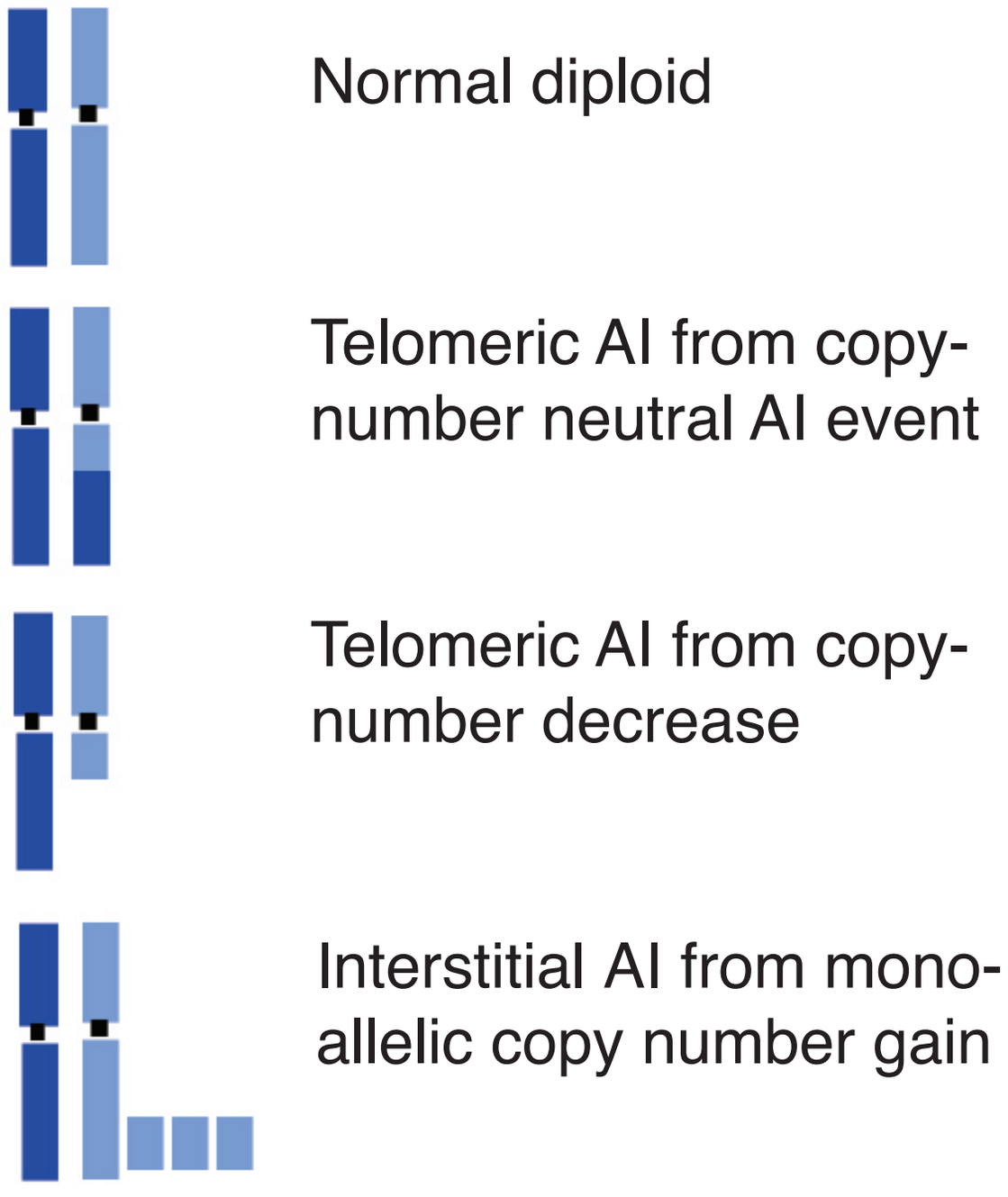


Figure S1. Definition of allelic imbalance.
The diagram shows normal bi-allelic chromosomes and three different ways in which allelic imbalance of a chromosomal region may occur.

