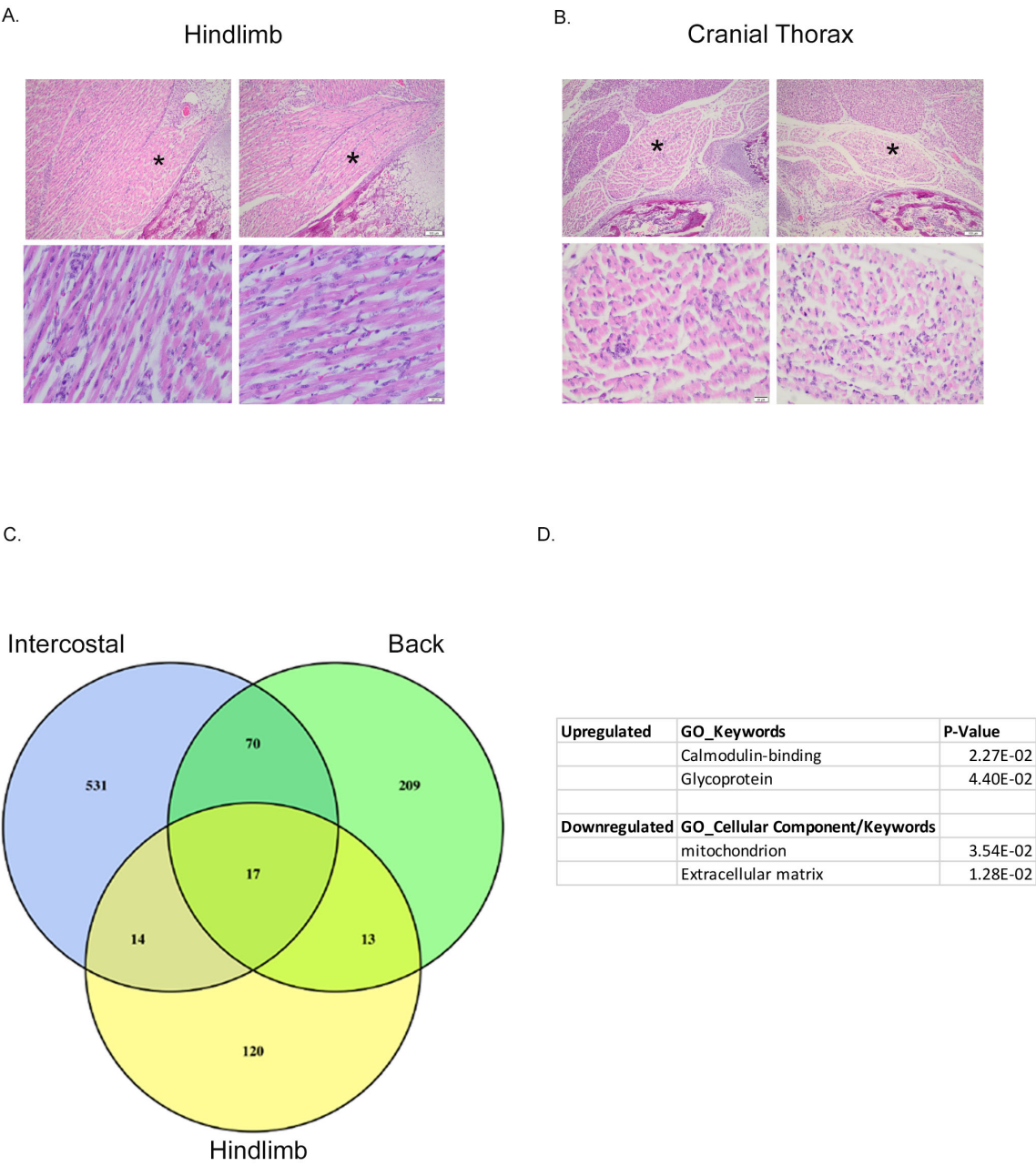


**The chromatin remodeler Mi2/CHD4 is required in skeletal muscle stem cells for normal
muscle development and regeneration**

Assia Derfoul, Iago Pinal-Fernandez, Wilson Huang, Cassie Parks, Katherine Pak, Victoria J.
Hoffmann, Katia Georgopoulos, and Andrew L. Mammen

Supplemental Figure 1. Deletion of CHD4 in satellite cells during myogenesis.



