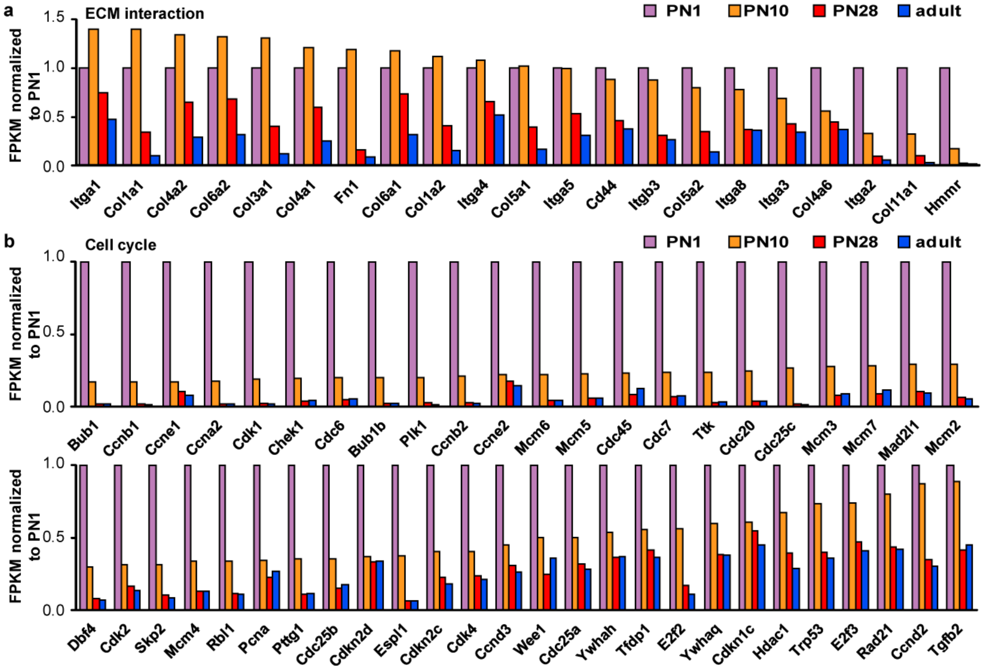


c

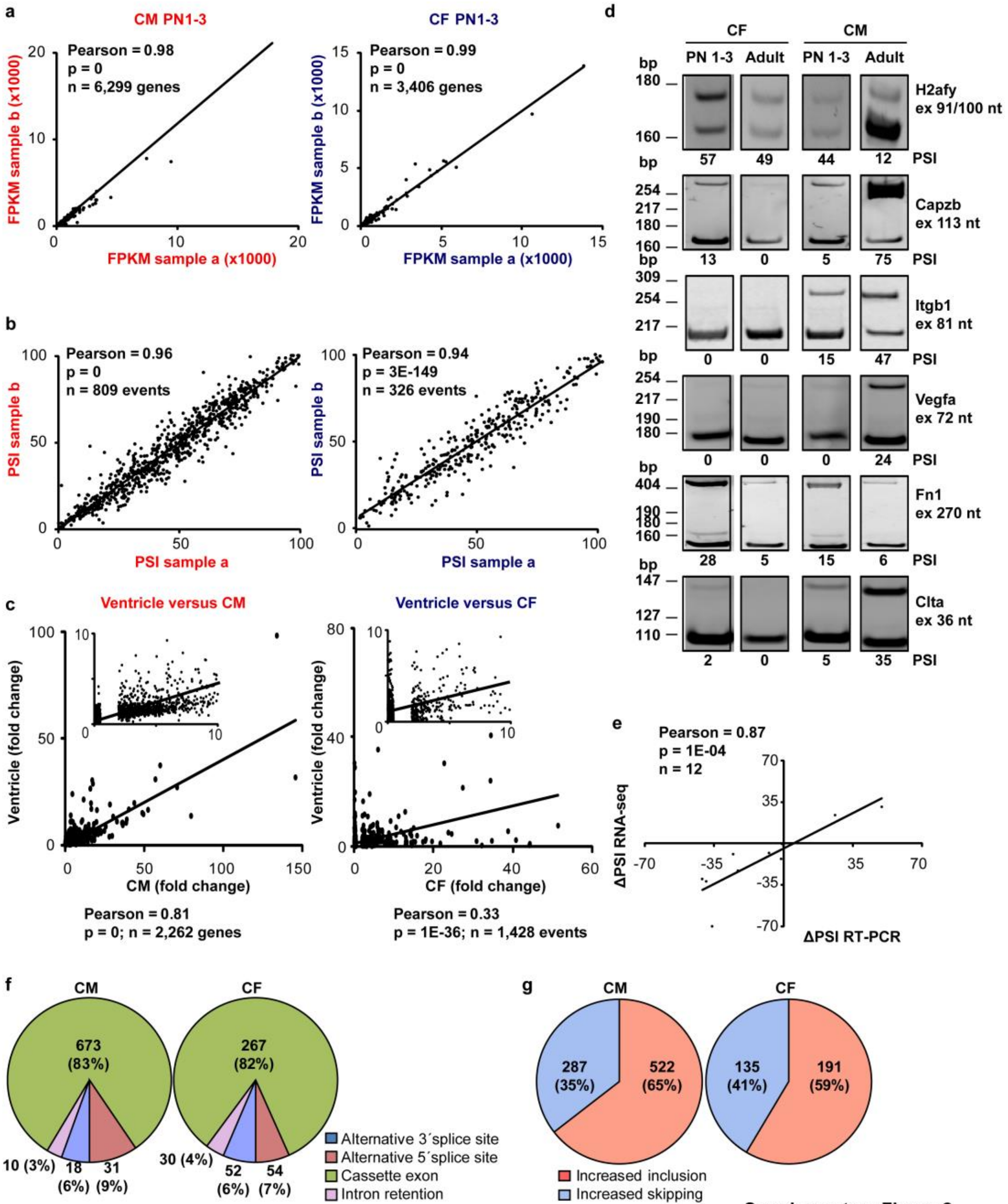
Gene name / Transcript ID	*p*	Site
Xdh / ENSMUST00000024866	9.4E-10	CAGUGGAAUA GUGUGUGUGUGUGUG UGGGGGGGGG
Hk2 / ENSMUST00000000642	9.4E-10	GUGUGUGUAU GUGUGUGUGUGUGU GUGUGUGUCUA
Prosc / ENSMUST00000033875	9.4E-10	CCAUGCCCUG GUGUGUGUGUGUGUG CAUGCCCUGU
Rilp / ENSMUST00000042972	1.6E-08	CCAGCTAACU GUGUGUGGAUGUGUG UGGGGGGGGG
Bdh1 / ENSMUST00000115227	1.1E-07	GCUCCCACAU GUGGGUGCGUGUGUG CAUGCACUCA
Aak1 / ENSMUST00000113278	1.8E-07	CUGAGAUUCA AGGUGUGUGUGUGGA CCUCCACCAC
Egln1 / ENSMUST00000034469	2.4E-07	AAGUAGAGCC GUGUGUGGAUGAGGG CCCACUCAGC
Bckdha / ENSMUST00000071329	2.6E-07	UUGGGGGCUG GGGUGUGUAUGUGGA GAGGAGGAGA
Nol3 / ENSMUST00000014920	3.0E-07	AAGACACAGU GUGUCUGUGUGAGUG AUAAAGAAAGG
Amacr / ENSMUST00000070877	3.8E-07	AUUGAGGAAA AUUUGUGUGUGUGUA CUGAUAGUAA
Slc25a33 / ENSMUST00000105686	5.4E-07	GACACUGAAU GGGGGUGGGGGUGGG GGUGGAGUGU
Gpt2 / ENSMUST00000034136	5.4E-07	GUCGCAGCAU GUGGGUGGGGCUGUG GAAACCUGGC
Pxmp2 / ENSMUST00000031472	6.1E-07	GAGGGAGGAA AUGUGUGGGUGUCAG AAUCAUGUGC
Mapk10 / ENSMUST00000112847	7.8E-07	CCCGCCCAGC AUGUGUGUGUCUCUA UCUCGCGUCU

