S5 Table. Statistical measures and raw counts.

genotype / treatment		Motoneuron phenotype observed n (3 trials)		Total N	p (normal/total)
		normal	disrupted		
Wild-type	Slc25a46 F0 CRISPR	10 (3,2,3)	23 (7,8,10)	33	0.24 (0.3, 0.2, 0.23)
	Slc25a46 F0 CRISPR + hRNA	19 (6,6,7)	9 (4,3,2)	28	0.68 (0.6, 0.67, 0.78)
	Control Cas9	30 (10,10,10)	0 (0, 0, 0)	30	1 (1,1,1)
	Slc25a46 ex3 MO	5 (2, 2, 1)	25 (8, 8, 9)	30	0.17 (0.20, 0.20, 0.10)
	Slc25a46 ex7 MO	10 (5, 2, 3)	19 (7, 6, 6)	29	0.33 (0.42, 0.25, 0.33)
	Control MO	24 (9, 9, 6)	0 (0, 0, 0)	24	1 (1,1,1)
	uninjected	20 (6,6,8)	0 (0, 0, 0)	20	1 (1,1,1)
slc25a46^{238s}	Slc25a46 CRISPR	17 (6, 6, 5)	0 (0, 0, 0)	17	1 (1,1,1)
	Slc25a46 ex3 MO	16 (6, 6, 4)	9 (3, 2, 4)	25	0.64 (0.67, 0.75, 0.50)
	Slc25a46 ex7 MO	43 (18, 16, 9)	2 (1, 0, 1)	45	0.96 (0.97, 1, 0.9)
	Control MO	30 (8, 13, 9)	1 (0, 1, 0)	31	0.97 (1, 0.92, 1)
	uninjected	33 (10, 13, 10)	0 (0, 0, 0)	33	1 (1,1,1)

Comparison Configuration	p1	n1	actual α	Odds ratio	Power
	p2	n2			
slc25a46 F0 CRISPR	0.24	33			
slc25a46 F0 CRISPR + hRNA	0.68	28	0.03	0.15	0.95
slc25a46 F0 CRISPR	0.24	33			
WT Control Cas9	1	30	0	0	1
slc25a46 F0 CRISPR	0.24	33			
slc25a46^{238s} uninjected	1	20	0	0	1
slc25a46 F0 CRISPR	0.24	33			
Slc25a46^{238s} CRISPR	1	17	0	0	1
Slc25a46^{238s} ex3 MO	0.64	25			
WT ex3 MO	0.17	30	0.03	8.68	0.97
WT ex7 MO	0.33	29			
WT Control MO	1	24	0	0	0.99
Slc25a46^{238s} ex7 MO	0.96	45			
WT ex7 MO	0.33	29	0.05	44.57	0.99