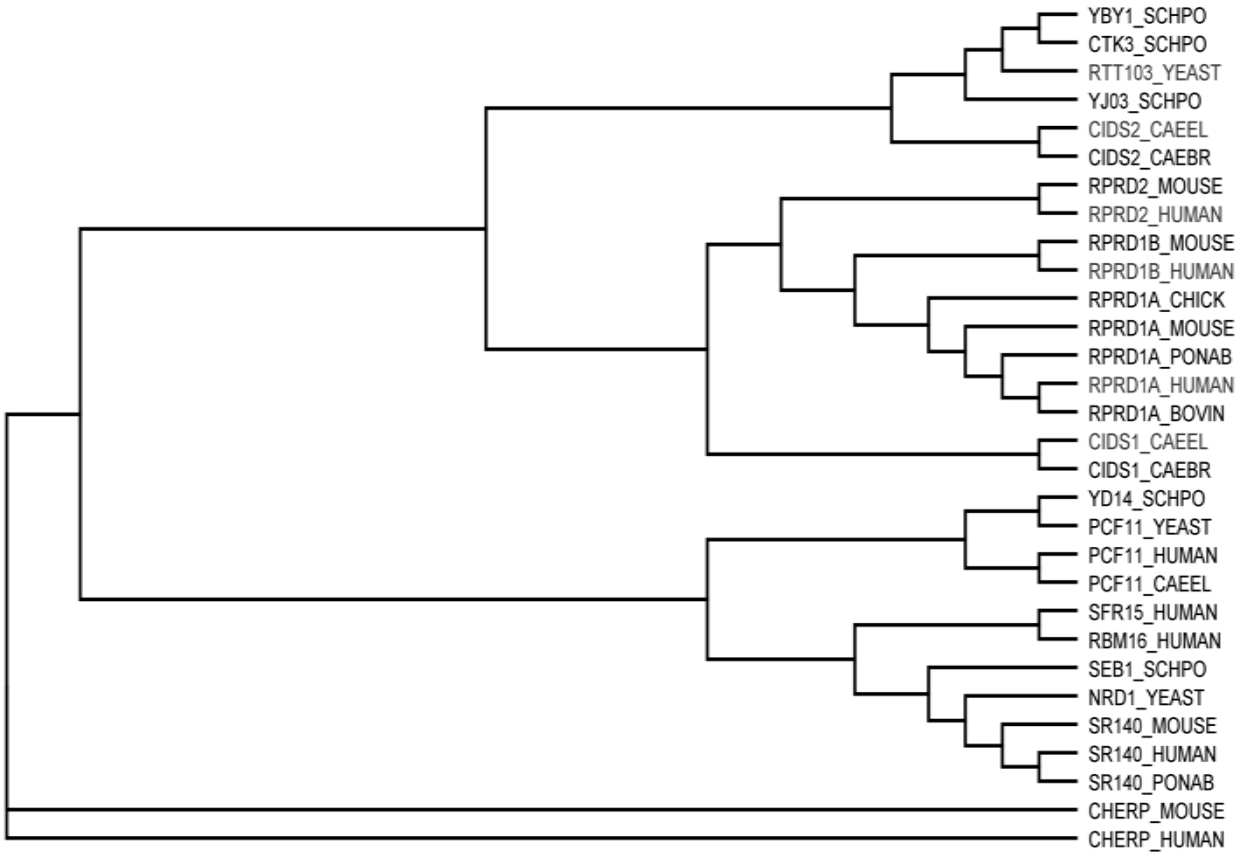
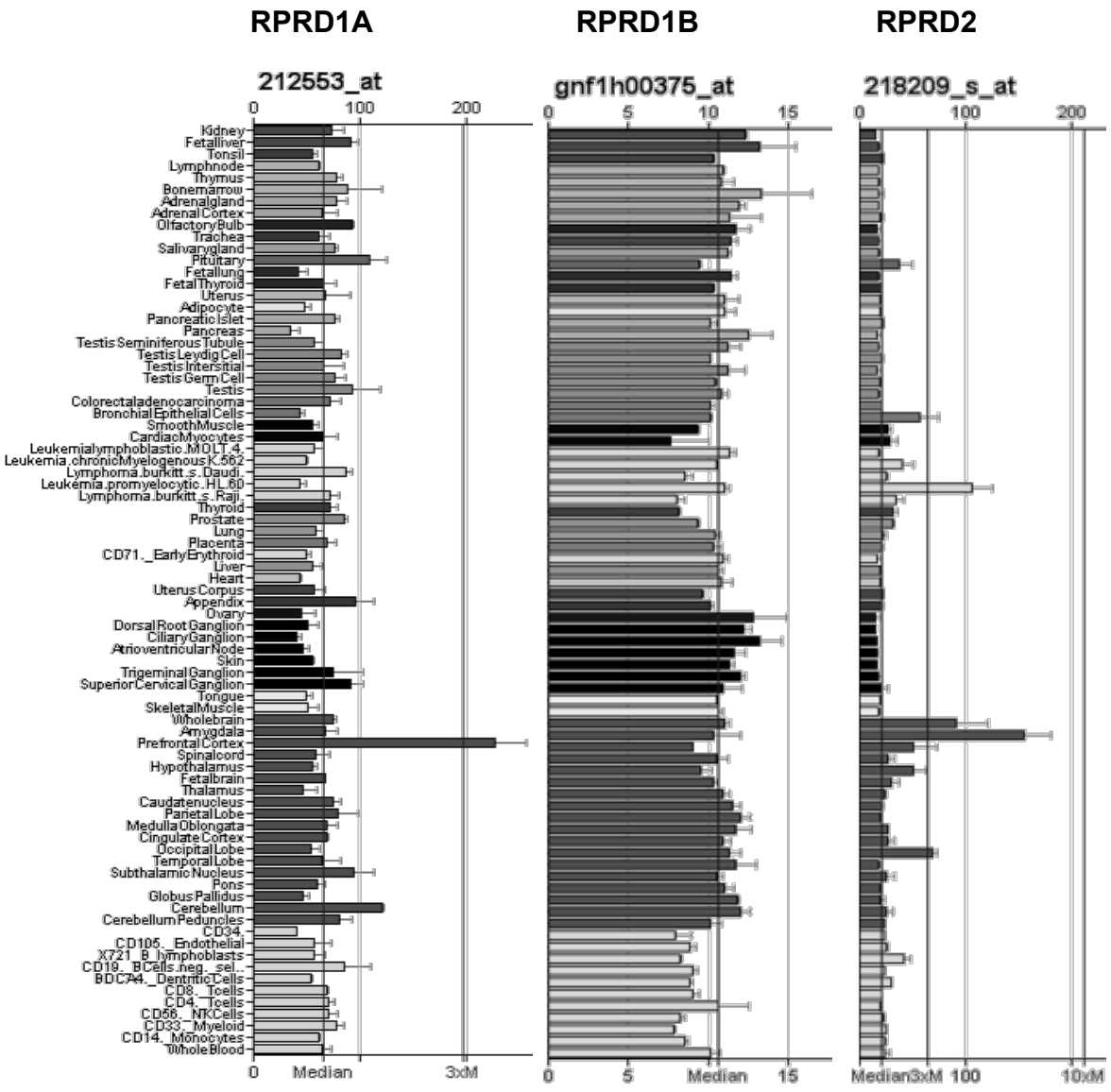
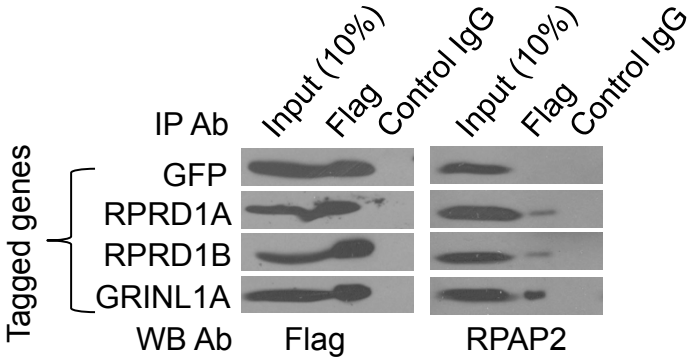