d

Motif	Enrich-ment	Count	Random set count
ACACACAC	85.8633	68	797
GAAGGAAG	53.1065	40	758
UUUUUUUU	42.8944	65	1,525
UCUCUCUC	37.8796	37	983
AAAAAAAA	34.5414	37	1,078
UGUGUGUG	27.2581	25	923
GGGGGGGG	22.3638	11	495
GGGAGGGA	21.1013	13	620
GGGGUGGG	16.4679	9	550
CACACACU	15.9546	13	820
GGGGAGGG	15.8069	9	573
CUACUACU	15.1106	15	999
GGGUGGGG	14.7274	9	615
AGGCUGUG	14.4707	11	765
GAGAGGGA	14.3996	9	629

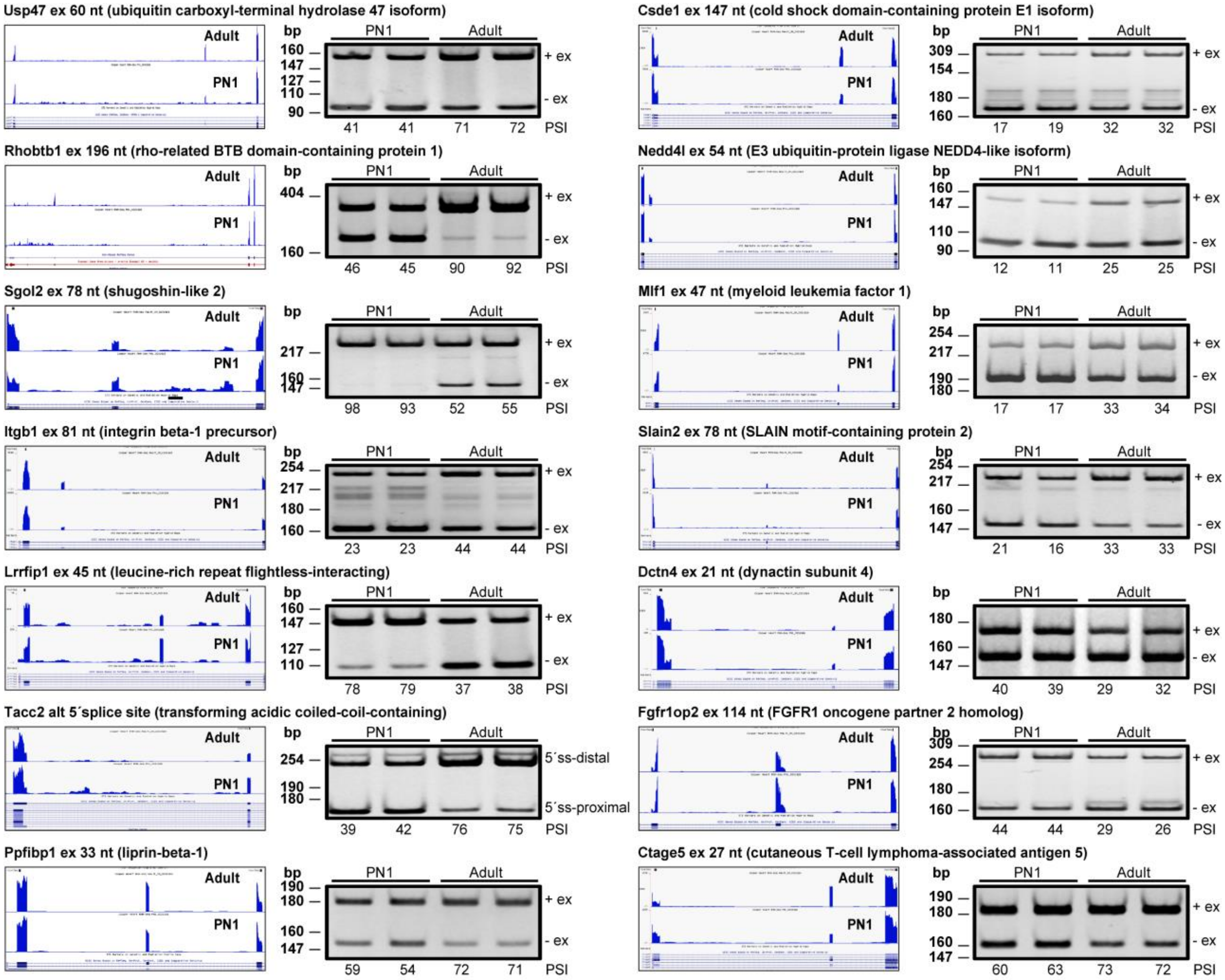
Supplementary Figure 1

Supplementary Figure 1. mRNA expression during development and potential role for CELF1. a-b. Expression of ECM-receptor interaction (**a**) and cell cycle (**b**) genes (KEGG-pathways) were analyzed by RNA-seq in ventricles during postnatal heart development. **c-d.** The 3´ UTRs of 58 genes belonging to oxidation-reduction and mitochondria categories (up-regulated during development and down-regulated after CELF1 induction) were analyzed for motif enrichment using MEME (**c**) and CLIPZ (**d**) bioinformatic tools. ECM: extracellular-matrix.



