

Figure S1. Scatter plot of β (the estimated slope from the regression model of coverage regressed on the total mapped reads in each exon) and scaling factors (standard deviation of all residuals in each regression model) between two sample preparation methods (robotic and manual).

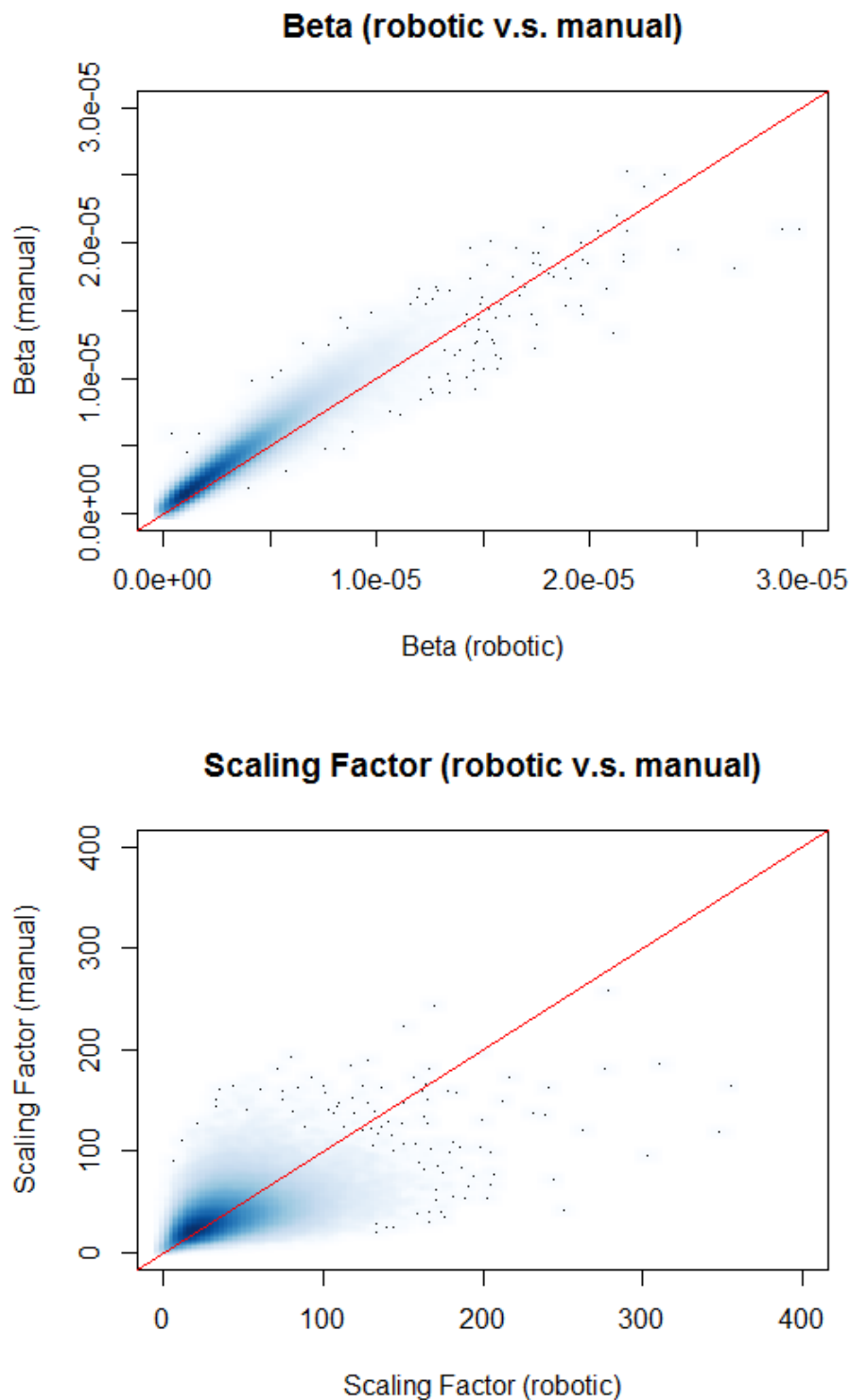


Figure S2. Median standardized residuals of all genes from replicates with manual preparation method.

