Supplementary Materials for

Laminopathies disrupt epigenomic developmental programs and cell fate

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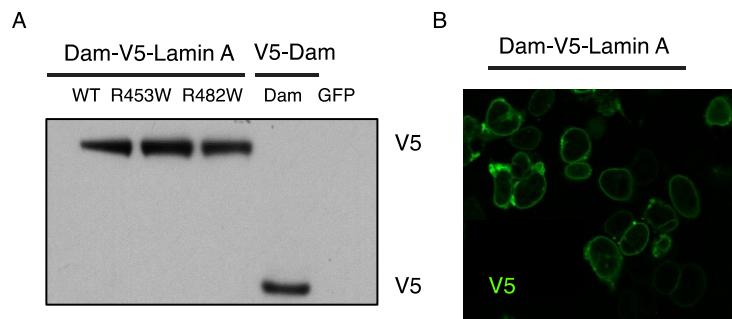
Fig. S1. Transfection of DamLMNA constructs into HEK293T cells. Panel A: Western blot shows using antibody against V5 shows the product size corresponding to the fusion (Dam-V5-LMNA) and V5-Dam alone proteins. Panel B: Immunofluorescence analysis confirms that fusion protein localizes to the nuclear envelope.
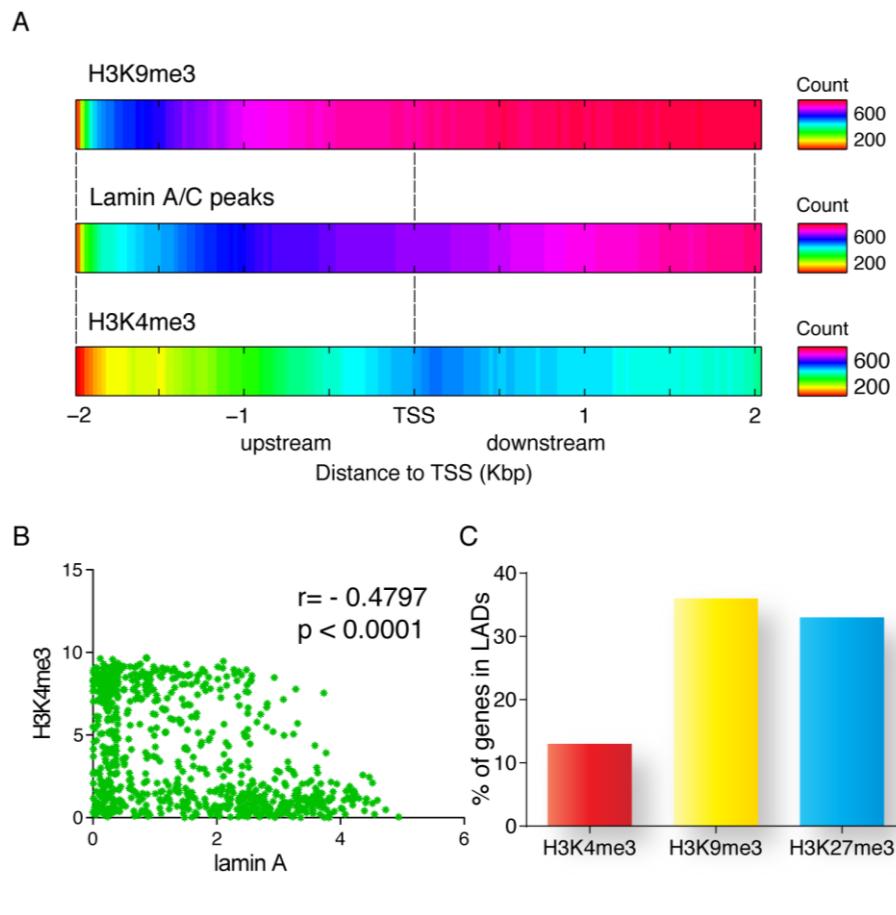
Fig. S2. LADs show enrichment for heterochromatin and are negatively correlated with euchromatin. Panel A: Distribution of H3K9me3 (top), lamin A (middle) and H3K4me3 (bottom) peaks around of transcription start site (2Kb +/-). Panel B: Scatter plot showing negative correlation between lamin A and H3K4me3 peaks. Panel C: Percentage of LAD genes that show enrichment for other chromatin marks (H3K4me3, H3K9me3, H3K27me3).
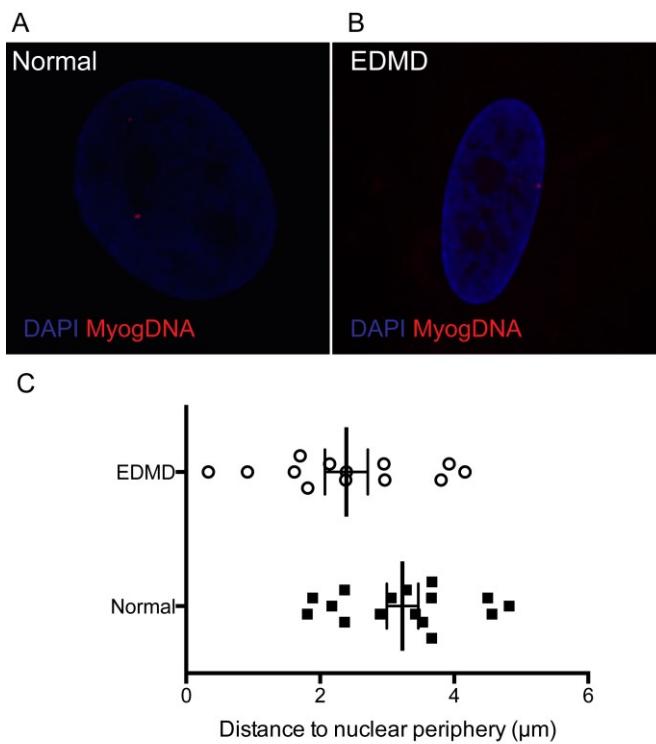
Fig. S3. Myogenin locus localized closer to the nuclear periphery in EDMD myotubes. FISH analysis showed that myogenin probe is abnormally localized peripherally in EDMD patient cells harboring LMNA p.H222P mutation (Panel B) relative to Normal control (Panel A). Panel C: Quantification analysis showing distribution of myogenin signal relative to nuclear periphery (Normal: n=16 nuclei; EDMD n= 13 nuclei; p value= 0.054).
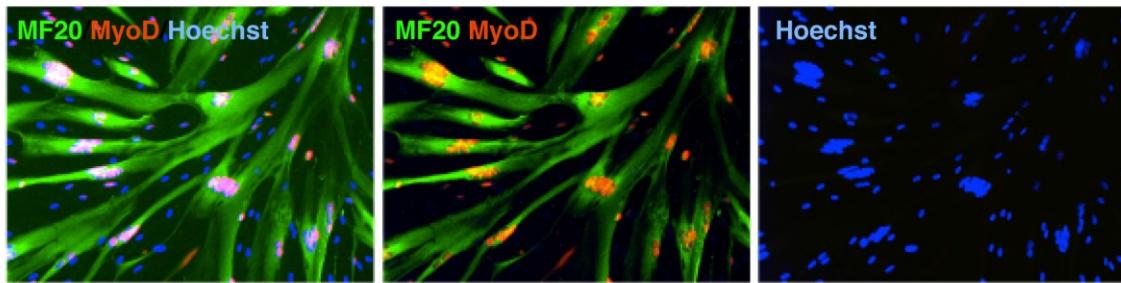
Fig. S4. Myogenic in vitro differentiation of MyoD-converted EDMD patient fibroblasts (p.H222P LMNA) into myoblasts. Immunostaining of EDMD patient fibroblasts show successful conversion into myogenic lineage capable of forming myotubes. Cells were stained for myogenic marker (myosin –MF20), MyoD and Hoechst (nuclear marker).
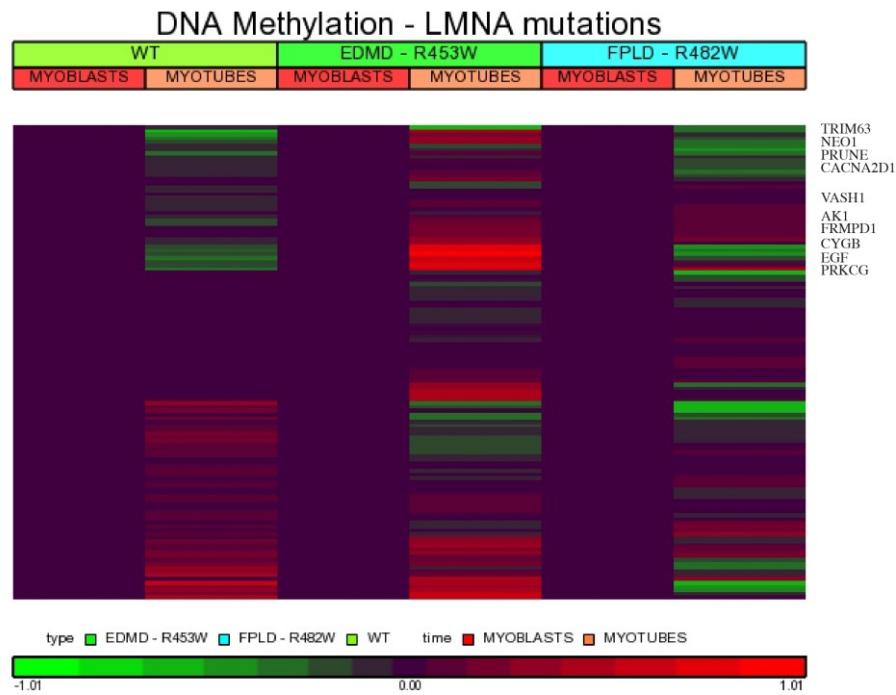
Fig. S5. **DNA methylation analysis of lamin A/C [wild-type, EDMD (LMNA p.R453W), and FPLD (LMNA p.R482W)] transduced human skeletal myogenic cells.** Genes involved in skeletal and cardiac muscle development and show persistent methylation in samples transduced with EDMD mutation are shown on the right.
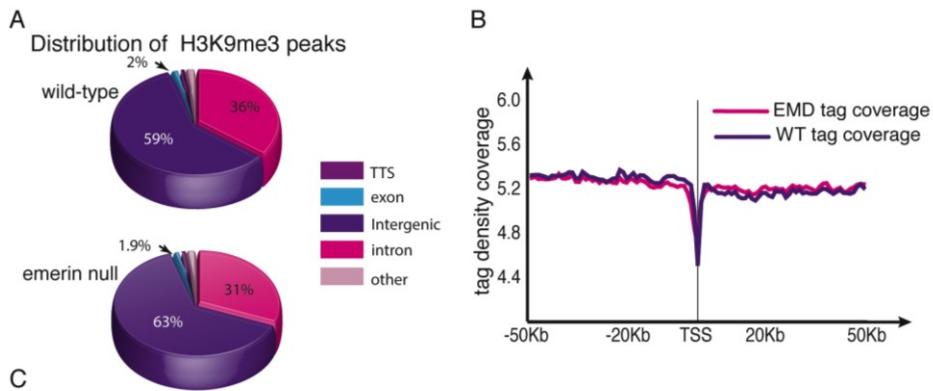
A Distribution of H3K9me3 peaks

wild-type: 2%, 59%, 36%

emerin null: 1.9%, 63%, 31%

Legend: TTS, exon, Intergenic, intron, other

B

EMD tag coverage / WT tag coverage

tag density coverage vs position (-50Kb, -20Kb, TSS, 20Kb, 50Kb)

C

sample	library size	genomic coverage	# of peaks called	# of peaks associated with genes
wt d 0	24,980,604	11.9	12261	5453
wt d 1	26,576,020	10.1	10083	6357
wt d 2	24,999,938	7.1	9100	5321
emerin null d0	36,231,223	8.7	9624	4869
emerin null d1	23,562,577	8.3	10843	6406
emerin null d2	18,563,298	6.7	9100	5052

Fig. S6. Genome-wide analysis of H3K9me3 peaks in wild-type and emerin-null (emd) differentiating mouse myoblasts shows similar peak distributions. Panel A: Distribution of H3K9me3 peaks in wild-type and emerin null myogenic cells. Panel B: Sequence tag density coverage shows similar profiles for H3K9me3 in wild-type and emerin null cells. Heterochromatin enrichment shows drop in tag density in both cell types. Panel C: Properties of heterochromatic domains in wild-type and emerin null cells during differentiation are shown in the table.
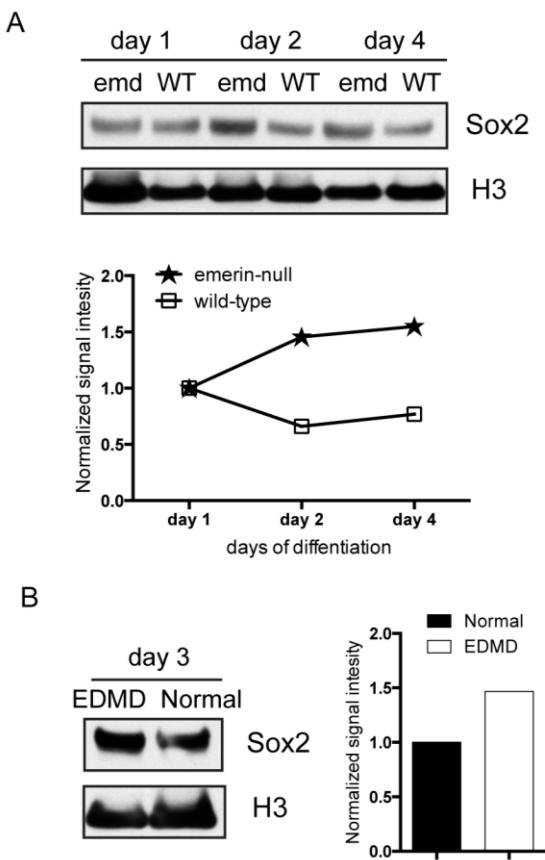
Fig. S7. Sox2 protein levels show abnormal up-regulation in emerin-null murine cells and EDMD patients harboring LMNA p.H222P mutation. Panel A: Wild-type and emerin null H2K cells were differentiated for 24 hrs (day 1), 48 hrs (day 2) and 96 hrs (day 4). Sox2 protein levels were queried using western blot analysis. Sox2 levels were normalized to loading control (H3) levels and day 1 for each condition to show changes in Sox2 expression over the course of differentiation. Panel B: Normal and EDMD MyoD converted myoblasts were harvested after 72 hrs (day 3) post differentiation. Sox2 protein levels were normalized to loading control (H3).
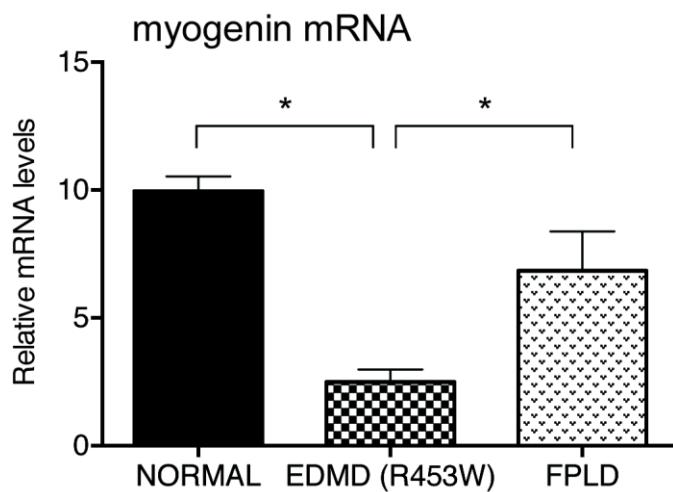
Fig S8. EDMD LMNA mutation significantly inhibits myogenin expression in human myogenic cells infected with LMNA constructs. Human skeletal myoblasts were infected with lenitiviral vectors carrying 3 different LMNA mutations (WT, p.R453W [EDMD]), p.R482W [FPLD]) and differentiated into myotubes. Myogenin mRNA levels were compared using qRT-PCR (* $p < 0.05$, Student t test).