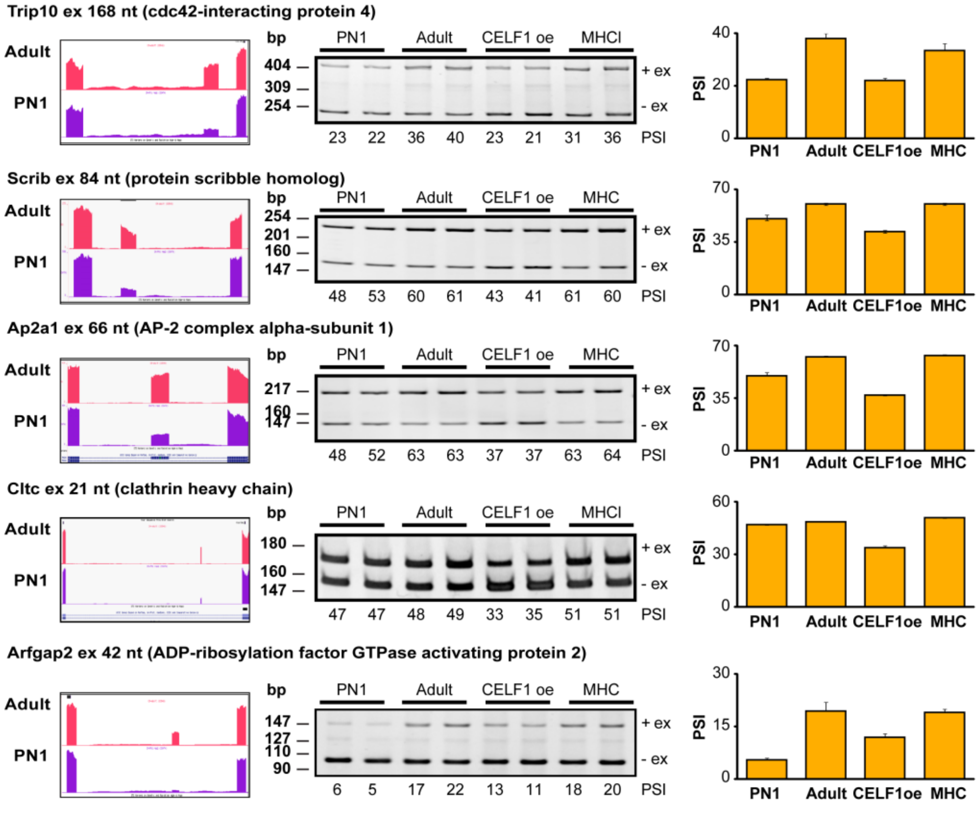
Supplementary Figure 2

Supplementary Figure 2. Gene expression and AS transitions during CM and CF development by RNA-seq. a-b. Analysis of CM (red) and CF (blue) duplicates (PN1-3) at the gene expression (**a**) or AS (**b**) levels. **c.** High correlation was detected between CM and ventricle gene expression changes during the first four week after birth (left panel). Similar analysis between CF and total ventricles showed a low correlation degree (right panel). **d.** Validation of AS transitions specifically in CM and CF during postnatal development by RT-PCR (*n*=2 biological replicates). Images from all the lanes came from one gel. **e.** Correlation between RNA-seq and RT-PCR data on CM and CF splicing transitions. **f.** Splicing was analyzed by type of event (alternative 3´ or 5´splice site, cassette exon or intron retention) from RNA-seq data (|ΔPSI|≥20% between adult and PN1-3). **g.** The same events were analyzed depending the developmental transition was an increment in inclusion of variable region in adult stage than in neonatal animals (increased inclusion) or a decrease (increased skipping). AS: alternative splicing. bp: base pairs. FPKM: fragments per kilobase per million mapped. PSI: percent spliced in.



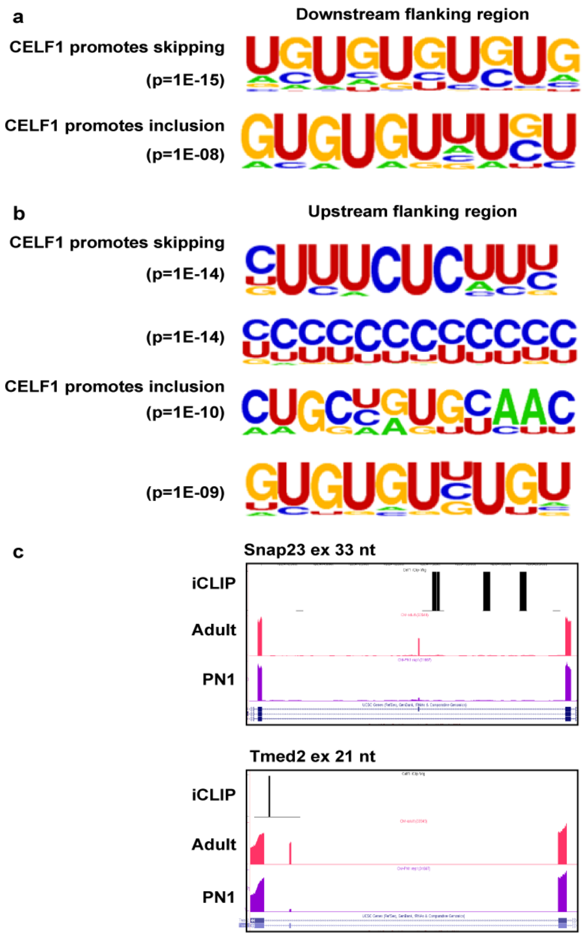
Supplementary Figure 3

Supplementary Figure 3. Validation of AS transitions during heart development by RT-PCR. RNA-seq data and RT-PCR validations (*n*=2 biological replicates) for different AS transitions during development in ventricles (+ex: exon included; -ex: exon skipped). 5´ss: 5´splice site. bp: base pairs. PSI: percent spliced in.



