

**Table S1 Summary of morphological and functional parameters of selected CC strains based on echocardiographic images  
12-week-old male mice in homeostasis**

Strain / Parameter*	BWT (g)	LV Mass (mg)	ENDarea;d (mm <sup>2</sup> )	ENDarea;s (mm <sup>2</sup> )	EPIarea;d (mm <sup>2</sup> )	EPIarea;s (mm <sup>2</sup> )	Heart Length;d (mm)	Heart Length;s (mm)	FAC (%)	EF (%)	Stroke Volume (μL)	LV Volume;d (μL)	LV Volume;s (μL)	LVPW;d (mm)	LVPW;s (mm)	PA Peak Pressure (mm Hg)
129X1/SvJArc (10)	28.6 ± 1.7	95.17 ± 7.27	13.30 ± 0.93	7.41 ± 1.12	24.64 ± 1.34	20.23 ± 1.60	7.29 ± 0.18	6.56 ± 0.16	44.44 ± 5.02	51.91 ± 4.80	34.94 ± 2.75	67.60 ± 4.78	32.65 ± 5.14	0.70 ± 0.03	1.00 ± 0.04	2.34 ± 0.34
A/JArc (11)	24.1 ± 1.1	69.42 ± 8.47	9.62 ± 0.46	5.09 ± 0.36	18.90 ± 1.25	15.61 ± 0.87	6.63 ± 0.19	6.06 ± 0.15	46.96 ± 4.39	53.29 ± 3.47	25.67 ± 2.04	48.20 ± 3.10	22.54 ± 2.47	0.65 ± 0.06	1.04 ± 0.08	2.32 ± 0.44
C57BL/6JArc (9)	26.3 ± 1.9	82.82 ± 7.05	13.13 ± 0.90	8.03 ± 0.92	22.30 ± 3.48	18.18 ± 3.75	6.97 ± 0.11	6.41 ± 0.16	38.86 ± 6.31	47.33 ± 4.91	32.04 ± 3.09	67.82 ± 4.01	35.78 ± 4.40	0.68 ± 0.06	0.97 ± 0.08	2.00 ± 0.38
NOD/ShiLtJArc (11)	26.3 ± 2.2	78.95 ± 11.10	11.34 ± 0.74	5.63 ± 0.84	21.31 ± 1.71	17.49 ± 1.67	7.05 ± 0.19	6.25 ± 0.26	50.37 ± 6.51	57.53 ± 5.76	32.77 ± 3.84	56.91 ± 3.55	24.14 ± 3.63	0.73 ± 0.07	1.14 ± 0.10	2.63 ± 0.54
BEM_AG (12)	30.7 ± 3.3	88.85 ± 5.60	10.80 ± 1.15	5.38 ± 1.11	22.16 ± 1.76	18.52 ± 1.42	6.99 ± 0.25	6.51 ± 0.17	50.57 ± 6.13	56.98 ± 6.05	30.99 ± 2.56	54.90 ± 6.71	23.91 ± 5.90	0.82 ± 0.06	1.42 ± 0.13	2.48 ± 0.49
BOM_GB (15)	23.1 ± 1.7	89.92 ± 9.01	11.57 ± 1.16	6.49 ± 0.90	23.81 ± 1.91	20.48 ± 1.85	6.42 ± 0.23	5.89 ± 0.23	43.93 ± 5.69	51.03 ± 4.89	30.99 ± 3.86	54.90 ± 5.47	23.91 ± 3.77	0.80 ± 0.09	1.16 ± 0.11	2.97 ± 0.55