Table S1. Genome-wide DamID-seq analysis of three lamin A proteins (wild-type, p.R453W LMNA causing EDMD, and p.R482W LMNA causing FPLD). Properties of lamina-associated domains are shown in the table.

	LADs						Non-LAD genome coverage (%)
	Genome coverage (%)	Number	Min size (kbp)	Max size (kbp)	Median size (kbp)	Mean size (kbp)	
DamLMNA	12.04	**11,607**	2	1070	26	**32.5**	87.96
DamLMNA-EDMD	13.88	**19,502**	2	245	17.9	**22.3**	86.12
DamLMNA-FPLD	14.6	**22,947**	2	194	15.9	**19.9**	85.4

Table S2. **Genes showing mRNA induction at myoblasts-myotube transition (ENCODE).** Gene names, fold change and p values (FDR corrected) are shown in the table. Genes are ranked by p value.

Gene ID	Fold change	p value
DCLK2	3.60	7.7E-06
PARM1	4.55	5.5E-05
TRIM54	4.53	8.2E-05
KCNA10	1.58	1.1E-04
HSPA12A	2.48	1.6E-04
ATXN1	2.10	2.0E-04
ATP1B4	66.71	2.0E-04
GPNMB	13.88	2.0E-04
RALGPS1	1.77	2.2E-04
DHCR24	2.39	2.4E-04
NBEA	4.10	2.5E-04
PDE7A	3.04	2.6E-04
ARMC9	2.76	2.7E-04
HDAC9	9.48	2.8E-04
MYOM1	24.49	2.8E-04
KBTBD5	3.05	3.2E-04
LRRC39	20.69	3.4E-04
CPEB4	3.51	3.5E-04
PLD1	2.61	3.5E-04
PRKCQ	4.12	3.8E-04
SGCD	2.19	4.4E-04
ABCG2	1.73	5.4E-04
ENAM	1.34	5.7E-04
SAMD4A	1.90	5.7E-04
TNNC2	7.63	5.8E-04
CAP2	2.41	6.0E-04

DIP2B	1.59	6.2E-04
TRIM63	2.88	6.3E-04
MYH6	2.81	6.5E-04
POLB	2.61	6.6E-04
ANKRD36BP1	1.41	7.0E-04
ASB14	7.24	7.2E-04
NEO1	2.25	7.4E-04
C10orf71	2.19	7.5E-04
FBXO30	2.00	7.5E-04
TNIK	2.85	7.7E-04
SOHLH2	16.67	7.8E-04
KIF2A	1.72	7.8E-04
MYOM2	11.89	8.0E-04
FRMPD1	2.65	8.0E-04
GRAMD3	2.83	8.0E-04
C7orf41	3.04	8.1E-04
LITAF	3.87	8.6E-04
POPDC2	3.26	8.8E-04
SULF2	1.42	8.9E-04
COLQ	2.00	8.9E-04
PGAP1	1.84	9.1E-04
MACROD2	1.93	9.6E-04
DENND1B	2.00	9.7E-04
PLN	8.32	9.8E-04
SRPK3	1.79	1.0E-03
RBM24	2.33	1.0E-03
EGF	7.14	1.1E-03
GSK3B	1.30	1.1E-03
ZNF148	1.59	1.3E-03
CPEB3	2.68	1.3E-03
GPR98	1.89	1.3E-03
P2RX5-TAX1BP3	2.27	1.3E-03
C12orf42	2.47	1.4E-03
SLCO2B1	1.31	1.4E-03
ICOSLG	2.56	1.4E-03
LDB3	5.27	1.4E-03
SPATA13	1.50	1.5E-03
TMEM229B	1.39	1.6E-03
SLC15A2	3.58	1.6E-03
LDLR	2.91	1.6E-03
ITGA6	2.47	1.6E-03
SGCG	27.31	1.6E-03
GGA2	1.69	1.6E-03
CACNA2D1	7.32	1.6E-03
HUNK	3.38	1.7E-03
ZNF643	1.51	1.7E-03
HMBOX1	2.88	1.8E-03
KCNN3	2.87	1.8E-03
PLP1	3.58	1.8E-03
DPYSL5	5.94	1.9E-03
NAV3	2.76	1.9E-03
CDKN1A	2.57	1.9E-03
STK38L	2.65	1.9E-03
CYSLTR1	14.35	2.0E-03
LOC646513	1.57	2.0E-03
BRF1	1.66	2.0E-03
PKIA	2.85	2.0E-03
C1orf105	4.42	2.1E-03
SVIL	5.23	2.1E-03
EXOC6	4.54	2.2E-03
MXRA5	4.89	2.2E-03
SEL1L3	3.07	2.2E-03

PTPRB	2.05	2.3E-03
RNF121	1.86	2.3E-03
A2M	44.09	2.3E-03
ELAVL2	3.54	2.3E-03
LRP8	1.97	2.3E-03
PKHD1	6.56	2.3E-03
PPFIBP2	4.64	2.3E-03
NIPSNAP3B	2.49	2.4E-03
LEPROTL1	1.47	2.4E-03
ANKRD50	1.36	2.4E-03
KIAA0922	1.83	2.4E-03
SCD	4.77	2.5E-03
REEP1	12.84	2.5E-03
TMEM38B	6.53	2.5E-03
FRK	3.38	2.5E-03
CLCN6	1.63	2.6E-03
ZNF323	2.80	2.7E-03
PPP1R15A	1.31	2.7E-03
AKNAD1	1.66	2.7E-03
RNF19B	1.72	2.8E-03
ZNF483	3.28	2.8E-03
GNA14	1.26	2.9E-03
SLC1A2	1.49	2.9E-03
PSEN2	1.91	2.9E-03
PLCXD2	1.40	2.9E-03
RBFOX1	2.54	2.9E-03
OLFML1	1.55	2.9E-03
DCX	4.99	2.9E-03
ZFP106	3.88	2.9E-03
TGFB3	4.39	3.0E-03
SYNPO2L	3.34	3.0E-03
FSD1L	4.70	3.1E-03
PRUNE	2.71	3.1E-03
PIK3C2B	4.02	3.1E-03
MYL1	28.66	3.1E-03
BHLHE40	4.25	3.2E-03
CXCL13	2.76	3.2E-03
SLCO5A1	6.28	3.3E-03
ATP1A1	1.88	3.3E-03
MED12L	2.94	3.4E-03
FBXO40	4.15	3.4E-03
NFKB2	1.35	3.4E-03
MOAP1	1.70	3.4E-03
CDK18	3.23	3.5E-03
CKMT2	8.76	3.5E-03
RNF152	3.20	3.5E-03
FADS2	6.23	3.5E-03
INPP4B	2.24	3.5E-03
TPRG1	3.21	3.7E-03
TMEM62	2.14	3.7E-03
NCF2	1.44	3.7E-03
DENND1B	1.78	3.8E-03
NECAB3	1.60	3.8E-03
AIF1L	3.15	3.8E-03
CHRM4	1.46	3.8E-03
KCTD7	1.83	3.8E-03
ASB4	3.13	3.9E-03
SNX18	1.61	3.9E-03
COL14A1	8.44	3.9E-03
SLN	44.72	3.9E-03
EGR2	2.48	3.9E-03
ENO3	6.73	3.9E-03

DCP2	2.35	3.9E-03
DACT1	4.92	3.9E-03
FAM213A	5.57	3.9E-03
DNAJA4	5.48	4.0E-03
CYP2J2	10.26	4.0E-03
PPM1K	5.08	4.0E-03
GRASP	2.16	4.0E-03
TTC33	1.74	4.0E-03
CLCN7	1.48	4.1E-03
PRAP1	1.35	4.1E-03
ERBB2	1.51	4.1E-03
EFCAB7	1.49	4.2E-03
HRC	5.34	4.3E-03
EAF2	2.19	4.3E-03
MGAT4A	1.49	4.4E-03
PADI2	2.64	4.4E-03
SHISA4	3.20	4.5E-03
MEF2A	2.96	4.6E-03
FGF13	1.90	4.6E-03
TTC13	2.39	4.7E-03
CSRP3	8.60	4.7E-03
MAPK8	1.51	4.8E-03
TSPAN9	2.81	4.8E-03
RNF115	2.01	4.8E-03
TOM1L2	1.53	4.8E-03
TRO	1.95	4.8E-03
MYOT	13.30	5.0E-03
NUDT9	1.44	5.0E-03
CDKN2B	1.88	5.0E-03
PLXDC1	1.66	5.0E-03
GXYLT2	1.64	5.1E-03
CD36	26.14	5.2E-03
FNDC5	3.02	5.2E-03
PGM5	7.10	5.2E-03
CCDC141	9.00	5.2E-03
HMGCS1	4.33	5.2E-03
MSMO1	3.80	5.2E-03
LOC158696	3.04	5.3E-03
FABP3	9.55	5.3E-03
ZSCAN16	1.40	5.3E-03
DYNC1I1	2.08	5.3E-03
NEK7	2.02	5.4E-03
ABLIM3	2.02	5.4E-03
SCAI	1.76	5.5E-03
MYOM3	9.03	5.5E-03
MYL3	2.03	5.6E-03
NEURL	1.62	5.6E-03
VASH1	2.40	5.6E-03
CDKL1	1.30	5.6E-03
DNAJB6	1.62	5.6E-03
ATP8A1	20.66	5.7E-03
CXCL12	3.69	5.7E-03
C16orf54	1.29	5.7E-03
KIFAP3	1.70	5.7E-03
GPRC5B	4.64	5.7E-03
NUP50	3.54	5.7E-03
OLFM2	2.44	5.7E-03
GPRC5C	2.66	5.8E-03
RRAGD	18.29	5.8E-03
TPM3	6.15	5.8E-03
AMZ2P1	1.23	5.8E-03
UAP1L1	1.46	5.9E-03

DPY19L2P4	1.42	5.9E-03
HRASLS2	1.49	5.9E-03
FAM189A2	2.34	6.0E-03
C13orf44	1.79	6.0E-03
AGL	4.18	6.0E-03
SQSTM1	1.71	6.0E-03
PCDHB11	2.35	6.1E-03
F13A1	3.99	6.1E-03
DMGDH	1.23	6.1E-03
FAM212B	1.42	6.2E-03
C5orf24	1.63	6.3E-03
USP13	2.72	6.4E-03
CARNS1	3.11	6.4E-03
JAM2	7.70	6.4E-03
CAMK2G	1.84	6.5E-03
SNN	1.44	6.5E-03
SORBS2	3.18	6.5E-03
TSPAN18	1.38	6.5E-03
VGLL2	3.99	6.5E-03
40789	2.63	6.5E-03
GALNT13	6.31	6.6E-03
APOBEC2	10.36	6.6E-03
KLHL31	10.10	6.7E-03
ITGA1	2.94	6.7E-03
FRMD7	2.35	6.8E-03
RAB15	2.23	6.8E-03
PMEPA1	1.57	6.8E-03
NCALD	3.37	7.0E-03
RRAGC	1.60	7.0E-03
LIMK2	2.06	7.0E-03
FAM69A	1.86	7.1E-03
OR1D5	1.53	7.1E-03
TMEM182	14.65	7.2E-03
PRKG1	10.09	7.3E-03
LGR4	4.42	7.3E-03
MAPK10	3.01	7.3E-03
JAZF1	1.48	7.3E-03
RAPGEF1	2.42	7.3E-03
CDK20	1.37	7.4E-03
ITGB1BP2	8.38	7.4E-03
FILIP1	11.09	7.4E-03
KPNA1	1.53	7.4E-03
KLHDC10	1.43	7.4E-03
AK1	2.46	7.5E-03
TMEM117	2.24	7.5E-03
SREBF2	1.98	7.5E-03
MYL6B	2.99	7.6E-03
CYGB	2.21	7.7E-03
CACNB4	1.41	7.8E-03
BAIAP2	1.23	7.8E-03
SLC40A1	4.21	7.8E-03
PDE2A	2.70	7.8E-03
FLRT2	3.16	7.9E-03
TAL2	3.51	7.9E-03
TRAK1	1.63	8.0E-03
VDR	2.77	8.1E-03
SLC41A2	3.42	8.1E-03
FAAH2	1.24	8.1E-03
MOB1B	2.64	8.1E-03
FBXO16	4.02	8.2E-03
ICAM1	2.67	8.2E-03
MYBPC1	62.04	8.2E-03

ABHD4	1.49	8.2E-03
CYB5R1	2.03	8.3E-03
ASAH1	2.11	8.3E-03
NRAP	14.11	8.3E-03
PHLDB1	1.76	8.4E-03
MAPRE3	8.22	8.4E-03
CASQ1	2.23	8.4E-03
NPY6R	5.37	8.4E-03
C21orf91	1.66	8.5E-03
ARL4C	1.98	8.5E-03
SLC4A4	3.58	8.5E-03
CELF1	1.45	8.6E-03
MLLT11	4.62	8.6E-03
AFAP1L1	2.69	8.6E-03
TRAF5	2.12	8.7E-03
IL34	2.11	8.7E-03
DTWD2	2.05	8.8E-03
FAM190B	1.54	8.8E-03
GFPT1	1.62	8.9E-03
PKP2	2.85	9.0E-03
PDE4DIP	1.94	9.1E-03
ZNF610	1.83	9.1E-03
MICU1	2.06	9.3E-03
PCDHB12	3.04	9.4E-03
YIPF7	4.22	9.4E-03
MAS1	2.28	9.4E-03
TBC1D1	1.72	9.4E-03
AKD1	2.63	9.5E-03
MBP	2.41	9.5E-03
DHCR7	3.44	9.5E-03
MYH7	17.04	9.6E-03
PREPL	2.38	9.6E-03
CACNB1	5.01	9.6E-03
AGBL1	7.84	9.7E-03
AFAP1	1.30	9.7E-03
SLC36A1	1.94	9.7E-03
TNNT1	5.11	9.7E-03
PPM1E	5.41	9.7E-03
IMPAD1	1.49	9.8E-03
KCND3	1.46	9.8E-03
COL19A1	5.93	9.8E-03
TNNC1	7.23	9.8E-03
ASB1	1.64	9.8E-03
UBE2D3	1.30	9.8E-03
HAGH	1.27	9.8E-03
CLIC5	1.62	9.8E-03
LIMCH1	6.90	9.9E-03
LRRN3	2.56	1.0E-02
MYL4	8.30	1.0E-02

Table S3. DNA methylation data of normal and EDMD patient MyoD-converted myoblasts normalized to d1. Genes queried were those showing mRNA upregulation with human myoblast –myotube transition (Encode), and then ranked by decrease of methylation at day 3 in wild-type cells.