Supplementary Figure 4

Supplementary Figure 4. AS of vesicular traffic genes reverts back to neonatal pattern after CELF1 induction in adult hearts. RT-PCR of AS events on genes involved in vesicle traffic during development and after CELF1 re-expression (CELF1 oe) in adult ventricles (+ex: exon included; -ex: exon skipped) (*n*=2 biological replicates). Left panels show RNA-seq data displayed on the UCSC browser for each AS event. Graph bars: mean±s.e.m (*n*=2 biological replicates). bp: base pairs. MHC: control animals. PSI: percent spliced in.



Supplementary Figure 5

Supplementary Figure 5. Motif analysis of AS events regulated during development and responsive to CELF1 re-expression in adults. a-b. AS events regulated during CM development and responsive to CELF1 re-expression in adult hearts were analyzed for motif enrichment within the 300 bp down- (**a**) and upstream (**b**) flanking regions. **c.** iCLIP-seq data from C2C12 differentiation were used to determine the presence of CELF1 binding sites within the flanking regions of CELF1-responsive AS events. Flanking intronic regions of the ex 33 nt from *Snap23* gene and the ex 21 nt from *Tmed2* gene are shown as examples with the iCLIP-tags.

SUPPLEMENTARY TABLES

<table>
<tr><th colspan="6">RNA-seq of ventricles during development (rRNA depletion)</th></tr>
<tr><th>Samples</th><th>Paired-end reads (nt)</th><th># reads</th><th># Mapped reads</th><th>Mapping rate</th><th>Strand specificity</th></tr>
<tr><td>E17</td><td>100 x 2</td><td>166,027,914 x 2</td><td>265,620,479</td><td>80.0 %</td><td>96.3 %</td></tr>
<tr><td>PN1</td><td>100 x 2</td><td>166,684,428 x 2</td><td>269,038,426</td><td>80.7 %</td><td>96.1 %</td></tr>
<tr><td>PN10</td><td>100 x 2</td><td>158,845,960 x 2</td><td>262,474,597</td><td>82.6 %</td><td>94.8 %</td></tr>
<tr><td>PN28</td><td>100 x 2</td><td>159,866,522 x 2</td><td>262,385,206</td><td>82.1 %</td><td>95.6 %</td></tr>
<tr><td>PN90 (adult)</td><td>100 x 2</td><td>154,600,222 x 2</td><td>247,130,461</td><td>80.0 %</td><td>95.4 %</td></tr>
<tr><th colspan="6">RNA-seq of CM and CF during development (polyA-selection)</th></tr>
<tr><th>Samples</th><th>Paired-end reads (nt)</th><th># reads</th><th># Mapped reads</th><th colspan="2">Mapping rate</th></tr>
<tr><td>CF. PN1-3</td><td>101 x 2</td><td>184,869,107 x 2</td><td>322,369,213</td><td colspan="2">87.2 %</td></tr>
<tr><td>CF. PN1-2</td><td>101 x 2</td><td>195,447,846 x 2</td><td>334,128,943</td><td colspan="2">85.5 %</td></tr>
<tr><td>CF. PN28</td><td>101 x 2</td><td>180,627,175 x 2</td><td>313,797,535</td><td colspan="2">86.9 %</td></tr>
<tr><td>CF. PN60 (adult)</td><td>101 x 2</td><td>190,932,847 x 2</td><td>329,018,420</td><td colspan="2">86.2 %</td></tr>
<tr><td>CM. PN1</td><td>101 x 2</td><td>163,947,033 x 2</td><td>295,559,466</td><td colspan="2">90.1 %</td></tr>
<tr><td>CM. PN1-2</td><td>101 x 2</td><td>171,862,237 x 2</td><td>310,403,120</td><td colspan="2">90.0 %</td></tr>
<tr><td>CM. PN30</td><td>101 x 2</td><td>190,376,627 x 2</td><td>337,974,976</td><td colspan="2">88.8 %</td></tr>
<tr><td>CM. PN67 (adult)</td><td>101 x 2</td><td>177,951,081 x 2</td><td>315,826,440</td><td colspan="2">88.7 %</td></tr>
</table>

Supplementary Table 1. Overall quality parameters of RNA-seq experiments on ventricles, CM and CF during mouse heart development. nt: nucleotides. rRNA: ribosomal RNA.

CF	**Term**	**# genes**	***p***	**- log *p***
Up-regulated	**immune response**	90	2E-45	45
	cytokine signaling	16	1E-10	10
	chemotaxis	21	1E-10	10
	cell proliferation regulation	46	2E-09	9
	transcription regulation	28	2E-05	5
	cell adhesion molecules	15	3E-03	3
Down-regulated	**mitochondria**	158	9E-29	28
	electron transport chain	25	2E-10	10
	oxidation-reduction	60	1E-06	6
	cellular respiration	14	2E-06	6
	cardiac contraction	22	3E-11	11
	fatty acid metabolism	11	3E-05	5
CM	**Term**	**# genes**	***p***	**- log *p***
Up-regulated	**mitochondria**	483	2E-198	198
	oxidation-reduction	171	8E-49	48
	electron transport chain	60	6E-37	36
	cellular respiration	33	4E-21	20
	fatty acid metabolism	48	4E-14	13
	mitochondria organization	27	7E-09	8
	cardiac contraction	30	4E-12	11
Down-regulated	**transcription regulation**	403	3E-17	16
	cell proliferation regulation	118	7E-10	9
	splicing	53	2E-07	7
	cytokine production	41	2E-07	7
	adherens junction	32	2E-09	9
	chemokine signaling	48	3E-06	6
	endocytosis	46	2E-04	4
	ECM-receptor interaction	19	2E-02	2

Supplementary Table 2. GO analysis summary of down- and up-regulated genes performed for the RNA-seq data from CM and CF (PN1-3 versus adult).

