Supplemental Table 1: Gene identifiers for the proteins shown in Table 1.

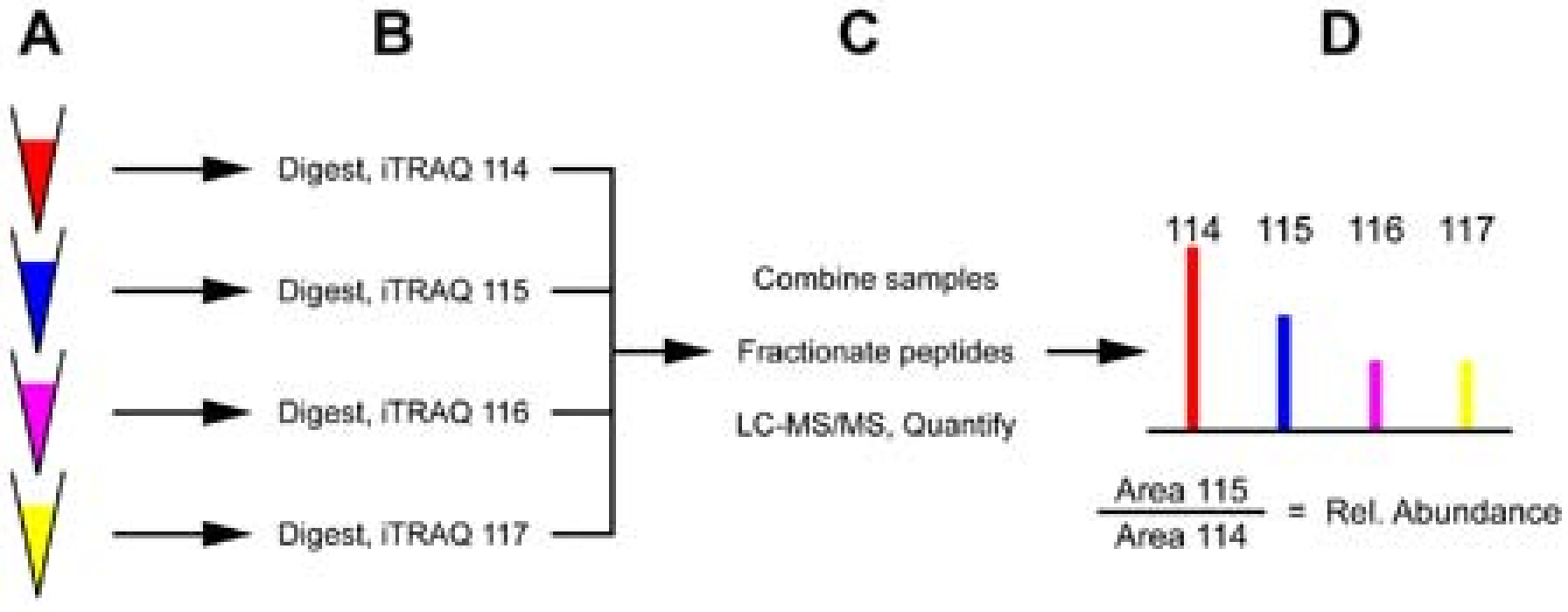
Protein Name	**Gene Identifier**
Oxidative stress	
Ferritin heavy polypeptide 1	66911979
Thioredoxin reductase 1	55250051
Prothymosin α	62201921
Membrane-cytoskeletal signaling	
Myristoylated alanine-rich C-kinase substrate-like 1, MARCKSL1	76363234
Brain abundant membrane attached signal protein 1 (BASP1/CAP-23)	730110
Gravin/A kinase anchor protein (AKAP12)	75905811
Tropomyosin 4 [1]	763182
Thymosin β4	78103212
Transcription regulation	
APEX nuclease	624915
Y box binding protein 1 (YBX1)	92373398
Neuropeptide signaling	
CGRP precursor [2]	76880491
Neurosecretory protein VGF [3]	13591864

