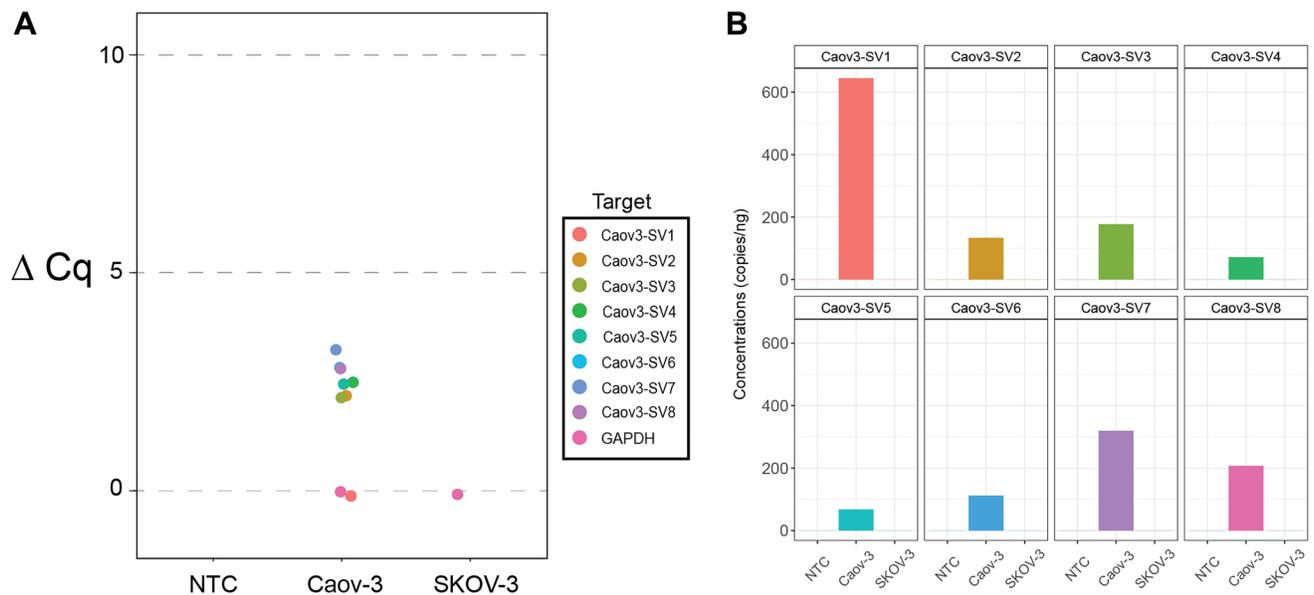
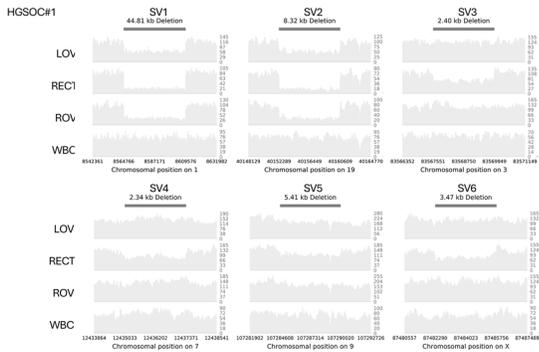
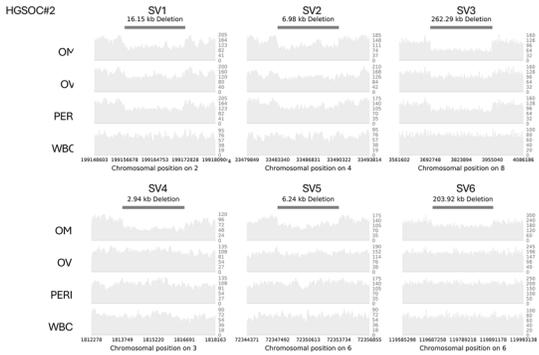
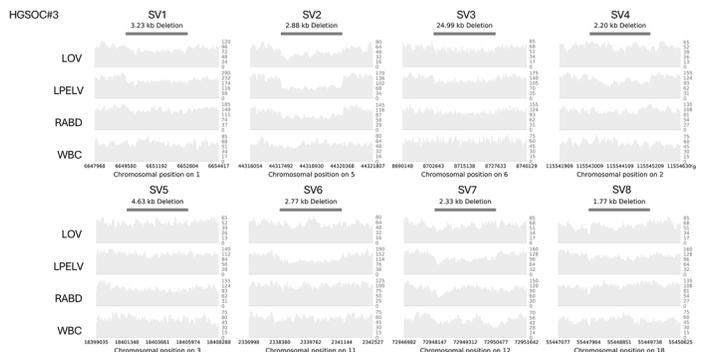
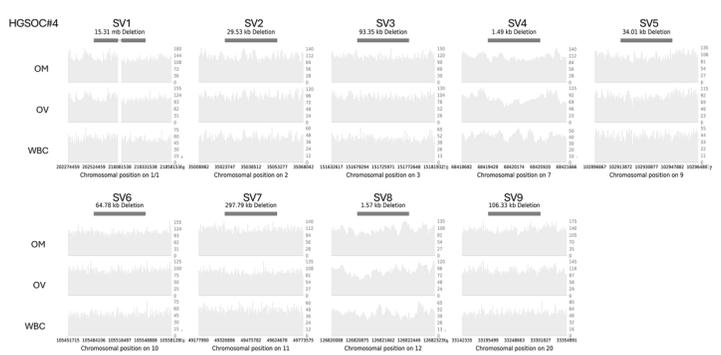


## Tumor-informed liquid biopsy detection of structural variants in high grade serous ovarian cancer

### SUPPLEMENTARY MATERIALS



**Supplementary Figure 1: Optimization of workflow by ovarian cancer cell lines.** (A) Real-time PCR results of targeted Caov-3 SVs.  $\Delta Cq$  ( $\Delta Cq = Cq_{\text{Target}} - Cq_{\text{GAPDH}}$ ) were calculated and compared in synthetic cfDNA of Caov-3 and SKOV-3 (serving as a control). Each dot represents the mean value of three duplicates. NTC (no template control) was used as a control. 8 Caov-3 SVs were tested. (B) Concentrations (copy numbers per ng sample input) of targeted Caov-3 SVs were measured by ddPCR (digital droplet PCR). Each column represents the mean value of three replicates. The same targets and samples were used as in Supplementary Figure 1A.

**A****B****C****D**

**Supplementary Figure 2: Visualization of large deletions using Samplots.** Sequence coverage across selected large deletions (SV) in HGSOC #1-#4 cases is shown for each sampling site (OM, OV, PERI, LOV, RECT, ROV, LPELV, RABD) and white blood cells (WBC). The Y-axis indicates coverage depth. Horizontal grey bars mark the deletion size. **(A)** HGSOC#1: Coverage for SV1–SV6 across four tissues (LOV, RECT, ROV, WBC). **(B)** HGSOC#2: Coverage for SV1–SV6 across four tissues (OM, OV, PERI, WBC). **(C)** HGSOC#3: Coverage for SV1–SV8 across four tissues (LOV, LPELV, RABD, WBC). **(D)** HGSOC#4: Coverage for SV1–SV9 across three tissues (OM, OV, WBC).