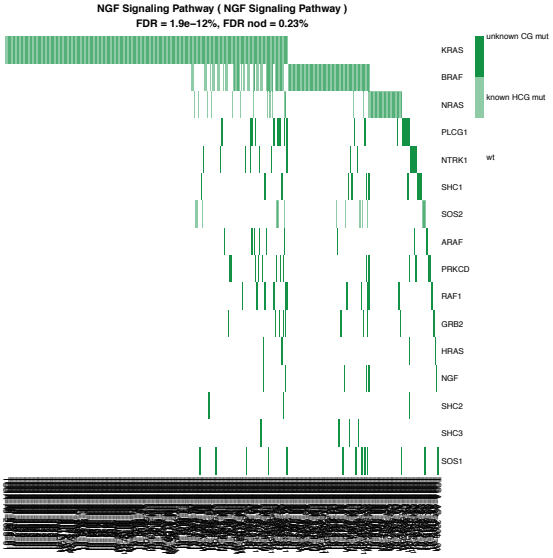

JNK Cascade (EGF Signaling Pathway Diagram)
JNK Cascade (PDGF Signaling Pathway)
FDR = 0.00054%, FDR nod = 0.0011%
MAP2K4
MAPK8
JUN
unknown CG mut
known HCG mut
wt

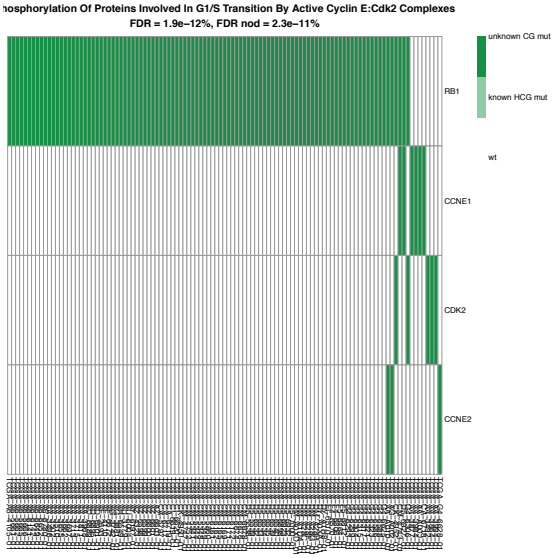

MAP3K8 (TPL2) Dependent MAPK1/3 Activation
FDR = 0.25%, FDR nod = 3.3%
MAP2K4
CHUK
CUL1
FBXW11
BTRC
NFKB1
IKBKB
TNIP2
UBC
MAP2K1
UBA52
IKBKG
MAP3K8
SKP1
unknown CG mut
known HCG mut
wt

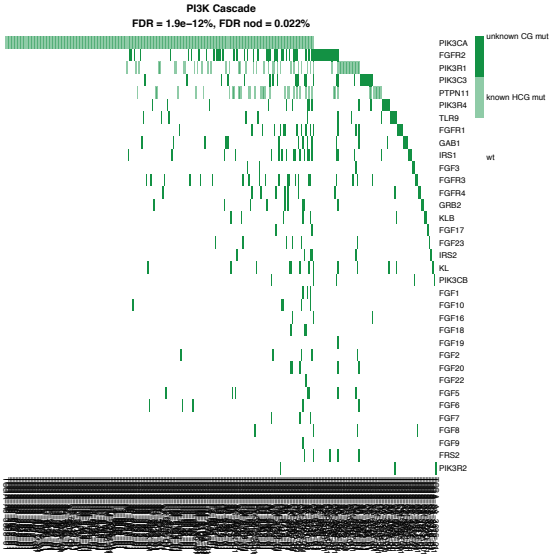

MAPK1 (ERK2) Activation
FDR = 1.2e−10%, FDR nod = 0.0054%
JAK2
PTPN11
JAK1
IL6ST
IL6R
TYK2
IL6
MAP2K2
MAPK1
unknown CG mut
known HCG mut
wt


MAPK3 (ERK1) Activation
FDR = 1.9e−12%, FDR nod = 3.6e−06%
JAK2
PTPN11
JAK1
IL6ST
MAP2K1
TYK2
IL6R
CDK1
MAPK3
IL6
unknown CG mut
known HCG mut
wt

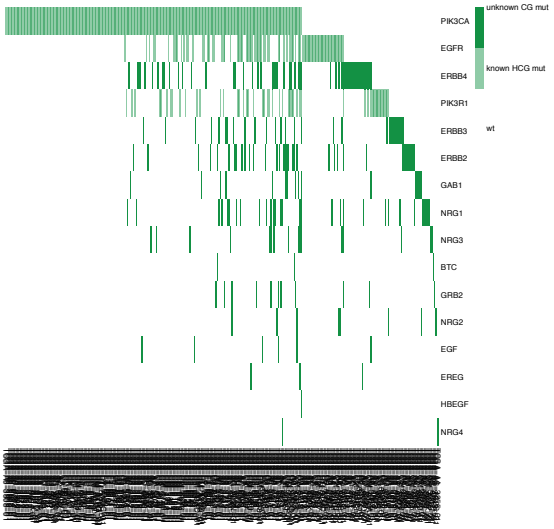

MyD88 Dependent Cascade Initiated On Endosome
TRAF6 Mediated Induction Of NFkB And MAP Kinases Upon TLR7/8 Or 9 Activation
FDR = 0.41%, FDR nod = 0.51%
TLR8
TLR7
TLR9
IRAK2
IRAK4
ECSIT
IRAK1
MYD88
TRAF6
unknown CG mut
known HCG mut
wt


NGF Signaling Pathway (NGF Signaling Pathway)
FDR = 1.9e−12%, FDR nod = 0.23%
KRAS
BRAF
NRAS
PLCG1
NTRK1
SHC1
SOS2
ARAF
PRKCD
RAF1
GRB2
HRAS
NGF
SHC2
SHC3
SOS1
unknown CG mut
known HCG mut
wt

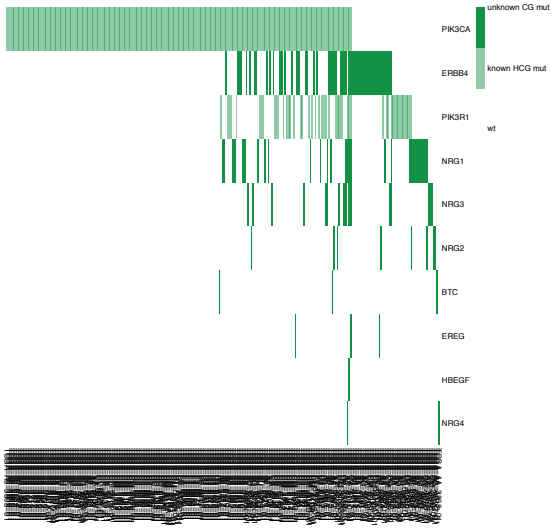

hosphorylation Of Proteins Involved In G1/S Transition By Active Cyclin E:Cdk2 Complexes
FDR = 1.9e−12%, FDR nod = 2.3e−11%
RB1
CCNE1
CDK2
CCNE2
unknown CG mut
known HCG mut
wt


PI3K Cascade
FDR = 1.9e−12%, FDR nod = 0.022%
PIK3CA
FGFR2
PIK3R1
PIK3C3
PTPN11
PIK3R4
TLR9
FGFR1
GAB1
IRS1
FGF3
FGFR3
FGFR4
GRB2
KLB
FGF17
FGF23
IRS2
KL
PIK3CB
FGF1
FGF10
FGF16
FGF18
FGF19
FGF2
FGF20
FGF22
FGF5
FGF6
FGF7
FGF8
FGF9
FRS2
PIK3R2
unknown CG mut
known HCG mut
wt

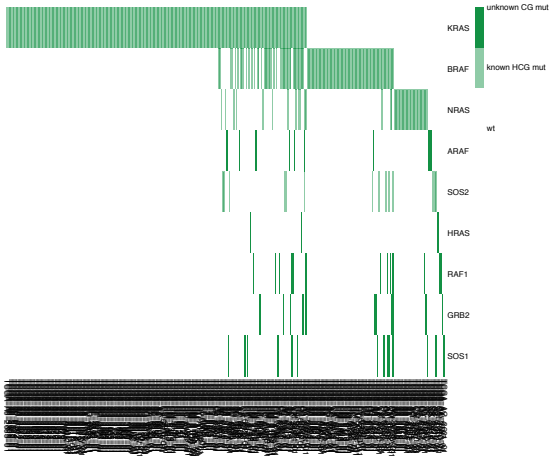
PI3K Events In ERBB2 Signaling
FDR = 1.9e−12%, FDR nod = 2.3e−11%



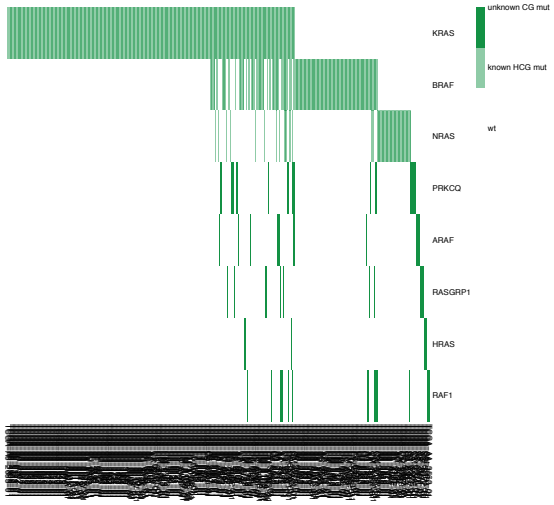
PI3K Events In ERBB4 Signaling
FDR = 1.9e−12%, FDR nod = 3.5e−06%



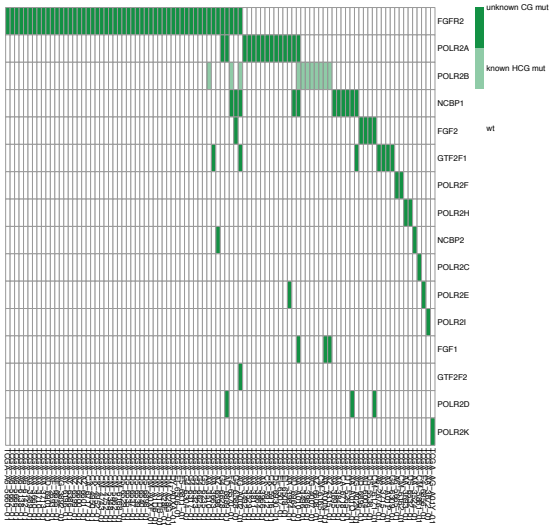
Raf Activation Signaling (through Grb2 And Sos) (B Cell Receptor Signaling)
Activation Signaling (through Grb2 And Sos) (CD4 T Cell Receptor Signaling (ERK Cascade))
Raf Activation Signaling (through Grb2 And Sos) (CD4 T Cell Receptor Signaling)
ivation Signaling (through Grb2 And Sos) (JAK STAT Pathway And Regulation Pathway Diagram)
FDR = 1.9e−12%, FDR nod = 2.5%



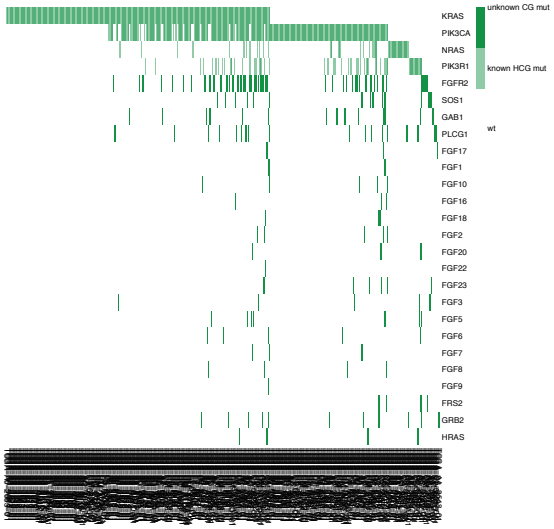
f Activation Signaling (through RasGRP) (CD4 T Cell Receptor Signaling (ERK Cascade))
Raf Activation Signaling (through RasGRP) (CD4 T Cell Receptor Signaling)
FDR = 1.9e−12%, FDR nod = 0.2%

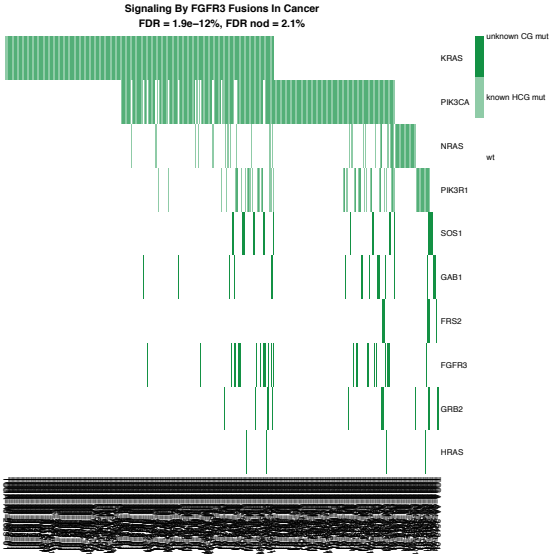


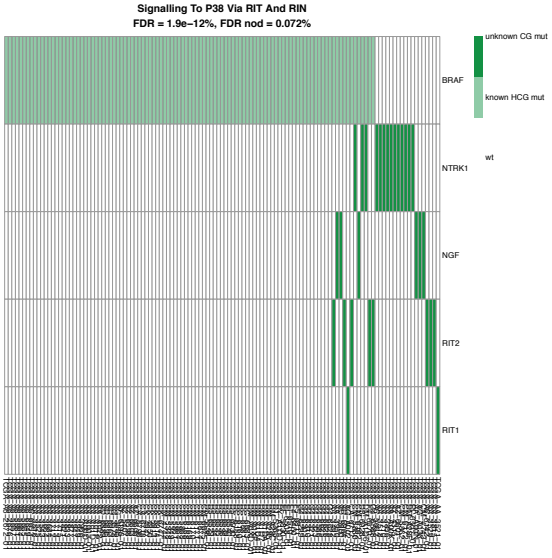
Signaling By FGFR2 IIIa TM
FDR = 4.8%, FDR nod = 4.8%

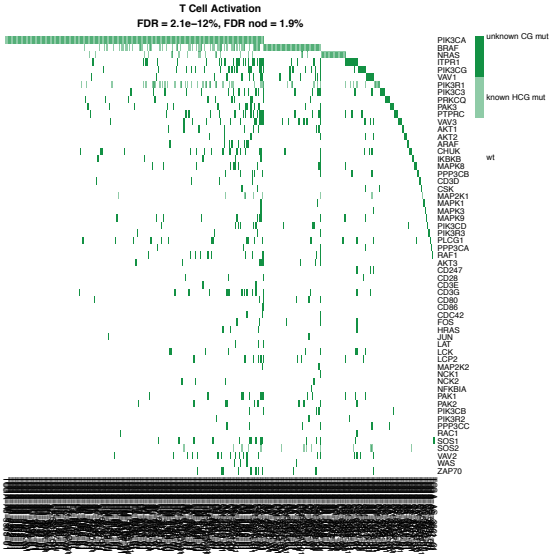


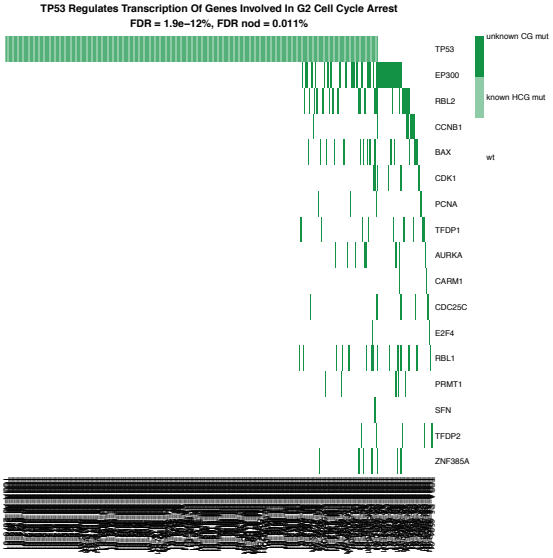
Signaling By FGFR2 In Disease
FDR = 1.9e−12%, FDR nod = 0.72%

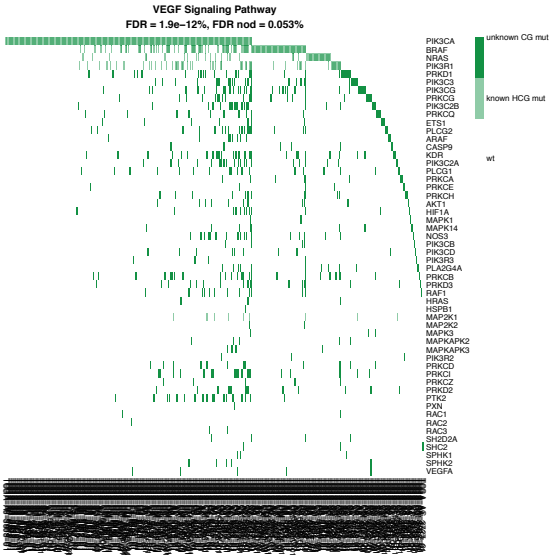


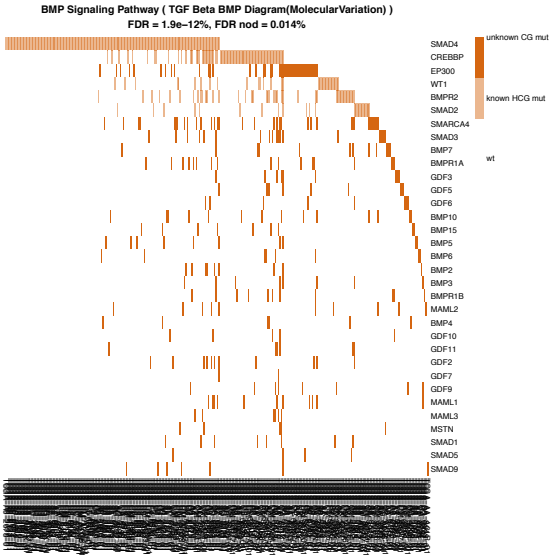

Signaling By FGFR3 Fusions In Cancer
FDR = 1.9e−12%, FDR nod = 2.1%
KRAS
PIK3CA
NRAS
PIK3R1
SOS1
GAB1
FRS2
FGFR3
GRB2
HRAS
unknown CG mut
known HCG mut
wt


Signalling To P38 Via RIT And RIN
FDR = 1.9e−12%, FDR nod = 0.072%
BRAF
NTRK1
NGF
RIT2
RIT1
unknown CG mut
known HCG mut
wt

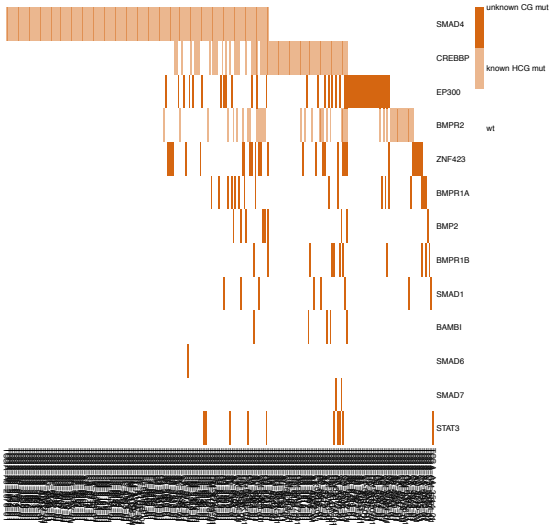

T Cell Activation
FDR = 2.1e−12%, FDR nod = 1.9%
PIK3CA
BRAF
NRAS
ITPR1
PIK3CG
VAV1
PIK3R1
PIK3C3
PRKCG
PIK3
PTPRC
VAV3
AKT1
AKT2
ARAF
CHUK
IKBKB
MAPK8
PPP3CB
CD3D
CSK
MAP2K1
MAPK1
MAPK3
MAPK9
PIK3CD
PIK3R3
PLCG1
PPP3CA
RAF1
AKT3
CD3Z47
CD28
CD3E
CD3G
CD80
CD86
CDC42
FOS
HRAS
JUN
LAT
LCK
LCP2
MAP2K2
NCK1
NCK2
NFKBIA
PAK1
PAK2
PIK3CB
PIK3R2
PPP3CC
RAC1
SOS1
SOS2
VAV2
WAS
ZAP70
unknown CG mut
known HCG mut
wt


TP53 Regulates Transcription Of Genes Involved In G2 Cell Cycle Arrest
FDR = 1.9e−12%, FDR nod = 0.011%
TP53
EP300
RBL2
CCNB1
BAX
CDK1
PCNA
TFDP1
AURKA
CARM1
CDC25C
E2F4
RBL1
PRMT1
SFN
TFDP2
ZNF385A
unknown CG mut
known HCG mut
wt

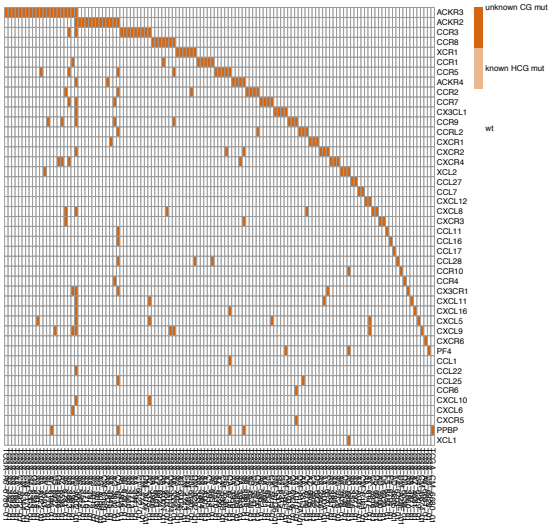

VEGF Signaling Pathway
FDR = 1.9e−12%, FDR nod = 0.053%
PIK3CA
BRAF
NRAS
PIK3R1
PRKD1
PIK3C3
PIK3CG
PRKCG
PIK3C2B
PRKCQ
ETS1
PLCG2
ARAF
CASP9
KDR
PIK3C2A
PLCG1
PRKCA
PRKCE
PRKCH
AKT1
HIF1A
MAPK1
MAPK14
NOS3
PIK3CB
PIK3CD
PIK3R3
PLA2G4A
PRKCB
PRKD3
RAF1
HRAS
HSPB1
MAP2K1
MAP2K2
MAPK3
MAPKAPK2
MAPKAPK3
PIK3R2
PRKCD
PRKCI
PRKCZ
PRKD2
PTK2
PXN
RAC1
RAC2
RAC3
SHD2D2A
SHC2
SPHK1
SPHK2
VEGFA
unknown CG mut
known HCG mut
wt


BMP Signaling Pathway (TGF Beta BMP Diagram(MolecularVariation))
FDR = 1.9e−12%, FDR nod = 0.014%
SMAD4
CREBBP
EP300
WT1
BMPR2
SMAD2
SMARCA4
SMAD3
BMP7
BMPR1A
GDF3
GDF5
GDF6
BMP10
BMP15
BMP5
BMP6
BMP2
BMP3
BMPR1B
MAML2
BMP4
GDF10
GDF11
GDF2
GDF7
GDF9
MAML1
MAML3
MSTN
SMAD1
SMAD5
SMAD9
unknown CG mut
known HCG mut
wt

