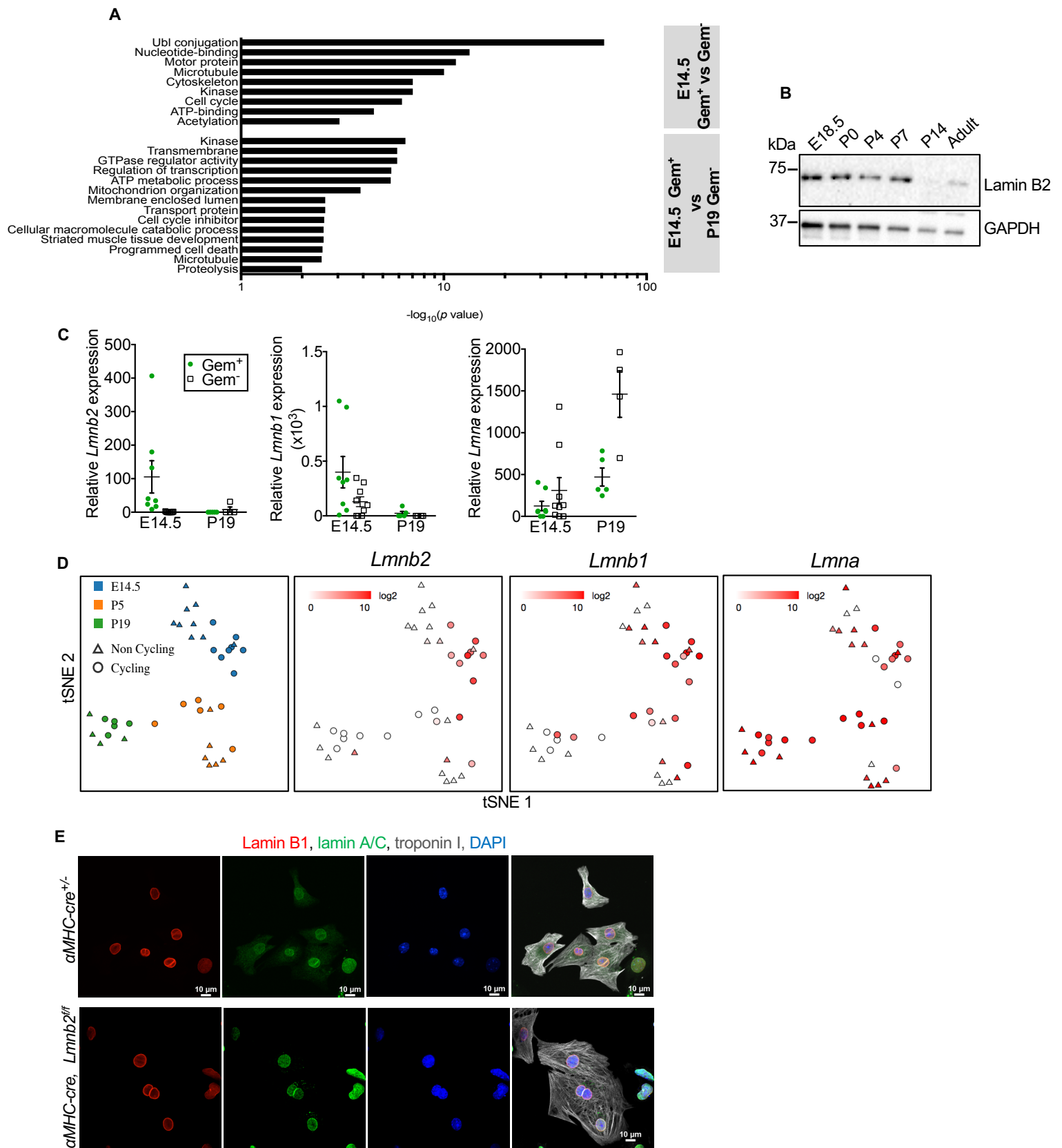


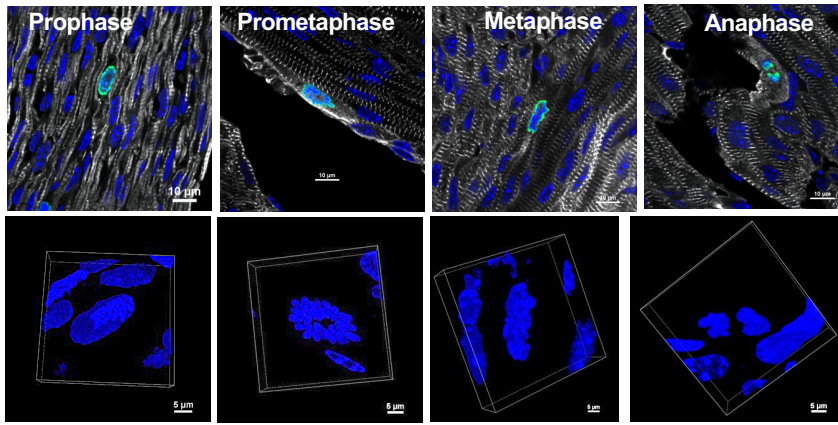
Supplemental Figure S1. Related to Figure 1. The Fucci cell cycle reporter system identifies cell cycle phases and can be used to quantify the percentage of cardiomyocytes in each phase (G1 vs. S vs. G2/M) in neonatal mice (P1). We isolated cardiomyocytes from P1 mice positive for both Fucci transgenes (Double, i.e., mKO2-Cdt1 and AG-hGeminin) to quantify the percentage of cardiomyocytes in the different phases of the cell cycle (G1 vs S vs G2/M) at birth (P1). **(A)** Immunofluorescence microscopy shows that neonatal (P1) cardiomyocytes express AG-Geminin. **(B)** Cells were analyzed by FACS. To increase the purity of the cardiomyocyte population, gates for size and granularity were applied and dead cells (by 7-AAD staining) and doublets were excluded. **(C)** The percentages of cells expressing mKO2 (indicating G1-phase), mKO2 + mAG (indicating S-phase), or mAG (indicating G2/M-phase) were calculated. The majority (45.7%) of cycling cardiomyocytes expressed mKO2, indicating cells in G1-phase; 15.3% of cardiomyocytes expressed both mKO2 and mAG, indicating S phase. Only 2.7% of cardiomyocytes expressed mAG only, indicating G2/M. **(D)** In addition, cardiomyocytes were isolated from pups positive for only the mKO2-hCdt1 (Red only) or mAG-hGem (Green only) transgene to evaluate the consistency of Fucci expression percentages at P1. It was found that 64.6% of cardiomyocytes isolated from Red only pups were expressing mKO2, indicating both G1 and S phase. This correlates with 45.7% (G1) + 15.3% (S) = 61% of cardiomyocytes expressing mKO2 from the Double isolation. As expected, only 3.1% of cardiomyocytes isolated from Green only pups were expressing mAG, indicating S phase and G2/M. As negative control, cardiomyocytes were isolated from P1 wild type C57BL6 pups, with 100% expressing no fluorophore. In conclusion, although the percentage of cardiomyocytes in G2/M at any given time is relatively low in neonatal mice, the mAG-Geminin reporter readily identifies it. **(E)** Time-lapse images of isolated cardiomyocytes from mKO2-hCdt1; mAG-hGem pup at P1. The cardiomyocytes are further validated by immunofluorescent staining with α -actinin. Scale bar 30 μ m.