	WT			EDMD		
Gene ID	Day 1	Day 3	Day 5	Day 1	Day 3	Day 5
DACT1	1.00	0.47	0.66	1.00	0.74	0.89
KCTD7	1.00	0.51	0.66	1.00	1.11	1.09
GSK3B	1.00	0.54	0.76	1.00	0.82	0.84
TPM3	1.00	0.56	0.68	1.00	0.57	0.73
JAM2	1.00	0.57	0.70	1.00	1.21	1.06
PADI2	1.00	0.57	0.78	1.00	0.93	0.88
SAMD4A	1.00	0.59	0.82	1.00	0.98	0.87
LIMCH1	1.00	0.60	1.05	1.00	1.01	0.92
GPRC5C	1.00	0.60	0.73	1.00	0.78	1.01
GNA14	1.00	0.61	0.52	1.00	0.84	1.17
FAAH2	1.00	0.62	0.60	1.00	0.97	0.94
PKP2	1.00	0.63	0.64	1.00	1.05	1.11
C10orf71	1.00	0.64	0.45	1.00	0.84	0.99
F13A1	1.00	0.65	0.74	1.00	1.14	1.02
HUNK	1.00	0.66	0.81	1.00	1.08	0.99
SC4MOL	1.00	0.66	0.88	1.00	0.74	0.83
FRMD7	1.00	0.67	1.30	1.00	0.54	0.79
ABHD4	1.00	0.68	0.64	1.00	0.99	1.36
PGAP1	1.00	0.69	0.85	1.00	0.68	0.96
CDK18	1.00	0.69	0.93	1.00	0.54	0.71
PPP1R15A	1.00	0.71	0.69	1.00	0.84	0.82
TTC13	1.00	0.71	0.85	1.00	1.39	1.29
SLCO5A1	1.00	0.72	0.71	1.00	1.07	1.06
PRKCQ	1.00	0.72	0.99	1.00	1.12	1.07
KLHDC10	1.00	0.73	1.03	1.00	0.91	0.93
ATP8A1	1.00	0.73	0.78	1.00	0.84	1.04
FABP3	1.00	0.74	0.92	1.00	1.19	1.11
CASQ1	1.00	0.74	0.63	1.00	0.94	0.87
TPRG1	1.00	0.76	0.98	1.00	0.98	0.97
TMEM182	1.00	0.77	0.99	1.00	0.87	0.89
PARM1	1.00	0.77	0.88	1.00	0.80	0.97
ANKRD50	1.00	0.77	0.52	1.00	0.65	1.00
HMGCS1	1.00	0.77	0.82	1.00	1.18	0.85
DYNC1I1	1.00	0.77	0.72	1.00	0.58	1.09
COL19A1	1.00	0.78	1.00	1.00	1.54	1.55
TOM1L2	1.00	0.79	0.65	1.00	0.93	0.92
CBARA1	1.00	0.79	0.95	1.00	0.90	1.05
OR1D5	1.00	0.80	0.85	1.00	0.57	0.96
YIPF7	1.00	0.80	0.88	1.00	0.83	1.10
SCD	1.00	0.81	1.00	1.00	0.85	0.84
CSRP3	1.00	0.81	0.73	1.00	0.98	1.59
TGFB3	1.00	0.81	0.91	1.00	1.08	1.05
FLJ32065	1.00	0.81	0.86	1.00	1.01	0.98
RAB15	1.00	0.82	0.95	1.00	0.88	0.54
CACNB4	1.00	0.82	0.90	1.00	0.87	0.99
TNNC1	1.00	0.82	0.98	1.00	0.81	0.96
NEURL	1.00	0.83	0.77	1.00	0.42	0.68
KIFAP3	1.00	0.83	0.90	1.00	0.90	0.89
LIMK2	1.00	0.83	0.94	1.00	0.74	0.77

MBP	1.00	0.84	0.79	1.00	0.98	1.00
ERBB2	1.00	0.85	0.91	1.00	0.90	0.80
NEO1	1.00	0.85	0.90	1.00	1.10	0.91
DHCR7	1.00	0.85	0.90	1.00	1.47	1.10
FBXO16	1.00	0.85	0.92	1.00	1.05	0.99
CYB5R1	1.00	0.85	1.15	1.00	1.81	1.28
CXCL12	1.00	0.86	0.68	1.00	1.00	1.11
LITAF	1.00	0.86	1.04	1.00	0.92	0.94
HDAC9	1.00	0.86	0.85	1.00	1.39	1.16
ZFP106	1.00	0.86	1.13	1.00	1.16	1.00
ZNF483	1.00	0.86	0.92	1.00	0.75	0.72
KPNA1	1.00	0.87	1.14	1.00	1.16	1.08
EFCAB7	1.00	0.87	0.97	1.00	1.05	0.96
ENAM	1.00	0.87	0.92	1.00	0.99	0.99
MYL1	1.00	0.88	1.00	1.00	0.78	0.70
ATXN1	1.00	0.88	0.94	1.00	0.95	0.95
HAGH	1.00	0.89	1.00	1.00	0.91	0.89
DPY19L2P4	1.00	0.89	0.98	1.00	0.89	0.94
SLC41A2	1.00	0.90	0.98	1.00	1.11	1.77
TAL2	1.00	0.90	0.98	1.00	0.98	0.96
SVIL	1.00	0.90	0.88	1.00	1.08	1.04
ATP1A1	1.00	0.90	1.06	1.00	1.08	0.97
ANKRD36BL1	1.00	0.90	0.92	1.00	1.03	1.10
FAM189A2	1.00	0.91	0.96	1.00	0.86	0.96
CACNB1	1.00	0.91	0.92	1.00	1.09	0.87
NECAB3	1.00	0.91	0.94	1.00	0.96	0.91
TRAK1	1.00	0.92	0.92	1.00	1.50	1.23
PTPRB	1.00	0.92	0.90	1.00	0.54	0.77
ATP1B4	1.00	0.92	0.94	1.00	0.46	0.62
MYL4	1.00	0.92	0.97	1.00	1.03	1.02
TNNT1	1.00	0.92	1.12	1.00	1.02	0.97
PDE4DIP	1.00	0.92	0.93	1.00	0.92	0.98
PIK3C2B	1.00	0.92	1.07	1.00	0.93	0.96
CXCL13	1.00	0.92	0.98	1.00	0.64	0.86
PPFIBP2	1.00	0.92	0.87	1.00	0.91	0.93
CHRM4	1.00	0.92	0.95	1.00	1.00	0.98
NRAP	1.00	0.93	0.87	1.00	1.09	1.04
ZNF610	1.00	0.93	1.04	1.00	1.24	1.24
MYH6	1.00	0.93	1.06	1.00	0.80	0.94
NEK7	1.00	0.93	0.97	1.00	0.99	0.96
RRAGD	1.00	0.93	0.95	1.00	0.87	0.99
DCP2	1.00	0.94	0.89	1.00	0.92	1.12
SOHLH2	1.00	0.94	0.95	1.00	0.97	1.03
IMPAD1	1.00	0.94	0.95	1.00	0.94	0.94
UAP1L1	1.00	0.94	1.14	1.00	0.89	0.98
LDLR	1.00	0.94	0.99	1.00	1.02	1.03
PGM5	1.00	0.94	0.90	1.00	0.72	1.03
FLRT2	1.00	0.94	1.13	1.00	0.83	0.93
FAM69A	1.00	0.95	0.96	1.00	0.98	0.99
SHISA4	1.00	0.95	1.04	1.00	1.23	1.06
KCNN3	1.00	0.95	1.14	1.00	0.99	0.98
GALNT13	1.00	0.95	0.99	1.00	0.89	0.94
OLFM2	1.00	0.95	1.01	1.00	1.06	1.04
ENO3	1.00	0.96	0.96	1.00	1.04	1.01
SGCD	1.00	0.96	0.99	1.00	0.96	0.96
APOBEC2	1.00	0.96	0.93	1.00	0.95	0.95
ARL4C	1.00	0.96	1.03	1.00	1.09	1.05
MXRA5	1.00	0.96	1.13	1.00	1.09	1.00
POLB	1.00	0.96	0.98	1.00	1.01	1.00
AKNAD1	1.00	0.96	1.02	1.00	0.99	0.94
MYOM3	1.00	0.96	1.05	1.00	1.04	0.93
ASB14	1.00	0.96	0.95	1.00	1.15	1.03

NAV3	1.00	0.97	1.04	1.00	1.14	1.13
PPM1K	1.00	0.97	0.99	1.00	0.99	0.99
KIF2A	1.00	0.97	1.70	1.00	0.85	0.86
SEL1L3	1.00	0.97	1.08	1.00	0.91	0.87
C1orf183	1.00	0.97	0.95	1.00	1.05	1.01
DNAJA4	1.00	0.97	0.95	1.00	1.04	1.04
TBC1D1	1.00	0.97	1.00	1.00	0.97	0.99
ITGA6	1.00	0.97	1.01	1.00	1.27	1.22
RNF19B	1.00	0.97	0.99	1.00	0.73	0.95
PCDHB12	1.00	0.98	1.05	1.00	1.05	0.93
LDB3	1.00	0.98	1.00	1.00	0.89	0.88
PKIA	1.00	0.98	0.91	1.00	0.98	0.98
SPATA13	1.00	0.98	1.00	1.00	1.07	1.04
SLC4A4	1.00	0.98	0.98	1.00	0.98	1.01
EGR2	1.00	0.98	1.00	1.00	0.80	0.95
CACNA2D1	1.00	0.98	1.00	1.00	0.99	0.97
CD36	1.00	0.98	0.98	1.00	0.93	0.91
CAP2	1.00	0.98	1.03	1.00	0.91	0.61
REEP1	1.00	0.98	0.98	1.00	1.29	1.25
LGR4	1.00	0.98	0.67	1.00	1.02	1.07
MYOM1	1.00	0.99	0.92	1.00	0.51	0.67
FBXO30	1.00	0.99	1.00	1.00	1.03	1.03
FRK	1.00	0.99	0.98	1.00	1.00	0.96
AK1	1.00	0.99	1.04	1.00	1.00	0.94
KCNA10	1.00	0.99	1.07	1.00	0.92	0.90
JAZF1	1.00	0.99	1.03	1.00	1.02	1.03
PPM1E	1.00	0.99	1.02	1.00	1.01	1.00
DMGDH	1.00	0.99	1.00	1.00	0.98	0.99
MGAT4A	1.00	0.99	1.06	1.00	0.89	0.94
TRIM63	1.00	0.99	0.95	1.00	0.86	0.82
GGA2	1.00	0.99	1.02	1.00	0.90	1.16
DTWD2	1.00	0.99	0.96	1.00	1.60	1.41
STK38L	1.00	0.99	0.98	1.00	1.01	0.98
TMEM62	1.00	1.00	1.02	1.00	1.02	0.99
RAPGEF1	1.00	1.00	1.03	1.00	0.93	1.02
TRIM54	1.00	1.00	1.02	1.00	0.99	0.99
TRAF5	1.00	1.00	0.99	1.00	1.08	1.12
PCDHB11	1.00	1.00	1.04	1.00	1.07	0.99
SLC36A1	1.00	1.00	0.98	1.00	1.01	0.97
RBM24	1.00	1.00	1.02	1.00	0.88	0.85
EGF	1.00	1.00	0.99	1.00	1.00	0.98
IL34	1.00	1.01	1.23	1.00	1.03	1.08
FAM190B	1.00	1.01	1.02	1.00	1.00	1.02
MAS1	1.00	1.01	1.06	1.00	1.09	1.31
TNNC2	1.00	1.01	1.02	1.00	1.09	1.08
FRMPD1	1.00	1.01	1.06	1.00	1.00	0.86
KLHL31	1.00	1.01	0.96	1.00	0.95	1.09
PLXDC1	1.00	1.01	1.02	1.00	0.82	0.94
HSPA12A	1.00	1.01	1.01	1.00	0.87	0.91
INPP4B	1.00	1.01	1.06	1.00	1.04	1.00
VDR	1.00	1.01	1.02	1.00	0.95	0.97
SYNPO2L	1.00	1.01	0.99	1.00	1.06	1.23
PDE7A	1.00	1.01	1.02	1.00	1.03	0.98
LRRN3	1.00	1.01	1.00	1.00	1.09	1.04
ASB4	1.00	1.02	1.04	1.00	0.96	0.98
LOC158696	1.00	1.02	1.16	1.00	0.90	0.89
CLIC5	1.00	1.02	0.99	1.00	0.95	0.98
GPNMB	1.00	1.02	0.98	1.00	0.99	1.01
HRASLS2	1.00	1.02	0.99	1.00	0.99	0.98
HRC	1.00	1.02	1.06	1.00	1.19	1.09
DHCR24	1.00	1.03	1.01	1.00	1.01	1.01
COL14A1	1.00	1.03	0.96	1.00	0.91	0.98

