Supplemental Figure 1

a

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  1 MKTFTLPASV LFCFLLLIRG LGAAPPGRSD VYPPPLGSEH NGQVAEDAVS RPKDDSVPEV
 61 RAARNSEPQD QGELFQGVDP RALAAVLLQA LDRPASPPAV PAGSQQGTPE EAAEALLTES
121 VRSQTHSLPA SEIQASAVAP PRPQTQDNDP EADDRSEELE ALASLLQELR DFSPSNAKRQ
181 QETAAAETET RTHTLTRVNL ESPGPERVWR ASWGEFQARV PERAPLPPSV PSQFQARMSE
241 NVPLPETHQF GEGVSSPKTH LGETLTPLSK AYQSLSAPFP KVRRLEGSFL GGSEAGERLL
301 QQGLAQVEAG RRQAEATRQA AAQEERLADL ASDLLLQYLL QAGARQRDLG GRGLQETQQE
361 RENEREEEAE QERRGGGEDE VGEEDEEAAE AEAEAEEAER ARQNALLFAE EEDGEAGAED
421 KRSQEEAPGH RRKDAEGTEE GGEEDDDDEE MDPQTIDSLI ELSTKLHLPA DDVVSIIEEV
481 EEKRKRKKNA PPEPVPPPRA APAPTHVRSP QPPPPAPARD ELPDWNEVLP PWDREEDEVF
541 PPGPYHPFPN YIRPRTLQPP ASSRRHFHH ALPPARHHPD LEAQARRAQE EADAEERRLQ
601 EQEELENYIE HVLLHRP
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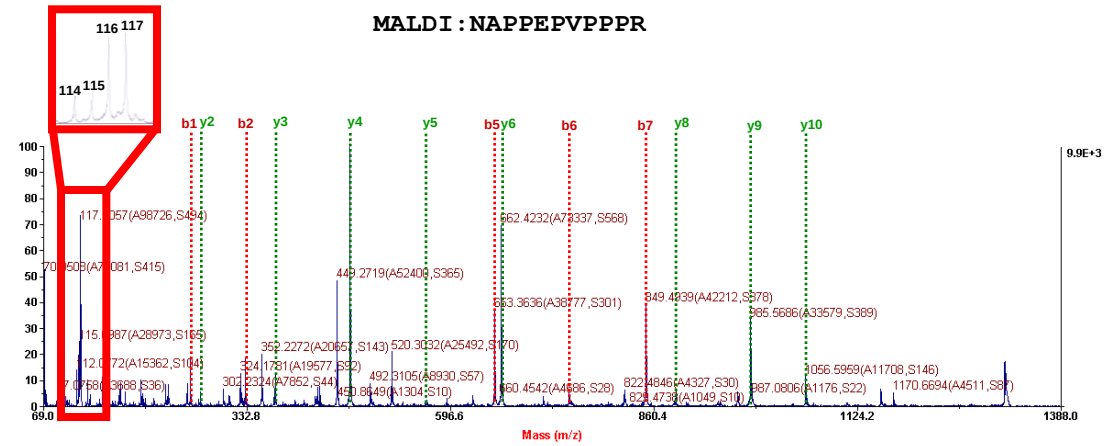
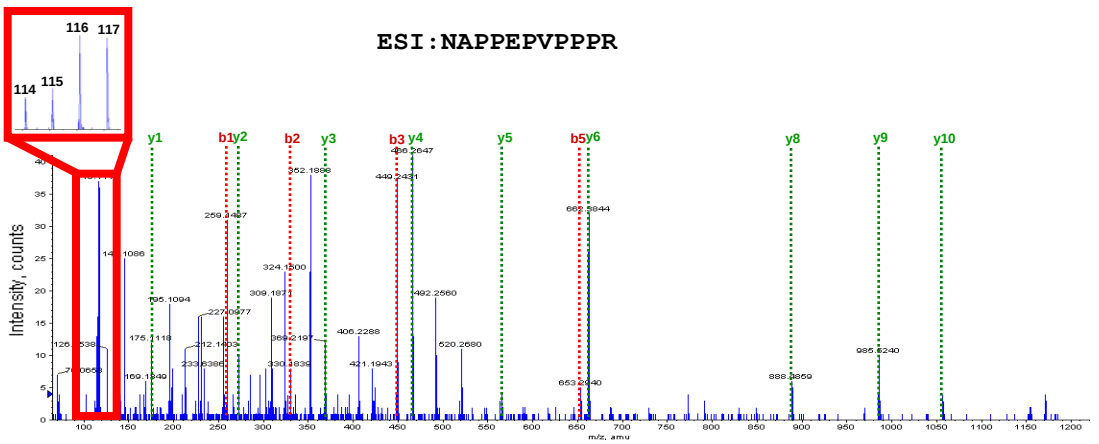
b

