**Supplementary Figure 1 Swimmer plot**

**Supplementary Figure 2 SV + DLP summary**

**Supplementary Figure 3 Study summary**

**Supplementary Figure 4 10kb vs 500kb copy number profiles**

**Supplementary Figure 5 Copy number heatmaps**

**Supplementary Figure 6 Clonal evolution trajectories Supplementary**

**Figure 7 Validation using WGS of plasma**

**Tables**

**Table S1 - cfDNA coverage statistics**

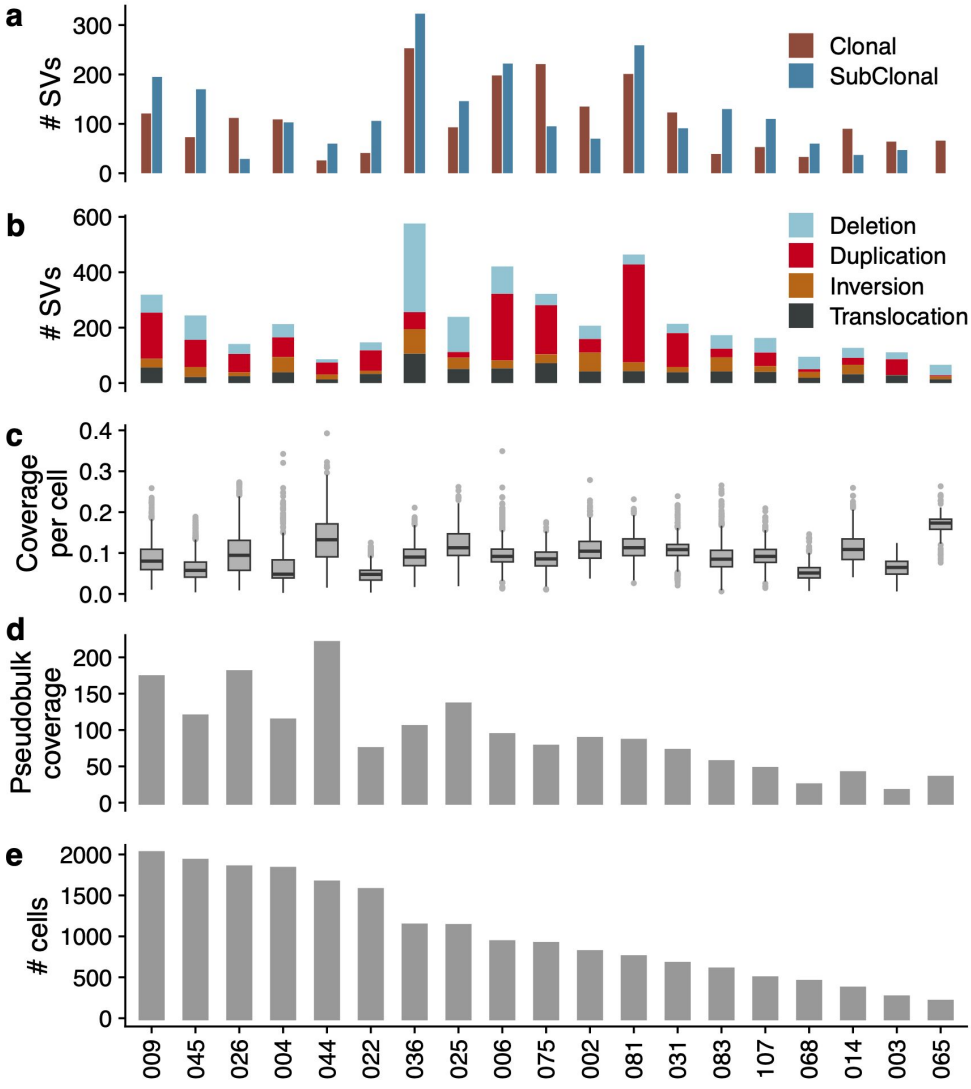
**Table S2 - cfDNA tumor fractions**

**Table S3 - Clone frequencies**

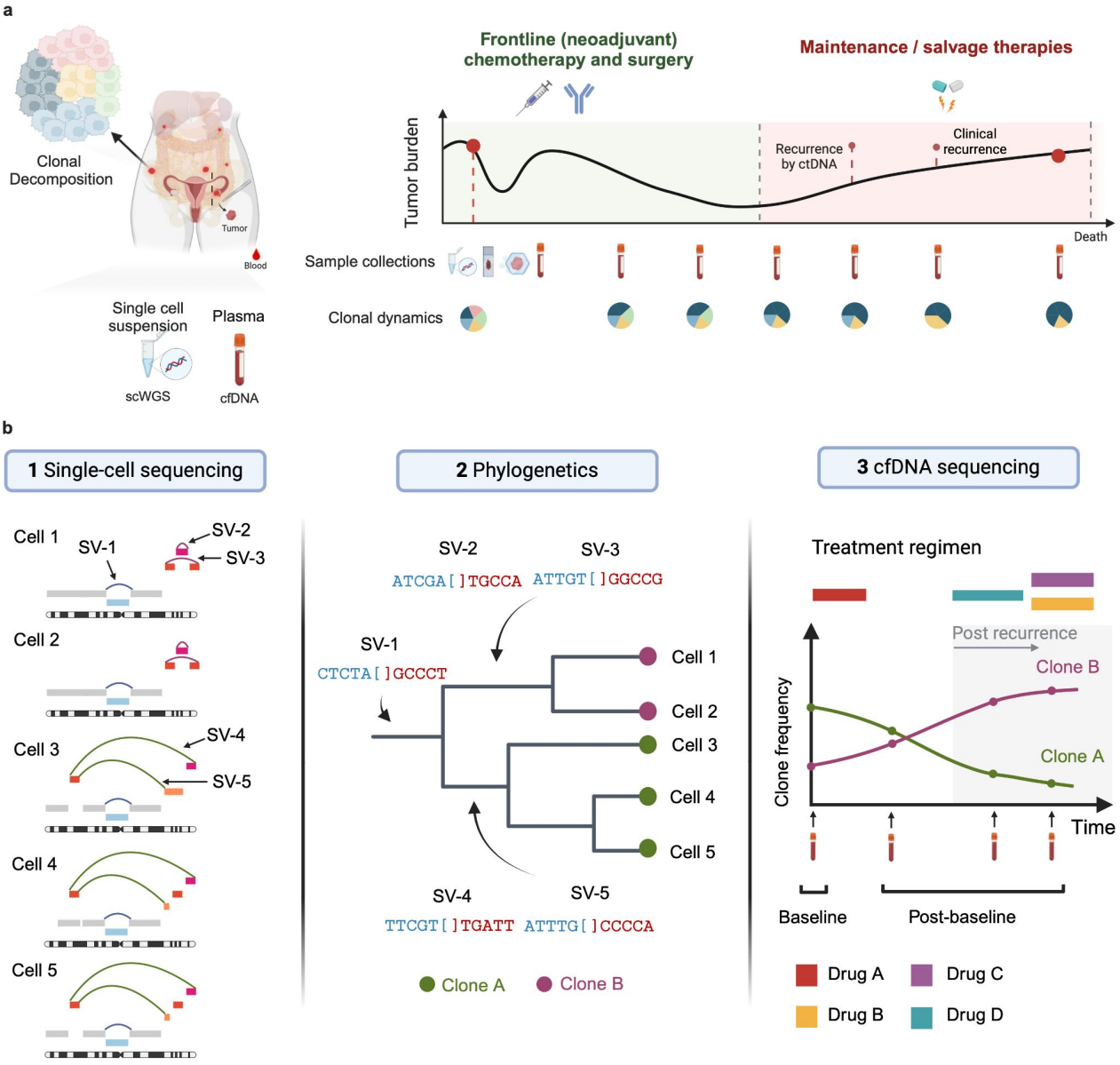
**Table S4 - Genomic features of clones**

