

Table 3 – Stat table

Table 3 - Stat table reporting all exact number of replicates, tests used and statistics. All data were analyzed with Prism (GraphPad 6 or 7) and all experiments were performed in at least three independent biological replicates. For all tests, the significance level was $\alpha = 0.05$, * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, **** $p \leq 0.0001$, ns: not significant.

Graph description	Figure no.	Normality test	TEST USED	n			AVERAGE, VARIANCE	P VALUE		DEGREES OF FREEDOM VALUE
				exact value	DEFINED	extra infos		REPORTED	exact value	
Precursors 181a-1 and 181a-2 expression level - EYE	S1E	N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	0.0286	
Precursors 181a-1 and 181a-2 expression level - ISOLATED AX	S1F	N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	0.0286	
RT-qPCR Drosha-MO vs co-MO vs WT	2E	yes	1-way Anova for multiple comparison (Tukey)	3	WT - 3 biological replicates	from 3 frogs (= indep. exp.)	mean +/- SEM	** (WT vs MO)	0.0041	6
		yes			co-MO - 3 biological replicates	from 3 frogs (= indep. exp.)	mean +/- SEM	* (co-MO vs MO)	0.0351	6
		yes			MO - 3 biological replicates	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (WT vs co-MO)	0.1871	6
Number of puncta/ μm with MO KD_WT - co-MO - MO	2F	no	Kruskall wallis (non parametric 1-way Anova) for multiple comparisons (Dunn)	61	(WT+ MB). 61 axons in which the total the number of particles was normalized on the axonal length measured in μm	from 4 frogs (= indep. exp.)	mean +/- SEM	**** (WT vs MO)	<0.0001	
		yes		15	(250 μM co-MO + MB). 15 axons in which the total the number of particles was normalized on the axonal length measured in μm	from 4 frogs (= indep. exp.)	mean +/- SEM	*** (co-MO vs MO)	0.0002	
		yes		35	(250 μM MO + MB). 35 axons in which the total the number of particles was normalized on the axonal length measured in μm	from 4 frogs (= indep. exp.)	mean +/- SEM	ns (WT vs co-MO)	0.8114	
Coloc exo-endo (#MB+pre-miR+)	2K	yes		32	32 single axons. (Compute relative % in each axon of coloc)	from 5 frogs (= indep. exp.)	mean +/- SEM			
Percentage of puncta moving antero and retro (ENDO and EXO)	3D		2-way ANOVA multiple comparisons (Sidak)	3	3 biological replicates (endo)	from 3 frogs (= indep. exp.) Compute relative % in each N and then compare endo exo, antero retro	mean +/- SEM	ns (endo antero vs exo antero)	0.8358	10
				4	4 biological replicates (exo)	from 4 frogs (= indep. exp.) Compute relative % in each N and then compare endo exo, antero retro	mean +/- SEM	ns (endo retro vs exo retro)	0.8358	10
							mean +/- SEM	ns (endo antero vs retro)	0.767	10
							mean +/- SEM	ns (exo antero vs retro)	0.9033	10
Puncta average speed antero and retro (ENDO and EXO)	3E	no	2-way ANOVA multiple comparison (Tukey)	72	MB antero particles <0.2 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	median with interquartile range	ns (antero endo vs exo <0.2 $\mu\text{m/s}$)	> 0.9999	825
		yes	2-way ANOVA multiple comparison (Tukey)	19	MB antero particles 0.2-0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	median with interquartile range	ns (antero endo vs exo 0.2-0.5 $\mu\text{m/s}$)	0.9882	825
		no	2-way ANOVA multiple comparison (Tukey)	86	MB antero particles > 0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	median with interquartile range	ns (antero endo vs exo >0.5 $\mu\text{m/s}$)	0.8911	825
		no	2-way ANOVA multiple comparison (Tukey)	67	MB retro particles <0.2 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	median with interquartile range	ns (retro endo vs exo <0.2 $\mu\text{m/s}$)	0.9998	825