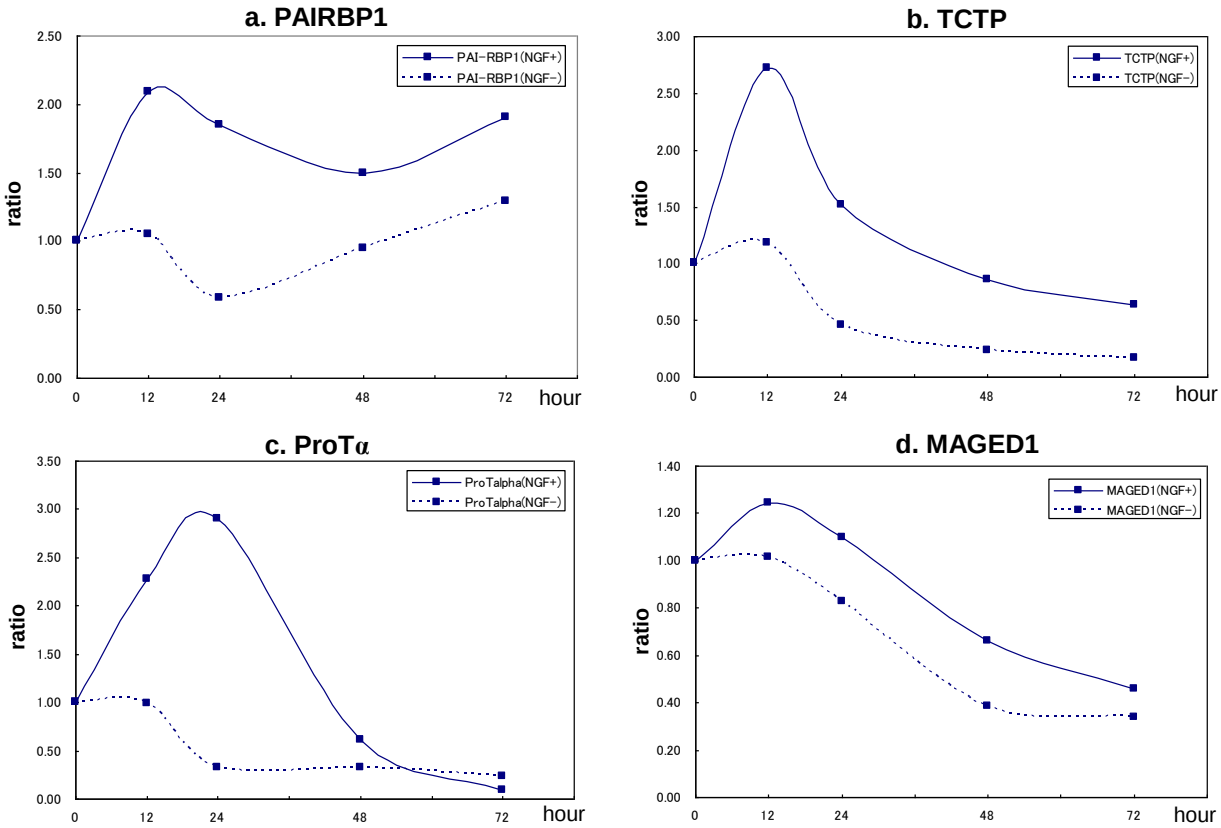


c



Quantitative analysis of differentially-expressed proteins in NGF-treated PC12 cells by iTRAQ method based on LC-MALDI or LC-ESI MS/MS analysis. (**A**) Amino acid sequence of VGF (Swiss-Prot accession number P20156) identified by LC-MALDI or LC-ESI MS/MS analysis. Green sequences were identified by both LC-MALDI and LC-ESI MS/MS analysis. Red and blue sequences were identified by only LC-MALDI and LC-ESI MS/MS analysis, respectively. (**B, C**) Example tandem mass (MS/MS) spectra of the precursor ion NAPPEPVPPPP identified as VGF by LC-MALDI (**B**) and LC-ESI (**C**) MS/MS analysis were shown. Expanded views of the low-m/z end of the MS/MS spectrum show relative abundances of the signature iTRAQ ions at 114.1, 115.1, 116.1, and 117.1 m/z.

Supplemental Figure 2



Quantitative time course analysis of PAIRBP1, TCTP, ProTα and MAGED1 by Western blotting in NGF-stimulated PC12 cells. Cell lysates were prepared at different time points as indicated. The ratios were calculated by the intensities of the protein bands shown in Fig. 4A. The intensities at 0 hours (before NGF stimulation) were determined to be the standard (the ratio = 1.0).