

Figure S1. Distribution of domains of various chromatin states relative to TSS. (A) – 4-state model of Lazurite, Aquamarine, Malachite And Ruby states [23,30]. (B) – 5-state model of Yellow, Red, Green, Blue and Black states [33]. Position relative to the TSS is plotted on the X axis. Y axis denotes the number of genes that were marked by a specific chromatin type at a certain position relatively to the TSS.

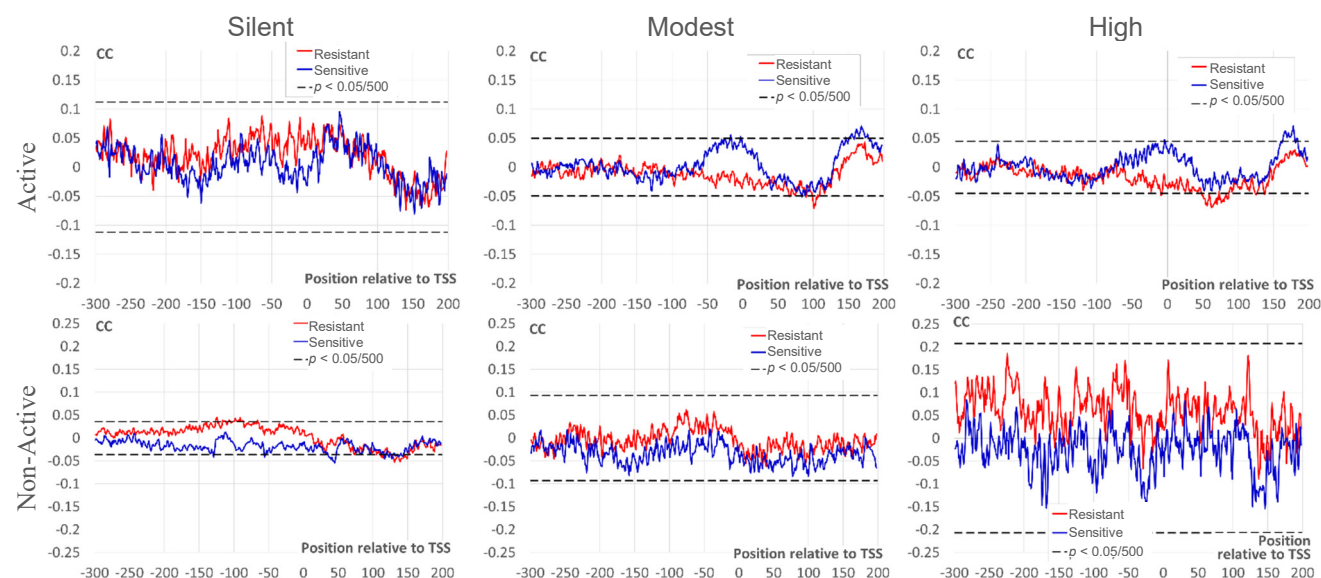


Figure S2. Correlation coefficients between BoE and the number of mapped nucleosomes. The top/bottom rows denote datasets of Active/Non-Active genes (see Materials and Methods). The left, middle and right columns mark intervals of the expression level (RPKM). Axes X show the position relative to TSS, axes Y imply the moving mean for Kendall's rank CC over a window of three nt. Red/blue lines denote resistant/sensitive sites [21]. Dashed black lines mark the threshold of Bonferroni corrected p-value for CC ($p < 0.05/500$). Genes were classified according to the chromatin map [23,30] (see Materials and Methods).

Among silent genes, only Non-Active genes revealed moderately significant positive CC for resistant sites, $[-120; -80]$. Active genes with modest/high RPKM values revealed moderately significant positive CC of sensitive sites just upstream and downstream TSS. Note that respective regions $[-20; +1]$ and $[+160; +180]$ respect to the centers of nucleosomes Nuc-1 and Nuc+1. The linker region $[+50; +85]$ between these nucleosomes shows the negative correlation of the number of resistant sites (high RPKM). Non-Active genes with modest/high RPKM do not show any significant correlations.

