

Table S1. Selected muscle diseases.

Disease	Disease description
Myotonic dystrophy (DM)	The most common adult muscular dystrophy, is characterized by autosomal dominant progressive myopathy. Two distinct forms caused by similar mutations in two different genes have been identified: myotonic dystrophy type 1 (DM1, with mutations in myotonin-protein kinase) and myotonic dystrophy type 2 (DM2 with mutations in the cellular nucleic acid-binding protein gene, <i>CNBP</i>).
Duchenne muscular dystrophy (DMD)	An X-linked recessive disorder in the dystrophin gene (1/5000 boys) presents in early childhood (age of 4) with proximal muscle weakness. Dystrophin function is linked with microtubule binding. The absence of dystrophin causes DMD.
Becker muscular dystrophy (BMD)	Mutations resulting in a reduced amount or shortened dystrophin protein cause BMD. BMD has a mean onset at 12 years, with loss of ambulation occurring around the third decade of life, and a life expectancy that is similar to the general population, contrasting DMD.
Pompe disease	A rare and deadly muscle disorder, combines a glycogen storage disorder, a lysosomal disorder, and an autophagic myopathy, caused by mutations in the gene coding for acid alpha-glucosidase (GAA, breaking down glycogen in the lysosome acidic milieu).
Tibial muscular dystrophy (TMD)	A late onset, autosomal dominant distal myopathy, results from mutations in the two last domains of titin (associated with the unfolded protein response and altered autophagy).
Dysferlinopathies	Harboring dysferlin mutations (<i>DYSF</i>). Dysferlin is responsible for membrane resealing, and mutations may result in a defect in membrane repair following mechanical or chemical stress, causing an influx of Ca^{2+} and affecting mitochondrial function.
Secondary dystroglycanopathies	Mutations in the fukutin related protein gene (<i>FKRP</i>) cause secondary dystroglycanopathies, muscular dystrophies that result from mutations in genes that participate in dystroglycan glycosylation, which is in turn essential for the muscle fibers to adhere to the muscle extracellular matrix.
Amyotrophic lateral sclerosis (ALS)	ALS patients also suffer from muscle wasting and our previous studies have shown brain tauopathy in the SOD1-G93A mouse model of ALS, which was corrected by NAP. (See main text, discussion).

Table S2. A tabular summary of the different patients and aged matched controls characterizations.

Disease	Pompe	DMD	DM2	TMD	BMD	DYSF	FKRP	ALS
Age of sampling	<u>Control:</u> 2m-2y 11 m <u>Patient:</u> 1 y 5 m	<u>Control:</u> 5-7 y <u>Patient:</u> 1-10 y	<u>Control:</u> 45-54 y <u>Patient:</u> 37-55 y	<u>Control:</u> 76-80 y <u>Patient:</u> 48-65 y	<u>Control:</u> N/A <u>Patient:</u> 10-32 y	<u>Control:</u> N/A <u>Patient:</u> 16-38 y	<u>Control:</u> N/A <u>Patient:</u> 12-55 y	<u>Control:</u> N/A <u>Patient:</u> 45-55 y
Muscle type	Biceps	Quadriceps	Vastus lateralis	Distal muscles	Typically, from the vastus lateralis	Typically, from the vastus lateralis	Typically, from the vastus lateralis	Typically, from the vastus lateralis
Sex	Males & Females	Males	Males & Females	Males	Males	Males & Females	Males & Females	Males

Table S3. G68 off targets. The vast majority have 4 mismatches with the G68 sequence, some have 3 and only 1-off target has 2 mismatches (intronic), making the effects of these targets mostly negligible.

offtargetSeq	mismatch hPos	mismatch Count	mitOfftarg etScore	cfOfftarg etScore	chr om	start	end	Stran d	locusDesc
GAGGGAAGAAGTAG GACTGTGGG	**...*..*	4	0.89998622	0.72527472 5	chr1 1	1.2E +08	1.2E +08	-	intron:Aspscr1
ATGGGTAGATGCAGA ACTGTGGG	**...* ..*.....	4	0.07795276 1	0.63688633 3	chr8	6.1E +07	6.1E +07	-	intron:2700029M09Rik
CTGGGAGGATACAAG ACTGTGGG	*.....** .*.....	4	0.06115766 3	0.60902255 6	chr9	1E+0 8	1E+0 8	+	intergenic:Gm5161-Ephb1
ACAGGAAGATGTAA GACTGTTGG	.**...*.... .*.....	4	0.15083093 2	0.48214285 7	chr7	1.3E +08	1.3E +08	+	exon:D430042O09Rik
AGGAGTGAAGTAG GACTGTTGG	.***...*..	4	0.76055280 2	0.46285714 3	chr9	2.6E +07	2.6E +07	-	intergenic:Gm26190-B3gat1
ATGGGGAGATGCAG GACTTTAGG	**...**	4	0.09626274 9	0.45112782	chr8	1E+0 8	1E+0 8	-	intergenic:Bean1-Tk2
AAGGGAGGATGAGG AACTGTGGG	.*.....* .*.....	4	0.07670389	0.41550265 6	chr3	2.8E +07	2.8E +07	-	intergenic:Tmem212-Pld1
ATTGGAAGATAAAG ACTGTGGG	..*...*.. *.....	4	0.26309417 4	0.4	chr1 9	2.2E +07	2.2E +07	+	intergenic:Gda-Gm3443
ACGGGGAGATGTGG GACTGTGGG	.*...**.... *.....	4	0.22879291 4	0.39929015 1	chr1 6	3.7E +07	3.7E +07	-	intron:Golgb1
GGGGGAGGAGGTAG AACTGTGGG	**.....*.. ..*.....	4	0.37102310 1	0.39529411 8	chr1 1	2.2E +07	2.2E +07	-	intergenic:Gm12047-Wdpcp
AGGGAAGGATGCAG GACTGAAGG	.*.*.....**	4	0.34314401 4	0.38794736 9	chr1 5	5.5E +07	5.5E +07	-	intron:Mal2
ATGAGAGTATATAGG ACTTTCGG	...*...*..*	4	0.27680625	0.375	chr7	7.4E +07	7.4E +07	+	intergenic:RP23-32A8.1-Gm26176
GGGGGAGGGTGTAG GACTTTTGG	**.....*..*	4	0.32190448 9	0.37333333 4	chr X	1.1E +08	1.1E +08	-	intergenic:Gm6377/Sh3bgrl-Gm14868
ATGGGAGAATAAAG GAATGTTGG	*..***	4	0.15040917 9	0.37333333 4	chr1 6	1.8E +07	1.8E +07	-	intergenic:Vpreb2-Dgcr6
AGAGGGGGATGAAG GACTGTAGG	.**...*.... *.....	4	0.41990681	0.36	chr1 8	7E+0 7	7E+0 7	+	intergenic:Rab27b-Dynap
CTGGGAGGGTGTAGA ACTTTTGG	*.....*.... .*...*	4	0.08627040 3	0.35854341 8	chr7	7.4E +07	7.4E +07	-	intergenic:Slco3a1-Gm7580

TTGGGAGGCTGTGGA ACTGTAGG	*.....*... *.*.....	4	0.09525625 3	0.35074899 5	chr X	1.7E +08	1.7E +08	+	intergenic:Gm15238-Frmpd4
ATGGAAGAATCTAGA ACTGTTGG	...*.*.*. ..*.....	4	0.21280572 3	0.34957983 3	chr1 6	8.4E +07	8.4E +07	+	intergenic:Rpl21-ps5-Gm24508
ATGGAGGGAAGTGG GACTGTAGG	...**.*.. *.....	4	0.29433393 4	0.34605146 4	chr1	4.2E +07	4.2E +07	-	intergenic:Gm5973-Gm9915
AAGGGACCATGTAGA ACTGTAGG	.*...**.... ..*.....	4	0.27514525 3	0.33693003 8	chr6	1E+0 8	1E+0 8	-	intergenic:Gm24248-Rybp
ATGAGAGGATAAAG GAATGTTGG	...*.....***...	4	0.15802483 4	0.336	chr1 3	1.2E +07	1.2E +07	+	intergenic:Gm25496-Ryr2
TGGGGAGGAGGAAG GACTGTGGG	**.....*. *.....	4	0.64830632 5	0.336	chr7	5.9E +07	5.9E +07	+	intergenic:Gm26288-Atp10a
ATGGGAGGGTGAAG AACTTTCGG	*.*. .*...*	4	0.03630840 6	0.33464052 3	chr2	6.9E +07	6.9E +07	-	intron:Lrp2
AAGGGAGGCAGAAG GACTGTGGG	.*.....**. *.....	4	0.39611516 5	0.33155416	chr3	2.6E +07	2.6E +07	+	intergenic:Gm24250-Nlgn1
GTGGAAGGCTGTAGG ACTTTGGG	*.*.*.*...*.	4	0.32190448 9	0.33015873	chr7	3.8E +07	3.8E +07	+	intergenic:Uri1-Ccne1
ATGGGAGAAGATGG GACTGTTGG	*.*. *.....	4	0.25814029 6	0.32608695 7	chr1 0	8.3E +07	8.3E +07	+	intergenic:Chst11-Slc41a2
ACAGGAGCATGAAG GACTGTGGG	.**....*... *.....	4	0.69406084 3	0.31648351 6	chr1 1	5.2E +07	5.2E +07	+	intron:Sec24a
ATGGGAATATAGAGG ACTGTGGG	*.*.* *.....	4	0.24337222 7	0.3125	chr3	1.3E +08	1.3E +08	-	intergenic:Gm23011-Gm26691
ATGAAAGGAGGAAG GACTGTGGG	...**....*. *.....	4	0.61849913 8	0.312	chr1 1	5.9E +07	5.9E +07	+	intron:Fam183b
AAGGGATGAAGTAA GACTGTGGG	.*...*.*.. .*.....	4	0.14088771 6	0.31083202 5	chr4	1.1E +08	1.1E +08	-	intron:Slc1a7
AGGGAAGGAGGAAG GACTGTAGG	.*.*.*.*. *.....	4	0.64830632 5	0.2912	chr1 5	4.3E +07	4.3E +07	+	intergenic:Gm17473-Rspo2
ATGAAAGGATGTGGG ACTGATGG	...**..... *.....*	4	0.25551675	0.28614130 4	chr1 2	3.3E +07	3.3E +07	-	intron:Gm11052
ATGGATGGATGAAGG ACTGAAGG	**.....**	4	0.19653001 5	0.27857142 9	chr8	9.5E +07	9.5E +07	-	exon:Cngb1
ACAGGAAGATCTAGG ACTGTAGG	.**.*.*.*	4	0.53474425 5	0.27551020 4	chr1 9	4.6E +07	4.6E +07	-	intron:Gbf1