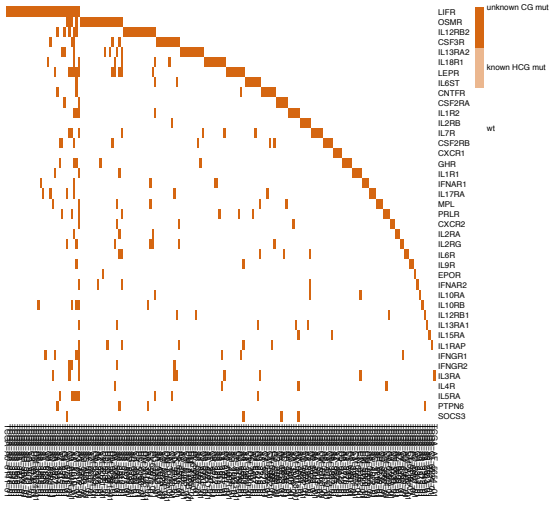
BMP2 Signaling Pathway(through Smad) (TGF Beta BMP Diagram(MolecularVariation))
FDR = 1.9e−12%, FDR nod = 0.095%



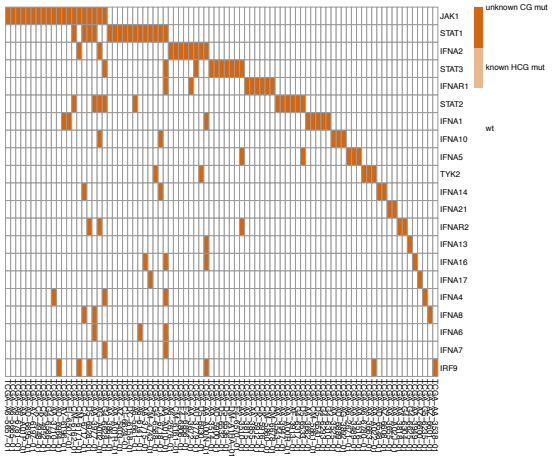
Chemokine Receptors Bind Chemokines
FDR = 4.8%, FDR nod = 3.9%



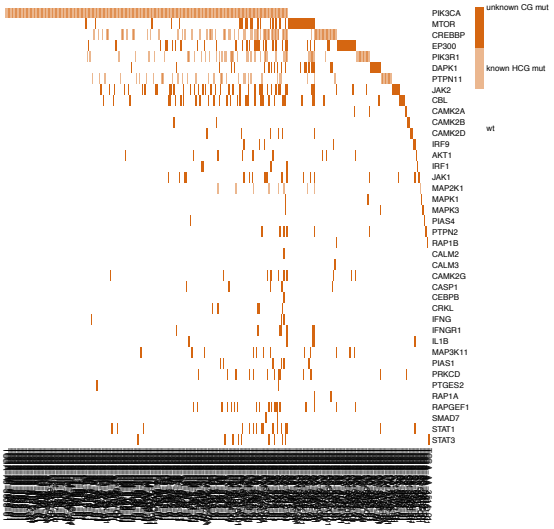
kine Receptor Degradation Signaling (JAK STAT Pathway And Regulation Pathway Diagram)
osphorylation Of Cytokine Receptor) In JAK STAT Pathway (JAK STAT Pathway And Regulation Pathway Diagram
FDR = 2.3%, FDR nod = 1.3%



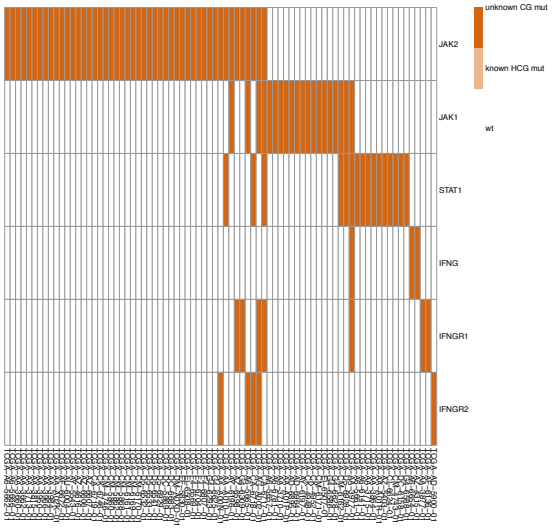
ignaling Pathway((JAK1 TYK2 STAT1 STAT2) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
ignaling Pathway(JAK1 TYK2 STAT1 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
a Signaling Pathway(JAK1 TYK2 STAT1) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
a Signaling Pathway(JAK1 TYK2 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
FDR = 2.5%, FDR nod = 2.5%



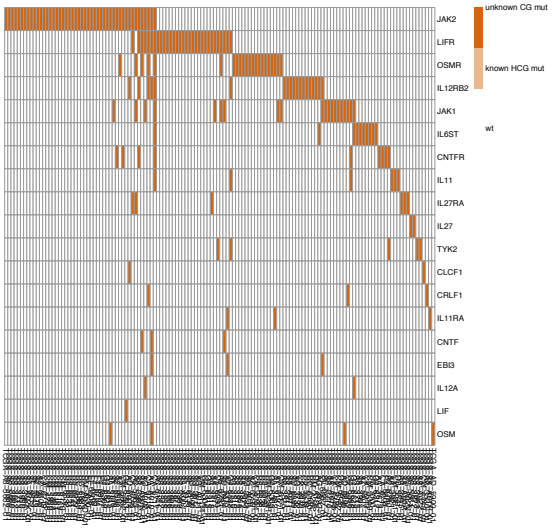
IFN Gamma Pathway
FDR = 1.9e−12%, FDR nod = 0.26%



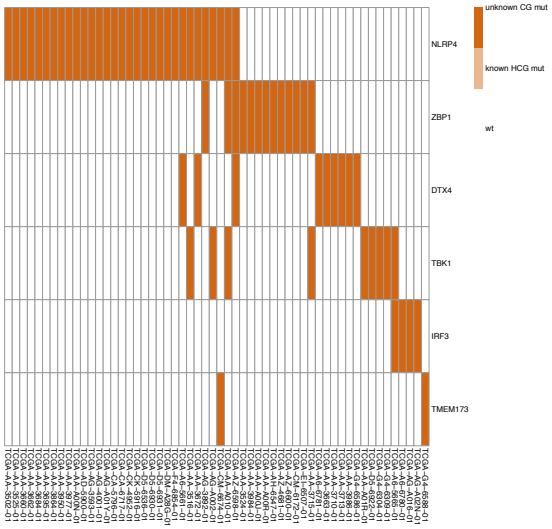
Gamma Signaling Pathway(JAK1 JAK2 STAT1) (IFN Gamma Signaling(JAK1 JAK2 STAT1))
FDR = 2.5e−12%, FDR nod = 2.3e−11%



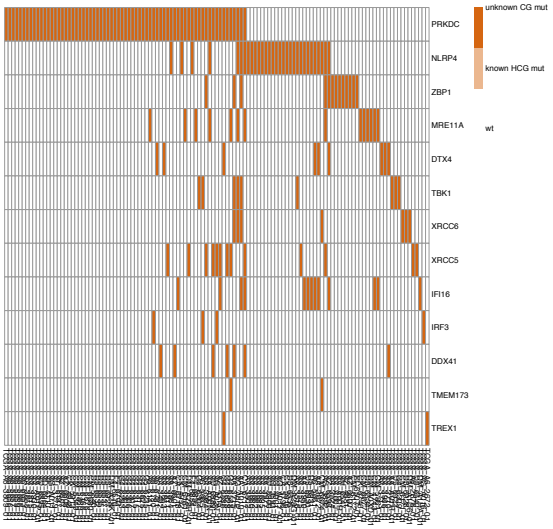
IL 6 Type Cytokine Receptor Ligand Interactions
FDR = 1.4e−09%, FDR nod = 1.2e−09%



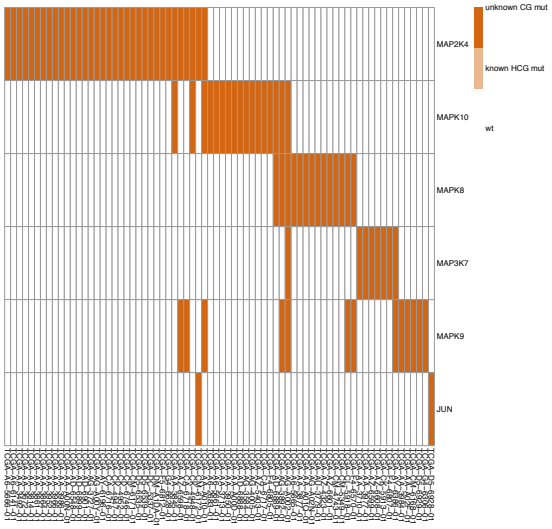
IRF3 Mediated Activation Of Type 1 IFN
FDR = 0.04%, FDR nod = 0.056%



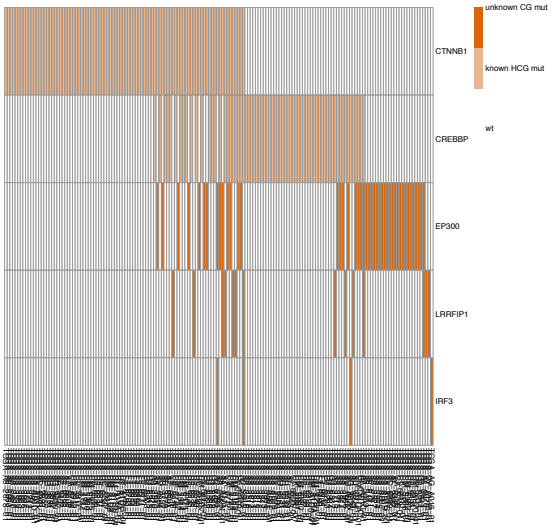
IRF3 Mediated Induction Of Type I IFN
FDR = 2.2e−07%, FDR nod = 2.2e−07%



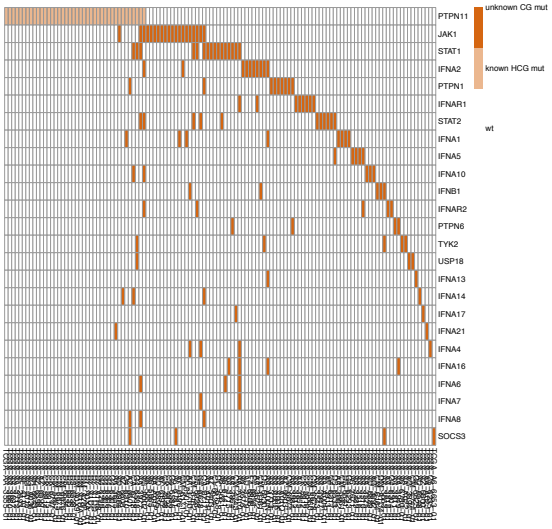
JNK Cascade (TGF Beta Signaling(through TAK1))
FDR = 0.38%, FDR nod = 0.45%



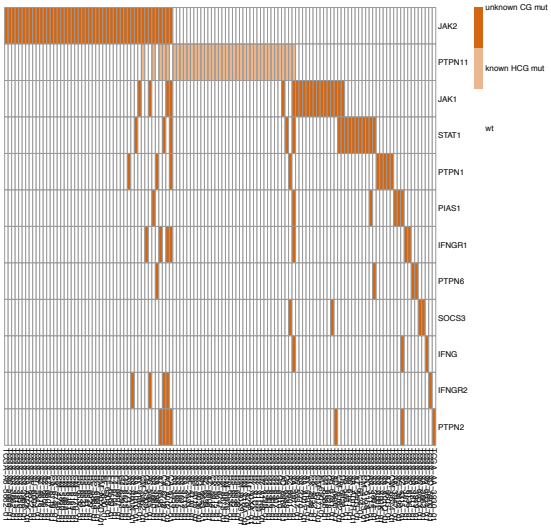
LRR FLII Interacting Protein 1 (LRRFIP1) Activates Type I IFN Production
FDR = 1.9e−12%, FDR nod = 0.021%



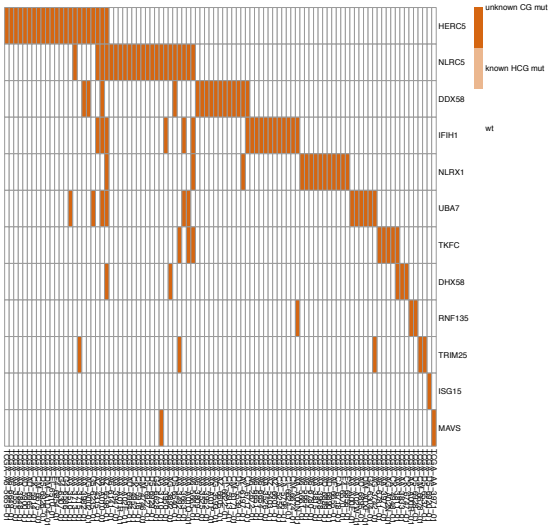
Regulation Of IFNA Signaling
FDR = 1.9e−07%, FDR nod = 0.54%



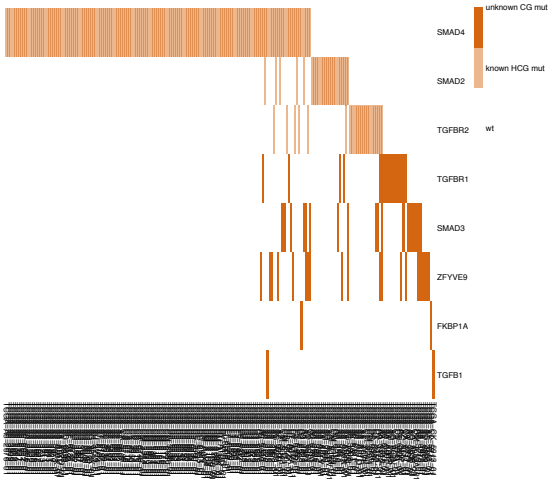
Regulation Of IFNG Signaling
FDR = 1.5e−11%, FDR nod = 0.0025%



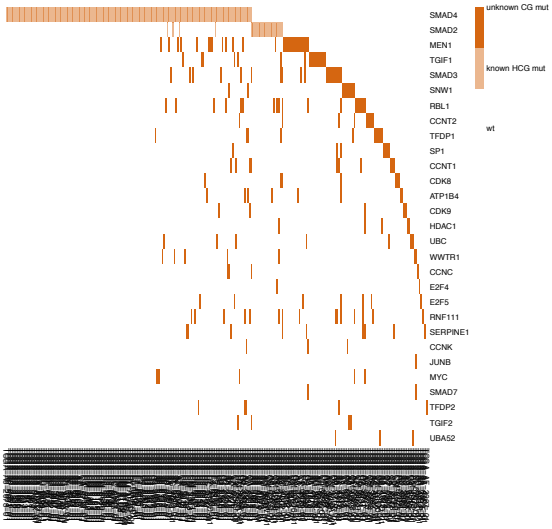
RIG I/MDA5 Mediated Induction Of IFN Alpha/beta Pathways
FDR = 0.8%, FDR nod = 0.78%



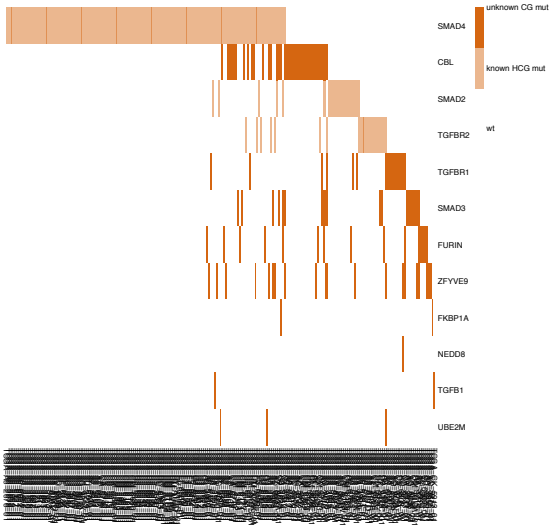
SMAD2/3 MH2 Domain Mutants In Cancer
SMAD2/3 Phosphorylation Motif Mutants In Cancer
TGFBR1 KD Mutants In Cancer
FDR = 2.1e−12%, FDR nod = 1.9%



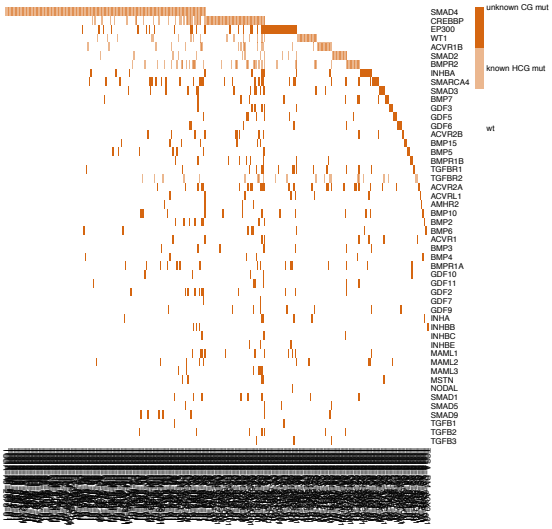
SMAD2/SMAD3:SMAD4 Heterotrimer Regulates Transcription
FDR = 1.9e−12%, FDR nod = 2.5%



TGF Beta Receptor Signaling Activates SMADs
FDR = 1.9e−12%, FDR nod = 0.00021%

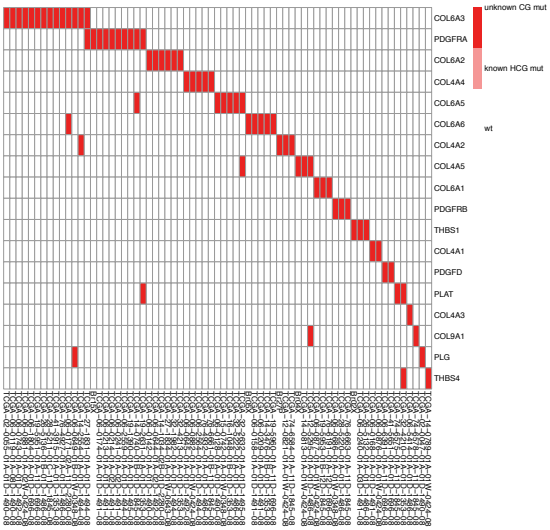


ta Super Family Signaling Pathway(canonical) (TGF Beta BMP Diagram(MolecularVariation))
FDR = 1.9e−12%, FDR nod = 0.31%

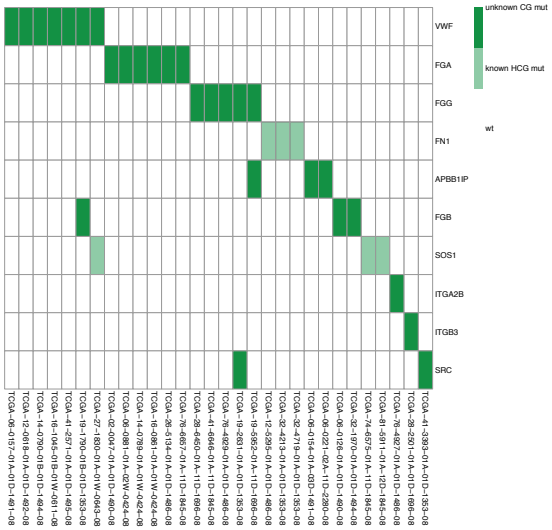


GBM

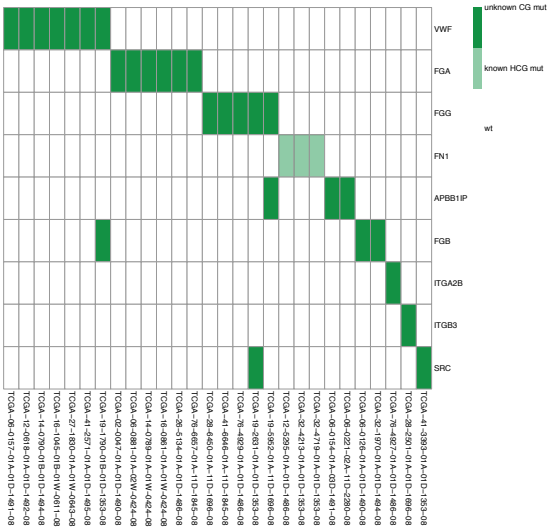
Signaling By PDGF
FDR = 0.0055%, FDR nod = 0.22%



GRB2:SOS Provides Linkage To MAPK Signaling For Integrins
FDR = 3.7%, FDR nod = 3.9%

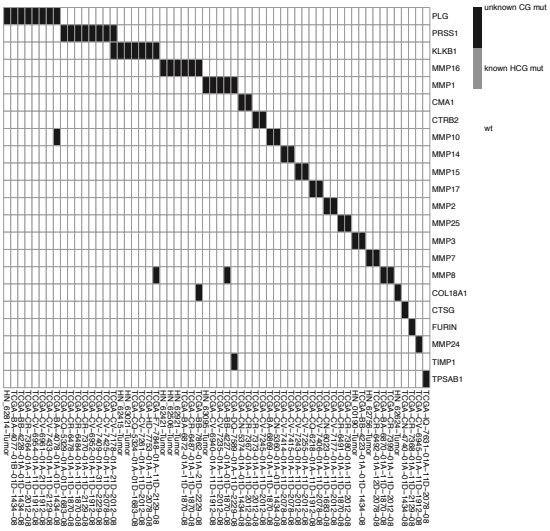


P130Cas Linkage To MAPK Signaling For Integrins
FDR = 1.9%, FDR nod = 3.9%

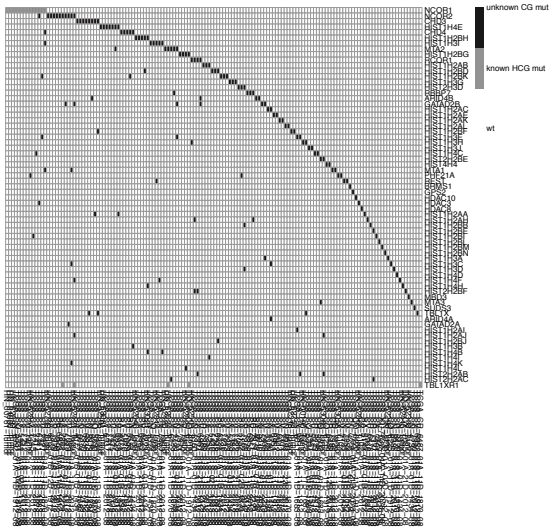


HSNC

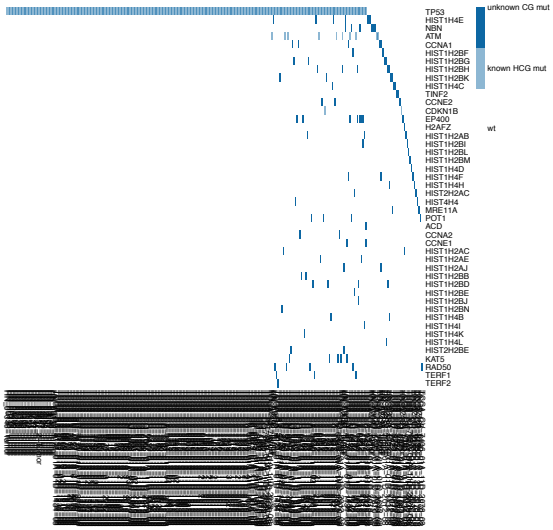
Activation Of Matrix Metalloproteinases
FDR = 0.53%, FDR nod = 3.1%



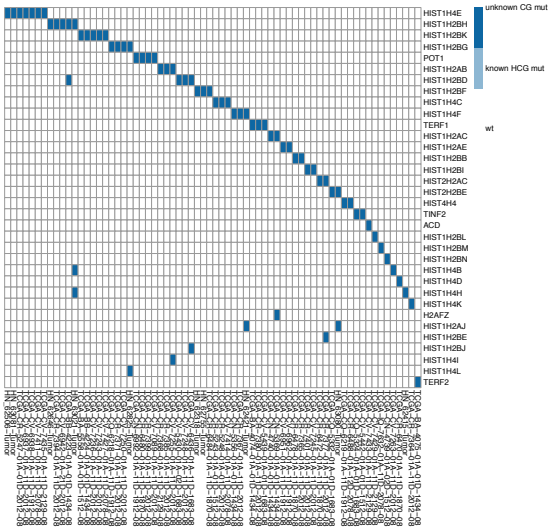
HDACs Deacetylate Histones
FDR = 0.00051%, FDR nod = 0.002%