**Table S5 - Error rates**

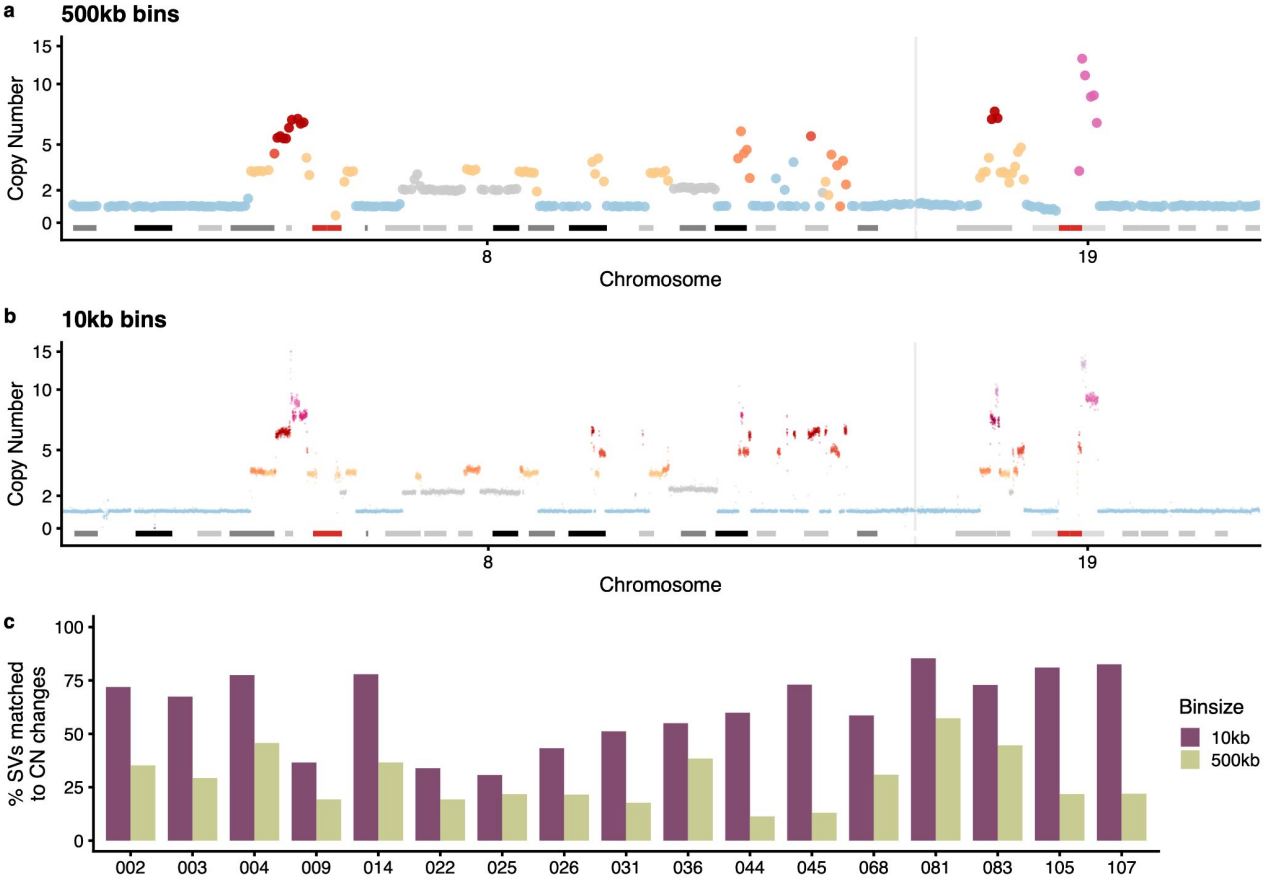

**Supplementary Figure 1**
Swimmer plot showing clinical history of all 19 patients included in the study. Shown are survival status, therapies, surgeries time of first clinical recurrence and data generation timepoints. Days are relative to day of first surgery, ie Day 0 is the date of primary debulking or laparoscopic biopsy.