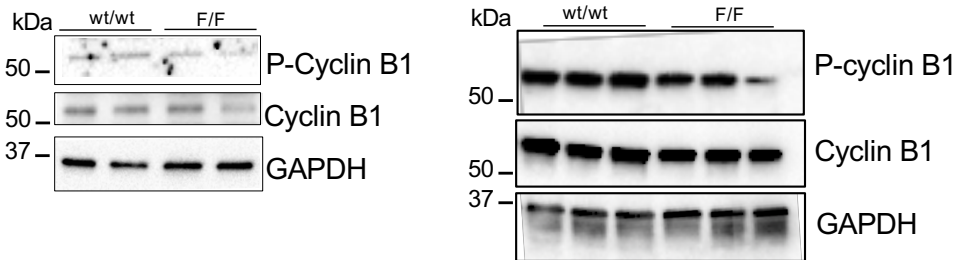
Supplementary Figure S2. Genome-wide transcriptional profiling reveals unique expression profile of *Lmnb2*, and *Lmnb2* gene inactivation does not alter the nuclear lamina filament Lamin B1 and Lamin A/C in cardiomyocytes. (a-d) Related to Figure 1 and 2. (A) Gene ontology (GO) analysis of differentially expressed genes between embryonic geminin positive and negative group, and between embryonic geminin positive and adult negative group shows regulation of different cellular processes. (B) Western blot of lysate (15 μ g) from isolated cardiomyocytes shows decrease of Lamin B2 protein after birth. GAPDH was used as a loading control. (C-D) Dot plot (C) and tSNE profile (D) show high expression of *Lmnb2* in cycling embryonic cardiomyocytes, whereas *Lmnb1* and *Lmna* expression was not confined to dividing cardiomyocytes and *Lmna* was also expressed in adult cardiomyocytes. Left panel corresponds to Figure 1B and serves as reference to indicate cardiomyocytes at different developmental ages. The intensity of red color indicates expression level according to the provided scales. (E) Immunofluorescence microscopy of P2 cardiomyocytes showed that α MHC-cre-induced *Lmnb2* KO does not affect Lamin B1 and Lamin A/C localization. Scale bars: 10 μ m. Error bars represent mean \pm SEM.

