S3 Table. Correlation between microsatellites, EWS/FLI binding enrichment and EWS/FLI-repressed genes.

Number of microsatellites	**6031**
Corr. of peak fold change and number of consecutive motifs, r (p-value)	0.46 (2.2e-16)
Corr. of peak fold change and total number of motifs, r (p-value)	0.23 (2.2e-16)
Repressed genes	
Number of genes	400
Number of microsatellites	477
Corr. of gene expression and peak fold change r (p-value)	-0.03 (0.51)
Corr. of peak fold change and number of consecutive motif, r (p-value)	0.39 (2.2e-16)
Corr. of peak fold change and total number of motif, r (p-value)	0.21 (3.1e-06)
Corr. of gene expression and number of consecutive motif r (p-value)	-0.06 (0.21)
Corr. of gene expression and number of total motif r (p-value)	-0.02 (0.62)
Promoter-like microsatellites	
Number of genes	49
Number of microsatellites	52
Corr. of gene expression and peak fold change, r (p-value)	0.12 (0.41)
Corr. of peak fold change and number of consecutive motif, r (p-value)	0.18 (0.19)
Corr. of peak fold change and total number of motif, r (p-value)	0.06 (0.66)
Corr. of gene expression and number of consecutive motif, r (p-value)	-0.22 (0.12)
Corr. of gene expression and total number of motif, r (p-value)	-0.04 (0.79)
Enhancer-like microsatellites	
Number of genes	357
Number of microsatellites	425
Corr. of gene expression and peak fold change, r (p-value)	-0.05 (0.33)
Corr. of peak fold change and number of consecutive motif, r (p-value)	0.40 (2.2e-16)
Corr. of peak fold change and total number of motif, r (p-value)	0.22 (3.0e-6)
Corr. of gene expression and number of consecutive motif, r (p-value)	-0.04 (0.43)
Corr. of gene expression and total number of motif, r (p-value)	-0.02 (0.68)