

Table S2. Biological process_Enriched GO terms for the functional annotation of NPM1-associated genes.

#	Enriched GO terms	Genes found in our data	EASE score	FDR
1	Translational elongation	35	6.80×10^{-51}	9.00×10^{-48}
2	Translation	38	3.20×10^{-36}	4.20×10^{-33}
3	Cellular protein metabolic process	53	6.00×10^{-18}	7.90×10^{-15}
4	RNA processing	23	8.60×10^{-12}	1.10×10^{-08}
5	RNA metabolic process	26	1.70×10^{-09}	2.20×10^{-06}
6	mRNA processing	14	2.40×10^{-07}	3.20×10^{-04}
7	RNA splicing	13	4.70×10^{-07}	6.20×10^{-04}
8	mRNA metabolic process	14	1.20×10^{-06}	1.60×10^{-03}

GO: gene ontology. EASE score: a modified Fisher exact test, Expression Analysis Systematic Explorer score. FDR: false discovery rate.

Table S3. Cellular component_Enriched GO terms for the functional annotation of NPM1-associated genes.

#	Enriched GO terms	Genes found in our data	EASE score	FDR
1	Ribonucleoprotein complex	51	6.40×10^{-49}	7.60×10^{-46}
2	Ribosome	35	1.80×10^{-39}	2.10×10^{-36}
3	Cytosolic ribosome	26	7.90×10^{-37}	9.40×10^{-34}
4	Ribosomal subunit	29	1.50×10^{-36}	1.80×10^{-33}
5	Cytosol	53	5.90×10^{-31}	7.10×10^{-28}
6	Cytosolic part	27	6.80×10^{-31}	8.10×10^{-28}
7	Cytosolic small ribosomal subunit	14	9.10×10^{-20}	1.10×10^{-16}
8	Small ribosomal subunit	15	1.40×10^{-18}	1.60×10^{-15}
9	Large ribosomal subunit	15	3.50×10^{-18}	4.10×10^{-15}
10	Intracellular non-membrane-bounded organelle	54	4.00×10^{-18}	4.80×10^{-15}
11	Intracellular organelle part	65	2.10×10^{-16}	2.70×10^{-13}

12	Cytosolic large ribosomal subunit	12	3.10×10^{-16}	4.00×10^{-13}
13	Cytoplasmic part	67	2.20×10^{-14}	2.60×10^{-11}
14	Cytoplasm	79	5.90×10^{-13}	7.00×10^{-10}
15	Intracellular organelle	82	2.50×10^{-09}	3.00×10^{-06}
16	Nuclear part	33	2.00×10^{-08}	2.30×10^{-05}
17	Nuclear lumen	29	2.90×10^{-08}	3.40×10^{-05}
18	Intracellular organelle lumen	32	4.30×10^{-08}	5.20×10^{-05}
19	Spliceosome	10	1.30×10^{-07}	1.50×10^{-04}
20	Nucleolus	19	2.40×10^{-07}	2.90×10^{-04}
21	Small nuclear ribonucleoprotein complex	5	1.40×10^{-05}	1.60×10^{-02}

GO: gene ontology. EASE score: a modified Fisher exact test, Expression Analysis Systematic Explorer score. FDR: false discovery rate.