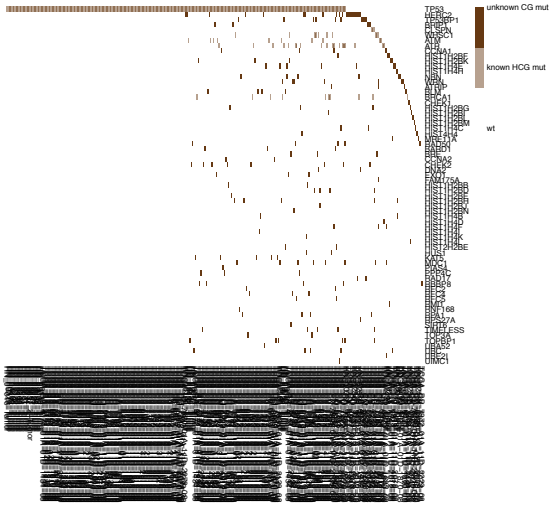
DNA Damage/Telomere Stress Induced Senescence
FDR = 2e−12%, FDR nod = 4e−04%



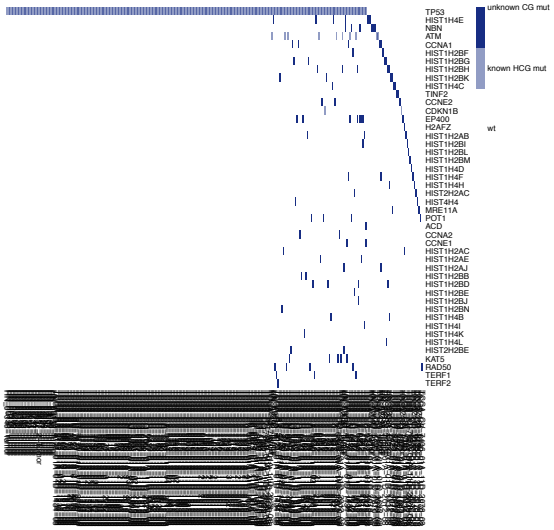
Packaging Of Telomere Ends
FDR = 1.2e−07%, FDR nod = 1.1e−06%

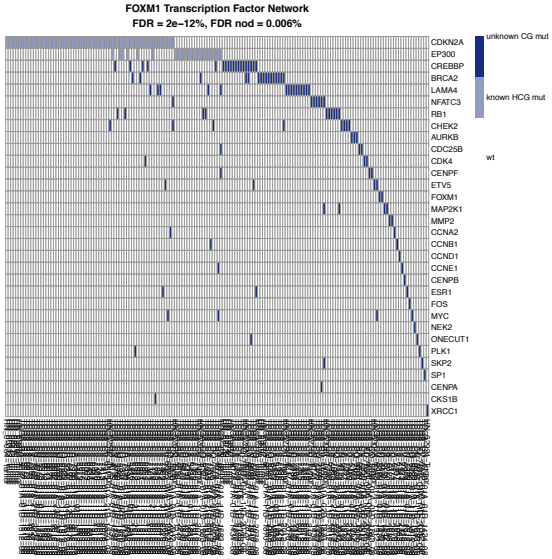


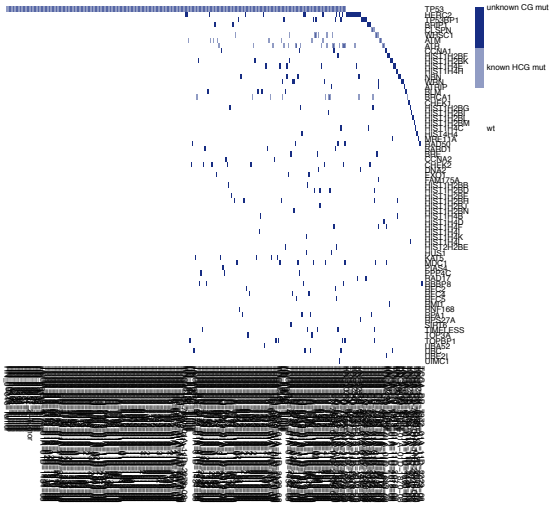
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 1.9e−12%, FDR nod = 0.12%

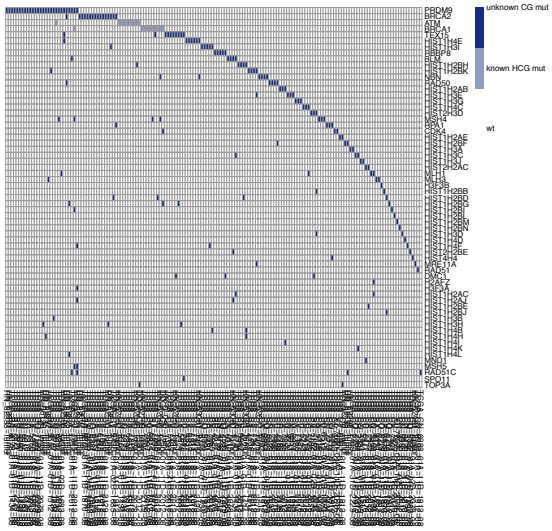


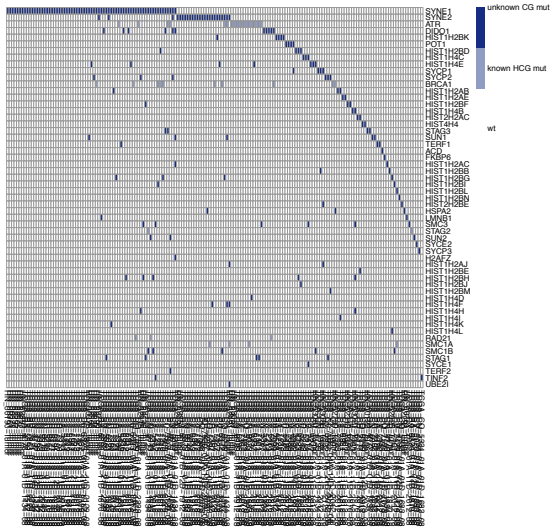
DNA Damage/Telomere Stress Induced Senescence
FDR = 2e−12%, FDR nod = 4e−04%

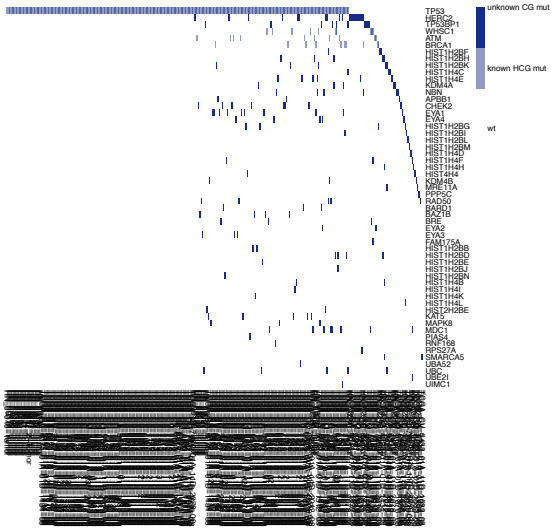


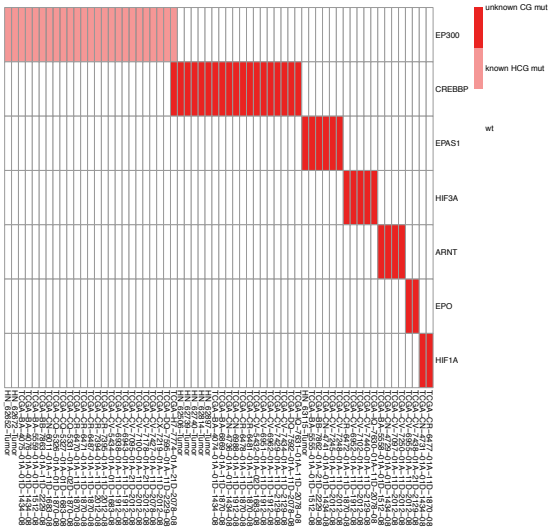

FOXM1 Transcription Factor Network
FDR = 2e−12%, FDR nod = 0.006%
unknown CG mut
known HCG mut
wt
CDKN2A
EP300
CREBBP
BRCA2
LAMA4
NFATC3
RB1
CHEK2
AURKB
CDC25B
CDK4
CENPF
ETV5
FOXM1
MAP2K1
MMP2
CCNA2
CCNB1
CCND1
CCNE1
CENPB
ESR1
FOS
MYC
NEK2
ONECUT1
PLK1
SKP2
SP1
CENPA
CKS1B
XRCC1


G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 1.9e−12%, FDR nod = 0.12%
unknown CG mut
known HCG mut
wt

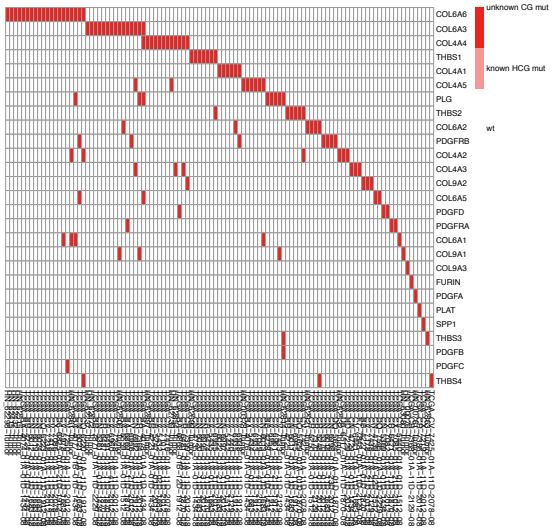

Meiotic Recombination
FDR = 1.7e−11%, FDR nod = 1.4e−10%
unknown CG mut
known HCG mut
wt


Meiotic Synapsis
FDR = 1.7e−07%, FDR nod = 9e−09%
unknown CG mut
known HCG mut
wt

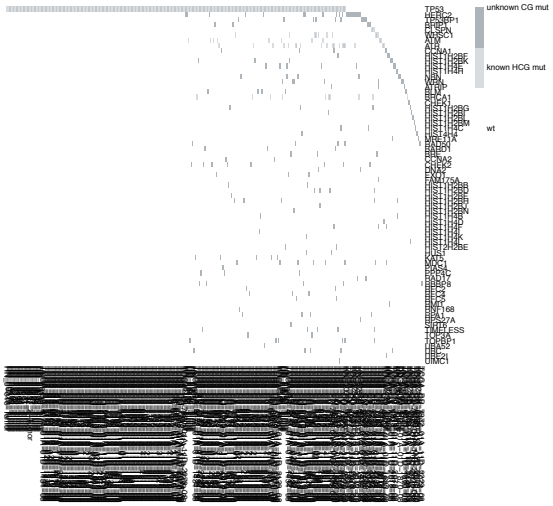

ınd ATM Mediated Phosphorylation Of Repair And Signaling Proteins At DNA Double Strand Breaks
FDR = 1.9e−12%, FDR nod = 0.028%
unknown CG mut
known HCG mut
wt


Regulation Of Gene Expression By Hypoxia Inducible Factor
FDR = 1.8e−06%, FDR nod = 2.3%
unknown CG mut
known HCG mut
wt
EP300
CREBBP
EPAS1
HIF3A
ARNT
EPO
HIF1A

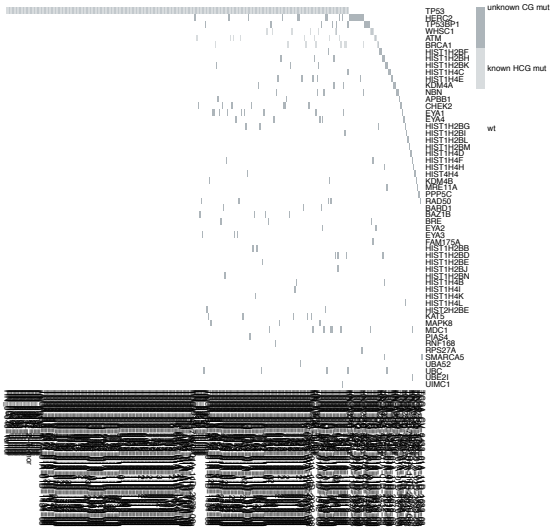
Signaling By PDGF
FDR = 0.65%, FDR nod = 3.1%



G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 1.9e−12%, FDR nod = 0.12%

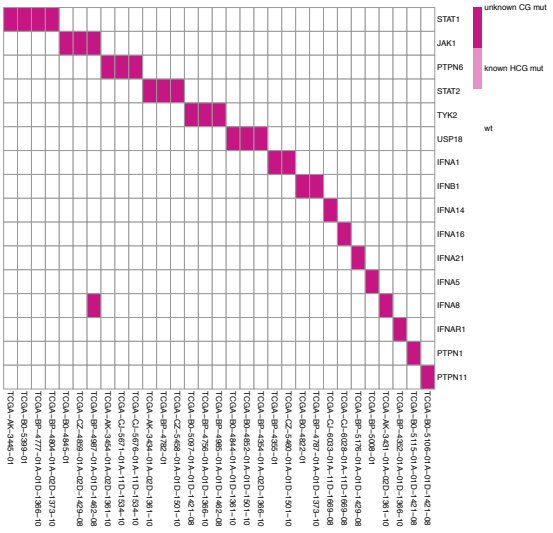


ınd ATM Mediated Phosphorylation Of Repair And Signaling Proteins At DNA Double Strand Breaks
FDR = 1.9e−12%, FDR nod = 0.028%

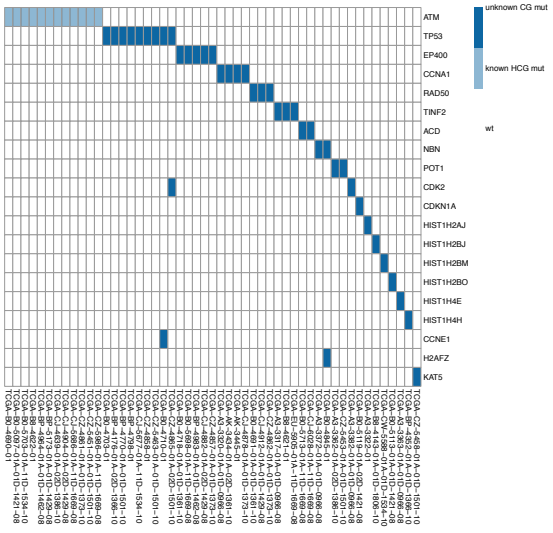


KIRC

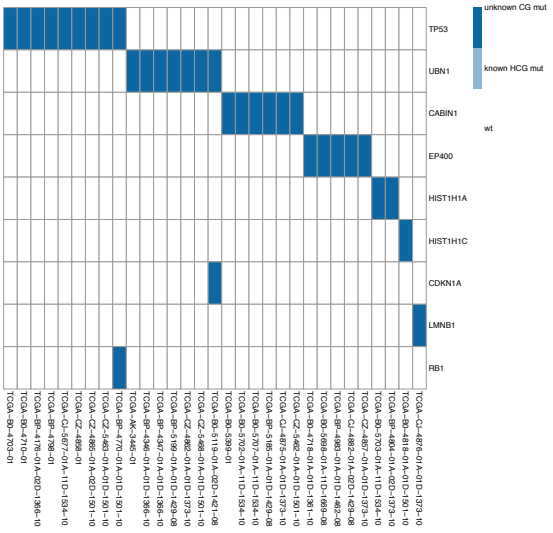
Regulation Of IFNA Signaling
FDR = 1.1%, FDR nod = 2.1%



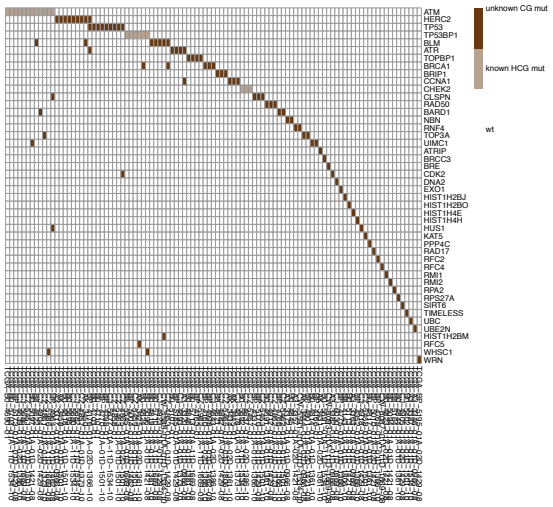
DNA Damage/Telomere Stress Induced Senescence
FDR = 0.14%, FDR nod = 1.9%



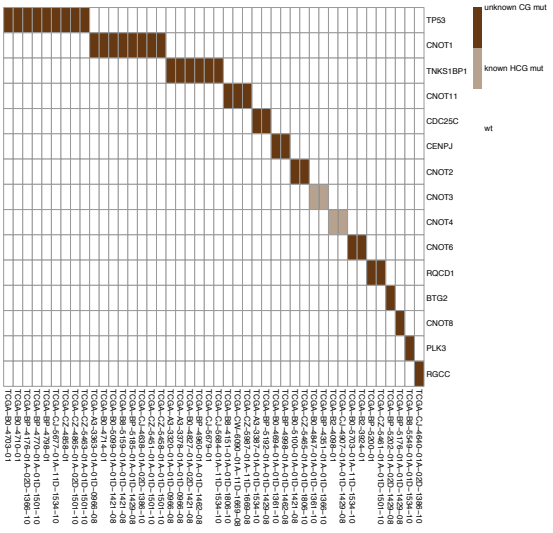
Formation Of Senescence Associated Heterochromatin Foci (SAHF)
FDR = 0.97%, FDR nod = 2.1%



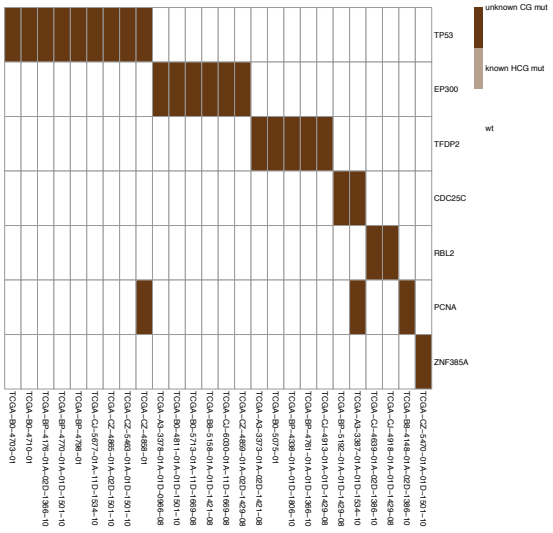
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 0.97%, FDR nod = 2.1%



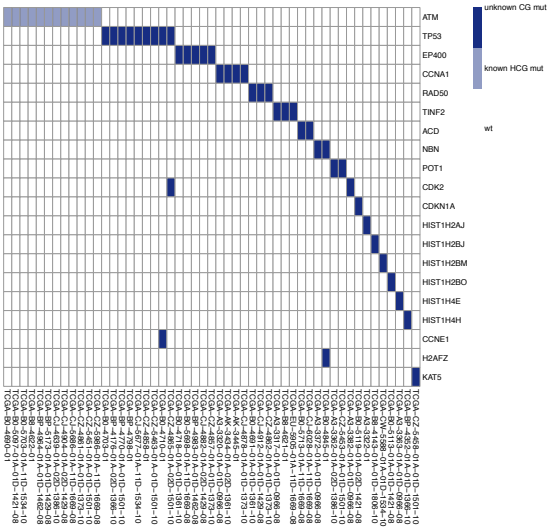
Transcription Of Additional Cell Cycle Genes Whose Exact Role In The P53 Pathway Remain Uncertain
FDR = 0.67%, FDR nod = 0.97%



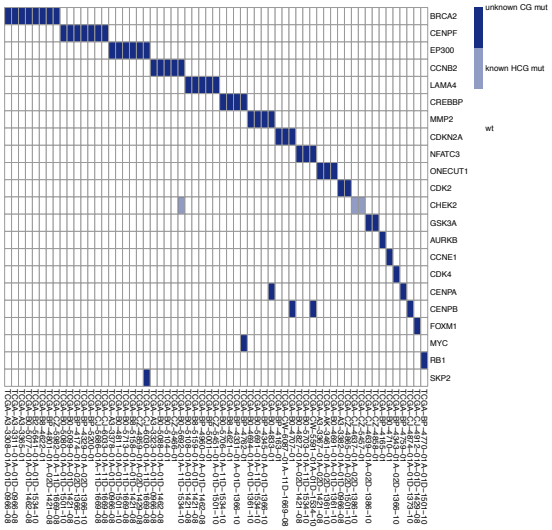
TP53 Regulates Transcription Of Genes Involved In G2 Cell Cycle Arrest
FDR = 1%, FDR nod = 2.1%



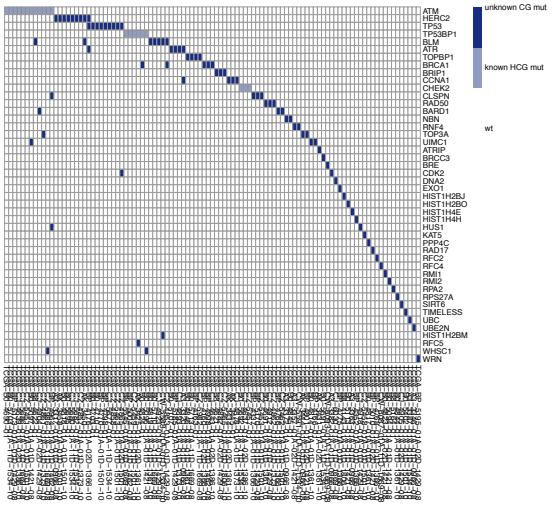
DNA Damage/Telomere Stress Induced Senescence
FDR = 0.14%, FDR nod = 1.9%



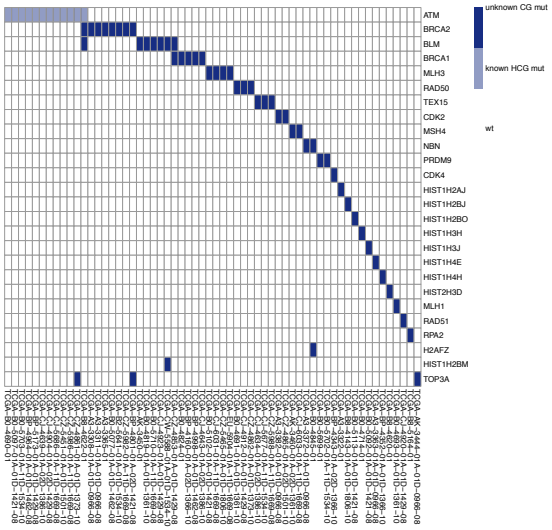
FOXM1 Transcription Factor Network
FDR = 0.29%, FDR nod = 1.2%



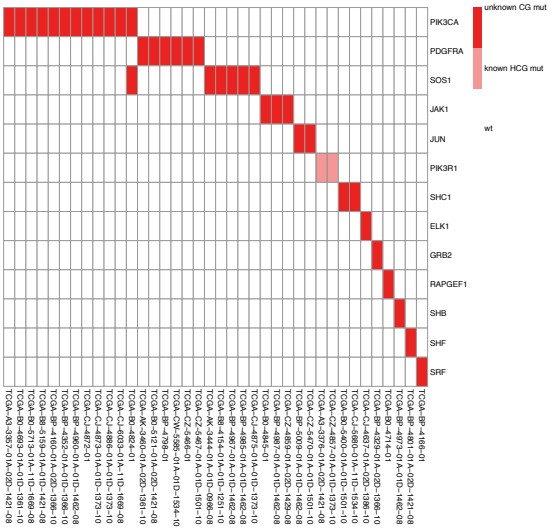
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 0.97%, FDR nod = 2.1%