AGGGAAGGATGAAG GATTGTAGG	.*. *.....**..	4	0.299915	0.27178666 7	chr5	1.1E +08	1.1E +08	-	intergenic:E130006D01Rik- Miat/MIAT_exon5_3/MIAT_exon5_2/G m26953/MIAT_exon5_1
AGGGGAGGAAGTAG GACAGAGGG	. *.....*...*.*	4	0.12590037 6	0.27	chr5	1.4E +08	1.4E +08	+	intron:Gna12
AAGGGAGGAGGCAG GACAGTAGG	. *.....*.**..	4	0.14062196 4	0.26720647 8	chr1 0	5.6E +07	5.6E +07	-	intergenic:Gm25602-Tbc1d32
ATGGGGGAATGAAG GAATGTAGG	*.* **..	4	0.16395955 6	0.26666666 7	chr1	2.3E +07	2.3E +07	-	intron:Rims1
CTGGGAAGATTAAGG ACTGTTGG	*.....*.* *.....	4	0.26682979 1	0.26373626 4	chr1 5	7E+0 7	7E+0 7	-	intergenic:Gm23987-Fam135b
GTGGGAGGTTGTGGG ACAGTGGG	*.....*... *...*..	4	0.07338048 9	0.26086956 5	chr4	1E+0 8	1E+0 8	+	intron:Dab1
AAGAAAGGATTTAGG ACTGTAGG	. *..*.....*	4	0.79405120 5	0.25384615 4	chr1	8.1E +07	8.1E +07	+	intron:Dock10
CTGGGAGTAGGCAGG ACTGTGGG	*.....*.* *.....	4	0.64830632 5	0.25375939 8	chr1 2	1.2E +08	1.2E +08	+	intron:Ptpn2
AGAGCAGGAGGTAG GACTGTGGG	. *..*.....*	4	1.2395125	0.2475	chr4	6.8E +07	6.8E +07	+	intergenic:Gm11249-Gm11751
AGGTCAAGATGTAGG ACTGTAGG	. *..*.....*	4	0.89127747 3	0.24	chr5	1.5E +08	1.5E +08	+	intergenic:Cdk8-Wasf3
GGGGGAGGTTGTAGG AATGTAGG	**.....*...*..	4	0.37245541 7	0.2352	chr1 3	8.8E +07	8.8E +07	-	intergenic:Gm27044-Gm8526
TTGGGAGGCTCTAGA ACTGTGGG	*.....*.* ..*.....	4	0.13660780 5	0.23049219 7	chr1 6	1E+0 7	1E+0 7	+	intergenic:Emp2-Tekt5
ATGGGAGTCTGCAGG ACTTTAGG	*.* **..	4	0.13547912 8	0.22556391	chr1 6	8395 956	8395 978	+	intergenic:Gm26159-Gm24579
AGGGGAGGGAGTAG GATTGTGGG	. *.....*.**..	4	0.34303143 9	0.224	chr1 1	5.4E +07	5.4E +07	-	intron:Rad50
AAGGGAAGATGTAG GAATGAGGG	. *.....*..... ...*.*	4	0.18339722 4	0.22211538 5	chr1 8	2.1E +07	2.1E +07	+	intergenic:Dsg2-Gm16090/Ttr
ATGGGGAGATGTGGG AATGTGGG	**..... *...*..	4	0.08808527 2	0.21739130 4	chr1 2	6.3E +07	6.3E +07	-	intergenic:Spanxn4-Gm7763
ATGGGGAGATGTGGG AATGTGGG	**..... *...*..	4	0.08808527 2	0.21739130 4	chr1 2	6.3E +07	6.3E +07	-	intergenic:Spanxn4-Gm7763
CTGGGAGGAAGTGG GACTCTGGG	*.....*.. *.....*	4	0.18778306 3	0.21479056 4	chr1 3	4E+0 7	4E+0 7	+	intergenic:Ofcc1-Gm9979

CTAGGAAGATGTAGG ACGGTTGG	*.*...*...*..	4	0.20899025 9	0.21428571 4	chr1 7	3.1E +07	3.1E +07	+	exon:Abcg1
AGGAGAGGTTGTAGG AATGTAGG	*.*...*...*..	4	0.37245541 7	0.21168	chr1 6	1.3E +07	1.3E +07	-	intergenic:Gm6327-Ercc4
ATTGGAAGATGTAGA ACTCTAGG	..*...*..... .*...*	4	0.09001509	0.21095334 7	chr4	2.5E +07	2.5E +07	+	intergenic:Gm11894-Gm25975
AGAGGAGGATGTAG GATTATAGG	.**..... ...*.*	4	0.18933048 8	0.21	chr1 6	2.7E +07	2.7E +07	-	intergenic:Gmnc-Ostn
ATGGGAGAATGTGGG AAAGTGGG	*...* ...**..	4	0.04178142 9	0.20289855 1	chr1 4	4.8E +07	4.8E +07	+	intron:Gm6498
GTTGGAGGAAGTAGG ATTGTGGG	*.*...*..*..	4	0.55356628 3	0.2	chr1 4	7.4E +07	7.4E +07	+	intergenic:Gm16409-Gm22164
ATGGGAGGATGTGAG ACTAATGG	* *...*	4	0.01033851 6	0.19652562 1	chr3	2E+0 7	2E+0 7	-	intergenic:Gyg-Cpa3
AGGGGAGGATAGAG GATTGTGGG	.*.....***..	4	0.16645282 5	0.196	chr1	1.7E +07	1.7E +07	-	intergenic:Gdap1-Gm25166
TGGGGAGGAGGTAG GAATGTGGG	**.....*..*..	4	0.56142625	0.196	chr1 5	2.6E +07	2.6E +07	+	intergenic:Gm5468-Myo10
CTTGGGGTATGTAGG ACTGTAGG	*.*...*...	4	0.81422916 7	0.19132653 1	chr9	1.1E +08	1.1E +08	+	intron:Susd5
GTGGGAGGATGCTGG ACAGTTGG	*.....* *...*	4	0.05908870 8	0.18947368 4	chr1 6	1.7E +07	1.7E +07	+	intergenic:Fgd4-Olfr19
ATGGAAGGACGCAG GACCGTTGG	...*...*.**..	4	0.13350186 5	0.18766917 3	chr1 0	4.3E +07	4.3E +07	-	intergenic:Scml4-Sobp
GTGGGAGGGTGGAG GACTGAGGG	*.....*.**	4	0.20966099 3	0.1875	chr1 1	8.2E +07	8.2E +07	+	exon:Ccl1
ATGGGAGGATTTAAA ACAGTGGG	*.. **..*..	4	0.00592904 1	0.18099547 5	chr1 4	5.3E +07	5.3E +07	-	intergenic:Trav6n-6-Trav12n-1
ATGGCAGGATGTGAG AATGTGGG	...*.....* *...*	4	0.03337063 6	0.17934782 6	chr1 4	2E+0 7	2E+0 7	+	intron:Gng2
ATGGGGGTAGGAAG GACTGTAGG	*.*.* *.....	4	0.37419197 8	0.17857142 9	chr1	4.1E +07	4.1E +07	-	intron:Slc9a2
ATGGGGGGGTGAAG GATTGTAGG	*.*.**..	4	0.10017928 9	0.17777777 8	chr6	2.4E +07	2.4E +07	-	intergenic:Cadps2-Gm24217
ATGGAAGGATGAATA ACTGTGGG	...*.....* **.....	4	0.02810876	0.17401307 2	chr1 5	8.8E +07	8.8E +07	+	intron:Fam19a5
TTGGGAGGATGCAGA GCTGTGGG	*.....*. .**....	4	0.03590878 4	0.17146939 7	chr8	2.7E +07	2.7E +07	+	intron:Poteg

TTGGGAGGTTCTAGG ACTTTTGG	*.....*.*.*.	4	0.17865699 2	0.17142857 2	chr6	1.5E +08	1.5E +08	+	intergenic:Klhl42-Gm7571
AAGAGAGGATGGAG GACTCTGGG	.*.*.....**.	4	0.245385	0.17068965 5	chr1 4	6.2E +07	6.2E +07	-	intergenic:Dleu2-Gm26969
ATGGGAGATTCTGGG ACTGTGGG	**.*. *.....	4	0.17125268 3	0.16770186 4	chr9	1.1E +08	1.1E +08	+	intron:Col7a1
CTGGGAGGACTCAGG ACTGTGGG	*.....** *.....	4	0.35981001 1	0.16657027 2	chr1	1.6E +08	1.6E +08	+	intergenic:Prrx1-Gorab
CTGATGGGATGTAGG ACTGTTGG	*..***.....	4	0.78949175 8	0.16530612 2	chr9	1.1E +08	1.1E +08	+	intron:Bsn
AGTGCAGGATGGAG GACTGTGGG	.*.*.*..... *.....	4	0.69406084 3	0.165	chr5	8367 472	8367 494	-	intron:Adam22
ATGGGGGCATGAAG GATTGTAGG	*.*...**..	4	0.16395955 6	0.16410256 4	chr4	8.8E +07	8.8E +07	+	intron:MIlt3
ATAGGAGGAGGTGG GACAGTGGG	..*.....*.. *....*..	4	0.10906262 2	0.16304347 8	chr1 4	6.1E +07	6.1E +07	+	exon:Spata13
ATGGGAGAAGGGGG GACTGTAGG	*.*.* *.....	4	0.22883788 4	0.16304347 8	chr1 4	6.3E +07	6.3E +07	-	intron:Gata4
ATGGGTGGATCTAGA ACTGAAGG	*.....*.. .*.....*	4	0.05640605 6	0.16206482 6	chr7	1.6E +07	1.6E +07	-	exon:Ccdc9
ATTGGAGGAAGAAG GATTGTAGG	..*.....*.**..	4	0.25856450 4	0.16	chr2	4.8E +07	4.8E +07	+	intergenic:Gm25264-Gm25959
ATGGAAGGATCCAGG ACTCTAGG	*.....***.	4	0.12929304 6	0.15773917 6	chr1 3	1.1E +08	1.1E +08	-	intergenic:Htr1a-Dph3b-ps
ATAAGAGGAGGTAG GAATGTGGG	..**.....*..*..	4	0.52553761	0.1575	chr7	9.7E +07	9.7E +07	+	intron:Tenn4
AGGGGAGGAGGAAG GATTGTGGG	.*.....*.**..	4	0.27622171 5	0.1568	chr1 0	8.5E +07	8.5E +07	+	intergenic:Cry1-AC100386.1
AGGGGAGGAGGAAG GATTGTGGG	.*.....*.**..	4	0.27622171 5	0.1568	chr1 7	3.7E +07	3.7E +07	+	intergenic:H2-M5-Zfp57
ATAGGAGGAAGTAG GACGATGGG	..*.....*..**.	4	0.08877190 2	0.15306122 4	chr3	1.4E +08	1.4E +08	-	intergenic:Rap1gds1-Gm4862
GTGGGTGGATGAATG ACTGTTGG	*.*.*.....* .*.....	4	0.06666736 2	0.15238095 3	chr5	1.1E +08	1.1E +08	-	intron:Crybb2
CTGTGAGGAGGCAGG ACTGTGGG	*.*.....*. *.....	4	0.64830632 5	0.14764183 2	chr1 3	8.3E +07	8.3E +07	-	intergenic:Gm24295-Mef2c
TTTGGAGGATGTAGG ACCTTTGG	*.*.....*..**.	4	0.10181665 1	0.14285714 3	chr X	1.6E +08	1.6E +08	+	intergenic:Gm26007-Gm7199