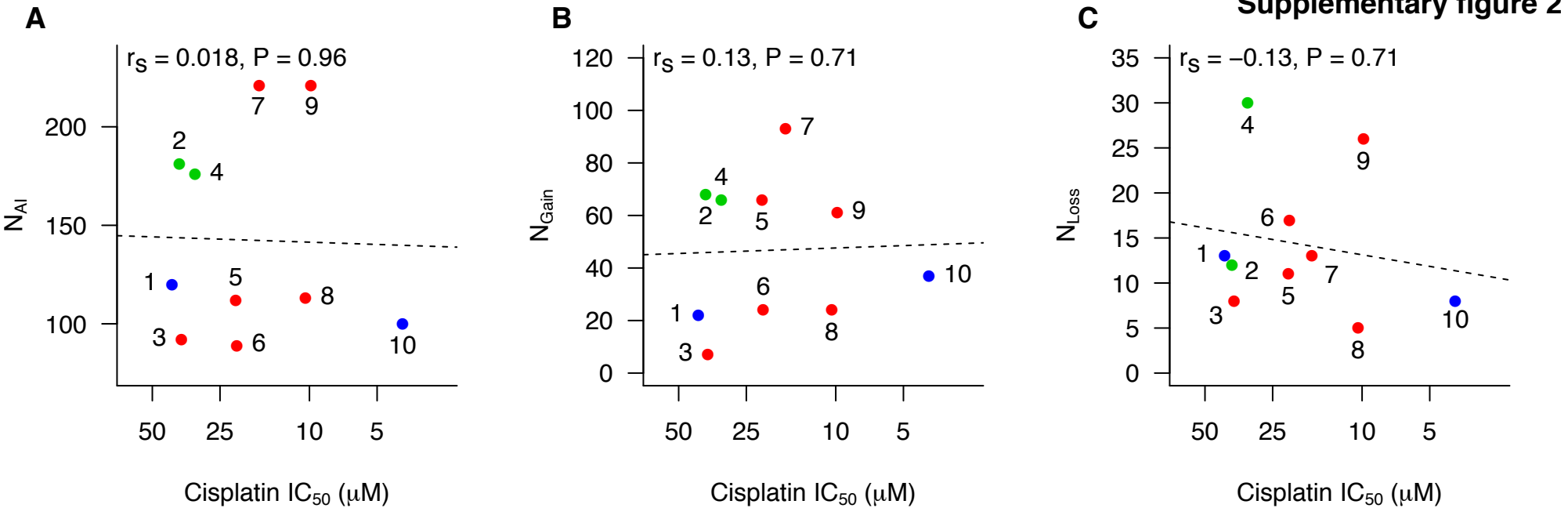


Figure S2. Association between cisplatin sensitivity and measures of genomic abnormalities in a panel of breast cancer cell lines. Cisplatin IC50 versus: **A.** total number of AI regions. **B.** total number of copy number gain regions. **C.** total number of copy number loss regions. Numbers represents the same cell lines as in Figure 1.

