Figure S1

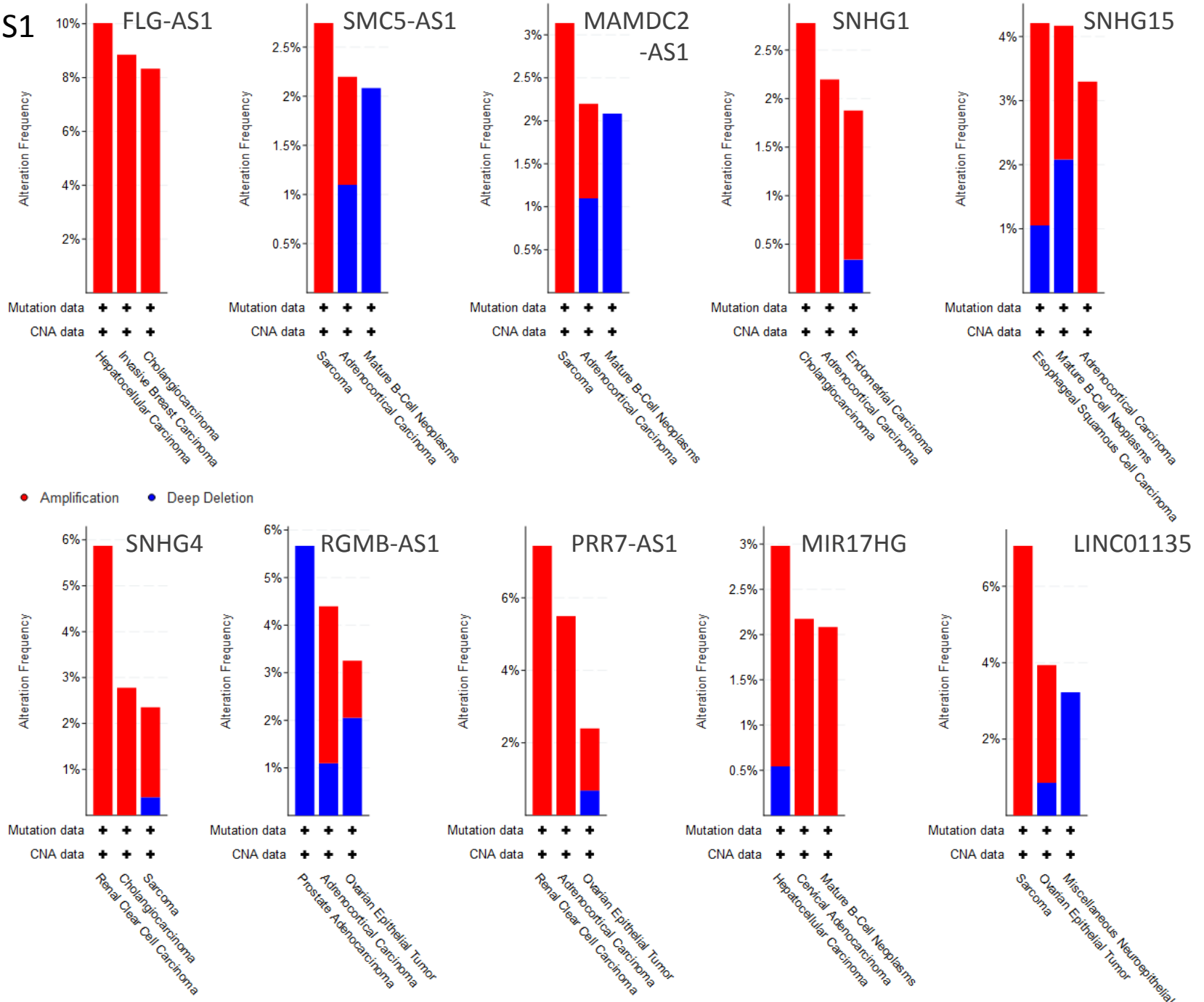
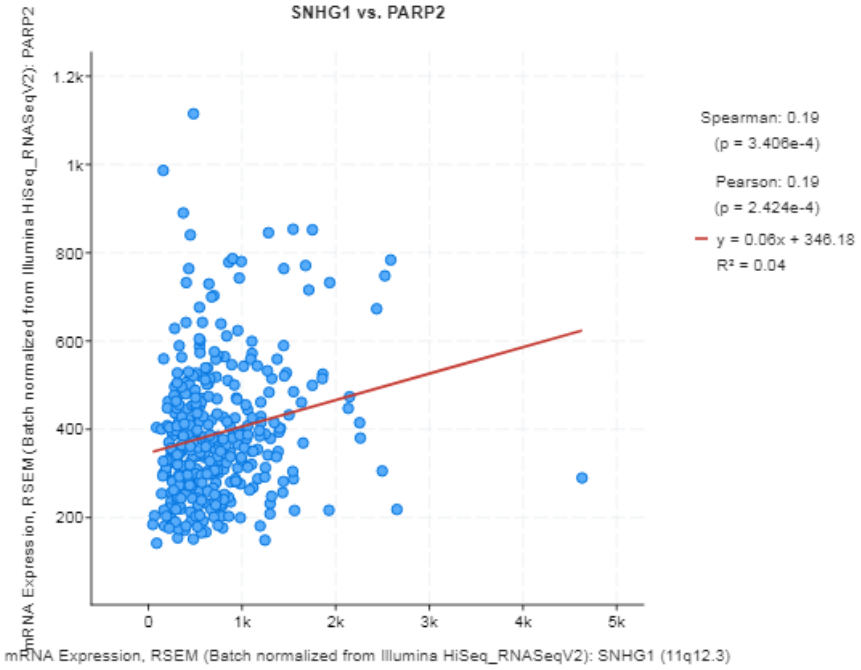

