Supplemental Materials

Molecular Biology of the Cell

Husedzinovic et al.

Table S1:

Primary hits of protein phosphatases scoring in the systematic screen for regulators of SMN function and localisation

Gene products identified as potential SMN regulators in the automated screen (left) as well as additional gene products identified by visual inspection (right). The identified genes are sorted according to the relative increase (%) in the proportion of cells showing no SMN accumulation in CB compared to the control (deviation from threshold, see methods for details). Serine/threonine phosphatases (PPM1G is indicated in bold font) are marked in yellow, tyrosine phosphatases (PTPN23: bold) in blue and dual specificity phosphatases in green. The list also indicates positions (plate and well) in the screen. The PPP1CC/PP1 regulatory subunits PPP1R8/NIPP1 (*italics*) was the only gene products whose knockdown caused cytoplasmic SMN accumulations.

Supplementary Figure 1:

Subcellular distribution of SMN after genome-wide knockdown of human phosphatases

72h after cell seeding and inverse siRNA transfection in 96well plates, HeLa cells were fixed and immunostained using an α-SMN antibody; nuclei were stained using DAPI. An Olympus ScanR High-content Screening Station was used to analyse the subcellular distribution of the SMN protein. Images were collected using a 10x objective. Inlets show sections displayed in Figure 1. Scalebar: 120µm.

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Plate	well	Gene	Number of cells without spots (%)	Deviation from treshold
pB1_1	F7	PPEF2	78,37023	35,975563
pA1_1	E8	PPP1R12B	80,39726	35,90111
pC1_2	C4	PTPRM	62,63628	32,541802
pC1_2	A5	PPP3R2	61,70373	31,609252
pC1_3	B6	PPP1R14D	77,02968	31,25886
pA1_2	A5	PPP3R2	64,15741	30,130764
pB1_1	**F11**	**PPM1G**	**68,39782**	**26,003153**
pB1_1	C5	CDC25C	66,71887	24,324203
pA1_1	A8	PPP1CC	68,02212	23,52597
pA1_4	B11	C3orf48	74,40848	23,160345
pA1_1	E9	NAP1L1	66,43797	21,94182
pA1_3	D10	DUSP16	77,05556	20,49891
pB1_1	C3	CDC25A	56,84	14,445333
pA1_1	H5	PPP2R3A	57,07415	12,578
pA1_2	A3	PPP3CB	45,49464	11,467994
pC1_1	F8	PPEF1	77,58797	11,46349
pB1_2	B8	PTPRD	45,16382	10,24404
pA1_3	B5	PPP1R12C	66,66421	10,10756
pC1_2	**H11**	**PTPN23**	**39,66659**	**9,572112**
pB1_2	B3	PTPN11	43,74117	8,82139
pB1_1	E9	NAP1L1	50,19887	7,804203
pB1_2	B1	PTPN7	41,33023	6,41045
pB1_4	C6	LOC283871	48,33502	5,22834
pC1_3	G1	PPTC7	46,24538	0,47456

Plate	well	Gene
pA1_1	C8	DUSP2
pC1_1	D2	DUSP7
pC1_1	C4	CDC25B
pC1_2	F3	CTDP1
pC1_1	*G9*	*PPP1R8*

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