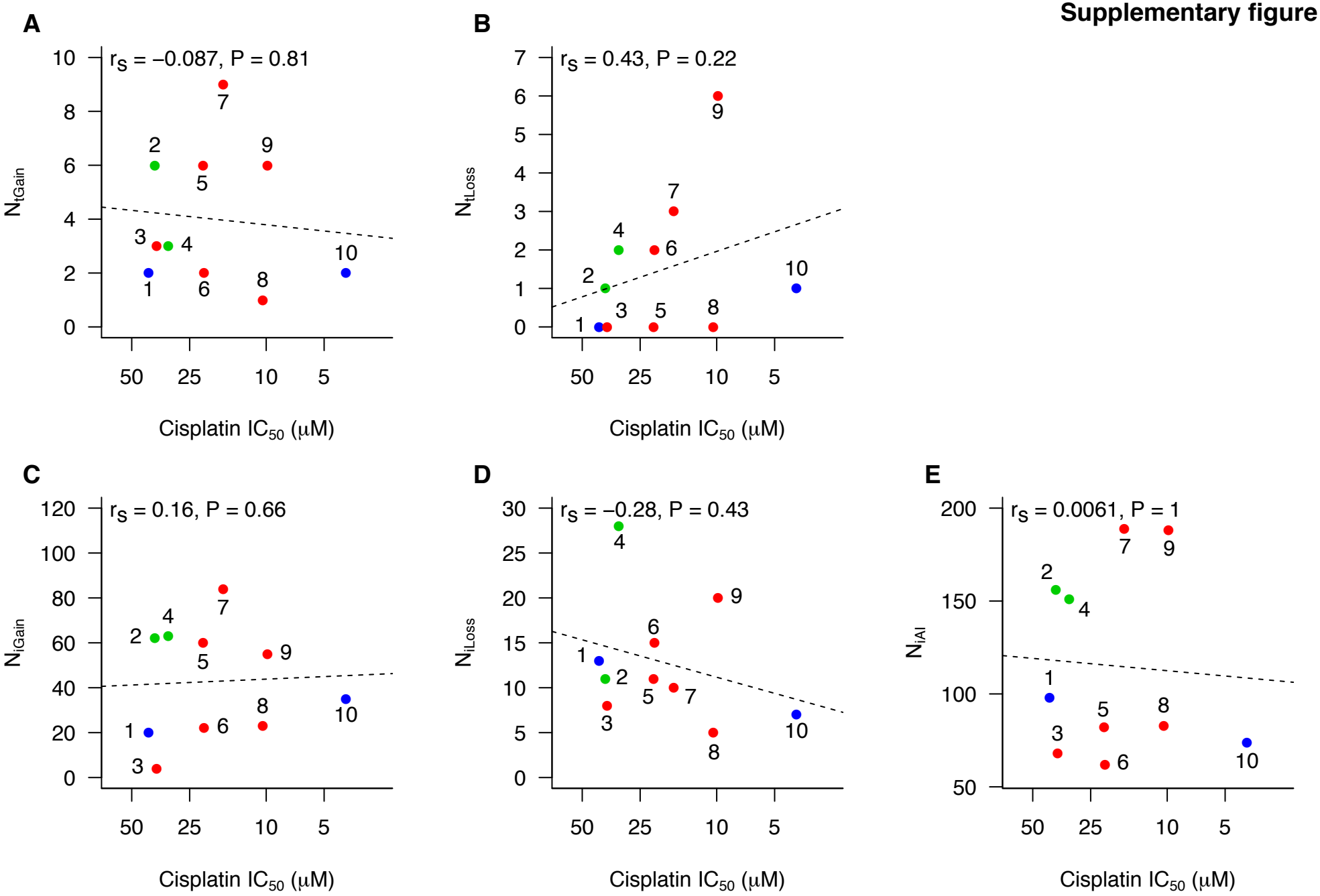


Figure S3. Association between cisplatin sensitivity and telomeric/interstitial gains and losses.
Cisplatin IC50 versus: **A.** number of telomeric copy number gain regions. **B.** number of telomeric copy number loss regions. **C.** number of interstitial copy number gain regions. **D.** number of interstitial copy number loss regions. **E.** number of interstitial AI regions. Numbers represents the same cell lines as in Figure 1.