MYOM2	1.00	1.03	0.90	1.00	1.22	1.16
VASH1	1.00	1.03	1.04	1.00	1.01	1.06
NPY6R	1.00	1.04	1.06	1.00	0.97	0.94
TTC33	1.00	1.04	0.99	1.00	0.55	1.01
MED12L	1.00	1.04	1.00	1.00	1.00	0.98
CYGB	1.00	1.05	1.04	1.00	0.98	0.96
AFAP1	1.00	1.06	1.00	1.00	0.98	1.01
ATPGD1	1.00	1.06	1.04	1.00	1.00	1.00
PRUNE	1.00	1.06	1.13	1.00	0.78	0.86
ABLIM3	1.00	1.07	1.13	1.00	1.05	1.39
FSD1L	1.00	1.07	1.11	1.00	0.97	1.10
NBEA	1.00	1.09	1.01	1.00	1.04	1.02
AGL	1.00	1.09	1.29	1.00	1.02	1.09
KIAA0922	1.00	1.09	1.13	1.00	1.26	1.34
ZNF148	1.00	1.10	1.10	1.00	0.74	0.89
PLP1	1.00	1.12	1.22	1.00	0.46	0.67
CCDC141	1.00	1.14	1.17	1.00	0.75	1.14
C5orf24	1.00	1.14	0.76	1.00	1.16	0.87
FILIP1	1.00	1.16	0.98	1.00	0.91	0.84
SLCO2B1	1.00	1.16	1.18	1.00	0.45	0.70
SNN	1.00	1.19	1.49	1.00	1.31	1.20
AGBL1	1.00	1.19	0.75	1.00	0.85	0.76
SNX18	1.00	1.20	1.52	1.00	0.77	1.06
RNF121	1.00	1.21	0.93	1.00	1.09	0.89
PMEPA1	1.00	1.22	1.25	1.00	0.86	1.01
AFAP1L1	1.00	1.23	1.11	1.00	1.29	1.41
DCX	1.00	1.23	1.52	1.00	1.12	1.06
BAIAP2	1.00	1.23	1.17	1.00	0.83	0.90
PSEN2	1.00	1.29	1.37	1.00	1.33	1.53
DCLK2	1.00	1.33	1.36	1.00	0.96	1.31
PKHD1	1.00	1.36	1.41	1.00	1.00	1.23
ICAM1	1.00	1.41	1.16	1.00	0.99	1.08
EXOC6	1.00	1.52	1.62	1.00	1.33	1.40
GPR98	1.00	1.54	1.17	1.00	1.15	0.91
VGLL2	1.00	1.66	0.86	1.00	0.86	1.23
42262	1.00	1.90	1.58	1.00	1.13	1.52

Table S4. Human myogenic cells infected with EDMD LMNA variant show differential DNA methylation levels on myogenic and cell cycle genes. Transcriptionally deregulated genes in EDMD *(3)* show differential methylation levels in EDMD when compared to WT (column 2 and 3), and FPLD LMNA mutation (column 3 and 4). Comparison between FPLD mutation and WT LMNA is shown column 5 and 6. Analysis was done using ANOVA (+/- 1.2 Fold Change with $p<0.05$ FDR corrected).

Gene Symbol	EDMD vs. WT		EDMD vs. FPLD		FPLD vs. WT	
	Fold Change	p-value (FDR)	**Fold Change**	p-value (FDR)	**Fold Change**	p-value (FDR)
HDAC1	-1.33872	1.09E-03	-1.32502	1.19E-03	-1.01034	3.46E-01
RB1	-1.22808	1.14E-03	-1.22007	1.22E-03	-1.00657	4.07E-01
MYOD1	1.46129	4.61E-03	1.41385	5.36E-03	1.03355	3.97E-01
CHRNG	-1.20232	1.13E-02	-1.21936	9.67E-03	1.01417	5.15E-01
MCM3	-1.2192	1.26E-02	-1.2243	1.21E-02	1.00418	8.57E-01

Table S5. Heterochromatin peaks (H3K9me3) showing decreased enrichment in emerin-null cell during myogenic transition (d0 to d1). Peaks for each condition were called using SICER (window size 1000bp,gap size 3000 bp and FDR1e-2) and merged to find union peaks. Union peak file was annotated with read counts and normalized to corresponding library sizes. Peaks showing decrease at day 0 and day 1 were annotated using GREAT to identify genes associated with these peaks.

Chromosomal position			Normalized read counts						Ratio			Great Annotation
chr	start	end	emd-d0	wt-d0	emd-d1	wt-d1	emd-d2	wt-d2	day 0	day 1	day 2	Gene Symbol
chr1	63957000	63972999	110.4	136.11	143.02	160.67	160.83	156.4	0.81	0.89	1.03	Fastkd2, Klf7
chr1	189262000	189276999	111.51	124.5	105.68	111.38	101.32	101.2	0.9	0.95	1	Esrrg, Gpatch2
chr1	35633000	35636999	31.19	38.43	32.25	34.24	37.53	41.2	0.81	0.94	0.91	Hs6st1, Plekhb2
chr1	38371000	38374999	30.64	35.63	30.56	33.49	34.31	28.8	0.86	0.91	1.19	Rev1, Aff3
chr1	58793000	58805999	160.08	236.98	193.95	229.15	194.6	181.2	0.68	0.85	1.07	Casp8, Cflar
chr1	91814000	91842999	237.36	270.21	286.05	307.04	315.76	275.6	0.88	0.93	1.15	Gbx2
chr1	122188000	122199999	92.74	111.69	94.64	100.09	92.21	88	0.83	0.95	1.05	C1ql2, Steap3
chr1	127283000	127288999	72.31	93.27	98.04	118.53	90.6	72	0.78	0.83	1.26	Actr3
chr1	156843000	156847999	42.78	48.44	43.29	47.41	41.28	38	0.88	0.91	1.09	Cacna1e, Mr1
chr1	163118000	163123999	48.58	59.25	50.5	62.46	64.87	60	0.82	0.81	1.08	Ankrd45, Prdx6
chr1	173421000	173430999	71.21	86.47	88.28	94.07	88.46	92	0.82	0.94	0.96	Refbp2, F11r
chr1	180678000	180687999	106.26	119.69	125.62	133.2	131.34	115.6	0.89	0.94	1.14	Kif26b, Smyd3
chr1	184636000	184659999	184.92	213.77	197.35	209.59	213.37	205.2	0.87	0.94	1.04	4922505E12Rik, Capn8
chr1	184610000	184631999	188.79	211.36	183.34	197.55	201.04	170.8	0.89	0.93	1.18	4922505E12Rik, Capn8
chr1	187316000	187322999	46.92	60.85	57.72	61.33	75.59	53.2	0.77	0.94	1.42	Slc30a10, Lyplal1
chr1	193887000	193891999	52.16	72.86	87	92.19	81.49	90.4	0.72	0.94	0.9	Traf5, Rd3
chr1	43077000	43081999	45.82	53.24	38.2	48.92	47.18	45.2	0.86	0.78	1.04	Gpr45, Tgfbrap1
chr1	63244000	63247999	36.16	46.44	33.95	60.96	56.29	60.4	0.78	0.56	0.93	Gpr1, Eef1b2
chr1	93019000	93025999	65.41	80.46	87	92.56	98.64	100.8	0.81	0.94	0.98	Rbm44, Lrrfip1
chr1	168963000	168965999	25.12	32.43	24.62	35.37	25.2	23.6	0.77	0.7	1.07	Fam78b, Uck2
chr1	194099000	194099999	10.21	14.01	8.06	9.41	13.4	12.8	0.73	0.86	1.05	Kcnh1, Hhat
chr10	84013000	84025999	111.51	129.7	133.69	146.75	153.32	123.2	0.86	0.91	1.24	Ckap4, Tcp11l2
chr10	120321000	120331999	78.94	112.09	95.07	105.73	120.09	109.2	0.7	0.9	1.1	Hmga2, Msrb3
chr10	121234000	121247999	96.05	111.69	106.1	114.77	106.15	101.2	0.86	0.92	1.05	BC048403, Srgap1
chr10	68434000	68450999	112.61	128.1	122.23	131.32	156	132	0.88	0.93	1.18	Rhobtb1, Tmem26
chr10	69446000	69456999	141.87	178.94	157.88	167.44	172.62	187.6	0.79	0.94	0.92	Ccdc6, Ank3
chr10	75609000	75613999	39.74	52.04	42.02	51.55	40.21	45.6	0.76	0.82	0.88	Slc5a4a, Prmt2
chr10	78520000	78535999	152.91	200.96	204.56	227.65	240.71	218.8	0.76	0.9	1.1	Olfr57, 2610008E11Rik
chr10	83122000	83132999	77.56	94.87	88.28	94.82	93.82	96.4	0.82	0.93	0.97	1500009L16Rik, Appl2
chr10	94343000	94369999	211.7	235.78	234.27	247.97	256.79	264.8	0.9	0.94	0.97	Plxnc1, Ccdc41
chr10	120607000	120643999	278.49	311.44	277.13	302.15	312.01	297.2	0.89	0.92	1.05	Tbc1d30, Wif1
chr10	121336000	121360999	175.54	216.97	197.77	214.1	220.34	177.2	0.81	0.92	1.24	Srgap1, BC048403
chr10	126057000	126062999	54.1	60.85	47.53	56.07	35.38	45.2	0.89	0.85	0.78	Xrcc6bp1, Lrig3
chr10	40250000	40253999	30.36	40.43	36.92	39.51	47.71	34.4	0.75	0.93	1.39	Slc22a16, Cdk19
chr10	41064000	41064999	8.56	12.41	6.79	10.91	8.58	9.2	0.69	0.62	0.93	Zbtb24, Fig4
chr10	42641000	42644999	40.3	45.24	35.65	43.65	46.64	50.4	0.89	0.82	0.93	Scml4, Sobp
chr10	63018000	63019999	20.7	26.82	23.34	24.83	33.77	18.4	0.77	0.94	1.84	Ctnna1, Lrrtm3
chr10	67453000	67465999	132.76	148.11	138.35	183.62	132.95	140.8	0.9	0.75	0.94	Rtkn2, Arid5b
chr10	67470000	67482999	141.31	217.37	168.06	200.56	175.84	183.2	0.65	0.84	0.96	Rtkn2, Arid5b
chr10	67554000	67565999	123.37	154.52	140.9	158.79	128.66	140	0.8	0.89	0.92	Rtkn2, Arid5b