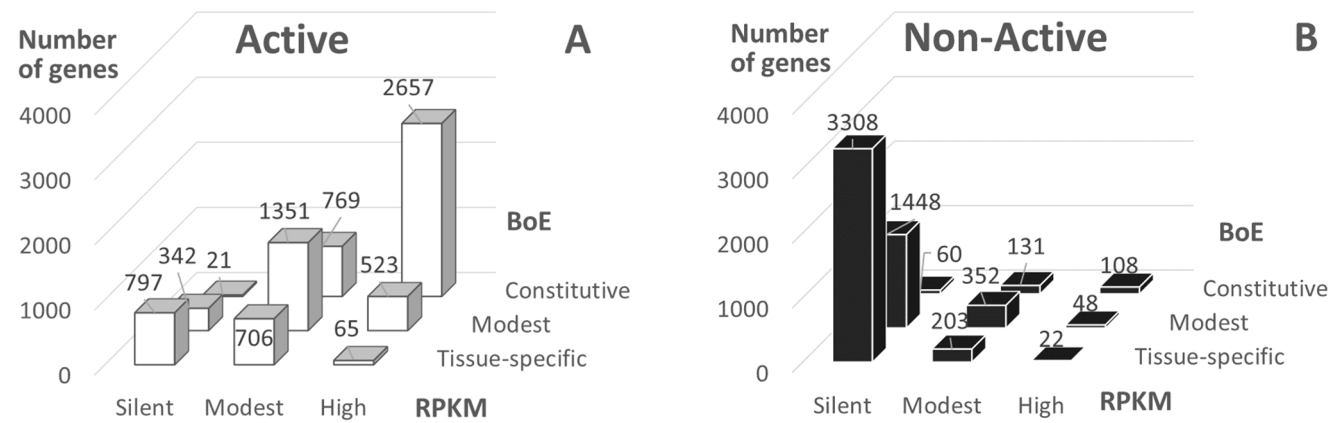


Figure S3. Classification of genes according to expression level (RPKM) and breadth of expression (BoE). BoE was computed for 29 tissues; RPKM values respected to S2 cells; panels (A) and (B) show Active and Non-Active genes classified according to the chromatin map [33] (see Materials and Methods).