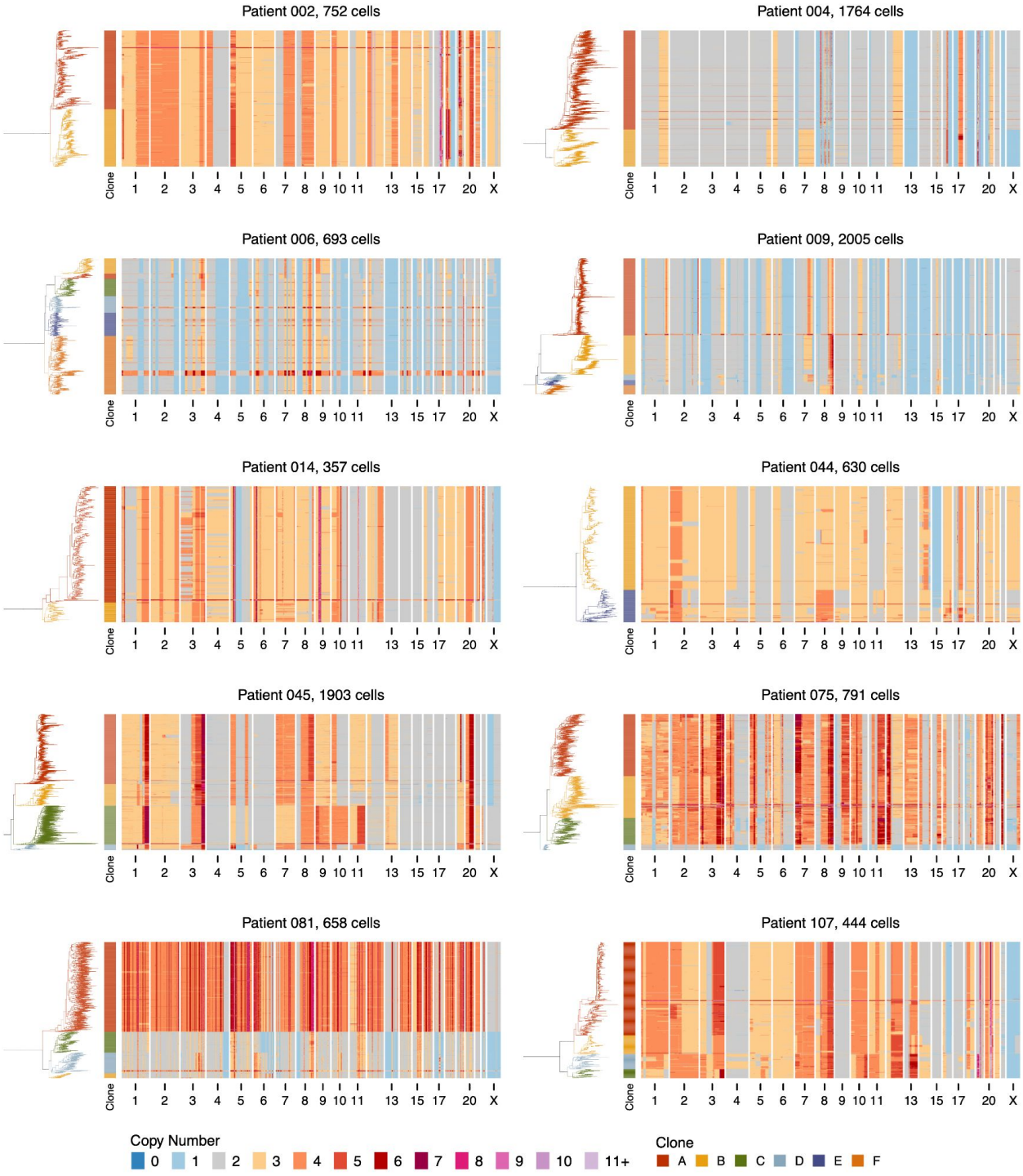

**Supplementary Figure 2**
a) Number of clonal and subclonal SVs per patient b) Total number of SVs called per patient by SV type c) Distribution of coverage per cell per patient d) Pseudobulk coverage per cell (summed coverage across all cells) e) Number of high quality cells per patient