Supplementary Figure 1. CID conservation. Phylogenetic tree of CIDs from the UniProt database. A clustalW alignment of CIDs was processed by the PHYML algorithm.

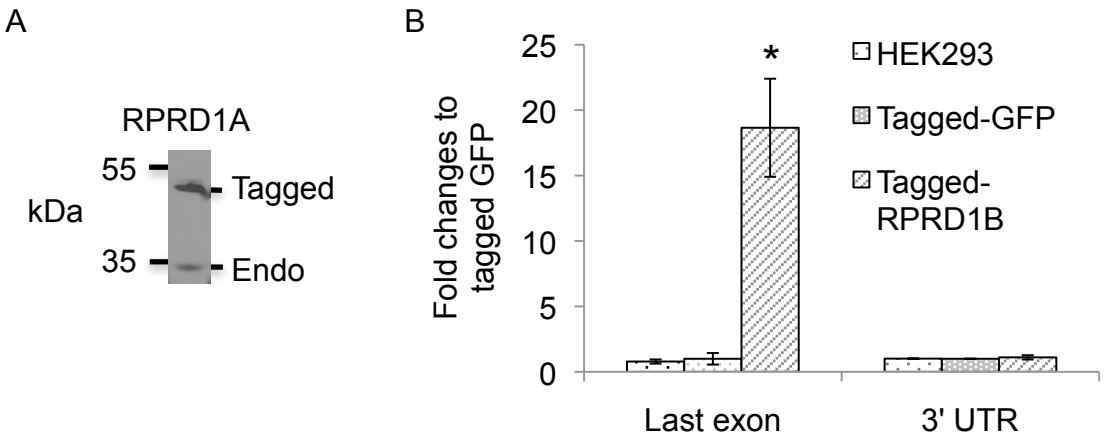


Supplementary Figure 2. Human tissue expression profile of the RPRD genes. RPRD1A and RPRD2 profiles were collected from public expression databases (BioGPS). Hybridization values are based on the HG-U113 Plus 2 (RPRD1A, RPRD2) and GNF1H (RPRD1B) chips.

