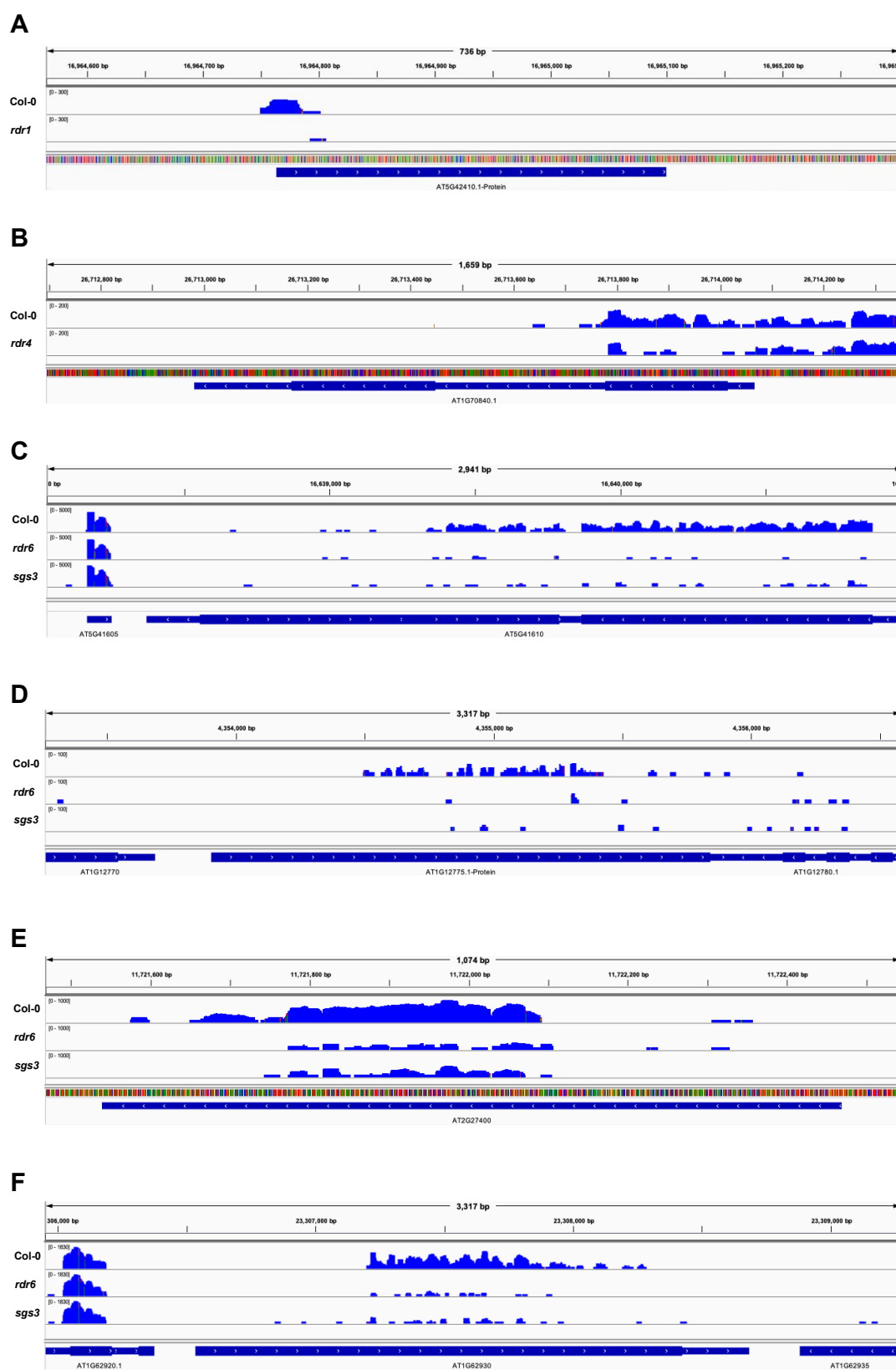
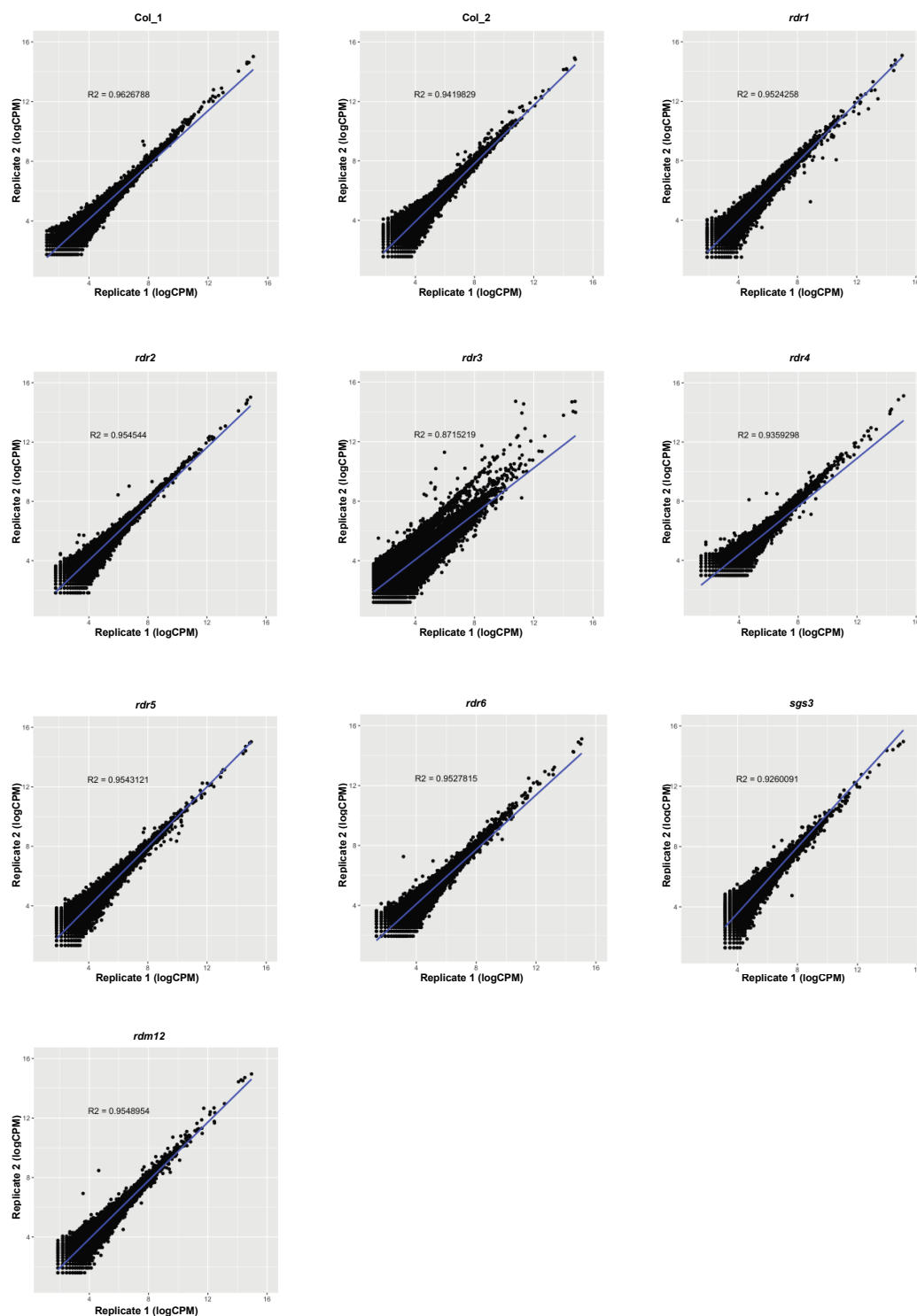


