**Supplementary Figure 1.** Molecular karyotype of patients with 11q deletion as represented by circos plots. Each patient code is indicated in the middle of each plot. Allele peaks (inner plots) and weighted Log2ratio (middle plots) information were obtained from Affymetrix software ChAS and further used to generate circos plots.

**Supplementary Figure 2.** Chromothripsis in 11qdel neuroblastoma patients. **A,** molecular karyotype reveals chromothripsis (at least 28 consecutive segmental breaks identified by changes in the Weighted Log2 Ratio coinciding with changes in the profile of Allele Peaks) on chromosome 5 in neuroblastoma TI\_423 and one segmental break in neuroblastoma NBX\_19. **B,** molecular karyotype reveals chromothripsis (at least 13 consecutive segmental breaks identified by changes in the Weighted Log2 Ratio coinciding with changes in the profile of Allele Peaks) on chromosome 17 in neuroblastoma NBX\_19 and two segmental breaks in neuroblastoma TI\_423.

**Supplementary Figure 3**. Molecular karyotype in circos plots of the indicated cell lines. Name of cell line is indicated in the middle of each plot. Allele peaks (inner plots) and weighted Log2ratio (middle plots) information were obtained from Affymetrix software ChAS and further used to generate circus plots.

**Supplementary Figure 4.** Treatment with olaparib and temozolomide induce cell death preferentially in IMR-32, NBL-S and LA-N-1 cell lines. Percentage of dead cells was determined at the indicated days by flow cytometry using LIVE/DEAD Fixable Near-IR Dead Cell Stain Kit (Invitrogen). Significance by t-test analysis was \* p<0.001, \*\* p<0.01.

**Supplementary Figure 5.** SK-N-AS cells have truncated *TP53* lacking exons 10 and 11. PCR from genomic DNA of the indicated cell lines was performed in the presence of 10% DMSO at the annealing temperature 63ºC using the following set of primers: 5’CCAGGGAGCACTAAGCGAGGTA3’, 5’TTTCTTCTTTGGCTGGGGAGAG3’ (exon 9); 5’CCTCCTCTGTTGCTGCAGATCC3’, 5’CAACCTAGGAAGGCAGGGGAGT3’ (exon 10) and 5’GGGCACAGACCCTCTCACTCAT3’, 5’GAGGCTGTCAGTGGGGAACAAG3’ (exon 11).

**Supplementary Table 1.** Summary of clinico-pathological features of 412 neuroblastoma patients included in the study.

**Supplementary Table 2.** Clinico-pathological features in relation to *MYCN* status and 11q status

**Supplementary Table 3.** Potential pathogenic variants detected by next generation sequencing in 17 11q-deleted neuroblastoma patients and functional effect predictions (see tab “Patients”) as well as in neuroblastoma cell lines used in this study (tab “cell lines”).