Supplementary figure 4

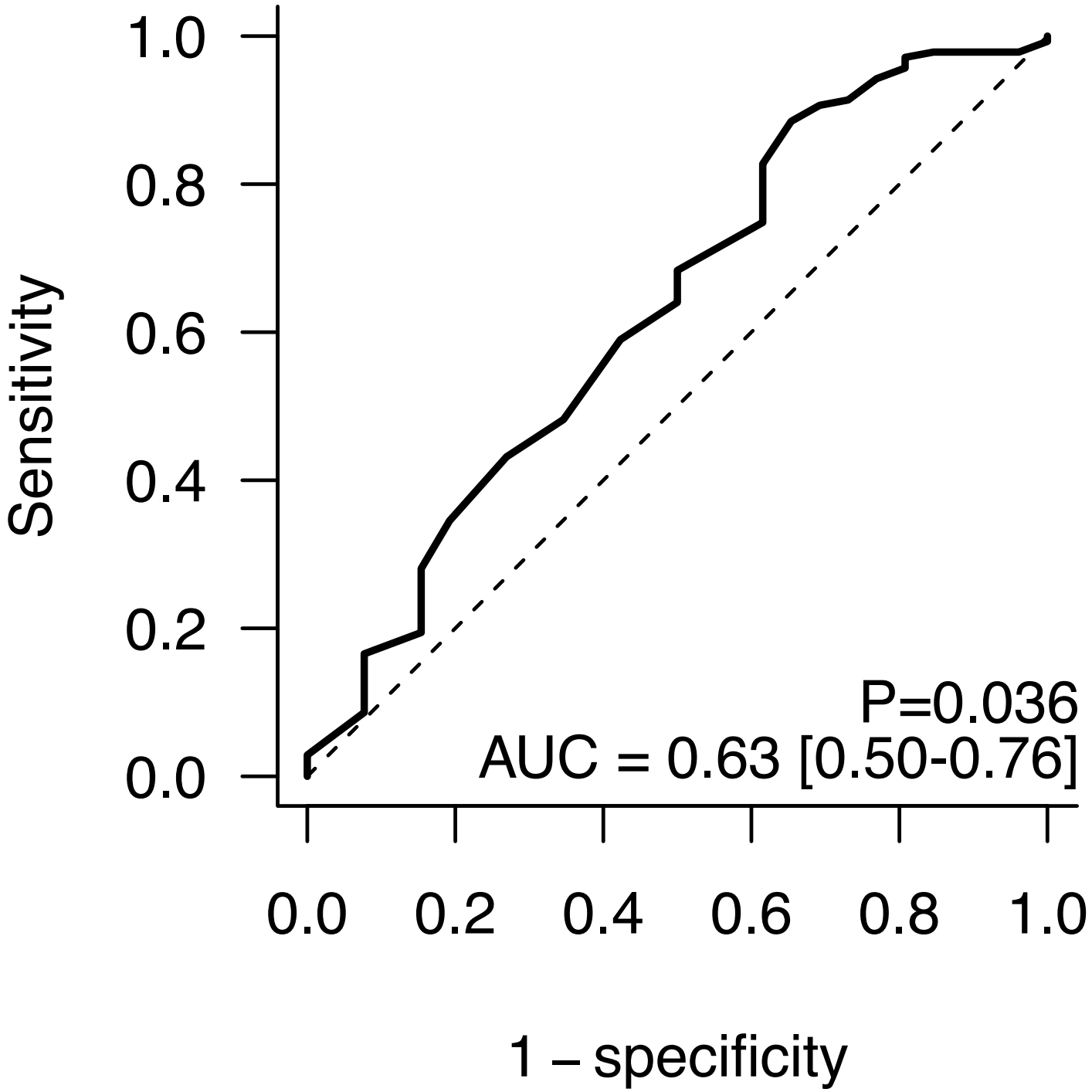


Figure S4. Receiver operating characteristic curve showing the ability of NtAI to predict for sensitivity to platinum-based therapy in wtBRCA serous ovarian cancer.