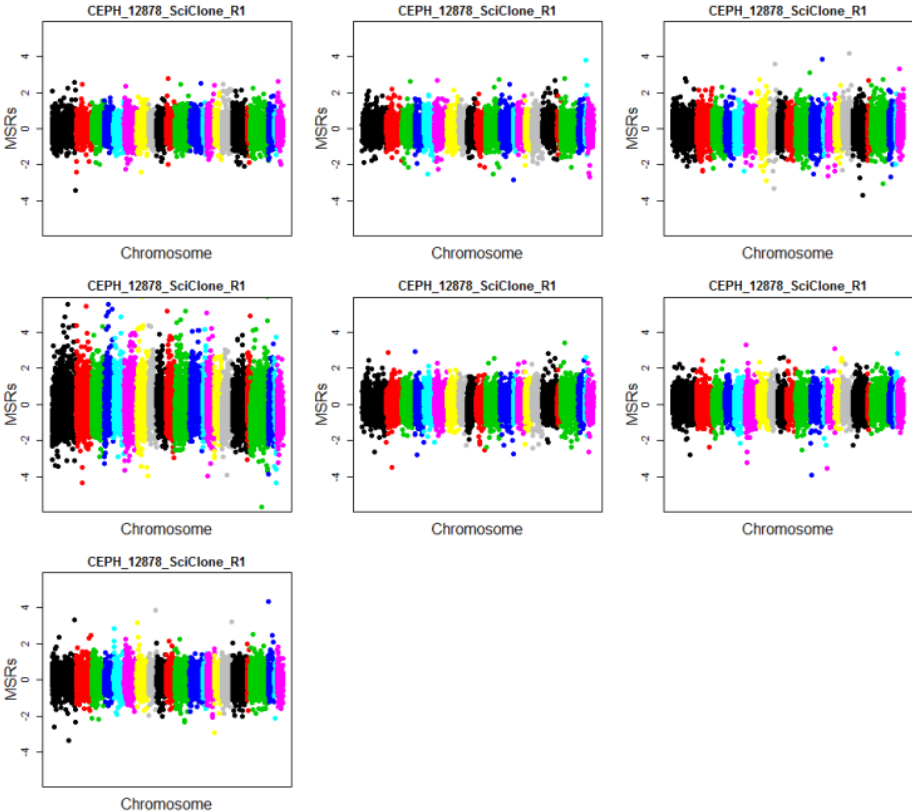


Figure S3. Median standardized residuals of all genes from replicates with robotic preparation method.