Supplementary Table 1. DNA primers used in studies.

Application	Gene name	Forward	Reverse
genomic DNA PCR	CHD4 WT	GGGCTACACAGAGAAACCT	GGAACTCGGGGACATAACCA
	CHD4 KO	GGGCTACACAGAGAAACCT	CTTCCACTGTGACGTCCAGAC
	CRE	TGATGAGGTTGGCAAGAA	CCATGAGTGAACGAACCT
RT-qPCR	CHD4 WT	CTGGGGACTTTGGTGGAGAT	TAGTGAACGTGGCCCGTCTT
	CHD4 KO	CTGGGGACTTTGGTGGAGAT	GGGGTTCCAGTCAGAGTCAT
	Myog	ATCGCGCTCCTCCTGGTTGA	CTGGGGACCCCTGAGCATTG
	MyH8	GAACTGAAGGAGAGGTCGA	GAGCACATTCTTGCGGTCTT
	18S	GGACCAGAGCGAAAGCATTG	GCCAGTCGGCATCGTTTATG

Supplementary Table 2. Antibodies used in studies.

Antibody	Catalog #	Source	Host	Application	Dilution
a7-integrin-PE	K0046-5	MBL	Mouse	FACS	1:100-1:200
Sca-1-FITC	557405	BD	Mouse	FACS	1:200
CD 11b-FITC	553310	BD	Rat	FACS	1:200
CD 31-FITC	553372	BD	Rat	FACS	1:200
CD 45-FITC	553080	BD	Rat	FACS	1:200
Pax7	Pax-7s	DSHB	Mouse	IF	1:10
CHD4-clone 16G4	MABE914	Millipore	Mouse	IHC	1:100
CHD4-clone 2G8	MABE915	Millipore	Mouse	IF	1:100
CHD4	Ab72418	Abcam	Rabbit	ChIP	7mg/300mg of chromatin
Laminin	L9393	Sigma	Rabbit	IHC	1:200
Myogenin	sc-576	Santa Cruz	Rabbit	IF	1:500
MyHC(emb)	F1.652	DSHB	Mouse	IHC	1:200
Myh fast	MF20	DSHB	Mouse	IHC	1:10
Myh (fast)	Ab91506	Abcam	Mouse	IHC	1:200
Actin	Sc-1616	Santa-Cruz	Rabbit	IF	1:200
anti-Mouse IgG ₁ Alexa594	A21125	Invitrogen	Goat	IF, IHC	1:1000
anti-Mouse IgG Alexa488	A11001	Invitrogen	Goat	IF, IHC	1:1000
anti-Rabbit Alexa555	A21429	Invitrogen	Goat	IF, IHC	1:1000

Supplementary Table 4. Differentially expressed genes in Tam-CRE CHD4 KO SCs cultured to the myoblast (MB) or myotube (MT) stage in vitro

