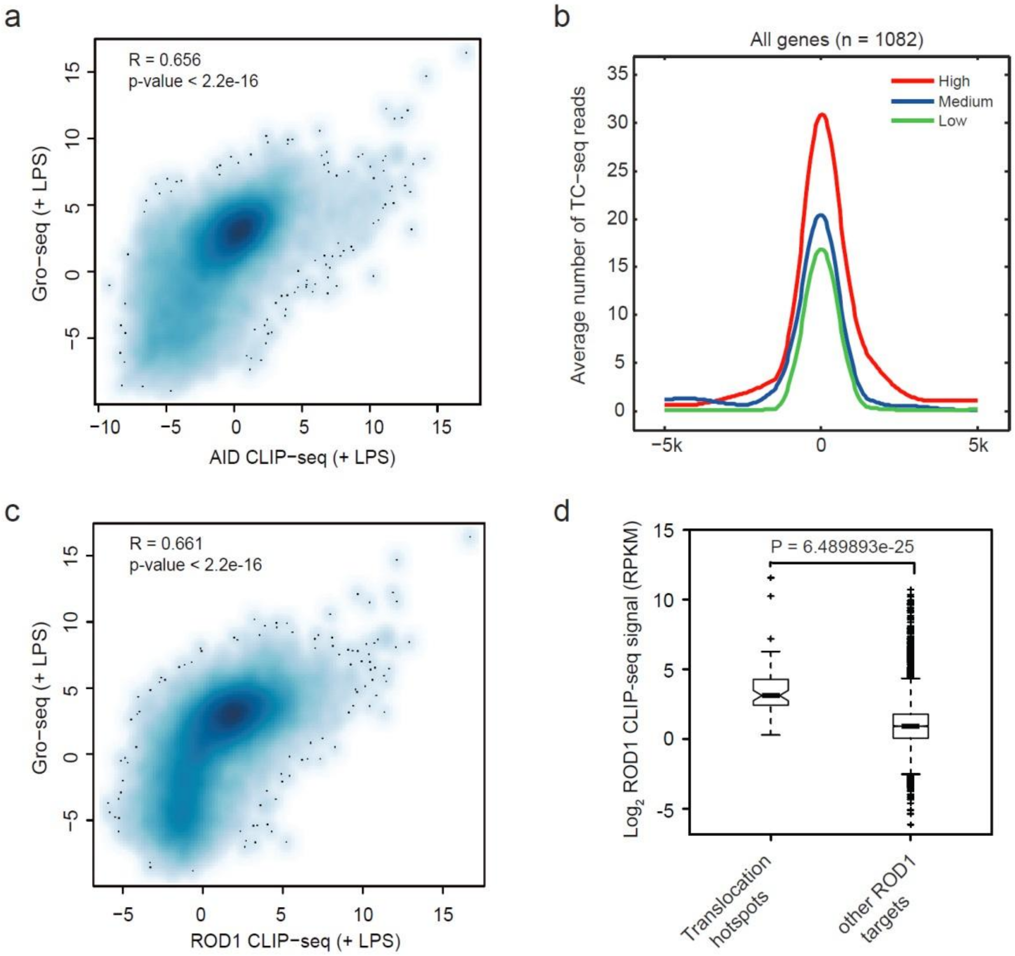

Supplementary Figure 15. ROD1 occupancy is highly correlated with TC-seq and Gro-seq signals. (**a**) The Pearson's correlation analysis of AID CLIP-seq to Gro-seq signals in LPS-activated B cells. Scatter plots represent the $\log_2$-normalized RPKM values of Refseq genes between the two datasets. The *P* value and R are indicated. (**b**) ROD1 binding profiles around the center of the translocation hotspots detected by TC-seq. TC-seq-detected genes (n = 1082) were subgrouped into low, medium or high based on ROD1 CLIP-seq signal. (**c**) Pearson's correlation analysis of ROD1 CLIP-seq to Gro-seq signals in LPS-activated B cells. (**d**) Enrichment of ROD1 CLIP-seq reads among translocation hotspots in LPS-activated B cells. The comparison is performed between 61 translocation hotspot genes and 5,219 other ROD1 targets. *P* value was determined by Wilcoxon rank-sum test.