SUPPLEMENTAL MATERIAL

Giessler et al., https://doi.org/10.1084/jem.20162017

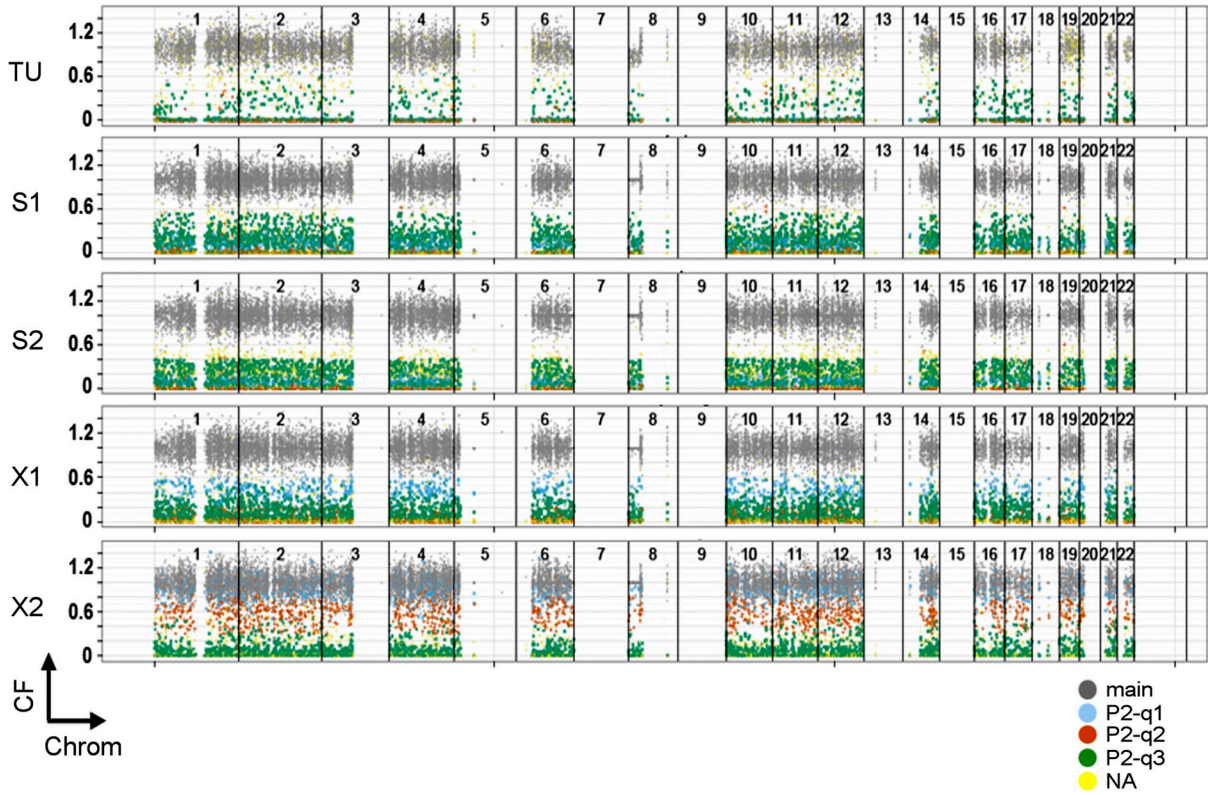

Figure S1. **Genome-wide distribution of SNVs.** Representative genomic location of the main SNV population and growth clones identified in P2. Gaps correspond to genomic regions with subclonal copy numbers or copy numbers ≥4 *n* and regions without allele-specific copy numbers, which were excluded from the analyses. All experiments were performed independently with tumor material from three CRC patients. Chrom., chromosome.