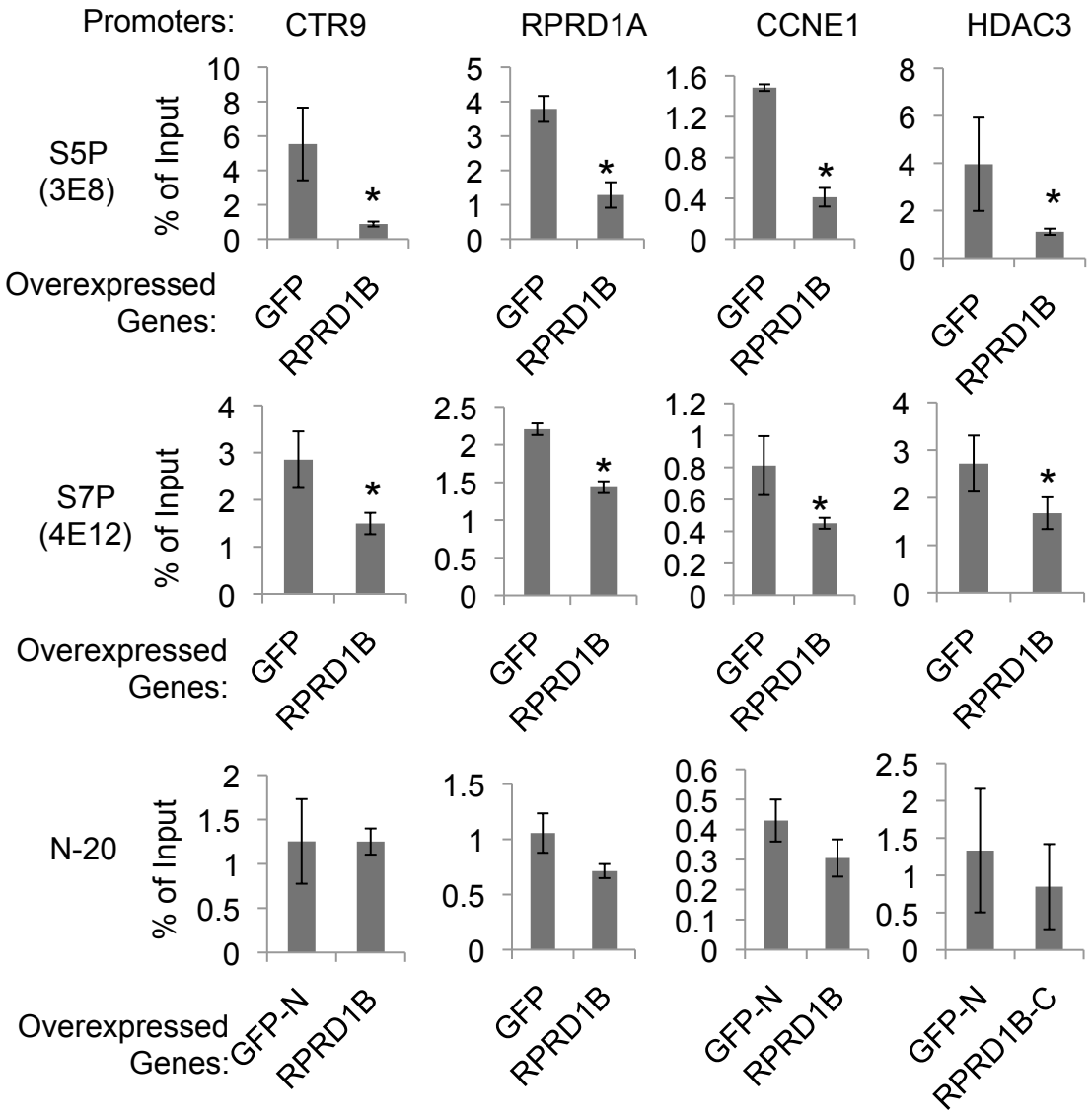


Supplementary Figure 3. Tagged RRPRD1A, RPRD1B and GRINL1A co-immunoprecipitated with endogenous RPAP2. Cell lysates from HEK293 cells stably expressing tagged RPRD1A, RPRD1B or GRINL1A were immunoprecipitated with anti-Flag antibodies followed by western blotting using the indicated antibodies.

Supplementary Figure 4. RPRD1A predominantly interacts with phosphorylated RNAPII. IP-WB was performed with soluble protein lysates from HEK293 cells expressing lentiviral encoded shRNA for the knockdown of RPRD1A (A), or HEK293 cells (B). IP with the indicated antibodies was followed by western blotting using the indicated probes. Control IgG: TBL1 antibody.



Supplementary Figure 5. Ectopic overexpression of RPRD1A and RPRD1B. A**.** Western blot was carried out using anti-RPRD1A antibody in HEK293 cells expressing tagged RPRD1A. Endo: endogenous RPRD1A, Tagged: tagged RPRD1A. B. RT-qPCR was performed using primers recognizing the indicated regions of the *RPRD1B* locus for total RNA extracted from HEK293 cells expressing tagged RPRD1B. Transcript levels were normalized to ß-TUBULIN and are the average of three experiments. *, statistically significant ($p<0.05$) as compared with tagged GFP.



Supplementary Figure 6. RPRD1B inhibits RNAPII CTD phosphorylation on S5 and S7. ChIP experiment using 3E8 and 4E12 phosphospecific antibodies, as well as antibody N-20, showing the total amount of RNAPII, was performed in HEK293 cells overexpressing the indicated genes**.** Immunoprecipitated DNA was quantified by qPCR with primers recognizing the indicated gene promoters. For 3E8 and 2E12 the levels of promoter occupancy were normalized to those of total RNAPII and represent an average of two biological replicates. *, statistically significant ($p<0.05$) compared with overexpressed GFP.

Supplementary Table 1. qPCR primers

Genes	Sites	Forward (5′ to 3′)	Reverse (5′ to 3′)
ß-TUBULIN	Last exon	CTTCGATGCCAAGAACATGA	AAGCATCTGCTCATCGACCT
CCNE1	Promoter	ACTCAGGGCCCGGAACTC	GAGCCAAGGGGATGTGTG
CTR9	Promoter	GGAGAGTCAGACGCCAGATG	GAAGCTTTTGTTGGCGTGTC
HDAC3	Promoter	AATGGCCCTCGCATCCTA	CTCAGCTCTCCCGGTATCTG
LEO1	Promoter	ATACCCAGGCGAGAACAGGT	GACAGTGTCGCAAAGATTCG
	Exon 2	GATGAAAAATGGGGCAGAGA	AGATCCTTGTGCCCTCTCCT
	Exon 3	AATCTGCAAGAGGCAGTGAT	GGCACCTCAGTGTCACTATCC
	Exon 5	GCCAATTCCTGAGACCAGAA	CACTGAGAAAGTTGGGCAGTT
	Exon 8	AACGTTTGAGGGCTTCCATA	TCCTCCTCCTCATCGTATCG
	Intron 9	CCCAGTCCAGAGAACACCAT	TAGCACCAAAATCGATGCAG
	Last exon	GTGAACCTTCCGGAAAGAGA	CCTCTTCATCGCTGATCACA
	3’ UTR	GTGAACCTTCCGGAAAGAGA	CCTCTTCATCGCTGATCACA
RPRD1A	Promoter	TGCTTCTTTGACAGAGTTTCCA	TGATGCCTGGGTTACTCTCA
	Last exon	TGGACATGGGCGTATCTTCT	GGGTTTGATATTTATTTTTAGCAGGA
RPRD1B	Exon 5	CAAAGAGGCAGCTGAACGTC	GACGGTCCTCCAGTTCTGC
	Last exon	CAAACAGAAGCTTGCACGAG	CTAAGCCCCCTGTGACGTT
	3’UTR	GGCTTCCACTAAGGCACTTG	TTATGGCAACGCTACGACAG