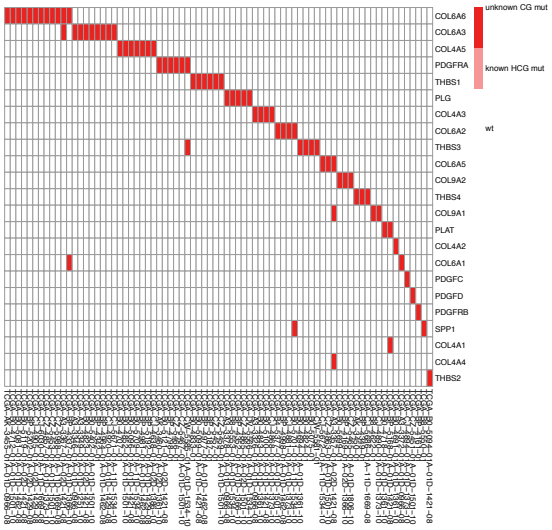
Meiotic Recombination
FDR = 0.22%, FDR nod = 1.8%



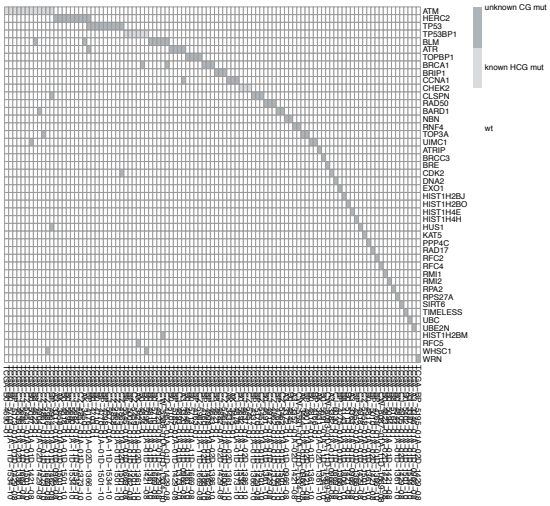
PDGFR Alpha Signaling Pathway
FDR = 3%, FDR nod = 2.1%



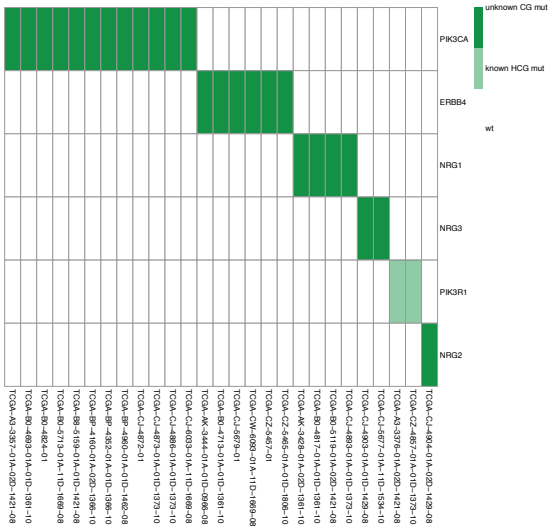
Signaling By PDGF
FDR = 0.21%, FDR nod = 0.97%



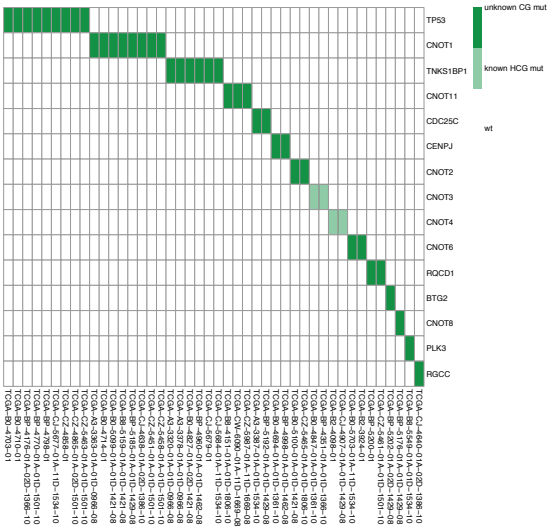
G2/M DNA Damage Checkpoint
Processing Of DNA Double Strand Break Ends
FDR = 0.97%, FDR nod = 2.1%



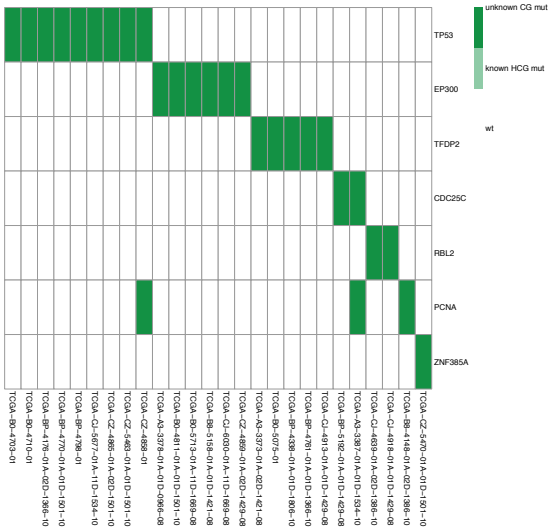
PI3K Events In ERBB4 Signaling
FDR = 4.8%, FDR nod = 3%



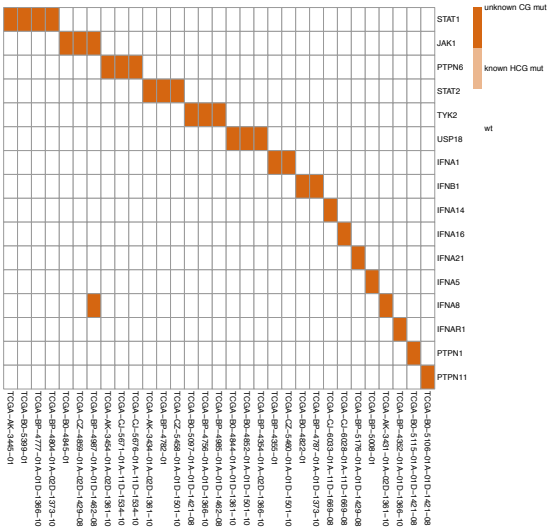
Transcription Of Additional Cell Cycle Genes Whose Exact Role In The P53 Pathway Remain Uncertain
FDR = 0.67%, FDR nod = 0.97%



TP53 Regulates Transcription Of Genes Involved In G2 Cell Cycle Arrest
FDR = 1%, FDR nod = 2.1%

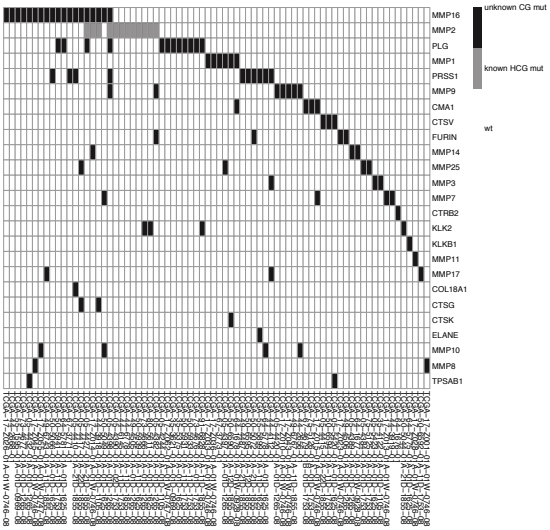


Regulation Of IFNA Signaling
FDR = 1.1%, FDR nod = 2.1%

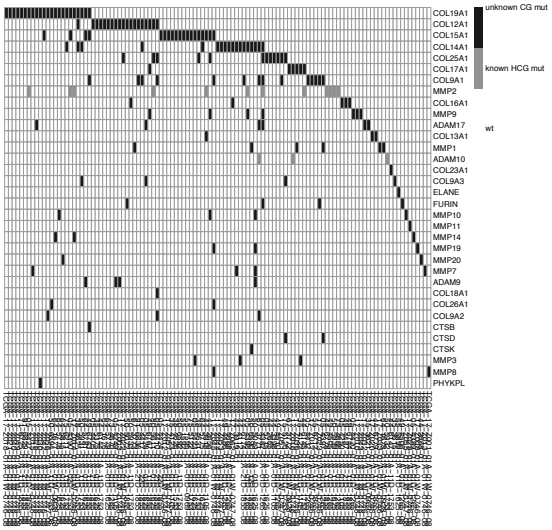


LUAD

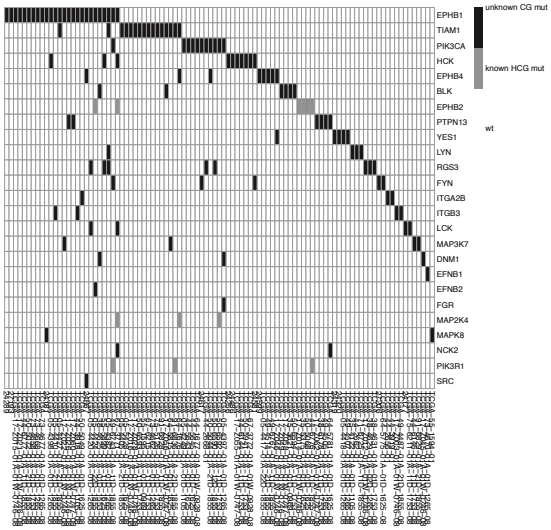
Activation Of Matrix Metalloproteinases
FDR = 0.11%, FDR nod = 0.93%



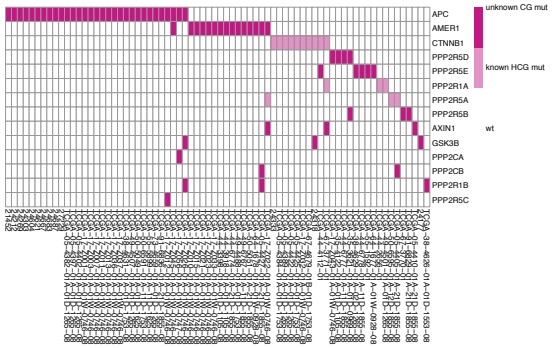
Collagen Degradation
FDR = 0.019%, FDR nod = 0.019%



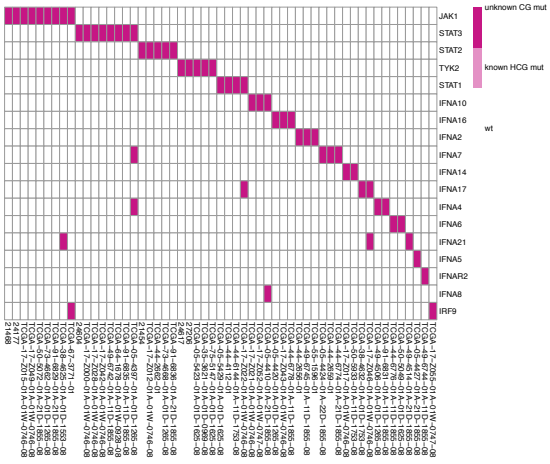
Ephrin B Reverse Signaling
FDR = 2.7%, FDR nod = 0.32%



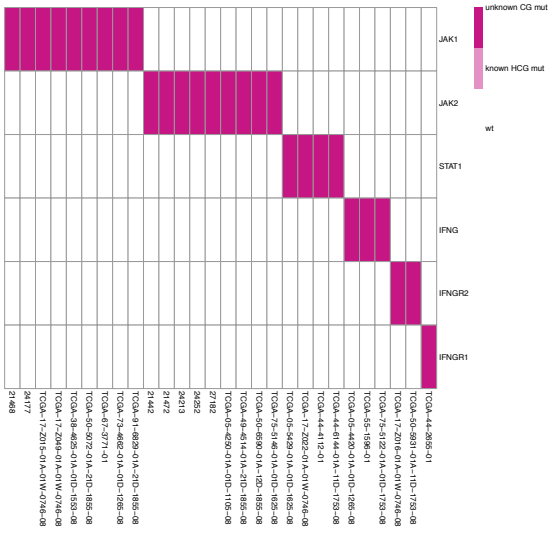
APC Truncation Mutants Have Impaired AXIN Binding
AXIN Missense Mutants Destabilize The Destruction Complex
Beta Catenin Phosphorylation Cascade
Misspliced GSK3beta Mutants Stabilize Beta Catenin
S33 Mutants Of Beta Catenin Aren't Phosphorylated
S37 Mutants Of Beta Catenin Aren't Phosphorylated
S45 Mutants Of Beta Catenin Aren't Phosphorylated
T41 Mutants Of Beta Catenin Aren't Phosphorylated
Truncations Of AMER1 Destabilize The Destruction Complex
FDR = 1.1%, FDR nod = 3.4%



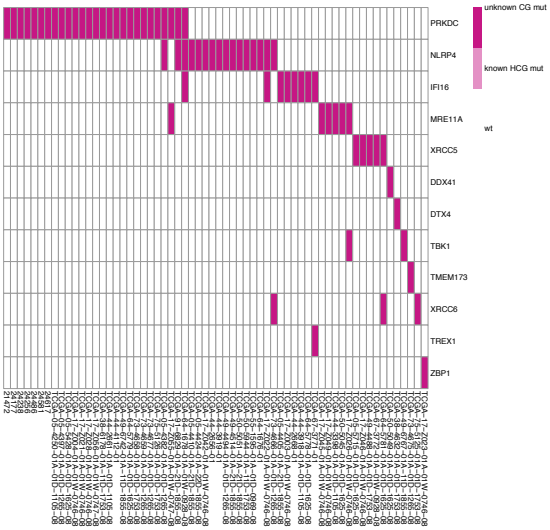
igналing Pathway((JAK1 TYK2 STAT1 STAT2) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
ıgnaling Pathway(JAK1 TYK2 STAT1 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
ıa Signaling Pathway(JAK1 TYK2 STAT1) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
ıa Signaling Pathway(JAK1 TYK2 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
FDR = 0.0085%, FDR nod = 0.037%



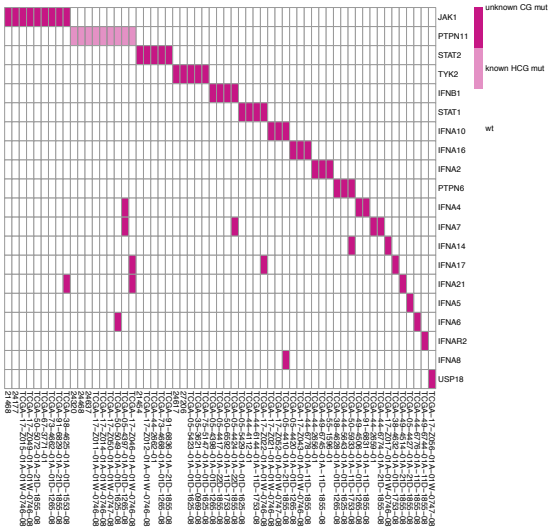
Gamma Signaling Pathway(JAK1 JAK2 STAT1) (IFN Gamma Signaling(JAK1 JAK2 STAT1))
FDR = 0.88%, FDR nod = 1.8%



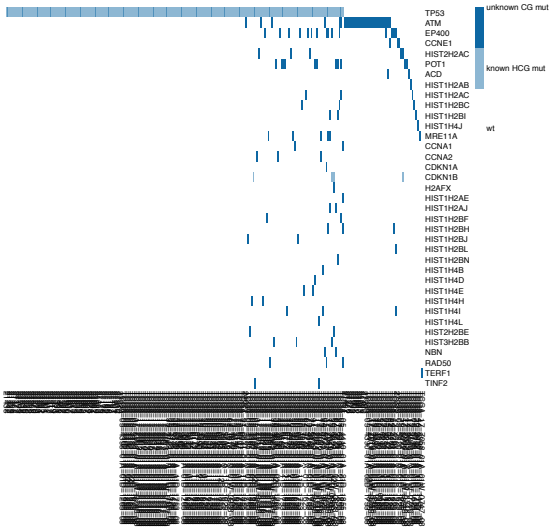
IRF3 Mediated Induction Of Type I IFN
FDR = 0.02%, FDR nod = 0.074%



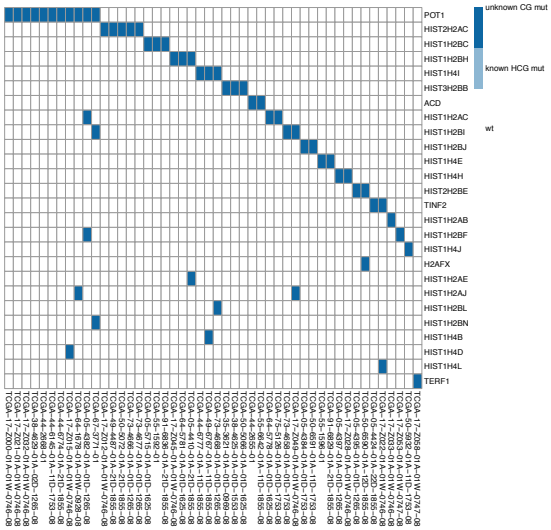
Regulation Of IFNA Signaling
FDR = 0.0013%, FDR nod = 0.019%



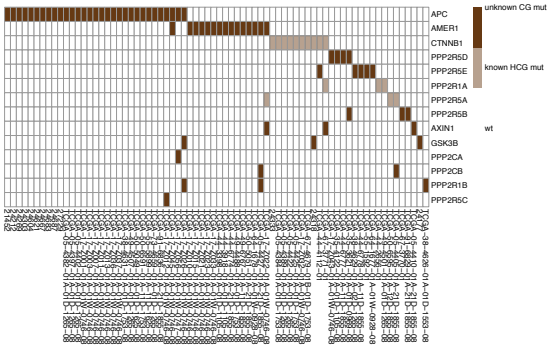
DNA Damage/Telomere Stress Induced Senescence
FDR = 2e−12%, FDR nod = 0.0053%



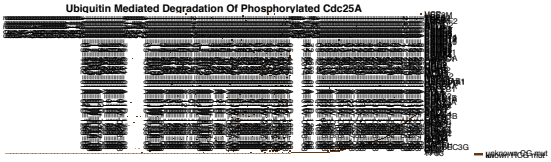
Packaging Of Telomere Ends
FDR = 0.07%, FDR nod = 0.2%

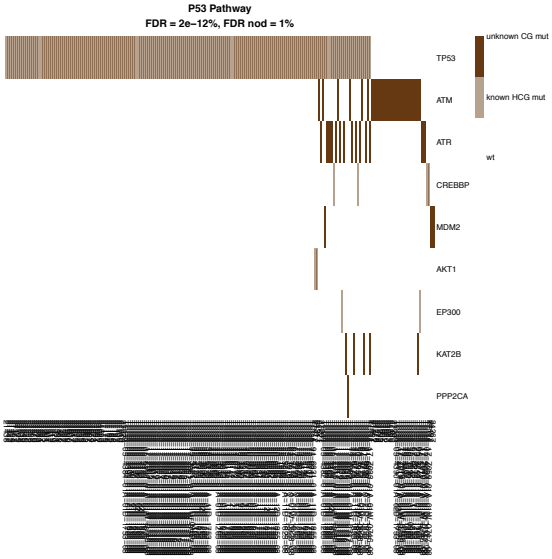


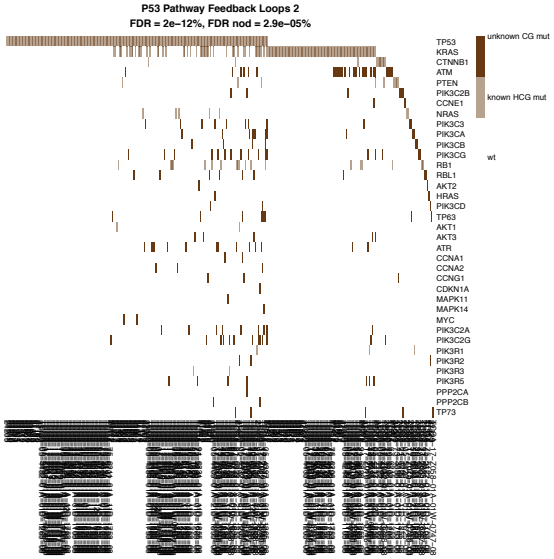
APC Truncation Mutants Have Impaired AXIN Binding
AXIN Missense Mutants Destabilize The Destruction Complex
Beta Catenin Phosphorylation Cascade
Misspliced GSK3beta Mutants Stabilize Beta Catenin
S33 Mutants Of Beta Catenin Aren't Phosphorylated
S37 Mutants Of Beta Catenin Aren't Phosphorylated
S45 Mutants Of Beta Catenin Aren't Phosphorylated
T41 Mutants Of Beta Catenin Aren't Phosphorylated
Truncations Of AMER1 Destabilize The Destruction Complex
FDR = 1.1%, FDR nod = 3.4%

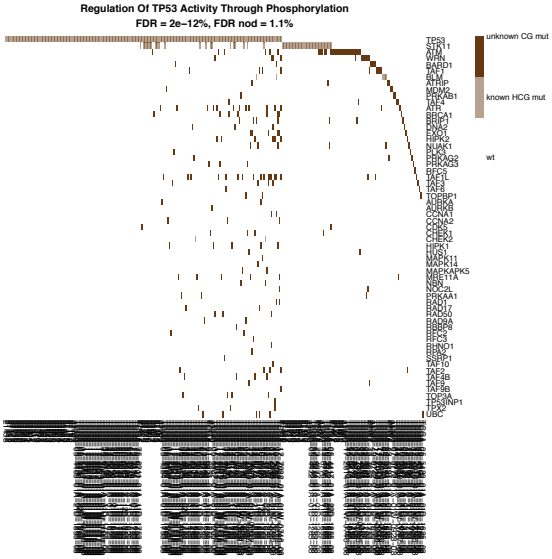


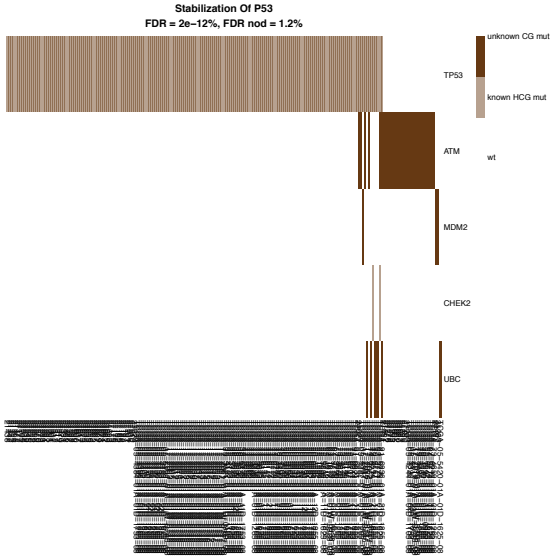
AUF1 (hnRNP D0) Binds And Destabilizes MRNA
Autodegradation Of The E3 Ubiquitin Ligase COP1
CDK Mediated Phosphorylation And Removal Of Cdc6
CDT1 Association With The CDC6:ORC:origin Complex
Cross Presentation Of Soluble Exogenous Antigens (endosomes)
Dectin 1 Mediated Noncanonical NF KB Signaling
Degradation Of AXIN
Degradation Of DVL
Degradation Of GLI1 By The Proteasome
Degradation Of GLI2 By The Proteasome
G2/M Checkpoints
GLI3 Is Processed To GLI3R By The Proteasome
Hedgehog Ligand Biogenesis
Hh Mutants That Don't Undergo Autocatalytic Processing Are Degraded By ERAD
NIK >noncanonical NF KB Signaling
Orc1 Removal From Chromatin
Regulation Of Activated PAK 2p34 By Proteasome Mediated Degradation
Regulation Of Ornithine Decarboxylase (ODC)
SCF Beta TrCP Mediated Degradation Of Emi1
The Role Of GTSE1 In G2/M Progression After G2 Checkpoint
Ubiquitin Dependent Degradation Of Cyclin D1
Ubiquitin Mediated Degradation Of Phosphorylated Cdc25A