ATATGAGGATGAGGG ACTGTGGG	..**.....* *.....	4	0.26860154 6	0.14229249	chr1 9	5157 231	5157 253	-	intron:Pacs1
ATTGGAGGATGCAGG ACACTGGG	..*.....*.**.	4	0.04742212 4	0.14156079 9	chr X	1E+0 8	1E+0 8	+	intron:Slc16a2
ATAGGAGGAGGAAG GATTGTAGG	..*.....*.*..	4	0.25856450 4	0.14	chr5	2.2E +07	2.2E +07	-	intergenic:Gm25459-n-R5s170
ATGGGAGTATGGGGG ACTTTTGG	*..* *.....*	4	0.08581083 9	0.13586956 5	chr1 4	8.4E +07	8.4E +07	-	intergenic:Gm24774-Pcdh17
ATGGGAGTATGGGGG ACTTTTGGG	*..* *.....*	4	0.08581083 9	0.13586956 5	chr1 4	9351 961	9351 983	+	intergenic:Gm9800-Fhit
AAGGTAGGATGAAG GACAGTTGG	..*.....**..	4	0.152684	0.13538461 5	chr1 6	4.5E +07	4.5E +07	-	intergenic:Boc-Mir3081
ATTGGAGGATGGAGA ACTGAGGG	..*.....*. .*....*	4	0.08583911 3	0.13235294 1	chr1 7	3.8E +07	3.8E +07	+	intergenic:Gm6726-Gm20410
ATTGGAGATTCTAGG ACTGTTGG	..*....**.*	4	0.45637881 3	0.12857142 9	chr4	7.2E +07	7.2E +07	+	intergenic:C630043F03Rik-Gm11235
ATTGGTGGATGGAGG ACTATAGG	..*.*.....**	4	0.14637951 4	0.12755102	chr8	3.1E +07	3.1E +07	+	intergenic:4933433F19Rik-Dusp26
CTGGGATGATGCAGC ACTGTTGG	*.....*..* ..*.....	4	0.13537146 5	0.12655014 2	chr1	1.6E +08	1.6E +08	+	intergenic:Dnm3-2810442N19Rik
GTGGGAGGCTGAAGC ACTGTGGG	*.....*..* ..*.....	4	0.12110097 3	0.12467532 5	chr6	7E+0 7	7E+0 7	+	exon:Igkv6-20
ATGGGAGGGGGAAG GATTGTGGG	**.**..	4	0.14549264 5	0.12444444 5	chr1 8	7.2E +07	7.2E +07	-	intron:Dcc
ACGGAAGGATGTAG AACTGGGGG	..*.*..... .*....*	4	0.18691584 5	0.12338111 7	chr5	5.1E +07	5.1E +07	-	intergenic:Gm22618-Gm22976
AGGGGAGGATGAAG CACAGTAGG	..*.....*. .*.*..	4	0.04091931 2	0.12218181 8	chr1 1	5.7E +07	5.7E +07	-	intron:Gria1
ATTGGAGGATGAGGG AATGTGGG	..*.....* *...*	4	0.10864762 6	0.12173913 1	chr1 3	8.9E +07	8.9E +07	-	intron:Edil3
ATGTGAGTGTGAAGG ACTGTTGG	...*...**.. *.....	4	0.41031810 3	0.12121212 1	chr4	1.5E +08	1.5E +08	+	intergenic:Fbxo2-Ptchd2
ATGTGAAGAGGTAGG ACTTTTGG	...*.*.*..*	4	0.31373519 6	0.12121212 1	chr1 3	9360 723	9360 745	-	intergenic:Dip2c-Gm26601
CTGATAGGAGGTAGG ACTGTTGG	*..**.*..*	4	1.31769578 3	0.11571428 6	chr X	9.2E +07	9.2E +07	-	intergenic:Mageb5-Gm14782
AAGGTCAGATGTAGG ACTGTAGG	..*..***....	4	0.53922287 1	0.11538461 5	chr9	1.2E +08	1.2E +08	-	intron:Ano10

ATGGGAGGGTGTGGG ATTGAGGG	*..* ...*..*	4	0.05431308 7	0.11413043 5	chr1 5	1E+0 8	1E+0 8	+	intergenic:Krt80-Krt7
ATGGAAGGATTTAGG ATTTTAGG	...*..... ...*..*	4	0.10117443 6	0.10370370 4	chr1 3	7.3E +07	7.3E +07	+	intergenic:Irx2-Irx4
ATGAGAGGATCTAGG AATGAAGG	...*..... ...*..*	4	0.14107891 9	0.10125	chr4	7E+0 7	7E+0 7	-	intergenic:Gm11404-Gm11221
CTGGGAGGCCTTAGG ACTGTGGG	*.....***	4	0.44683722 9	0.10047095 8	chr X	9E+0 7	9E+0 7	+	intergenic:Gm6027-Gm4746
ATGGGAAGATCGAG GATTGTGGG	*..* ...*..*	4	0.10272946 9	0.1	chr4	9.3E +07	9.3E +07	-	intergenic:Gm12642-Tusc1
ATAGGATGAGGTAGG AATGTGGG	..*..*..* ...*..*	4	0.35894218 8	0.1	chr8	9E+0 7	9E+0 7	-	intergenic:Gm24212-Tox3
AGGGGAGGATATAG GACAGGTGG	.*.***** ...*..*	4	0.07586830 5	0.09882352 9	chr X	1.3E +08	1.3E +08	+	intergenic:4921511C20Rik-Gm22636
AGGAGAGGATGTAG GGCAGTGGG	.*.***** ..*..*	4	0.05337733 3	0.09692307 7	chr1 1	3.2E +07	3.2E +07	+	intergenic:Nsg2-Gm12108
AGTGGAGGAAGTATG ACTGTTGG	**.....* .*.....	4	0.20338988	0.096	chr1	1.1E +08	1.1E +08	+	intergenic:2310035C23Rik-Tnfrsf11a
ATGGGAGGAGGTTGA ACTTTCGG	*..* .*..*	4	0.04304983 3	0.09411764 7	chr1 2	6.7E +07	6.7E +07	+	intergenic:MDGA2/Mdga2-Mdga2
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm8320-Gm15114
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm8303-Gm15107
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm15085-Gm15086
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm15085-Gm15086
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm8346-Gm15093
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm8366-Gm15100
ATGGCAGGATTTAGG ATAGTAGG	...*..... ...*..*	4	0.06295298 3	0.09401709 4	chr X	1.5E +08	1.5E +08	-	intergenic:Gm8334-Gm15127
ATGGCAGGATGTAAC ACTGAGGG	...*..... **....*	4	0.02636510 3	0.09040178 6	chr1 6	4.3E +07	4.3E +07	-	intron:Zbtb20
CGGGGAGGAAGTAG TACTGTGGG	**.....* ..*.....	4	0.37102310 1	0.08816326 5	chr2	1.1E +08	1.1E +08	-	exon:Ccdc73

ATGGCAGGAAGTAG GGCAGTAGG	...*...*... ..*..	4	0.04667138 4	0.08634222 9	chr1 2	5.3E +07	5.3E +07	+	intron:Akap6
CTGGGAGGTTGCAGG ACTGGGGG	*.....*.**	4	0.20966099 3	0.08597965 5	chr1 2	7.3E +07	7.3E +07	+	intergenic:D830013O20Rik-Tmem30b
ACGGGAGGATGGAG GATCGTTGG	.*.....*. ...*..	4	0.05878334	0.08571428 6	chr1 6	9.4E +07	9.4E +07	-	intergenic:Dopey2- 2310043M15Rik/Dopey2
CAGGGAGGATGTGG GACTGGGGG	**..... *.....*	4	0.26991206	0.08347151 6	chr1 6	3.2E +07	3.2E +07	-	intergenic:Nrros-Bex6
AAGGGAGGAAGTGG GACTGGAGG	.*.....*.. *.....*	4	0.24858900 7	0.08347151 6	chr1	2.1E +07	2.1E +07	+	intergenic:Gm24723-6720483E21Rik
AAGGGATGCTGTTGG ACTGTGGG	.*...*.*... *.....	4	0.23106193 4	0.08288854	chr1 7	8210 086	8210 108	+	intergenic:Fgfr1op-Ccr6
AGGGGTGGATGTTGG ACTCTAGG	.*...*..... *.....*	4	0.11677483 1	0.08068965 5	chr5	1.2E +08	1.2E +08	-	intergenic:Gm16338-Pitpnm2
ATGGGTGGAGGGAG GACTCTGGG	*...*.**	4	0.12980672 4	0.08004926 1	chr4	1.5E +08	1.5E +08	-	intron:Slc25a33
CTGGGAGGAAGTAG GGCTGAGGG	*.....*... ..*..*	4	0.11048400 3	0.07947409 7	chr4	1.4E +08	1.4E +08	+	intron:Rap1gap
ATGGGAAGAAATAG GACTGCTGG	*...*.**	4	0.21883455 4	0.07792207 8	chr1 0	9051 158	9051 180	-	intergenic:Gm26674/Sash1-Gm9930
ATGGGAAGATGGAG GAAGTTGG	*...*.. ...*..	4	0.03627923 6	0.07777777 8	chr5	1.5E +08	1.5E +08	-	intron:Slc7a1
AGGGGAGGACTTAG GACTCTGGG	.*.....*.**	4	0.25493855 6	0.07724137 9	chr9	5.5E +07	5.5E +07	-	intergenic:Cib2-Idh3a
TTGGGAGGATTTAGG ATCGTAGG	*.....*.. ...*..	4	0.06631047 5	0.07692307 7	chr4	1.1E +08	1.1E +08	-	intron:BC055111
AGGGGAGGAGGCAG GGCTGTGGG	.*.....*.* ...*....	4	0.11715469 7	0.07651821 8	chr1 7	2.6E +07	2.6E +07	-	intergenic:Sstr5-Sox8
AGGGGAGGATTGAG GATTGTAGG	.*.....***..	4	0.16645282 5	0.07538461 6	chr X	1.6E +08	1.6E +08	-	intron:Txlng
CTGGGAGGATCTAGG ACCCTAGG	*.....*..*.*	4	0.05731059	0.07057404 3	chr1 1	1.6E +07	1.6E +07	+	intergenic:Gm12010-Gm12011
ATGGAAGGATTTAGG ATTCTTGG	*...*.. ...*.*	4	0.10117443 6	0.06973180 1	chr2	4.3E +07	4.3E +07	+	intergenic:Gm24350-Gm13464
ATGTGTGGATATATG ACTGTAGG	...*...*.* .*.....	4	0.07157974 6	0.06926406 9	chr1 0	2E+0 7	2E+0 7	+	intron:Pex7
AAGAGAGAATGTAG GACTGCGGG	.*.***....*	4	0.69744718 3	0.06923076 9	chr1 1	6.9E +07	6.9E +07	+	intron:Alox8