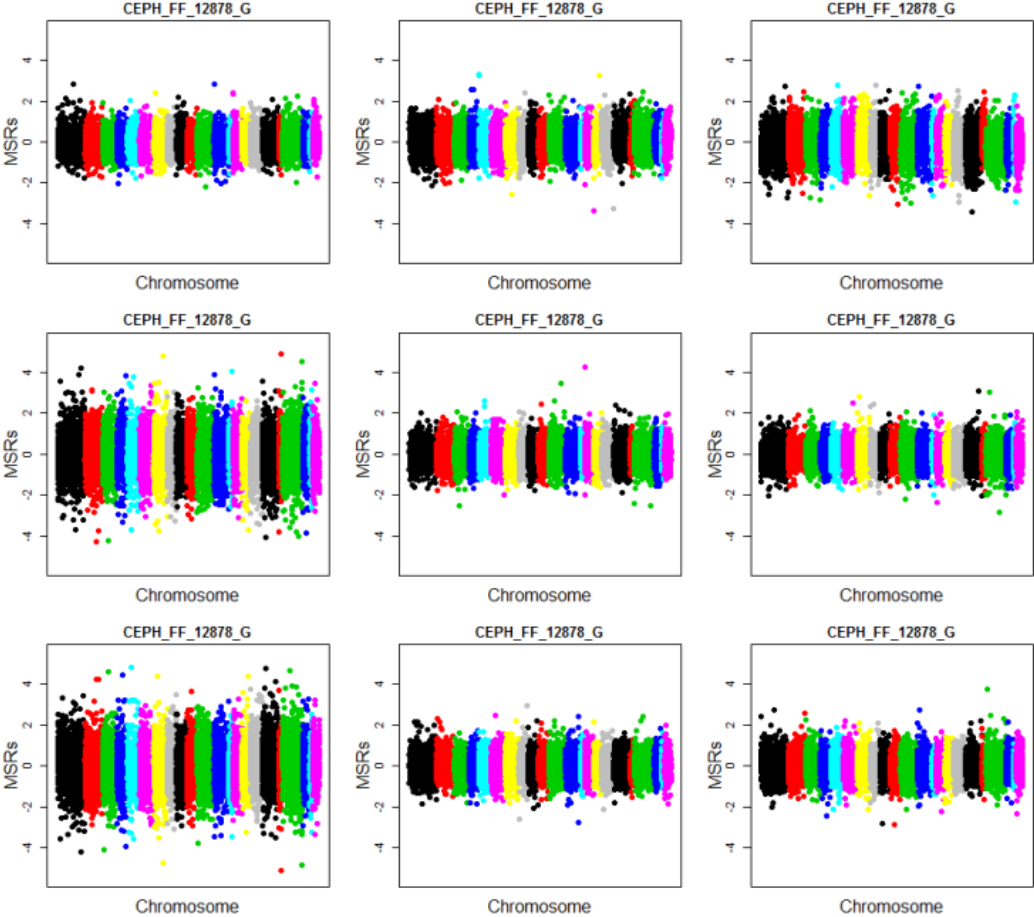


Figure S4. Scatter plot and Spearman's correlation of MSR values and copy numbers reported by CCLE of 10 cancer cell lines. CNV estimates by RefCNV: red (deletion), black (normal) and blue (amplification).