H3P, Troponin I, DAPI

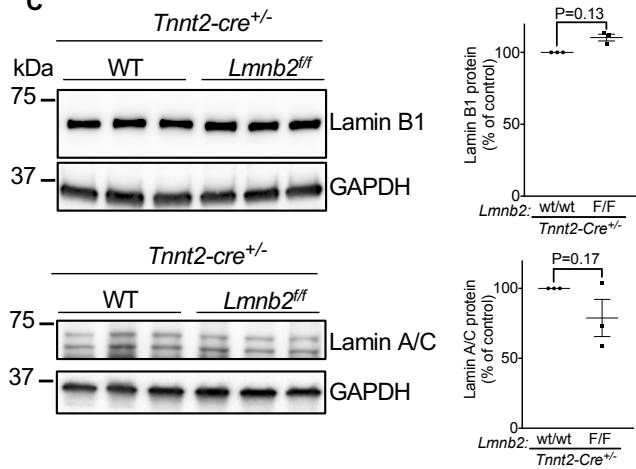
A



B *aMHC-Cre^{+/-}*

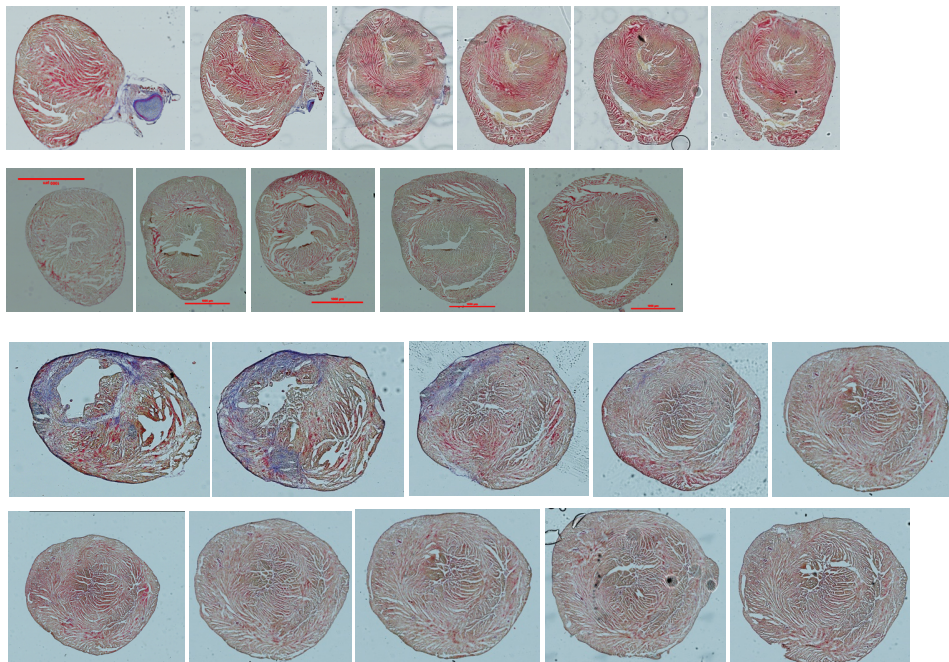


C

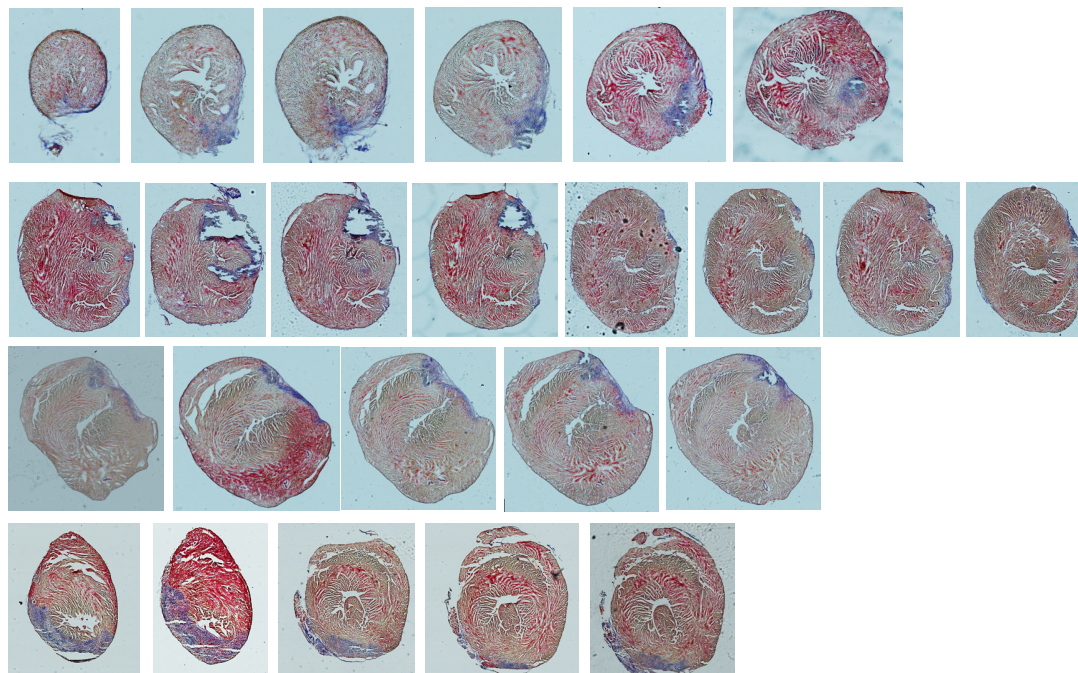


Supplementary Figure S3. Related to Figure 2 and 5. *Lmn2* gene inactivation inhibits prometaphase-to-metaphase transition. (A) Example photomicrographs (top) and three-dimensional nuclear volume view (bottom) of mitotic sub-phases *in-vivo* in P2 *Lmn2* KO heart sections. Scale bar, 10 μ m (top) 5 μ m (bottom). (B) Additional Western blot results of