Up in MBs	log2 Fold Change	padj	Down in MB	log2 Fold Change	padj	Up in MT	log2 Fold Change	padj	Down in MT	log2Fold Change	padj
Ndufb8	8.408976441	2.21E-22	Zdhc18	-0.65023646	3.21E-03	Bea2	6.102293207	2.53E-11	Ndufb6	-6.315076994	7.51E-15
Pacsin1	6.501609114	5.13E-22	Eno1	-0.65123079	2.95E-02	Snhg11	6.014509314	2.56E-15	Xist	-3.758772058	1.15E-02
Tcf15	6.355549746	2.62E-26	Abcb10	-0.653298396	1.22E-02	Tcf15	5.176993382	3.37E-10	Myoz3	-3.485278176	2.09E-02
Lincenc1	5.210351918	2.54E-08	1600002H07Ril	-0.655451479	3.17E-02	Col2a1	4.754205537	4.28E-04	Cd300c	-3.104304223	1.01E-02
Bmp8b	5.075202925	1.51E-11	Hmnpab	-0.657399912	3.30E-02	Icam1	4.585461402	2.41E-06	Card11	-2.999513704	2.25E-02
Snhg11	5.020665388	1.73E-22	Asph	-0.660629368	3.19E-03	Lincenc1	4.405530006	2.47E-04	Ankrd23	-2.955722754	4.93E-08
Chd5	4.811888509	8.06E-37	Fastkd5	-0.661673561	1.97E-02	Zkscan4	4.09951106	6.52E-05	Msln	-2.95476954	5.23E-06
Lum	4.648791047	1.53E-22	Pxylp1	-0.663521	3.16E-02	Lum	4.043431151	9.68E-05	Asb14	-2.889679999	8.21E-02
Fhad1	4.542180371	6.01E-05	Ppil1	-0.665226921	3.30E-02	Spint1	4.009102936	9.43E-04	2700094K13f	-2.883241374	3.73E-02
Sbk2	4.470674045	1.08E-07	Nudc	-0.665562936	3.17E-03	Pnma2	3.974271119	5.60E-04	Hacd1	-2.681729155	2.90E-07
Tex19.2	4.440028948	2.70E-05	Slc25a39	-0.666659893	4.33E-03	Cnma1g	3.956915787	3.32E-05	Ptges3l	-2.624918232	5.85E-05
Dtx1	4.371211197	4.64E-05	Txndc12	-0.6691256	4.82E-03	Emilin2	3.868464973	2.48E-07	4930539J05R	-2.617056306	1.14E-01
Camk2b	4.267782937	3.50E-26	Sgpl	-0.669487259	2.56E-03	Chd5	3.817222707	2.84E-09	Susd3	-2.611320574	9.47E-02
Kankd5	4.263477766	5.81E-12	Ppargc1b	-0.670016883	4.36E-02	Don1	3.811910029	2.91E-03	Gabrd	-2.593705814	1.20E-01
Camkv	4.195175074	3.48E-06	Elof1	-0.670267946	1.51E-02	Procr	3.809087243	2.83E-03	Fsd2	-2.558226818	1.92E-03
Lama3	4.185005026	1.65E-04	Tfpid1	-0.671269188	6.22E-04	Col6a3	3.72076341	1.67E-05	Ckmt2	-2.530838162	1.13E-02
Guca1a	4.154975857	6.13E-04	Rexo2	-0.672320897	3.87E-02	Rtn4r2	3.706275691	1.53E-03	Rcsd1	-2.52844507	5.02E-02
Cyp26a1	4.07705823	1.70E-04	Gypc	-0.673887351	1.70E-03	Hmha1	3.62874815	7.12E-05	Fam98c	-2.455482934	1.46E-01
Pygm	4.06614033	1.55E-35	Nono	-0.675353614	1.48E-06	Irf5	3.582001476	1.59E-03	Slc5a1	-2.443660411	1.18E-02
Gm4371	4.011639812	4.71E-06	Gsr	-0.675644263	7.48E-03	Dguuq	3.575757397	2.03E-03	Ppp1r3a	-2.437540003	4.34E-03
Padl3	3.971003902	3.51E-25	Trim37	-0.675970853	2.06E-03	Fibcd1	3.559788352	7.74E-07	Bckhnb	-2.396204344	1.68E-01
Grasp2	3.923768537	1.33E-48	Zmiz2	-0.676765325	2.57E-03	Cpxm1	3.485988237	2.12E-02	Dnajb11	-2.37512697	1.06E-06
Traf3ip3	3.921147775	1.73E-06	Paps1	-0.677102834	4.27E-02	Gpsm3	3.436212033	5.19E-05	1700123M08	-2.338146353	1.89E-02
Cacna1g	3.874931762	2.48E-07	Magi3	-0.679640187	4.35E-02	Alpl	3.425772862	2.17E-02	Nr4a3	-2.327040488	3.20E-03