**Figure S1. Correlation analysis of smRNA-seq libraries.** X-axis and y-axis indicate logCPM (Counts Per Million mapped reads) of smRNA-seq libraries using the R package edgeR. Genotypes for the smRNA-seq libraries are shown above each scatter plot, Col\_1 are Col-0 samples prepared with *rdr1*, 2, 4 – 6, *sgs3*, and *rdm12*, Col\_2 are Col-0 samples prepared with *rdr3* mutants. Coefficient of correlation ( $R^2$ ) are shown on each plot.



**Figure S2.** Browser views at example transcripts demonstrating loss of smRNA enrichment in mutants compared to Col-0. Each mutant genotype is indicated on the left of each browser window. Example transcripts are (A) *AT5G42410*, (B) *AT1G70840*, (C) Antisense of a gene *AT5G41610*, (D) *AT1G12775*, (E) *AT2G27400*, and (F) *AT1G62930*.



**Figure S3. Correlation analysis of total RNA-seq libraries.** X-axis and y-axis indicate logCPM (Counts Per Million mapped reads) of total RNA-seq libraries using the R package edgeR. Genotypes for the total RNA-seq libraries are shown above each scatter plot, Col\_1 are Col-0 samples prepared with *rdr1*, 2, 4 – 6, *sgs3*, and *rdm12*, Col\_2 are Col-0 samples prepared with *rdr3* mutants. Coefficient of correlation ( $R^2$ ) are shown on each plot.