Gene symbol	**loci**	**ΔPSI**	
		RT-PCR	**RNA-seq**
4932438A13Rik	chr3:36921305-36925265	-3%	-27%
ap2a1	chr7:52158208-52158343.	7%	13%
Arfgap1	chr2:180702239-180702519	-13%	-13%
arhgap17	chr7:130428933-130428981	1%	7%
Cacna2d1	chr5:15828356-15828413	14%	33%
Clta	chr4-44044271-44044307	18%	14%
cltc	chr11:86509151-86509192	3%	8%
Csde1	chr3:102840497-102840644	14%	33%
Ctage5_27	chr12:60247322-60247349	11%	28%
Dctn4	chr18:60705010-60705031	-9%	-25%
eps15L1	chr8:74880062-74880110	20%	16%
erc1	chr6:119723751-119729650	6%	0%
Fgfr1op2	chr6:146541155-146541269	-17%	-28%
Frmd6	chr12:71978226-71978250	-11%	-20%
gapvd1	chr2:34572772-34572835	5%	3%
Heatr7a	chr15:76262801-76262828	-7%	-1%
Itgb1	chr8:131250882-131250963	21%	33%
itsn2	chr12:4647718-4647799	4%	8%
Kif3a	chr11:53404218-53404227	-42%	-55%
Lrrfip1	chr1:92987031-92987076	-41%	-34%
Mif1	chr3:67194899-67194944	16%	36%
Ndrg4	chr8:98236224-98236263	34%	48%
Nedd4l	chr18:65341136-65341190	14%	31%
Plekha6	chr1:135171369-135171456	12%	31%
Ppfibp1	chr6:146948183-146948216	14%	25%
Rhobtb1	chr10:68682194-68682287	45%	86%
Scrib	chr15:75892168-75892231	-17%	-14%
Sgol2	chr1:58056807-58059823	-42%	-20%
Slain2	chr5:73357042-73357120	22%	32%
Spna2	chr2:29869677-29869692	22%	35%
Tacc2	chr7:137878664-137878742	31%	28%
Tmed2	chr5:124993495-124993516	31%	53%
Tmem188	chr8:90648980-90649054	-16%	-29%
Tnnt2	chr1:137746955-137746964	31%	52%
Traf6	chr2:101520982-101521184	30%	49%
Usp47	chr7:119190440-119190500	31%	51%

Supplementary Table 3. Developmentally AS transitions detected by RNA-seq and validated by RT-PCR.

Gene symbol	id	loci	ΔPSI		
			Adult-PN1/3 (CM)	Mbnl1 (wild type-KO)	CELF1 (control-oe)
Antagonistic regulation by Mbnl1 and CELF1					
1110007C09Rik	CA-CA-13-49299297-49299357.0	chr13:49299086-49300714	-24%	16%	16%
4833439L19Rik	CA-CA-13-54665545-54665633.1	chr13:54663053-54666717	-41%	-27%	-27%
Abi1	CA-CA-2-22818733-22818748.0	chr2:22817920-22826779	36%	18%	29%
Aplp2	CA-CA-9-30963774-30963810.0	chr9:30960998-30965432	24%	17%	18%
Arfip1	CA-CA-3-84333091-84333187.0	chr3:84331607-84338617	31%	63%	14%
Arhgef9	CA-CA-X-92249567-92249629.0	chrX:92246861-92250350	-30%	-30%	-36%
Atp11a	CA-CA-8-12863758-12863862.0	chr8:12859313-12868728	21%	43%	16%
Bnip3l	CA-CA-14-67607736-67607778.0	chr14:67604075-67608121	28%	17%	38%
Bptf	CA-CA-11-106956315-106956504.0	chr11:106943826-106957239	34%	14%	12%
Cd99l2	CA-CA-X-68703113-68703182.0	chrX:68694248-68703848	-28%	-20%	-16%
Clta	CA-CA-4-44044271-44044307.1	chr4:44038320-44045718	26%	15%	22%
Ctage5	CA-CA-12-60247322-60247349.0	chr12:60245685-60247944	36%	28%	24%
D19Wsu162e	CA-CA-19-46681201-46681249.0	chr19:46673618-46718945	-24%	28%	27%
Dcun1d2	CA-CA-8-13258946-13259043.0	chr8:13255962-13271720	35%	-10%	-20%
Erbb2ip	CA-CA-13-104617986-104618103.1	chr13:104614799-104625108	25%	10%	15%
Exoc7	CA-CA-11-116158884-116158977.0	chr11:116156857-116161747	27%	-18%	-16%
Fbln2	CA-CA-6-91209623-91209764.0	chr6:91207718-91213467	63%	13%	18%
Fgfr1	CA-CA-8-26665979-26666246.0	chr8:26642721-26668286	-27%	-22%	-12%
Gnas	CA-CA-2-174162247-174162292.0	chr2:174159712-174167208	-23%	-10%	-20%
Gopc	CA-CA-10-52077147-52077171.0	chr10:52074377-52078743	28%	16%	10%
Immt	CA-CA-6-71803166-71803262.1	chr6:71802723-71807042	-20%	-10%	-19%
Kif21a	CA-CA-15-90779436-90779475.0	chr15:90774195-90786940	35%	10%	14%
Lpin1	CA-CA-12-16577969-16578068.0	chr12:16575195-16580591	21%	11%	38%
Map4k4	CA-CA-1-40065175-40065184.0	chr1:40064277-40066708	34%	17%	18%
Mark2	CA-CA-19-7354475-7354502.0	chr19:7352531-7355745	28%	-17%	-15%
Mbnl2	CA-CA-14-120803859-120803954.0	chr14:120795672-120830919	-44%	-15%	-24%
Nab2	CA-CA-10-127099786-127099978.0	chr10:127097973-127100320	26%	11%	18%
Palm	CA-CA-10-79279536-79279668.0	chr10:79277929-79283641	31%	15%	12%
Ppp3cb	CA-CA-14-21322468-21322498.0	chr14:21319089-21327943	44%	15%	19%
R3hdm2	CA-CA-10-126918748-126918850.0	chr10:126913575-126921274	39%	12%	41%
Rps24	CA-CA-14-25312838-25312841.0	chr14:25312604-25312988	26%	18%	25%
Tnrc6b	CA-CA-15-80713373-80713532.0	chr15:80709296-80714812	27%	19%	30%
Usp15	CA-CA-10-122590096-122590183.0	chr10:122583849-122605428	35%	-14%	-19%
Zfp346	CA-CA-13-55231894-55231988.0	chr13:55223690-55236186	28%	25%	19%
Zfp672	CA-CA-11-58133368-58133456.0	chr11:58132825-58136231	20%	-28%	-31%
Same regulation by Mbnl1 and CELF1					
4833439L19Rik	CA-CA-13-54665875-54665982.3	chr13:54663053-54666664	-58%	-34%	37%
Ankhd1	CA-CA-18-36784162-36784921.0	chr18:36774368-36791866	-33%	33%	-14%
Ap1b1	CA-CA-11-4933244-4933265.0	chr11:4932420-4933845	32%	-30%	22%
Ccnc	CA-CA-4-21674629-21674723.0	chr4:21673802-21677693	28%	-10%	12%
Ctsa	CA-CA-2-164659223-164659350.0	chr2:164658372-164659708	-37%	10%	-37%
Dmtf1	CA-CA-5-9126539-9126749.0	chr5:9124441-9128108	30%	-20%	23%
Ehbp1l1	CA-CA-19-5720971-5721007.0	chr19:5720808-5721584	45%	-16%	36%
Enah	AA-AA-1-183851899-183852631.0	chr1:183851788-183853971	-28%	-16%	28%
Fbxo25	CA-CA-8-13938921-13938948.0	chr8:13935145-13940521	40%	-15%	25%
Fez2	CA-CA-17-78786330-78786411.0	chr17:78784083-78800238	29%	-11%	16%
Golga2	CA-CA-2-32152145-32152241.0	chr2:32148834-32152528	-22%	-19%	31%
Lsm14b	CA-CA-2-179763662-179763779.0	chr2:179762604-179766233	25%	-12%	32%