FLG-AS1
Alteration Frequency
10%
8%
6%
4%
2%
Mutation data
CNA data
Hepatocellular Carcinoma
Invasive Breast Carcinoma
Cholangiocarcinoma
SMC5-AS1
2.5%
2%
1.5%
1%
0.5%
Sarcoma
Adrenocortical Carcinoma
Mature B-Cell Neoplasms
MAMDC2-AS1
3%
2.5%
2%
1.5%
1%
0.5%
Sarcoma
Adrenocortical Carcinoma
Mature B-Cell Neoplasms
SNHG1
2.5%
2%
1.5%
1%
0.5%
Cholangiocarcinoma
Adrenocortical Carcinoma
Endometrial Carcinoma
SNHG15
4%
3%
2%
1%
Esophageal Squamous Cell Carcinoma
Mature B-Cell Neoplasms
Adrenocortical Carcinoma
Amplification
Deep Deletion
SNHG4
6%
5%
4%
3%
2%
1%
Renal Clear Cell Carcinoma
Cholangiocarcinoma
Sarcoma
RGMB-AS1
6%
5%
4%
3%
2%
1%
Prostate Adenocarcinoma
Adrenocortical Carcinoma
Ovarian Epithelial Tumor
PRR7-AS1
6%
4%
2%
Renal Clear Cell Carcinoma
Adrenocortical Carcinoma
Ovarian Epithelial Tumor
MIR17HG
3%
2.5%
2%
1.5%
1%
0.5%
Hepatocellular Carcinoma
Cervical Adenocarcinoma
Mature B-Cell Neoplasms
LINC01135
6%
4%
2%
Sarcoma
Ovarian Epithelial Tumor
Miscellaneous Neuroepithelial Tumor

Fig S2

A


SNHG1 vs. PARP2
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PARP2
1.2k
1k
800
600
400
200
0
1k
2k
3k
4k
5k
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SNHG1 (11q12.3)
Spearman: 0.19
(p = 3.406e-4)
Pearson: 0.19
(p = 2.424e-4)
y = 0.06x + 346.18
R² = 0.04

