

1 **Supplementary Table 1. Significantly enriched exonic motifs in cardiac**
2 **hypertrophy.**

Exon exclusion			Exon inclusion			
Motif	<i>p</i> -value*		Motif	<i>p</i> -value*		
	3'UTR	Alternative terminal exon		5'UTR	Alternative promoter	Intron retention
AATAAA	3.19E-171	2.03E-10	GGCGGC	2.19E-61	0.190828	9.09E-06
TTTTTA	4.33E-119	7.05E-08	GCGGCG	1.58E-58	0.199917	0.001268
TTTTAA	5.71E-118	5.02E-07	CGCCGC	1.12E-52	0.228677	0.001352
TTTTCT	7.83E-113	5.24E-06	GCGCGG	1.35E-51	0.412408	0.000755
TTTAAA	5.83E-112	3.11E-05	CGGCGG	1.11E-48	0.437487	8.19E-05
ATTTTT	4.30E-110	1.71E-07	CGGCCG	3.44E-46	1	0.00374
TGTTTT	7.97E-110	1.13E-05	CCGCCG	3.62E-46	0.686154	0.024498
TATTTT	2.53E-104	5.15E-08	GGGCGG	3.92E-46	0.369626	0.000499
TTTTGT	5.99E-104	3.43E-07	GCGGCC	5.95E-46	0.575761	0.019626
TTTTTT	2.15E-102	1.13E-05	GCGGGC	1.47E-45	0.14722	0.006008
CTTTTT	2.93E-98	1.43E-05	GGCCGC	2.31E-43	0.554333	6.16E-08
TTTCTT	3.72E-98	2.30E-07	GCCGGG	3.02E-42	0.547038	0.016482
TTCTTT	6.85E-98	3.06E-06	GCGGGG	2.64E-41	0.206065	0.010655
TTAAAA	2.66E-94	2.77E-06	GGCGGG	2.83E-38	0.67022	0.00254
TTTTAT	3.97E-94	1.49E-07	GGCCGG	5.44E-38	0.158473	0.000755
TAAAAT	1.22E-93	2.02E-07	GCGGAG	2.46E-37	0.773159	4.17E-06
GTTTTT	1.07E-90	2.85E-06	CCGGGC	5.18E-37	0.14722	0.006008
TTGTTT	2.23E-89	1.33E-06	CGGAGC	5.90E-36	0.237493	0.013686
TTTGTT	3.49E-89	1.28E-07	CGGGGC	1.70E-35	0.027484	0.002408
TTATTT	2.75E-88	3.64E-06	CCCGGG	5.63E-35	0.023481	0.270354
TTTTTC	1.20E-87	3.73E-08	CCGGAG	1.05E-33	0.296193	0.020468
TTTTTG	3.21E-87	1.13E-05	CGGGCC	4.91E-33	0.8283	0.00177
TAAAAA	2.26E-86	1.02E-04	GCCCGG	9.79E-31	0.038378	0.038533
TTTGTA	1.94E-85	2.67E-03	CGCAGC	1.25E-27	0.130908	0.035114
CATTTT	2.06E-82	4.75E-03				
ATTTTA	4.52E-82	5.26E-06				
TCTTTT	5.25E-82	1.61E-05				
AATTTT	2.54E-75	1.43E-02				
AAAAAA	3.65E-68	2.77E-06				

3 *p*-value* indicates the significance value for enrichment analysis (Fisher's exact test)

1 **Supplementary Table 2. Summary of the intronic motifs significantly enriched**
 2 **in excluded or included exons in cardiac hypertrophy**

	Motif	Position	p-value¹	p-value²	Splicing factors	PMID	
	AGAGGG	143~147 (R4)	0.045103	0.0315			
	AGGCTG	0~4 (R1)	0.01287	0.03587			
	CAGCTG	208~212 (R2)	0.025321	0.013109	USF2delta	90370211	
	CCCTCC	488~492 (R4)	0.037716	0.046382	hnRNP K/J	12003487	
	CCTGGC	8~12 (R3)	0.046465	0.042673			
	GCTGCT	61~65 (R1)	0.036453	0.020548	MBNL	20071745	
	GGAGAG	15~19 (R1)	0.006351	0.022109	SRp30c	11875052	
	GGAGGG	38~42 (R2)	0.007296	0.017052	SRp40	9037021	
	GGGCAG	1~5 (R1)	0.016084	0.03938			
Exon exclusion		13~17 (R1)	0.014523	0.038004			
		20~24 (R1)	0.016389	0.048258			
	★GGTGGG	34~38 (R1)	0.040825	0.029634	SC35, ASF/SF2, ESRP	15247216, 11421362, 20711167 22354987	
		11~15 (R2)	0.012338	0.011898			
		19~23 (R3)	0.038408	0.035493			
		20~24 (R1)	0.038327	0.047022			
		18~22 (R3)	0.037389	0.034898			
		TCCCCA	73~77 (R1)	0.048935	0.024412	hnRNP K	11278705
			74~78 (R2)	0.039366	0.048444		19258514
		★TTCTTC	26~30 (R3)	0.020511	0.016068	9G8 PTB	10094314 17626050
	CTCTCC	485~489 (R2)	0.025637	0.019643			
	GTGCTG	3~7 (R1)	0.013583	0.04021			
Exon inclusion		TCCCCT	493~497 (R2)	0.022936	0.016185	SC30 PyRo 1	10629063 10871347
		TCTCCC	486~490 (R2)	0.032101	0.014864		
		TCTCCT	486~490 (R2)	0.040956	0.045046		
		TTGTCT	490~494 (R2)	0.046875	0.049789		
		TTGTGT	488~492 (R2)	0.038801	0.022055	CUGBP2	19680430

