Supplementary Table 2. Genes differentially downregulated in carvedilol-treated mouse hearts.

Seqname	GeneSymbol	Microarray	Real-time PCR
		(Carv/DMSO)	Fold Change
NM_001098230	Pdp1	0.50	UT
NM_177580	Baiap2l2	0.50	UT
NM_001033369	Acvr1c	0.50	UT
NM_172378	BC026439	0.50	UT
NM_001159319	Cacnb1	0.50	0.65*
NM_010254	Galr2	0.51	UT
NM_001172107	Gramd1c	0.51	UT
NM_028667	D3Ertd751e	0.52	UT
NM_001168404	Ankrd55	0.52	UT
NM_001199785	Zfp839	0.52	UT
NM_177823	Ubash3a	0.52	UT
NM_212436	Olfr301	0.52	UT
NM_181750	R3hdm1	0.53	UT
NM_053079	Slc15a1	0.53	UT
NM_001167996	1110032F04Rik	0.53	UT
NM_007418	Adra2c	0.53	UT
NM_010774	Mbd4	0.53	UT
NM_001005370	Spin2	0.53	UT
NM_183262	Stk35	0.53	UT
NM_009301	Svs5	0.53	UT
NM_001008798	Whrn	0.54	UT
NM_001161539	Islr2	0.54	UT
NM_013905	Heyl	0.54	UT
NM_023709	Capn9	0.55	UT
NM_008171	Grin2b	0.55	UT
NM_001039243	Gm7092	0.55	UT
NM_026253	Lrrc18	0.55	UT
NM_028889	Efhd1	0.55	UT
NM_146162	Tmem119	0.55	UT
NM_001111027	Runx1t1	0.55	1.03
NM_172961	Abat	0.55	UT
NM_027548	Serpinb7	0.55	UT
NM_001037878	Tcf25	0.55	UT
NM_001001496	Gja6	0.56	UT
NM_028176	Cda	0.56	UT
NM_025673	Golph3	0.56	0.89

NM_030137	Cstad	0.56	UT
NM_001115009	Synrg	0.56	UT
NM_001081441	Wdr86	0.56	UT
NM_080637	Nme5	0.56	UT
NM_029628	Ppp1r3g	0.56	UT
NM_177625	Ttc5	0.57	UT
NM_018763	Chst2	0.57	0.1***
NM_199148	BC051665	0.57	UT
NM_001164169	Pias2	0.57	UT
NM_001109764	Ctnna2	0.57	UD
NM_026252	Cpeb4	0.57	UT
NM_001029985	Kcp	0.57	UT
NM_001134465	Fam116a	0.57	UT
NM_025807	Slc16a9	0.57	UT
NM_001163581	Prom1	0.58	UT
NM_153382	Lats2	0.58	UT
NM_001014390	Dyrk2	0.58	UT
NM_173391	Tph2	0.58	UT
NM_007511	Atp7b	0.58	UT
NM_001101431	2510049J12Rik	0.58	UT
NM_007705	Cirbp	0.59	UT
NM_172588	Serinc5	0.59	UT
NM_001034059	Ccdc160	0.59	UT
NM_177348	Ifne	0.59	UT
NM_008245	Hhex	0.60	UT
NM_001162926	Fam84b	0.60	UT
NM_010921	Nkx3-1	0.60	UT
NM_001168578	Tceal8	0.60	UT
NM_023143	C1ra	0.60	UT
NM_053144	Pcdhb19	0.60	UT
NM_016905	Galk1	0.60	1.02
NM_028331	C1qtnf6	0.61	UT
NM_177391	Fam109b	0.61	UT
NM_177186	Slc35e2	0.61	UT
NM_145395	Duoxa1	0.61	UT
NM_178218	Hist3h2a	0.61	UT
NM_198647	Tbc1d22b	0.61	UT
NM_144520	Sec14l2	0.61	UT
NM_177394	A730011L01Rik	0.61	UT
NM_194060	Foxo6	0.61	UT
NM_009661	Alox8	0.62	UT