TTGGGGGGAGGTAGG GCTGTGGG	*...*... ...*	4	0.15174549 5	0.06868131 9	chr1	1.3E +07	1.3E +07	-	intergenic:Ncoa2-AC121538.1
TTGGGAGGATGAAGA ACTGCAGG	*.....* .*...*	4	0.09196259 6	0.06844919 8	chr5	1.4E +08	1.4E +08	-	intron:Baz1b
ATTGGAGGATGTGAC ACTGTGGG	..*.....* **.....	4	0.02290421 8	0.06669960 5	chr8	1.1E +08	1.1E +08	-	intergenic:Wwox-Gm16116
GTGGGGGGATGTGGT ACTGTCGG	*...*..... .*.....	4	0.09432084	0.06654835 9	chr1 7	4.4E +07	4.4E +07	-	intergenic:Gm24532-Rcan2
CTGGGAGGATGCTGC ACTGTTGG	*.....* .*.....	4	0.07670389	0.06643882 4	chr6	1.2E +08	1.2E +08	-	intergenic:Rpl28-ps4-Gm9946
GTGGGGGGATGTAGG GTTGTGGG	*...*..... ..**..	4	0.06343324 2	0.06410256 4	chr2	6837 162	6837 184	-	intron:Celf2
ATGGGAGGAGGTGG GACCCTGGG	*..**.	4	0.03148420 6	0.06264724 8	chr7	1.1E +08	1.1E +08	-	intron:Cyb5r2
ATGGGAGGATGAAG AAATGGAGG	*.. .*...*	4	0.02889422 5	0.06200692	chr1 8	8.4E +07	8.4E +07	+	intergenic:Gm24720-Tshz1
ATGGGTGGATGAAGG GCTGAAGG	*.....* ..**..	4	0.03209161	0.06181318 7	chr1 5	7.1E +07	7.1E +07	+	intergenic:Gm23987-Fam135b
ATGTGAGGACGTAGG ATAGTAGG	...*.....* ...**..	4	0.10446792 2	0.0603367	chr1 6	4.7E +07	4.7E +07	-	intergenic:Pvrl3-Gm6912
AGGGGAGGATCGAG GACGGTTGG	.*.....***	4	0.08473962	0.06	chr6	4747 105	4747 127	-	exon:Sgce
ATGGGAGGACCCAGC ACTGTGGG	*** ..*.....	4	0.08795180 1	0.05905673 3	chr4	1.4E +08	1.4E +08	+	intergenic:Myom3-Gm13000
ATGTGATGTTGTAGG ATTGTGGG	...*..*...*...	4	0.24150669 3	0.05818181 8	chr5	2E+0 7	2E+0 7	+	intron:Magi2
AAGGGAGGAGGGAG CACTGTCGG	.*.....* .*.....	4	0.18254336 6	0.05769230 8	chr1 3	1E+0 8	1E+0 8	-	intron:Mccc2
ATGGAAGGATGAAG GAATGGAGG	*.....* ...*...*	4	0.12506455 5	0.05709803 9	chr7	1.4E +08	1.4E +08	+	intergenic:Gm9358-Jakmip3
ATGGGAGGATGAAG GATGCTGGG	*.. ..***.	4	0.01596271 7	0.05578544 1	chr4	1.3E +08	1.3E +08	-	intron:Grik3
ATGGGTGGATGTACC ACAGTAGG	*..... **..*..	4	0.00711768 9	0.05565862 7	chr1 4	1.2E +08	1.2E +08	-	intergenic:Clybl-Gm5089
AGGGGAGGATGAAG GAATGGAGG	.*.....* ...*...*	4	0.13211044 5	0.05534117 6	chr5	1.3E +08	1.3E +08	-	intron:Glt1d1
CTGATAGGAAGTAGG ACTGTAAG	*..**...*	4	0.26353915 7	0.05142857 1	chr3	1.8E +07	1.8E +07	-	intergenic:Cyp7b1-Gm6369

ATGGGAGGCTTTTAG ACTGTTGG	*.* **.....	4	0.02551665 9	0.04945054 9	chr4	3.9E +07	3.9E +07	-	intergenic:Gm12381-Gm25581
AAGGGAGGAGGAAG TACTGTGGG	.*.***.* ..*.....	4	0.18254336 6	0.04835164 8	chr6	2.8E +07	2.8E +07	+	intron:Zfp800
ATGGTTGGATGTTAG ACTGTGGG	...**..... **.....	4	0.04991236 3	0.04821428 6	chr1	1.2E +08	1.2E +08	+	intergenic:Gm25578-Actr3
ATGGCAGGTTGTTGG ACGGTGGG	...*...*.. *...*..	4	0.06966502 1	0.04714285 7	chr1 8	7.9E +07	7.9E +07	-	intergenic:Setbp1-Gm25824
ATGGGAGGAGGAAG GACAGGAGG	*.* ...*.*	4	0.05298737 3	0.04705882 3	chr1 1	8.5E +07	8.5E +07	-	intron:Bcas3
GTGGGAGGATGTTGG AAGGTTGG	*.....* ...**..	4	0.04623811 5	0.04666666 7	chr1 5	8.5E +07	8.5E +07	-	exon:Phf21b
AAGTTAGGAGGTAGG ACTGTAGG	.*.**...*.	4	1.25711206 9	0.04615384 6	chr1 5	4.4E +07	4.4E +07	-	intergenic:Tmem74-Trhr
AAGAGAGGATGTTGG GCTGTGGG	.*.*..... *.*.....	4	0.10005664 6	0.04393491 1	chr1 1	3E+0 7	3E+0 7	+	intron:Eml6
ATGGGAGGATGGAG GAAGGAAGG	*.. ..**.*	4	0.02113159 7	0.04375 7	chr1	3.3E +07	3.3E +07	-	intergenic:Gm24901-Gm25792
ATCAGAGGATGTGGG GCTGTAGG	..**..... *.*.....	4	0.09865585 3	0.04341394 4	chr6	1.2E +08	1.2E +08	+	exon:Kdm5a
ATGGGGGGGGGTAG GACTGGAGG	*.*..*	4	0.21340215 3	0.04201680 7	chr1 3	1E+0 8	1E+0 8	+	intron:Mast4
ATACGAGGATTTAGC ACTGTAGG	..**.....*. ..*.....	4	0.22045056 6	0.04164952 7	chr1 2	1.1E +08	1.1E +08	-	intron:Atg2b
GTGGGAGGATGTATC ACTGAAGG	*..... **....*	4	0.02785046 1	0.04090909 1	chr9	5.4E +07	5.4E +07	+	intergenic:Cyp19a1-1700104A03Rik
ATGACAGGATGTTGG GCTGTAGG	...**..... *.*.....	4	0.10005664 6	0.04079670 3	chr1 5	7.4E +07	7.4E +07	-	intergenic:Gm6569/Mroh5-Gm7935
CTGTTAGGATCTAGG ACTGTGGG	.*.**.....*	4	0.79405120 5	0.04007421 2	chr5	1.1E +08	1.1E +08	+	intron:Ssh1
ATTGCAGGGTGTAGT ACTGTGGG	..*.*...*.. ..*.....	4	0.24269422 7	0.03741496 6	chr Y	3969 512	3969 534	+	intergenic:Gm8521-Gm20918
AATGGAGGATGGAG GACTGGGGG	.*.*.....**	4	0.33833999 8	0.03733031 7	chr1 0	3.8E +07	3.8E +07	+	intergenic:Gm26535-Gm24710
ATGGGAGGGTGGAG GGCTGAGGG	*.* ..*.*	4	0.03084795 2	0.03605769 2	chr9	2.2E +07	2.2E +07	-	intron:Cnn1
ATGGGAAGATCTAGG ATTGGAGG	*.*.. ...*.*	4	0.09147807 1	0.03529411 8	chr1 7	1.3E +07	1.3E +07	+	intron:Sod2

ATGGGAGGATATTCC ACTGTGGG	*.* **.....	4	0.01119224 6	0.03506493 5	chr6	8.5E +07	8.5E +07	+	intergenic:Spr-ps1-Emx1
ATGGGAGGAGGAAG GATTGGGGG	*.* ...*.*	4	0.10408233 9	0.03294117 6	chr8	8.8E +07	8.8E +07	-	intergenic:Brd7-Nkd1
AGCTGAGGATGTAGC ACTGTTGG	.***..... ..*.....	4	0.39720822 8	0.03204068 7	chr7	5.2E +07	5.2E +07	+	intergenic:Gm22211-Gm6181
AGCTGAGGATGTAGC ACTGTGGG	.***..... ..*.....	4	0.39720822 8	0.03204068 7	chr1 4	1.2E +08	1.2E +08	-	intergenic:Tm9sf2-Clybl
ATGGGAGAATGCAG GAGTGATGG	*.*. ...*.*	4	0.11873217 2	0.03134674 9	chr1	1.9E +08	1.9E +08	+	intron:Eprs
ATGGGAGCATGTTGG AAGGTAGG	*.* ...**..	4	0.04178142 9	0.02871794 9	chr1 2	1.1E +08	1.1E +08	+	intergenic:BC022687-Cdca4
AGCGGAGGATGGAG GACTGGAGG	.***.....**	4	0.33833999 8	0.02850678 7	chr X	1.2E +07	1.2E +07	+	intergenic:Gm14513-Gm26314
ATTGGAGTATGCAGG ACTGCCGG	..*....*.**	4	0.32029519 8	0.02691387 6	chr7	6.6E +07	6.6E +07	+	intron:Aldh1a3
GGGTTAGGATGTAGG ACTGTTAG	**.*.*.....	4	0.26098901 1	0.02375757 6	chr7	1.4E +08	1.4E +08	-	intergenic:Tcerg1l-Mapk1ip1
GTGGGTGGATGTAGG AGTGATGG	*....*..... ...*.*	4	0.16245288 5	0.02363445 4	chr1 6	1.4E +07	1.4E +07	+	intron:Myh11
ATTGTAGGATGTAGG ATGGTAGG	..*.*..... ...**..	4	0.11780563 7	0.02333333 3	chr X	4.2E +07	4.2E +07	-	intergenic:Gria3-Gria3/Gm22413
ATGGCAGAATGGAG GAGTGTGGG	*.*.**	4	0.28472943 4	0.02310924 4	chr1 5	5.9E +07	5.9E +07	-	intron:Fer1l6
ATGGAAGGGTGTAGG AGTTTGGG	*.*.* ...*.*	4	0.11138302 8	0.02265795 2	chr4	9.4E +07	9.4E +07	-	intron:Gm12649
GTGGGAGGCTGTGGG AGTGTGGG	*.....*... *...*	4	0.14414024 6	0.02192181 2	chr4	1.2E +08	1.2E +08	-	intron:Gm12923
ATAGAAGGATGTAGG AGTGAGGG	..*.*..... ...*.*	4	0.25063750 3	0.02150735 3	chr4	3.1E +07	3.1E +07	+	intergenic:4930556G01Rik-Gm25705
TTGGGAGGAGGTAGG AATGCAGG	*.....*... ...*.*	4	0.24730430 9	0.02121212 1	chr2	1.5E +08	1.5E +08	+	intergenic:Gm14216-Gm14214
GTGGGTGGATGGAGG AGTGTGGG	*....*.**	4	0.18144857 5	0.02100840 3	chr X	1.1E +08	1.1E +08	-	intergenic:Gm6377/Sh3bgrl-Gm14868
ATGGGAGGGTGTCTAG GCTGTGGG	*.* *.*.....	4	0.00827144 3	0.02024291 5	chr1 2	5.7E +07	5.7E +07	-	intergenic:Nkx2-9-Gm15524
AATGGAGGATGTATG ACTGGTGG	.***..... *.....*	4	0.10246475 5	0.01990950 2	chr7	9.9E +07	9.9E +07	+	intergenic:Prkrir-Wnt11