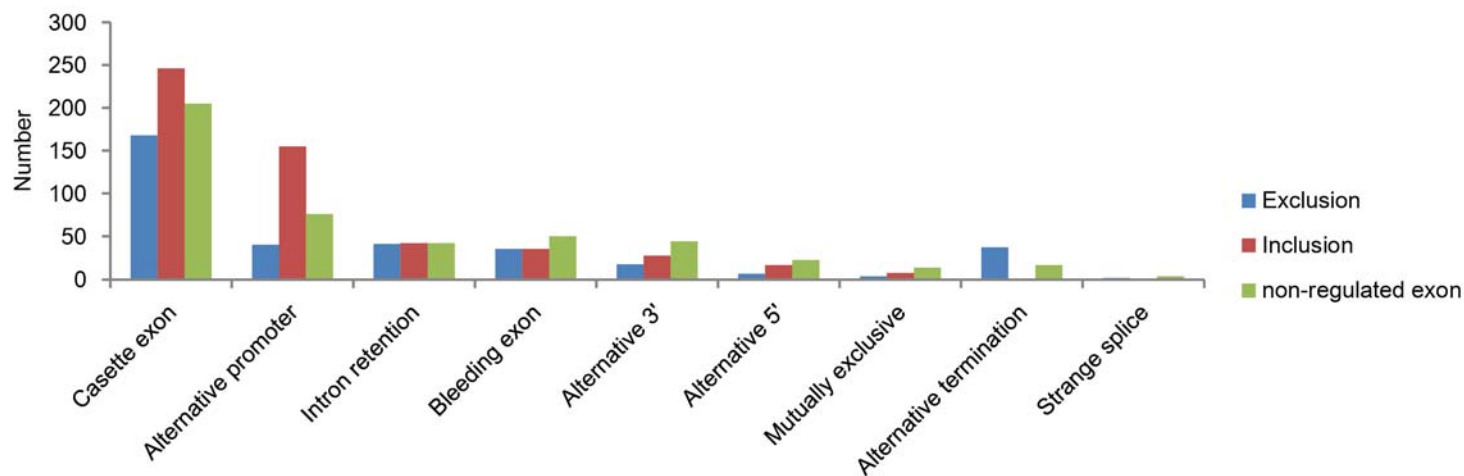
3 *p*-value¹ indicates the significance value for the comparison between exclude exons and
 4 included exons

5 *p*-value² indicates the significance value for the comparison between exon variants and non-
 6 regulated exons.

7 R1~R4 indicates the intronic region surrounding the exon variants. Schematic view of
 8 R1~R4 is illustrated in Fig. 2A.

9 ★, representative motifs displayed in Fig. 2B-2C.

1 **Supplementary Figure 1**

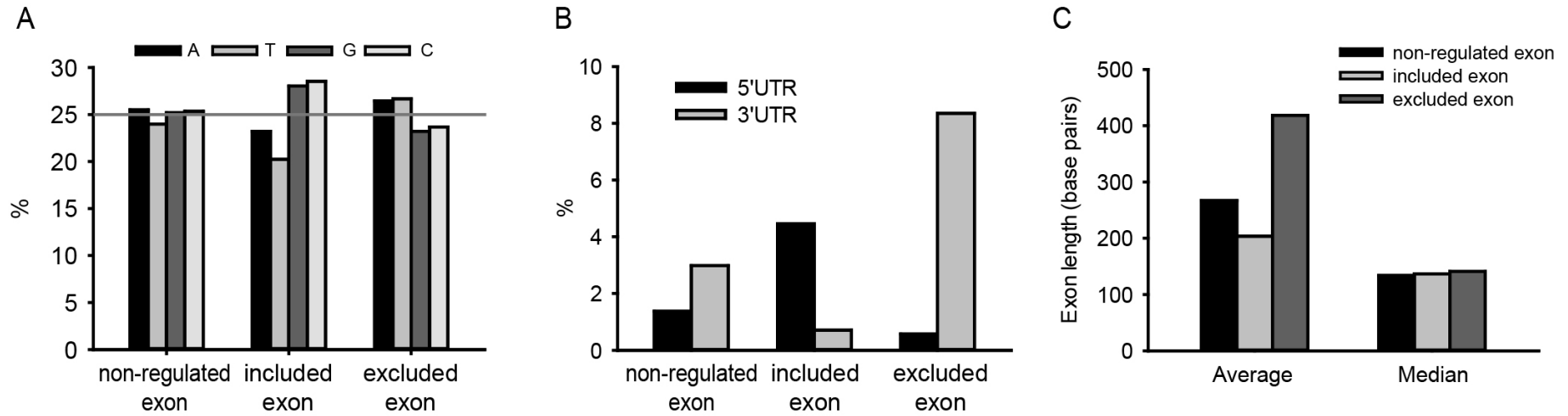


2

3 Supplementary Figure 1. Distribution of alternative splicing types of the exons excluded, included and non-regulated. Alternative
4 splicing types were analyzed based on UCSC 'knownAlt' track and ASTD (Alternative Splicing and Transcript Diversity Database)
5 information.