Mast2	CA-CA-4-116041340-116041389.0	chr4:116025577-116064239	58%	-19%	25%
Mknk1	CA-CA-4-115527506-115527612.0	chr4:115520824-115529738	30%	-19%	31%
Ndel1	CA-CA-11-68639671-68639706.0	chr11:68635611-68643568	37%	-27%	35%
Ndrg2	CA-CA-14-52530760-52530802.0	chr14:52530354-52531221	42%	15%	-21%
Phldb1	CA-CA-9-44509028-44509169.0	chr9:44507638-44511975	32%	-22%	15%
Psap	CA-CA-10-59760284-59760293.0	chr10:59758693-59761977	40%	-18%	12%
Repin1	CA-CA-6-48544860-48544975.0	chr6:48543898-48549080	-22%	25%	-17%
Uap1	CA-CA-1-172078126-172078177.0	chr1:172073527-172079590	33%	-10%	12%
Vegfa	CA-CA-17-46159225-46159297.0	chr17:46157939-46161043	26%	10%	-24%
Zfp207	CA-CA-11-80206585-80206678.0	chr11:80205336-80208033	45%	-18%	29%

Supplementary Table 4. Developmentally AS transitions regulated by CELF1 and Mbnl1. AA: alternative 3´splice site. CA: alternative cassette exon. Chr: chromosome. KO: knock-out. Oe: CELF1-exoressing mice. PSI: percent spliced in.

CELF1 response (#events)	iCLIP-tags (#) within the upstream flanking region	iCLIP-tags (#) within the downstream flanking region	Total iCLIP-tags (#)
Inclusion (13 events)	5	2	5
Skipping (58 events)	21	27	33
Total (71 events)	26	29	38 (54%)

Supplementary Table 5. iCLIP-tags present within the flanking intronic regions of AS exons regulated during CM development which responds to CELF re-expression in adults.

Mouse	**Genotype**	**D;s (mm)**	**D;d (mm)**	**SV (vol)**	**EF (%)**	**FS (%)**	**IVSd (mm)**	**LVIDd (mm)**	**IVSs (mm)**	**LVIDs (mm)**
#1	***MHC***	3.0	4.3	47	57	30	0.8	4.3	0.9	3.0
#2	***MHC***	2.5	3.9	43	66	36	0.7	3.8	0.8	2.5
#3	***TRECUGBP1 / MHC***	3.6	4.6	41	43	21	0.8	4.5	0.9	3.7
#4	***TRECUGBP1 / MHC***	3.6	4.2	25	31	14	0.7	4.2	0.7	3.6

Supplementary Table 6. Echocardiogram parameters of bitransgenic (*TRECUGBP1/MHC*) and *MHC* adult animals after four days on 2 g/kg doxycycline. EF: ejection fraction. FS: fractional shortening. IVSd: interventricular septal thickness at diastole. IVSs: interventricular septal thickness at systole. LVIDd: left ventricle internal diameter at diastole. LVIDs: left ventricle internal diameter at systole.

Mouse	**Genotype**	**HR (bpm)**	**HRV (bpm)**	**CV (%)**	**RR (ms)**	**PQ (ms)**	**PR (ms)**	**QRS (ms)**	**QT (ms)**	**ST (ms)**	**QTC (ms)**
#1	***MHC***	634	13	2.0	94.8	17.5	25.4	11.4	44.5	33.5	45.7
#2	***MHC***	663	14	2.1	90.6	12.6	18.3	9.8	48.7	39.5	51.3
#3	***TRECUGBP1 / MHC***	590	12	2.0	101.8	23.4	30.6	10.5	34.0	24.0	33.7
#4	***TRECUGBP1 / MHC***	323	3	0.9	185.7	30.8	46.4	23.3	95.1	72.3	69.8

Supplementary Table 7. Electrocardiogram parameters of bitransgenic (*TRECUGBP1/MHC*) and MHC adult animals after four days on 2 g/kg doxycycline. bpm: beats per minute. HR: heart rate. HRV: heart rate variability. ms: millisecond.