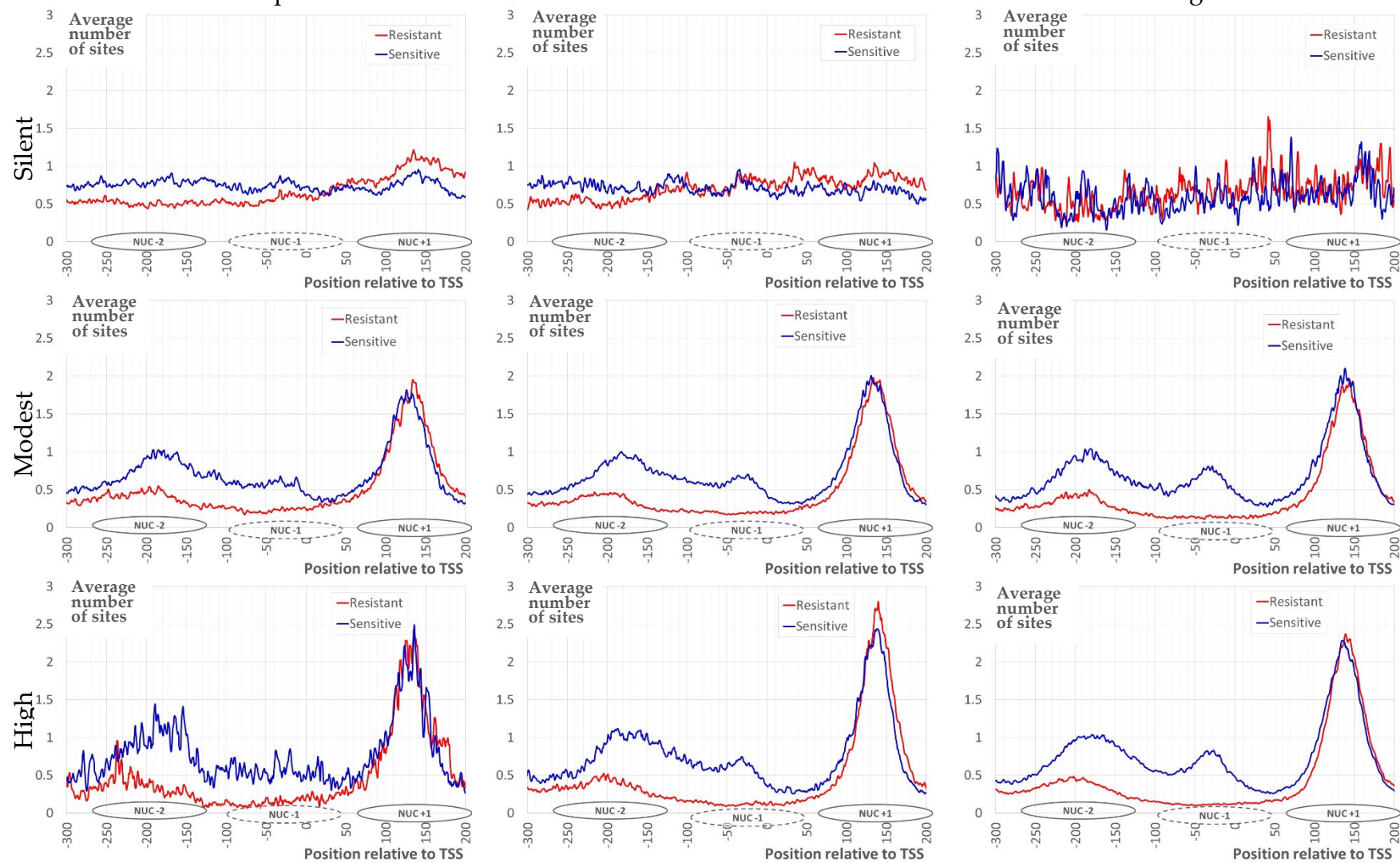
Active

A

Modest

High

Tissue-specific



Non-Active

B

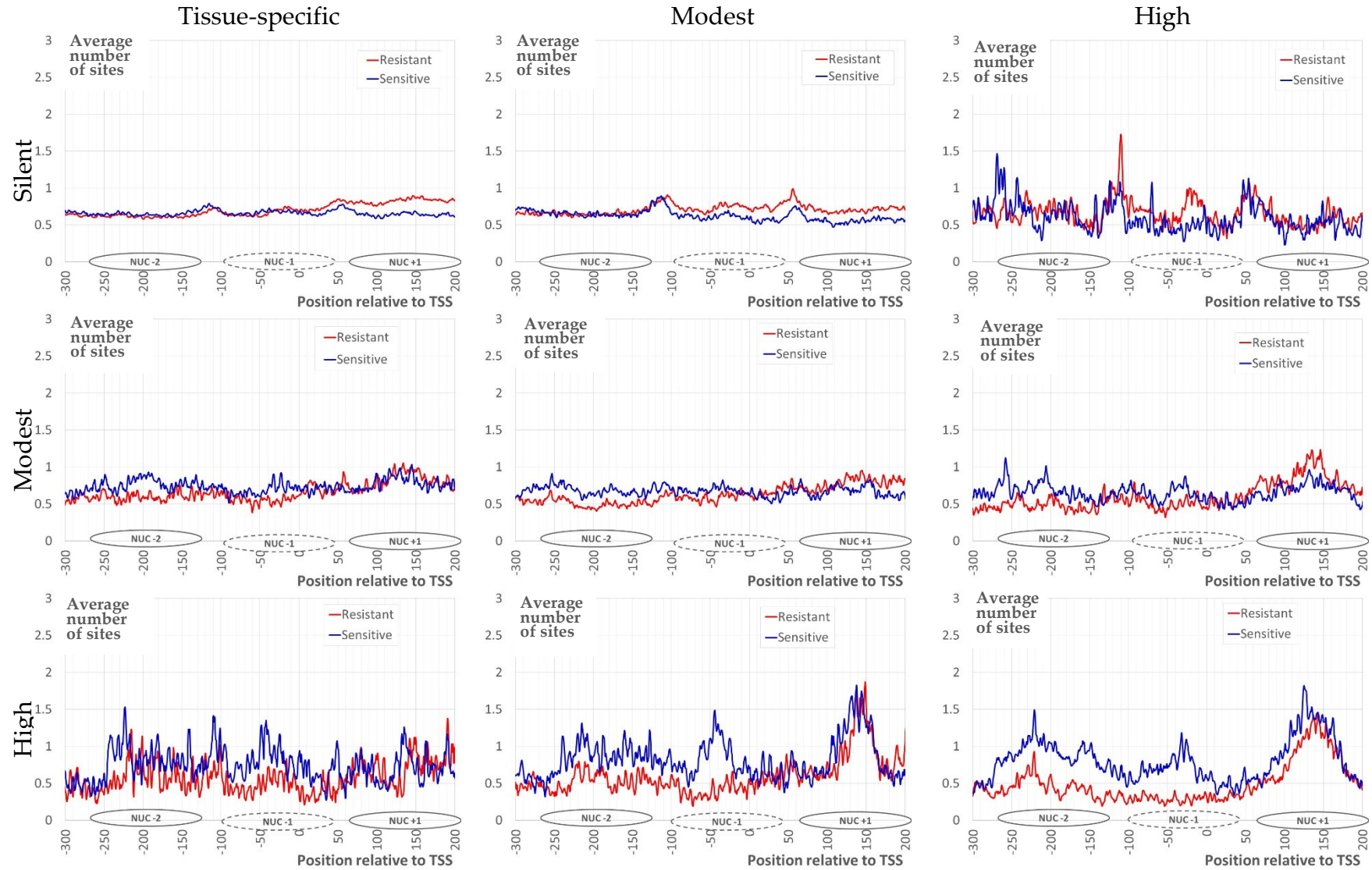


Figure S4. Average numbers of mapped nucleosome sites for Active (A) and Non-Active (B) genes classified according to the chromatin map [33] (see Materials and Methods). Red/blue lines mark resistant/sensitive nucleosomes [21]. Axes X denote the position relative to TSS. Axes Y show the moving mean over a window of 3 nt for average number of nucleosome sites. The headers of columns/rows mean the classification of genes by BoE/RPKM. Ovals near axes X denote approximate positions of nucleosomes upstream (Nuc-2, Nuc-1) and downstream (Nuc+1) TSS.