cyclin B1 and cyclin B1 phosphorylation in *Lmn2* KO cardiomyocytes. (C) Western blot shows that *Tnnt2-Cre*-induced *Lmn2* KO does not alter the protein amount of Lamin B1 and Lamin A/C at P0. Fifteen μ g lysate loaded per lane and normalized against GAPDH. One heart per lane. Statistical significance was tested with two-tailed Student's *t*-test (C). Lamin B1: P=0.13; Lamin A/C; P=0.17.

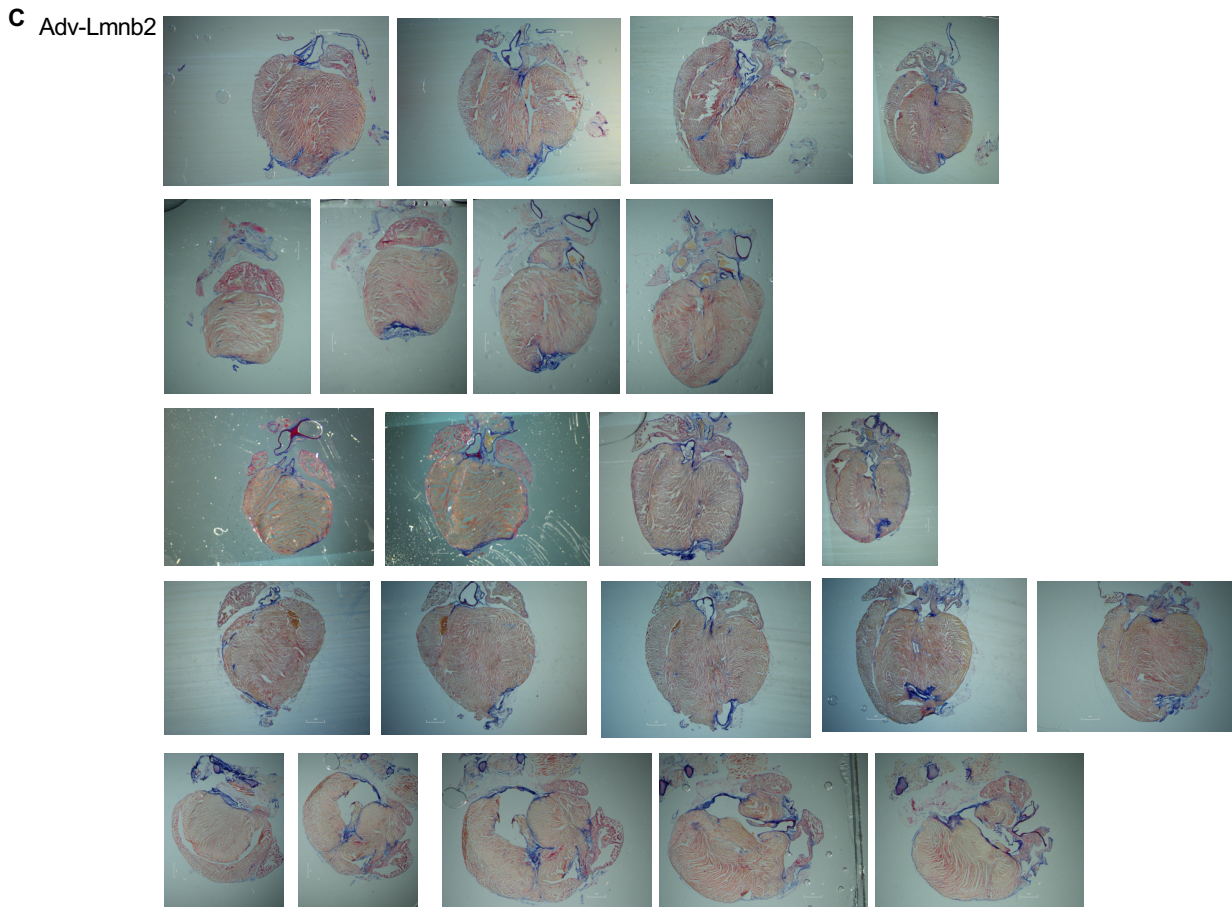
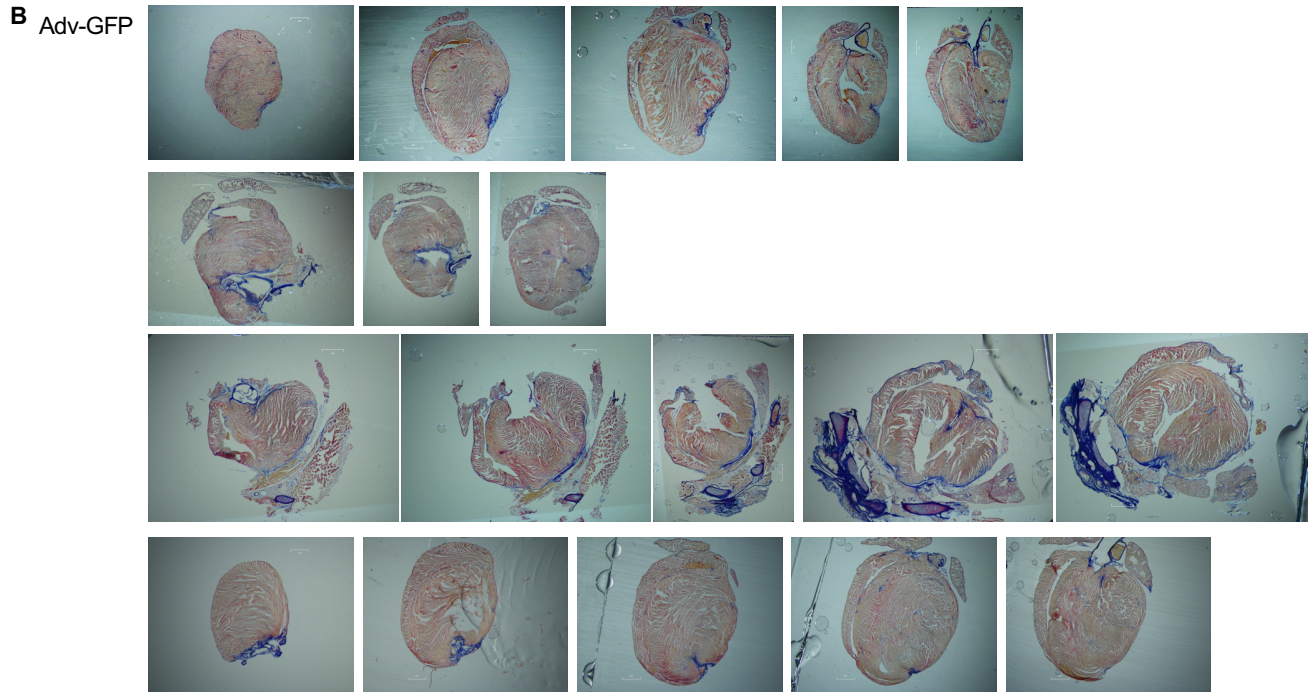
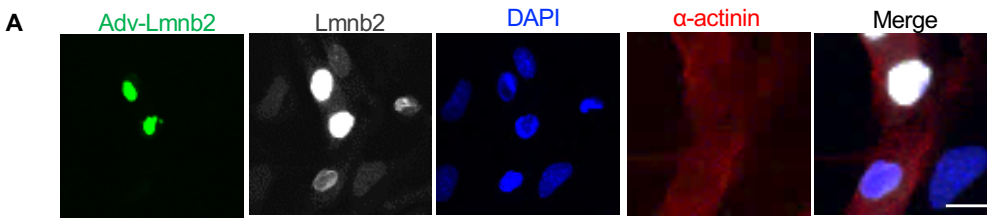
A TNT-Cre WT



