




rRNA	Version/ID	Articles using this version
5.8S	U13369.1:6623-6779 , NR_046235.3:6601-6757	snoRNABase , snoRNA Atlas , snOPY , Gumienny et al. (2017) , Incarnato et al. (2017) , Zhu et al. (2017)
18S	X03205.1	snoRNABase , snoRNA Atlas
18S	NR_003286	snOPY , Gumienny et al. (2017)
18S	NR_145820.1	Incarnato et al. (2017) , Zhu et al. (2017)
28S	U13369.1:7935-12969	snoRNABase , snoRNA Atlas , snOPY , Gumienny et al. (2017)
28S	NR_003287.4	Incarnato et al. (2017) , Zhu et al. (2017)

Table S1. Most widely used rRNA versions in the literature.

136,726,104	136,726,239	Ensembl ID	RefSeq ID	HGNC ID	Rfam ID
		ENSG00000280496	-	-	RF00416
136,726,105	136,726,234	Ensembl ID	RefSeq ID	HGNC ID	Rfam ID
		ENSG00000276161	-	HGNC:32636	RF00416
136,726,104	136,726,237	Ensembl ID	RefSeq ID	HGNC ID	Rfam ID
		-	NR_002975	HGNC:32636	-



snoDB0971


136,726,104	136,726,239	Ensembl ID	RefSeq ID	HGNC ID	Rfam ID
		ENSG00000280496;ENSG00000276161	NR_002975	HGNC:32636	RF00416

Figure S1. SnoRNAs from different sources are merged to give at most one entry per chromosomal position in snoDB 2.0. Example of three independent overlapping entries from Ensembl (first two) and one from RefSeq (last one) for the snoRNA SNORA17B. The merged entry groups together all useful ids and information.

Compilation of 2'-O-methylation levels for the 18S rRNA in all studies for position Cm174

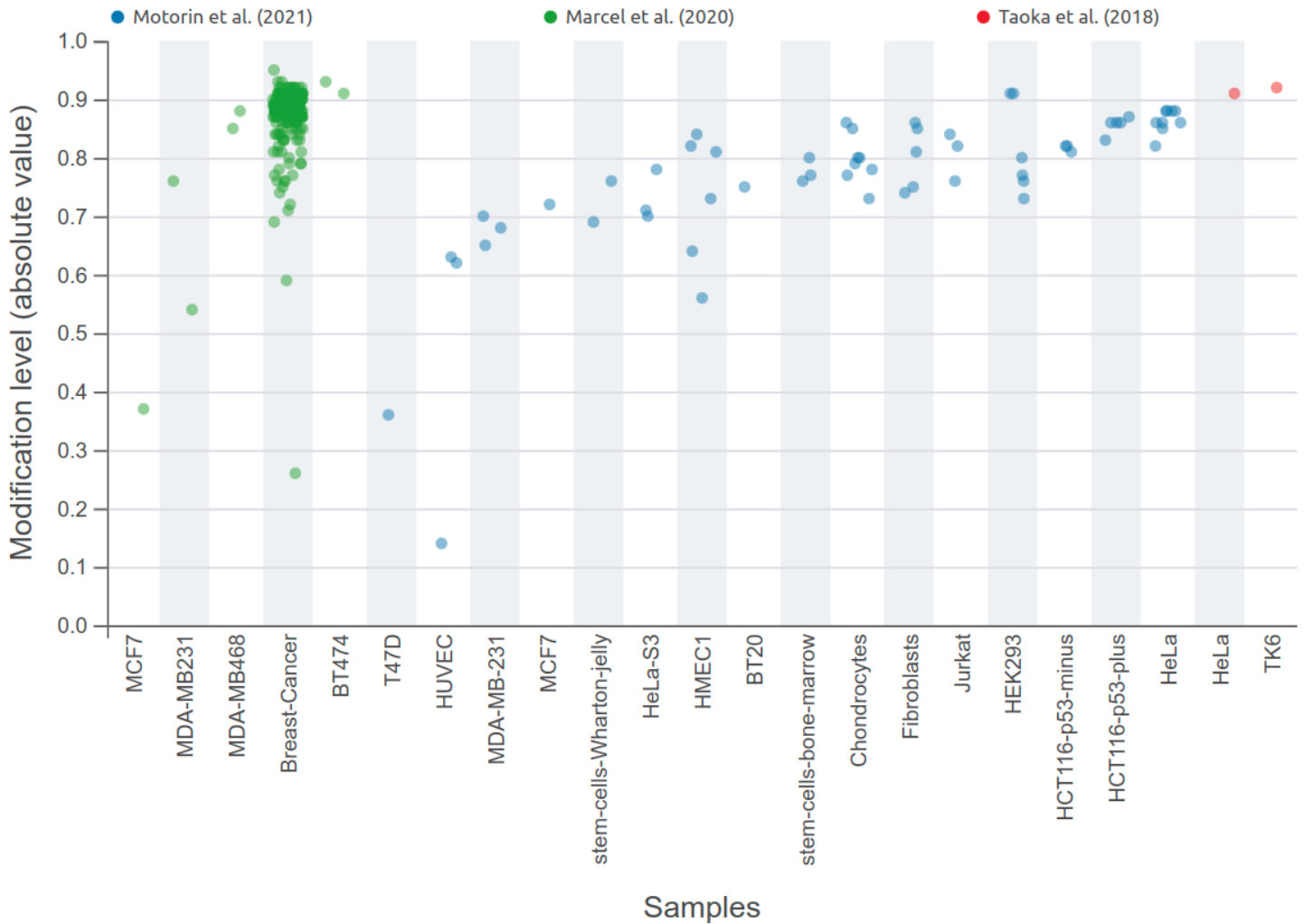


Figure S2. Screenshot of the detailed dot plot for a specific position in the "modification levels" subsection. Each value (modification level ranging from 0 to 1) from a sample is represented as a dot, and grouped by cell type. Colors represent different studies. The dot plot can also be reordered according to the mean value, tissue - cell lines, alphabetical order of the samples or by the studies (default).