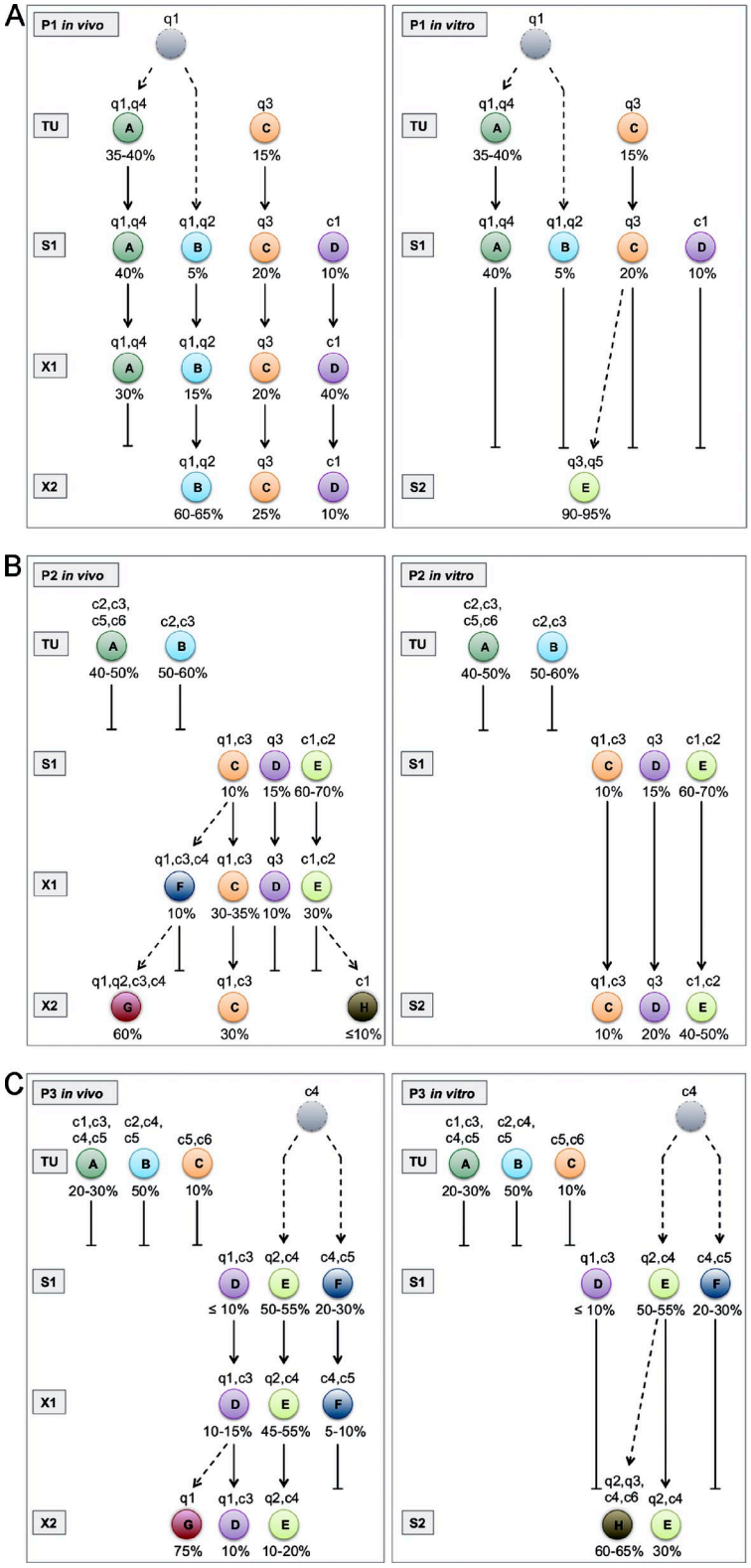

Figure S2. **Model of genomic subclones in primary tumors, spheroid cultures, and xenografts.** (A–C) Underlying growth clones are indicated on top of each genomic subclone for P1 (A), P2 (B), and P3 (C). The respective CFs are indicated below each subclone. Gray circles indicate common ancestors. Dashed lines indicate phylogeny constructed applying maximum parsimony. All experiments were performed independently with tumor material from three CRC patients.