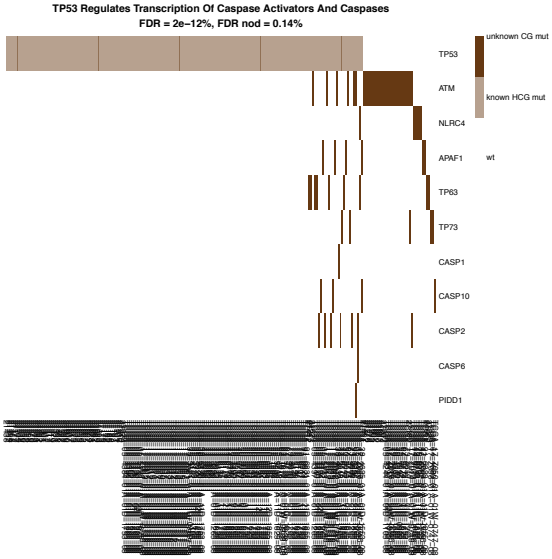


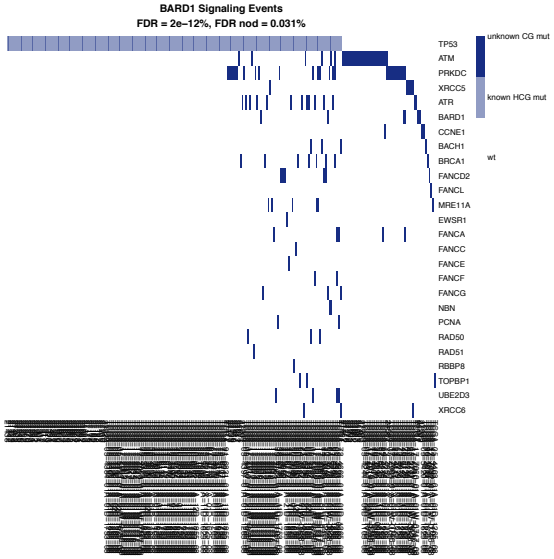

P53 Pathway
FDR = 2e−12%, FDR nod = 1%
TP53
ATM
ATR
CREBBP
MDM2
AKT1
EP300
KAT2B
PPP2CA
unknown CG mut
known HCG mut
wt


P53 Pathway Feedback Loops 2
FDR = 2e−12%, FDR nod = 2.9e−05%
TP53
KRAS
CTNNB1
ATM
PTEN
PIK3C2B
CCNE1
NRAS
PIK3C3
PIK3CA
PIK3CB
PIK3CG
RB1
RBL1
AKT2
HRAS
PIK3CD
TP63
AKT1
AKT3
ATR
CCNA1
CCNA2
CCNG1
CDKN1A
MAPK11
MAPK14
MYC
PIK3C2A
PIK3C2G
PIK3R1
PIK3R2
PIK3R3
PIK3R5
PPP2CA
PPP2CB
TP73
unknown CG mut
known HCG mut
wt

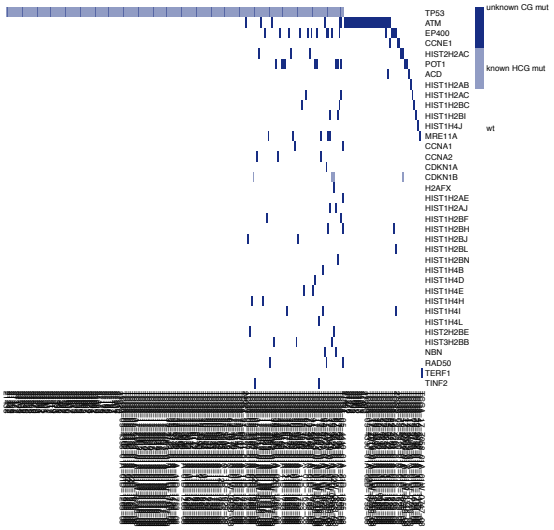

Regulation Of TP53 Activity Through Phosphorylation
FDR = 2e−12%, FDR nod = 1.1%
unknown CG mut
known HCG mut
wt


Stabilization Of P53
FDR = 2e−12%, FDR nod = 1.2%
TP53
ATM
MDM2
CHEK2
UBC
unknown CG mut
known HCG mut
wt

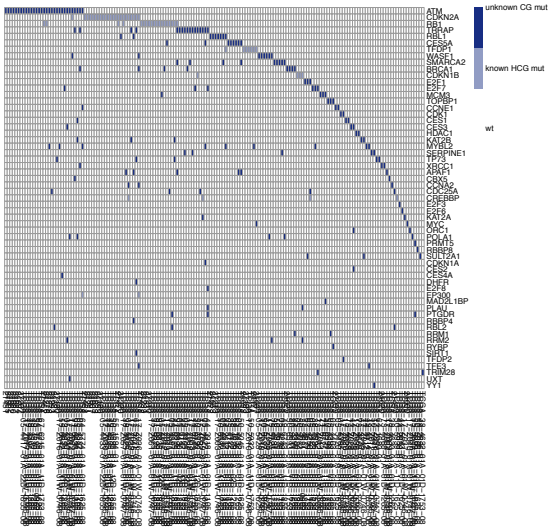

TP53 Regulates Transcription Of Caspase Activators And Caspases
FDR = 2e−12%, FDR nod = 0.14%
TP53
ATM
NLRC4
APAF1
TP63
TP73
CASP1
CASP10
CASP2
CASP6
PIDD1
unknown CG mut
known HCG mut
wt


BARD1 Signaling Events
FDR = 2e−12%, FDR nod = 0.031%
TP53
ATM
PRKDC
XRCC5
ATR
BARD1
CCNE1
BACH1
BRCA1
FANCD2
FANCL
MRE11A
EWSR1
FANCA
FANCC
FANCE
FANCF
FANCG
NBN
PCNA
RAD50
RAD51
RBBP8
TOPBP1
UBE2D3
XRCC6
unknown CG mut
known HCG mut
wt

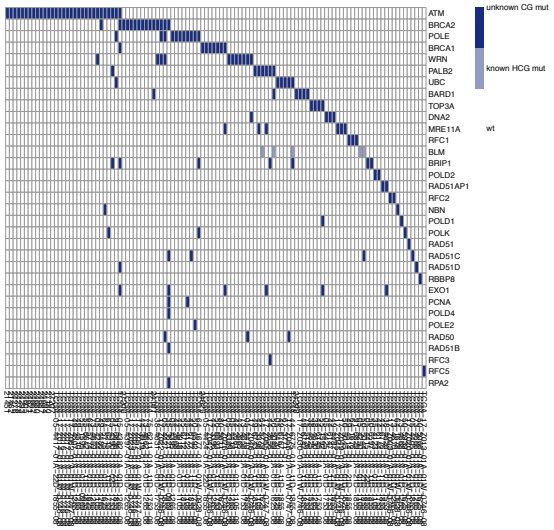
DNA Damage/Telomere Stress Induced Senescence
FDR = 2e−12%, FDR nod = 0.0053%



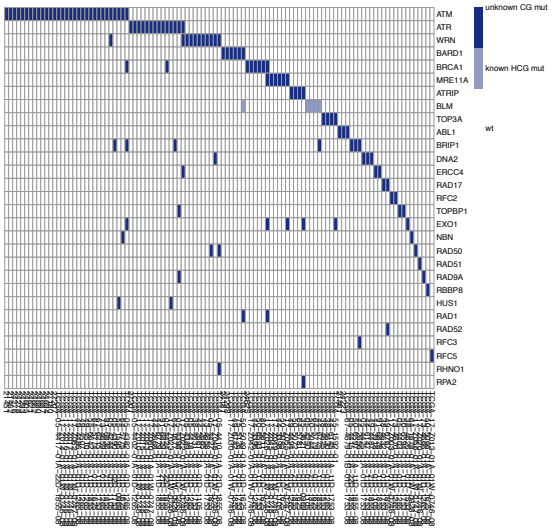
E2F Transcription Factor Network
FDR = 9.5e−07%, FDR nod = 1.1%



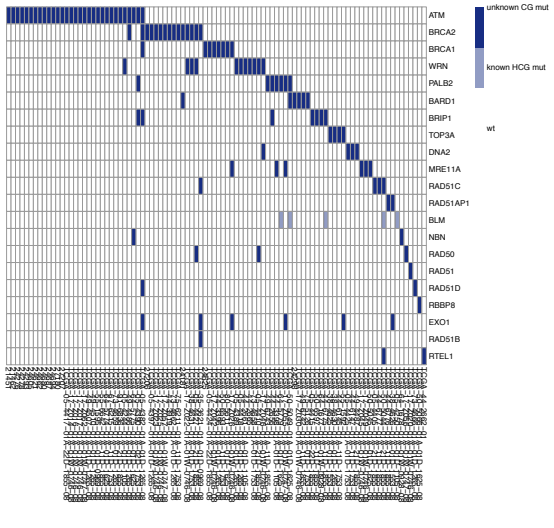
HDR Through Homologous Recombination (HRR)
FDR = 1.2%, FDR nod = 1.3%



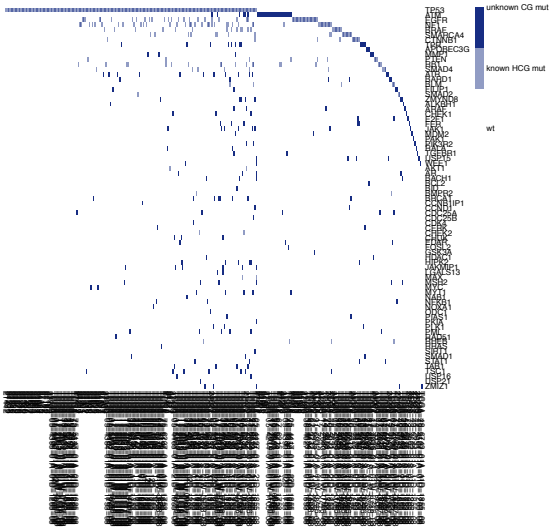
HDR Through Single Strand Annealing (SSA)
FDR = 0.14%, FDR nod = 0.41%

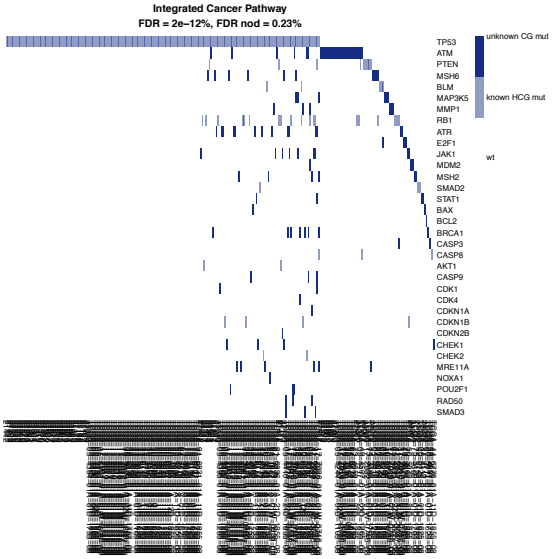


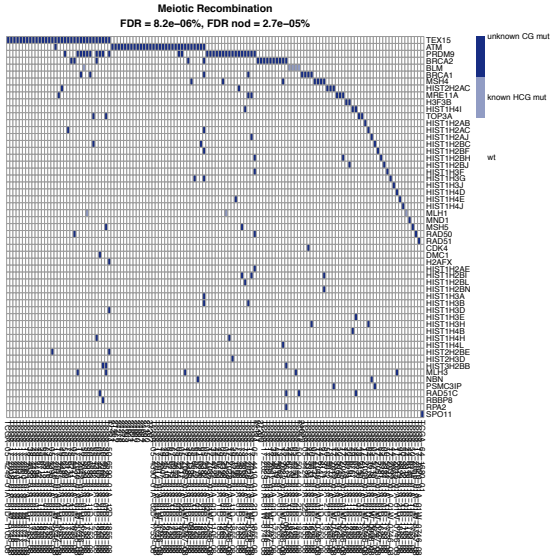
Homologous DNA Pairing And Strand Exchange
esolution Of D Loop Structures Through Synthesis Dependent Strand Annealing (SDSA)
FDR = 1.1%, FDR nod = 1.1%

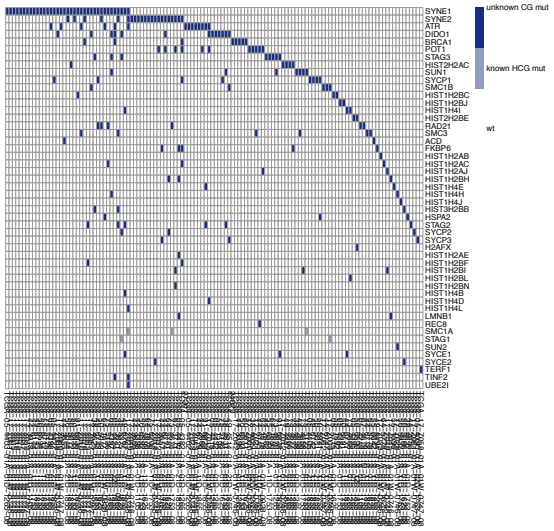


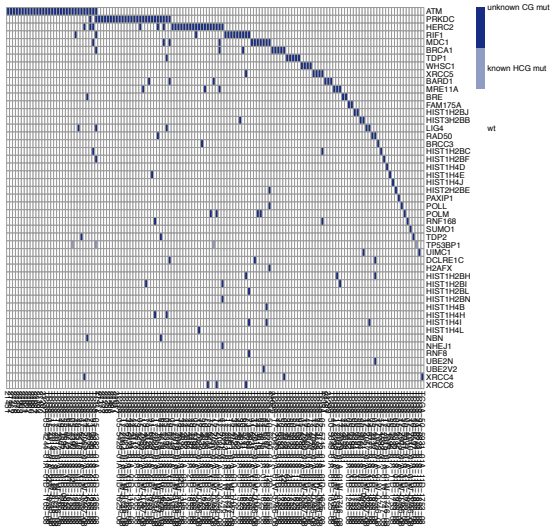
Integrated Breast Cancer Pathway
FDR = 2e−12%, FDR nod = 0.23%

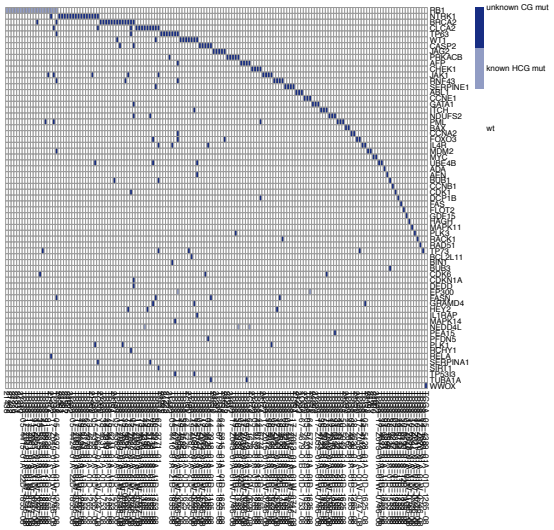


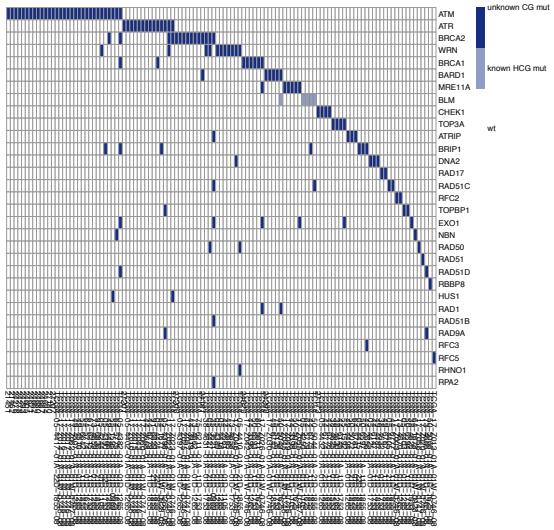

Integrated Cancer Pathway
FDR = 2e−12%, FDR nod = 0.23%
TP53
ATM
PTEN
MSH6
BLM
MAP3K5
MMP1
RB1
ATR
E2F1
JAK1
MDM2
MSH2
SMAD2
STAT1
BAX
BCL2
BRCA1
CASP3
CASP8
AKT1
CASP9
CDK1
CDK4
CDKN1A
CDKN1B
CDKN2B
CHEK1
CHEK2
MRE11A
NOXA1
POU2F1
RAD50
SMAD3
unknown CG mut
known HCG mut
wt

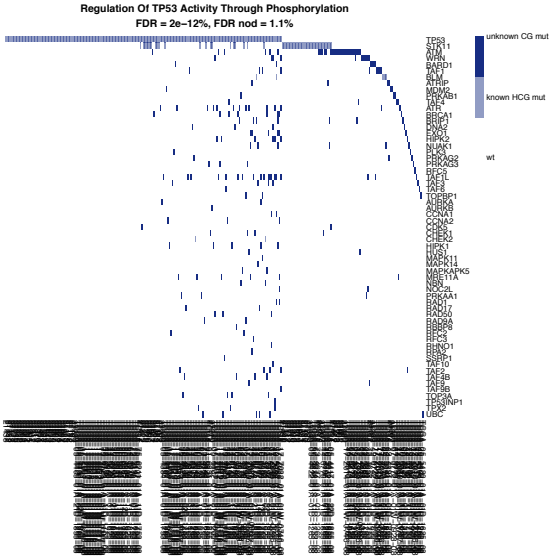

Meiotic Recombination
FDR = 8.2e−06%, FDR nod = 2.7e−05%
TEX15
ATM
PRDM9
BRCA2
BLM
BRCA1
MSH3
HIST2H2AC
MRE11A
H3F3B
HIST1H4I
TOP3A
HIST1H2AB
HIST1H2AC
HIST1H2AJ
HIST1H2BC
HIST1H2BF
HIST1H2BH
HIST1H2BJ
HIST1H3E
HIST1H3G
HIST1H3J
HIST1H4D
HIST1H4E
HIST1H4J
MLH1
MND1
MSH5
RAD50
RAD51
CDK4
DMC1
H2AFX
HIST1H2AE
HIST1H2BF
HIST1H2BL
HIST1H2BN
HIST1H3A
HIST1H3B
HIST1H3D
HIST1H3E
HIST1H3H
HIST1H3I
HIST1H4H
HIST1H4L
HIST2H2BE
HIST2H3D
HIST3H2BB
MLH3
NBN
PSMC3IP
RAD51C
RBBP8
RPA3
SPO11
unknown CG mut
known HCG mut
wt

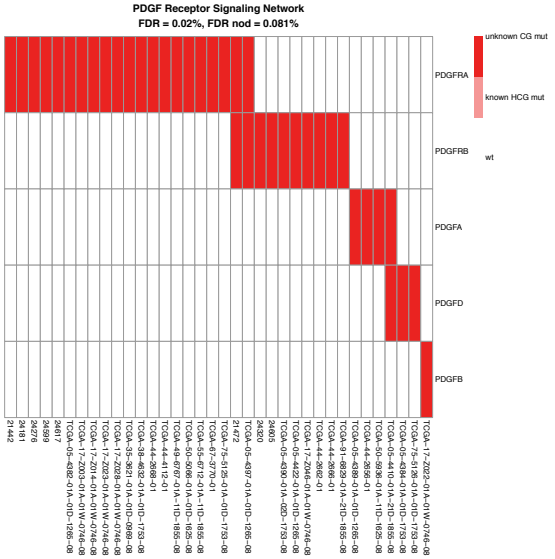

Meiotic Synapsis
FDR = 5.3%, FDR nod = 1.4%
SYNE1
SYNE2
ATR
DIDO1
BRCA1
POT1
STAG3
HIST2H2AC
SUN1
SYCP1
SMC1B
HIST1H2BC
HIST1H2BJ
HIST1H4I
HIST2H2BE
RAD21
SMC3
ACD
FKBP6
HIST1H2AB
HIST1H2AC
HIST1H2AJ
HIST1H2BH
HIST1H4E
HIST1H4H
HIST1H4J
HIST3H2BB
HSPA2
STAG2
SYCP2
SYCP3
H2AFX
HIST1H2AE
HIST1H2BF
HIST1H2BI
HIST1H2BL
HIST1H2BN
HIST1H4B
HIST1H4D
HIST1H4L
LMNB1
REC8
SMC1A
STAG1
SUN2
SYCE1
SYCE2
TERF1
TINF2
UBE2I
unknown CG mut
known HCG mut
wt

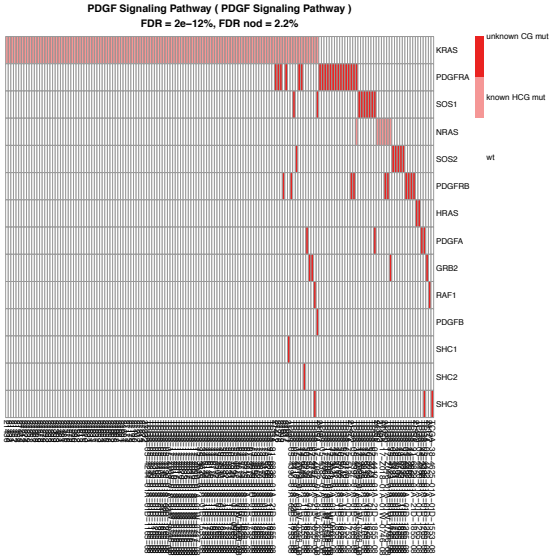

Nonhomologous End Joining (NHEJ)
FDR = 0.35%, FDR nod = 0.23%
ATM
PRKDC
HERC2
RIF1
MDC1
BRCA1
TOP1
WHSC1
XRCC5
BARD1
MRE11A
BRE
FAM175A
HIST1H2BJ
HIST3H2BB
LIG4
RAD50
BRCC3
HIST1H2BC
HIST1H2BF
HIST1H4D
HIST1H4E
HIST1H4J
HIST2H2BE
PAXIP1
POLL
POLM
RNF168
SUMO1
TDP2
TP53BP1
UIMC1
DCLRE1C
H2AFX
HIST1H2BH
HIST1H2BI
HIST1H2BL
HIST1H2BN
HIST1H4B
HIST1H4H
HIST1H4I
HIST1H4L
NBN
NHEJ1
RNF8
UBE2N
UBE2V2
XRCC4
XRCC6
unknown CG mut
known HCG mut
wt

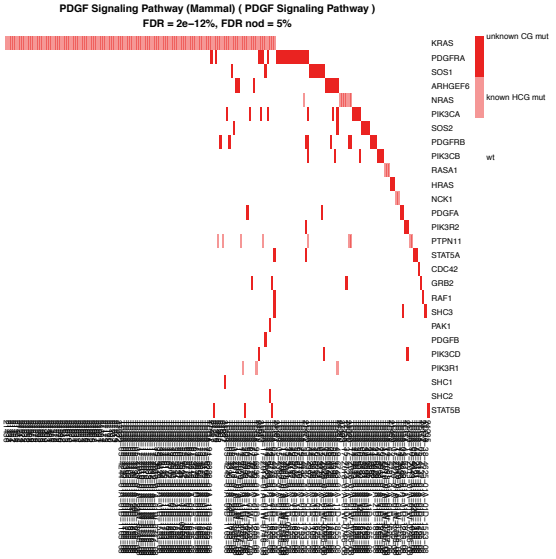

P73 Transcription Factor Network
FDR = 0.11%, FDR nod = 1.2%
unknown CG mut
known HCG mut
wt

