Figure S5
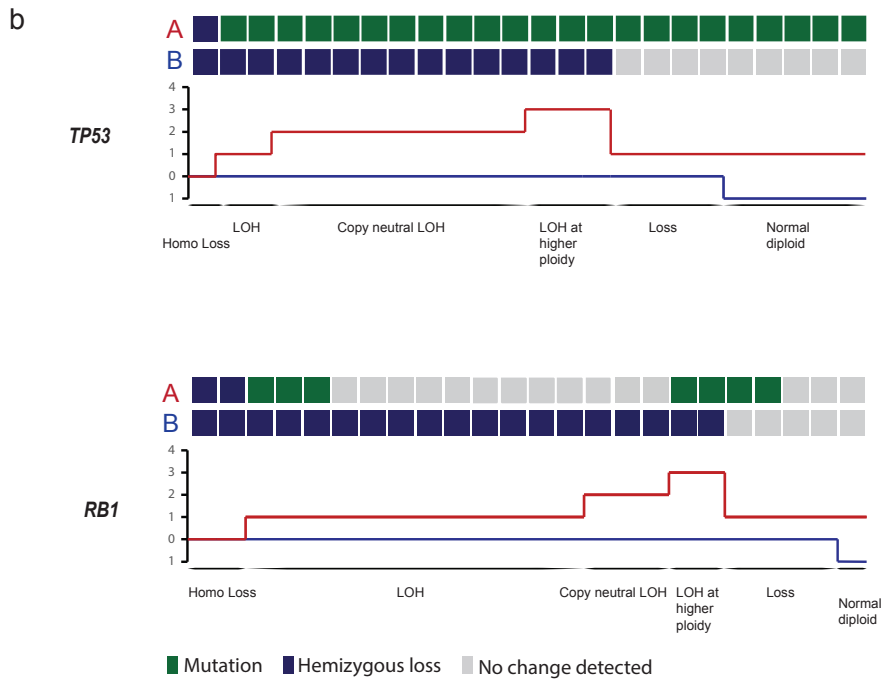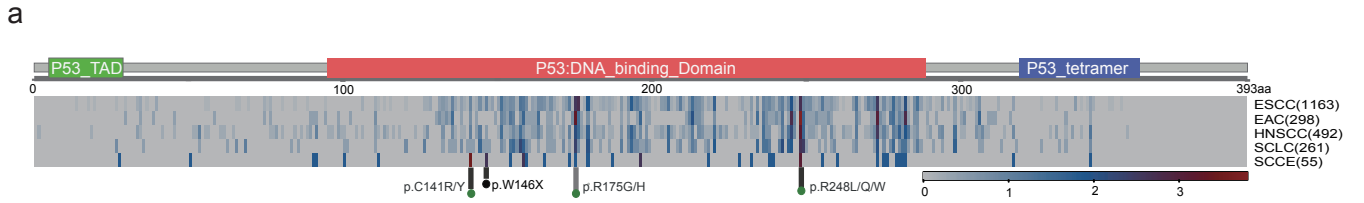
a

b

■ Mutation ■ Hemizygous loss ■ No change detected

Supplementary information, Figure S5 Characterization of *TP53* and *RB1*

mutations. **a** Heat map of *TP53* coding mutation. Upper panel shows the protein

structure of *TP53* with domains labelled in different colors. Lower panel (heat map)

denotes the mutation fraction of each amino acid. Mutations with high fraction are

marked. Except SCCE, all mutation data of the other cancers are adopted from the

IARC TP53 mutation database[1]. **b** Bi-allelic inactivation of *TP53* and *RB1* in SCCE.

Somatic mutations and copy number alterations of *TP53* and *RB1* were determined for

the 24 patients who had both whole exome sequencing data and OncoScan CNV

FFPE assay data. Samples are plotted from left to right. Alleles A and B are

represented for each case and color-coded according to the somatic mutations and

copy number alterations. The integral copy number (iCN) state of each allele is

plotted; hemizygous losses are annotated as loss of heterozygosity (LOH), copy-

neutral LOH or LOH at higher ploidy. Samples retaining allele A and B show

alterations on both alleles (bi-allelic alterations).

Reference

1. Bouaoun L, Sonkin D, Ardin M *et al.* TP53 Variations in Human Cancers: New

Lessons from the IARC TP53 Database and Genomics Data. *Hum Mutat* 2016;

37:865-876.