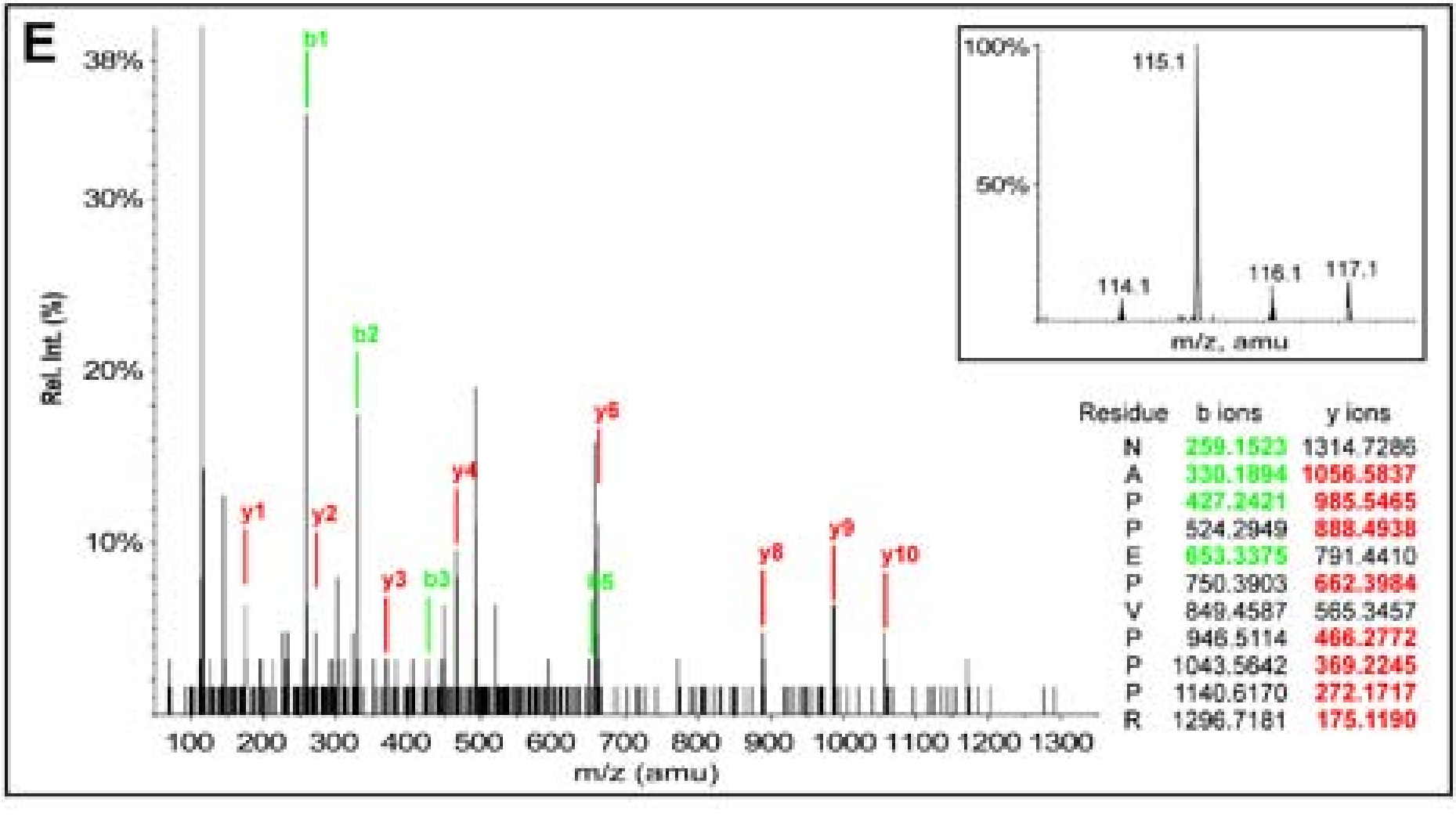
Other	
Diazepam binding inhibitor (DBI)	62201921
Proteasome P20 subunit (PSMB7)	9719458
α-Galactosidase	34881493
Palmytoyl-protein thioesterase 1	11968070
Acetyl-Coenzyme A acetyltransferase 2	33086552
Cell cycle exit and neuronal differentiation 1 (CEND1)	81882797
LSM3 homolog, U6 small nuclear RNA associated	27712626

Supplemental Table 2: Colocalization of VGF-ir and TrkA-ir in DRG neurons

		% VGF+ of Total	% TrkA+ of Total	% TrkA+ of VGF+
L4	Naïve	21.3 ± 2.4	46.8 ± 3.9	58.3 ± 4.5
	Sham	42.1 ± 2.6 [a]	49.6 ± 1.6	56.5 ± 3.2
	SNL	61.9 ± 5.3 [a.b]	53.3 ± 4.7	53.3 ± 4.4
L5	Naive	17.7 ± 1.8	43.4 ± 4.2	54.7 ± 2.4
	Sham	36.8 ± 3.2 [a]	47.6 ± 4.1	52.7 ± 4.2
	SNL	76.5 ± 1.8 [a,b]	53.3 ± 1.7	51.9 ± 1.4
	CFA	28.2 ± 0.3 [a]	50.1 ± 3.2	65.5 ± 5.2

[a] Significantly different from naïve; [b] significantly different from sham


A
B
C
D
Digest, iTRAQ 114
Digest, iTRAQ 115
Digest, iTRAQ 116
Digest, iTRAQ 117
Combine samples
Fractionate peptides
LC-MS/MS, Quantify
114 115 116 117
Area 115
Area 114
= Rel. Abundance


E
Rel. Int. (%)
38%
30%
20%
10%
b1
b2
b3
y1
y2
y3
y4
y5
y6
y8
y9
y10
100 200 300 400 500 600 700 800 900 1000 1100 1200 1300
m/z (amu)
100%
50%
115.1
114.1
116.1
117.1
m/z, amu
Residue b ions y ions
N 259.1523 1314.7286
A 330.1894 1056.5837
P 427.2421 985.5465
P 524.2949 888.4938
E 653.3375 791.4410
P 750.3903 662.3984
V 849.4587 565.3457
P 946.5114 466.2772
P 1043.5642 369.2245
P 1140.6170 272.1717
R 1296.7181 175.1190

Supplemental Figure 1: Identification and relative quantification of VGF using iTRAQ. A, The four samples (cytoplasmic t0, cytoplasmic t24, nuclear t0, nuclear t24) were each digested with trypsin and labeled with an iTRAQ reagent (B). C, The peptide samples were combined and fractionated into fourteen fractions. Each fraction was then analyzed by LC-MS/MS to identify peptides and quantify the four iTRAQ labels. D, The relative iTRAQ label areas correspond to the relative peptide abundance. Relative protein abundance was calculated by ProteinPilot based on the abundance of all peptides mapped to a given protein. E, During MS/MS the peptide of 585.77 m/z (z = 2+) was fragmented generating a spectrum of b-ions (containing the N-terminus of peptides) and y-ions (containing the C-terminus of peptides). In ProteinPilot, the masses of the b- and y-ions were used to deduce the amino acid sequence of the peptide as NAPPEPVPPPR, corresponding to amino acids 489-499 of VGF (99% confidence of identification). The inset shows the iTRAQ reporter tags, which were fragmented from this peptide in the t0 (tag 114) and t24 (tag 115) samples. The ratio between the 114 and 115 tags was calculated as 1:45, indicating that the relative abundance of this VGF peptide was substantially increased at t24 and suggesting upregulation of the VGF protein.