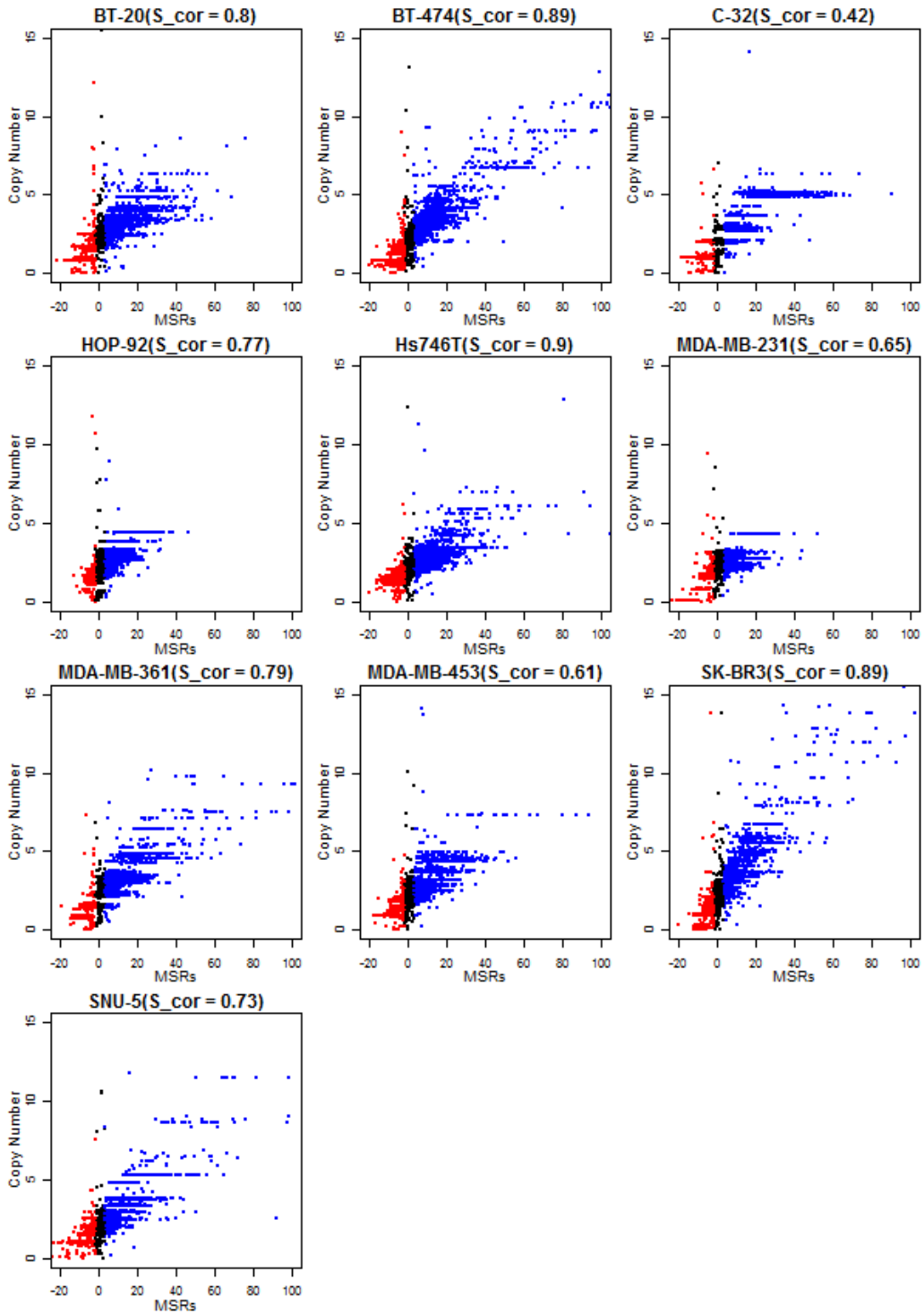


Figure S5. Scatter plot and Spearman's correlation of copy number values of CONTRA and copy numbers reported by CCLE of 10 cancer cell lines.

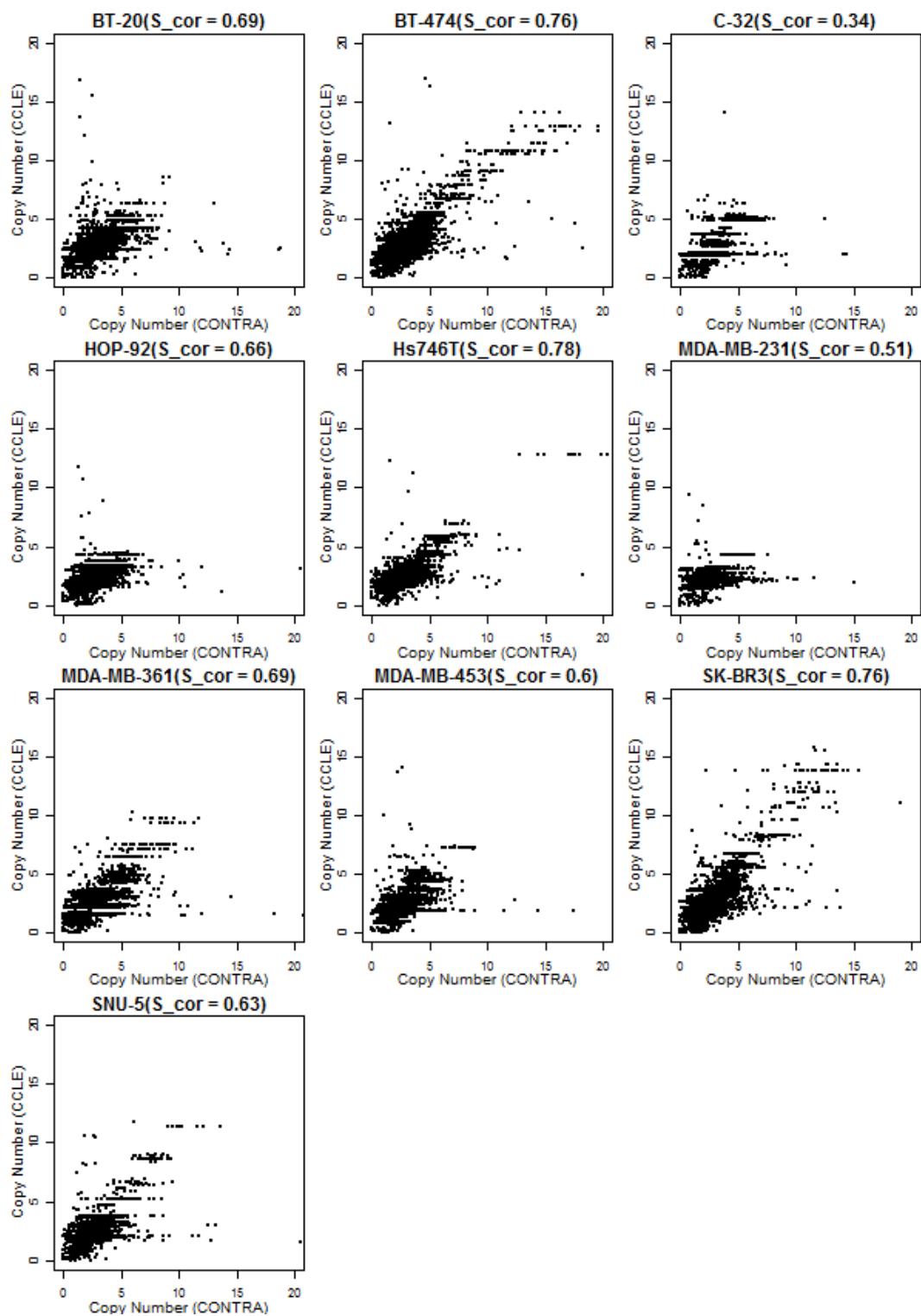


Figure S6. Scatter plot and Spearman's correlation of copy number values of ExomeCNV and copy numbers reported by CCLE of 10 cancer cell lines.