Gpsm3	3.827747643	8.34E-13	Clic1	-0.680558319	3.98E-02	Sfrp4	3.421896072	1.83E-02	Firp	-2.284360328	1.54E-01
Nos1	3.805182424	2.75E-13	Eef1a1	-0.681511745	3.50E-05	Bic1c1	3.374544881	5.06E-03	Prlc4	-2.23437404	9.93E-04
9430018G01	3.777004675	2.15E-07	Six2	-0.682421737	3.52E-02	H2-Q7	3.348074953	4.76E-03	D830046C22l	-2.229587226	4.94E-02
Esx1	3.739064342	1.52E-03	Galc	-0.68349315	2.09E-02	Akr1c13	3.300994304	2.20E-02	Mylh14	-2.214018839	1.06E-01
Tbtkbp1	3.738185333	8.02E-16	Gxylt1	-0.684402939	1.59E-03	MT3	3.297741079	1.08E-02	Il11ra1	-2.196770955	8.11E-03
Tex40	3.710542308	1.82E-03	Cnpy4	-0.684667198	3.50E-02	Dtx1	3.279485973	2.73E-02	Ucp3	-2.190725002	1.28E-01
Draxin	3.706625235	6.69E-05	Rfwd3	-0.684678963	6.93E-04	Oasl1	3.261483933	4.12E-03	Slc25a34	-2.184367753	1.20E-01
Chrm4	3.684788368	1.27E-05	Pitrm1	-0.684679482	4.02E-03	Nr1h3	3.224308662	1.49E-02	P2ry2	-2.160372375	3.04E-03
Icam1	3.679624573	4.20E-11	Tspan12	-0.687069994	1.01E-03	Tex19.2	3.207308762	3.10E-02	Cmya5	-2.151224849	1.56E-01
PK5	3.67485411	4.04E-04	Abhd17c	-0.689613543	1.53E-03	Dpt	3.199964237	1.72E-02	Hras	-2.140625792	2.38E-01
Trp63	3.63055826	2.67E-07	Rnf168	-0.690667448	5.05E-04	F13a1	3.153752597	3.20E-02	Oplah	-2.120131995	2.52E-01
Ndufv2	3.620443782	6.56E-05	Rpp38	-0.690858875	1.30E-02	5033406O09	3.119815835	2.68E-02	Gpr146	-2.107023743	1.01E-04
Prl1	3.618644519	7.24E-04	Lsm4	-0.691207995	3.88E-02	Tubb4a	3.119593723	1.88E-04	Casq1	-2.106763584	7.67E-02
Lmtk3	3.598878305	1.58E-06	Ugcg	-0.693093629	4.41E-05	Acan	3.110591707	4.91E-02	Tsacc	-2.102704558	2.37E-01
Knip3	3.59776702	2.59E-18	Sigmar1	-0.694518559	2.17E-03	Ltbp2	3.106200087	1.24E-08	Tg	-2.087323622	2.47E-01
Ache	3.583134936	3.97E-17	Slc9a5	-0.694725704	3.49E-02	Trnp1	3.08497932	1.83E-02	Slc16a9	-2.082098743	2.17E-01
2610037D02l	3.582189898	2.98E-03	Rhou	-0.694981349	3.26E-02	Cd68	3.08400274	2.44E-02	Dnrtt	-2.080842877	2.17E-01
Rbp4	3.579746864	1.65E-03	Anapc11	-0.695651168	2.42E-03	Thy1	3.027107348	1.28E-03	Cnbl	-2.07788068	9.99E-02
Hmha1	3.54717064	8.51E-12	Zfp41	-0.695863196	2.57E-02	Srgn	3.002735952	3.81E-02	LOC1052465f	-2.066894435	8.70E-02
Fam83a	3.531243034	3.48E-04	Senp1	-0.697597071	5.32E-03	Ugt1a7c	3.000873919	5.37E-02	Cd24a	-2.031822836	9.16E-02
Blnk	3.491053804	3.36E-04	Rsrc1	-0.698073302	1.96E-02	Efn3	2.973003516	3.96E-02	Wfdc1	-2.027982113	2.47E-01
Slc30a2	3.451899442	1.12E-06	Slc16a1	-0.699147581	7.06E-03	Mmp2	2.961029304	1.20E-08	5930438M14	-2.025466305	2.37E-01
Fibcd1	3.400967363	1.32E-13	Rnf219	-0.699777635	3.41E-02	Thbs3	2.959974978	1.34E-02	Mgst3	-2.007787408	2.72E-01
C1qtnf4	3.389887052	2.18E-04	Suv39h2	-0.704138331	3.25E-02	Cxx1c	2.956476955	3.90E-07	Rgs11	-2.005456006	1.60E-01
Mmel1	3.382281959	1.88E-03	Phlpp2	-0.704494622	1.75E-02	Igln5	2.945789599	2.54E-02	Cldn5	-1.99955586	2.17E-01