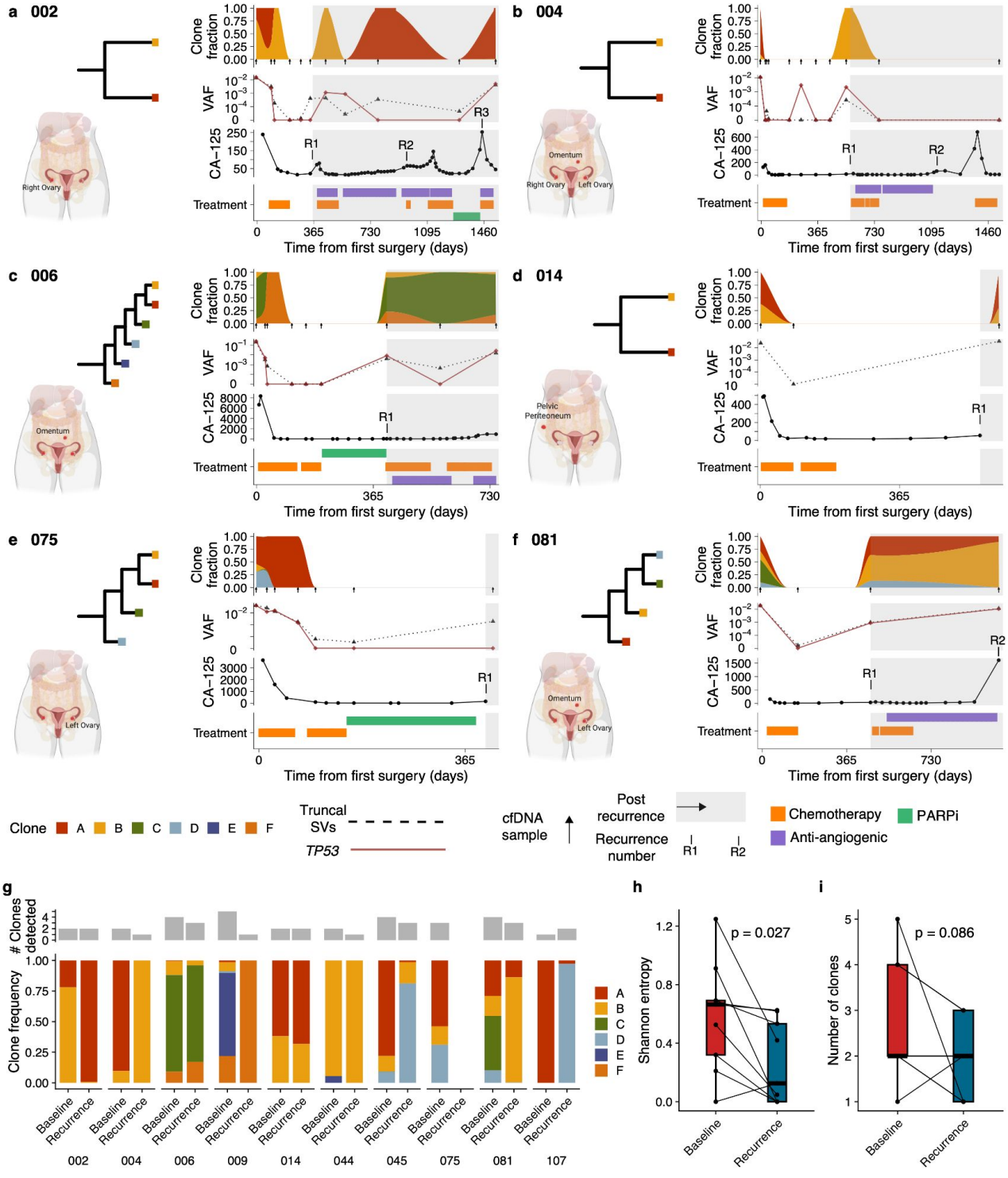

**Supplementary Figure 3**
a) Study summary, showing typical clinical history of HGSOC patient, specimen sample collection protocol. b) Workflow showing clonal evolution tracking using structural variants identified in single-cell whole genome sequencing and assigned to clones using single-cell phylogenetics. These clone specific SVs are then followed in cfDNA using deep duplex error corrected sequencing.



