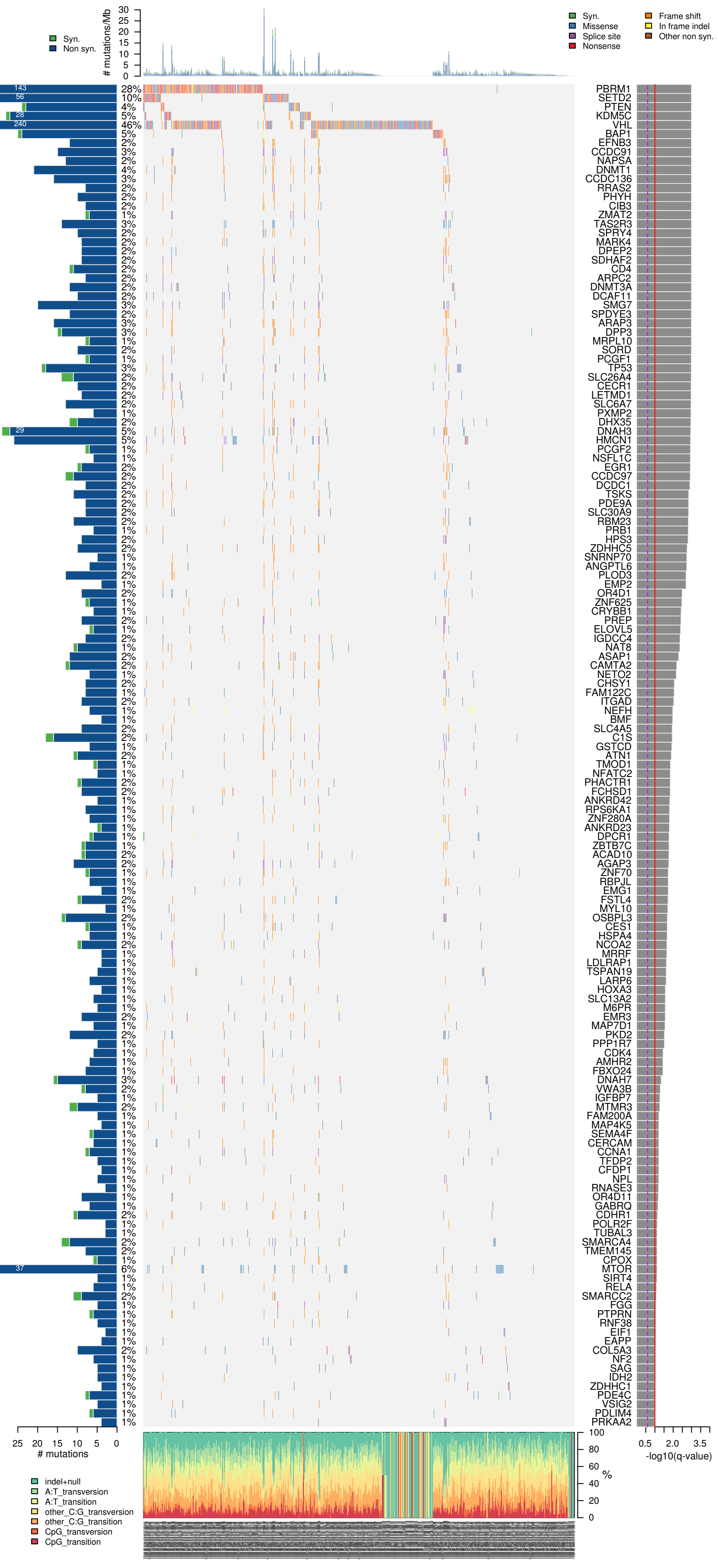

Syn.
Non syn.
# mutations/Mb
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
143 28% PBRM1
56 10% SETD2
4% PTEN
28 5% KDM5C
240 46% VHL
5% BAP1
2% EFNB3
3% CCDC91
2% NAPSA
4% DNMT1
3% CCDC136
2% RRAS2
2% PHYH
2% CIB3
1% ZMAT2
3% TAS2R3
2% SPRY4
2% MARK4
2% DPEP2
2% SDHAF2
2% CD4
2% ARPC2
2% DNMT3A
2% DCAF11
3% SMG7
2% SPDYE3
3% ARAP3
3% DPP3
1% MRPL10
2% SORD
1% PCGF1
3% TP53
2% SLC26A4
2% CECR1
2% LETMD1
2% SLC6A7
1% PXMP2
2% DHX35
29 5% DNAH3
5% HMCN1
1% PCGF2
1% NSFL1C
2% EGR1
2% CCDC97
2% DCDC1
2% TSKS
2% PDE9A
2% SLC30A9
2% RBM23
1% PRB1
2% HPS3
2% ZDHHC5
1% SNRNP70
1% ANGPTL6
2% PLOD3
1% EMP2
2% OR4D1
1% ZNF625
1% CRYBB1
2% PREP
1% ELOVL5
2% IGDCC4
1% NAT8
2% ASAP1
2% CAMTA2
1% NETO2
2% CHSY1
1% FAM122C
2% ITGAD
1% NEFH
1% BMF
2% SLC4A5
2% C1S
1% GSTCD
2% ATN1
1% TMOD1
1% NFATC2
2% PHACTR1
2% FCHSD1
1% ANKRD42
1% RPS6KA1
1% ZNF280A
1% ANKRD23
1% DPCR1
1% ZBTB7C
2% ACAD10
2% AGAP3
1% ZNF70
1% RBPJL
1% EMG1
2% FSTL4
1% MYL10
2% OSBPL3
1% CES1
1% HSPA4
2% NCOA2
1% MRRF
1% LDLRAP1
1% TSPAN19
1% LARP6
1% HOXA3
1% SLC13A2
1% M6PR
2% EMR3
1% MAP7D1
2% PKD2
1% PPP1R7
1% CDK4
1% AMHR2
1% FBXO24
3% DNAH7
2% VWA3B
1% IGFBP7
2% MTMR3
1% FAM200A
1% MAP4K5
1% SEMA4F
1% CERCAM
1% CCNA1
1% TFDP2
1% CFDP1
1% NPL
1% RNASE3
1% OR4D11
1% GABRQ
2% CDHR1
1% POLR2F
1% TUBAL3
2% SMARCA4
2% TMEM145
1% CPOX
37 6% MTOR
1% SIRT4
1% RELA
2% SMARCC2
1% FGG
1% PTPRN
1% RNF38
1% EIF1
1% EAPP
2% COL5A3
1% NF2
1% SAG
1% IDH2
1% ZDHHC1
1% PDE4C
1% VSIG2
1% PDLIM4
1% PRKAA2
25 20 15 10 5 0
# mutations
0.5 2.0 3.5
-log10(q-value)
100 80 60 40 20 0
%
indel+null
A:T_transversion
A:T_transition
other_C:G_transversion
other_C:G_transition
CpG_transversion
CpG_transition