TTTGGAGGATGTGGG AGTGTGG	*.*..... *...*	4	0.23260602 8	0.01918158 6	chr X	2.3E +07	2.3E +07	-	intergenic:Gm26131-Klhl13
ATTGGGTGATGTAGG ACTGCTGG	..*.*...*	4	0.26900565 1	0.01855287 6	chr2	3.2E +07	3.2E +07	+	intergenic:Prcc2b-AL808027.1
ATTGGAGGAGGTATC ACTGTGGG	..*.....* **.....	4	0.05450848 8	0.01818181 8	chr1 3	5.9E +07	5.9E +07	+	intergenic:Slc28a3-Ntrk2
ATGGGATGATGTGGG AATGCTGG	*..... ...*..*	4	0.06378741 2	0.01581027 7	chr3	1E+0 8	1E+0 8	+	intron:Casq2
ATGGTAGAATGTAGC GCTGTGGG	*.*..... .**....	4	0.06595060 2	0.01573426 6	chr1	8.3E +07	8.3E +07	+	intergenic:Slc19a3-Ccl20
ATGGGTGGAGGTAGG ATTGCTGG	*.*..... ...*..*	4	0.13446780 5	0.01515151 5	chr1 6	4327 553	4327 575	-	intron:Adcy9
ATGGGAGAATGTACG AGTGAGGG	*..... *..*.*	4	0.03595750 8	0.01418067 2	chr5	3218 881	3218 903	-	intergenic:Gm8715-Gm15772
ATGGGAAGATGATGG AGTGTGG	*..... *..*.....	4	0.07163298 1	0.01411764 7	chr4	1.2E +08	1.2E +08	-	intergenic:Mast2-Gm12950
ATGGGAGGATGGAG GATGGGAGG	*.. ..*.*	4	0.02113159 7	0.01372549	chr3	1.2E +08	1.2E +08	+	intergenic:Mir760-Bcar3
ATGGGAGGATGGAG GATGGGAGG	*.. ..*.*	4	0.02113159 7	0.01372549	chr1 8	8.4E +07	8.4E +07	+	intergenic:Gm24720-Tshz1
ATGGGAGGATGGAG GATGGGAGG	*.. ..*.*	4	0.02113159 7	0.01372549	chr3	1.2E +08	1.2E +08	+	intergenic:Mir760-Bcar3
ATGGGAGGATGGAG GATGGGAGG	*.. ..*.*	4	0.02113159 7	0.01372549	chr3	1.2E +08	1.2E +08	+	intergenic:Mir760-Bcar3
ATGGGAGGATGGAG GATGGGAGG	*.. ..*.*	4	0.02113159 7	0.01372549	chr3	1.2E +08	1.2E +08	+	intergenic:Mir760-Bcar3
ATGGGAGGAGGTTGG GATGTGGG	*.. ..*.*	4	0.03221618 7	0.01346153 8	chr1 7	4.6E +07	4.6E +07	+	intron:Tmem63b
ATGTGAGGATGTAGA AGAGTTGG	..*..... *.*..	4	0.03039891 8	0.01342141 1	chr1 7	4315 096	4315 118	-	intergenic:Nox3-Gm23186
ATGGGAGGGTGGGG GAGTGTGGG	*.. *..*.....	4	0.06113534 6	0.01278772 4	chr9	1E+0 8	1E+0 8	-	intron:Stag1
ATGGGAGGGTGGGG GAGTGTGGG	*.. *..*.....	4	0.06113534 6	0.01278772 4	chr3	1.6E +08	1.6E +08	+	intergenic:Gm23038-4930570G19Rik
ATGGGAGGATGGCTG ACTCTGGG	** *...*	4	0.01219796 1	0.01258318 2	chr1 0	8E+0 7	8E+0 7	+	exon:Cirbp
ATGGGTGGAGGGAG GAGTGTAGG	*.*..*	4	0.15100675 1	0.01050420 2	chr2	1.2E +07	1.2E +07	-	intergenic:Pfkfb3-Rbm17

ATGGGAGGAGGGAG GAGAGTAGG	*.* ...**..	4	0.04667194 5	0.00980392 2	chr X	6.9E +07	6.9E +07	-	intergenic:Gm14700-Gm14705
ATGGTAGGATGGAGG ACAGCTGG	...*.....**.*	4	0.06366922 8	0.00909090 9	chr9	3.3E +07	3.3E +07	+	intergenic:RP24-86O15.2-Gm10698
TTGGCAGGATGTAGG GGTGTGGG	*..*..... ..**..	4	0.10484833 3	0.00888817 1	chr4	1.8E +07	1.8E +07	-	intron:Mmp16
ATGGGAGGAAGCAG GAGTGGGGG	*.* ...*.*	4	0.10408233 9	0.00842937 8	chr1 2	1.1E +08	1.1E +08	+	intron:D430019H16Rik
CTGGGAGGATGGAG GAGGGTAGG	*.....*. ...**..	4	0.05878334	0.00840336 1	chr X	1.1E +07	1.1E +07	+	intergenic:Mid1ip1/Gm14493-Gm14473
ATGAGAGGATGTCAG AGTGTGG	...*.....* *..**..	4	0.03337063 6	0.00835913 3	chr1 5	9.5E +07	9.5E +07	-	intron:Tmem117
ATGGTAGGATGTGGG AGTTTGGG	...*.....* ...*.*	4	0.07054866 1	0.00767263 4	chr1 4	1.2E +08	1.2E +08	+	intergenic:Hs6st3-Oxgr1
GTGGGAGGATGTGGG GGTGTGGG	*.....* ..**..	4	0.04057630 5	0.00737753 3	chr2	5045 493	5045 515	+	intron:Optn
TTGGGAGGATGTAGG AGAGGGGG	*..... ..**.*	4	0.05262936 4	0.00692041 5	chr2	7E+0 7	7E+0 7	+	intron:Ppig
GGGTTAGGATGTAGG ACTGTTGA	**.*.....	4	0.26098901 1	0.00636363 6	chr1 3	8.9E +07	8.9E +07	+	intron:Edil3
AGGGGAGGATGTAG GAGAGGAGG	.*..... ..**.*	4	0.05262936 4	0.00581314 9	chr1 1	3.2E +07	3.2E +07	-	intergenic:Bod1-D630024D03Rik
GTGGGAGGACGTAG GAGTGGGGG	*.....*.. ...*.*	4	0.24730430 9	0.00553633 2	chr1 3	5.8E +07	5.8E +07	-	intron:Klhl3
ATGGGAGGATGAGG GAGTGGTGG	** ...*.*	4	0.04172412 3	0.00541597 7	chr1 7	6.1E +07	6.1E +07	-	intergenic:Gm5496-Gm4518
ATGGGTTGATGTAGG GGTGTGGG	**..... ..**..	4	0.03914901	0.00461723 1	chr1 3	1.6E +07	1.6E +07	-	exon:Gli3
ATGGGAGGAGGTGG GAGTGGAGG	*.* ...*.*	4	0.08186964 5	0.00338498 6	chr8	1.2E +08	1.2E +08	-	intron:2310022B05Rik
ATTGGAGGATGTAGG TTTCTGGG	.*..... **.*	4	0.03256484 4	0	chr1 2	1.1E +08	1.1E +08	-	intergenic:Cep170b-Pld4
ATTGGAAGATGTAGC CCTGTTGG	..*..*..... **....	4	0.04666243 4	0	chr2	5.3E +07	5.3E +07	-	intron:Fmn12
ACGGGAGGCTGCAG GCCTGTGGG	.*.....*.* ...*....	4	0.07772152	0	chr1 7	2.5E +07	2.5E +07	-	exon:Mapk8ip3
ATGAGAGGATGCATG TCTGTTGG	...*.....* *.*....	4	0.01895336 6	0	chr1 1	1.2E +08	1.2E +08	-	intron:Aatk

ATGGCAGAATGGAG GTCTGTCGG	*..*..* ...*....	4	0.12107349 4	0	chr1 3	1.1E +08	1.1E +08	+	intron:4930544M13Rik
ATGGCAGGATGTAGA CCGGTCGG	*..... **.*..	4	0.01358081 5	0	chr9	4.4E +07	4.4E +07	+	intergenic:Gm23326-Thy1
ATGGGACTATGTAGG TCTGCAGG	**.... ..*..*	4	0.07363626 2	0	chr1 7	8.2E +07	8.2E +07	+	intergenic:Rpl31-ps25-AC135509.1
TTGGGATGATGGAGG CCTGTGG	*....*....* ...*....	4	0.09151380 4	0	chr1 2	8.6E +07	8.6E +07	-	exon:Mfsd7c
ATAAAAGGATGTAGG TCTGTGGG	..***..... ...*....	4	0.25492468 4	0	chr5	4086 116	4086 138	+	intron:Cyp51
ATGGGAGGAAGTAA GCTTGTGGG	*... *.*.*..	4	0.01240364 8	0	chr1	3.6E +07	3.6E +07	+	intergenic:Gm25096-Gm25634
ATGCTAGGGTGTAGG TCTGTGGG	...**.*... ...*....	4	0.15797057	0	chr6	9E+0 7	9E+0 7	-	intron:Ccdc37
AAGGGAGGATGAAG ATCTGTGGG	.*.....*. .*.*....	4	0.03409061 8	0	chr1	1.5E +08	1.5E +08	+	intergenic:Gm9931-Gm22966
ATGGGATGAAGTAGG TCTGAAGG	*.*... ..*..*	4	0.06781899 7	0	chr2	1.5E +08	1.5E +08	-	intergenic:A530006G24Rik-Gm25516
GTGGGAGGATGTATG TGTGTGG	*..... *.*.*..	4	0.01562240 2	0	chr3	8.7E +07	8.7E +07	-	intron:Kirrel
ATTAGAGGATGTAGC CCTGTGG	..**..... .*.*....	4	0.06831981 5	0	chr1	2.3E +07	2.3E +07	+	intron:Rims1
ATGGGATGATGTAGG TCTAGAGG	*..... .*.*..	4	0.02319542 2	0	chr1 5	6.7E +07	6.7E +07	-	intergenic:Lrrc6-Tmem71
ATGGGAGGAAGTAG GTGTGGGGG	*.... .*.*.*	4	0.03638650 9	0	chr5	1.2E +08	1.2E +08	-	intron:Vsig10
AGCGGAGGATGTAG GTCAGTAGG	.*.*..... ..*.*..	4	0.05263005 1	0	chr2	1.5E +08	1.5E +08	+	intergenic:A530006G24Rik-Gm25516
ATGGGAGGTTTTAGG TCTTTGGG	*.*.. ..*.*.	4	0.02628625 5	0	chr1 6	3.2E +07	3.2E +07	+	intergenic:Bdh1-Gm26053
GTGGGTGTATGTAGG CCTGTGGG	*....*.*.... ...*....	4	0.16476166 7	0	chr3	8.5E +07	8.5E +07	+	intron:Fbxw7
ATGGAAGGATGGAG GCCAGTGGG	*.....*. ..*.*..	4	0.02493194 4	0	chr7	3.5E +07	3.5E +07	-	intron:Pepd
ATGGGAGGATGTTGG TGTCTGGG	*.*. .*.*.*.	4	0.01101856 6	0	chr1 8	7.4E +07	7.4E +07	+	intergenic:Ccdc11-Myo5b
ATGGGTGGGTGTTGG CCTGTGGG	*.*... *.*.*..	4	0.03520396	0	chr X	1.7E +08	1.7E +08	-	intron:Gla2