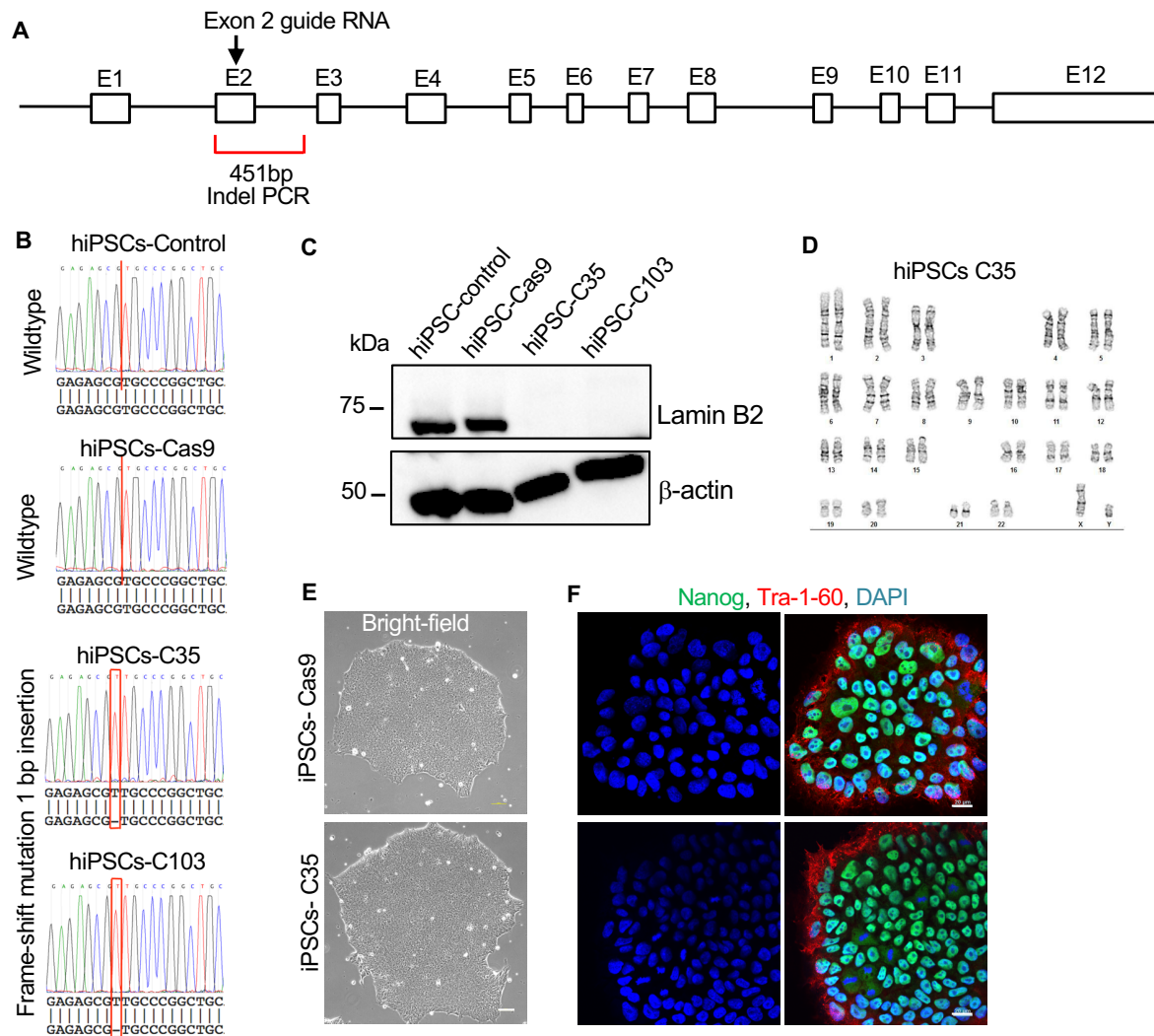
B TNT-Cre Lmnb2 KO hearts



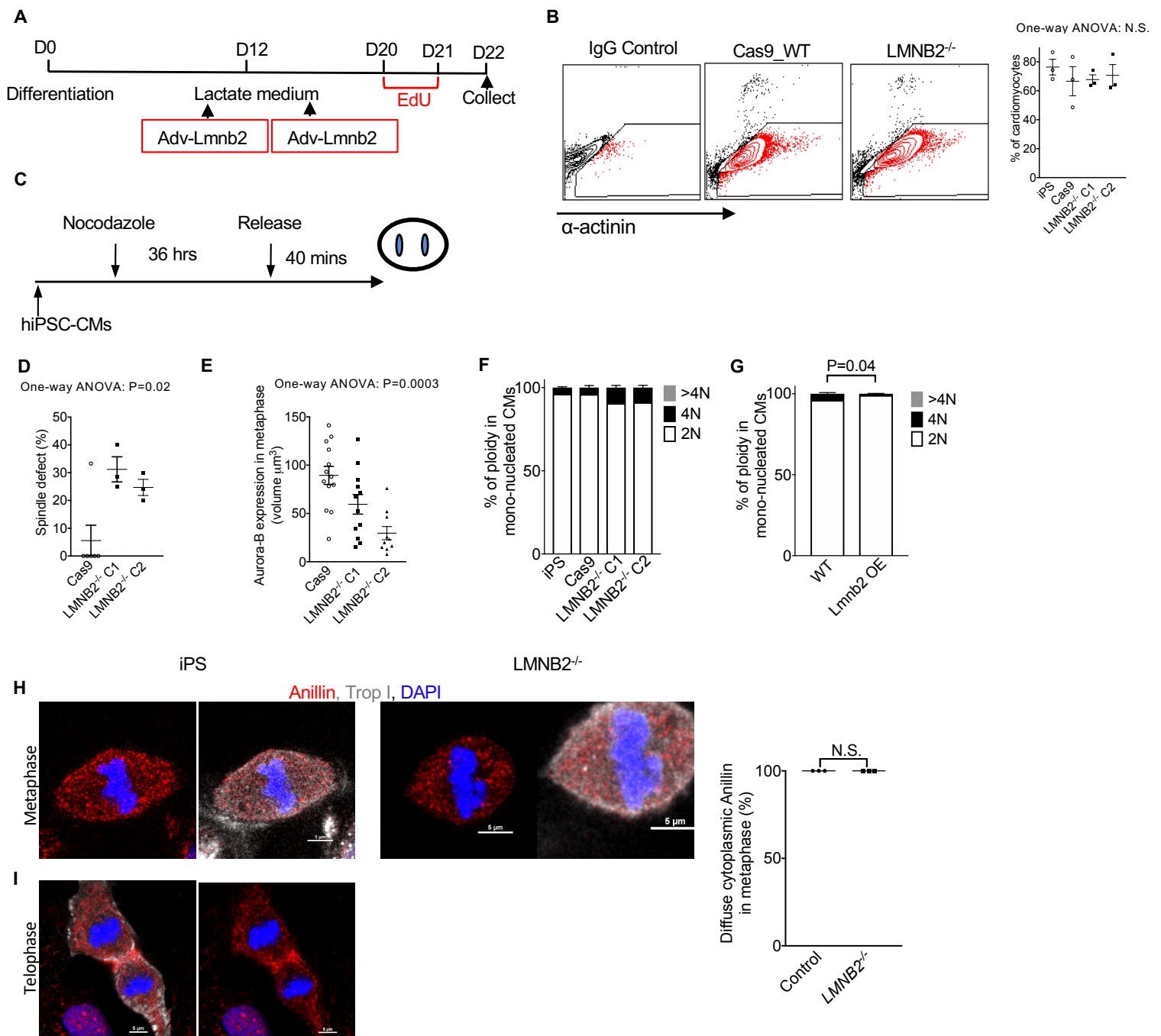
Supplementary Figure. S4. Relate to Figure 6. (A-B) Example of Scar formation visualized by AFOG staining of *Tnnt2-cre* (A) and *Tnnt2-cre, Lmnb2^{fl/fl}* mice (B) 9 dpi post cryoinjury. Four out of nine hearts from each group were shown. Scale bar 1 mm.



Supplementary Figure S5. Related to Figure 7. Validation of nuclear expression of Adv-Lmnb2 and examples of scar analysis by AFOG staining. (A) Adenoviral transduction with type V replication-deficient adenovirus increases lamin B2 protein expression in the nucleus. Mice received retro-orbital injection of Ad-GFP (control) or Ad-Lmnb2 (test) on the day of birth and cardiomyocytes were isolated and subjected to immunofluorescence microscopy. Scale bar 20 μ m. **(B, C)** Examples of scar formation visualized by AFOG staining of control and Lmnb2 adenoviral-transduced groups. Scale bar 1 mm. Note one heart from Ad-GFP group had adherent to the chest post injury, thus both scar and chest tissue are stained by AFOG.



Supplementary Figure S6. *LMNB2* gene is successfully inactivated with CRISPR/Cas9 in human iPSCs (hiPSCs). Related to Fig. 8 A-D. (A) Strategy for creating indel in human *LMNB2* gene. CRISPR-Cas9 mediated deletion using guide RNA targeting *LMNB2* exon 2. SURVEYOR PCR primers amplify 451 bp of exon 2 including indel region. (B) Sanger sequencing of PCR products from controls and *LMNB2* guide RNA transduced clones. hiPSCs-Control: hiPS cell line (CiPS0001-013) with no transduction; Cas9-control: hiPS cells transduced with no specific guide RNA; C35 and C103: *LMNB2*^{-/-} clones. Sequencing revealed a 1 bp insertion causing frame-shift mutation in clones C35 and C103. (C) Western blot of cell extracts labeled with Lamin B2 antibody shows no protein expression in *LMNB2*^{-/-} hiPS clone C35. (D) *LMNB2*^{-/-} hiPS clone C35 has normal karyotype and was used for further experimentation. (E-F) Each clone maintained normal morphology (bright-field) (E) and expressed pluripotency markers NANOG (green) and TRA-1-60 (red) determined by immunofluorescence microscopy (F). Scale bars 100 μm (E), 20 μm (F).