		no	2-way ANOVA multiple comparison (Tukey)	30	MB retro particles 0.2-0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	median with interquartile range	ns (retro endo vs exo 0.2-0.5 $\mu\text{m/s}$)	0.9998	825
		no	2-way ANOVA multiple comparison (Tukey)	79	MB retro particles >0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	median with interquartile range	ns (retro endo vs exo >0.5 $\mu\text{m/s}$)	0.96	825
		no	2-way ANOVA multiple comparison (Tukey)	50	Cy3 antero particles <0.2 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)	median with interquartile range	ns (antero vs retro endo <0.2 $\mu\text{m/s}$)	0.9996	825
		no	2-way ANOVA multiple comparison (Tukey)	28	Cy3 antero particles 0.2-0.5 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)	median with interquartile range	ns (antero vs retro endo 0.2-0.5 $\mu\text{m/s}$)	0.9998	825
		no	2-way ANOVA multiple comparison (Tukey)	157	Cy3 antero particles > 0.5 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)	median with interquartile range	**** (antero vs retro endo >0.5 $\mu\text{m/s}$)	< 0.0001	825
		no	2-way ANOVA multiple comparison (Tukey)	83	Cy3 retro particles <0.2 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)	median with interquartile range	ns (antero vs retro exo <0.2 $\mu\text{m/s}$)	0.9912	825
		no	2-way ANOVA multiple comparison (Tukey)	62	Cy3 retro particles 0.2-0.5 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)	median with interquartile range	ns (antero vs retro exo 0.2-0.5 $\mu\text{m/s}$)	0.9718	825
		no	2-way ANOVA multiple comparison (Tukey)	106	Cy3 retro particles > 0.5 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)	median with interquartile range	**** (antero vs retro exo >0.5 $\mu\text{m/s}$)	< 0.0001	825
MSD fitting curve (ENDO and EXO)	3F	yes	Non linear regression - comparisons of fit (anomalous diffusion equation), B1	67	endogenous_tracked particles	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (H0: B1 same for all data sets, endo vs exo)	0.9795	
		yes		82	exogenous_tracked particles	from 4 frogs (= indep. exp.)	mean +/- SEM			
MSD alpha coefficient distribution (ENDO and EXO)	3G	no	Mann-Whitney 2-tailed	67	endogenous_tracked particles	from 3 frogs (= indep. exp.)	median with interquartile range	ns (endo vs exo MSD alpha values)	0.8797	
		no		82	exogenous_tracked particles	from 4 frogs (= indep. exp.)	median with interquartile range			
Distribution MSD alpha coefficient per categories (ENDO and EXO)	3H		2-way ANOVA multiple comparison (Tukey)	3	endogenous_tracked particles	from 3 frogs (= indep. exp.) Compute relative % in each N and then compare endo exo, antero retro	mean +/- SEM	ns (endo vs exo MSD_alpha<0.5)	0.7915	15
				4	exogenous_tracked particles	from 4 frogs (= indep. exp.) Compute relative % in each N and then compare endo exo, antero retro	mean +/- SEM	ns (endo vs exo 0.9-MSD_alpha<1.1)	0.9981	15
							mean +/- SEM	ns (endo vs exo MSD_alpha>1.5)	0.846	15
Percentage per velocity categories _antero (ENDO and EXO)	S3C		2-way ANOVA multiple comparison (Tukey)	3	3 biological replicates (endo)	from 3 frogs (= indep. exp.) Compute relative % in each N and then compare antero endo vs antero exo	mean +/- SEM	ns (endo antero vs exo antero <0.2 $\mu\text{m/s}$)	0.2363	30
				4	4 biological replicates (exo)	from 4 frogs (= indep. exp.) Compute relative % in each N and then compare antero endo vs antero exo	mean +/- SEM	ns (endo antero vs exo antero 0.2-0.5 $\mu\text{m/s}$)	0.9923	30
							mean +/- SEM	ns (endo antero vs exo antero >0.5 $\mu\text{m/s}$)	0.1433	30
Percentage per velocity categories _retro (ENDO and EXO)	S3D		2-way ANOVA multiple comparison (Tukey)	3	3 biological replicates (endo)	from 3 frogs (= indep. exp.) Compute relative % in each N and then compare retro endo vs antero exo	mean +/- SEM	ns (endo retro vs exo retro <0.2 $\mu\text{m/s}$)	0.9479	30