ATGGAAGGAGGTAGT CCTGTGGG	*...*... ..**....	4	0.06074050 5	0	chr1 1	1.2E +08	1.2E +08	-	intron:Rbfox3
CTGGGAGGAAGTAG GCCTATGGG	*.....*... ..*..*	4	0.08345913 9	0	chr8	7.3E +07	7.3E +07	+	intergenic:Nwd1-Sin3b
ATTGGAGGATGTAGG TCCCTTGG	..*..... ..***.	4	0.01657846 6	0	chr1 3	4.1E +07	4.1E +07	-	intergenic:Elovl2-Smim13
ATGGGAGGATGTATG CCTACTGG	* ..**	4	0.00459489 6	0	chr8	1E+0 8	1E+0 8	+	intergenic:Gm8730-Cdh5
GTGGGAGAATGTATG CCTGTTGG	*.....*... **....	4	0.04057766 7	0	chr1 2	8E+0 7	8E+0 7	+	intergenic:Rad51b-Zfp3611/Gm26669
AGGTGAGGATGTAGG CCAGTTGG	..*..... ..*..*	4	0.05337733 3	0	chr2	2E+0 7	2E+0 7	-	intergenic:Etl4-Gm13335
CTGAGAGGATGTTGG CCTGTCGG	*.....*... **....	4	0.105393	0	chr7	1.2E +08	1.2E +08	+	exon:Ern2
GTGGGAGGATGGAG GTCTGCTGG	*.....*. ..**	4	0.05902077	0	chr5	4.1E +07	4.1E +07	-	intergenic:Gm23022-Rab28
ATGGGAGGATGTTGG TCCATGGG	*. ..***.	4	0.00560945 2	0	chr1 2	8E+0 7	8E+0 7	+	intergenic:Rad51b-Zfp3611/Gm26669
ATGGGAGAAAGTAG GTCTATTGG	*... ..*..*	4	0.07139275 8	0	chr1 3	4.6E +07	4.6E +07	-	intergenic:Stmnd1-Rbm24
TTGGGAGCAGGTAGG CCTGTGGG	*.....*... ...*	4	0.250819	0	chr8	7.7E +07	7.7E +07	+	intergenic:Gm7069-Gm10649
ATGGGAGGATGTCTGG TGTCTCGG	*. ..**.	4	0.01101856 6	0	chr1 5	7.7E +07	7.7E +07	-	intergenic:Mb-Apol6
TTGGGAGGATGTAGA ACTTTTGG	*..... *...*	3	0.30206779 7	0.62745098 1	chr1 9	2.4E +07	2.4E +07	+	intergenic:Pip5k1b-4930418C01Rik
CTGGGAGGATGTAGA ACTTTTGG	*..... *...*	3	0.30206779 7	0.53781512 6	chr6	4.3E +07	4.3E +07	+	intergenic:Olfr455-Fam115e
ATGGGAGGATATAGA AATGTTGG	*... *...*	3	0.14565369 5	0.43921568 7	chr X	1E+0 8	1E+0 8	+	intergenic:Gm14828-Mir676
ATGGGAGGACAAAG GACTGTAGG	***	3	0.58342819 8	0.42666666 6	chr1 9	2.2E +07	2.2E +07	-	intergenic:Gm22506-RP23-448C3.1
ATGAGAGCATGTGGG ACTGTTGG	...*...*... *.....	3	1.03417721 5	0.36120401 3	chr X	5.1E +07	5.1E +07	+	intergenic:Gm14621-Hs6st2
ATGGGAGGGTGTGGG ACTTTTGG	*...**	3	0.20965854 3	0.28985507 3	chr4	3.7E +07	3.7E +07	+	intergenic:Gm23314-Lingo2
CTGGGAGGATGGAG GACTGATGG	*.....*.*	3	0.73410847 5	0.24107142 9	chr7	1.1E +08	1.1E +08	-	intron:Tead1

ATGGGAGGATGTAGG AATAAAGG	***	3	0.11732134 6	0.1875	chr4	1.3E +08	1.3E +08	+	intron:Wdtd1
ATGGGAGGGTGGAG GATTGTGGG	*.. ...*	3	0.30927943 5	0.15555555 6	chr3	7.8E +07	7.8E +07	-	intergenic:Gm23644-Gm15442
AGAGGAGGAAGTAG GACTGTAAG	.**.....*..	3	0.48534497 9	0.14	chr X	1.6E +08	1.6E +08	+	intron:Cnksr2
ATGTGAGGATTCAGG ACTGTTGG	...*.....**	3	0.72969620 3	0.13249908	chr1 9	2.3E +07	2.3E +07	+	intron:Trpm3
ATGTGAGGATTTAGA ACTGTTGG	...*.....*.. .*.....	3	0.41867555 6	0.13163307 3	chr7	1.1E +08	1.1E +08	-	intergenic:Gm9105- Stk33/1700095J03Rik
ATGGAGGGATGTAGG GCTGTGGG	...**..... ..*....	3	0.29290963 9	0.11904761 9	chr1 9	3E+0 7	3E+0 7	+	intergenic:Ranbp6-Il33
ACAGGAGGATGTGG GACTGTCAG	.**..... *.....	3	0.21481653 3	0.10869565 2	chr1	1.2E +08	1.2E +08	+	intergenic:Dpp10-Gm10543/Dpp10
AAGGAAGGAGGTAG GACTGTGAG	.**.*.....*..	3	0.49223628 7	0.09506172 8	chr3	8.8E +07	8.8E +07	-	intron:Slc25a44
ATGGGAGAATGTAGG GTTGTGGG	*..... .**...	3	0.17695921 2	0.08974359	chr1 1	1E+0 7	1E+0 7	+	intergenic:Eif3s6-ps1-Gm11995
ATGGGAGTCAGTAGG ACTGTCAG	***..	3	0.26109619 9	0.07936507 9	chr7	5.2E +07	5.2E +07	-	intergenic:Gm22211-Gm6181
AGGGGAAGATGTAG GACTGCTGG	.**.*.....*	3	1.01909774 6	0.07636363 6	chr4	1.4E +08	1.4E +08	-	exon:Emc1
ATGTGTGGATGTATG ACTGTGGG	...*.*..... *.....	3	0.25374148 1	0.06926406 9	chr4	1.2E +08	1.2E +08	-	intron:Ndufs5
ATGGTAGGATGTTGG ACTTTGGG	...*.....**.	3	0.38411194	0.06	chr2	7.8E +07	7.8E +07	+	intron:Gm14461
ATGGGAGGATGTAGG AAAGGAGG	**.*	3	0.07299994 9	0.05490196 1	chr1 0	9.6E +07	9.6E +07	+	intergenic:Gm24433-Eea1
AAGGAAGGATGTAG GAGTGTAGG	.**.*..... ...*	3	1.21310116 1	0.04313725 5	chr3	5.4E +07	5.4E +07	+	intron:Frem2
CTGGAAGGATGAAG GACTGTAGA	*.*.....*	3	0.27697777 8	0.04126984 1	chr1 3	1.1E +08	1.1E +08	+	intron:Elovl7
ATGGGAGGAGGTAG GACTACAGG	*....**	3	0.34053054 2	0.03246753 2	chr1 6	9.4E +07	9.4E +07	-	intron:Ttc3
ATGGGAGCATGTAGG CCCGTAGG	*..... .*.*..	3	0.09489303 7	0	chr4	8.2E +07	8.2E +07	-	intergenic:Gm5860-Nfib
ATGGAAGGATGTAGG CCAGTGGG	*..... .*.*..	3	0.10023912 4	0	chr1 0	8.1E +07	8.1E +07	-	exon:Adat3/Scamp4

CTGGGGGGATGTAGG TCTGTGGG	*...*..... ..*....	3	0.32788391 4	0	chr8	9.4E +07	9.4E +07	-	exon:Nlrc5
GTGGGAGGAAGTAG GTCTGTGGG	*.....*... ..*....	3	0.49914228 9	0	chr1 7	8.2E +07	8.2E +07	-	intergenic:Rpl31-ps25-AC135509.1
ATGGGTGGATGTAGG ACTATTGG	*.....*	2	2.10518895 3	0.51020408 1	chr1	9E+0 7	9E+0 7	+	intron:Iqca

Table S4. Summary of significant fold-changes in reference to the tested parameters in CatWalk gait analysis affected by *Adnp* knockdown, NAP treatment and sex.

