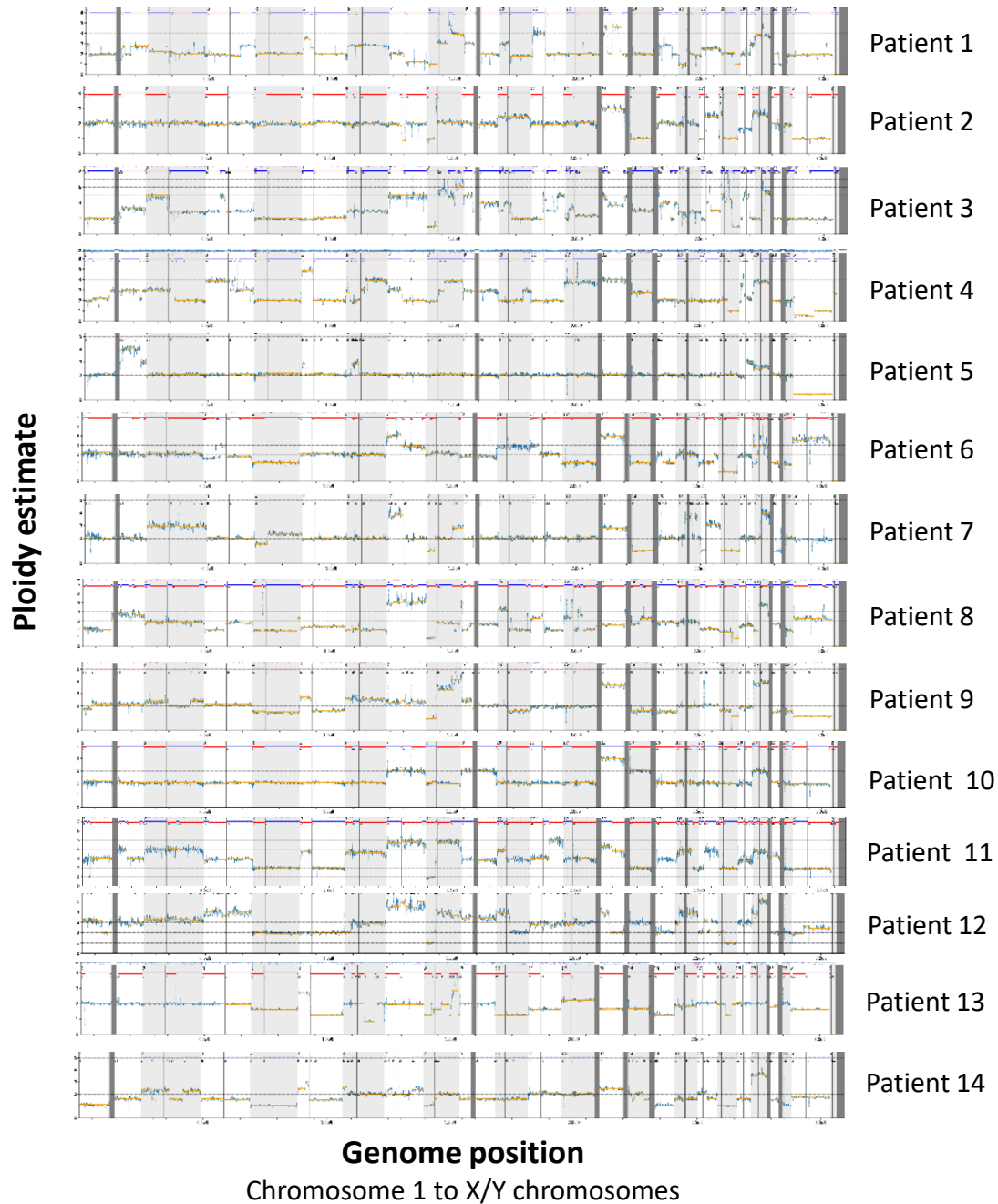
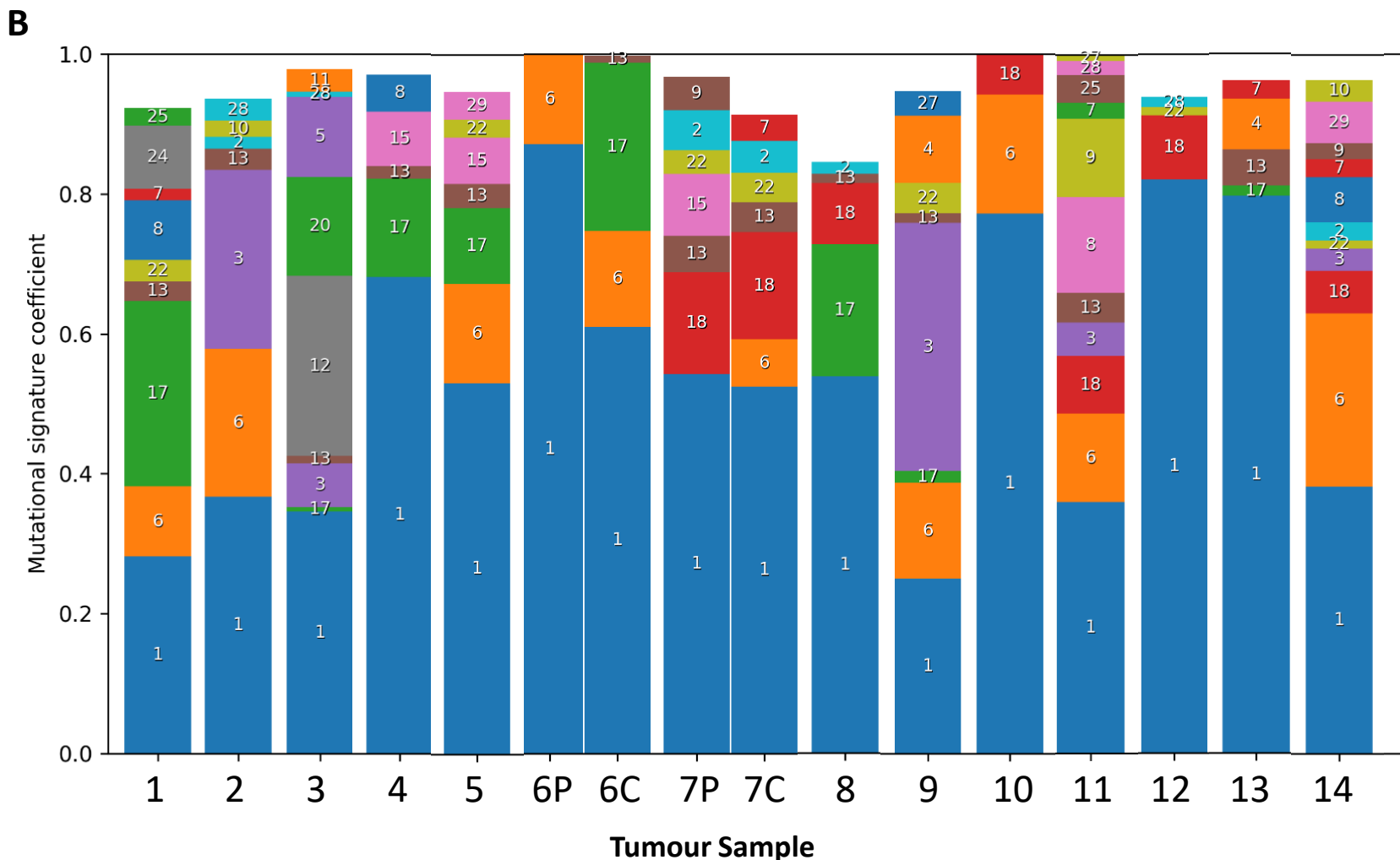


A

Supplementary Figure 2. (A) Ploidy estimate plots from WES across genome show that some peritonoids from the cohort have relatively normal chromosomal copy numbers across the genome, with gains and losses of specific regions (eg patient 5), but the majority have widespread variation in ploidy.



Supplementary Figure 2 (B) Cosmic DNA mutation signature v2 generated from WES of peritonoids, or CRPM tissue for patient 13. Colours in the bar graph indicate different mutation signatures with different etiologies. By signature these are: 1 aging; 2 cytidine deaminase fault; 3 BRCA- failure of dsDNA break repair; 4 exposure to tobacco mutagens; 6 mismatch repair fault/microsatellite instability; 7 UV light exposure; 9 polymerase η fault; 10 polymerase POLE fault; 11 alkylating agent exposure/fault in transcription-coupled nucleotide excision repair; 13 cytidine deaminase fault; 15 & 20 DNA mismatch repair fault; 22 exposure to aristolochic acid; 24 exposure to aflatoxin; 29 tobacco chewing; signatures 5, 8, 12, 17, 18, 25, 27 & 28 unknown etiologies. The estimated proportion by which signature each contributes to the total mutation profile found in each sample is indicated by the height of each coloured bar.