

Figure S1. Summary of coding somatic variants found on NS-TGCT cohort. **(A)** Frequency and classification of variants found (missense). **(B)** Types of mutational variants most frequently found (SNP). **(C)** Transversions and transitions represented in the cohort **(D)** Variants found per sample (median 27 variants). **(E)** Distribution of variant types found per sample (color scheme is the same as a). **(F)** Top 10 genes mutated on the cohort and mutation types.

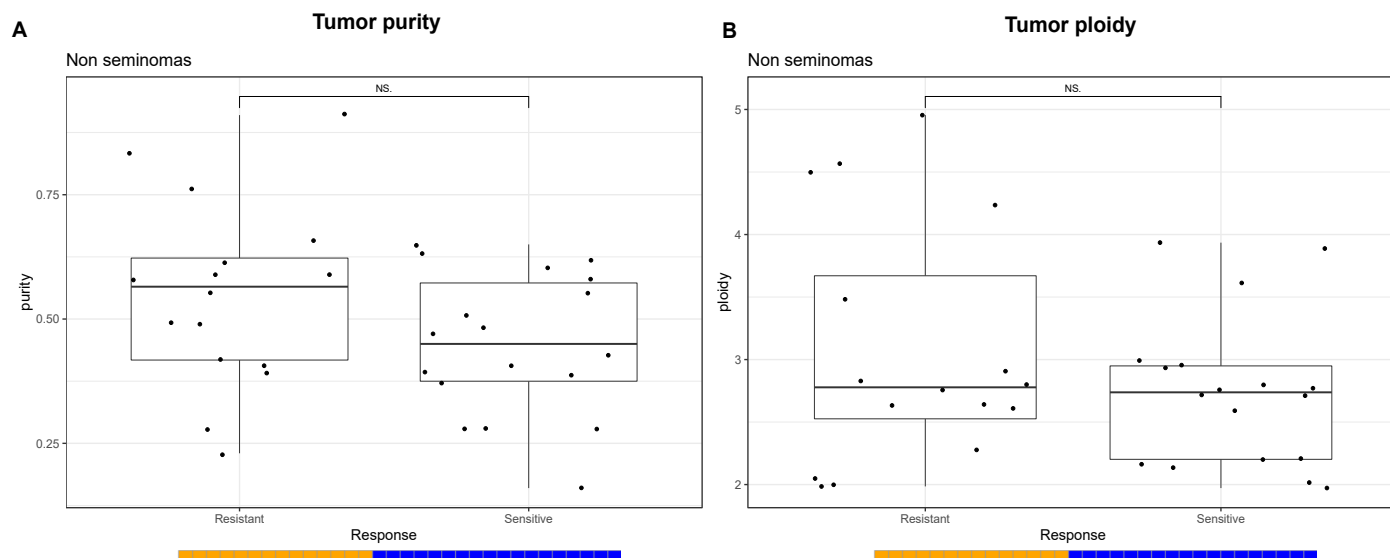
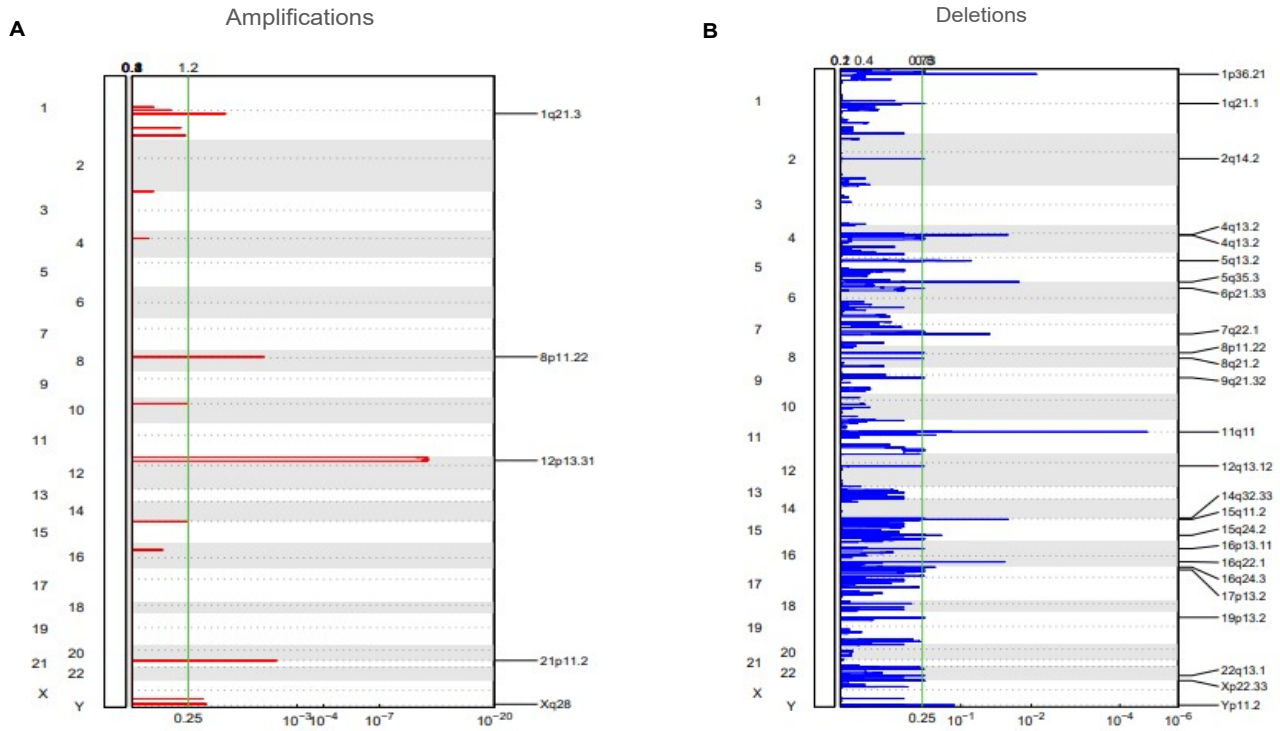