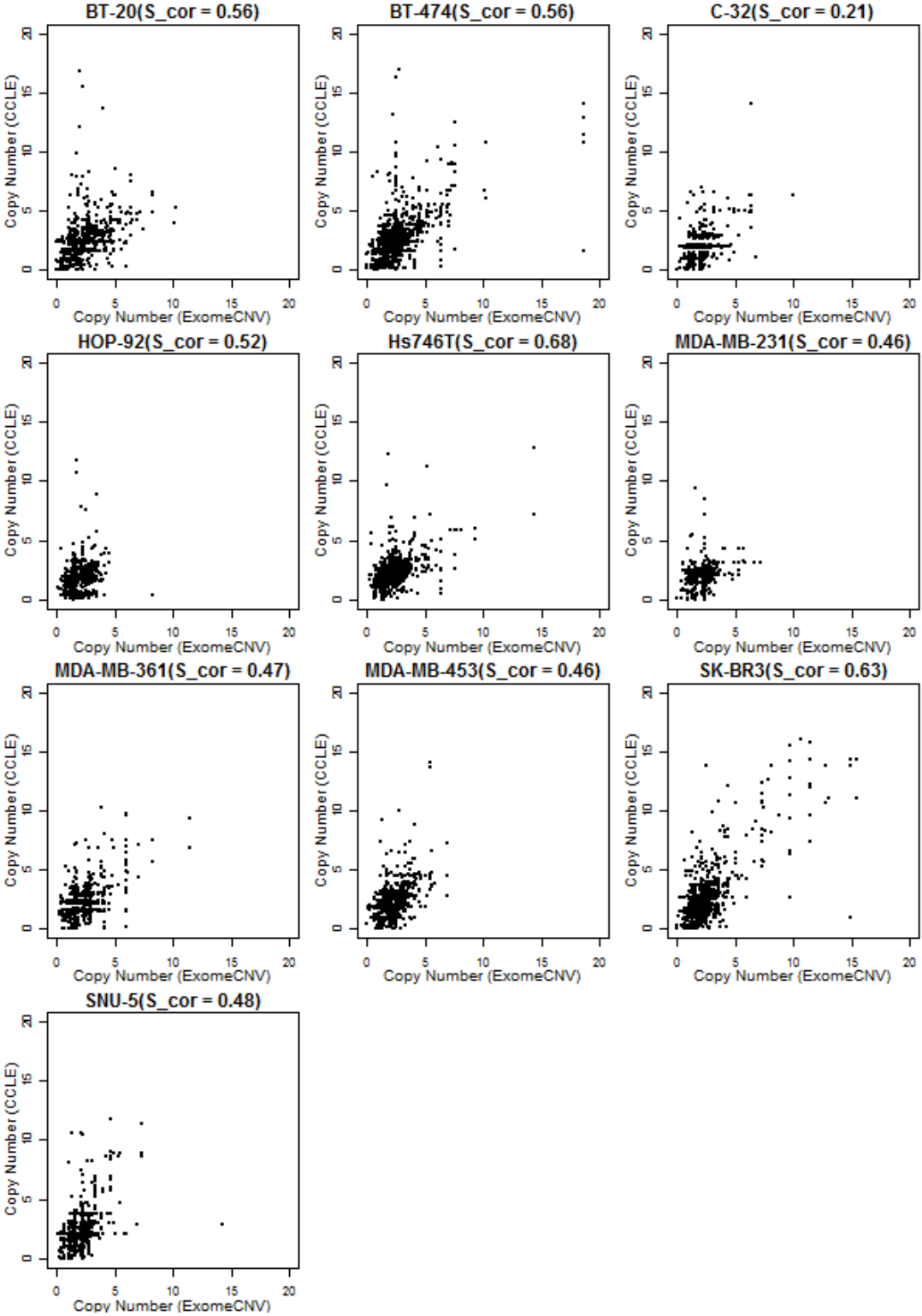


Figure S7. Scatter plot and Spearman's correlation of copy number values of cn.MOPS and copy numbers reported by CCLE of 10 cancer cell lines.

