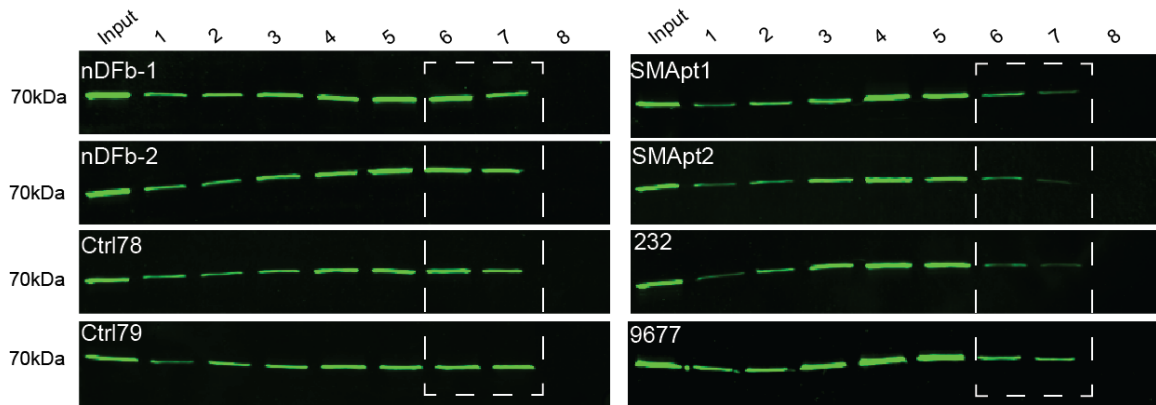A

B

C

D

1

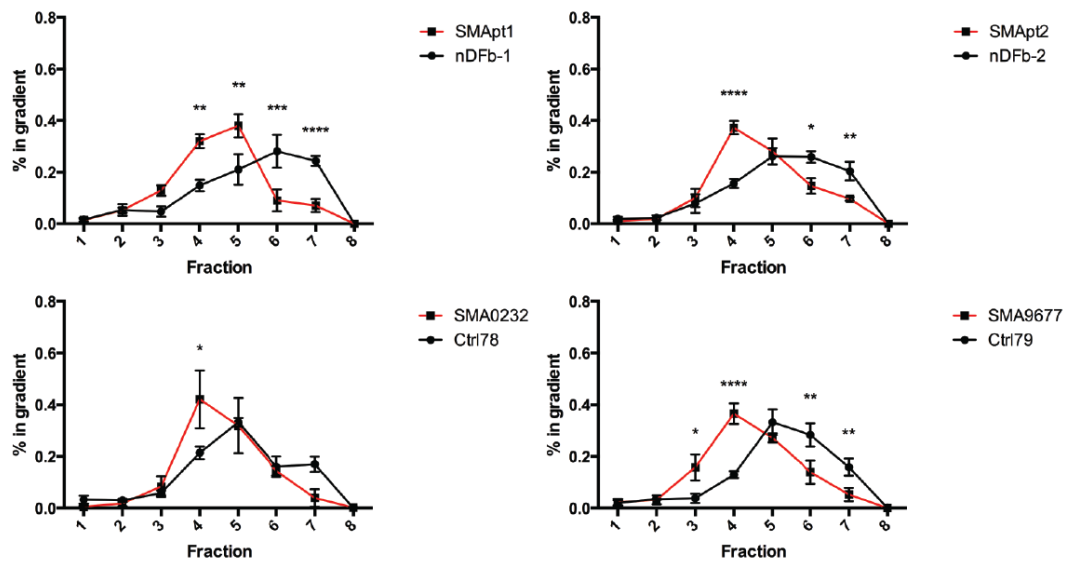**Supplemental Figure 1. Relates to figure 5.:**

Cytoskeletal proteins show unaltered distributions in SMA fibroblasts relative to controls.

A. Cytoplasmic lysates from fibroblasts were fractionated via Optiprep gradient centrifugation and fractions were analyzed for the presence of tubulin by western blot analysis. SMA lysates (SMApt1, 232) shows unaltered distribution of tubulin relative to control fractions (nDFb-1, Ctrl78). **B.** Distributions plotted as enrichment in % of the total signal in all fractions found in one particular faction. n=3, analyzed by Sidak's multiple comparisons test. Error bars +/- SEM. **C.** Cytoplasmic lysates from fibroblasts were fractionated via Optiprep gradient centrifugation and fractions were analyzed for the presence of actin. SMA lysates shows unaltered distribution of actin relative to control fractions. **D.** Distributions plotted as enrichment in % of the total signal in all fractions found in one particular faction. n=3, analyzed by Sidak's multiple comparisons test. Error bars +/- SEM.