Figure S2. Comparison of tumor ploidy and purity median from the sequenced samples obtained by PureCN analyses. **(A)** Tumoral purity reported for chemoresistant (left, orange) and chemosensitive (right, blue) NS-TGCT. Each dot represents the tumoral purity of the sample where >0.75 implies high tumoral purity and <0.25 represents low purity. **(B)** Tumoral ploidy reported for chemoresistant (left, orange) and chemosensitive (right, blue) NS-TGCT. Each dot represents the tumoral ploidy of the sample where >1 implies high tumoral ploidy and <1 represents low ploidy.

Platinum resistant



Platinum sensitive

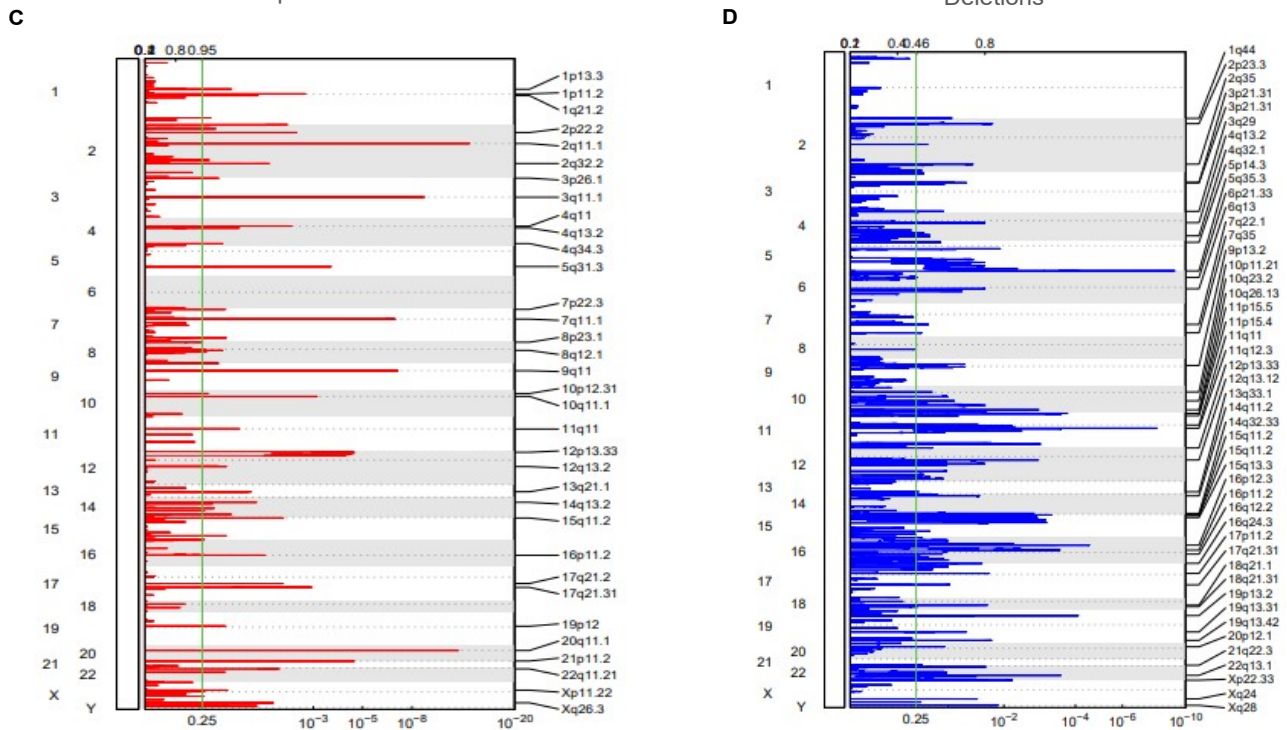


Figure S3. Comparison of amp/del per segment over resistant (up) and sensitive (down) from GISTIC analysis. **(A) & (B)** Amp/Del events (red/blue, respectively) in resistant samples. Left bar represents a total chromosome array, each line indicated are labeled genomic segments and its longitude represents the frequency of each event. G-Score corresponds to the peaks with higher incidences, estimated for gain or loss in those genomic segments. Scheme is the same for **(C) & (D)**. Broadly, the GISTIC plot reveals that platinum-sensitive samples have more gain and loss sites than resistant, and copies are lost in different segments more frequently than are lost.