Qrfp	3.343179029	8.10E-07	Ogfrp1	-0.705820117	2.46E-02	Eph3	2.945044975	3.39E-02	Klf15	-1.968406057	1.70E-01
Art5	3.342939987	2.22E-04	Iqsec3	-0.706860113	4.29E-03	Fabp7	2.937132561	5.06E-02	F2	-1.967830335	2.71E-01
Mag	3.342062962	8.35E-03	Acs14	-0.70780616	2.44E-04	Lingo3	2.931220293	4.78E-04	Sypl2	-1.955012137	1.70E-04
Sncg	3.333774237	5.94E-11	Hs6st1	-0.710350133	1.69E-03	Zfp941	2.926148489	2.98E-02	Prr15	-1.94929762	3.16E-01
Cnga3	3.300404021	6.50E-07	Lin5a	-0.711408968	4.93E-02	Tfpl2	2.922348065	2.42E-03	Ip6k3	-1.928509527	2.52E-01
Rorc	3.284412378	4.44E-04	Adam9	-0.714055651	6.39E-03	Adgrf4	2.921103071	2.82E-02	Cited4	-1.924907707	2.28E-01
Sowahb	3.277312721	1.83E-04	Ndn	-0.718363716	5.27E-03	Smoc2	2.919655321	7.00E-02	Esrrg	-1.92353823	1.31E-02
9030619P08f	3.266774341	9.54E-03	Lmnb2	-0.719067939	3.69E-04	Glrp1	2.918775769	2.23E-02	Kbtbd13	-1.921141015	1.92E-01
H1foo	3.264841197	1.11E-02	Sall2	-0.719208825	6.71E-03	Sp7	2.896455744	4.52E-03	Ppp2r2c	-1.921028878	2.85E-01
Akr1c13	3.263743291	1.34E-03	Sfpq	-0.719805158	2.34E-03	Serpine2	2.890951178	3.41E-21	Mybpcc2	-1.907559864	1.91E-01
Chrd	3.238380876	4.88E-04	Crtap	-0.719870773	4.68E-03	Hmgcd1	2.879538776	4.79E-02	Krt80	-1.905898145	2.03E-01
Pak6	3.236801886	4.52E-10	Cdk4	-0.721739852	1.98E-02	Ngb	2.878391958	4.56E-02	Lrrc30	-1.885153559	1.18E-01
Meg3	3.221383044	1.86E-09	Taldo1	-0.722795359	3.30E-02	Ptgsl	2.870517363	9.85E-04	Slc2a4	-1.880723724	3.20E-02
Mirg	3.203975699	6.84E-04	Pfas	-0.724515264	2.39E-04	Adam23	2.864047199	9.51E-04	Kcna7	-1.878460996	1.32E-01
Plxn4	3.180864883	2.58E-13	Prps1l3	-0.725345778	2.47E-04	Mbp	2.852865743	2.37E-06	Pm20d2	-1.866603639	2.73E-02
Palms3	3.178787238	3.89E-09	Pdc5a	-0.725872348	8.86E-03	Scara5	2.852792397	5.18E-02	Enho	-1.855011589	3.95E-02
Rspo1	3.177715984	9.61E-03	9430015G10Ri	-0.730113367	2.08E-03	Abca8a	2.851412434	6.03E-02	Syng1	-1.851736539	1.59E-01
Mir7688	3.173987707	8.58E-03	Ubpap2	-0.730517885	2.05E-02	Crbp1	2.848566883	4.70E-02	Cdc24	-1.849823685	3.15E-01
Heyl	3.164066908	4.52E-13	Zbtb45	-0.731277069	1.51E-02	Kif1a	2.843255193	4.91E-03	H2-ke6	-1.827938998	1.41E-02
Tub	3.160671993	3.36E-05	Rpa3	-0.73474545	3.52E-02	Ly6a	2.832076379	7.76E-02	Aes	-1.817103234	3.20E-03
4933403O08	3.149869468	2.74E-03	Col4a1	-0.735308966	1.85E-02	Rpl30	2.825269307	7.78E-02	Capn3	-1.81198924	1.09E-03
Cldn4	3.146360389	1.82E-07	Erl1	-0.735122996	1.05E-02	Cadm2	2.81847692	5.38E-02	Atp1a2	-1.803917211	5.67E-03
Hif3a	3.129573447	3.73E-05	Hart1	-0.735742423	2.44E-03	Tmem154	2.812506044	1.79E-02	Myadml2	-1.796867956	1.47E-01
Thpo	3.125603438	2.93E-03	Smo	-0.736113715	5.72E-04	9430018G01	2.805153109	1.44E-02	Stac2	-1.789328132	1.13E-02
Neurl1a	3.123424546	2.14E-27	Mcmcbp	-0.738316229	1.75E-03	Isoc2b	2.798844693	5.80E-02	Trpt1	-1.787241999	2.35E-01