B

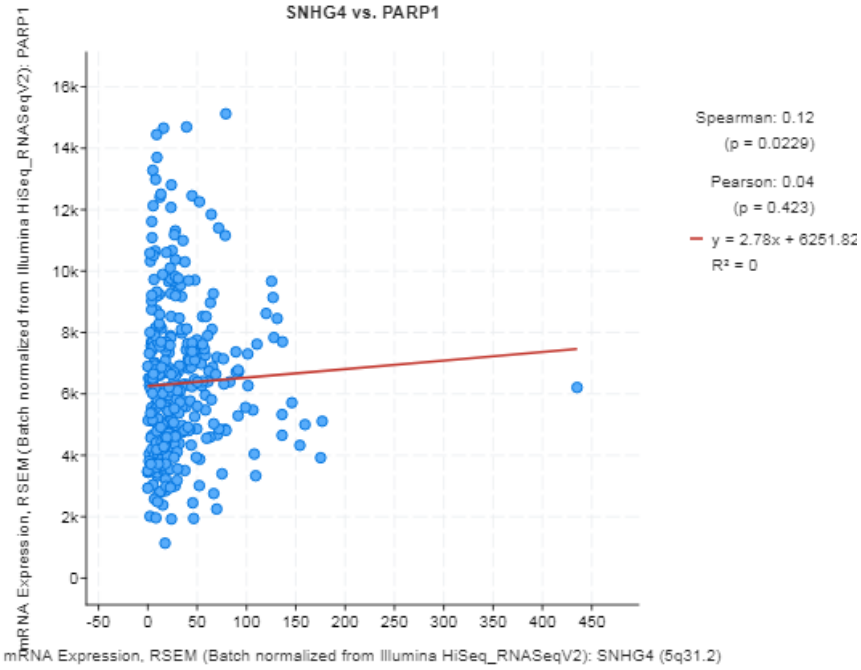

SNHG4 vs. PARP1
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): PARP1
16k
14k
12k
10k
8k
6k
4k
2k
0
-50
0
50
100
150
200
250
300
350
400
450
mRNA Expression, RSEM (Batch normalized from Illumina HiSeq_RNASeqV2): SNHG4 (5q31.2)
Spearman: 0.12
(p = 0.0229)
Pearson: 0.04
(p = 0.423)
y = 2.78x + 6251.82
R² = 0