Supplementary Figure S7. *LMNB2* gene inactivation with CRISPR/Cas9 in human iPSCs (hiPSCs) does not affect differentiation to cardiomyocytes and does not alter Anillin localization in metaphase of hiPSC-CMs. Related to Fig. 8 A-D. (A) Experimental design for cardiomyocyte differentiation, and important time points for treatments corresponding to the experiments in Figure 8. (B) Two clones are analyzed and show consistent differentiation efficiency. The CMs were collected and stained with cardiac marker α -actinin at day 12 before Lactate treatment. N.S. not significant. (C) Experimental design to enrich prometaphase and metaphase cardiomyocytes *in vitro*. (D) *LMNB2* KO hiPSC-CMs have disorganized spindles. Cas9 control: 25 cells; *LMNB2* KO: clone 1: 20 cells; clone 2: 24 cells; 3 biological replicates. $P=0.02$ (E) Expression of Aurora B kinase, a chromosomal passenger protein, is decreased on centromeres in *LMNB2* KO hiPSC-CMs indicating decreased microtubule attachment in metaphase. $n=13$ cells from Cas 9, $n=12$ cells from clone 1, and $n=10$ from clone 2, 3 biological replicates. $P=0.0003$ (F) *LMNB2* gene inactivation increases nuclear ploidy in hiPSC-CMs in both clones. (G) Overexpression of *Lmnb2* decreases nuclear ploidy in hiPSC-CMs. $P=0.04$ (H-I) Anillin is present in the cytoplasm of control and *LMNB2*^{-/-} cardiomyocytes in metaphase (H). Anillin marks the contractile ring in telophase of wildtype hiPSC-CMs, which validates the specificity of Anillin antibody for contractile ring (I). iPSC and Cas9 WT: $n=14$ cardiomyocytes in metaphase; *LMNB2*^{-/-}: $n=10$ cardiomyocytes in metaphase. N.S. not significant. Statistical significance was tested with One-way ANOVA (B, C, D, E, F) and Student's *t*-test (G, H). Error bars represent mean \pm SEM. Scale bar, 5 μ m.

Supplementary Tables

Supplementary Table S1. *Related to Figure 1. List of differentially expressed genes between E14.5 cycling and non-cycling cardiomyocytes.* 163 genes were differentially expressed between E14.5 cycling and non-cycling cardiomyocytes. These genes have a p-value of ≤ 0.05 and false discovery rate (FDR) of $\leq 10\%$. (See **Supplementary Table 1_163** differentially expressed genes.xlsx).

Supplementary Table 1. List of differentially expressed genes between E14.5 cycling and non-cycling cardiomyocytes. 163 genes were differentially expressed between E14.5 cycling and non-cycling cardiomyocytes. These genes have a p-value of ≤ 0.05 and false discovery rate (FDR) of $\leq 10\%$.