Supplemental Figure 2. Relates to Figure 5:

PABPC1 granules show reduced complexity in SMA patient samples. **A.** Cytoplasmic lysates from fibroblasts were subjected to Optiprep gradient centrifugation and fractions were analyzed for the presence of PABPC1. SMA lysates shows altered distribution of PABPC1 complexes relative to control fractions. **B.** Distributions are plotted as enrichment in % of the total signal in all fractions found in one particular faction. n=3, analyzed by Sidak's multiple comparisons test, *p<.05, **p<.01., ***p<.001, ****p<.0001. Error bars +/- SEM.

Number of families	1			
Number of comparisons per family	6			
Alpha	0.05			

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
No UTR vs. ΔBox UTR	0.004453	-0.5897 to 0.5986	No	ns
No UTR vs. ΔZip UTR	-0.7825	-1.377 to -0.1883	Yes	**
No UTR vs. Full UTR	-2.899	-3.432 to -2.366	Yes	****
ΔBox UTR vs. ΔZip UTR	-0.787	-1.381 to -0.1928	Yes	**
ΔBox UTR vs. Full UTR	-2.904	-3.437 to -2.370	Yes	****
ΔZip UTR vs. Full UTR	-2.117	-2.650 to -1.583	Yes	****

Supplemental Table 1. Relates to Figure 1D:

Statistical comparisons for figure 1D. Values for cell body TriFC signals were assessed using a one way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 6 comparisons per family and an alpha of .05. ns: not significant, *: $p<.05$, **, $p<.01$, ***: $p<.001$, ****: $p<.0001$.

Number of families	1			
Number of comparisons per family	6			
Alpha	0.05			

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
No UTR vs. ÄBox UTR	0.03454	-0.2570 to 0.3260	No	ns
No UTR vs. ÄZip UTR	-0.6792	-0.9707 to -0.3877	Yes	****
No UTR vs. Full UTR	-1.928	-2.219 to -1.636	Yes	****
ÄBox UTR vs. ÄZip UTR	-0.7137	-1.005 to -0.4222	Yes	****
ÄBox UTR vs. Full UTR	-1.962	-2.254 to -1.671	Yes	****
ÄZip UTR vs. Full UTR	-1.249	-1.540 to -0.9571	Yes	****

Supplemental Table 2. Relates to Figure 1E:

Statistical comparisons for figure 1E. Values for axonal TriFC signals were assessed using a one way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 6 comparisons per family and an alpha of .05. ns: not significant, *: $p < .05$, **, $p < .01$, ***: $p < .001$, ****: $p < .0001$.

Compare column means (main column effect)

Number of families	1	
Number of comparisons per family	28	
Alpha	0.05	

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
Ctrl78 vs. Ctrl79	-0.1228	-0.6174 to 0.3718	No	ns
Ctrl78 vs. nDFb-1	0.1645	-0.3301 to 0.6590	No	ns
Ctrl78 vs. nDFb-2	-0.1168	-0.6113 to 0.3778	No	ns
Ctrl78 vs. SMApt1	0.8463	0.3517 to 1.341	Yes	****
Ctrl78 vs. SMApt2	0.9857	0.4911 to 1.480	Yes	****
Ctrl78 vs. SMA0232	1.01	0.5150 to 1.504	Yes	****
Ctrl78 vs. SMA9677	1.061	0.5660 to 1.555	Yes	****
Ctrl79 vs. nDFb-1	0.2873	-0.2073 to 0.7818	No	ns
Ctrl79 vs. nDFb-2	0.006054	-0.4885 to 0.5006	No	ns
Ctrl79 vs. SMApt1	0.9691	0.4745 to 1.464	Yes	****
Ctrl79 vs. SMApt2	1.108	0.6139 to 1.603	Yes	****
Ctrl79 vs. SMA0232	1.132	0.6378 to 1.627	Yes	****
Ctrl79 vs. SMA9677	1.183	0.6889 to 1.678	Yes	****
nDFb-1 vs. nDFb-2	-0.2812	-0.7758 to 0.2133	No	ns
nDFb-1 vs. SMApt1	0.6818	0.1872 to 1.176	Yes	***
nDFb-1 vs. SMApt2	0.8212	0.3266 to 1.316	Yes	****
nDFb-1 vs. SMA0232	0.8451	0.3506 to 1.340	Yes	****
nDFb-1 vs. SMA9677	0.8962	0.4016 to 1.391	Yes	****
nDFb-2 vs. SMApt1	0.963	0.4685 to 1.458	Yes	****
nDFb-2 vs. SMApt2	1.102	0.6079 to 1.597	Yes	****
nDFb-2 vs. SMA0232	1.126	0.6318 to 1.621	Yes	****
nDFb-2 vs. SMA9677	1.177	0.6828 to 1.672	Yes	****
SMApt1 vs. SMApt2	0.1394	-0.3552 to 0.6340	No	ns
SMApt1 vs. SMA0232	0.1633	-0.3313 to 0.6579	No	ns
SMApt1 vs. SMA9677	0.2143	-0.2802 to 0.7089	No	ns