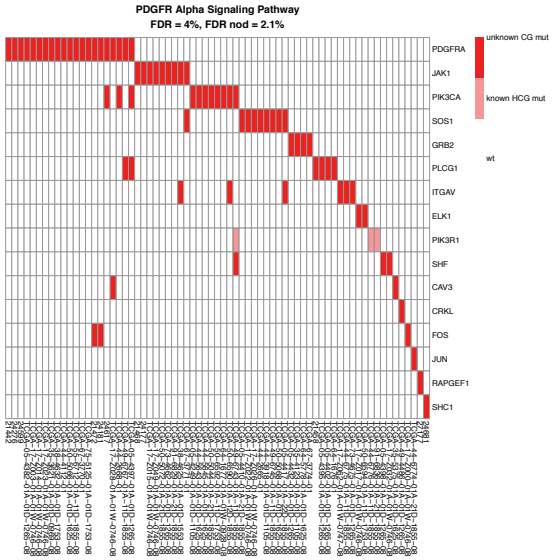

Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange
FDR = 0.13%, FDR nod = 0.23%
ATM
ATR
BRCA2
WRN
BRCA1
BARD1
MRE11A
BLM
CHEK1
TOP3A
ATRIP
BRIP1
DNA2
RAD17
RAD51C
RFC2
TOPBP1
EXO1
NBN
RAD50
RAD51
RAD51D
RBBP8
HUS1
RAD1
RAD51B
RAD9A
RFC3
RFC5
RHNO1
RPA2
unknown CG mut
known HCG mut
wt

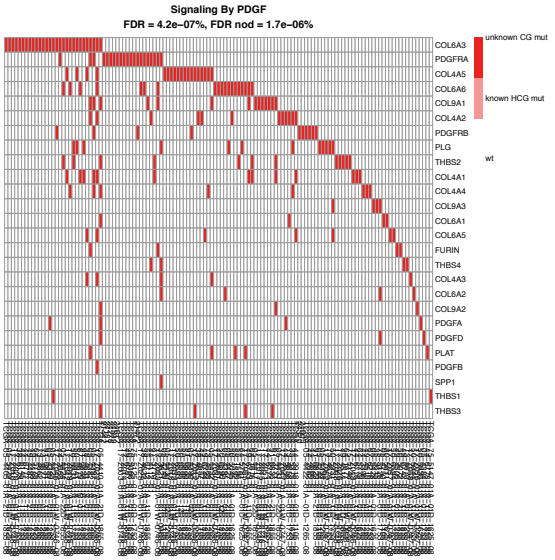

Regulation Of TP53 Activity Through Phosphorylation
FDR = 2e−12%, FDR nod = 1.1%
unknown CG mut
known HCG mut
wt
TP53
STK11
ATRN
BARD1
BLM
ATRIP
MDM2
PRKAB1
IGF4
ATR
BRCA1
BRCA1
DNA2
TOP1
RPK2
NUAK1
PLK4
PRKAG2
PRKAG3
DEF2
TAF1L
TAF6
TOPBP1
AURKA
AURKB
CCNA1
CCNA2
CHEK1
CHEK2
HIPK1
ITCH
MAPK11
MAPK14
MAPKAPK5
NBE11A
NBN
PPM1D
PRKAA1
RAD1
RAD17
RAD50
RAD9A
RBBP8
RFC4
RFC5
RHNO1
SSBP1
TAF10
TAF2
TAF4B
TAF9
TAF9B
TOP3A
TOPBP1
TP53
UBC

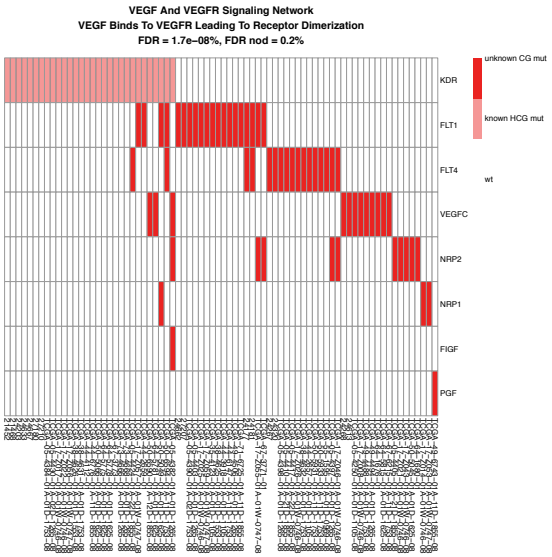

PDGF Receptor Signaling Network
FDR = 0.02%, FDR nod = 0.081%
unknown CG mut
known HCG mut
wt
PDGFRA
PDGFRB
PDGFA
PDGFD
PDGFB

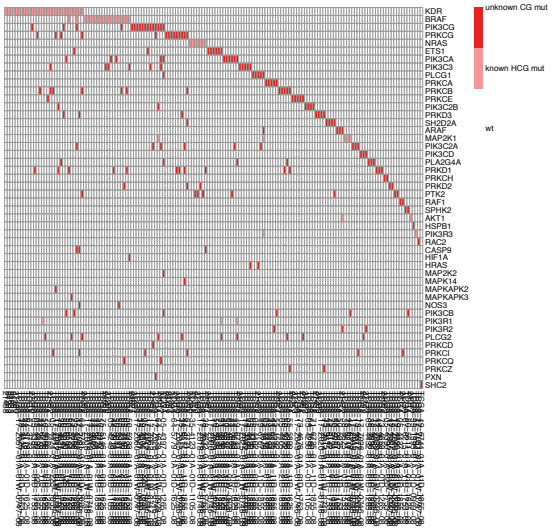

PDGF Signaling Pathway (PDGF Signaling Pathway)
FDR = 2e−12%, FDR nod = 2.2%
unknown CG mut
known HCG mut
wt
KRAS
PDGFRA
SOS1
NRAS
SOS2
PDGFRB
HRAS
PDGFA
GRB2
RAF1
PDGFB
SHC1
SHC2
SHC3

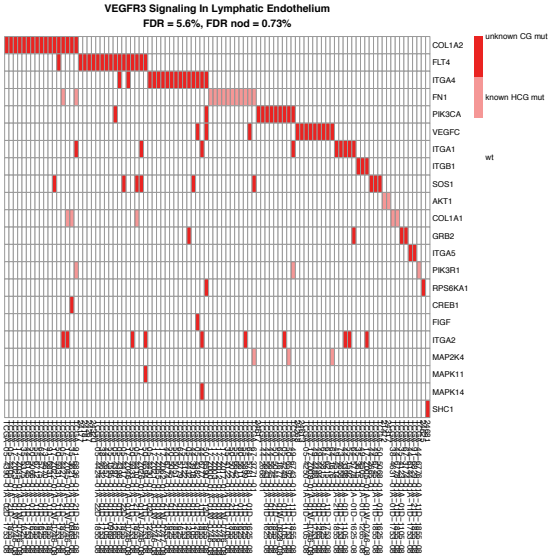

PDGF Signaling Pathway (Mammal) (PDGF Signaling Pathway)
FDR = 2e−12%, FDR nod = 5%
unknown CG mut
known HCG mut
wt
KRAS
PDGFRA
SOS1
ARHGEF6
NRAS
PIK3CA
SOS2
PDGFRB
PIK3CB
RASA1
HRAS
NCK1
PDGFA
PIK3R2
PTPN11
STAT5A
CDC42
GRB2
RAF1
SHC3
PAK1
PDGFB
PIK3CD
PIK3R1
SHC1
SHC2
STAT5B

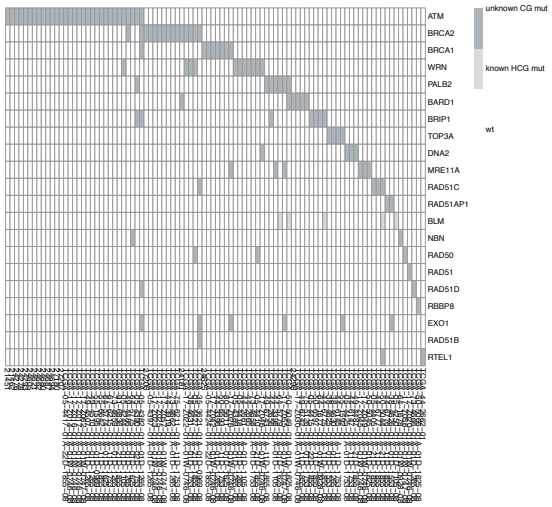

PDGFR Alpha Signaling Pathway
FDR = 4%, FDR nod = 2.1%
unknown CG mut
known HCG mut
wt
PDGFRA
JAK1
PIK3CA
SOS1
GRB2
PLCG1
ITGAV
ELK1
PIK3R1
SHF
CAV3
CRKL
FOS
JUN
RAPGEF1
SHC1

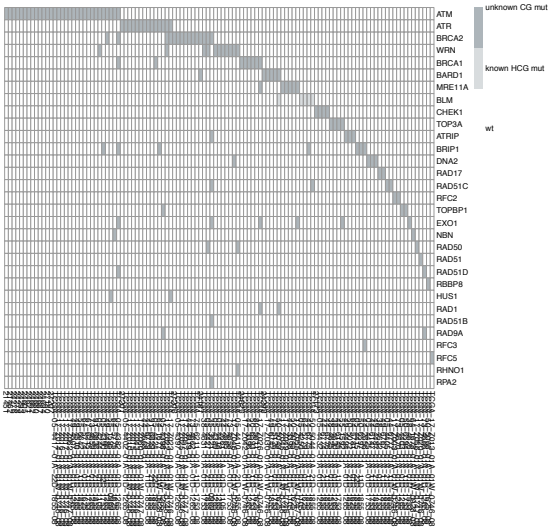

Signaling By PDGF
FDR = 4.2e−07%, FDR nod = 1.7e−06%
unknown CG mut
known HCG mut
wt
COL6A3
PDGFRA
COL4A5
COL6A6
COL9A1
COL4A2
PDGFRB
PLG
THBS2
COL4A1
COL4A4
COL9A3
COL6A1
COL6A5
FURIN
THBS4
COL4A3
COL6A2
COL9A2
PDGFA
PDGFD
PLAT
PDGFB
SPP1
THBS1
THBS3

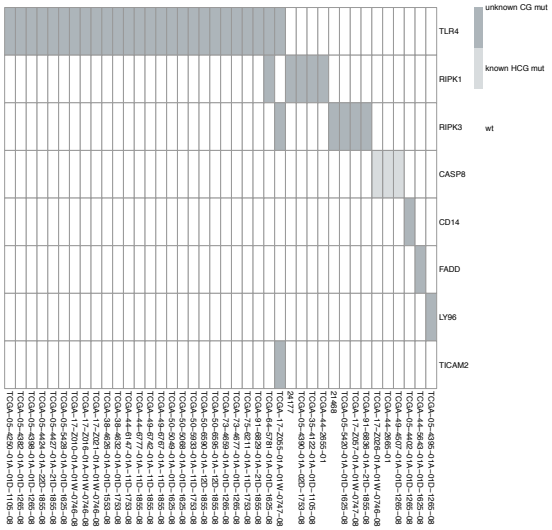

VEGF And VEGFR Signaling Network
VEGF Binds To VEGFR Leading To Receptor Dimerization
FDR = 1.7e−08%, FDR nod = 0.2%
unknown CG mut
known HCG mut
wt
KDR
FLT1
FLT4
VEGFC
NRP2
NRP1
FIGF
PGF


VEGF Signaling Pathway
FDR = 9e−06%, FDR nod = 0.14%
unknown CG mut
known HCG mut
wt
KDR
BRAF
PIK3CG
PRKCG
NRAS
ETS1
PIK3CA
PIK3C3
PLCG1
PRKCA
PRKCB
PRKCE
PIK3C2B
PRKD3
SH2D2A
ARAF
MAP2K1
PIK3C2A
PIK3CD
PLA2G4A
PRKD1
PRKCH
PRKD2
PTK2
RAF1
SPHK2
AKT1
HSPB1
PIK3R3
RAC2
CASP9
HIF1A
HRAS
MAP2K2
MAPK14
MAPKAPK2
MAPKAPK3
NOS3
PIK3CB
PIK3R1
PIK3R2
PLCG2
PRKCD
PRKCI
PRKCQ
PRKCZ
PXN
SHC2

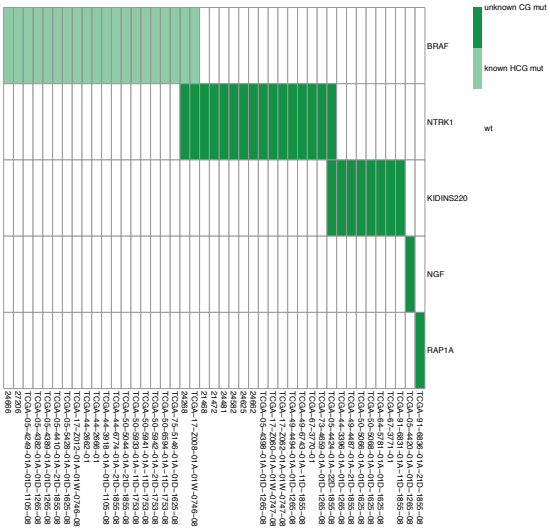

VEGFR3 Signaling In Lymphatic Endothelium
FDR = 5.6%, FDR nod = 0.73%
unknown CG mut
known HCG mut
wt
COL1A2
FLT4
ITGA4
FN1
PIK3CA
VEGFC
ITGA1
ITGB1
SOS1
AKT1
COL1A1
GRB2
ITGA5
PIK3R1
RPS6KA1
CREB1
FIGF
ITGA2
MAP2K4
MAPK11
MAPK14
SHC1


Homologous DNA Pairing And Strand Exchange
esolution Of D Loop Structures Through Synthesis Dependent Strand Annealing (SDSA)
FDR = 1.1%, FDR nod = 1.1%
unknown CG mut
known HCG mut
wt
ATM
BRCA2
BRCA1
WRN
PALB2
BARD1
BRIP1
TOP3A
DNA2
MRE11A
RAD51C
RAD51AP1
BLM
NBN
RAD50
RAD51
RAD51D
RBBP8
EXO1
RAD51B
RTEL1

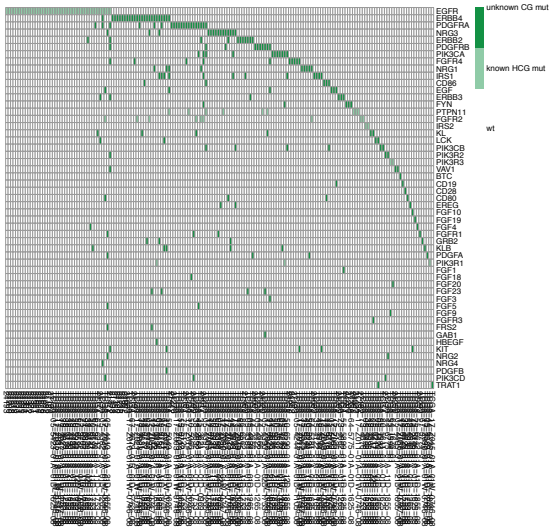

Presynaptic Phase Of Homologous DNA Pairing And Strand Exchange
FDR = 0.13%, FDR nod = 0.23%
unknown CG mut
known HCG mut
wt
ATM
ATR
BRCA2
WRN
BRCA1
BARD1
MRE11A
BLM
CHEK1
TOP3A
ATRIP
BRIP1
DNA2
RAD17
RAD51C
RFC2
TOPBP1
EXO1
NBN
RAD50
RAD51
RAD51D
RBBP8
HUS1
RAD1
RAD51B
RAD9A
RFC3
RFC5
RHNO1
RPA2


TRIF Mediated Programmed Cell Death
FDR = 0.00019%, FDR nod = 2.7e−05%
unknown CG mut
known HCG mut
wt
TLR4
RIPK1
RIPK3
CASP8
CD14
FADD
LY96
TICAM2

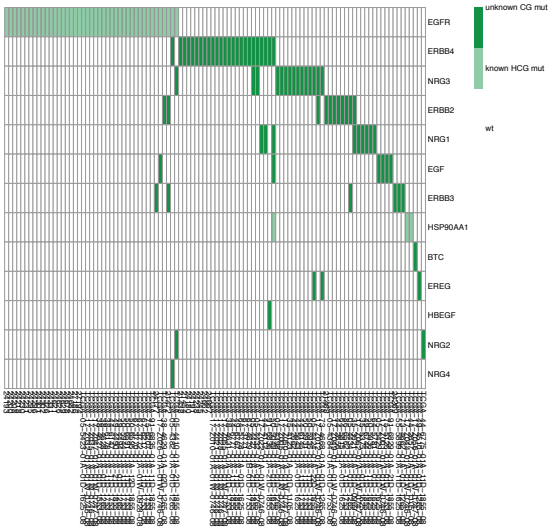
ARMS Mediated Activation
FDR = 0.00051%, FDR nod = 2.1%



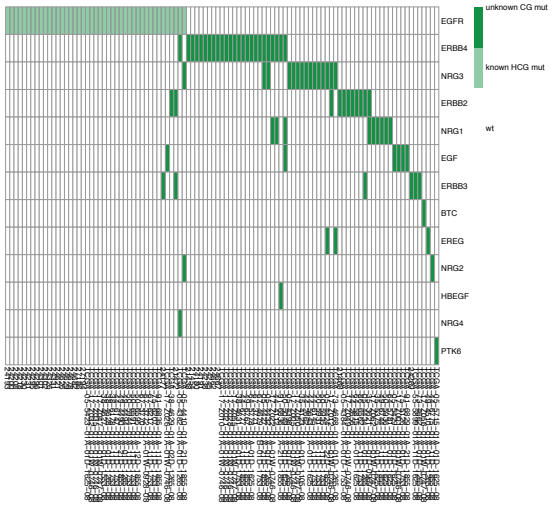
Constitutive Signaling By Aberrant PI3K In Cancer
FDR = 2e−12%, FDR nod = 0.08%



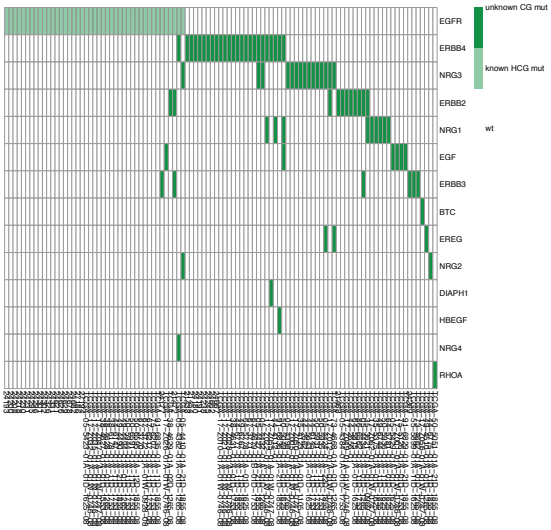
ErbB Receptor Signaling Network
FDR = 2.3e−12%, FDR nod = 0.16%



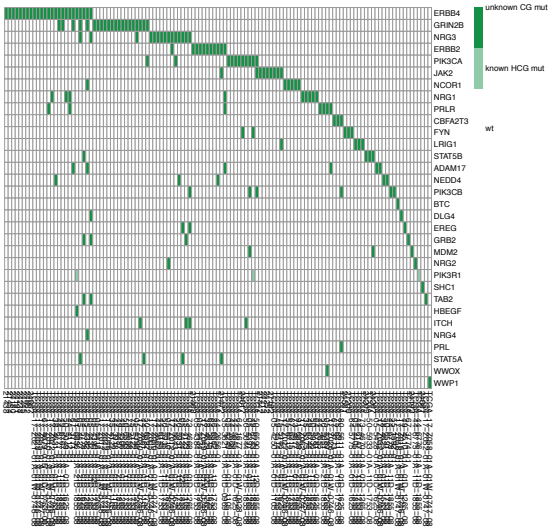
ERBB2 Activates PTK6 Signaling
Signaling By ERBB4
FDR = 2.2e−12%, FDR nod = 0.2%



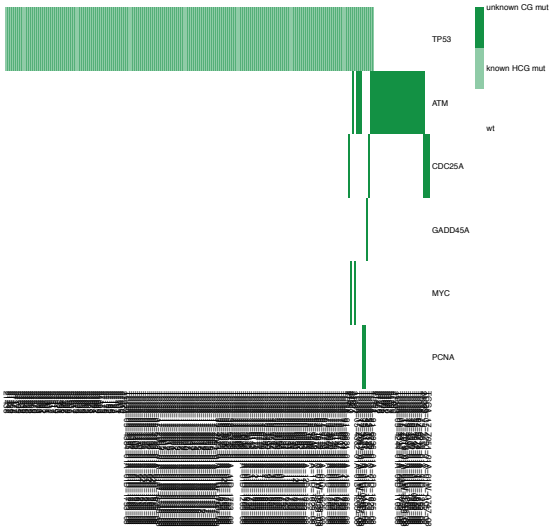
ERBB2 Regulates Cell Motility
FDR = 9.4e−12%, FDR nod = 1%



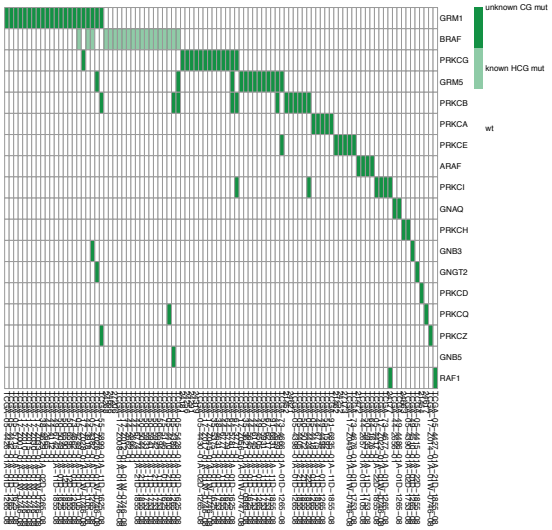
ErbB4 Signaling Events
FDR = 3%, FDR nod = 2.1%



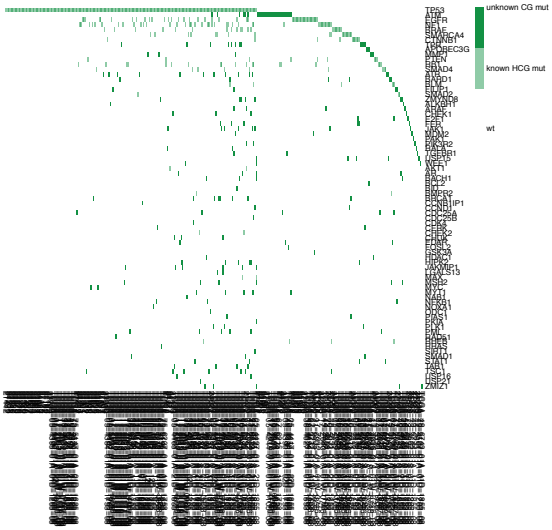
G1 To S Cell Cycle Control
FDR = 2e−12%, FDR nod = 0.046%