				4	4 biological replicates (exo)	from 4 frogs (= indep. exp.) Compute relative % in each N and then compare retro endo vs antero exo	mean +/- SEM	ns (endo retro vs exo retro 0.2-0.5 $\mu\text{m/s}$)	0.2699	30
							mean +/- SEM	ns (endo retro vs exo retro >0.5 $\mu\text{m/s}$)	0.5842	30
Percentage categories velocities +/- Nocodazole	4C		2-way ANOVA multiple comparison (Tukey)	162	no Noco MB particles <0.2 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (no Noco vs Noco <0.2 $\mu\text{m/s}$)	< 0.0001	
				62	no Noco MB particles 0.2-0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (no Noco vs Noco 0.2-0.5 $\mu\text{m/s}$)	0.167	
				134	no Noco MB particles > 0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)	mean +/- SEM	** (no Noco vs Noco >0.5 $\mu\text{m/s}$)	0.0011	
				428	Noco MB particles <0.2 $\mu\text{m/s}$	from 4 frogs (= indep. exp.)				
				29	Noco MB particles 0.2-0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)				
				46	Noco MB particles > 0.5 $\mu\text{m/s}$	from 3 frogs (= indep. exp.)				
Mean velocities +/- Nocodazole	4D	no	Mann-Whitney 2-tailed	358	no Noco particles trafficked	from 3 frogs (= indep. exp.)	median with interquartile range	**** (no Noco vs Noco)	< 0.0001	
		no		503	Noco particles trafficked	from 3 frogs (= indep. exp.)	median with interquartile range			
Percentage of co-trafficking: % MB+/CD63+ s126+40h	4I	yes		22	#MB/CD63+ 22 single axons	from 5 frogs (=indep.exp.)	mean +/- SEM			
Percentage of co-trafficking: % MB+/CD63+ s126+40h (ANTERO vs RETRO)	4J	yes	Unpaired t test 2-tailed	22	22 single axons	from 5 frogs (=indep.exp.) 92 anterograde particles and 78 retrograde particles on a total of 170 co-trafficked MB+/CD63+ particles.	mean +/- SEM	ns (% MB+/CD63+ antero vs retro)	0.7404	
		yes		22	22 single axons		mean +/- SEM			

Percentage of co-trafficking: % MB+/CD63+ s137/38	S4E	yes		17	17 single axons (#MB/CD63+)	from 5 frogs (=indep. exp.)	mean +/- SEM			
Percentage of co-trafficking: % MB+/CD63+ s137/38 (ANTERO vs RETRO)	S4F	yes	Unpaired t test 2-tailed	17	17 single axons	from 5 frogs (=indep. exp.) 57 anterograde particles and 50 retrograde particles on a total of 116 co-trafficked MB+/CD63+ particles.	mean +/- SEM	ns (% MB+/CD63+ antero vs retro)	0.9162	
		yes		17	17 single axons		mean +/- SEM			
Sema3A vs PBS (2 ^o -dCI) norm to PBS)	S5D									
miR-181a-5p		N too small	Mann-Whitney 2-tailed	6	4 biological replicates + 2 technical replicates	from 4 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	**	0.0022	
miR-181a-1-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	*	0.0286	
miR-181a-2-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	*	0.0286	
pre-miR-181a-1		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	*	0.0286	
pre-miR-181a-2		N too small	Mann-Whitney 2-tailed	5	4 biological replicates + 1 technical replicate	from 4 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	*	0.0317	
pre-miR-182		N too small	Mann-Whitney 2-tailed	3	3 biological replicates	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.9	
Sil12 vs PBS (2 ^o -dCI) norm to PBS)	S5E									
miR-181a-5p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.8571	
miR-181a-1-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.8286	
miR-181a-2-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.4286	
pre-miR-181a-1		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.8286	
pre-miR-181a-2		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.8286	
pre-miR-182		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns	0.8286	