Figure S3

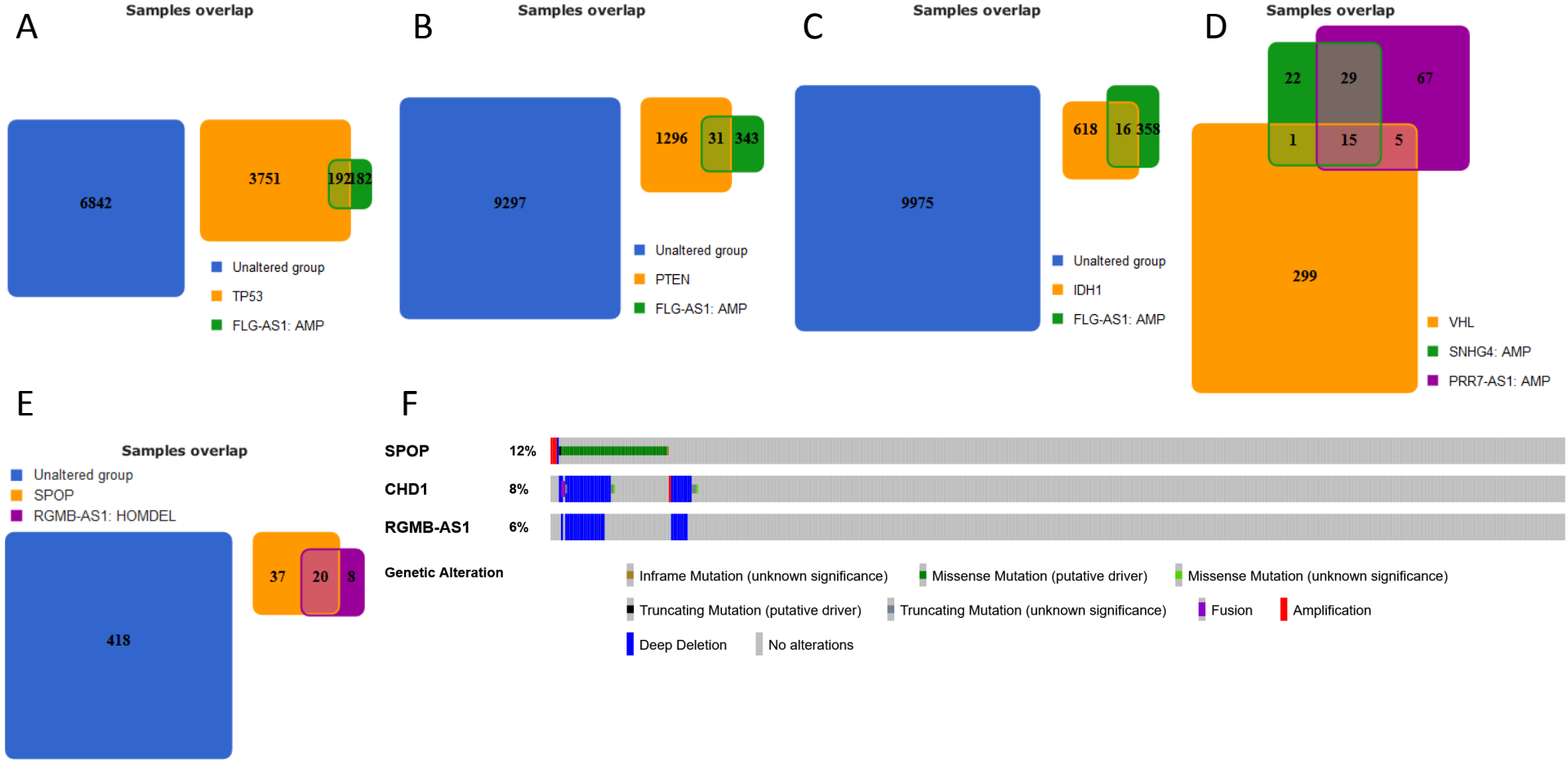
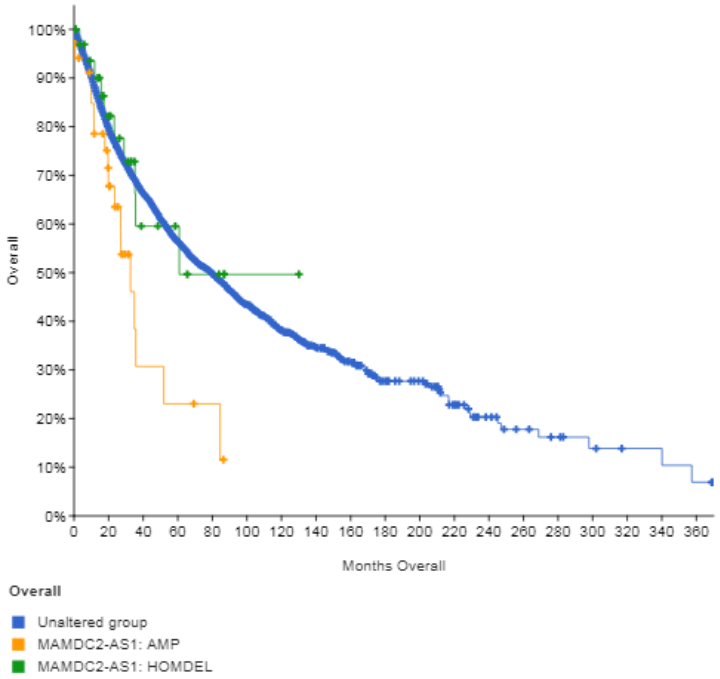
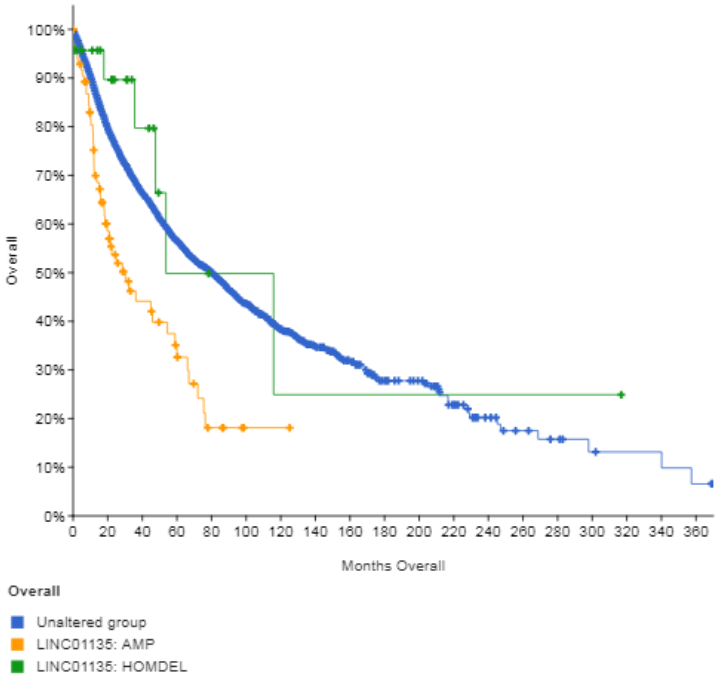
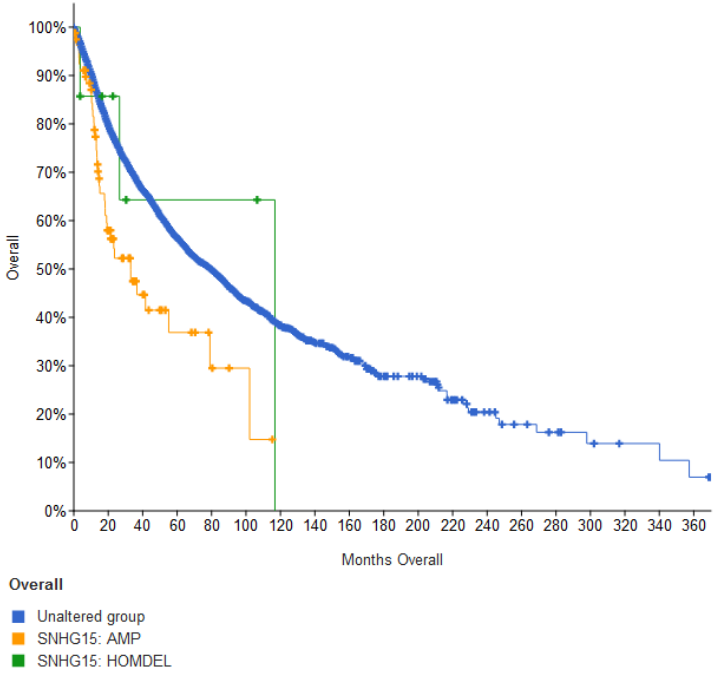

A
Samples overlap
6842
3751
192
82
Unaltered group
TP53
FLG-AS1: AMP
B
Samples overlap
9297
1296
31
343
Unaltered group
PTEN
FLG-AS1: AMP
C
Samples overlap
9975
618
16
358
Unaltered group
IDH1
FLG-AS1: AMP
D
Samples overlap
22
29
67
1
15
5
299
VHL
SNHG4: AMP
PRR7-AS1: AMP
E
Samples overlap
Unaltered group
SPOP
RGMB-AS1: HOMDEL
418
37
20
8
F
SPOP
12%
CHD1
8%
RGMB-AS1
6%
Genetic Alteration
Inframe Mutation (unknown significance)
Missense Mutation (putative driver)
Missense Mutation (unknown significance)
Truncating Mutation (putative driver)
Truncating Mutation (unknown significance)
Fusion
Amplification
Deep Deletion
No alterations

Figure S4

A



B



C