chr10	70306000	70311999	70.93	92.87	84.03	92.56	82.02	81.2	0.76	0.91	1.01	Phyhipl, Bicc1
chr10	75097000	75103999	61.83	69.25	69.6	80.15	69.69	68.8	0.89	0.87	1.01	Susd2, Ggt5
chr10	75536000	75539999	43.88	52.44	47.11	50.42	53.61	50	0.84	0.93	1.07	Slc5a4b, Zfp280b
chr10	78550000	78555999	49.4	61.65	46.68	58.7	60.58	60.8	0.8	0.8	1	2610008E11Rik, Olfr57
chr10	84692000	84696999	37.81	44.43	37.35	44.4	40.21	42.8	0.85	0.84	0.94	Btbd11, Cry1
chr10	89211000	89215999	50.78	59.65	52.63	62.84	56.83	53.2	0.85	0.84	1.07	Anks1b, Uhrf1bp1l
chr10	94443000	94450999	60.45	79.26	67.9	77.89	65.94	66.4	0.76	0.87	0.99	Plxnc1, Cradd
chr10	116910000	116912999	35.05	39.23	39.89	47.03	52.54	42	0.89	0.85	1.25	Cpm, Cpsf6
chr10	119440000	119447999	66.24	73.66	66.63	71.12	70.76	56.4	0.9	0.94	1.25	Helb, Grip1
chr10	119479000	119479999	8.28	9.21	8.06	10.16	10.72	8	0.9	0.79	1.34	Helb, Grip1
chr10	127410000	127415999	50.78	59.25	53.9	63.59	67.55	66.8	0.86	0.85	1.01	Hsd17b6, Sdr9c7
chr10	128437000	128446999	84.18	110.49	122.65	129.44	135.63	150	0.76	0.95	0.9	Olfr763, Olfr9
chr11	64486000	64492999	71.21	80.46	67.9	71.87	69.69	72	0.89	0.94	0.97	Elac2, Hs3st3a1
chr11	49637000	49648999	96.88	107.68	100.16	114.39	91.14	84.4	0.9	0.88	1.08	Mapk9, Gfpt2
chr11	59274000	59279999	65.97	92.47	96.76	103.1	124.91	116.8	0.71	0.94	1.07	Zfp867, Jmjd4
chr11	94318000	94325999	58.24	66.45	60.27	66.6	64.33	52.8	0.88	0.9	1.22	Abcc3, Cacna1g
chr11	96109000	96142999	277.66	316.25	344.19	370.26	324.88	369.6	0.88	0.93	0.88	Hoxb9, AK078566
chr11	96221000	96237999	154.84	188.15	172.31	200.93	189.24	198.8	0.82	0.86	0.95	Skap1, Hoxb1
chr11	108759000	108779999	176.37	198.55	187.16	203.94	211.22	197.2	0.89	0.92	1.07	Axin2, Ccdc46
chr11	113258000	113263999	69.28	85.27	74.27	74.13	61.65	70	0.81	0.78	0.88	Slc39a11, Sox9
chr11	120619000	120626999	66.24	86.87	98.04	112.13	107.22	94.8	0.76	0.87	1.13	Cbr2, Rfng
chr11	3000000	3004999	153.46	1921.89	150.66	1906.61	165.65	1698.4	0.08	0.08	0.1	Sfi1
chr11	11897000	11897999	6.07	7.21	5.09	9.41	7.51	8	0.84	0.54	0.94	Ddc, Grb10
chr11	52537000	52539999	20.15	25.22	26.31	27.84	20.37	28.8	0.8	0.94	0.71	Fstl4, 9530068E07Rik
chr11	63652000	63657999	45.26	53.64	44.56	52.3	50.93	50	0.84	0.85	1.02	Hs3st3b1, Pmp22
chr11	63937000	63942999	48.3	54.04	48.81	52.68	61.12	40.8	0.89	0.93	1.5	Hs3st3a1, Cox10
chr11	64751000	64759999	58.79	66.05	59.42	66.23	59.51	49.2	0.89	0.9	1.21	Elac2, Hs3st3a1
chr11	81555000	81555999	12.14	14.01	7.64	12.42	8.58	10	0.87	0.62	0.86	Ccl2, 1700071K01Rik
chr11	95787000	95789999	27.88	35.63	28.86	45.15	40.74	28	0.78	0.64	1.46	B4galnt2, Igf2bp1
chr11	96213000	96216999	30.64	39.23	40.74	45.15	31.63	50	0.78	0.9	0.63	Hoxb1, Hoxb2
chr11	96341000	96353999	87.49	105.28	99.31	111.38	113.12	114.8	0.83	0.89	0.99	Skap1, Snx11
chr11	96358000	96358999	8	9.21	8.06	11.29	9.11	9.6	0.87	0.71	0.95	Skap1, Snx11
chr11	96395000	96398999	24.84	34.03	28.43	30.48	27.34	37.2	0.73	0.93	0.73	Skap1, Snx11
chr12	71489000	71499999	78.39	87.27	82.76	88.05	78.27	74.4	0.9	0.94	1.05	Tmx1, Trim9
chr12	110848000	110856999	109.02	126.1	112.47	129.82	107.22	101.6	0.86	0.87	1.06	Dio3, Rtl1
chr12	111034000	111047999	125.03	159.72	150.24	160.29	138.31	140.8	0.78	0.94	0.98	Dio3, Rtl1
chr12	3109000	3110999	1206.69	1406.29	1214.64	1375.68	1313.44	1384	0.86	0.88	0.95	Rab10
chr12	27837000	27837999	7.18	10.01	4.67	9.78	9.65	7.2	0.72	0.48	1.34	Sox11, Cmpk2
chr12	57368000	57375999	60.72	68.05	77.67	82.03	65.4	62.8	0.89	0.95	1.04	Mbip, Brms1l
chr12	75904000	75905999	245.92	274.61	235.12	274.31	267.51	279.2	0.9	0.86	0.96	Kcnh5, Dbpht2
chr12	81645000	81648999	35.33	39.63	37.35	39.51	27.34	36.8	0.89	0.95	0.74	Galntl1, Erh
chr12	85525000	85527999	55.2	68.05	78.51	84.66	80.41	85.2	0.81	0.93	0.94	Pnma1, C130039O16Rik
chr13	43150000	43163999	87.22	100.08	95.49	101.97	92.74	98.4	0.87	0.94	0.94	Tbc1d7, Phactr1
chr13	45187000	45187999	11.32	12.81	8.06	9.41	17.16	9.6	0.88	0.86	1.79	Mylip, Dtnbp1
chr13	47095000	47109999	154.29	206.56	178.67	191.53	204.25	191.6	0.75	0.93	1.07	Kif13a, Nhlrc1
chr13	54531000	54545999	115.92	131.3	123.5	140.73	152.79	141.2	0.88	0.88	1.08	Thoc3, Cplx2
chr13	54848000	54854999	56.31	63.25	61.96	76.76	67.55	72	0.89	0.81	0.94	Gprin1
chr13	56246000	56250999	37.54	46.84	42.44	54.56	51.47	50.8	0.8	0.78	1.01	H2afy, Tifab
chr13	60305000	60326999	177.75	200.56	236.82	249.85	264.83	236.4	0.89	0.95	1.12	Dapk1, Gas1
chr13	67174000	67178999	33.12	43.63	38.62	41.77	41.82	47.2	0.76	0.92	0.89	Zfp712, Zfp708
chr13	83855000	83872999	115.37	133.7	152.78	177.6	165.12	182.4	0.86	0.86	0.91	Tmem161b, Mef2c
chr13	84375000	84377999	30.64	42.03	35.23	37.25	52	43.6	0.73	0.95	1.19	Ccnh, Tmem161b
chr13	13018000	13024999	102.95	148.92	108.22	146.37	109.36	133.2	0.69	0.74	0.82	Prl2c3, Prl2c2

chr13	38241000	38247999	60.45	71.66	58.14	75.63	73.98	73.6	0.84	0.77	1.01	Snrnp48, Dsp
chr13	45171000	45177999	51.89	64.05	58.14	61.33	75.05	55.2	0.81	0.95	1.36	Mylip, Dtnbp1
chr13	45714000	45721999	115.92	144.51	129.87	151.64	137.24	136	0.8	0.86	1.01	Gmpr, Atxn1
chr13	46129000	46130999	14.9	18.01	16.98	18.06	13.4	16.8	0.83	0.94	0.8	Gm1574, Atxn1
chr13	48580000	48593999	122.82	148.52	138.35	153.15	157.61	146.4	0.83	0.9	1.08	Zfp169, Id4
chr13	53760000	53767999	77.01	87.27	77.67	84.29	75.05	66.8	0.88	0.92	1.12	Msx2, Drd1a
chr13	67591000	67597999	49.96	61.65	57.29	64.34	65.4	62.4	0.81	0.89	1.05	Zfp874b, Zfp58
chr13	99238000	99249999	96.6	126.5	114.16	123.04	134.02	117.6	0.76	0.93	1.14	Foxd1, Tmem174
chr13	99570000	99570999	17.39	19.62	14.43	18.06	23.05	24.8	0.89	0.8	0.93	Tmem171, Fcho2
chr13	107942000	107947999	43.61	49.24	39.47	46.28	40.74	42	0.89	0.85	0.97	Kif2a, Zswim6
chr13	112396000	112406999	75.63	89.27	78.94	89.18	80.41	78	0.85	0.89	1.03	Gpbp1, Mier3
chr13	112464000	112473999	72.04	97.28	83.61	88.05	99.18	81.6	0.74	0.95	1.22	Gpbp1, Mier3
chr13	115165000	115167999	26.22	34.83	30.98	33.11	33.24	31.2	0.75	0.94	1.07	Ndufs4, Arl15
chr14	48641000	48647999	50.51	58.85	52.2	60.2	65.4	51.6	0.86	0.87	1.27	Peli2, Ktn1
chr14	76053000	76054999	19.04	24.82	16.98	19.94	15.55	18.4	0.77	0.85	0.84	4930564B18Rik, Cog3
chr14	104870000	104873999	42.5	57.64	49.66	58.32	50.93	50.8	0.74	0.85	1	Pou4f1
chr14	118831000	118833999	24.29	32.83	24.19	30.48	24.12	25.2	0.74	0.79	0.96	Sox21, Abcc4
chr14	25419000	25423999	43.33	51.24	44.56	47.41	52.54	45.2	0.85	0.94	1.16	Zmiz1, Rps24
chr14	28238000	28241999	36.71	54.44	50.93	54.94	56.29	61.2	0.67	0.93	0.92	D14Abb1e
chr14	37859000	37861999	16.56	22.82	19.1	21.45	22.52	20.4	0.73	0.89	1.1	Fam190b, Rgr
chr14	46685000	46687999	23.74	28.42	29.28	31.61	23.05	28	0.84	0.93	0.82	Ddhd1, Gm15217
chr14	55826000	55827999	30.91	34.43	30.98	36.88	42.89	40	0.9	0.84	1.07	Jph4, Dhrs2
chr14	58952000	58962999	86.67	130.1	91.67	100.47	105.08	87.2	0.67	0.91	1.2	Fgf9, 1700129C05Rik
chr14	61823000	61831999	93.29	120.89	84.88	107.24	92.74	125.2	0.77	0.79	0.74	Sacs, Sgcg
chr14	64691000	64699999	62.65	72.06	70.03	73.75	71.3	77.6	0.87	0.95	0.92	Prss55, Rp1l1
chr14	65198000	65199999	24.29	27.62	18.67	24.83	20.37	24.8	0.88	0.75	0.82	Msra, Kif13b
chr14	73401000	73403999	34.22	41.63	37.35	42.9	46.1	35.2	0.82	0.87	1.31	Fndc3a, Cysltr2
chr14	75476000	75478999	19.32	26.02	22.07	28.22	24.66	21.2	0.74	0.78	1.16	Lrrc63, 5031414D18Rik
chr14	79057000	79061999	58.24	75.26	58.57	66.23	77.2	60.4	0.77	0.88	1.28	Akap11, Dgkh
chr14	120835000	120839999	43.88	52.44	55.17	59.83	53.07	56.4	0.84	0.92	0.94	Rap2a, Mbnl2
chr14	121347000	121351999	46.64	52.44	52.2	63.21	58.97	46.8	0.89	0.83	1.26	Farp1, Ipo5
chr14	122229000	122240999	109.57	137.71	113.74	123.42	134.02	124.4	0.8	0.92	1.08	Dock9, Ubac2
chr14	122737000	122739999	21.25	28.42	23.77	27.09	20.37	19.2	0.75	0.88	1.06	Zic5, Clybl
chr15	79690000	79708999	112.89	134.5	131.99	142.61	149.04	134.8	0.84	0.93	1.11	Npcd, Apobec3
chr15	25744000	25758999	120.34	158.52	132.41	154.65	149.57	144.8	0.76	0.86	1.03	Fam134b, Myo10
chr15	56075000	56082999	52.72	60.45	68.33	75.26	68.62	78	0.87	0.91	0.88	Sntb1, Has2
chr15	96446000	96455999	104.05	116.89	105.25	127.56	134.02	119.6	0.89	0.83	1.12	Scaf11, Slc38a1
chr15	97466000	97476999	107.37	125.7	105.68	114.39	112.04	107.6	0.85	0.92	1.04	Amigo2, Rpap3
chr15	25763000	25770999	81.42	106.08	87.43	108.74	119.55	107.2	0.77	0.8	1.12	Fam134b, Myo10
chr15	25775000	25786999	115.65	140.91	128.59	142.99	128.13	135.2	0.82	0.9	0.95	Zfp622, Fam134b
chr15	38644000	38648999	59.89	78.06	61.11	65.85	69.69	70	0.77	0.93	1	Baalc, Atp6v1c1
chr15	58447000	58457999	76.45	86.87	78.94	93.69	94.89	90.8	0.88	0.84	1.05	Tmem65, D15Ertd621e
chr15	86625000	86625999	11.04	12.41	8.06	13.17	11.26	12	0.89	0.61	0.94	Fam19a5, Tbc1d22a
chr16	56095000	56100999	44.99	58.85	61.96	69.24	82.02	59.6	0.76	0.89	1.38	Impg2, Senp7
chr16	44448000	44454999	56.58	63.65	63.24	69.24	63.8	60.4	0.89	0.91	1.06	Wdr52, Boc
chr16	48297000	48303999	43.06	53.64	54.75	64.72	58.43	57.2	0.8	0.85	1.02	Dppa2, Dppa4
chr16	87587000	87601999	120.06	144.11	141.75	162.93	134.02	159.2	0.83	0.87	0.84	Bach1, ORF63
chr16	90353000	90363999	73.42	86.47	83.18	90.68	112.04	100	0.85	0.92	1.12	Scaf4, Hunk
chr16	90616000	90619999	30.08	35.23	22.49	28.6	29.49	29.2	0.85	0.79	1.01	2610039C10Rik, Hunk
chr16	92473000	92509999	308.85	346.27	369.23	390.2	393.5	367.2	0.89	0.95	1.07	Rcan1, Clic6
chr16	17270000	17271999	24.29	30.02	31.83	35.75	40.21	34	0.81	0.89	1.18	Tmem191c, Hic2
chr16	22184000	22195999	79.49	90.47	87	93.32	107.76	89.2	0.88	0.93	1.21	Igf2bp2, Tra2b
chr16	23178000	23179999	18.77	21.62	20.8	24.83	19.3	14.8	0.87	0.84	1.3	St6gal1, Adipoq