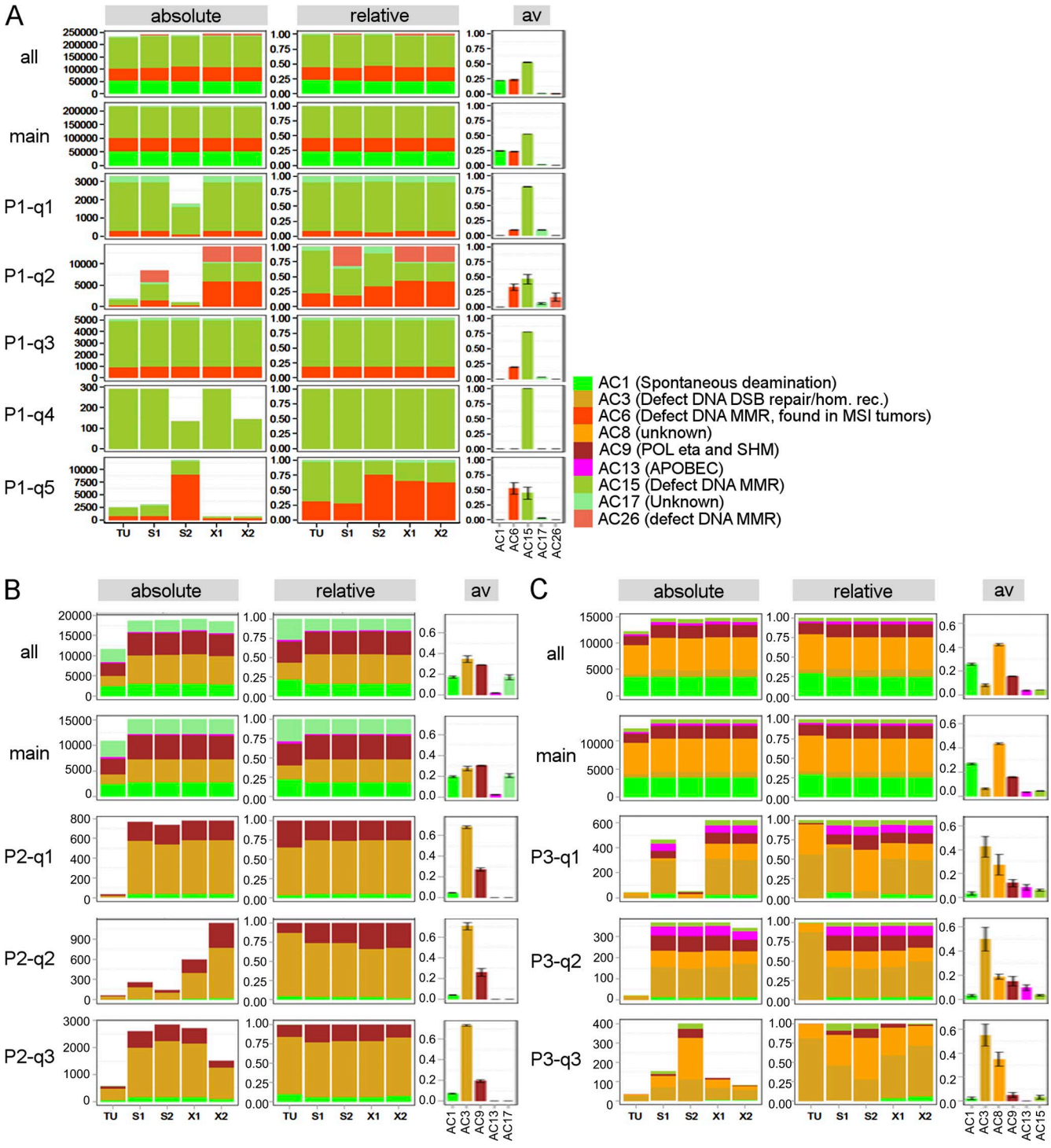

Figure S3. **SNV-based growth clones harbor distinct mutational signatures.** (A–C) Mutational profiles for growth clones from P1 (A), P2 (B), and P3 (C). The first row of plots corresponds to an unstratified analysis including all SNVs; the other rows of the plots correspond to SNV-based growth clones underlying genomic subclone heterogeneity. Each small panel shows the absolute (left), relative (middle), or average (av) of the relative (right) signature exposures of one SNV-based growth clone. All experiments were performed independently with tumor material from three CRC patients. AC: Alexandrov COSMIC (nomenclature referring to http://cancer.sanger.ac.uk/cosmic/signatures; Alexandrov et al., 2013). hom. rec., homologous recombination; POL eta and SHM, DNA polymerase eta and somatic hypermutation.

Table S1, included in a separate Excel file, shows mutations in CRC-associated and mismatch repair genes in SNV-based growth clones.

REFERENCE

Alexandrov, L.B., S. Nik-Zainal, D.C. Wedge, S.A. Aparicio, S. Behjati, A.V. Biankin, G.R. Bignell, N. Bolli, A. Borg, A.L. Børresen-Dale, et al. ICGC PedBrain. 2013. Signatures of mutational processes in human cancer. *Nature.* 500:415–421 (published erratum appears in *Nature.* 2013 502:258). http://dx.doi.org/10.1038/nature12477