	g1	g2	g5	g6	g8	g25	g27	g28	g29	n3	n5	n7	n8	n10	n21	n23	n24	n25	n28	n30	Pvalue	q	
Fam64a	74.7803772	189.443014	1269.18413	163.393132	1224.39001	498.59193	729.333942	895.604214	842.366801	578.853982	0	0	0	0.104693264	0	0	0	25.5932047	0	0.47824666	3.081E-11	2.9132E-07	
Aspm	709.983811	723.43551	3572.74128	738.536958	3496.48405	1222.79107	5777.80339	260.020794	207.297439	1698.11676	0	0	0	0	0	0	0	44.0990604	0	0.95649331	3.9522E-11	2.9132E-07	
Penpe	2226.22042	306.660879	1296.8778	1681.85998	4088.60111	165.821298	5294.42417	2768.45669	4240.11645	1022.90024	0	0	0	2.61733159	0	0	0	2.36244967	0	0.95649331	5.7326E-10	2.817E-06	
Cdc2a	1190.46922	287.716578	411.822554	374.714917	820.640651	1058.09781	5272.62472	1327.38755	2326.55218	1528.53591	0	0	0	0	0	0	0	163.79651	0	0	2.0672E-09	5.0126E-06	
Nusap1	2954.25467	201.283203	3449.91701	893.21579	8778.81066	1178.79766	14914.1446	4526.80081	4167.80339	8584.8833	0	0	2.53051607	80.5773655	3.14079791	0	0	59.0612416	0	0.286947994	2.3802E-09	5.0126E-06	
Ccnb1	997.93124	151.554411	5517.4589	610.001027	2038.45969	721.943066	18323.8637	11476.2596	3636.86483	14646.1663	0	0	0	0	0	0	14.5496074	0	0.95649331	2.2533E-09	5.0126E-06		
Slc6a6	1509.36026	1258.61203	964.531772	1977.0569	129.228999	1166.38927	351.634688	39.6852087	3011.7586	1394.54484	0	0	0	0	19.8966229	0	0	0.78748322	0	0	1.9247E-09	5.0126E-06	
Sgol1	670.444761	140.898242	34.9206259	1236.34137	1103.9223	887.764364	1665.76271	2260.81673	93.2034996	476.21258	0	0	0	0	0	0	0	21.6557886	0	0	1.9247E-09	5.0126E-06	
Fam83d	1783.55497	574.249137	15096.5478	781.019172	6538.84134	758.040219	9473.28492	3407.14052	3322.54406	7032.56811	0	0	0	27.4559912	3.14079791	0	0	251.246879	0	0.286947994	7.4429E-09	1.0972E-05	
Racgap1	989.335795	207.203297	1267.97997	621.98319	1412.7577	180.485766	1414.12117	1216.39298	1949.88149	1043.82316	0	0	1.26252804	6.56556311	1.04693264	0	4.85904315	14.5684396	0	85.3168567	3.3477266	7.204E-09	1.0972E-05
Hmnr	2266.61902	184.706939	10234.1517	250.536136	5535.67385	3640.1723	6429.41754	2402.81537	3428.60322	4195.96599	0	0	0	0	0	0	0	0	0	0.95649331	9.9338E-09	1.3313E-05	
Ckap2l	5342.06947	1915.74248	12353.4725	2733.02246	2954.74441	7685.30954	13052.6607	5990.39957	5850.60864	4662.74861	0	0	0	0	0	0	0	506.745453	0	0	2.39123328	1.1869E-08	1.4581E-05
Prc1	1303.92911	329.157237	2516.69339	291.929063	2502.07786	1223.9191	7549.71997	5172.92561	3236.73257	6621.63981	0	0	0	0	0	0	0	20.0808222	0	1.11162028	25.8253195	1.5183E-08	1.7218E-05
Anln	4309.75645	5255.85963	31770.5446	10588.9643	11156.0402	24925.0843	18930.9311	4815.55204	4789.37431	7054.32954	0	0	0	0.59686937	5.23466318	0	0	1.11162028	0	0	2.7653E-08	2.9118E-05	
Kif20b	2505.57241	290.084615	1994.08816	502.16156	7574.13355	3853.37111	4818.15347	916.686982	5455.61864	8424.21142	0	0	0	323.503201	6.28159581	0	0	10.2372819	26.2602671	0	0.95649331	3.9703E-08	3.9021E-05
Aurkb	445.244083	693.835039	14.4499142	223.303947	1517.16305	661.02912	704.69108	845.584316	802.51427	531.341531	0	0	0	0	0	0	0	213.801695	0	0	4.2572E-08	3.9225E-05	
Kif23	1354.64223	242.723862	72.661216	623.072478	2691.17566	2579.81842	6513.77195	2805.54039	2129.86066	4581.86864	0	0	0	0	0	0	0	891.824749	0	0	5.197E-08	4.5067E-05	
Dlga5	1049.50391	47.3607535	3178.98112	520.679448	1436.12114	495.207822	4119.6231	4333.7488	717.024164	3635.24653	0	0	0	0	0	0	0	531.157433	0	0	1.91298663	6.3367E-07	5.1898E-05
C330027C09	850.089575	607.401664	7450.13492	2327.80749	5632.77813	3784.56092	12576.8639	1787.90133	1349.84379	4059.95706	0	1042.48275	0	3.58121624	1.04693264	0	0	20.0808222	0	1.38952535	0.1672E-07	0.00012973	
Penf	3642.74987	187.074977	13476.9533	3283.11267	6465.1005	4620.43562	13378.7047	4965.61174	7662.61323	11528.8418	0	0	0.506103215	0	0.209386527	0	0	100.010369	0	0	993.796553	1.8192E-07	0.00013409
Nek2	650.675236	188.258995	4932.23737	466.215071	2203.46395	793.009336	1301.33269	1305.6847	898.610292	2640.38658	0	0	0	0	0	0	0	871.350185	0	0.55581014	0.19145E-07	0.00013409	
Mki67	6645.13903	1334.38923	36105.5189	5074.99069	3894.39255	8261.73596	8979.95378	3293.87232	17786.4416	10192.3274	0	0	0	0	0	0	0	4400.84999	0	0.55581014	0.47824666	2.2758E-07	0.0001525
Shcp1	2532.21829	1605.52955	9951.17423	6238.34979	10243.406	3768.76841	10252.3785	1412.54524	2525.81484	2156.5575	2.32935081	0	0	0	4.18773054	0	0	2095.8866	0	0	1.91298663	7.2749E-07	0.00016887
Kif4	685.916563	78.152434	77.066209	359.464891	2004.87476	894.53258	2180.41941	642.817703	16.3909603	1197.9666	0	0	0	0	0	0	0	217.739111	0	0	2.6513E-07	0.00016887	
Mxd3	30.9436043	21.3123391	80.678675	32.6786265	73.7408414	42.8653695	279.127805	230.256888	278.646325	23.2121897	0	0	0	0	0	0	0	0	0	0	3.0713E-07	0.00017415	
Ndc80	3547.34042	597.929514	668.308531	140.518094	5446.60076	2236.89547	3161.39488	3902.79224	7233.87713	2711.11122	0	0	0	0	0	0	0	1865.94149	0	1.11162028	3.309E-07	0.00017415	
Ttk	182.223448	333.893313	2187.95784	786.46561	1845.71136	489.567641	778.145765	240.798271	2278.02209	394.607226	0	0	0	0	0	0	0	725.665789	0	0	3.593E-07	0.00019618	
Kif2c	305.997865	40.2566405	1411.27495	17.4286008	1035.29221	720.81503	920.790025	2201.49561	776.80296	276.370134	0	0	0	0	0	0	0	0	0	0.95649331	5.9262E-07	0.00031202	
Ncapg	710.843355	104.193658	564.750813	364.911329	522.756856	462.494777	603.750125	314.79465	449.947929	47.8751431	0	0	0	0	0	0	0	368.935889	0	0	9.4544E-07	0.00048061	
Ccna2	3071.15273	863.149733	6226.95819	11188.895	1714.61478	5969.25947	3493.95191	3641.38286	2637.12237	0	0	0	0	0	0	0	0	1466.29376	0	0.47824666	1.0096E-06	0.00049609	
Gtse1	120.336239	22.4963579	827.257857	150.321682	407.399896	316.977127	745.446583	146.959288	352.24495	128.029734	0	0	0	0	0	0	0	361.061057	1.4194739	0	1.1532E-06	0.00054862	
C79407	1950.30662	7.10411303	12437.7636	416.107844	11177.2133	318.106163	3200.72868	1837.50784	4458.34119	5852.37334	0	0	0	0	0	0	0	11.8122483	0	0.47824666	1.2082E-06	0.00054862	
4930547N16	22.3481587	24.8643956	7203.28222	214.589647	216.84188	188.382019	619.388664	744.725453	132.091856	569.78672	0	0	0	1.19373875	4.18773054	1.42118735	0	0	0	0	1.3697E-06	0.00061128	
Bub1	1412.23172	303.108823	1345.04618	2710.14742	1877.10597	1031.02494	4930.94195	1261.86562	1912.92148	1374.23417	0	0	0	0	0	0	0	975.29797	0	0	1.4405E-06	0.00062446	
Arhgap11a	771.87102	253.380031	14655.5135	1760.28868	5722.58133	2311.34585	1403.22144	913.379881	1169.54322	1096.05058	0	0	0	0	0	0	0	1409.20123	0.70973695	0	1.4924E-06	0.00062862	
Neur1b	239.812934	67.4890738	416.63192	21.785751	156.782756	399.324758	167.634548	90.6323685	541.134173	0	0	0	2.3874775	0	0	0	0	376.023238	0	0	1.5579E-06	0.00063795	
Arhgap19	80.7791891	69.8571115	160.153215	2.1785751	676.079397	99.2671715	51.1813293	148.406145	99.3177609	98.6518064	0	0	0	14.324865	18.4754356	0	0	0	0	0	1.6389E-06	0.00065299	
Nuf2	307.716954	183.52292	1213.79279	1017.39457	1266.73624	268.472578	1396.11293	4333.54211	1872.42617	1821.06882	0	0	0	0	0	0	0	2449.46656	0.70973695	0	1.952E-06	0.00073786	
Kif18a	2117.05826	189.443014	3286.15132	4.35715019	11226.1305	464.750849	2274.25184	6388.90521	4486.94503	2095.6255	0	0	0	0	0	0	0	14.9621812	0	0	333.33792	1.9054E-06	0.00073786
Incepp	1944.28981	679.626813	930.815305	240.732548	778.294425	874.227931	1521.69674	419.38171	3794.34661	2144.58872	0	0	0	0	0	0	0	2255.35195	2.83894779	1.11162028	2.266E-06	0.00083515	
Cntrob	229.498399	372.965934	964.531772	160.12527	202.969841	684.717876	151.174482	467.954752	361.243909	924.860685	0	1.62127956	0	2.3874775	0	0	0	1.57496644	0	0	7.4557E-06	0.00101875	
Aurka	165.032557	59.2009419	434.701585	3.26786265	844.004086	241.399713	1532.12257	597.138374	312.071028	1167.50061	0	0	0	0	0.52346632	0	0	0	0	0	3.2291E-06	0.0010819	
Spc25	6345.15798	2616.68163	7112.97026	6128.33175	14775.1822	4328.27429	20493.8573	41731.0639	28192.1303	11296.7199	0	0	0	410.646129	3.14079791	0	0	6002.59086	1.4194739	0	0.47824666	3.0933E-06	0.0010819
Sgol2	1273.84505	439.270989	4859.9878	2421.48622	6261.40055	2171.46938	7307.55645	2205.42279	515.833161	2481.16547	27.9522098	6.48511822	0	0	0	0	0	3.1407					

