

## Suppl Fig. S4

1 **MDGIVPDI**AV **GTK**RGSDLEF STCVTNGPFI MSSNSASAAN GNSKFKFGD SRSAGVPSRV IHIR**KL**PIDV **TEGEVISLGL**  
81 **PF**GKVTNLLM LKGKNQAFIE MNTEEAANTM VNYYSVTPV LR**GQPIYIQF** **SNH**KELKTDSPNQAR**AQA**LQAVNSVQSG  
161 **NLALAASAAA** **VDAGMAMAGQ** **SPVLR**IIIVEN LFYPVTLDEL HQIFSKFGTV LKIITFTK**NN** **QFQALLQYAD** **PVSAQHAKLS**  
241 LDGQNIYNAC CTLRIDFSKL TSLNVKYNNND KSRDYTRPDL PSGDSQPSLD QTMAAAFGLS VPNVHGALAP LAIPSAAAAA  
321 AAAGR**IAIPG** **LAGAGNSVLL** **VSNLNPER**VT PQSLFILFGV YGDVQRVKIL FNKK**ENALVQ** **MADGNQAQLA** **MSHLNGHKLH**  
401 GKPIRITLSK HQNVQLPREG QEDQGLTKDY GNSPLHRFKK PGSKNFQNIFF PPSATLHLSN IPPSVSEEDL KVLFSNNGGV  
481 VKGFKFFQKD RKMALIQMGS VEEAVQALID LHNHDLGENH HLRVSFSKST I

Mass spectrometric analysis of the protein precipitated with MACC1-AS1 identified PTBP1. The coverage rate of the seven peptide sequence reached 29% for PTBP1 with 100% matching. Highlighted sequences in the figure show the peptides that completely matched the sequence of the PTBP1 protein.