

Table S12. Frequency (%) of METTL genetic amplifications, deep deletions and mutations in more than 1,000 CCLE tumor lines

METTL Gene	Amplification	Deep Deletion	Mutation
METTL1	3.11	0.47	0.00
METTL2A	4.47	0.57	1.66
METTL2B	6.31	2.59	1.21
METTL3	2.43	4.34	2.04
METTL4	4.37	5.90	1.97
METTL5	1.26	0.47	0.89
METTL6	1.17	6.78	1.34
METTL7A	1.17	0.76	0.70
METTL7B	0.97	0.47	0.83
METTL8	1.46	0.47	1.97
METTL9	1.17	2.30	1.15
EEF1AKMT2	0.78	5.41	0.45
NTMT1	0.78	2.20	1.15
METTL11B	4.27	0.28	0.96
CSKMT	0.58	1.14	0.76
EEF1AKNMT	4.17	0.09	2.36
METTL14	0.49	2.79	1.08
METTL15	1.84	2.30	2.10
METTL16	0.29	11.84	3.31
METTL17	2.91	4.24	1.97
METTL18	4.08	0.19	2.17
TRMT44	0.58	6.49	3.12
ETFBKMT	6.31	1.72	1.53
METTL21A	0.29	1.24	0.96
EEF1AKMT3	3.11	0.47	0.76
METTL21C	5.05	5.89	1.15
VCPKMT	3.88	3.17	1.02
METTL22	0.97	2.00	2.36
METTL23	4.08	0.47	0.70
METTL24	0.58	7.37	1.59
METTL25	0.97	2.20	2.87
RRNAD1	4.95	0.28	1.91
METTL26	0.39	3.46	1.46
METTL27	5.15	2.10	0.64