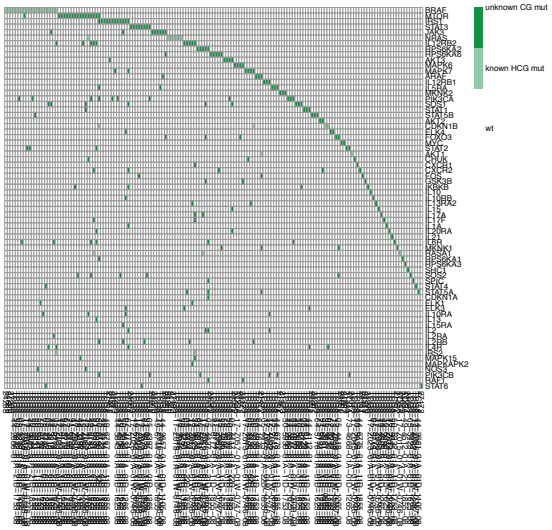
thway (through Glutamate, G Alpha Q And PLC Beta) (GPCR Groupl Metabotropic Glutamate Receptor Signaling I
FDR = 0.00071%, FDR nod = 0.46%



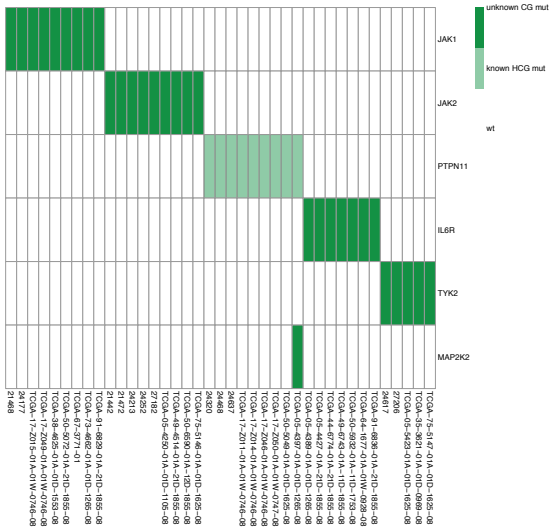
Integrated Breast Cancer Pathway
FDR = 2e−12%, FDR nod = 0.23%



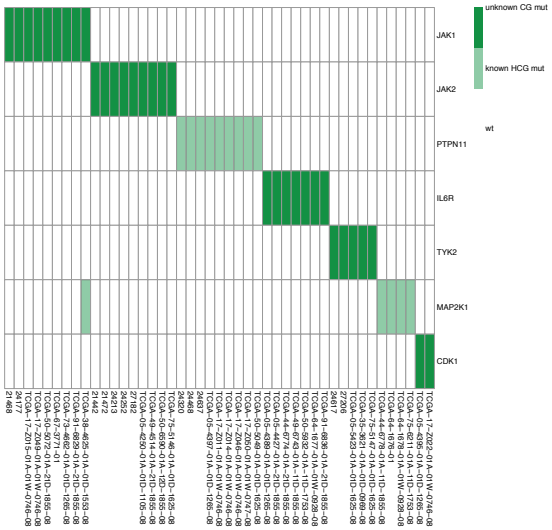
Interleukin Signaling Pathway
FDR = 0.24%, FDR nod = 4.8%

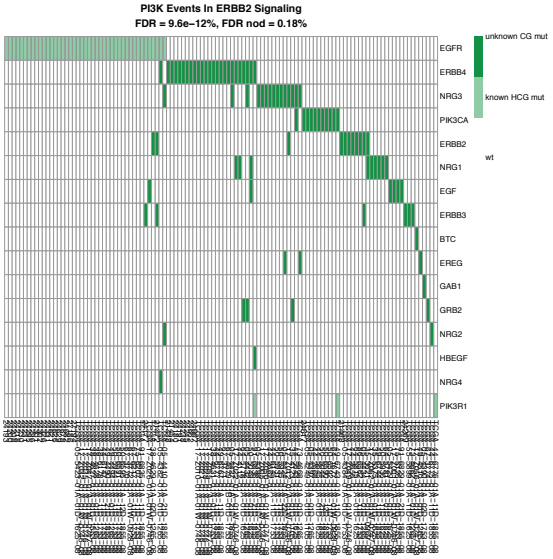


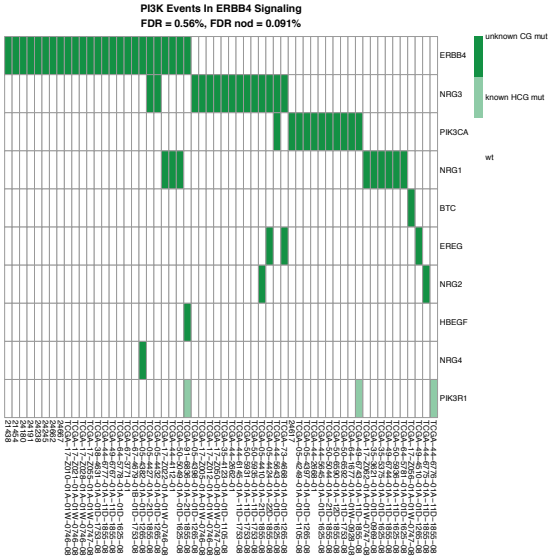
MAPK1 (ERK2) Activation
FDR = 0.23%, FDR nod = 2.8%

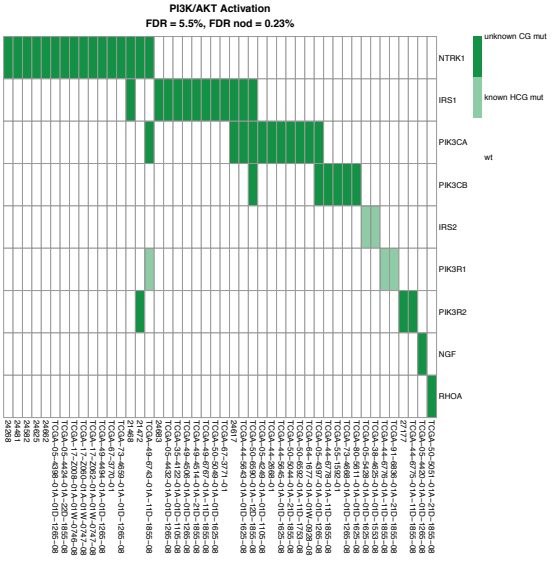


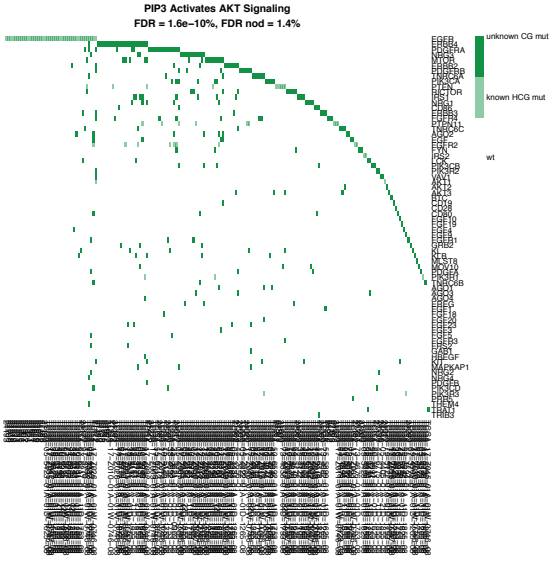
MAPK3 (ERK1) Activation
FDR = 0.012%, FDR nod = 1%

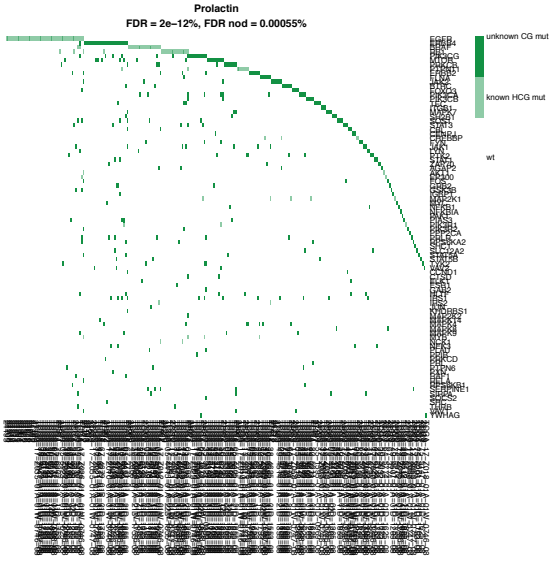


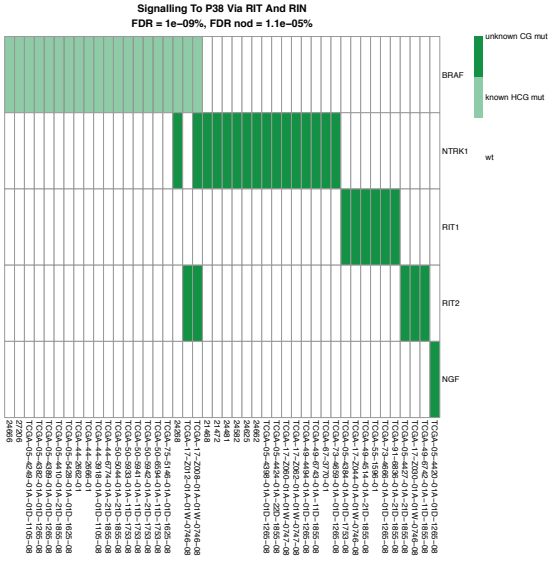

PI3K Events In ERBB2 Signaling
FDR = 9.6e−12%, FDR nod = 0.18%
EGFR
ERBB4
NRG3
PIK3CA
ERBB2
NRG1
EGF
ERBB3
BTC
EREG
GAB1
GRB2
NRG2
HBEGF
NRG4
PIK3R1
unknown CG mut
known HCG mut
wt

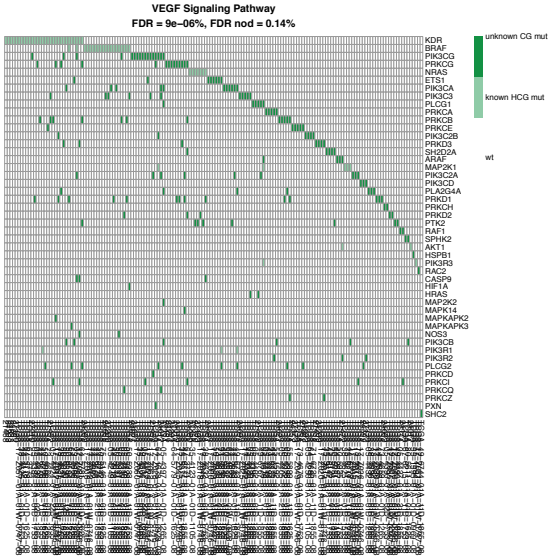

PI3K Events In ERBB4 Signaling
FDR = 0.56%, FDR nod = 0.091%
ERBB4
NRG3
PIK3CA
NRG1
BTC
EREG
NRG2
HBEGF
NRG4
PIK3R1
unknown CG mut
known HCG mut
wt

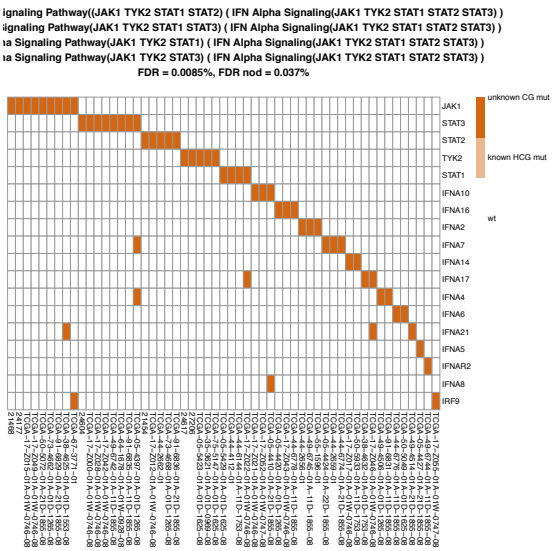

PI3K/AKT Activation
FDR = 5.5%, FDR nod = 0.23%
NTRK1
IRS1
PIK3CA
PIK3CB
IRS2
PIK3R1
PIK3R2
NGF
RHOA
unknown CG mut
known HCG mut
wt

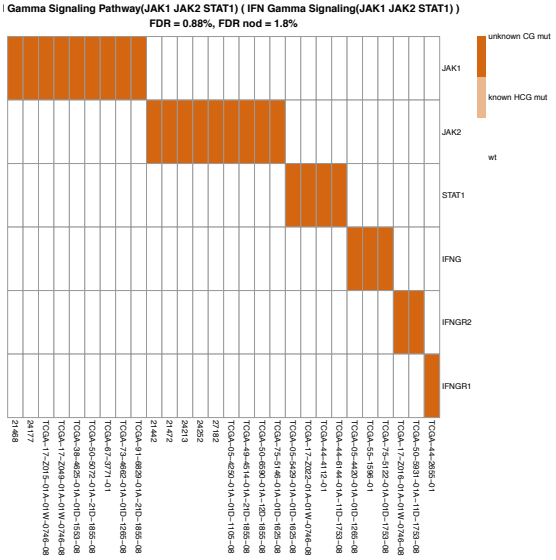

PIP3 Activates AKT Signaling
FDR = 1.6e−10%, FDR nod = 1.4%
unknown CG mut
known HCG mut
wt

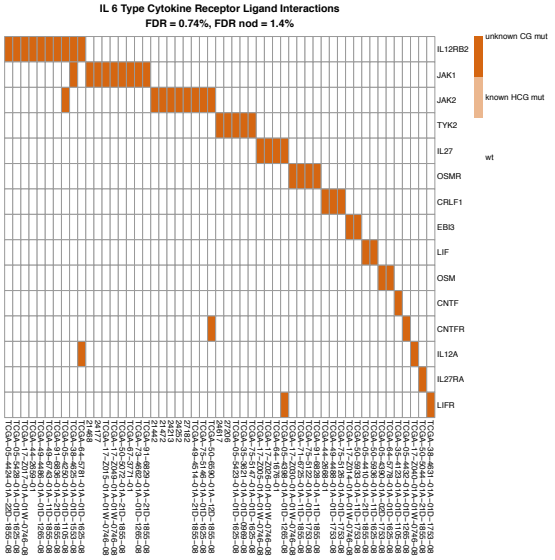

Prolactin
FDR = 2e−12%, FDR nod = 0.00055%
unknown CG mut
known HCG mut
wt

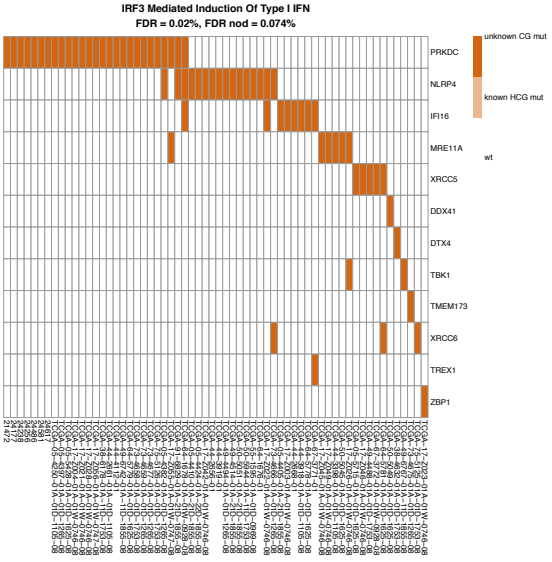

Signalling To P38 Via RIT And RIN
FDR = 1e−09%, FDR nod = 1.1e−05%
BRAF
NTRK1
RIT1
RIT2
NGF
unknown CG mut
known HCG mut
wt

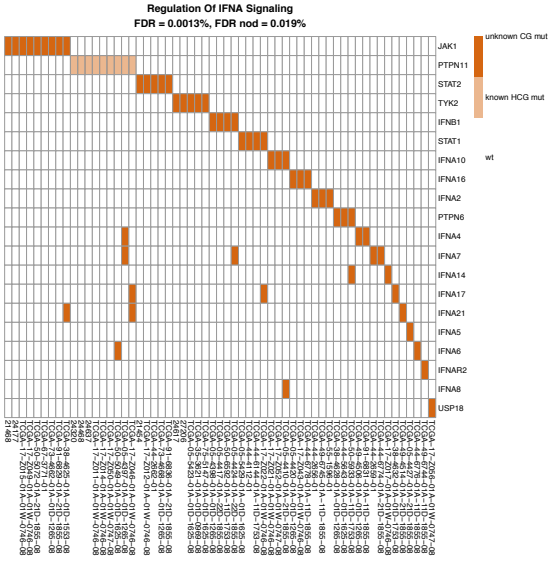

VEGF Signaling Pathway
FDR = 9e−06%, FDR nod = 0.14%
unknown CG mut
known HCG mut
wt
KDR
BRAF
PIK3CG
PRKCG
NRAS
ETS1
PIK3CA
PIK3C3
PLCG1
PRKCA
PRKCB
PRKCE
PIK3C2B
PRKD3
SH2D2A
ARAF
MAP2K1
PIK3C2A
PIK3CD
PLA2G4A
PRKD1
PRKCH
PRKD2
PTK2
RAF1
SPHK2
AKT1
HSPB1
PIK3R3
RAC2
CASP9
HIF1A
HRAS
MAP2K2
MAPK14
MAPKAPK2
MAPKAPK3
NOS3
PIK3CB
PIK3R1
PIK3R2
PLCG2
PRKCD
PRKCI
PRKCQ
PRKCZ
PXN
SHC2


ignaling Pathway((JAK1 TYK2 STAT1 STAT2) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
ignaling Pathway(JAK1 TYK2 STAT1 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
a Signaling Pathway(JAK1 TYK2 STAT1) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
a Signaling Pathway(JAK1 TYK2 STAT3) (IFN Alpha Signaling(JAK1 TYK2 STAT1 STAT2 STAT3))
FDR = 0.0085%, FDR nod = 0.037%
unknown CG mut
known HCG mut
wt
JAK1
STAT3
STAT2
TYK2
STAT1
IFNA10
IFNA16
IFNA2
IFNA7
IFNA14
IFNA17
IFNA4
IFNA6
IFNA21
IFNA5
IFNAR2
IFNA8
IRF9


Gamma Signaling Pathway(JAK1 JAK2 STAT1) (IFN Gamma Signaling(JAK1 JAK2 STAT1))
FDR = 0.88%, FDR nod = 1.8%
unknown CG mut
known HCG mut
wt
JAK1
JAK2
STAT1
IFNG
IFNGR2
IFNGR1

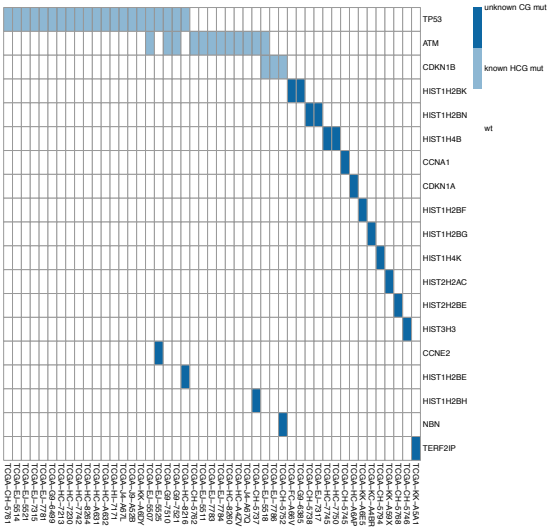

IL 6 Type Cytokine Receptor Ligand Interactions
FDR = 0.74%, FDR nod = 1.4%
unknown CG mut
known HCG mut
wt
IL12RB2
JAK1
JAK2
TYK2
IL27
OSMR
CRLF1
EBI3
LIF
OSM
CNTF
CNTFR
IL12A
IL27RA
LIFR


IRF3 Mediated Induction Of Type I IFN
FDR = 0.02%, FDR nod = 0.074%
unknown CG mut
known HCG mut
wt
PRKDC
NLRP4
IFI16
MRE11A
XRCC5
DDX41
DTX4
TBK1
TMEM173
XRCC6
TREX1
ZBP1

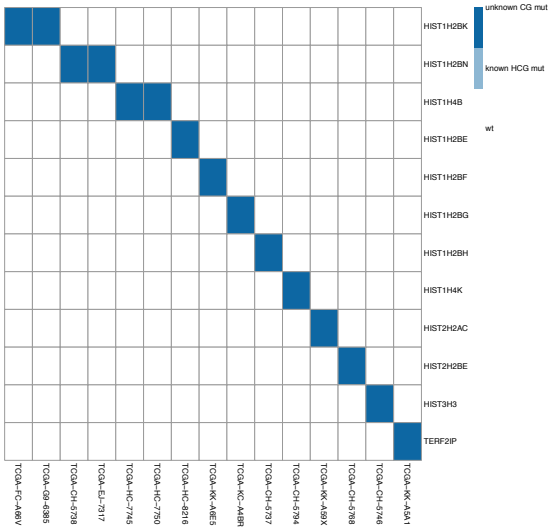

Regulation Of IFNA Signaling
FDR = 0.0013%, FDR nod = 0.019%
unknown CG mut
known HCG mut
wt
JAK1
PTPN11
STAT2
TYK2
IFNB1
STAT1
IFNA10
IFNA16
IFNA2
PTPN6
IFNA4
IFNA7
IFNA14
IFNA17
IFNA21
IFNA5
IFNA6
IFNAR2
IFNA8
USP18

PRAD

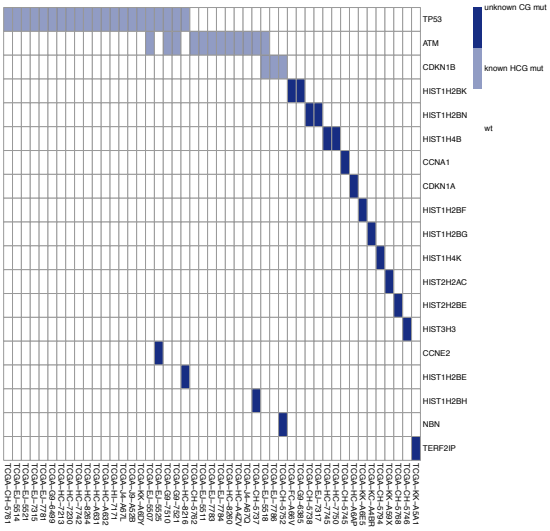
DNA Damage/Telomere Stress Induced Senescence
FDR = 6.7e−09%, FDR nod = 3.9%



Packaging Of Telomere Ends
FDR = 0.066%, FDR nod = 1%

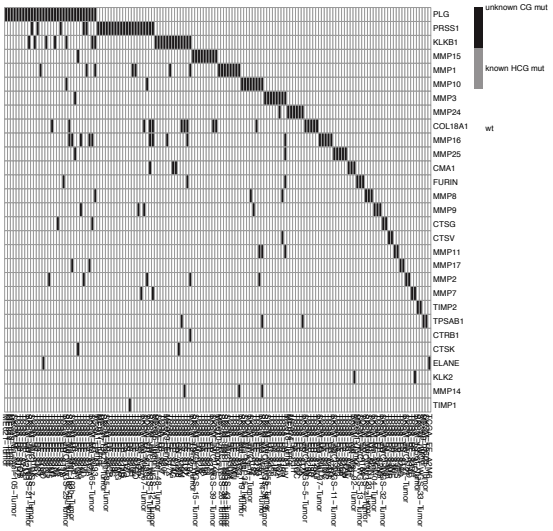


DNA Damage/Telomere Stress Induced Senescence
FDR = 6.7e−09%, FDR nod = 3.9%

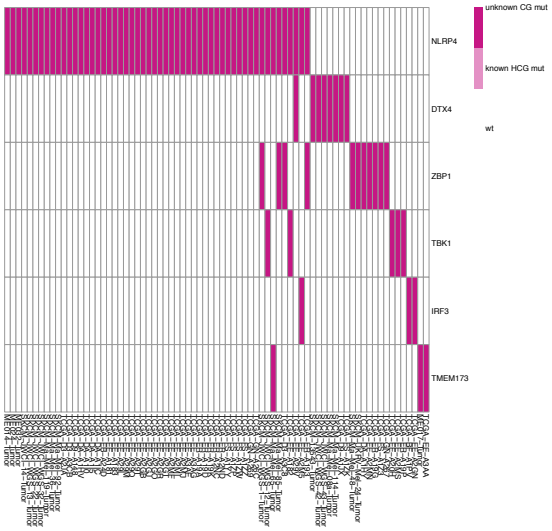


SKCM

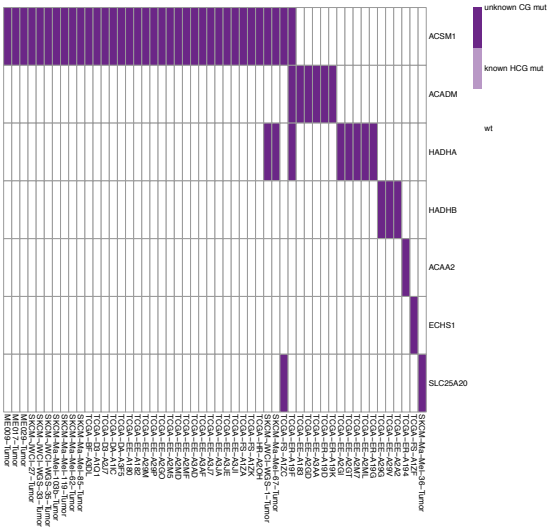
Activation Of Matrix Metalloproteinases
FDR = 0.022%, FDR nod = 0.093%