Collapse assay – Sema3A with or without CHX	S5C									
PBS no CHX			2-way ANOVA multiple comparison (Tukey)	1380	counted axons	from 3 frogs (= indep. exp.) each time 1 or 2 plates	mean +/- SEM	**** (PBS vs Sema no CHX)	<0.0001	16
Sema3A no CHX			2-way ANOVA multiple comparison (Tukey)	1125	counted axons	from 3 frogs (= indep. exp.) each time 1 or 2 plates	mean +/- SEM	**** (Sema no CHX vs CHX)	<0.0001	16
PBS CHX			2-way ANOVA multiple comparison (Tukey)	729	counted axons	from 3 frogs (= indep. exp.) each time 1 or 2 plates	mean +/- SEM	*** (PBS vs Sema CHX)	0.0002	16
Sema3A CHX			2-way ANOVA multiple comparison (Tukey)	852	counted axons	from 3 frogs (= indep. exp.) each time 1 or 2 plates	mean +/- SEM	ns (PBS CHX vs PBS no CHX)	> 0.9999	16
miR-181 mature isoforms in isolated axons (upon Sema3A exposure)	S5D									
miR-181a-5p		yes	1-way ANOVA multiple comparison (Tukey)	6	4 biological replicates + 2 technical replicates	from 4 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	**** (miR-181a-5p vs miR-181a-1-3p)	<0.0001	11
miR-181a-1-3p		yes	1-way ANOVA multiple comparison (Tukey)	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	**** (miR-181a-5p vs miR-181a-2-3p)	<0.0001	11
miR-181a-2-3p		yes	1-way ANOVA multiple comparison (Tukey)	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.). 40 explants per N.	mean +/- SEM	ns (miR-181a-1-3p vs miR-181a-2-3p)	0.9318	11
Collapse assay axonal transfection MOs 5p	S6D									
PBS co-MO			2-way ANOVA multiple comparison (Tukey)	743	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (PBS co-MO vs. PBS MO)	0.2361	8
Sema3A co-MO			2-way ANOVA multiple comparison (Tukey)	907	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	*** (PBS co-MO vs. Sema3A co-MO)	0.0001	8
PBS MO			2-way ANOVA multiple comparison (Tukey)	848	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (PBS MO vs. Sema3A MO)	0.8605	8
Sema3A MO			2-way ANOVA multiple comparison (Tukey)	518	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	** (Sema3A co-MO vs. Sema3A MO)	0.0022	8
Collapse assay axonal transfection MOs 3p	S6E									
PBS co-MO			2-way ANOVA multiple comparison (Tukey)	354	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (PBS co-MO vs. PBS MO)	0.5602	8
Sema3A co-MO			2-way ANOVA multiple comparison (Tukey)	405	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (PBS co-MO vs. Sema3A co-MO)	<0.0001	8
PBS MO			2-way ANOVA multiple comparison (Tukey)	317	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	** (PBS MO vs. Sema3A MO)	0.0096	8
Sema3A MO			2-way ANOVA multiple comparison (Tukey)	324	number of counted axons	from 3 frogs (= indep. exp.)	mean +/- SEM	** (Sema3A co-MO vs. Sema3A MO)	0.0038	8
miRNA expression level after MOs 5p microinjection	S6B									
miR181 co-MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-5p MO vs co-MO)	0.0286
miR181 MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-1-3p MO vs co-MO)	0.0286
miR181a-1-3p co-MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-1-3p MO vs co-MO)	0.0286
miR181a-1-3p MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-1-3p MO vs co-MO)	0.0286
miR181a-2-3p co-MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-2-3p MO vs co-MO)	0.0286
miR181a-2-3p MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-2-3p MO vs co-MO)	0.0286
miRNA expression level after MOs 3p microinjection	S6C									
miR181 co-MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-5p MO vs co-MO)	0.0286
miR181 MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-1-3p MO vs co-MO)	0.0286
miR181a-1-3p co-MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-1-3p MO vs co-MO)	0.0286