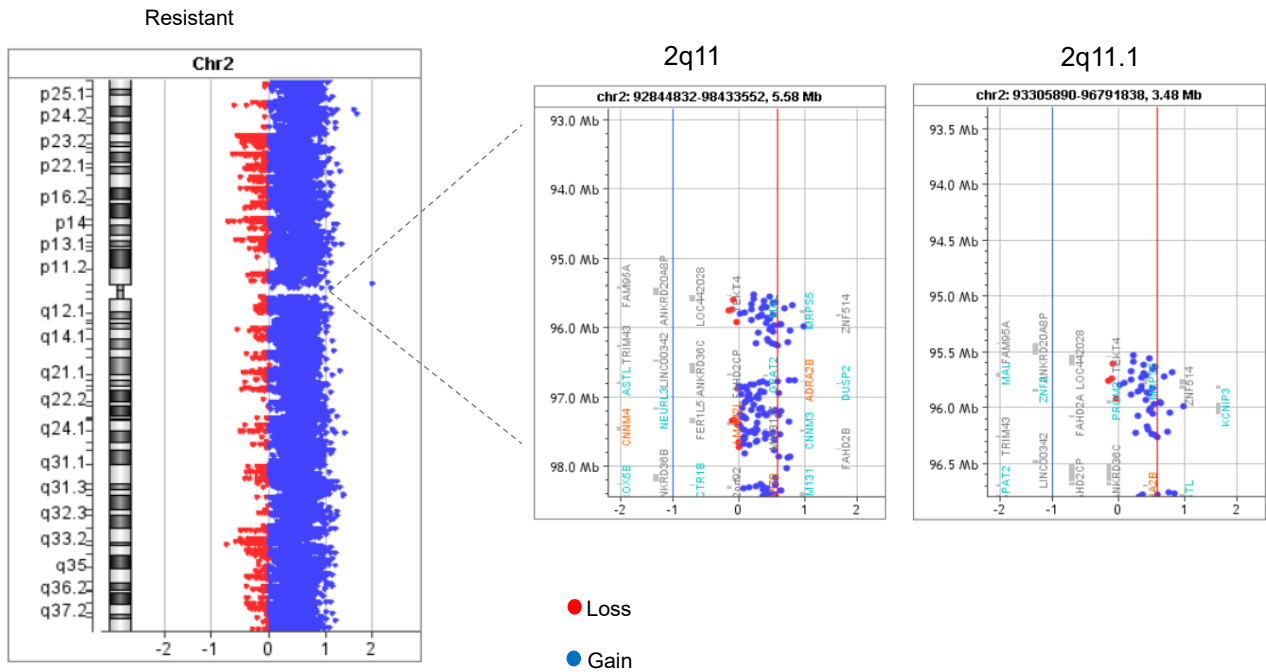
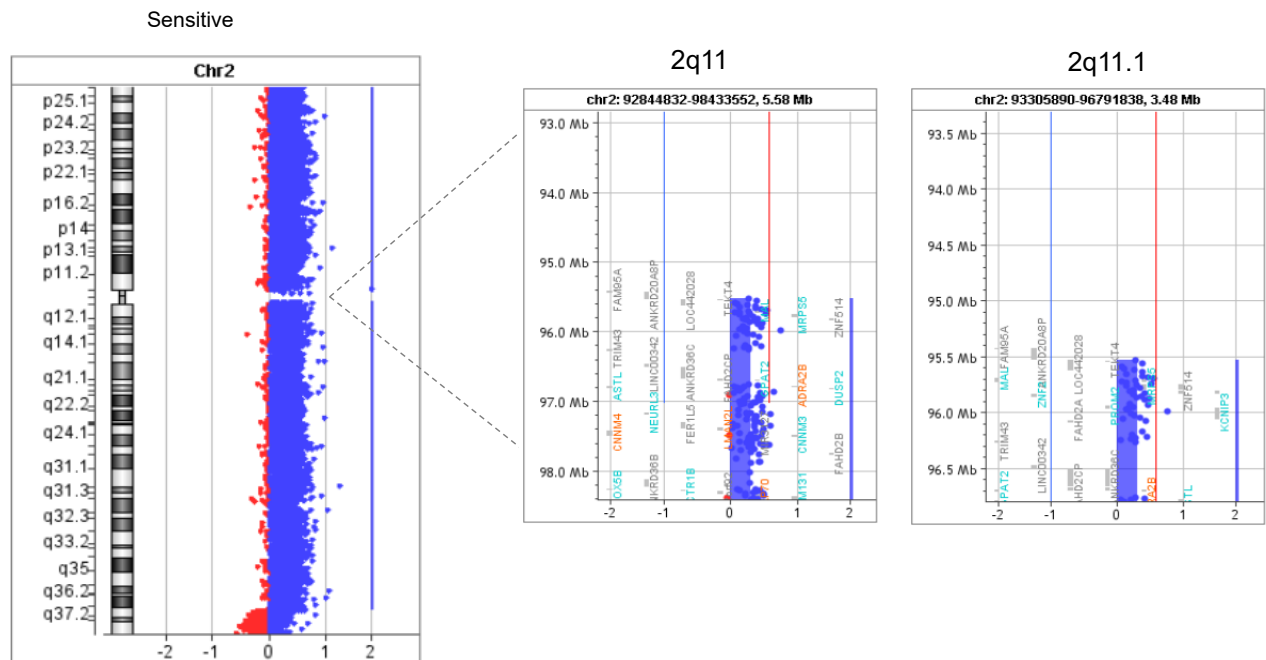
A**B**

Figure S4. Visualization of aCGH in Chr2 region in two samples to compare focal-CNVs in 2q11.1 segment. **(A)** A resistant sample (up) included in aCGH, shows the 2q11.1 segment without gains or losses (blue and red, respectively), **(B)** A sensitive sample (down) included in aCGH shows the constant gains in the 2q11.1 segment in sensitive samples. Both **(A)** and **(B)** shows in right a zoom with the genes contained in the 2q11.1 region.