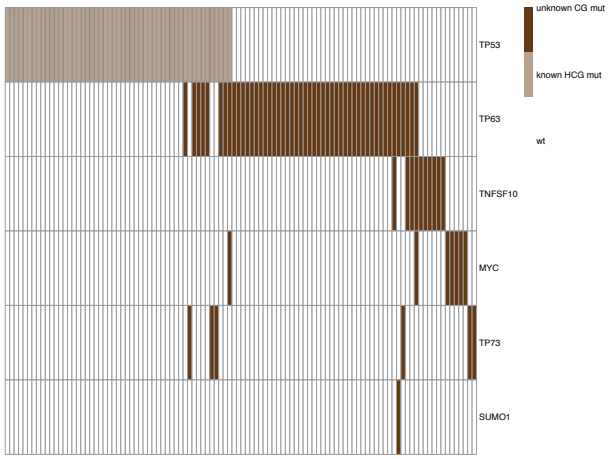
IRF3 Mediated Activation Of Type 1 IFN
FDR = 1.2e−06%, FDR nod = 1.2e−05%



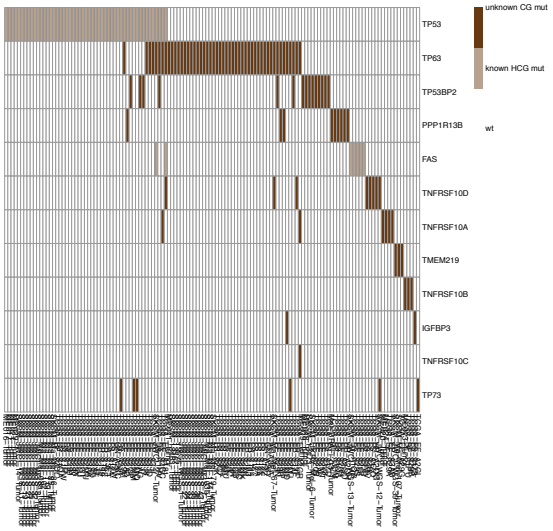
Mitochondrial Beta Oxidation Of Medium Chain Saturated Fatty Acids
FDR = 0.42%, FDR nod = 1.5%



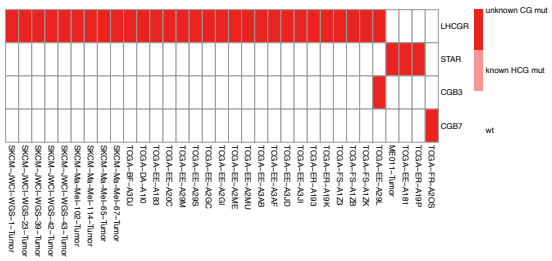
TP53 Network
FDR = 4.2e−12%, FDR nod = 2.1e−05%



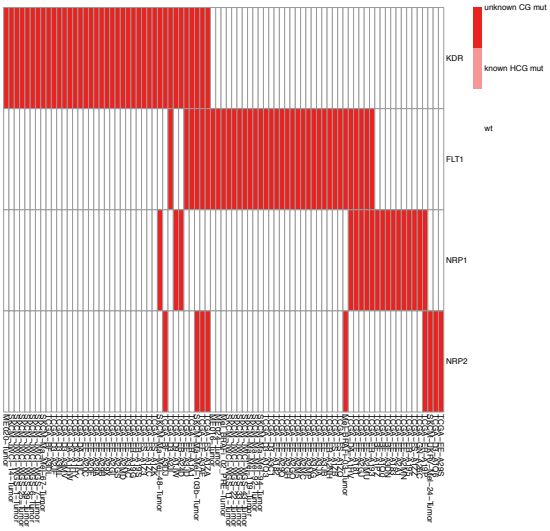
TP53 Regulates Transcription Of Death Receptors And Ligands
FDR = 1.6e−11%, FDR nod = 0.43%



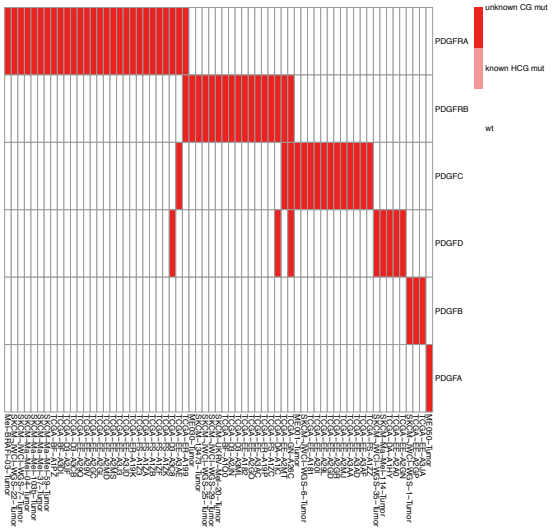
[CGB Protein Results In Increased Activity Of LHCGR Protein]
de Results In Decreased Activity Of PTGS2 Protein] Inhibits The Reaction [CGB Protein Results In Increased Chen
ı(3, 2 F)quinazoline 1,3 Diamine Binds To F2R Protein] Promotes The Reaction [CGB Protein Results In Increased
ne Inhibits The Reaction [CGB Protein Results In Increased Chemical Synthesis Of Androgens]
ıtrazine Inhibits The Reaction [CGB Protein Results In Increased Secretion Of Cyclic AMP]
forsin Promotes The Reaction [CGB Protein Results In Increased Abundance Of Cyclic AMP]
Reaction [[Gonadotropins, Equine Co Treated With CGB Protein] Results In Increased Abundance Of Progesteron
hibits The Reaction [[CGB Protein Co Treated With Colforsin] Results In Increased Abundance Of Cyclic AMP]
Protein Promotes The Reaction [CGB Protein Results In Increased Abundance Of Progesterone]
ole Metabolite Inhibits The Reaction [CGB Protein Results In Increased Abundance Of Testosterone]
se Chloride Inhibits The Reaction [CGB Protein Results In Increased Expression Of STAR Protein]
terone Promotes The Reaction [CGB Protein Results In Increased Expression Of VEGFA MRNA]
one Enanthate Inhibits The Reaction [CGB Protein Results In Increased Abundance Of Androgens]
FDR = 0.19%, FDR nod = 0.72%



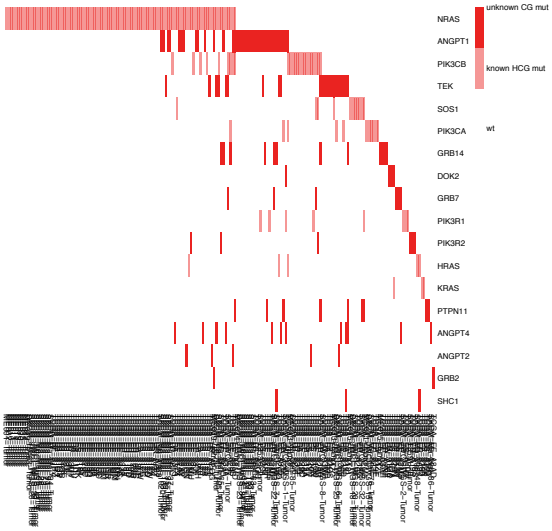
Neurophilin Interactions With VEGF And VEGFR
FDR = 0.05%, FDR nod = 0.21%



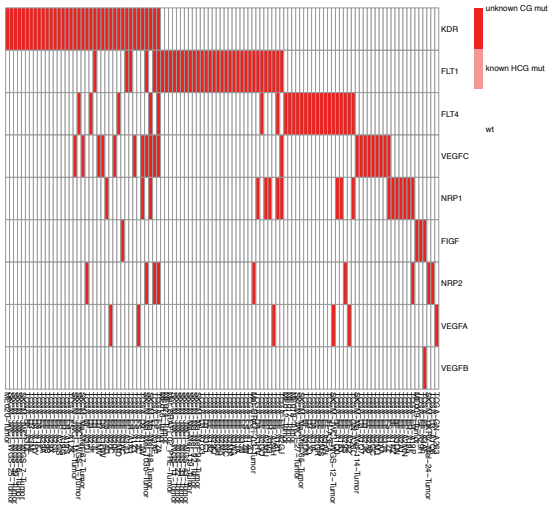
PDGF Receptor Signaling Network
FDR = 0.82%, FDR nod = 2.7%



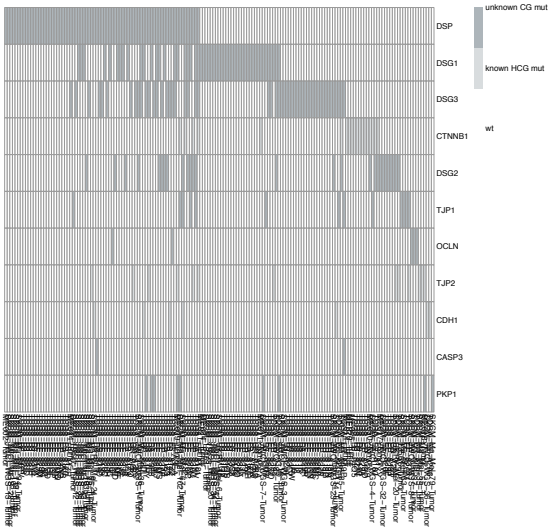
Tie2 Signaling
FDR = 5.6e−12%, FDR nod = 3.7%



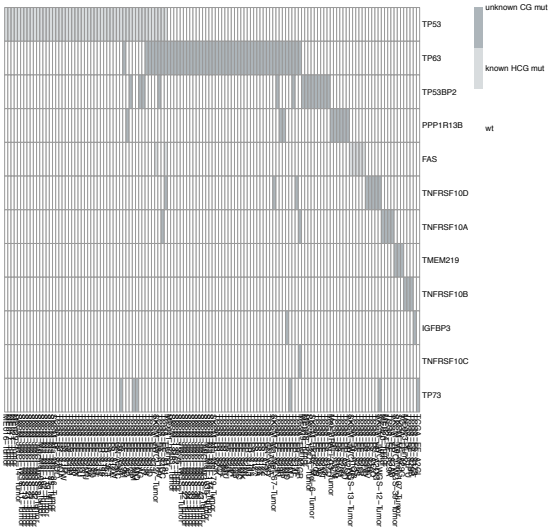
VEGF And VEGFR Signaling Network
VEGF Binds To VEGFR Leading To Receptor Dimerization
FDR = 0.71%, FDR nod = 2.3%



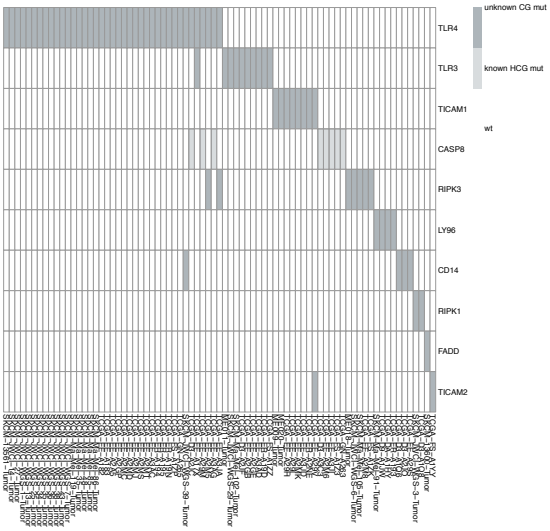
Apoptotic Cleavage Of Cell Adhesion Proteins
FDR = 4.6e−12%, FDR nod = 9.4e−11%



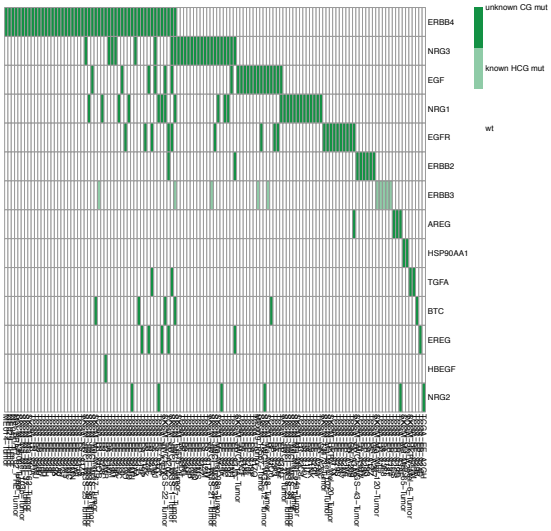
TP53 Regulates Transcription Of Death Receptors And Ligands
FDR = 1.6e−11%, FDR nod = 0.43%



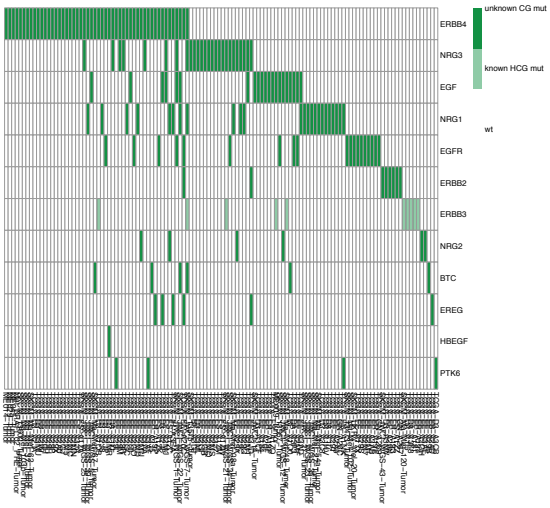
TRIF Mediated Programmed Cell Death
FDR = 0.007%, FDR nod = 0.001%



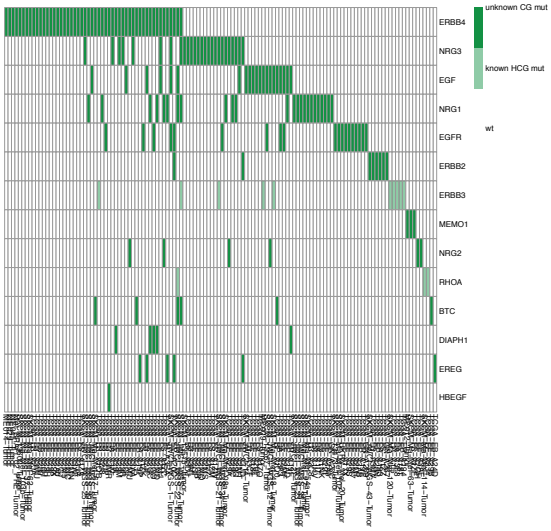
ErbB Receptor Signaling Network
FDR = 1.1%, FDR nod = 1.5%



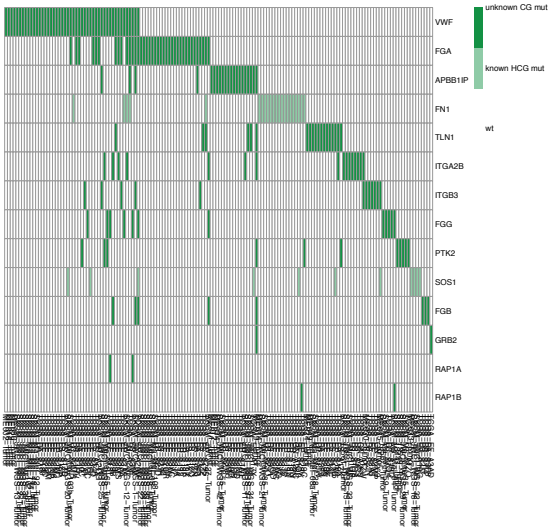
ERBB2 Activates PTK6 Signaling
Signaling By ERBB4
FDR = 0.43%, FDR nod = 0.48%



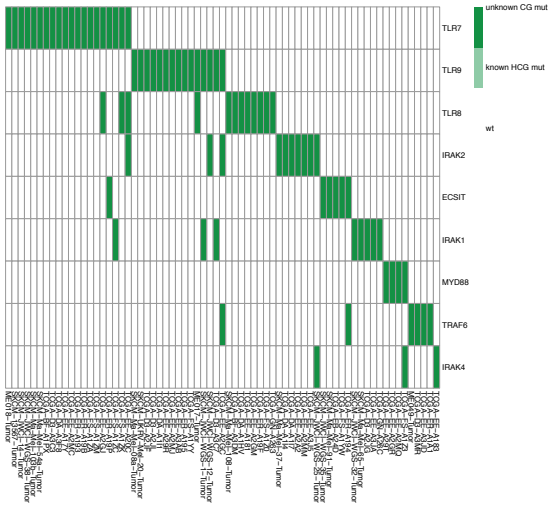
ERBB2 Regulates Cell Motility
FDR = 3.5%, FDR nod = 4.6%



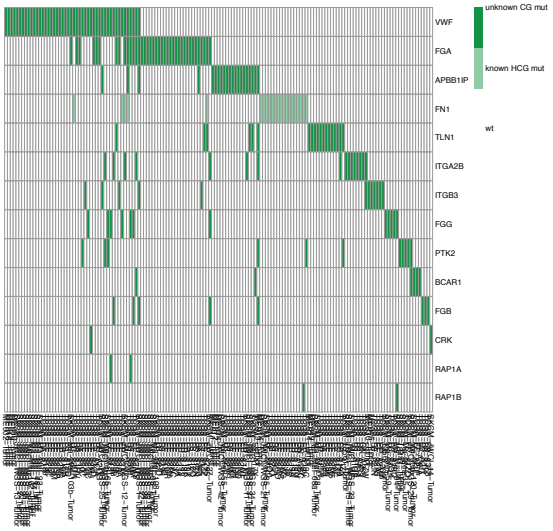
GRB2:SOS Provides Linkage To MAPK Signaling For Integrins
FDR = 0.0059%, FDR nod = 0.0064%



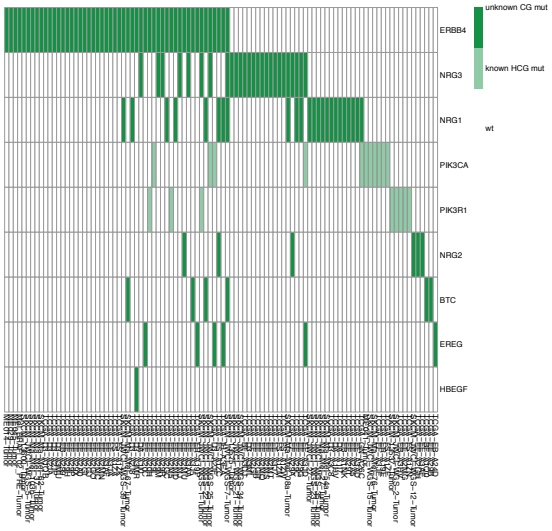
MyD88 Dependent Cascade Initiated On Endosome
TRAF6 Mediated Induction Of NFkB And MAP Kinases Upon TLR7/8 Or 9 Activation
FDR = 0.85%, FDR nod = 2.7%



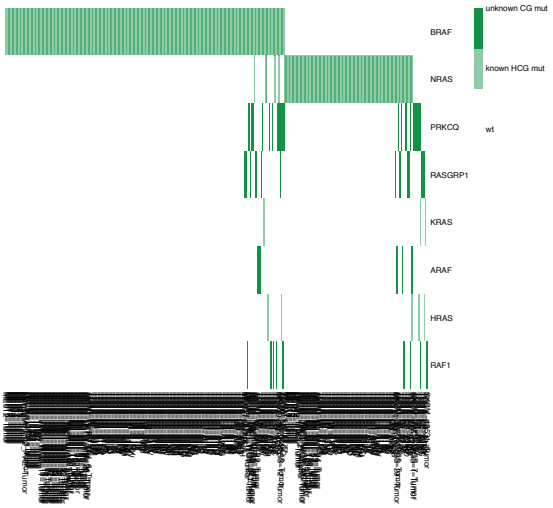
P130Cas Linkage To MAPK Signaling For Integrins
FDR = 0.0074%, FDR nod = 0.066%



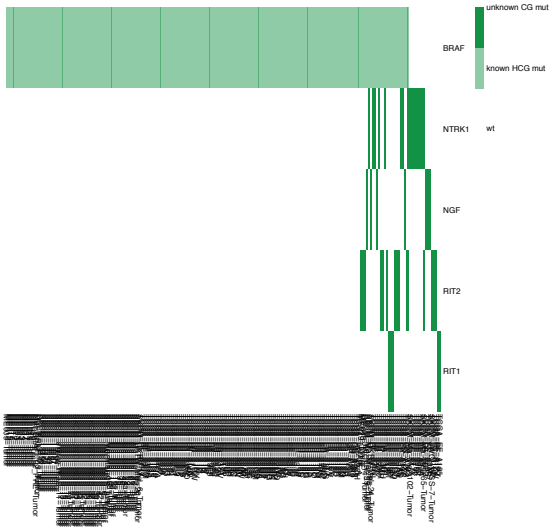
PI3K Events In ERBB4 Signaling
FDR = 1.1%, FDR nod = 0.02%



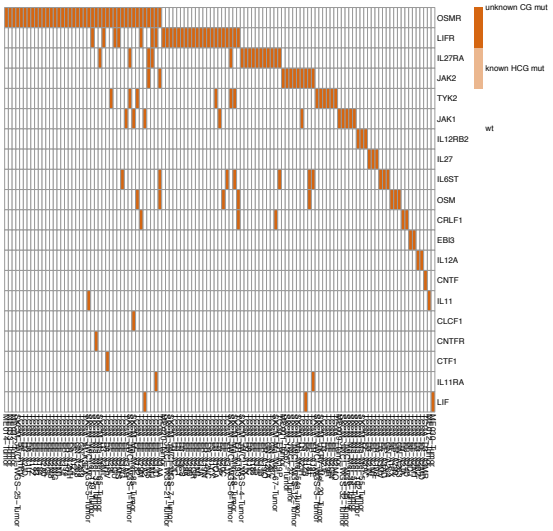
f Activation Signaling (through RasGRP) (CD4 T Cell Receptor Signaling (ERK Cascade))
Raf Activation Signaling (through RasGRP) (CD4 T Cell Receptor Signaling)
FDR = 3.9e−12%, FDR nod = 1.1%



Signalling To P38 Via RIT And RIN
FDR = 3.9e−12%, FDR nod = 7.5e−05%



IL 6 Type Cytokine Receptor Ligand Interactions
FDR = 1.7%, FDR nod = 4.6%



IRF3 Mediated Activation Of Type 1 IFN
FDR = 1.2e−06%, FDR nod = 1.2e−05%