Supplementary information

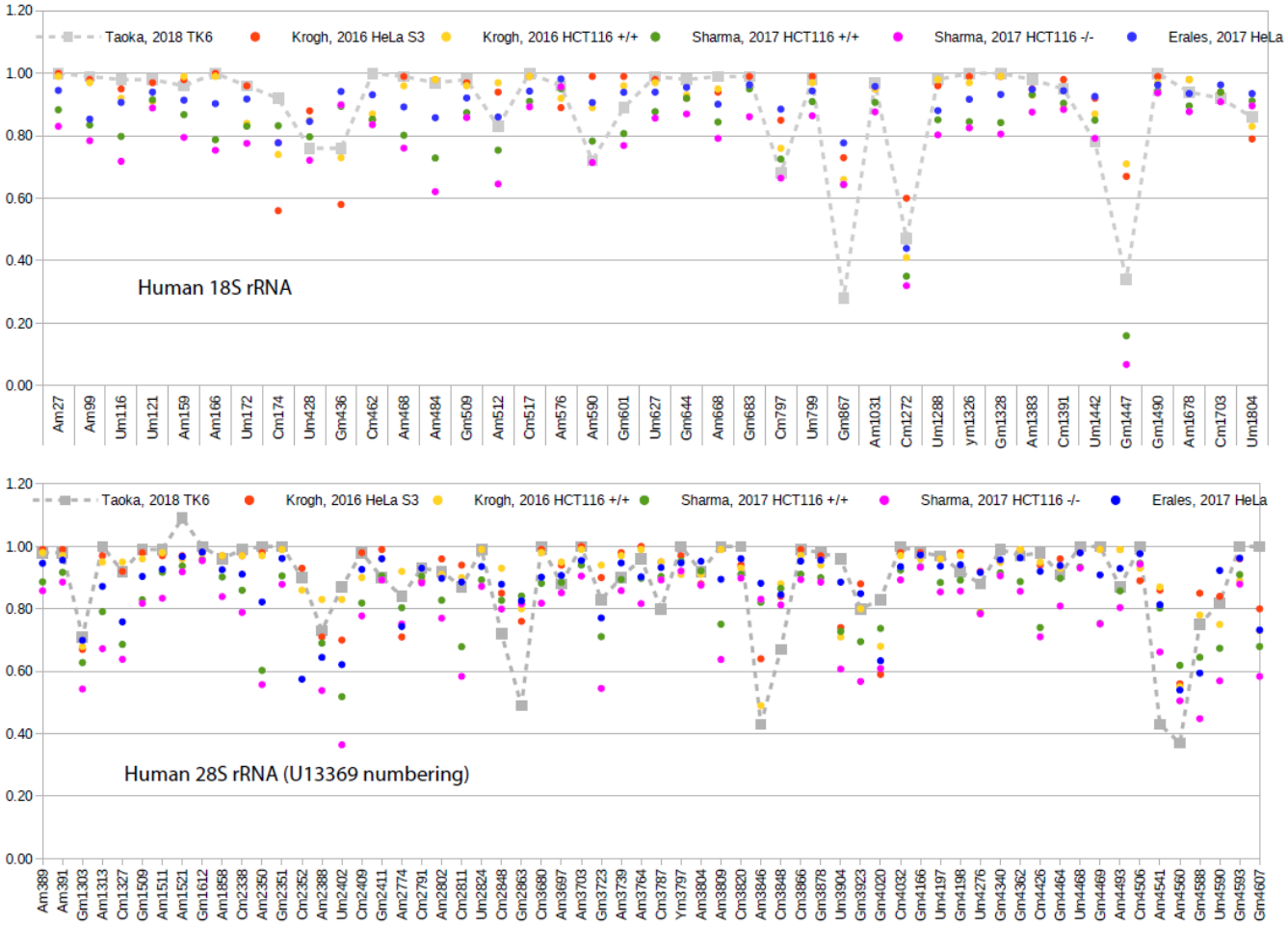

Figure S1. Comparative analysis of the 2′-O-methylation levels obtained by mass-spectrometry analysis and MethScore for the same position provided by various RiboMethSeq protocols. Direct comparison seems to be difficult since different cell lines were used and culture conditions are not necessarily identical. Cell lines used:

TK6 human lymphoblast cell from spleen, Epstein-Barr virus transformed [1], cervix adenocarcinoma cell HeLa S3 (ATCC CCL-2.2) and colorectal carcinoma cell line HCT116 (ATCC CCL-247) [2], colorectal carcinoma cell line HCT116 (ATCC CCL-247) (HCT +/+) and isogenous cell line in which endogenous alleles of p53 were disrupted sequentially by homologous recombination (HCT -/-) [3], cervix adenocarcinoma cell line HeLa [4].

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