SMApt2 vs. SMA0232	0.02392	-0.4706 to 0.5185	No	ns
SMApt2 vs. SMA9677	0.07495	-0.4196 to 0.5695	No	ns
SMA0232 vs. SMA9677	0.05102	-0.4435 to 0.5456	No	ns

Supplemental Table 3. Relates to Figure 3B:

Statistical comparisons for figure 3B. Values for fibroblast TriFC signals were assessed using a two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 28 comparisons per family and an alpha of .05. ns: not significant, *: p<.05, **, p<.01, ***: p<.001, ****: p<.0001.

Compare column means (main column effect)

Number of families	1			
Number of comparisons per family	28			
Alpha	0.05			

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
Ctrl78 vs. Ctrl79	0.01659	-0.1318 to 0.1649	No	ns
Ctrl78 vs. nDFb-1	0.004521	-0.1438 to 0.1529	No	ns
Ctrl78 vs. nDFb-2	0.01596	-0.1324 to 0.1643	No	ns
Ctrl78 vs. SMApt1	0.01914	-0.1292 to 0.1675	No	ns
Ctrl78 vs. SMApt2	-0.032	-0.1804 to 0.1164	No	ns
Ctrl78 vs. SMA0232	0.02831	-0.1200 to 0.1767	No	ns
Ctrl78 vs. SMA9677	0.08215	-0.06621 to 0.2305	No	ns
Ctrl79 vs. nDFb-1	-0.01207	-0.1604 to 0.1363	No	ns
Ctrl79 vs. nDFb-2	-0.0006256	-0.1490 to 0.1477	No	ns
Ctrl79 vs. SMApt1	0.002552	-0.1458 to 0.1509	No	ns
Ctrl79 vs. SMApt2	-0.04859	-0.1969 to 0.09978	No	ns
Ctrl79 vs. SMA0232	0.01173	-0.1366 to 0.1601	No	ns
Ctrl79 vs. SMA9677	0.06556	-0.08280 to 0.2139	No	ns
nDFb-1 vs. nDFb-2	0.01144	-0.1369 to 0.1598	No	ns
nDFb-1 vs. SMApt1	0.01462	-0.1337 to 0.1630	No	ns
nDFb-1 vs. SMApt2	-0.03652	-0.1849 to 0.1118	No	ns
nDFb-1 vs. SMA0232	0.02379	-0.1246 to 0.1722	No	ns
nDFb-1 vs. SMA9677	0.07763	-0.07074 to 0.2260	No	ns
nDFb-2 vs. SMApt1	0.003178	-0.1452 to 0.1515	No	ns

nDFb-2 vs. SMApt2	-0.04796	-0.1963 to 0.1004	No	ns
nDFb-2 vs. SMA0232	0.01235	-0.1360 to 0.1607	No	ns
nDFb-2 vs. SMA9677	0.06619	-0.08218 to 0.2145	No	ns
SMApt1 vs. SMApt2	-0.05114	-0.1995 to 0.09722	No	ns
SMApt1 vs. SMA0232	0.009173	-0.1392 to 0.1575	No	ns
SMApt1 vs. SMA9677	0.06301	-0.08535 to 0.2114	No	ns
SMApt2 vs. SMA0232	0.06031	-0.08805 to 0.2087	No	ns
SMApt2 vs. SMA9677	0.1141	-0.03422 to 0.2625	No	ns
SMA0232 vs. SMA9677	0.05383	-0.09453 to 0.2022	No	ns

Supplemental Table 4. Relates to Figure 4B:

Statistical comparisons for IMP1 protein levels for figure 4B. Values for steady state

IMP1 levels were assessed using a two way ANOVA and Tukey's multiple comparisons

test. Test was conducted with 1 family, 28 comparisons per family and an alpha of .05.

ns: not significant.