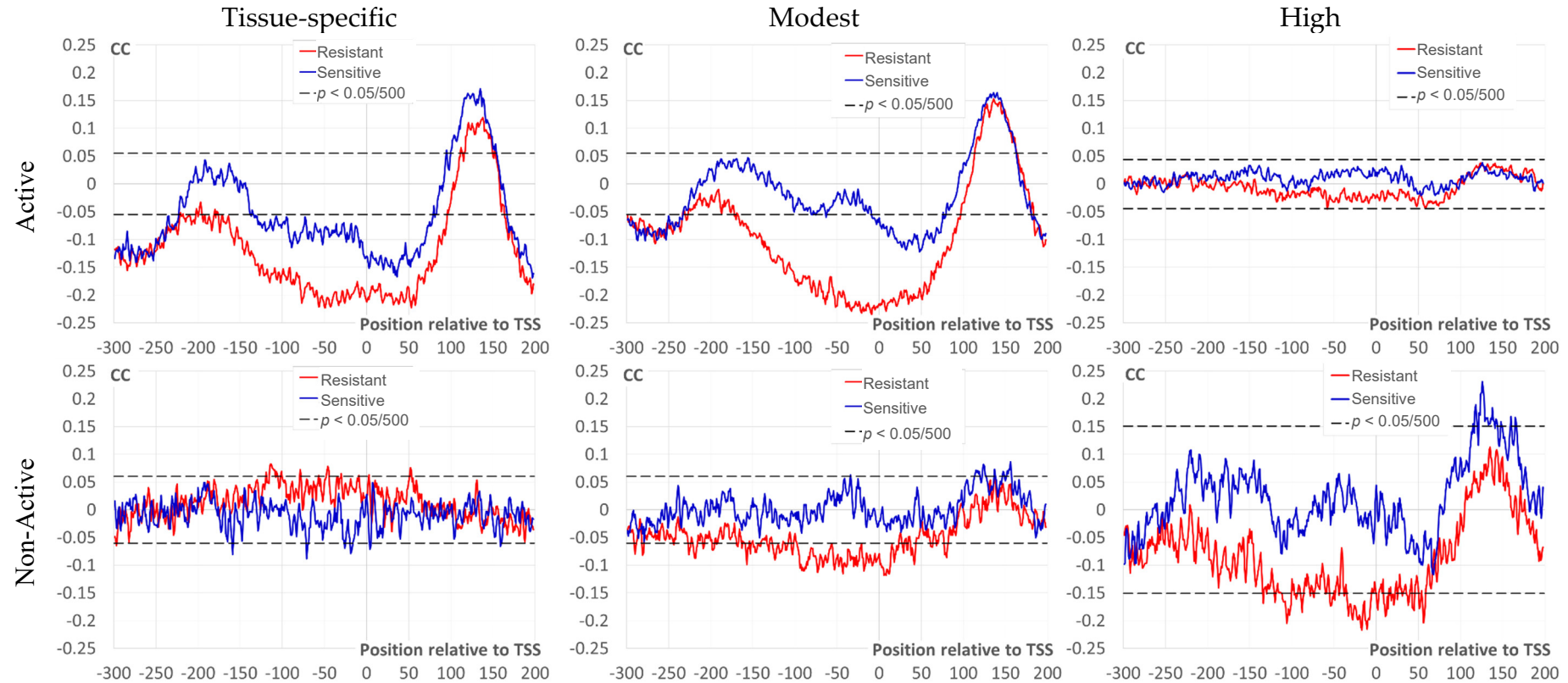


Figure S5. Kendall's rank correlation coefficients between the transcription level (RPKM) and the number of nucleosome sites. The top/bottom rows denote datasets compiles from genes referred to domains of Active (Yellow or Red) / not-Active (Green, Blue or Black) chromatin states [33]. The left, middle and right columns mark intervals of the expression breadth (BoE). Axes X – position relative to TSS, axes Y – the moving mean over a window of 3 nt for the correlation coefficient. Red/blue lines denote resistant/sensitive sites. Dashed black lines mark the threshold of Bonferroni corrected p -value for correlation coefficient ($p < 0.05/500$).