chr16	38220000	38221999	26.5	46.44	35.65	39.51	30.56	30.4	0.57	0.9	1.01	Nr1i2, Gsk3b
chr16	91165000	91166999	10.76	14.81	12.73	14.3	16.62	11.2	0.73	0.89	1.48	4932438H23Rik, Olig2
chr17	4961000	4969999	56.03	65.25	64.93	73.37	77.2	59.2	0.86	0.88	1.3	Arid1b
chr17	8575000	8585999	85.84	95.67	96.34	103.1	109.36	106.8	0.9	0.93	1.02	T, Prr18
chr17	12644000	12654999	76.73	88.07	87.85	94.82	90.06	91.2	0.87	0.93	0.99	Slc22a3, Plg
chr17	23754000	23760999	45.82	64.05	50.5	57.19	55.75	57.2	0.72	0.88	0.97	Zscan10, Mmp25
chr17	28518000	28526999	81.97	98.48	96.34	115.52	102.39	108.4	0.83	0.83	0.94	Tulp1, Fkbp5
chr17	33471000	33475999	35.6	42.03	31.41	46.66	41.28	39.6	0.85	0.67	1.04	Zfp81, Zfp955b
chr17	47980000	47996999	126.69	148.11	151.94	168.95	171.55	168	0.86	0.9	1.02	Mdfi, Foxp4
chr17	84000000	84011999	81.15	91.67	78.09	89.18	81.49	82	0.89	0.88	0.99	Cox7a2l, Kcng3
chr17	7821000	7825999	60.17	76.06	84.03	89.93	120.62	117.2	0.79	0.93	1.03	Gm9992, Fndc1
chr17	30533000	30536999	37.26	51.64	36.5	39.51	40.21	39.2	0.72	0.92	1.03	Btbd9, Zfand3
chr17	50432000	50433999	20.7	32.83	27.16	38.38	24.12	30.4	0.63	0.71	0.79	Dazl
chr17	66307000	66313999	77.01	120.49	117.98	141.86	116.33	120.8	0.64	0.83	0.96	Twsg1, Ankrd12
chr17	69182000	69182999	9.94	14.81	10.61	12.42	9.65	12.8	0.67	0.85	0.75	Epb4.1l3, L3mbtl4
chr17	71066000	71068999	32.57	46.44	38.62	43.65	45.03	44.4	0.7	0.88	1.01	Tgif1, Dlgap1
chr17	78989000	78995999	63.48	72.46	72.15	76.01	73.45	63.6	0.88	0.95	1.15	Vit, Strn
chr17	79823000	79826999	35.6	48.84	47.96	54.18	49.32	46.4	0.73	0.89	1.06	Fam82a1, Cdc42ep3
chr17	80364000	80370999	56.86	75.66	57.72	71.49	79.34	60.4	0.75	0.81	1.31	Atl2, Hnrpll
chr17	85595000	85599999	45.26	50.44	47.11	55.31	60.58	49.6	0.9	0.85	1.22	Six3, 1700106N22Rik
chr17	88241000	88243999	30.64	36.43	33.53	38.38	38.6	40	0.84	0.87	0.96	Msh6, Kcnk12
chr18	24322000	24330999	74.8	87.67	83.18	89.55	102.93	86	0.85	0.93	1.2	Ino80c, Galnt1
chr18	34130000	34156999	186.58	209.36	196.07	211.85	216.05	197.2	0.89	0.93	1.1	D0H4S114, Epb4.1l4a
chr18	60454000	60461999	51.34	61.25	65.36	73	64.33	73.2	0.84	0.9	0.88	Iigp1, Gm4841
chr18	65930000	65948999	165.33	203.76	176.98	187.76	191.92	177.2	0.81	0.94	1.08	Sec11c, 5330437I02Rik
chr18	74670000	74679999	100.19	112.09	98.04	105.36	85.24	92.4	0.89	0.93	0.92	Acaa2, Myo5b
chr18	76503000	76521999	137.45	156.52	142.17	157.28	155.47	149.2	0.88	0.9	1.04	Skor2, Smad2
chr18	78969000	78976999	64.86	74.86	64.08	68.86	83.63	74.8	0.87	0.93	1.12	Slc14a2, Setbp1
chr18	85076000	85083999	61.27	70.05	61.54	70.74	64.33	62	0.87	0.87	1.04	Fbxo15, Cyb5
chr18	10856000	10860999	51.89	64.05	58.99	60.58	70.76	61.2	0.81	0.94	1.16	Gata6, Mib1
chr18	13127000	13132999	45.82	68.85	47.96	56.44	67.01	67.2	0.67	0.85	1	Impact
chr18	37678000	37682999	42.23	47.24	37.35	44.02	44.5	44.8	0.89	0.85	0.99	Pcdhb22, Slc25a2
chr18	61760000	61764999	67.9	90.47	84.03	89.55	91.14	86.8	0.75	0.94	1.05	Il17b, Csnk1a1
chr18	75949000	75953999	44.71	62.85	51.35	63.21	64.87	58	0.71	0.81	1.12	Gm672, Zbtb7c
chr18	81601000	81601999	8.28	10.81	6.37	8.28	6.97	8	0.77	0.77	0.87	Sall3, Galr1
chr18	83219000	83220999	23.74	29.22	20.8	23.33	19.3	27.2	0.81	0.89	0.71	Zfp516
chr19	30260000	30266999	50.23	58.05	56.87	66.6	64.87	52	0.87	0.85	1.25	Mbl2, Gldc
chr19	37780000	37784999	47.47	58.05	62.39	68.11	77.2	68.4	0.82	0.92	1.13	Cyp26a1, Myof
chr19	55242000	55247999	46.92	61.25	59.42	63.59	64.33	54.4	0.77	0.93	1.18	Gpam, Tectb
chr19	37760000	37762999	52.72	65.65	55.6	66.98	83.1	75.2	0.8	0.83	1.1	Cyp26a1, Cyp26c1
chr19	56242000	56242999	11.59	14.01	14.43	15.43	23.05	8.4	0.83	0.94	2.74	Habp2, Ppnr
chr2	71038000	71042999	42.78	52.04	41.17	48.54	51.47	50.8	0.82	0.85	1.01	Dync1i2, Cybrd1
chr2	92693000	92804999	927.65	1065.63	1128.06	1217.64	1164.94	1168	0.87	0.93	1	Syt13, Chst1
chr2	143911000	143932999	208.38	265.01	240.21	267.53	274.48	282	0.79	0.9	0.97	Banf2, Snx5
chr2	147061000	147065999	48.85	54.84	41.59	44.78	30.56	40.8	0.89	0.93	0.75	Pax1, Nkx2-2
chr2	166035000	166068999	299.74	335.46	345.46	369.88	327.02	318.4	0.89	0.93	1.03	Sulf2, Prex1
chr2	5137000	5158999	169.19	190.15	182.07	194.54	202.65	180	0.89	0.94	1.13	Ccdc3, Camk1d
chr2	52264000	52266999	42.5	60.85	65.78	71.49	62.19	89.6	0.7	0.92	0.69	Neb, Arl5a
chr2	70464000	70477999	113.99	129.7	124.77	136.21	151.18	121.2	0.88	0.92	1.25	Gorasp2, Gad1
chr2	74873000	74875999	28.7	32.83	23.34	26.34	23.05	33.6	0.87	0.89	0.69	Hnrnpa3, Mtx2
chr2	120960000	120965999	42.78	52.44	50.5	54.18	46.1	64	0.82	0.93	0.72	Adal, Lcmt2
chr2	127722000	127765999	329.83	375.09	362.44	420.3	380.09	386.8	0.88	0.86	0.98	Bcl2l11, Acoxl
chr2	152337000	152351999	119.51	135.71	136.66	147.5	143.14	142.4	0.88	0.93	1.01	Defb28

chr2	157377000	157389999	138.83	179.74	155.76	181.37	202.65	204.8	0.77	0.86	0.99	Peg5, Nnat
chr2	165155000	165168999	98.53	125.3	97.61	112.51	117.41	121.6	0.79	0.87	0.97	Elmo2, Zfp663
chr2	5654000	5658999	49.96	57.64	58.99	73.37	65.4	65.2	0.87	0.8	1	Camk1d, Cdc123
chr2	9803000	9813999	101.29	125.7	125.62	133.58	131.34	135.2	0.81	0.94	0.97	Gata3, Taf3
chr2	49824000	49835999	81.42	90.87	95.49	102.72	96.5	90	0.9	0.93	1.07	Lypd6, Lypd6b
chr2	52271000	52274999	38.92	51.64	54.32	58.32	62.72	56.4	0.75	0.93	1.11	Neb, Arl5a
chr2	59156000	59157999	23.74	44.03	31.41	33.11	33.77	40.8	0.54	0.95	0.83	Dapl1, Pkp4
chr2	61641000	61650999	87.22	97.68	115.44	121.91	119.55	110.8	0.89	0.95	1.08	Slc4a10, Tbr1
chr2	70256000	70265999	79.49	88.47	85.73	97.83	84.17	78.8	0.9	0.88	1.07	Sp5, Myo3b
chr2	73784000	73784999	9.38	11.61	8.49	11.29	10.19	7.2	0.81	0.75	1.41	Atp5g3, Lnp
chr2	74944000	74944999	8.56	10.81	8.06	8.65	6.43	10	0.79	0.93	0.64	Hnrnpa3, Mtx2
chr2	77816000	77820999	51.34	58.85	49.66	61.71	60.04	51.6	0.87	0.8	1.16	Ube2e3, Cwc22
chr2	80283000	80284999	25.12	30.82	23.77	32.74	27.88	31.2	0.81	0.73	0.89	Frzb, Dnajc10
chr2	93423000	93427999	32.57	40.03	32.25	35.75	39.14	39.2	0.81	0.9	1	Cd82, Alx4
chr2	103811000	103813999	26.5	31.22	36.5	39.89	38.06	36.8	0.85	0.92	1.03	Fbxo3, Lmo2
chr2	104990000	104990999	9.11	13.21	8.06	11.29	11.26	11.6	0.69	0.71	0.97	0610012H03Rik, Wt1
chr2	165243000	165243999	8.56	10.41	10.61	11.66	8.58	12.8	0.82	0.91	0.67	4833422F24Rik, Slc13a3
chr2	170353000	170357999	48.3	57.24	42.44	45.91	50.39	53.2	0.84	0.92	0.95	Dok5, Pfdn4
chr3	35141000	35150999	60.45	70.85	66.21	77.89	58.43	70.4	0.85	0.85	0.83	Atp11b, Sox2
chr3	36251000	36258999	55.48	77.26	64.51	68.11	68.08	69.6	0.72	0.95	0.98	Qrfpr, Anxa5
chr3	51004000	51023999	168.09	207.36	209.65	243.83	204.25	219.6	0.81	0.86	0.93	Slc7a11, Ccrn4l
chr3	57705000	57730999	182.44	202.96	197.35	223.89	195.68	190.4	0.9	0.88	1.03	Tsc22d2, Pfn2
chr3	57741000	57754999	88.87	103.68	99.31	109.12	124.37	116	0.86	0.91	1.07	Tsc22d2, Pfn2
chr3	82900000	82919999	158.15	192.55	167.21	179.49	166.19	205.6	0.82	0.93	0.81	Sfrp2, Plrg1
chr3	87055000	87066999	97.43	109.28	97.61	107.24	96.5	91.6	0.89	0.91	1.05	Kirrel, Fcrls
chr3	87383000	87393999	85.29	98.88	79.36	98.21	93.82	79.6	0.86	0.81	1.18	Arhgef11, Etv3
chr3	98081000	98100999	147.66	171.33	155.76	164.81	171.55	158.4	0.86	0.95	1.08	Hmgcs2, Phgdh
chr3	104005000	104005999	18.77	23.62	18.25	25.21	25.2	20.8	0.79	0.72	1.21	Magi3, Phtf1
chr3	131415000	131416999	28.43	34.83	28.86	32.74	38.6	30.8	0.82	0.88	1.25	Dkk2, Papss1
chr3	138305000	138325999	166.16	202.56	204.56	230.66	229.45	213.2	0.82	0.89	1.08	Tspan5, Eif4e
chr3	152533000	152540999	81.42	95.67	63.66	77.51	67.55	66	0.85	0.82	1.02	St6galnac5, Pigk
chr3	8639000	8646999	66.24	78.06	73	91.44	72.91	67.6	0.85	0.8	1.08	Hey1, Stmn2
chr3	37989000	37991999	30.08	42.03	36.92	39.89	44.5	46	0.72	0.93	0.97	Gm5148, Ankrd50
chr3	52221000	52226999	48.85	66.45	56.02	60.96	78.27	67.6	0.74	0.92	1.16	Foxo1, Cog6
chr3	66774000	66778999	42.23	60.85	52.63	63.97	51.47	54	0.69	0.82	0.95	Veph1, Shox2
chr3	88549000	88553999	61.83	68.85	66.21	85.42	71.3	73.6	0.9	0.78	0.97	Syt11, Rit1
chr3	98223000	98234999	108.19	184.94	151.94	167.82	180.13	179.2	0.59	0.91	1.01	Zfp697, Hsd3b4
chr3	105658000	105658999	7.45	8.81	4.67	7.53	6.97	8	0.85	0.62	0.87	Rap1a, Adora3
chr3	129174000	129178999	46.09	66.45	50.93	59.83	57.9	40.8	0.69	0.85	1.42	Enpep, Elovl6
chr3	138749000	138750999	21.8	29.22	24.19	29.73	27.88	28	0.75	0.81	1	B930007M17Rik, Rap1gds1
chr3	146541000	146546999	48.85	64.85	58.99	67.35	80.95	67.6	0.75	0.88	1.2	Ttll7
chr4	129879000	129894999	138	154.92	132.84	159.54	122.23	145.6	0.89	0.83	0.84	Tinagl1, Gm853
chr4	150062000	150080999	204.52	244.19	230.45	250.23	247.68	221.6	0.84	0.92	1.12	Errfi1, Slc45a1
chr4	33040000	33086999	338.38	389.5	402.33	452.66	457.83	471.6	0.87	0.89	0.97	Ankrd6, Rragd
chr4	46847000	46863999	141.59	164.13	151.09	168.2	159.22	156.4	0.86	0.9	1.02	Tbc1d2, Gabbr2
chr4	57863000	57873999	143.25	168.93	144.72	188.89	159.22	159.6	0.85	0.77	1	Akap2, D630039A03Rik
chr4	117079000	117135999	456.24	514.8	491.03	529.05	567.19	484.8	0.89	0.93	1.17	Rnf220, Tmem53
chr4	117981000	118006999	229.91	261.8	305.57	325.11	355.97	345.6	0.88	0.94	1.03	Hyi, Ptprf
chr4	119074000	119083999	72.59	102.48	80.64	91.06	92.74	97.2	0.71	0.89	0.95	Ppih, Ccdc30
chr4	128550000	128567999	135.52	152.92	168.91	185.88	166.19	162.8	0.89	0.91	1.02	Trim62
chr4	140812000	140826999	123.93	160.12	145.15	170.83	169.94	173.2	0.77	0.85	0.98	Epha2, Arhgef19
chr4	145661000	145677999	154.56	181.34	150.24	161.8	150.11	154.8	0.85	0.93	0.97	Gm13251, Gm13242