Gene symbol	**id**	**AS region (nt)**	**Forward primer**		**Reverse primer**	
Rhobtb1	CA-CA-10-68682194-68682287.0	196	**Rhobtb1-F**	CGCAGGAACTCCTGTTCTTC	**Rhobtb1-R**	CTCCTGGCAGACACGGTACT
Aak1	CA-CA-6-86933805-86933916.0	111	**Aak1-F**	CAAAGCTGATGTTGCTGTTGA	**Aak1-R**	CATCTTCTGCCACCTTTTCG
Kif3a	CA-CA-11-53404218-53404227.0	9	**Kif3a-F**	TGACATCAGTGGGTCAGAGG	**Kif3a-R**	GGTCCTTCTCCCGTCTCTCT
Tmed2	CA-CA-5-124993495-124993516.0	21	**Tmed2-F**	GGATGTCCACTATGACTCCAAA	**Tmed2-R**	TCCCGGACTTCCATGTACTC
Tnnt2	CA-CA-1-137746955-137746964.0	9	**Tnnt2b-F**	ACAGGAGGAAGGCTGAGGAT	**Tnnt2b-R**	CTTCATTCAGGTGGTCGATG
Usp47	CA-CS-7-119190440-119190500.0	60	**Usp47-F**	AGAACCAACTGGTCCCGAAG	**Usp47-R**	GTTCACTCACTGTCTTCGAGTTAG
Ndrg4	CA-CA-8-98236224-98236263.0	39	**Ndrg4-F**	CCAGGGAAGCTGACTGAGG	**Ndrg4-R**	AGGGACGCGGTACGTGAG
Mlf1	CA-CA-3-67194899-67194944.0	47	**Mif1-F**	TGCACACCGAGAAAGTATGC	**Mif1-R**	TTCGCATATTTGCCATCATC
Itgb1	CA-CA-8-131250882-131250963.0	81	**Itgb1-F**	TTCTTATTGGCCTTGCCTTG	**Itgb1-R**	CTTCGGATTGACCACAGTTG
Lrrfip1	CA-CS-1-92987031-92987076.0	45	**lrrfip1-F**	GGACTCTCCTGCTCCAACCT	**lrrfip1-R**	CATAGAGGCTGCTCTCATCCA
Cacna2d1	CA-CA-5-15828356-15828413.0	57	**Cacna2d1-F**	TCCCAATGGCTACTATTTTGC	**Cacna2d1-R**	TTCATTCTCTAACTCAGCATCGAG
Csde1	CA-CA-3-102840497-102840644.0	147	**Csde1-F**	TCCTTTGGAACTTGTGCTGA	**Csde1-R**	AACCCCAGTTTCACGAAGTG
Nedd4l	CA-CA-18-65341136-65341190.0	54	**Nedd4l-F**	CTGGCTGGGAAGAGAGGAT	**Nedd4l-R**	TGATGGCTGGGTTCTGTAGTC
Sgol2	CA-CA-1-58058061-58058139.0	78	**Sgol2-F**	CTACCGAAAAGATGCAATTACAGA	**Sgol2-R**	CAGGCTTGCACTGCTTACTG
Tacc2	AD-AD-7-137878664-137878742.0	78	**Tacc2-F**	GCCAGAAGTGGACGTGTATG	**Tacc2-R**	GAGGAGCCAAGCTTTTCCAT
Dctn4	CA-CA-18-60705010-60705031.0	21	**Dctn4-F**	TTACCAGCAGCTTGCTCAGA	**Dctn4-R**	CCAGCAAGTGTACTGATGGATG
Frmd6	AD-AD-12-71978226-71978250.0	24	**Frmd6-F**	TGAACATGTATATATGGAATTGTCAC	**Frmd6-R**	GATCAGCTTCCCATTCTCCA
Fgfr1op2	CA-CA-6-146541155-146541269.0	114	**Fgfr1op2-F**	CAGTCTGCCCTGGAACTGAT	**Fgfr1op2-R**	TCATTACTGCTGCCATCTCG
Ppfibp1	CA-CA-6-146948183-146948216.0	33	**Pfibp1-F**	GAGCAACTGGAGGAGAAGGA	**Pfibp1-R**	TTCTTCATTCGCTGCCATC
Heatr7a	CA-CA-15-76262801-76262828.0	27	**Heatr7a-F**	TGTCTGATCCTGTGCTACGG	**Heatr7a-R**	CACCAGCTCTGTTTTCCTCA
4932438A13Rik	AD-AD-3-36921396-36921954.0	63	**13rik-F**	GTTACAGCCGATCGAAGAGC	**13rik-F**	GTGGTTTTGGGAGAGCTGAA
Ctage5	CA-CA-12-60247320-60247349.0	27	**Ctage5-F**	TAAAGGAGGCCAGCTTTGAG	**Ctage5-R**	CAGCTCGTCTTGTTCAGAATG
Plekha6	CA-CA-1-135171369-135171456.1	87	**Plekha6-F**	ACCTAGCGCCCGTTTTGAT	**Plekha6-R**	TGCTGGTCCAAATACTCTAGGTT
Tmem188	CA-CA-8-90648980-90649054.0	74	**Tmem188-F**	AATATATTCATTGCTTGCAACCTG	**Tmem188-R**	AGCTAATAGTGAAAAACGGATGG
Slain2	CA-CA-5-73357042-73357120.0	78	**Slain2-F**	CAAGTGCCAAATGGAGGAAT	**Slain2-R**	TTGGCTACCAGAACCAGAGC
Spna2	CA-CA-2-29869677-29869692.0	15	**Spna2-F**	TGAAGCCTGGATCAGTGAGA	**Spna2-R**	CTCAAAGGCTTGGTGCTTCT
Eps15L1	CA-CA-8-74880062-74880110.0	48	**Eps15l1-Fa**	GCAAATGGATCTTTGCCACT	**Eps15l1-Ra**	ACAGGACACTCCTGCTCTGC
Scrib	CA-CS-15-75892168-75892231.0	63	**Scrib-Fa**	TGTAGGGGGTAGAGCCTTTTC	**Scrib-Ra**	GAGGAGGAGGAGGAGGAGAA
Traf6	CA-CA-2-101520982-101521184	203	**Traf6-F**	AAGCCTTCCCAGTTGGTTGT	**Traf6-R**	GCAGTCACTGGACGACTGG
Arfgap1	AA-AA-2-180702238-180702306.0	213 (281)	**Arfgap1-F**	CTAGTCCAGCTTGGCACCTC	**Arfgap1-R**	ATCCTGTGCCCGGACTTC
Clta	CA-CA-4-44043086-44043140.1	54+36	**Clta-F**	GGAGCTGGAAGAGTGGTATGC	**Clta-R**	CTGGGGATGACTCGTCAATG
Erc1	CA-CS-6-119728005-119728089.0	84	**Erc1-Fa**	GGGACTCTTTCAGCACCTCA	**Erc1-Ra**	GGGAGGAAGAGATGAAGCAA
Gapvd1	AD-AD-2-34572772-	63	**Gapvd1-Fa**	AGCTGCAGTGCTT	**Gapvd1-Ra**	AAACATGCAGCT