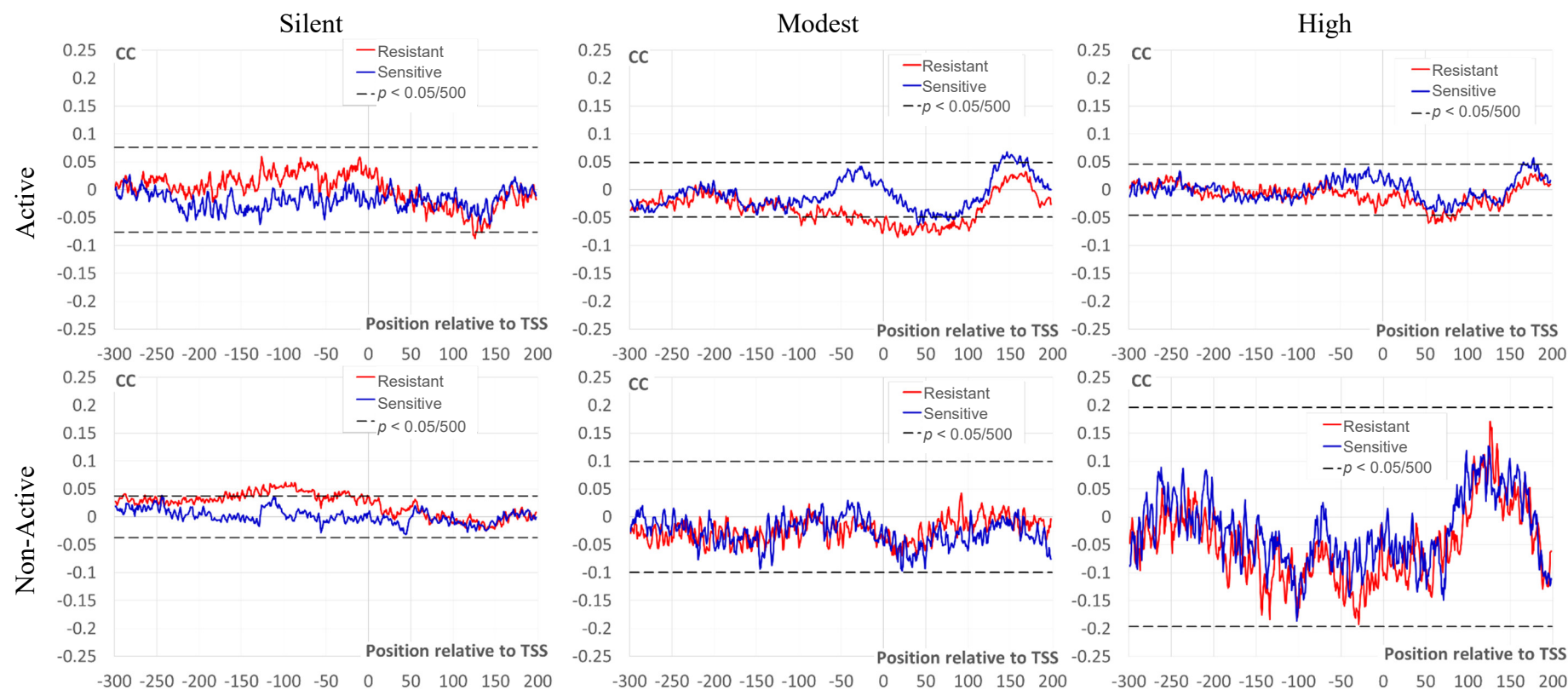


Figure S6. Kendall's rank correlation coefficients between the breadth of expression (BoE) and the number of nucleosome sites. The top/bottom rows denote datasets compiles from genes referred to domains of Active (Yellow or Red) / (Green, Blue or Black) chromatin states [33]. The left, middle and right columns mark intervals of the transcription level (RPKM). Axes X – position relative to TSS, axes Y – the moving mean over a window of 3 nt for the correlation coefficient. Red/blue lines denote resistant/sensitive sites. Dashed black lines mark the threshold of Bonferroni corrected p-value for correlation coefficient ($p < 0.05/500$).