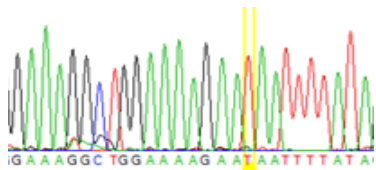
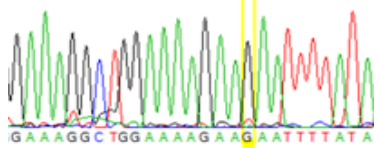
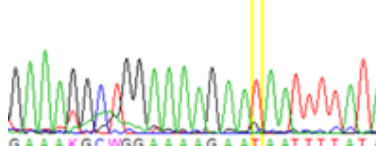
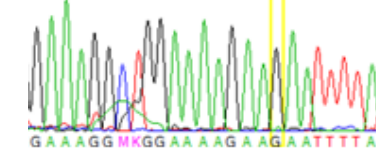
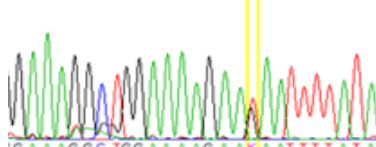
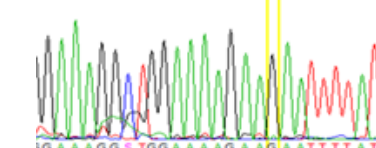
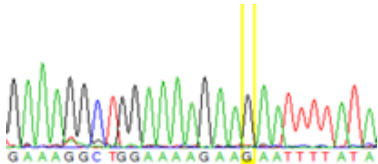
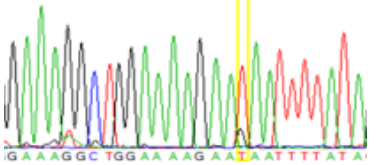
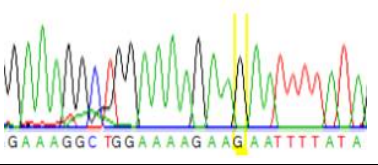
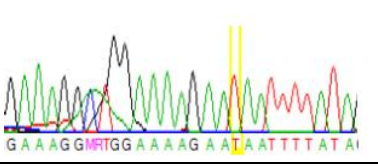
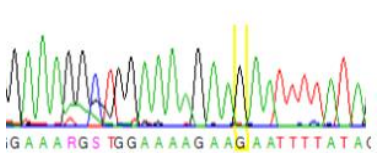


The Combination of Single-Cell and Next-Generation Sequencing Can Reveal Mosaicism for *BRCA2* Mutations and the Fine Molecular Details of Tumorigenesis

Alexandra Gráf, Márton Zsolt Enyedi, Lajos Pintér, Éva Kriston-Pál, Gábor Jaksa, Árpád Bálint, Éva Ezer, Péter Horváth, Farkas Sükösd, Ernő Kiss, and Lajos Haracska

Table S1. The result of Sanger sequencing in the rest of the single normal cells and bulks of 5-10 tumor cells

| Sample type (Approximate number of cells) | Sanger sequencing (yellow box indicates position 7795 of <i>BRCA2</i>) | Presenting allele(s) (At position 7795 of <i>BRCA2</i>) |
|---|---|---|
| Normal (single cell) |  | T |
| Normal (single cell) |  | G |
| Normal (single cell) |  | T |
| Normal (single cell) |  | G |
| Normal (single cell) |  | G/T |
| Normal (single cell) |  | G |

| | | |
|----------------------|---|-----|
| Normal (single cell) |  G A A A G G C T G G A A A A G A A G A A T T T T A T A | G |
| Tumor (5-10 cells) |  G A A A G G C T G G A A A A G A A G A A T T T T A T A | G/T |
| Tumor (5-10 cells) |  G A A A G G C T G G A A A A G A A G A A T T T T A T A | G |
| Tumor (5-10 cells) |  G A A A G G M T G G A A A A G A A T A A T T T T A T A | T |
| Tumor (5-10 cells) |  i G A A A R G S T G G A A A A G A A G A A T T T T A T A | G |