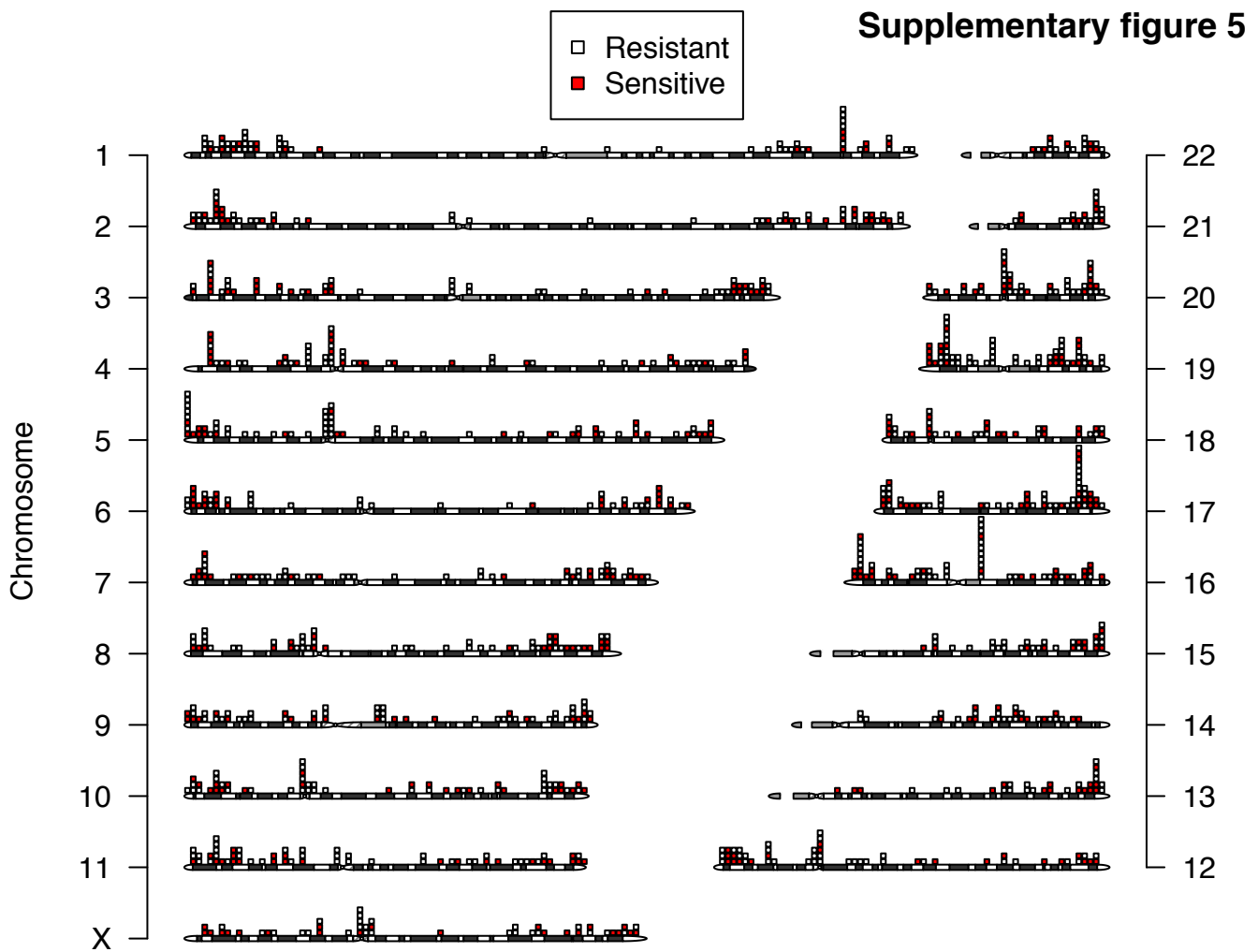