Poc1a	101.426259	134.978148	169.786492	87.1430039	61.3290166	121.827892	2.36950598	406.566695	15.4267861	311.188419	0	0	0	5.96869374	0	29.1343407	41.3018668	14.9621812	0	0	76.9977118	0.00057101	0.05995681
Neil3	3340.19018	176.418807	0	5877.79561	806.038504	1758.60819	6.63461676	6040.41947	2145.60884	257.51023	0	0	0	0	0	0	875.437608	149.621812	0	0	0	0.00057346	0.05995681
Kif1Bb	145.263032	0	439.518223	0	669.508431	90.2428832	67.2939699	374.942544	683.920852	883.876662	0	0	0	0	0	0	0	178.36495	0	0	0	0.00058232	0.06045512
Ccdc99	283.649707	1031.28041	2.40831903	954.215893	1560.23939	1279.19287	937.850468	894.777439	866.149763	0.72538093	0	423.964604	0	0	0	0	0	452.015369	0	0	0	0.00059327	0.0611607
Taf8	390.233233	1018.2562	2402.29823	52.2858023	150.402112	119.57182	111.840682	0	597.466571	0	0	59.9873435	0	0	0	0	0	0	0	0	0	0.00060451	0.06188662
Wee1	1263.53051	533.992496	1127.09331	401.947105	1222.19969	329.386524	505.178676	816.440491	1725.55031	3129.65602	0	91.6022949	87.3028046	1283.86602	2.09386527	0	0	1459.60015	19.1628976	0	0	0.00062658	0.06370331
Stk17b	1126.86292	1520.28019	16299.5032	1196.03773	9165.76755	3289.35309	7280.07019	5546.00791	878.362636	5510.71892	7477.21611	0	2.53051607	389.755701	2.09386527	0	0	2652.24349	0	1.11162028	682.457979	0.00063837	0.06445794
Lrrc10	532.91763	670.154663	131.253387	640.501079	309.565512	271.856686	396.655302	974.147857	89.346803	101.19064	1409.25724	842.254729	2448.2743	1676.0092	1224.91118	2258.2667	275.075832	845.363239	744.15919	1547.09753	2386.92906	0.00071237	0.07095761
Cks2	2708.42492	992.207787	8297.86322	2069.64634	10076.2114	1581.50653	10043.3881	10619.7205	7162.52825	6905.26376	0	693.90765	0	503.757752	39.2599738	1.42118735	858.700904	655.186041	483.68573	107.549262	1064.09881	0.00070765	0.07095761
Kifc1	292.245152	8.28813187	8.42911661	0	32.8548303	226.735244	126.057718	0.41338759	136.269944	343.46787	0	0	0	0	1.04693264	0	0	0	0	0	0	0.00075591	0.07432706
Rfc4	116.898061	73.409168	122.824271	435.715019	68.63009	160.181118	253.063239	378.456339	243.936056	8.34188069	0	0	0	47.1526805	0	0	0	303.18104	289.217806	0.55581014	0	0.00075628	0.07432706
Chek2	205.431151	14.2082261	0	150.321682	290.582721	0	52.1291316	95.6992272	42.7450533	831.286545	0	0	0	0	0	0	0	19.6870805	0	0	0.47824666	0.00078453	0.07659295
Tmem194	126.353051	7.10411303	0	421.554281	186.907479	760.296291	821.744675	639.510602	561.792128	1184.90975	0	0	0	94.9022305	1.04693264	880.425564	0.53989368	0	0	0	0	0.0008405	0.08151748
Lcorl	4853.84816	1564.08889	2924.90346	1826.73522	1355.07922	959.95867	1648.70226	1043.59697	4574.68487	672.065431	0	522.862657	0	2662.63428	5.23466318	2250.45017	0.53989368	45.6740269	3.54868474	1.11162028	124.344131	0.00085987	0.08197665
Csrp3	6383.83749	10726.0267	6758.94736	4081.56045	6352.66397	5957.15833	8786.60209	5330.42628	6680.11979	8002.03972	7363.07792	11426.7783	19228.1264	13913.622	33278.8477	21771.8796	12892.3912	8929.666	8339.764	9102.50269	12091.5102	0.00086192	0.08197665
Lnx1	4040.719	589.641382	13426.3786	3730.80985	3645.42595	5704.47826	12.7953323	1254.01126	1255.35472	0	0	0	235.763403	3.14079791	0	0	0	1.57496644	2.12921084	0	4649.514	0.0008551	0.08197665
Igap3	572.45668	26.0484145	146.907461	297.375501	196.398875	54.1457299	297.609952	183.957478	82.9189755	668.438526	0	0	0	105.645879	0	0	0	142.534463	0	0	956.97156	0.00087943	0.08310635
Cit	179.644814	2.36803768	0	216.768222	29.934401	4.51214416	4.73901197	68.2089524	7.71339307	374.65925	0	0	0	0	0	0	0	0	0	0	0	0.00091078	0.08517937
Gm6682	24.9267924	9.47215071	172.194811	7.62501284	70.820412	42.8653695	196.668997	161.014466	117.307853	213.624684	4.65870163	38.9107093	0	2.3874775	92.6535382	4.97415573	22.6755347	1.18122483	10.2911857	0	0.95649331	0.00091293	0.08517937
4931417G12	117.757605	0	0	191.714609	253.347247	107.163424	1.89560479	1209.3654	779.374091	262.225206	0	0	0	0	0	0	0	0	0	0	0	0.00098371	0.09120651
Tubb5	18285.9511	6922.95815	23605.139	15867.6517	15405.995	16819.0174	38907.7622	45434.6033	33794.3034	29022.491	2382.92588	1900.95028	6269.35358	7917.47225	6246.0001	2327.90488	11995.3579	22322.3932	10948.4022	8469.43493	14143.6666	0.00102803	0.09472006
Nup155	804.533713	181.154882	774.274568	1470.53819	691.411651	300.057587	740.233669	3934.2097	1682.48386	624.19029	0	0	0	10.4693264	54.715713	957.771395	289.793826	114.977386	19.73126	0.95649331	0.0010364	0.0948983	
Tsr1	0	318.501068	0	0	0	0	0	0	0	0	0	0	0	2624.13665	5242.04954	1.07978737	1006.00982	1714.01473	7419.78748	202.298336	0.00109896	0.0993922	
2810006K231	422.895926	248.643956	20.4707118	0	177.416084	21.4326848	458.736359	13.8484843	34.0674861	9.42995208	0	0	0	0	16.2274558	0	0	127.572282	0	0	0	0.00109499	0.0993922