NM_008269	Hoxb6	0.62	UT
NM_027721	Katnal2	0.62	UT
NM_183088	Scand3	0.62	UT
NM_176838	Esrp2	0.62	UT
NM_133853	Magi3	0.62	UT
NM_177748	Kir3dl2	0.62	UT
NM_145379	Mrgprf	0.62	UT
NM_023898	Pde6h	0.62	UT
NM_181490	Cldn17	0.62	UT
NM_152814	Zfp566	0.62	UT
NM_025739	Rnf220	0.63	UT
NM_015799	Trfr2	0.63	UT
NM_001110337	Gprc5c	0.63	UT
NM_207668	Acpp	0.63	UT
NM_001012324	Ecm2	0.63	UT
NM_027026	Lrrc46	0.63	UT
NM_001005424	Gm996	0.63	UT
NM_001164523	Omt2a	0.63	UT
NM_172264	Chdh	0.63	UT
NM_145124	Mib2	0.63	UT
NM_172565	Klhl11	0.63	UT
NM_009189	Six1	0.63	UT
NM_001159354	Magi3	0.63	UT
NM_054042	Cd248	0.63	UT
NM_001007578	Armcx6	0.64	UT
NM_001083118	Terf2	0.64	UT
NM_027046	Ccdc54	0.64	UT
NM_027195	Casz1	0.64	UT
NM_001145390	Gm766	0.64	UT
NM_001177600	Adam23	0.64	UT
NM_001083894	Liph	0.64	UT
NM_027120	Itgb1bp3	0.64	UT
NM_024290	Tnfrsf23	0.65	UT
NM_033264	Arpp21	0.65	UT
NM_001081060	Slc9a3	0.65	0.82
NM_001191004	Lsm6	0.65	UT
NM_026075	Srek1ip1	0.65	UT
NM_134028	Tubg2	0.65	UT
NM_001033158	Rasl12	0.65	UT
NM_001141983	Golga7b	0.65	UT
NM_001163144	Pcsk5	0.65	UT

NM_008538	Marcks	0.65	UT
NM_178879	B3gnt9-ps	0.65	UT
NM_153049	Mkl1	0.65	UT
NM_010690	Lats1	0.65	UT
NM_023850	Chst1	0.65	UT
NM_177049	Jph4	0.65	UT
NM_017377	B4galt2	0.65	0.79
NM_175331	Nt5dc3	0.65	UT
NM_199200	Fam171a2	0.65	UT
NM_025285	Stmn2	0.65	UT
NM_027061	Zpbp2	0.66	UT
NM_018862	Agpat1	0.66	UT
NM_173027	Ip6k3	0.66	UT
NM_175525	D630042P16Rik	0.66	UT
NM_027622	Tex19.2	0.66	UT
NM_001166537	Hmga1	0.66	UT
NM_175546	Wdfy2	0.66	UT
NM_001166250	Mgll	0.66	UT
NM_009056	Rfx2	0.66	UT
NM_007453	Prdx6	0.66	UT
NM_145399	Scgn	0.66	UT
NM_009751	Bfsp1	0.66	UT
NM_001198971	BC049352	0.66	UT
NM_013796	Nagpa	0.66	UT
NM_028426	3110007F17Rik	0.66	UT
NM_198160	Smarcc2	0.67	UT
NM_177632	Fam43a	0.67	UT

The expression of eight indicated genes, which were identified by microarray analysis (Figure 1) and categorized into pathways involved in transcriptional misregulation [runx1t1 and golph3], galactose metabolism [galk1], mineral absorption [slc9a3], glycosaminoglycan biosynthesis-keratan sulfate [chst2 and b4galt2], or arrhythmogenic right ventricular cardiomyopathy [cacnb1 and ctnna2] (Figure 6B), was verified by using real-time RT-PCR analysis. Fold change values represent mean of expression levels from three (microarray) or six (real-time PCR) independent mice per group. Red color means that those genes are significantly downregulated by carvedilol (Carv) compared to vehicle control (DMSO) in both microarray and real-time PCR analyses. UD: undetectable; UT: untested. *, $P < 0.05$ vs. DMSO; . ***, $P < 0.001$ vs. DMSO.