chr4	33953000	33955999	32.84	45.24	30.13	37.25	41.28	33.6	0.73	0.81	1.23	Cnr1, Rngtt
chr4	43632000	43639999	65.41	88.47	73.85	80.9	98.11	76	0.74	0.91	1.29	Msmp, Npr2
chr4	47111000	47111999	6.62	11.61	10.19	12.04	8.58	13.2	0.57	0.85	0.65	Col15a1, Galnt12
chr4	53217000	53226999	66.24	77.26	65.78	76.76	64.87	75.2	0.86	0.86	0.86	Slc44a1, Abca1
chr4	57041000	57044999	33.67	38.83	34.38	43.65	41.28	33.2	0.87	0.79	1.24	6430704M03Rik, Epb4.1l4b
chr4	57035000	57036999	13.8	21.22	19.95	23.71	19.84	20.4	0.65	0.84	0.97	6430704M03Rik, Epb4.1l4b
chr4	58159000	58161999	29.53	47.64	42.44	45.15	47.71	34.4	0.62	0.94	1.39	Txndc8, Svep1
chr4	98644000	98646999	33.95	48.84	51.78	55.31	47.71	38.8	0.7	0.94	1.23	Angptl3, Usp1
chr4	111166000	111171999	53.27	59.25	44.14	50.42	45.57	55.2	0.9	0.88	0.83	Spata6, Bend5
chr4	121689000	121696999	87.22	98.08	84.88	92.56	64.87	77.2	0.89	0.92	0.84	9530002B09Rik, Gm12887
chr5	21495000	21497999	31.46	37.23	30.98	32.74	35.92	32	0.85	0.95	1.12	Slc26a5, Reln
chr5	23195000	23215999	158.43	194.15	167.64	192.28	167.26	161.2	0.82	0.87	1.04	Srpk2, ENSMUSG00000073777
chr5	100532000	100535999	28.7	33.63	24.62	30.48	25.73	28.8	0.85	0.81	0.89	Tmem150c, Enoph1
chr5	144834000	144847999	94.39	117.69	104.83	111	114.19	107.6	0.8	0.94	1.06	Ocm, Lmtk2
chr5	20460000	20471999	88.32	110.09	98.89	112.51	130.27	116.4	0.8	0.88	1.12	Rsbn1l, Ptpn14
chr5	27735000	27741999	46.64	53.24	54.32	57.95	65.94	59.6	0.88	0.94	1.11	Speer4b, Dpp6
chr5	33387000	33392999	51.89	60.05	57.29	60.96	69.69	63.6	0.86	0.94	1.1	Slc5a1, Ywhah
chr5	65288000	65293999	51.34	66.85	54.75	78.27	68.62	74	0.77	0.7	0.93	Tlr1, Klf3
chr5	67272000	67283999	94.95	112.09	100.16	103.48	105.61	103.2	0.85	0.95	1.02	Limch1, Phox2b
chr5	72957000	72961999	45.26	57.24	42.86	50.42	52	44.8	0.79	0.85	1.16	Nfxl1, Zar1
chr5	110556000	110562999	63.48	89.67	75.97	85.04	102.39	70	0.71	0.89	1.46	Chfr, Zfp605
chr5	120104000	120117999	136.35	154.12	157.45	168.57	136.71	136	0.88	0.93	1.01	Tbx3
chr5	127171000	127175999	37.54	48.04	39.47	44.78	28.95	31.2	0.78	0.88	0.93	Tmem132c
chr5	137283000	137312999	237.92	269.81	288.59	320.97	330.24	335.2	0.88	0.9	0.99	Emid2, Myl10
chr5	144718000	144722999	55.75	62.85	47.11	59.08	55.22	51.6	0.89	0.8	1.07	Rsph10b2, Ccz1
chr5	150355000	150362999	77.28	91.67	75.12	80.52	87.92	78.8	0.84	0.93	1.12	Wdr95, Hsph1
chr5	75383000	75393999	73.97	92.47	83.18	95.95	117.41	87.2	0.8	0.87	1.35	Lnx1, Chic2
chr5	104602000	104606999	38.36	47.24	41.17	46.28	48.78	49.2	0.81	0.89	0.99	Dmp1, Dspp
chr5	104943000	104949999	58.51	75.66	69.18	76.76	100.79	76	0.77	0.9	1.33	BC005561, Zfp951
chr5	106431000	106437999	61.83	68.85	54.75	61.71	54.15	55.6	0.9	0.89	0.97	Zfp326, Barhl2
chr5	106974000	106981999	72.04	80.86	60.69	70.74	48.25	60	0.89	0.86	0.8	Barhl2, Zfp644
chr5	119312000	119321999	109.85	125.7	114.59	126.81	120.62	121.2	0.87	0.9	1	Tbx3, Med13l
chr5	126310000	126318999	81.42	95.27	76.82	81.65	61.65	71.2	0.85	0.94	0.87	Tmem132b
chr5	126425000	126433999	87.77	100.88	86.58	94.45	69.16	76.4	0.87	0.92	0.91	Tmem132b
chr5	131336000	131339999	40.85	45.64	39.89	44.78	37.53	36	0.9	0.89	1.04	A330070K13Rik, Wbscr17
chr5	135730000	135732999	35.33	41.63	34.38	39.13	53.61	47.6	0.85	0.88	1.13	Fzd9
chr5	148538000	148551999	123.65	146.91	145.57	158.41	136.71	132.8	0.84	0.92	1.03	Pomp, Flt1
chr5	150702000	150702999	6.35	8.01	7.64	12.42	9.65	7.2	0.79	0.62	1.34	Rxfp2, B3galtl
chr6	145613000	145630999	150.42	180.14	165.94	175.72	185.49	183.2	0.84	0.94	1.01	Rassf8, Tuba3b
chr6	37630000	37638999	76.73	88.47	81.49	90.31	98.64	85.2	0.87	0.9	1.16	Atp6v0c, Akr1d1
chr6	37822000	37830999	98.26	126.9	139.2	147.5	137.78	118.8	0.77	0.94	1.16	Trim24, Svopl
chr6	87389000	87405999	115.37	135.71	125.62	139.6	133.49	148.4	0.85	0.9	0.9	Bmp10, Arhgap25
chr6	87638000	87668999	240.68	273.01	247.43	298.77	292.17	276	0.88	0.83	1.06	Aplf, Ccdc48
chr6	117257000	117270999	108.19	132.9	137.51	154.27	127.59	136	0.81	0.89	0.94	Zfp637, Cxcl12
chr6	144816000	144819999	35.88	42.43	30.56	34.99	38.06	42.4	0.85	0.87	0.9	Sox5, Bcat1
chr6	8570000	8572999	29.81	36.83	36.5	44.02	47.18	44.4	0.81	0.83	1.06	Glcci1, Ica1
chr6	28887000	28892999	37.26	47.64	42.86	46.28	56.29	44	0.78	0.93	1.28	Lep, Lrrc4
chr6	31593000	31594999	14.35	17.21	17.4	18.44	16.62	19.2	0.83	0.94	0.87	1700012A03Rik, Podxl

chr6	37685000	37690999	41.4	51.24	55.17	59.83	42.89	42	0.81	0.92	1.02	Atp6v0c, Akr1d1
chr6	52152000	52156999	87.49	107.68	102.28	114.01	85.78	92	0.81	0.9	0.93	Hoxa4
chr6	85074000	85077999	47.75	56.84	47.53	54.18	55.75	44.8	0.84	0.88	1.24	Gm5878
chr6	118379000	118380999	26.5	40.03	40.74	43.27	58.97	55.2	0.66	0.94	1.07	Bms1, Zfp248
chr6	136391000	136393999	30.91	41.23	29.28	40.64	41.28	37.6	0.75	0.72	1.1	Atf7ip, LOC100502936
chr6	142830000	142833999	27.05	35.63	25.89	37.25	40.21	22.8	0.76	0.69	1.76	Gm766, St8sia1
chr6	143314000	143316999	40.02	50.04	41.59	46.28	43.96	36	0.8	0.9	1.22	Etnk1, Sox5
chr6	144433000	144437999	40.85	48.44	39.89	49.29	50.93	39.2	0.84	0.81	1.3	Sox5, Bcat1
chr6	144452000	144452999	8.56	10.41	7.64	9.41	8.04	7.6	0.82	0.81	1.06	Sox5, Bcat1
chr7	122550000	122572999	191.27	212.97	179.95	198.3	154.93	169.2	0.9	0.91	0.92	Sox6, Insc
chr7	19447000	19453999	65.41	73.26	65.36	69.24	83.63	60.4	0.89	0.94	1.38	Pglyrp1, Mill2
chr7	28766000	28776999	118.41	166.53	140.05	155.03	173.16	162	0.71	0.9	1.07	Zfp780b, Psmc4
chr7	29047000	29052999	49.96	68.45	65.36	75.26	60.04	58	0.73	0.87	1.04	Eid2
chr7	29457000	29462999	43.06	59.65	53.47	63.97	69.69	71.2	0.72	0.84	0.98	C330005M16Rik, Fbxo27
chr7	31539000	31540999	29.53	35.23	25.04	30.85	29.49	31.2	0.84	0.81	0.95	Dmkn, Sbsn
chr7	89436000	89440999	50.51	62.45	52.63	58.32	57.9	54.8	0.81	0.9	1.06	Adamtsl3, Sh3gl3
chr7	108962000	108969999	66.52	87.67	64.51	81.65	80.95	89.2	0.76	0.79	0.91	Phox2a
chr7	145161000	145171999	103.78	116.09	84.03	102.35	71.3	86.4	0.89	0.82	0.83	Tcerg1l, Glrx3
chr7	145307000	145320999	138.28	158.92	105.68	125.68	99.71	116.4	0.87	0.84	0.86	Tcerg1l, Glrx3
chr7	145420000	145426999	61.55	71.66	59.42	74.88	49.86	66	0.86	0.79	0.76	Tcerg1l, Glrx3
chr7	149089000	149095999	46.64	53.64	54.75	61.71	61.12	58	0.87	0.89	1.05	Tollip
chr7	6264000	6269999	41.95	49.24	50.93	55.69	66.48	62.4	0.85	0.91	1.07	Zfp583, Zfp667
chr7	16539000	16543999	68.45	84.47	71.3	87.3	71.3	75.2	0.81	0.82	0.95	Gltscr2, Ehd2
chr7	26486000	26487999	25.94	29.62	32.68	31.61	35.92	38.8	0.88	0.89	0.93	Tgfb2, Ccdc97
chr7	28813000	28816999	44.99	53.64	46.68	56.07	54.68	49.2	0.84	0.83	1.11	Zfp780b, Psmc4
chr7	29475000	29487999	118.13	138.11	152.78	165.94	157.08	190.8	0.86	0.92	0.82	Fbxo17, Fbxo27
chr7	31257000	31259999	27.32	30.42	25.89	27.84	40.74	32.4	0.9	0.93	1.26	Prodh2, Nphs1
chr7	31837000	31837999	10.21	11.61	10.19	11.66	12.33	10.4	0.88	0.87	1.19	Fxyd7
chr7	73502000	73509999	87.49	126.5	121.38	132.45	105.08	107.6	0.69	0.92	0.98	Lrrk1, Chsy1
chr7	74206000	74209999	32.84	41.23	25.89	28.97	36.99	38	0.8	0.89	0.97	Lysmd4, Adamts17
chr7	89446000	89451999	60.72	68.05	54.75	71.12	81.49	64	0.89	0.77	1.27	Adamtsl3, Sh3gl3
chr7	118360000	118367999	60.72	72.46	75.97	83.53	90.06	81.2	0.84	0.91	1.11	Eif4g2, Galntl4
chr7	120827000	120827999	8	10.01	4.67	7.53	11.79	5.6	0.8	0.62	2.11	Spon1, Far1
chr7	122532000	122533999	16.01	20.42	14.43	16.56	11.26	21.2	0.78	0.87	0.53	Sox6, Insc
chr7	124398000	124398999	11.32	14.41	10.19	12.04	8.04	6.4	0.79	0.85	1.26	Xylt1, Nucb2
chr7	143368000	143372999	46.37	51.64	44.14	50.8	47.71	50.8	0.9	0.87	0.94	Mgmt, Mki67
chr7	149296000	149305999	70.38	84.07	66.21	77.51	75.59	62	0.84	0.85	1.22	Dusp8, Krtap5-2
chr8	10479000	10488999	61.55	77.26	58.57	65.47	79.88	67.2	0.8	0.89	1.19	Myo16, Irs2
chr8	127007000	127014999	58.51	67.25	64.08	70.36	66.48	63.6	0.87	0.91	1.05	Pgbd5, Cog2
chr8	27363000	27384999	151.25	186.95	165.52	182.5	169.41	173.6	0.81	0.91	0.98	Zfp703, Thap1
chr8	27432000	27454999	211.14	248.19	227.48	249.47	205.86	208.8	0.85	0.91	0.99	Zfp703, Thap1
chr8	46093000	46115999	237.09	292.63	224.93	293.87	239.64	229.6	0.81	0.77	1.04	Mtnr1a, Fat1
chr8	46120000	46129999	95.5	108.48	75.97	106.49	82.56	88.4	0.88	0.71	0.93	Mtnr1a, Fat1
chr8	47361000	47366999	49.13	56.04	50.08	53.06	63.26	58	0.88	0.94	1.09	Slc25a4, Helt
chr8	63913000	63923999	80.04	96.47	89.97	98.59	107.22	100	0.83	0.91	1.07	Cbr4, Sh3rf1
chr8	85553000	85561999	72.87	93.27	70.88	77.14	69.16	65.6	0.78	0.92	1.05	Tbc1d9, Rnf150
chr8	85917000	85918999	10.21	14.81	10.61	17.31	14.47	17.6	0.69	0.61	0.82	Clgn, Scoc
chr8	112797000	112803999	59.89	74.46	56.45	63.59	50.93	58	0.8	0.89	0.88	Vac14, Hydin
chr8	14592000	14597999	59.62	68.85	61.54	67.73	71.3	71.2	0.87	0.91	1	Cln8, Dlgap2
chr8	27007000	27016999	67.62	79.26	76.39	85.04	85.78	76	0.85	0.9	1.13	Kcnu1, Hgsnat
chr8	37488000	37490999	21.8	24.42	27.59	31.61	33.77	23.6	0.89	0.87	1.43	Lonrf1, 6430573F11Rik
chr8	48121000	48125999	40.57	46.84	36.92	46.66	43.96	37.2	0.87	0.79	1.18	Enpp6, Stox2
chr8	80617000	80619999	26.5	31.22	25.89	31.23	28.41	22.4	0.85	0.83	1.27	Ednra, Ttc29

