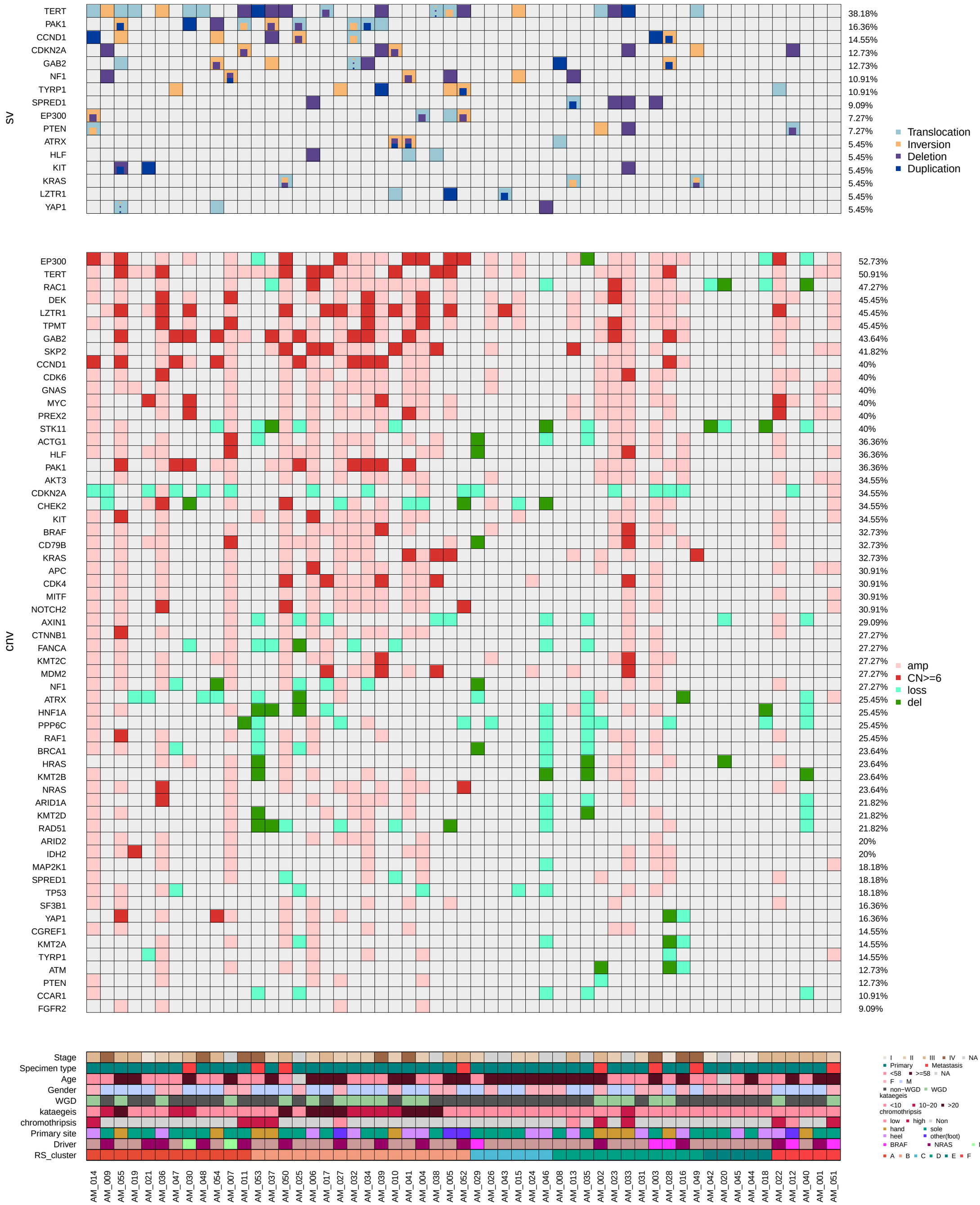
SV
TERT 38.18%
PAK1 16.36%
CCND1 14.55%
CDKN2A 12.73%
GAB2 12.73%
NF1 10.91%
TYRP1 10.91%
SPRED1 9.09%
EP300 7.27%
PTEN 7.27%
ATRX 5.45%
HLF 5.45%
KIT 5.45%
KRAS 5.45%
LZTR1 5.45%
YAP1 5.45%
Translocation
Inversion
Deletion
Duplication
cnv
EP300 52.73%
TERT 50.91%
RAC1 47.27%
DEK 45.45%
LZTR1 45.45%
TPMT 45.45%
GAB2 43.64%
SKP2 41.82%
CCND1 40%
CDK6 40%
GNAS 40%
MYC 40%
PREX2 40%
STK11 40%
ACTG1 36.36%
HLF 36.36%
PAK1 36.36%
AKT3 34.55%
CDKN2A 34.55%
CHEK2 34.55%
KIT 34.55%
BRAF 32.73%
CD79B 32.73%
KRAS 32.73%
APC 30.91%
CDK4 30.91%
MITF 30.91%
NOTCH2 30.91%
AXIN1 29.09%
CTNNB1 27.27%
FANCA 27.27%
KMT2C 27.27%
MDM2 27.27%
NF1 27.27%
ATRX 25.45%
HNF1A 25.45%
PPP6C 25.45%
RAF1 25.45%
BRCA1 23.64%
HRAS 23.64%
KMT2B 23.64%
NRAS 23.64%
ARID1A 21.82%
KMT2D 21.82%
RAD51 21.82%
ARID2 20%
IDH2 20%
MAP2K1 18.18%
SPRED1 18.18%
TP53 18.18%
SF3B1 16.36%
YAP1 16.36%
CGREF1 14.55%
KMT2A 14.55%
TYRP1 14.55%
ATM 12.73%
PTEN 12.73%
CCAR1 10.91%
FGFR2 9.09%
amp
CN>=6
loss
del
Stage
Specimen type
Age
Gender
WGD
kataegeis
chromothripsis
Primary site
Driver
RS_cluster
AM_014 AM_009 AM_055 AM_019 AM_021 AM_036 AM_047 AM_030 AM_048 AM_054 AM_007 AM_011 AM_053 AM_037 AM_050 AM_025 AM_006 AM_017 AM_027 AM_032 AM_034 AM_039 AM_010 AM_041 AM_004 AM_038 AM_005 AM_052 AM_029 AM_026 AM_043 AM_015 AM_024 AM_046 AM_008 AM_013 AM_035 AM_002 AM_023 AM_033 AM_031 AM_003 AM_028 AM_016 AM_049 AM_042 AM_020 AM_045 AM_044 AM_018 AM_022 AM_012 AM_040 AM_001 AM_051
I II III IV NA
Primary Metastasis
<58 >=58 NA
F M
non−WGD WGD
kataegeis
<10 10−20 >20
chromothripsis
low high Non
hand sole
heel other(foot)
BRAF NRAS NF1 Triple WT
A B C D E F