Tested parameters		Genotype Effect G68 vs. Poly T		NAP Treatment Effect G68 NAP vs. G68		Sex Effect Females vs. Males		
		Males	Females	Males	Females	Poly T	G68	G68 NAP
Run Characterization	Run duration				0.77			
	Cadence	1.20	0.81			1.27		
Interlimb Coordination	Swing speed-RF		0.77		1.174			
	Swing speed-LF		0.74		1.23			
	Swing speed-LH		0.78		1.40		0.75	
	Body speed-RF		0.75		1.20			
	Body speed-LF		0.74		1.21			
	Body speed-RH		0.75					
	Body speed-LH		0.72		1.24			
	Step cycle-RF		1.30			0.826		
	Step cycle-LF					0.80		
	Step cycle-RH		1.35			0.792		
	Step cycle-LH	0.81	1.32		0.82	1.12	0.88	

	BOS- front paws						0.87	
	BOS- hind paws		0.84		1.10			
	Step Sequence				0.913			
	Support Three	0.85						
	Support Diagonal	1.29						
	Support Lateral							9.12
Temporal Parameters	Single Stance-RF		1.33			0.84		
	Single Stance-RH		1.27		0.82		1.20	
	Initial Dual Stance-RF	0.58	1.50			0.55		
	Initial Dual Stance-RH		1.87			0.47		
	Terminal Dual Stance-RH					0.52		
	Terminal Dual Stance-LH	0.60				0.61		
	Max Intensity AT		0.90			1.10		
Spatial Parameters	Mean Intensity Of The 15 Most Intense Pixel-RF		0.93			0.94	0.91	0.92
	Mean Intensity Of The 15 Most Intense Pixel-LF		0.93		1.10		0.91	
	Mean Intensity Of The 15 Most Intense Pixel-RH							0.82
	Mean Intensity Of The 15 Most Intense Pixel-LH					0.86		0.86
	Print Width-RH					0.86		
	Print Width-LH		0.92				0.91	

Supplemental Figures:

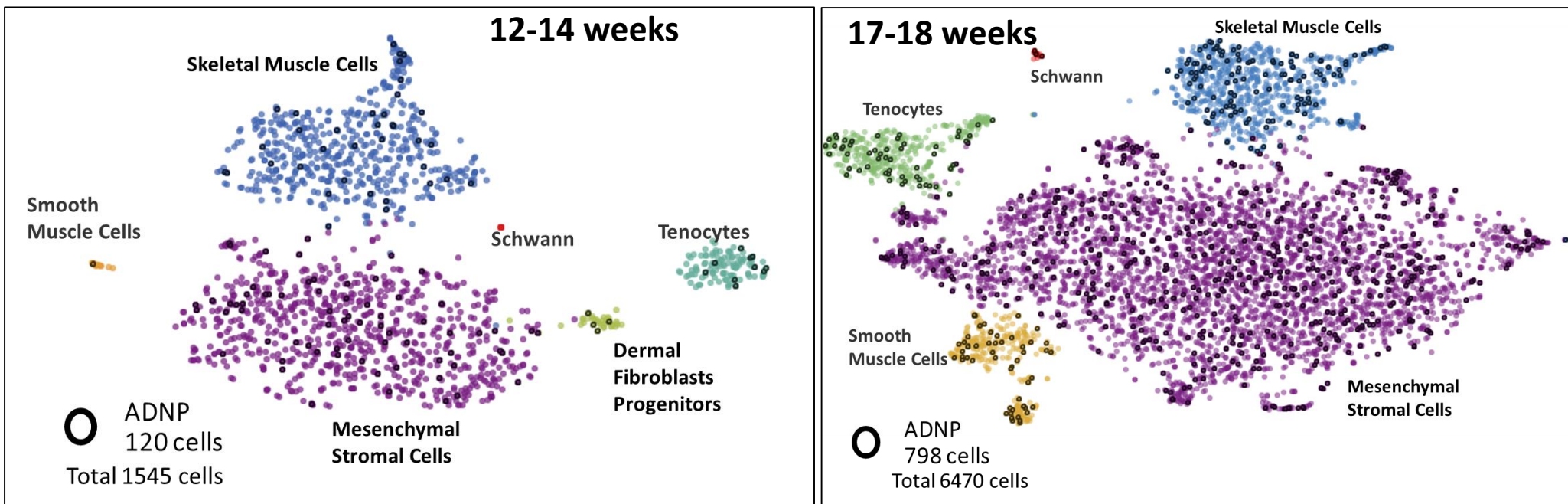


Figure S1. Single human muscle cell ADNP cellular distribution at different time points during gestation.

As in Figure 1, assessing human embryo limbs at 12-14 and 17-18 weeks of gestations.

Expression levels

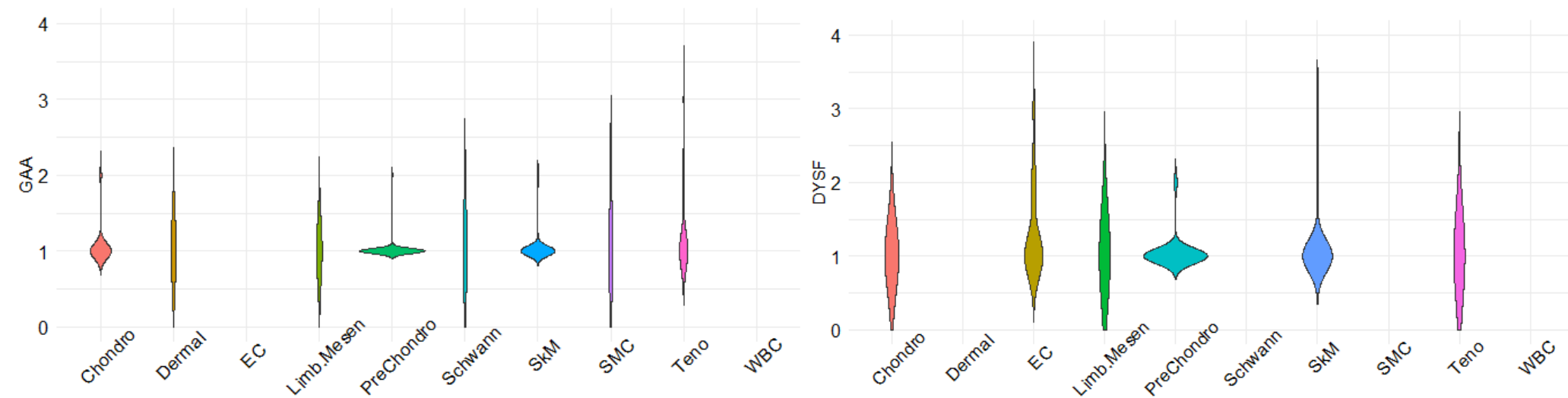


Figure S2 Single cell specific gene transcriptomes of hind limbs from human fetuses of 9 weeks

Violin graphs as in Figure 1, representative transcripts as per diseases depicted in Figure 2.

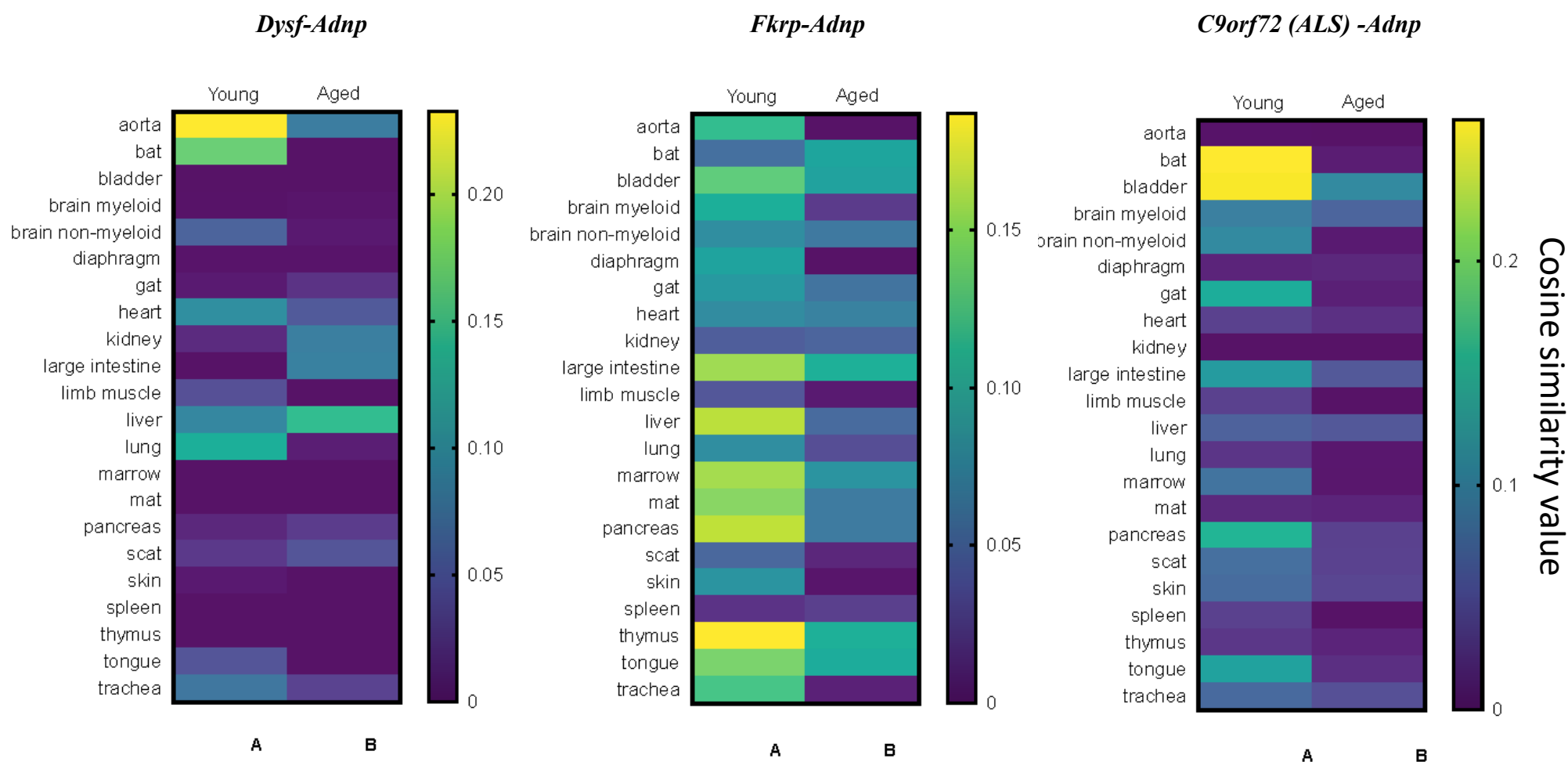


Figure S3. Overall systemic loss of correlation of expression of *Adnp* and disease genes at the single cell level.

Heatmaps plotting cosine similarity values (indicating co-expression at the single cell level) for the genes of interest (indicated above each heatmap) and *Adnp* in young (3 months) and aged mice (18 and 24 months) in 22 tissues (indicated in rows). GAT, SCAT, MAT and BAT stand for gonadal-, subcutaneous-, mesenteric- and brown- adipose tissue.