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1 **Supplementary Figure 2**

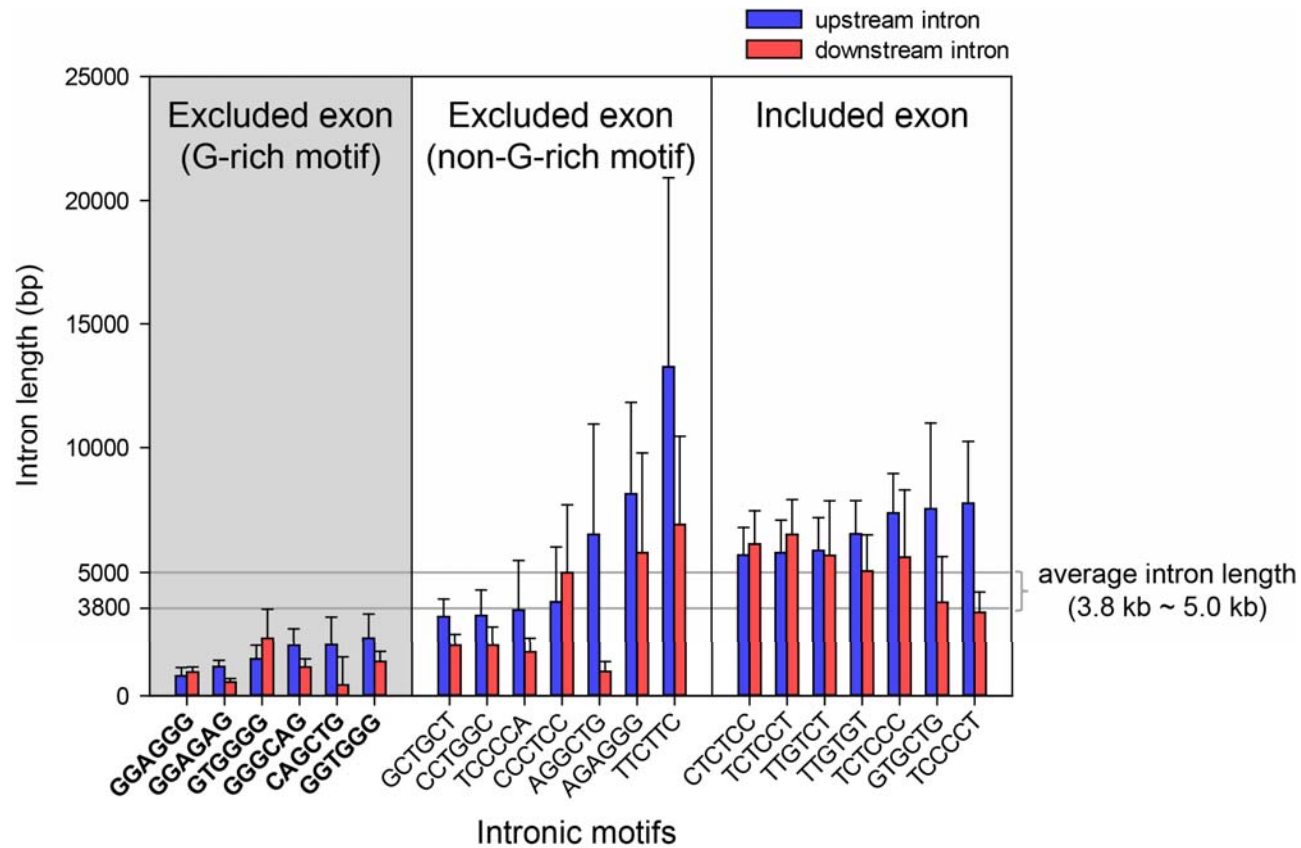


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3 Supplementary Figure 2. The properties of exon variants and non-regulated exons. (A) Nucleotide composition of the exon
4 variants and non-regulated exons. (B) Percentage of 5' or 3'UTR in exon variants and non-regulated exons. (C) Average and
5 median length of exon variants and non-regulated exons.

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1 **Supplementary Figure 3**



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3 Supplementary Figure 3. Length of upstream and downstream introns of excluded/included exons containing the intronic motifs.
 4 Bars represent means \pm SEM. Lengths of the introns, which are flanking the excluded exon and contain the G-rich intronic motifs,
 5 are much shorter than the average intron length of mouse.