miR181a-1-3p MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-1-3p MO vs co-MO)	0.0286
miR181a-2-3p co-MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-2-3p MO vs co-MO)	0.0286
miR181a-2-3p MO		N too small	Mann-Whitney 2-tailed	4	4 biological replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(miR-181a-2-3p MO vs co-MO)	0.0286
qPCR axonal transfection MOs 5p	S6E									
PBS co-MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	6	4 biological replicates + 2 technical replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	*	(181a-1-3p PBS co-MO vs 181a-1-3p Sema co-MO)	0.0411
Sema3A co-MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	6	4 biological replicates + 2 technical replicates	from 4 frogs (= indep. exp.)	mean +/- SEM			
PBS MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	6	4 biological replicates + 2 technical replicates	from 4 frogs (= indep. exp.)	mean +/- SEM	ns	(181a-1-3p PBS MO vs 181a-1-3p Sema MO)	0.6753
Sema3A MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	6	4 biological replicates + 2 technical replicates	from 4 frogs (= indep. exp.)	mean +/- SEM			
qPCR axonal transfection MOs 3p	S6F									
PBS co-MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.)	mean +/- SEM	*	(181a-5p PBS coMO vs 181a-5p Sema coMO)	0.0286
Sema3A co-MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.)	mean +/- SEM			
PBS MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.)	mean +/- SEM	ns	(181a-5p PBS MO vs 181a-5p Sema MO)	0.9714
Sema3A MO 181a-1-3p		N too small	Mann-Whitney 2-tailed	4	3 biological replicates + 1 technical replicate	from 3 frogs (= indep. exp.)	mean +/- SEM			
Ratio of misprojecting axons co-MO vs miR-181 MO stage 40	7C									
co-MO		no	Mann-Whitney 2-tailed	45	numbers of brains, hence of embryos	from 4 frogs (= indep. exp.)	mean +/- SEM	**** (co-MO vs miR-181 MO family)	< 0.0001	
miR-181 family		no	Mann-Whitney 2-tailed	52	numbers of brains, hence of embryos	from 4 frogs (= indep. exp.)	mean +/- SEM			

Ratio of misprojecting axons rescue experiment with mimics stage 40		7E										
	co-MO+ctrl mimics	yes	1-way ANOVA multiple comparison (Tukey)	96	number of co-electroporated axons	from 4 frogs (= indep. exp.)	mean +/- SEM	** (co-MO + ctrl mimics vs. miR-181-MO + ctrl mimics)	0.0055			
	miR-181 MO + ctrl mimics	yes	1-way ANOVA multiple comparison (Tukey)	101	number of co-electroporated axons	from 4 frogs (= indep. exp.)	mean +/- SEM	ns (co-MO + ctrl mimics vs. miR-181-MO + miR-181ab mimics)	0.9431			
	miR-181 MO + miR181ab mimics	yes	1-way ANOVA multiple comparison (Tukey)	134	number of co-electroporated axons	from 4 frogs (= indep. exp.)	mean +/- SEM	** (miR-181-MO + ctrl mimics vs. miR-181-MO + miR-181ab mimics)	0.0089			
Ratio of misprojecting axons co-MO vs miR-181 MO stage 44/45		7G										
	co-MO	no	Mann-Whitney 2-tailed	21	numbers of brains, hence of embryos	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (co-MO vs miR-181 MO family)	< 0.0001			
	miR-181	yes	Mann-Whitney 2-tailed	31	numbers of brains, hence of embryos	from 3 frogs (= indep. exp.)	mean +/- SEM					
In vivo behavioural assay stage 44/45		7I										
		no	Mann-Whitney 2-tailed	43	numbers of brains, hence of embryos	from 4 frogs (= indep. exp.)	mean +/- SEM	* (co-MO vs miR-181 MO)	0.0323			
		no	Mann-Whitney 2-tailed	45	numbers of brains, hence of embryos	from 4 frogs (= indep. exp.)	mean +/- SEM					
In vivo behavioural assay stage 44/45 blind control		7D										
		no	Mann-Whitney 2-tailed	15	number of embryos	from 4 frogs (= indep. exp.)	mean +/- SEM	**** (WT vs blind)	< 0.0001			
		no	Mann-Whitney 2-tailed	14	number of embryos	from 4 frogs (= indep. exp.)	mean +/- SEM					
