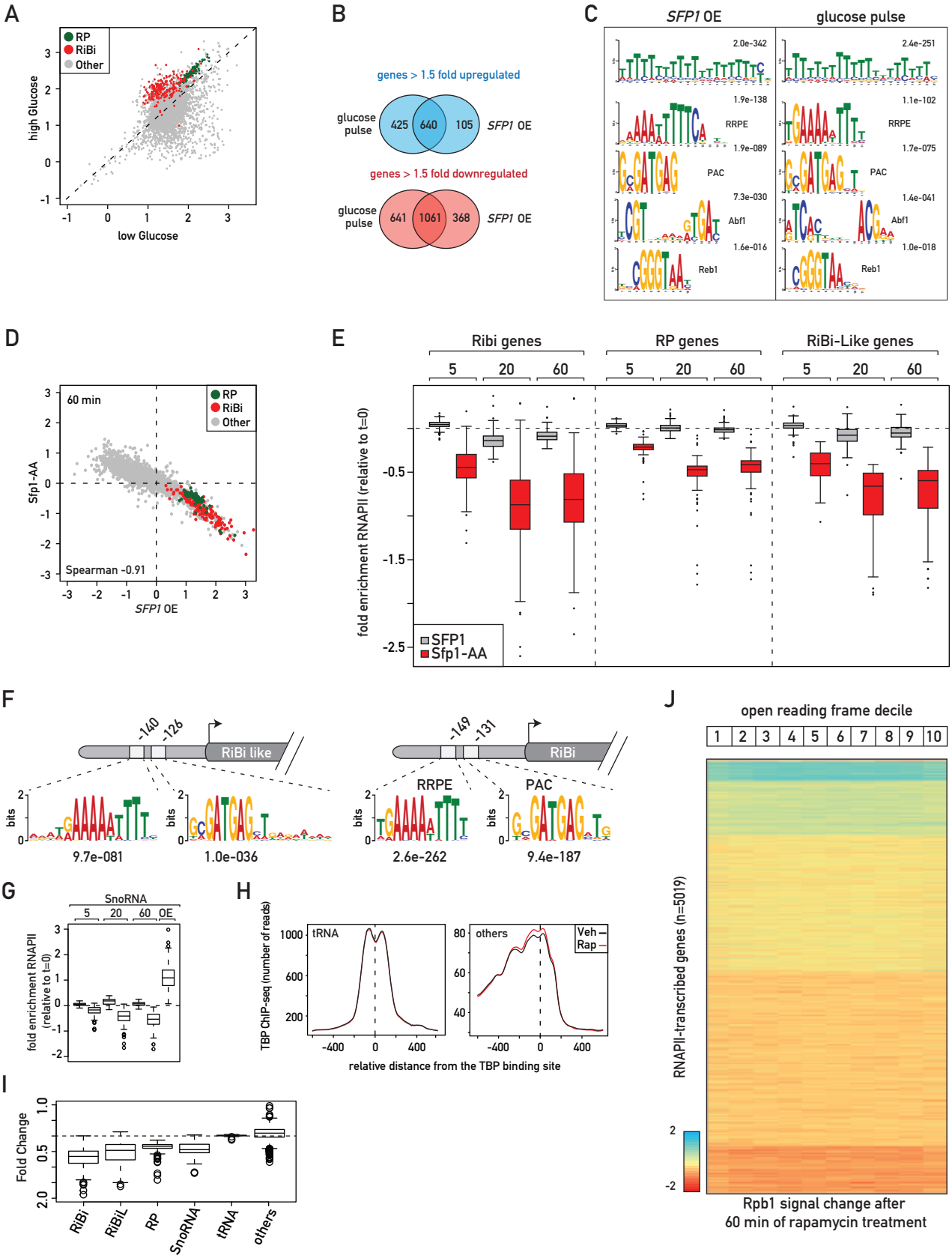

Figure S1. (A) Scatter plot comparing RNAPII (Rpb1) ChIP-Seq signal in low glucose (0.05%; x-axis) and 10 minutes after glucose addition to 2% (y-axis). (B) Venn diagram showing overlap between genes downregulated (red) or upregulated (blue) after Sfp1 overexpression (Sfp1-OE) or glucose pulse. (C) Most significant motifs found in genes that are upregulated > 1.5-fold after Sfp1 overexpression or following a 10 min glucose pulse. E values and motif name or associated TF are indicated where known. (D) Scatter plots comparing RNAPII ChIP-seq fold-change (log2) at 20 (left) and 60 (right) min following rapamycin addition in a Sfp1 anchor-away strain (y axes) to Rpb1 ChIP-seq change 60 min following galactose addition in a pGAL-SFP1 strain (x-axes). (E) Box plots showing log2 fold Rpb1-ChIP change on different categories of genes (RiBi, RP, RiBi-like) relative to t=0 for cell treated during 5, 20, 60 min of rapamycin (red) in Sfp1-FRB or in SFP1 rapamycin-resistant cells (black). (F) Schematic representation of RiBi and RiBi-like gene promoters with average position of PAC and RRPE motif relative to the transcription start site (TSS) and E values for occurrence indicated. (G) Box plots showing RNAPII ChIP-seq fold-change (log2) at snoRNA genes relative to t=0 for cells treated for 5, 20 or 60 min with rapamycin (red) or vehicle (grey) in a Sfp1 anchor-away strain (Sfp1-FRB), or 60 minutes following galactose addition to pGAL1-SFP1 cells (SFP1 OE). (H) Average TBP binding profiles, centered on the TATA or TATA-like element, at 20 min following vehicle or rapamycin addition to a Sfp1 anchor-away strain at all tRNA genes (left panel) or all genes other than RiBi, RiBi-like, RP, and snoRNA ("others", right panel). (I) Box plots showing log2 fold TBP-ChIP change on different categories of genes (RiBi, RP, RiBi-like, snoRNA, tRNA, others) for cells treated for 20 min with rapamycin relative to vehicle-treated cells. (J) Heat maps representing RNAPII ChIP-seq signal obtained after 1h Sfp1 anchor-away, normalized to the t = 0 sample. Cluster analysis was performed for all protein coding genes based on the RNAPII changes observed compared to the t = 0 sample. Rpb1 occupancy was measured by dividing each open reading frame (ORF) into 10 equal regions (bins 1-10, as shown at the top of the panel) and summing the reads in each bin.