	34572835.0			CAACTCC		TTCGGATG
Itsn2	CA-CA-12-4647718-4647799.0	93	**Itsn2-Fa**	GAAAAGGAAGAATTATGCCAAAGA	**Itsn2-Ra**	TGTTCAAGGGCTAACTGCTG
Cltc	CA-CS-11-86509151-86509192.0	21	**Cltc-Fa**	GGGCTGTGTCTCTGTAGCTTG	**Cltc-Ra**	CAGATGTCGTCCTGGAAACC
Arhgap17	CA-CA-7-130428933-130428981.1	47	**Arhgap17-Fa**	TGTCATTGTCTATGTCCAGCAG	**Arhgap17-Ra**	TTACATCCTCAGTGCCCACA
Ap2a1	IR-IR-7-52158208-52158343.0	66	**Ap2a1-Fa**	GAATGGGAGGGCCTATGTC	**Ap2a1-Ra**	CCTCCTGGTGGATGTCTTCT

Supplementary Table 8. Sequences of the primers (SIGMA) used for validation in ventricles.

Gene symbol	**id**	**AS region (nt)**	**Forward primer**		**Reverse primer**	
Ap1b1	CA-CA-11-4933244-4933265.1	21	**Ap1b1-F**	TCAGCCTGATGTCATTCCTG	**Ap1b1-R**	CTGATGGGTGCTCCAAGTCT
Ap2a1	CA-CA-7-52158831-52158897.0	66	**Ap2a1-F**	GTAGGCGGGAACCTCCTG	**Ap2a1-R**	TTATTCAACAGTTCATCTGCTTCTG
Arfgap1	CA-CA 2-180702239-180702519	213 (281)	**Arfgap1-F**	CTAGTCCAGCTTGGCACCTC	**Arfgap1-R**	ATCCTGTGCCCGGACTTC
Arfgap2	CA-CA-2-91109226-91109268.0	42	**Arfgap2-F**	CCTGAACAAGGCCCTAACAC	**Arfgap2-R**	TAGCGGCTGCTGGCTTCT
Arhgap17	CA-CA-7-130437985-130438219.0	234	**Arhgap17-F**	ATTTGTGCCACTTGCTACCC	**Arhgap17-R**	TCTGGTTGCTGTTCCTTCCT
Asap1	CA-CA-15-63942468-63942638	171	**Asap1-F**	CACAGATTTGCCCACATCAC	**Asap1-R**	ACAGCCCCTCAAACTTGTTG
Clta	CA-CA-4-44044271-44044307.1	54+36	**Clta-F**	GCGATAAAGGAGCTGGAAGA	**Clta-R**	GTTTGCTGGACTTGGGGTTA
Cltc	CA-CA-11-86514562-86514583.0	21	**Cltc-F**	GAAACCGCATGGAGACATAA	**Cltc-R**	AAACAATGGGCTGTGTCTCTG
Dnm1l	CA-CA-16-16341515-16341561	47 (+39)	**Dnm1l-F**	AGAGCTCAGTGCTGGAAAGC	**Dnm1l-R**	TTTTCAATTTCTTGTCGAATTTCA
Erc1	CA-CS-6-119728005-119728089.0	84	**Erc1-F**	GGGAGGAAGAGATGAAGCAA	**Erc1-R**	GGGACTCTTTCAGCACCTCA
Gapvd1	AD-AD-2-34572772-34572835.0	63	**Gapvd1-F**	AAACATGCAGCTTTCGGATG	**Gapvd1-R**	AGCTGCAGTGCTTCAACTCC
Itsn2	CA-CA-12-4647718-4647799.0	93	**Itsn2-F**	GAAAAGGAAGAATTATGCCAAAGA	**Itsn2-R**	TGTTCAAGGGCTAACTGCTG
Mdm2	CA-CA-10-117146756-117146840	131 or 85	**Mdm2-F**	GGACCCTCTCGGATCACC	**Mdm2-R**	CGCTCCAACGGACTTTAACA
Nedd4l	CA-CA-18-65341136-65341190.0	54	**Nedd4l-F**	CTGGCTGGGAAGAGAGGAT	**Nedd4l-R**	TGATGGCTGGGTTCTGTAGTC
Scrib	CA-CA-15-75879886-75879970.0	84	**Scrib-F**	GACCACCGGAGGGAAGAC	**Scrib-R**	CTGGGTAGCACTGTTCTCAGG
Snap23	CA-CA-2-120416398-120416431.0	33	**Snap23-F**	AGAAGAAGGCATGGACCAAA	**Snap23-R**	AGTTTGCTGAGGCTGACCAT
Tmed2	CA-CA-5-124993495-124993516.0	21	**Tmed2-F**	GGATGTCCACTATGACTCCAAA	**Tmed2-R**	TCCCGGACTTCCATGTACTC
Traf6	CA-CA-2-101520982-101521184	203	**Traf6-F**	AAGCCTTCCCAGTTGGTTGT	**Traf6-R**	GCAGTCACTGGACGACTGG
Trip10	CA-CA-17-57396282-57396450.0	168	**Trip10-F**	CCAGGGGACTTGGAATTTG	**Trip10-R**	CCTTCTGCAACTCTCGGTTC

Supplementary Table 9. Sequences of the primers (SIGMA) used for validation of AS events on vesicular trafficking related genes.