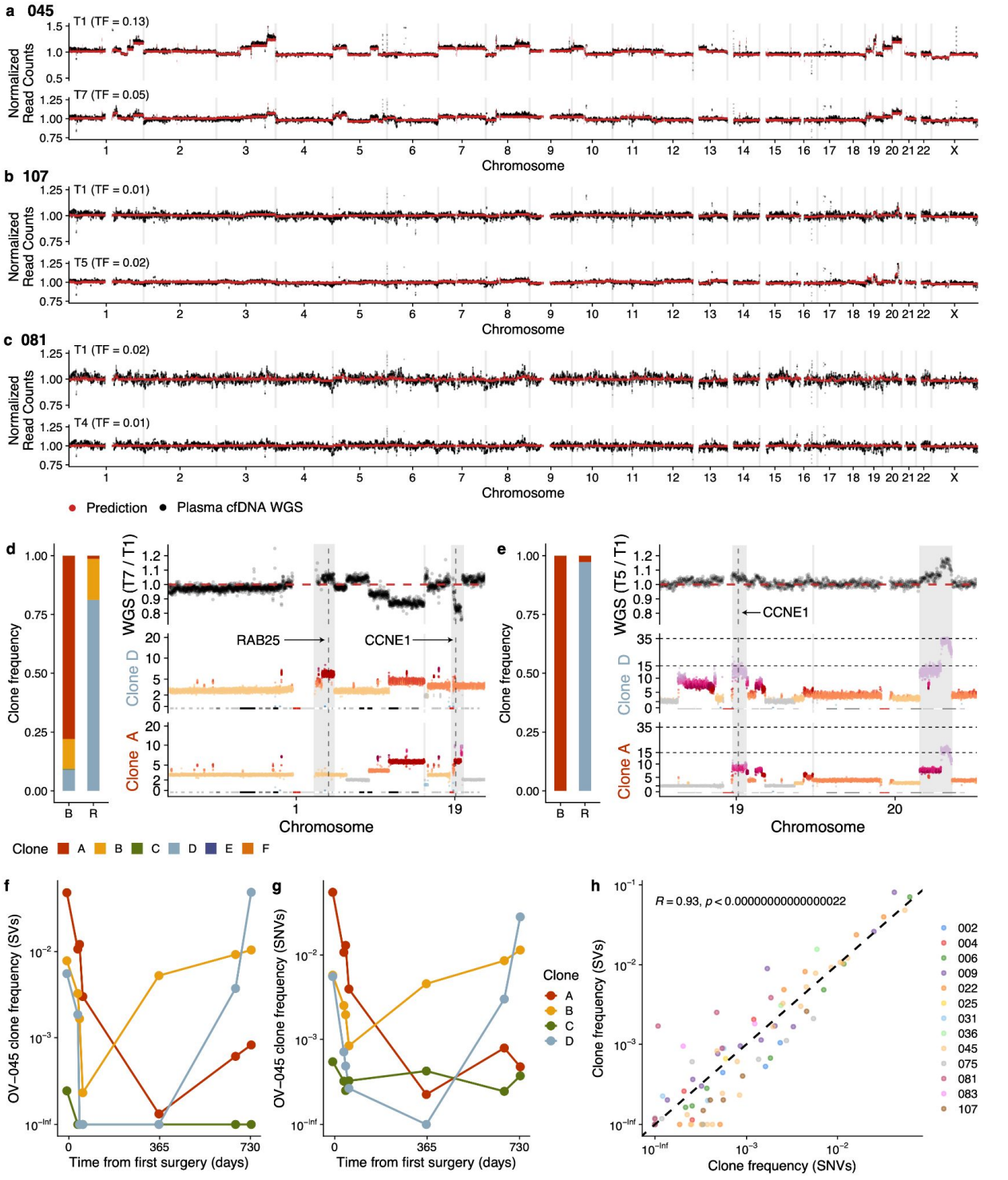

**Supplementary Figure 4**
Copy number plots of chromosome 8 and 19 from OV-004 using 500kb bins a) and 10kb bins b). c) proportion of SVs that could be matched to copy number transitions at 10kb and 500kb bins




**Supplementary Figure 5** scWGS copy number heatmaps and phylogenetic trees for the 10 patients with longitudinal tracking data. The title of each plot gives the patient ID and the total number of cells. Each row shows the copy number profile of a cells, rows are ordered by the MEDICC2 derived phylogenetic tree shown on the left of each plot. Trees are coloured by clone assignments.




**Supplementary Figure 6** Clonal evolution tracking in 6 patients a)-f). For each patient we show the anatomical sites sequenced with DLP, a phylogenetic tree of the clones, then clonal fractions, mean truncal SV VAF and TP53 VAF, CA-125 and treatment history over time. g) Summary of the clonal composition at baseline and recurrence (final time point if more than one post-recurrence time point) for 9 patients. h) Distribution of shannon entropy at baseline and recurrence i) Number of clones detected at baseline and recurrence.




**Supplementary Figure 7** Normalized read counts at baseline and recurrence from whole-genome sequencing of cfDNA from 3 patients a)-c). Black dots are the data, red dots are predictions based on copy number profiles from DLP and inferred tumor and clone fractions from targeted sequencing. The text above each plot denotes the time point and the tumor fraction (TF) based on TP53 mutation. d) Zoom in on regions with high level amplifications in patients 045, left hand bar plots show the clone fractions at T1 and T7 then right hand side show copy number profiles of 2 most abundant clones from DLP at the bottom and ratio of normalized read counts of plasma WGS at T7 vs T1. Shaded areas highlight copy number amplification specific to one of the clones. e) Zoom in on regions with high level amplifications in patient 107. Clone frequencies over time calculated from SVs (f) and SNVs (g) for patient OV-045. c) Scatter plot of all clone frequencies calculated using SNVs and SVs, dashed line indicates y-x line. Included in this plot are clone frequency estimates from samples with purity > 0.1% and clones with at least 4 SVs and SNVs.