Compare column means (main column effect)

Number of families		1		
Number of comparisons per family		28		
Alpha		0.05		

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant ?	Summary
Ctrl78 vs. Ctrl79	0.03468	-0.1714 to 0.2408	No	ns
Ctrl78 vs. nDFb-1	0.01609	-0.1900 to 0.2222	No	ns
Ctrl78 vs. nDFb-2	-0.05117	-0.2573 to 0.1549	No	ns
Ctrl78 vs. SMApt1	0.5046	0.2985 to 0.7107	Yes	****
Ctrl78 vs. SMApt2	0.4638	0.2577 to 0.6699	Yes	****
Ctrl78 vs. SMA0232	0.4742	0.2681 to 0.6803	Yes	****
Ctrl78 vs. SMA9677	0.4794	0.2733 to 0.6855	Yes	****
Ctrl79 vs. nDFb-1	-0.01859	-0.2247 to 0.1875	No	ns
Ctrl79 vs. nDFb-2	-0.08585	-0.2920 to 0.1203	No	ns
Ctrl79 vs. SMApt1	0.4699	0.2638 to 0.6761	Yes	****
Ctrl79 vs. SMApt2	0.4291	0.2230 to 0.6353	Yes	****
Ctrl79 vs. SMA0232	0.4395	0.2334 to 0.6456	Yes	****
Ctrl79 vs. SMA9677	0.4447	0.2386 to 0.6508	Yes	****
nDFb-1 vs. nDFb-2	-0.06727	-0.2734 to 0.1389	No	ns
nDFb-1 vs. SMApt1	0.4885	0.2824 to 0.6947	Yes	****
nDFb-1 vs. SMApt2	0.4477	0.2416 to 0.6538	Yes	****
nDFb-1 vs. SMA0232	0.4581	0.2520 to 0.6642	Yes	****
nDFb-1 vs. SMA9677	0.4633	0.2572 to 0.6694	Yes	****
nDFb-2 vs. SMApt1	0.5558	0.3497 to 0.7619	Yes	****

nDFb-2 vs. SMApt2	0.515	0.3089 to 0.7211	Yes	****
nDFb-2 vs. SMA0232	0.5254	0.3193 to 0.7315	Yes	****
nDFb-2 vs. SMA9677	0.5306	0.3244 to 0.7367	Yes	****
SMApt1 vs. SMApt2	-0.04081	-0.2469 to 0.1653	No	ns
SMApt1 vs. SMA0232	-0.03042	-0.2365 to 0.1757	No	ns
SMApt1 vs. SMA9677	-0.02524	-0.2314 to 0.1809	No	ns
SMApt2 vs. SMA0232	0.01039	-0.1957 to 0.2165	No	ns
SMApt2 vs. SMA9677	0.01557	-0.1906 to 0.2217	No	ns
SMA0232 vs. SMA9677	0.005178	-0.2009 to 0.2113	No	ns

Supplemental Table 5. Relates to Figure 4B:

Statistical comparisons for SMN protein levels for figure 4B. Values for steady state SMN levels were assessed using a two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 28 comparisons per family and an alpha of .05. ns: not significant. *: p<.05, **, p<.01, ***: p<.001, ****: p<.0001.

Supplemental Table 6. Relates to Figure 4E:

Statistical comparisons for IMP1 association with mRNA levels for figure 4E. Values for IMP1 pulldown/IMP1 input were assessed using a two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 120 comparisons per family and an alpha of .05. ns: not significant. *: p<.05, **, p<.01, ***: p<.001, ****: p<.0001.

Supplemental Table 7. Relates to Figure 6D & 6F:

Statistical comparisons for figure 6D, worksheet 1. IMP1 granule volume values were assessed using a two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 28 comparisons per family and an alpha of .05. ns: not significant, *: p<.05, **, p<.01, ***: p<.001, ****: p<.0001. Statistical comparisons for figure 6F, worksheet 2. IMP1 granule volumes after transfection with expression constructs for either mCherry, SMN-mCherry or SMNΔtudor-mCherry were assessed using two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 66 comparisons per family and an alpha of .05. ns: not significant, *: p<.05, **, p<.01, ***: p<.001, ****: p<.0001.