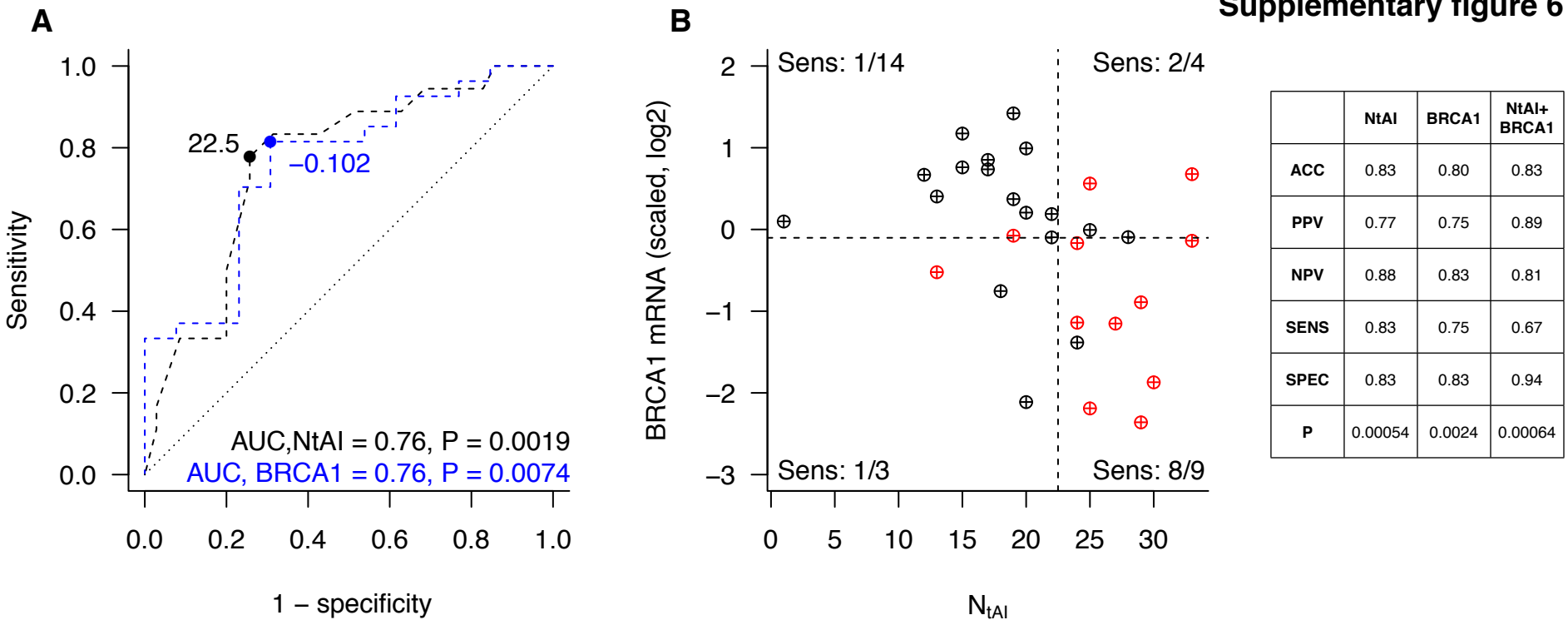