Note: Remaining pages for this table can be provided upon request.

Supplementary Table 5. Differentially expressed genes in Tam-CRE CHD4mKO injured muscles at day 7 through 28 (D7, D10, D14 AND D28) post CTX.

Up in D7			Down in D7			Up in D10			Down in D10			Up in D14			Down in D14			Up in D28			Down in D28		
Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj	Gene	log2 Fold Change	padj
Cyp19b1	4.88	1.53E-02	Fgf10	-2.55	4.33E-02	Wdr69	5.70	3.89E-11	Ser2	-4.80	1.56E-05	Krt15	3.42	2.40E-02	Atg16l1	-1.18	2.39E-02	Arf2	2.73	4.88E-02			
Ctsc	3.16	6.38E-03	Nr6a	-1.58	1.17E-02	R2h	1.19	1.05E-05	Rarb	-3.48	1.42E-02	Ser11	3.32	1.02E-02									
Krt4	2.74	1.13E-02	Vgfa	-1.44	2.11E-02	Krt14	2.82	3.49E-02	Krt14	-3.47	1.81E-05	Gsk3	3.31	2.20E-02									
Trop2	2.70	1.12E-03	Foxl1	-1.37	2.18E-03	Cxcl4	2.82	1.78E-02	Ucp1	-3.02	1.13E-03	Mmp1	1.90	1.20E-02									
Tuba1b	2.43	6.75E-15	Wdr2	-1.33	6.05E-03	Cxcl5	1.79	1.47E-02	Gli3	-2.69	3.49E-02	Atg16l1	-1.18	2.39E-02									
Mmp1	2.11	1.48E-04	Prrxl1	-1.32	1.02E-02				Ser11	-2.33	3.49E-02												
Tuba1a	1.98	6.70E-04	Tnfrsf1	-1.16	7.12E-03				Ser11	-2.02	2.89E-02												
Krt11	1.63	6.71E-03	Krt1	-1.10	7.53E-03				Gsk3	-1.96	4.47E-02												
Scl2a4	1.60	8.84E-04	Tnfrsf1	-1.06	2.46E-02				Atg16l1	-1.48	1.13E-02												
Foxl1	1.59	1.10E-03	Nr6a	-1.05	3.14E-02				Prrxl1	-1.20	2.74E-02												
Ahr	1.58	3.82E-05							Rarb	-1.29	5.13E-04												
Atg16l1	1.56	2.12E-03																					
Atg16l1	1.26	1.18E-02																					
Gli1	1.24	8.88E-03																					
Cxcl4	1.24	1.18E-02																					
Gsk3	1.23	4.27E-02																					
Rarb	1.22	3.56E-02																					
Tnfrsf1	1.22	1.10E-02																					
Krt1	1.19	1.70E-02																					
Rarb	1.18	1.18E-02																					
Prrxl1	1.14	2.38E-02																					
Dhh	1.14	2.28E-02																					
Atg16l1	1.07	1.17E-02																					