Compare column means (main column effect)

Number of families	1	
Number of comparisons per family	28	
Alpha	0.05	

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Ctrl78 vs. Ctrl79	116	-319.6 to 551.6	No	ns	0.9923
Ctrl78 vs. nDFb-1	1.446	-434.2 to 437.1	No	ns	>0.9999
Ctrl78 vs. nDFb-2	52.8	-382.8 to 488.4	No	ns	>0.9999
Ctrl78 vs. SMA0232	-44.04	-479.7 to 391.6	No	ns	>0.9999
Ctrl78 vs. SMA9677	-110.3	-546 to 325.3	No	ns	0.9943
Ctrl78 vs. SMApt1	-252.6	-688.2 to 183.1	No	ns	0.6402
Ctrl78 vs. SMApt2	-104.2	-539.9 to 331.4	No	ns	0.996
Ctrl79 vs. nDFb-1	-114.6	-550.2 to 321.1	No	ns	0.9928
Ctrl79 vs. nDFb-2	-63.2	-498.8 to 372.4	No	ns	0.9998
Ctrl79 vs. SMA0232	-160	-595.7 to 275.6	No	ns	0.9516
Ctrl79 vs. SMA9677	-226.3	-662 to 209.3	No	ns	0.7578
Ctrl79 vs. SMApt1	-368.6	-804.2 to 67.06	No	ns	0.1661
Ctrl79 vs. SMApt2	-220.2	-655.9 to 215.4	No	ns	0.7826
nDFb-1 vs. nDFb-2	51.35	-384.3 to 487	No	ns	>0.9999
nDFb-1 vs. SMA0232	-45.49	-481.1 to 390.2	No	ns	>0.9999
nDFb-1 vs. SMA9677	-111.8	-547.4 to 323.9	No	ns	0.9938
nDFb-1 vs. SMApt1	-254	-689.7 to 181.6	No	ns	0.6334
nDFb-1 vs. SMApt2	-105.7	-541.3 to 330	No	ns	0.9956
nDFb-2 vs. SMA0232	-96.84	-532.5 to 338.8	No	ns	0.9975
nDFb-2 vs. SMA9677	-163.1	-598.8 to 272.5	No	ns	0.9464
nDFb-2 vs. SMApt1	-305.4	-741 to 130.3	No	ns	0.3912
nDFb-2 vs. SMApt2	-157	-592.7 to 278.6	No	ns	0.9562
SMA0232 vs. SMA9677	-66.29	-501.9 to 369.3	No	ns	0.9998
SMA0232 vs. SMApt1	-208.5	-644.2 to 227.1	No	ns	0.8267
SMA0232 vs. SMApt2	-60.2	-495.8 to 375.4	No	ns	0.9999
SMA9677 vs. SMApt1	-142.3	-577.9 to 293.4	No	ns	0.9745
SMA9677 vs. SMApt2	6.095	-429.5 to 441.7	No	ns	>0.9999
SMApt1 vs. SMApt2	148.3	-287.3 to 584	No	ns	0.9678

Supplemental Table 8. Relates to Figure 7B:

Statistical comparisons for figure 7B. IMP1 levels in the lamellipodia were assessed using two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 6 comparisons per family and an alpha of .05. ns: not significant, *: $p<.05$, **, $p<.01$, ***: $p<.001$, ****: $p<.0001$.

Compare column means (main column effect)