FRAP on TUBB3 ex vivo wt, mut, Sema3A		8B										
	TUBB3 wt		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 5 frogs (= indep. exp.)	mean +/- SEM					
	TUBB3 wt + Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 5 frogs (= indep. exp.)	mean +/- SEM					
	TUBB3 mut		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	14	number of single FRAP axon	from 5 frogs (= indep. exp.)	mean +/- SEM	Table 4 reported FRAP experiment stat				
	TUBB3 mut + Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 5 frogs (= indep. exp.)	mean +/- SEM					
	TUBB3 mut + Sema3A + CHX		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	12	number of single FRAP axon	from 5 frogs (= indep. exp.)	mean +/- SEM					
	no UTR		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	12	number of single FRAP axon	from 5 frogs (= indep. exp.)	mean +/- SEM					
FRAP on TUBB3 ex vivo - isolated axons		8C										
	TUBB3 mut - isolated axons		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	12	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	ns (mut vs mut+Sema3A)	0.5053			
	TUBB3 mut + Sema3A - isolated axons		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	Table 4 reported FRAP experiment stat				
FRAP on TUBB3 ex vivo co-MO vs MO		8D										
	TUBB3 co-MO Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	14	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (TUBB3 coMO vs MO)	< 0.0001			
	TUBB3 MO Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	16	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	Table 4 reported FRAP experiment stat				
FRAP on TUBB3 in vivo		8E										
	TUBB3 wt		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	12	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	** (TUBB3 wt vs TUBB3 mut in vivo)	0.005			
	TUBB3 mut		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	14	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (TUBB3 mut vs no UTR)	< 0.0001			
	no UTR		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	8	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (TUBB3 wt vs no UTR)	< 0.0001			
								Table 4 reported FRAP experiment stat				
FRAP on APP ex vivo wt, mut, Sema3A		8F										
	APP wt		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 4 frogs (= indep. exp.)	mean +/- SEM					
	APP wt + Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 4 frogs (= indep. exp.)	mean +/- SEM	Table 4 reported FRAP experiment stat				
	APP mut		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 4 frogs (= indep. exp.)	mean +/- SEM					
	APP mut + Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	13	number of single FRAP axon	from 4 frogs (= indep. exp.)	mean +/- SEM					
FRAP on THBS1 ex vivo wt, mut, Sema3A		8G										
	THBS1 wt		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	11	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM					
	THBS1 wt + Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	11	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	Table 4 reported FRAP experiment stat				
	THBS1 mut		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	11	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM					
	THBS1 mut + Sema3A		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	11	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM					
FRAP on ACTB ex vivo		8C										
	ACTB		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	9	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	**** (ACTB vs ACTB + CHX)	< 0.0001			
	ACTB + CHX		Non linear regression - comparisons of fit (one phase decay) Y0, Plateau, K	9	number of single FRAP axon	from 3 frogs (= indep. exp.)	mean +/- SEM	Table 4 reported FRAP experiment stat				