Figure S5. Distribution of dsDNA breaks resulting in telomeric allelic imbalance and association with common CNVs according to cisplatin response

Squares indicate inferred chromosomal location of dsDNA breaks resulting in tAI, pooled from both trials. Stacked squares represent multiple tumors with dsDNA breaks at the same position.

Supplementary figure 6



	NtAI	BRCA1	NtAI+ BRCA1
ACC	0.83	0.80	0.83
PPV	0.77	0.75	0.89
NPV	0.88	0.83	0.81
SENS	0.83	0.75	0.67
SPEC	0.83	0.83	0.94
P	0.00054	0.0024	0.00064

Figure S6. BRCA1 expression and N_tAI versus response to cisplatin in Cisplatin-1 and Cisplatin-2 combined.
A. Identification of the optimum cut-off for N_{tAI} (black) and BRCA1 mRNA (blue) to predict cisplatin response separately. Filled circles represent optimum cut-points. **B.** This panel shows how the combination of BRCA1 expression and N_{tAI} may improve prediction of cisplatin response. Red indicates samples sensitive to cisplatin. Lines represents the optimum cut-off for prediction of response based on N_{tAI} and BRCA1 mRNA, as determined in panel A. “Sens” represents the number of sensitive per total cases shown in each quadrant defined by the N_{tAI} and BRCA1 mRNA cut-offs. The table shows the prediction accuracy based on the defined cut-offs for N_{tAI} alone, BRCA1 mRNA alone, and the two measurements combined. ACC: accuracy. PPV: positive predictive value. NPV: negative predictive value. SENS: sensitivity. SPEC: specificity. P: p-value based on Fishers exact test. This table is based only on the samples shown in panel B.

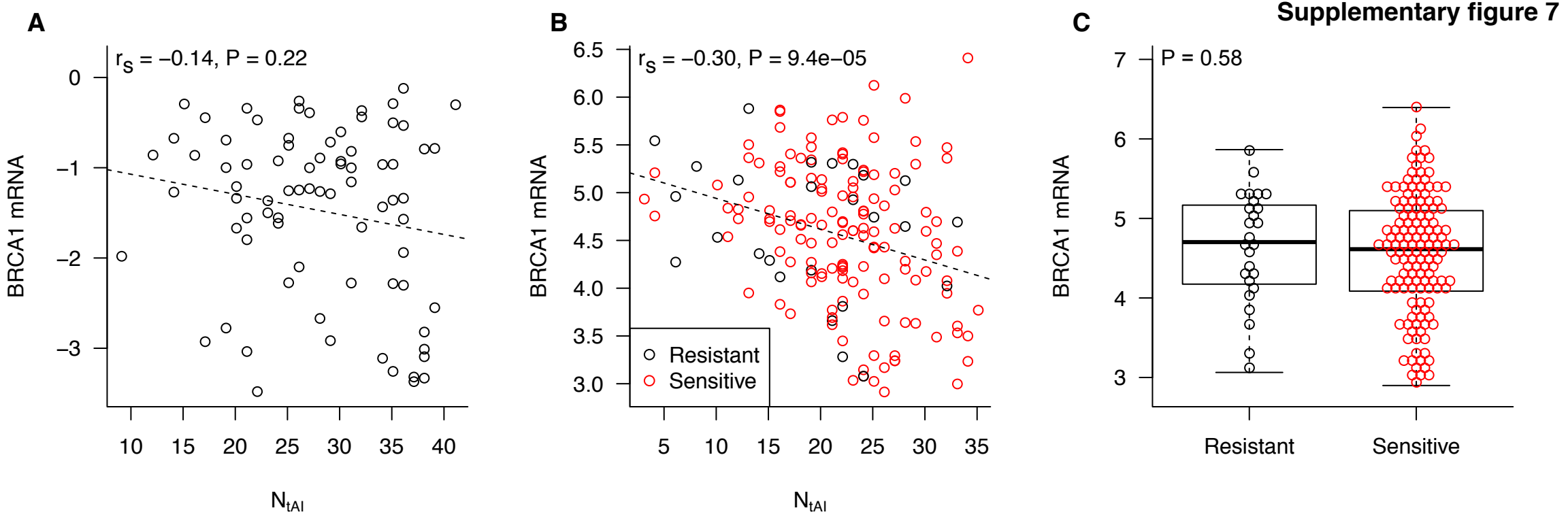


Figure S7. BRCA1 expression by gene expression micro array in TCGA cohorts.
A. BRCA1 mRNA expression versus N_{tAI} in the TCGA ER-/HER2- breast cancers (n=78). **B.** BRCA1 mRNA expression versus N_{tAI} in the TCGA wtBRCA serous ovarian cancers (n=165). **C.** BRCA1 mRNA expression versus treatment response in the TCGA wtBRCA serous ovarian cancers.