

Description of Additional Supplementary Files

Supplementary Dataset 1: μ score and amplification frequency for each tumor type at 1 and 36 Mbp and arm-level.

Supplementary Dataset 2: aggregation estimates computed with TANGO.

Supplementary Dataset 3: protected and unprotected genes, gene ontology analysis and CRISPR common essential and non-essential.

Supplementary Dataset 4: number of genes and mutations in each subset of Fig. 2.