14-month-old male mice

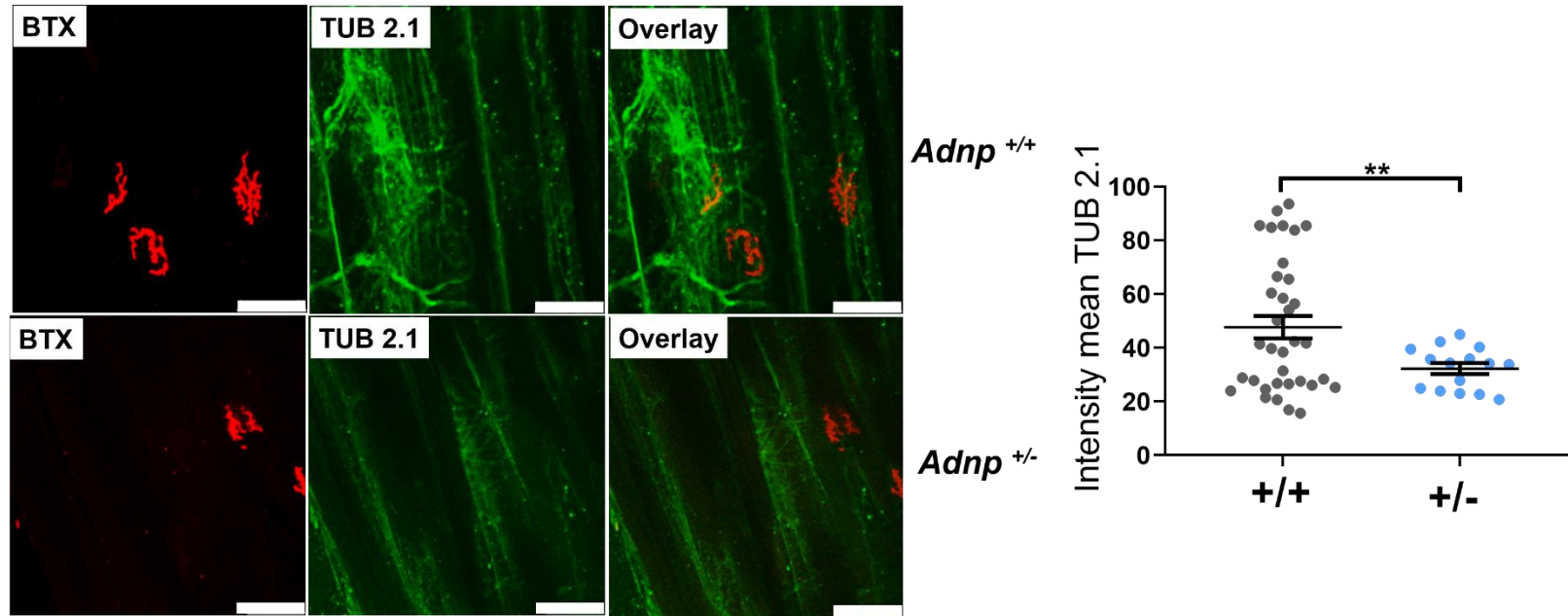


Figure S4. Representative whole-mount NMJ immunostaining of 14-month-old (*Adnp*^{+/+} CB n=4; *Adnp*^{+/-} CB n=2) male mice. The post-synaptic marker bungarotoxin was labeled by BTX (red) and the pre-synaptic marker Tubulin was labeled by Tub 2.1 (green). Decreased tubulin intensity was observed in *Adnp*^{+/-} CB, compared with *Adnp*^{+/+} CB, (**p<0.01). The images were acquired by confocal microscope at X20 magnification. Scale bar, 50 μ m. The intensity mean is expressed as mean $\pm$ SEM.

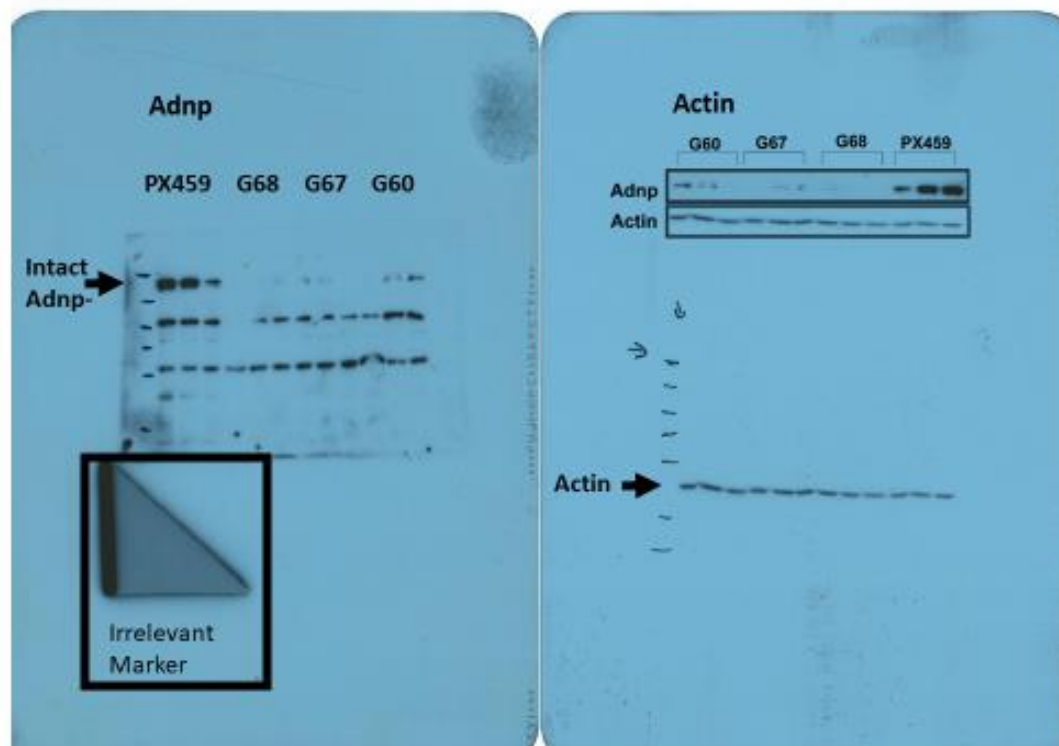


Figure S5. A successful knockdown of Adnp in culture by the CRISPR-Cas9 technology: Full Western blot control for Figure 7B. The left hand panel depicts the full Adnp Western blot results (an irrelevant marker was inserted for placement). Intact Adnp is indicated by a black arrow (experiments were performed in triplicates, as shown in the main text and in the insert – on the right side of the figure). The lower molecular weight bands identified by the Adnp antibody may represent breakdown products or non-specific antibody label. Regardless, complete knockdown of the intact Adnp is shown for the G68 sgRNA. The actin detecting antibody is highly specific (right hand panel).

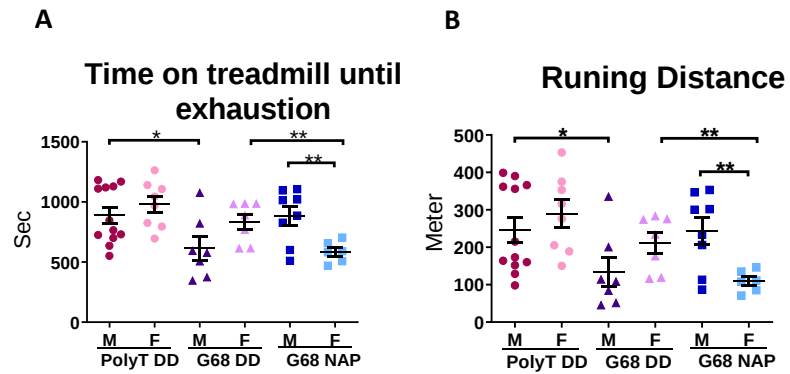
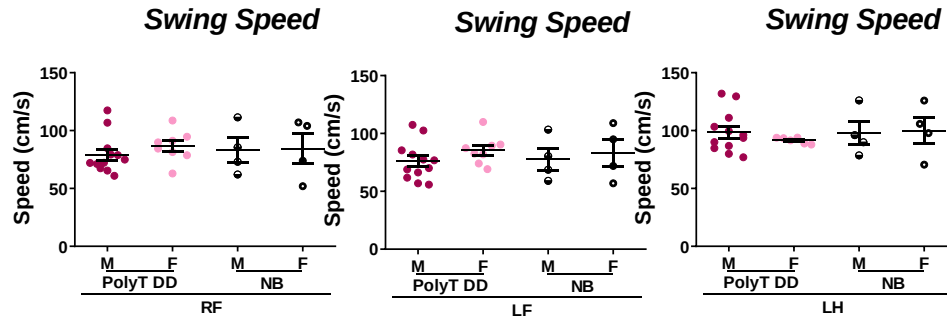


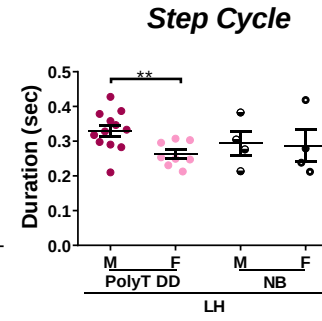
Figure S6. G68 male mice displayed a significantly reduced max ability to run on treadmill compared with the Poly T DD group. An unpaired Student's t-test revealed a significant reduction in time until exhaustion (A) and the running distance (B) in G68 male mice group compared to the control group (Poly T DD) (* $p < 0.05$). Also, sex differences were observed in NAP treated G68 group (** $p < 0.01$). Poly T (males $n=12$; females $n=8$), G68 DD (males $n=7$; females $n=7$) and G68 NAP groups (males $n=8$; females $n=7$). All the results are expressed as mean $\pm$ SEM.

Interlimb Coordination:

A

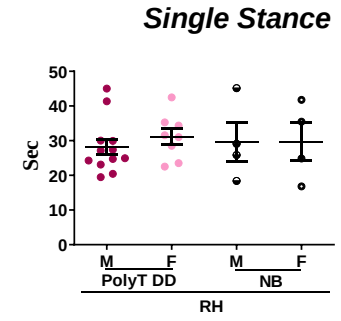


C

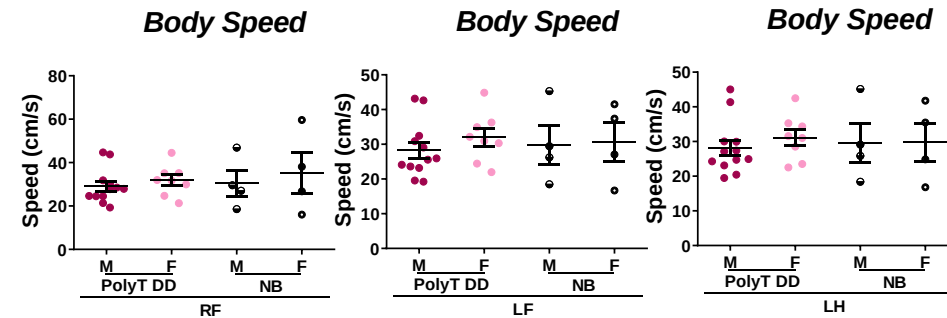


Temporal Parameters:

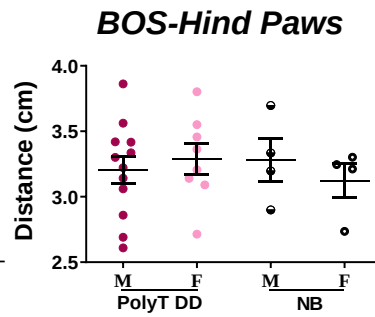
E



B



D



Spatial Parameters:

F

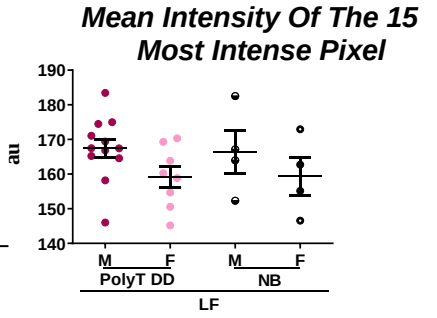


Figure S7. No significant differences were found between the Poly T DD and the neurobasal (NB) medium injected groups. Poly T (males n=12; females n=8), G68 DD (males n=7; females n=7) and G68 NAP groups (males n= 8; females n=7). All the results are expressed as mean $\pm$ SEM.