chr8	83478000	83479999	20.98	26.02	17.82	20.7	23.05	16.8	0.81	0.86	1.37	Gab1, Usp38
chr8	87070000	87074999	42.5	47.24	40.32	45.91	42.35	46	0.9	0.88	0.92	Ier2, Cacna1a
chr8	94883000	94891999	137.73	198.55	154.48	182.5	136.71	180.8	0.69	0.85	0.76	Irx6, Irx5
chr8	111316000	111319999	63.48	73.26	58.57	66.98	86.31	82.4	0.87	0.87	1.05	Pmfbp1, Zfhx3
chr8	114169000	114178999	71.76	93.67	87	91.81	114.19	116.8	0.77	0.95	0.98	Zfp1, Ctrb1
chr8	128184000	128185999	14.08	19.21	15.28	17.69	20.91	18.4	0.73	0.86	1.14	Sipa1l2, 4933403G14Rik
chr9	27069000	27085999	117.3	134.9	118.41	126.81	113.12	111.2	0.87	0.93	1.02	Jam3, Igsf9b
chr9	40330000	40342999	114.82	136.51	124.77	137.34	122.23	124	0.84	0.91	0.99	9030425E11Rik, Gramd1b
chr9	121392000	121407999	125.03	139.71	129.87	158.41	158.69	146	0.89	0.82	1.09	Cck, Trak1
chr9	20241000	20243999	50.23	60.85	63.24	67.35	57.9	53.2	0.83	0.94	1.09	Zfp560, Zfp26
chr9	22010000	22010999	10.49	14.41	9.76	11.29	17.16	13.2	0.73	0.86	1.3	Zfp809, Zfp872
chr9	34625000	34625999	7.45	8.81	8.49	9.78	6.97	8	0.85	0.87	0.87	St3gal4, Kirrel3
chr9	40589000	40590999	28.43	36.43	29.71	39.51	30.02	33.6	0.78	0.75	0.89	Hspa8, 9030425E11Rik
chr9	41832000	41835999	28.43	36.03	32.68	34.99	31.09	30.4	0.79	0.93	1.02	Ubash3b, Sorl1
chr9	42747000	42747999	6.9	8.41	7.21	7.9	7.51	7.6	0.82	0.91	0.99	Tbcel, Grik4
chr9	51708000	51715999	66.79	75.26	66.63	71.12	88.99	65.2	0.89	0.94	1.36	Fdx1, Arhgap20
chr9	60003000	60003999	10.49	12.01	8.06	8.65	8.58	7.2	0.87	0.93	1.19	Thsd4, Thsd4
chr9	69016000	69020999	33.95	38.83	33.1	38.76	33.77	36	0.87	0.85	0.94	Narg2, Rora
chr9	77518000	77520999	32.29	37.23	33.95	36.12	45.57	42.8	0.87	0.94	1.06	Gclc, Klhl31
chr9	98784000	98785999	30.36	40.43	33.53	39.51	20.37	31.2	0.75	0.85	0.65	7420426K07Rik, 2410012M07Rik
chr9	100994000	101000999	48.02	62.45	51.78	61.71	61.65	64.8	0.77	0.84	0.95	Msl2, Ppp2r3a
chr9	103777000	103783999	48.85	62.45	47.96	57.57	57.9	47.6	0.78	0.83	1.22	Nphp3, Tmem108
chr9	108726000	108737999	122.55	154.52	151.09	174.59	171.55	160.8	0.79	0.87	1.07	Slc26a6, Celsr3
chr9	110578000	110582999	67.62	78.06	78.94	96.7	91.67	75.6	0.87	0.82	1.21	Ccdc12, Pth1r
chr9	114019000	114024999	54.93	65.25	68.33	84.29	68.08	80	0.84	0.81	0.85	Bcl2a1c, Fbxl2
chr9	116400000	116404999	44.16	49.24	53.47	45.91	55.75	42	0.9	0.9	1.33	Tgfbr2
chr9	119761000	119761999	10.49	12.41	8.06	10.16	11.79	6.4	0.85	0.79	1.84	Wdr48, Scn11a
chr9	122493000	122499999	64.59	74.86	51.35	65.85	54.15	68.8	0.86	0.78	0.79	Gm9524, Abhd5
chr9	123259000	123261999	37.54	50.04	40.32	51.55	64.33	48.4	0.75	0.78	1.33	Tmem158, Lars2
chrY	1635000	1637999	63.48	70.85	44.56	53.81	40.21	47.2	0.9	0.83	0.85	Gm6026, Zfy2

Table S6. Characteristics of the patient muscle biopsies used for mRNA profiling. EDMD-AD (n=3), EDMD-XR (n=4) and FPLD (n=7) muscle biopsies are shown in the table. Genes affected and the specific mutations for each patient are shown in last two columns.

Sample ID	Diagnosis	File Name [Profile]	Sex	Age	Gene	Mutation
ED-L-2	EDMD-AD	HUD-EDMD-2aUA-s2	F	2	*LMNA*	c.IVS7-1G>T (c.1381G>T)
ED-E-1	EDMD-XR	HUD-EDMD-3aUA-s2	M	16	*EMD*	exon 4; 18 bp intronic duplication
ED-L-3	EDMD-AD	HUD-EDMD-4aUA-s2	M	2	*LMNA*	R249Y/+
ED-L-4	EDMD-AD	HUD-EDMD-5aUA-s2	M	23	*LMNA*	exon 4/+
ED-E-2	EDMD-XR	HUD-EDMD-6aUA-s2	M	35	*EMD*	exon 6; g.1675-1678delTCCG
ED-E-3	EDMD-XR	HUD-EDMD-7aUA-s2	M	37	*EMD*	exon 6; g.1675-1678delTCCG
ED-E-4	EDMD-XR	HUD-EDMD-8aUA-s2	M	42	*EMD*	exon 6; g.1675-1678delTCCG
FKRP-1a	LGMD2I (FKRP)	HUD-FKRP-1aUA-s2	F	14	*FKRP*	L276I/L276I
FKRP-1b	LGMD2I (FKRP)	HUD-FKRP-1bUA-s2	F	14	*FKRP*	L276I/L276I
FKRP-3	LGMD2I (FKRP)	HUD-FKRP-3aUA-s2	F	12	*FKRP*	L276I/L276I
FKRP-6a	LGMD2I (FKRP)	HUD-FKRP-6aUA-s2	M	45	*FKRP*	L276I/L276I
FKRP-6b	LGMD2I (FKRP)	HUD-FKRP-6bUA-s2	M	45	*FKRP*	L276I/L276I
FKRP-7a	LGMD2I (FKRP)	HUD-FKRP-7aUA-s2	M	55	*FKRP*	L276I/L276I
FKRP-7b	LGMD2I (FKRP)	HUD-FKRP-7bUA-s2	M	55	*FKRP*	L276I/L276I

Table S7. ChIP-seq targets show up-regulation in muscle biopsies from EDMD patients.

Shown in bold are the transcirpts that show disease specific upregulation in EDMD. Red marked transcripts are shared between EDMD-XR and EDMD-AD.

	EDMD-XR		FKRP			EDMD-AD		FKRP	
gene ID	**FC**	**FDR**	**FC**	**FDR**	**gene ID**	**FC**	**FDR**	**FC**	**FDR**
ACTR3	**1.617**	3.1E-03	1.368	ns	*ACTR3*	**2.302**	5.2E-05	1.368	ns
ADIPOQ	**7.255**	1.0E-03	3.777	ns	*ADIPOQ*	**10.788**	1.8E-03	3.777	ns
ANXA5	**1.723**	1.8E-03	1.745	ns	*ANXA5*	**2.694**	1.9E-04	1.745	ns
CHIC2	**1.651**	1.4E-05	1.043	ns	*CHIC2*	**1.812**	5.3E-05	1.043	ns
EHD2	**2.210**	3.3E-04	1.242	ns	*EHD2*	**3.431**	3.1E-04	1.242	ns
GCLC	**1.607**	1.1E-03	-1.077	ns	*GCLC*	**1.587**	5.2E-03	-1.077	ns
ID4	**1.532**	2.1E-03	1.297	ns	*ID4*	**1.678**	6.5E-04	1.297	ns
KIF2A	**1.432**	2.4E-03	1.124	ns	*KIF2A*	**1.687**	5.3E-05	1.124	ns
MBIP	**1.384**	5.6E-04	-1.105	ns	*MBIP*	**1.980**	7.9E-05	-1.105	ns
SOX2	**1.519**	7.0E-05	-1.070	ns	*SOX2*	**1.329**	0.04	-1.070	ns
STRN	**1.517**	2.3E-04	-1.007	ns	*STRN*	**1.424**	2.6E-03	-1.007	ns
TGFB1	**1.952**	4.9E-04	1.911	6.92E-05	*TGFB1*	**3.090**	1.4E-04	1.911	ns
TGIF1	**1.665**	1.0E-03	1.880	2.01E-06	*TGIF1*	**2.512**	1.6E-08	1.880	5.7E-07
TMEM158	**2.560**	1.9E-04	1.812	9.46E-03	*TMEM158*	**3.010**	7.5E-05	1.812	ns
ATP6V1C1	**1.396**	2.9E-03	-1.222	ns	*ADAMTSL3*	**2.067**	1.7E-03	1.015	ns
ATXN1	**1.533**	9.0E-04	-1.021	ns	*ARID5B*	**1.673**	2.8E-03	1.145	ns
CASP8	**1.513**	8.9E-05	1.109	ns	*ATP11B*	**1.902**	6.2E-03	1.019	ns
CHFR	**1.454**	6.3E-05	1.410	1.40E-05	*BACH1*	**1.577**	1.5E-03	1.050	ns
DAPK1	**1.523**	1.1E-03	-1.200	ns	*BEND5*	-1.670	5.4E-03	-1.229	ns
DYNC1I2	**1.422**	3.1E-03	1.252	ns	*CCL2*	**7.725**	2.2E-03	3.098	ns
FBXO17	**1.872**	8.6E-04	-1.026	ns	*CDC42EP3*	**1.920**	2.8E-03	1.172	ns
FGF9	**1.644**	2.7E-03	1.109	ns	*CDK19*	**1.598**	4.2E-03	-1.196	ns
GFPT2	**1.331**	2.2E-03	-1.078	ns	*CHST1*	-1.226	9.5E-04	1.067	ns
GPATCH2	**1.433**	4.9E-04	1.031	ns	*CHSY1*	**2.022**	8.4E-06	1.112	ns
GSK3B	**1.507**	4.1E-03	-1.075	ns	*DAZL*	-1.718	5.2E-03	-1.614	6.3E-04
HOXA5	**1.462**	8.3E-05	-1.316	5.89E-03	*DNAJC10*	1.506	4.7E-03	-1.044	ns
HSD17B6	**1.415**	1.5E-03	1.161	ns	*ELOVL6*	-1.312	6.5E-03	-1.092	ns
KIF13A	**1.436**	3.7E-03	-1.218	ns	*ERH*	1.448	5.9E-04	1.261	3.63E-03
MSRA	**1.434**	1.8E-03	1.113	ns	*FAT1*	**3.878**	2.0E-04	1.686	ns
PHACTR1	-1.801	2.3E-03	-1.260	ns	*FOXO1*	**2.086**	1.8E-03	1.128	ns
RAP2A	**2.221**	2.7E-04	1.162	ns	*GAS1*	**3.551**	3.4E-04	1.781	ns

Gene					Gene				
RIT1	**1.334**	3.2E-03	1.015	ns	HGSNAT	**1.944**	1.3E-03	1.048	ns
SLC30A10	**1.501**	3.5E-03	-1.374	ns	IMPG2	-1.388	4.0E-03	-1.199	ns
SLC44A1	**1.914**	1.8E-04	-1.136	ns	JAM3	**3.226**	6.7E-05	1.759	ns
SNTB1	-1.857	1.4E-03	-1.243	ns	LRRK1	**1.818**	2.4E-03	1.424	ns
TBC1D2	**3.800**	4.1E-04	-5.939	ns	MSX2	**1.461**	3.5E-03	1.055	ns
THAP1	**1.435**	4.1E-03	-1.119	ns	PAPSS1	**1.724**	2.1E-03	1.013	ns
TINAGL1	-1.617	3.1E-03	1.263	ns	PELI2	**2.346**	1.1E-03	-1.064	ns
TRAK1	**1.412**	2.4E-03	1.116	ns	PMP22	**2.077**	5.7E-03	1.353	ns
TSPAN5	-1.342	4.1E-03	-1.179	ns	PNMA1	**2.184**	1.8E-03	1.453	ns
ZFHX3	**1.789**	7.2E-04	1.017	ns	RAP1GDS1	**1.572**	4.3E-03	-1.079	ns
					SH3GL3	**1.754**	2.7E-03	-1.657	ns
					SHOX2	**2.320**	3.9E-04	1.130	ns
					SLC38A1	**3.180**	1.3E-05	-1.812	ns
					SLC7A11	**1.360**	4.4E-03	-1.473	6.1E-04
					SPON1	**5.373**	7.8E-04	1.077	ns
					TBX3	**2.088**	1.9E-03	-1.563	ns
					TGFBR2	**2.639**	6.8E-04	1.966	3.7E-03
					TMX1	**1.783**	3.2E-03	1.035	ns
					TRIM9	**3.543**	1.1E-04	1.682	ns
					VAC14	**1.588**	1.6E-04	-1.209	ns
					XYLT1	**2.006**	1.2E-03	-1.071	ns
					ZMIZ1	**2.597**	1.2E-05	1.193	ns

Table S8. Primer sequences used for RT-qPCR and ChIP-qPCR experiments.

Mouse primers

RT-qPCR primers

Name	Forward primer	Reverse primer
Tk1	CTCAGGGAAAAGCACAGAGC	CAAGGACTCCTGGGTCACAT
myogenin	CTACAGGCCTTGCTCAGCTC	ACGATGGACGTAAGGGAGTG
Cdk1	TCAAGAGTCAGTTGGCGCCC	CACACCGCAGTTCCGGACTG

ChIP-qPCR primer

Name	Forward primer	Reverse primer
Tk1	AGACCCCGCACCTGAATCTG	TTCACGTAGCTGAGAGGTGG
Myog	GAATCACATGTAATCCACTGGA	ACGCCAACTGCTGGGTGCCA
Cdk1	TCAAGAGTCAGTTGGCGCCC	CACACCGCAGTTCCGGACTG

Human primers

RT-qPCR primers

Name	Forward primer	Reverse primer
SOX2	TAGTGGTACGTTAGGCGCTT	TCTTGCCAGTACTTGCTCTC
HOXB1	TCAGAAGGAGACGGAGGCTA	CAGGGTGTTTCCTTGTCCTC
GATA6	TTGTGGACTCTACATGAAACTCCA	TTATGTTCTTAGGTTTTCGTTCCTG

ChIP-qPCR primers

Name	Forward primer	Reverse primer
HOXB1	AAGGCAGCTGGTGCTATTGT	TCCTCCTTTCCCTTCCAACT
GATA6	GGGACAGGGATTCTTTTGTTGG	TGATTCACCAGAGGTCTCAAGCC

DamID-qPCR primers

Name	Forward primer	Reverse primer
SOX2	TGGTACGGTAGGAGCTTTGC	GCAAGAAGCCTCTCCTTGAA