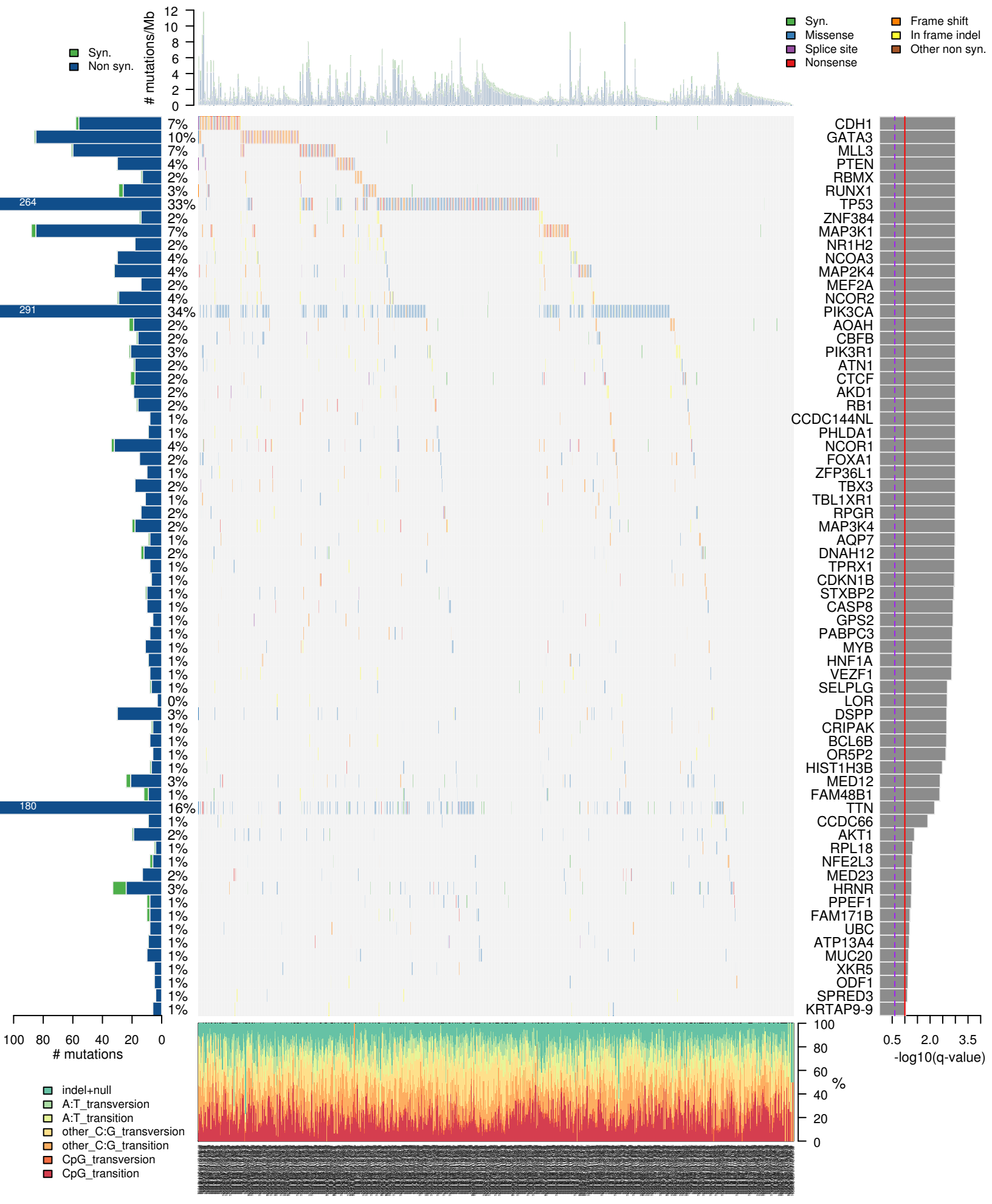
Syn.
Non syn.
mutations/Mb
0
2
4
6
8
10
12
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
7%
10%
7%
4%
2%
3%
264
33%
2%
7%
2%
4%
4%
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4%
291
34%
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3%
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0%
3%
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3%
1%
180
16%
1%
2%
1%
1%
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3%
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1%
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1%
1%
1%
CDH1
GATA3
MLL3
PTEN
RBMX
RUNX1
TP53
ZNF384
MAP3K1
NR1H2
NCOA3
MAP2K4
MEF2A
NCOR2
PIK3CA
AOAH
CBFB
PIK3R1
ATN1
CTCF
AKD1
RB1
CCDC144NL
PHLDA1
NCOR1
FOXA1
ZFP36L1
TBX3
TBL1XR1
RPGR
MAP3K4
AQP7
DNAH12
TPRX1
CDKN1B
STXBP2
CASP8
GPS2
PABPC3
MYB
HNF1A
VEZF1
SELPLG
LOR
DSPP
CRIPAK
BCL6B
OR5P2
HIST1H3B
MED12
FAM48B1
TTN
CCDC66
AKT1
RPL18
NFE2L3
MED23
HRNR
PPEF1
FAM171B
UBC
ATP13A4
MUC20
XKR5
ODF1
SPRED3
KRTAP9-9
100
80
60
40
20
0
mutations
0.5
2.0
3.5
-log10(q-value)
indel+null
A:T_transversion
A:T_transition
other_C:G_transversion
other_C:G_transition
CpG_transversion
CpG_transition
100
80
60
40
20
0
%