Supplementary Figure legends

SF1. Reactome-based pathway overrepresentation analysis of genes altered by CNV events in all distant metastases (A) and brain only (B). A binomial test is used to calculate the probability shown for each result, and the p-values are corrected for the multiple testing (Benjamini–Hochberg procedure) that arises from evaluating the submitted list of identifiers against every pathway.

SF2. Differences in the number of altered genes in focused gene lists between CNV "sensitive" and "resistant" IFN-treated samples. Two-sided Mann-Whitney U-test was used for statistical analysis (*p≤0.05, **p≤0.01). The "immune mimicry" pattern 1 is consisted of genes found by Papp et al. (2021) (27), whereas the "immune mimicry" pattern 2 is consisted of genes listed by Timar et al. (2023) (28). Abbreviations: CN- copy number, CNV- copy number variation, DDR – DNA damage response, MMR – mismatch repair, HDR – homologous directed repair, BER – base excision repair, NER – nucleotide excision repair, NHEJ – non-homologous end joining repair

SF3. A) Association of the IFN signature mRNA expression with the overall survival (OS) in immune checkpoint inhibitor (ICI) on-treatment primary melanoma samples (N=87). Data was extracted from the GEO Database under the following GSE accession numbers: GSE91061, GSE115821, GSE2019, GSE165278 and GSE158403. Kaplan-Meier and Cox regression analyses were used, and P-value ≤0.05 is considered statistically significant. B) Downregulation of BCORL1 in prospectively collected ICI-treated lymph node metastases (N=5) compared to naive ones (N=26). P-value ≤0.05 is considered statistically significant.