Number of families	1				
Number of comparisons per family	28				
Alpha	0.05				

Tukey's multiple comparisons test	Mean Diff.	95.00% CI of diff.	Significant?	Summary	Adjusted P Value
Ctrl78 vs. Ctrl79	96.75	-485.4 to 678.9	No	ns	0.9996
Ctrl78 vs. nDFb-1	123.6	-458.5 to 705.7	No	ns	0.9981
Ctrl78 vs. nDFb-2	40.76	-541.4 to 622.9	No	ns	>0.9999
Ctrl78 vs. SMA0232	549	-33.17 to 1131	No	ns	0.0806
Ctrl78 vs. SMA9677	655.3	73.19 to 1237	Yes	*	0.0154
Ctrl78 vs. SMApt1	550.5	-31.6 to 1133	No	ns	0.0789
Ctrl78 vs. SMApt2	457.9	-124.3 to 1040	No	ns	0.2443
Ctrl79 vs. nDFb-1	26.83	-555.3 to 609	No	ns	>0.9999
Ctrl79 vs. nDFb-2	-56	-638.1 to 526.1	No	ns	>0.9999
Ctrl79 vs. SMA0232	452.2	-129.9 to 1034	No	ns	0.259
Ctrl79 vs. SMA9677	558.6	-23.56 to 1141	No	ns	0.0705
Ctrl79 vs. SMApt1	453.8	-128.4 to 1036	No	ns	0.2549
Ctrl79 vs. SMApt2	361.1	-221 to 943.3	No	ns	0.5556
nDFb-1 vs. nDFb-2	-82.83	-665 to 499.3	No	ns	0.9999
nDFb-1 vs. SMA0232	425.4	-156.8 to 1008	No	ns	0.336
nDFb-1 vs. SMA9677	531.7	-50.39 to 1114	No	ns	0.1017
nDFb-1 vs. SMApt1	426.9	-155.2 to 1009	No	ns	0.3311
nDFb-1 vs. SMApt2	334.3	-247.8 to 916.4	No	ns	0.6516
nDFb-2 vs. SMA0232	508.2	-73.93 to 1090	No	ns	0.1375
nDFb-2 vs. SMA9677	614.6	32.43 to 1197	Yes	*	0.0303
nDFb-2 vs. SMApt1	509.8	-72.36 to 1092	No	ns	0.1348
nDFb-2 vs. SMApt2	417.1	-165 to 999.2	No	ns	0.3618
SMA0232 vs. SMA9677	106.4	-475.8 to 688.5	No	ns	0.9993
SMA0232 vs. SMApt1	1.571	-580.6 to 583.7	No	ns	>0.9999
SMA0232 vs. SMApt2	-91.08	-673.2 to 491	No	ns	0.9997
SMA9677 vs. SMApt1	-104.8	-686.9 to 477.3	No	ns	0.9994
SMA9677 vs. SMApt2	-197.4	-779.6 to 384.7	No	ns	0.9685
SMApt1 vs. SMApt2	-92.65	-674.8 to 489.5	No	ns	0.9997

Supplemental Table 9. Relates to Figure 7C:

Statistical comparisons for figure 7C. IMP1 levels in the leading edge were assessed using two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 6 comparisons per family and an alpha of .05. ns: not significant, *: $p<.05$, **, $p<.01$, ***: $p<.001$, ****: $p<.0001$.

Number of families	1			
Number of comparisons per family	6			
Alpha	0.05			

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
nDFb-1 vs. nDFb-2	0.9786	-1.717 to 3.674	No	ns
nDFb-1 vs. SMApt1	5.77	3.075 to 8.465	Yes	****
nDFb-1 vs. SMApt2	5.597	2.902 to 8.292	Yes	****
nDFb-2 vs. SMApt1	4.791	2.096 to 7.486	Yes	****
nDFb-2 vs. SMApt2	4.619	1.923 to 7.314	Yes	***
SMApt1 vs. SMApt2	-0.1727	-2.868 to 2.523	No	ns

Supplemental Table 10. Relates to Figure 7E:

Statistical comparisons for figure 7E. IMP1 granule association with the actin cytoskeleton was assessed using two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 6 comparisons per family and an alpha of .05. ns: not significant, *: $p < .05$, **, $p < .01$, ***: $p < .001$, ****: $p < .0001$.

Number of families	1			
Number of comparisons per family	6			
Alpha	0.05			

Tukey's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
nDFb-1 vs. nDFb-2	0.1362	-6.724 to 6.996	No	ns
nDFb-1 vs. SMApt1	9.296	2.437 to 16.16	Yes	**
nDFb-1 vs. SMApt2	8.106	1.246 to 14.97	Yes	*
nDFb-2 vs. SMApt1	9.16	2.300 to 16.02	Yes	**
nDFb-2 vs. SMApt2	7.969	1.110 to 14.83	Yes	*
SMApt1 vs. SMApt2	-1.191	-8.051 to 5.669	No	ns

Supplemental Table 11. Relates to Figure 7G:

Statistical comparisons for figure 7G. IMP1 granule association with the microtubule cytoskeleton was assessed using two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 6 comparisons per family and an alpha of .05. ns: not significant, *: $p < .05$, **, $p < .01$.

Supplemental Table 12. Relates to Figure 7I:

Statistical comparisons for figure 7I. Values for IMP1 pellet/IMP1 soluble fraction were assessed using a two way ANOVA and Tukey's multiple comparisons test. Test was conducted with 1 family, 120 comparisons per family and an alpha of .05. ns: not significant, *: p<.05, **, p<.01, ***: p<.001, ****: p<.0001.