

Supplementary Table I Identification of the 36kDa PKB substrate as methyltransferase-like protein-1 (METTL1). The 36 kDa protein was purified, digested with trypsin and analysed on a Perspective Biosystems (Framingham, MA) Elite SR matrix-assisted laser desorption time of flight (MALDI-TOF) mass spectrometer. The tryptic mass ions obtained were scanned against the Swiss-Prot and GenPep databases using the MS-FIT program of Protein Prospector. 41 peptides were detected, 15 of which could be matched with the sequence of human methyltransferase-like protein-1, giving 36% coverage of the protein.

Masses submitted	Masses matched	Start	End	Peptide Sequence
864.4907	864.4732	251	257	NFPAIFR
981.4954	981.4641	112	119	VSDYVQDRI
1065.5664	1065.5522	144	151	HLPNFFYKG
1178.6303	1178.6170	7	18	NVAGAEAPPQKR
1334.7069	1334.7181	7	19	NVAGAEAPPQKRY
1349.6474	1349.6384	25	36	AHSNPMADHTLRY
1365.6310	1365.6334	25	36	AHSNPMADHTLRY
1425.7079	1425.7029	157	167	MFFLFPDPHFKR
1441.7236	1441.6979	157	167	MFFLFPDPHFKR
1445.7471	1445.7323	125	138	AAPAGGFQNIACLR
1721.9882	1721.9842	175	189	IISPTLLAEYAYVLRV
1890.9521	1890.9925	259	276	IQDPVLQAVTSQTSPLGH
2047.0644	2047.0936	258	276	RIQDPVLQAVTSQTSPLGH
2408.2297	2408.1833	220	242	VPLEDLSEDPVVGHLGTSTEEGKK
3737.5671	3737.7110	37	37	YPVKPEEMDWSELYPEFFAPLTQNSHDDPKD