BOON_HF (10)	30.2 ± 2.0	98.57 ± 10.19	12.14 ± 0.88	7.27 ± 0.49	23.97 ± 1.36	20.11 ± 0.99	7.36 ± 0.17	6.85 ± 0.19	39.90 ± 4.46	46.14 ± 3.61	31.34 ± 3.49	67.06 ± 5.65	35.72 ± 3.80	0.78 ± 0.07	1.14 ± 0.09	2.44 ± 0.33
CIS_AD (8)	24.9 ± 2.4	99.55 ± 9.10	11.23 ± 1.21	5.94 ± 1.05	23.19 ± 1.96	19.39 ± 1.59	7.40 ± 0.31	6.69 ± 0.20	47.35 ± 5.44	55.03 ± 5.01	33.80 ± 4.64	61.54 ± 7.99	27.74 ± 5.24	0.87 ± 0.06	1.27 ± 0.11	2.37 ± 0.40
DAVIS_BA (6)	23.8 ± 0.9	93.59 ± 9.51	12.04 ± 0.49	7.73 ± 0.23	23.45 ± 0.71	19.54 ± 1.26	7.29 ± 0.11	6.61 ± 0.15	35.68 ± 4.25	43.30 ± 5.05	29.44 ± 5.22	67.58 ± 4.73	38.14 ± 0.58	0.71 ± 0.08	1.07 ± 0.09	3.02 ± 0.40
DOD_AH (6)	32.0 ± 2.3	106.97 ± 8.96	12.28 ± 1.37	6.67 ± 0.64	24.79 ± 2.12	21.32 ± 2.26	7.66 ± 0.19	7.12 ± 0.31	45.55 ± 1.40	52.16 ± 1.49	32.75 ± 5.31	59.21 ± 6.49	28.11 ± 2.50	0.97 ± 0.09	1.41 ± 0.13	1.97 ± 0.45
DONNELL_HA (7)	26.4 ± 2.1	74.51 ± 10.31	9.18 ± 0.78	5.49 ± 0.72	19.47 ± 1.53	17.10 ± 1.43	6.37 ± 0.27	5.87 ± 0.19	40.05 ± 5.58	46.13 ± 6.33	20.52 ± 2.41	44.67 ± 3.01	24.15 ± 3.87	0.79 ± 0.13	1.24 ± 0.19	1.61 ± 0.49
FEW_FD (11)	24.8 ± 1.5	101.91 ± 7.96	11.32 ± 1.02	6.00 ± 0.93	23.79 ± 1.82	20.15 ± 2.18	7.36 ± 0.22	6.82 ± 0.23	47.17 ± 4.81	53.13 ± 4.95	33.38 ± 3.54	63.14 ± 7.64	29.76 ± 6.09	0.98 ± 0.07	1.55 ± 0.15	2.56 ± 0.47
FIM_DF (11)	23.9 ± 2.5	73.15 ± 11.41	10.06 ± 1.71	6.45 ± 1.13	19.66 ± 3.05	17.04 ± 2.38	6.75 ± 0.31	6.06 ± 0.27	35.70 ± 6.49	44.28 ± 6.57	22.94 ± 6.65	51.46 ± 9.85	28.52 ± 4.94	0.68 ± 0.09	0.98 ± 0.16	2.58 ± 1.09
FIV_AC (10)	25.8 ± 2.3	95.20 ± 7.56	9.98 ± 0.98	4.74 ± 0.54	22.07 ± 0.99	18.80 ± 1.24	6.95 ± 0.23	6.26 ± 0.24	58.88 ± 4.80	58.85 ± 4.73	29.17 ± 3.08	49.53 ± 2.83	20.36 ± 2.46	0.83 ± 0.06	1.34 ± 0.10	1.60 ± 0.32
GALASUPREME_CE (9)	28.1 ± 3.6	92.20 ± 11.20	9.92 ± 0.55	6.35 ± 0.19	20.80 ± 1.31	19.49 ± 1.21	7.56 ± 0.16	7.18 ± 0.27	35.81 ± 3.98	41.05 ± 4.65	20.87 ± 3.42	50.70 ± 3.78	29.83 ± 2.25	0.87 ± 0.06	1.14 ± 0.10	1.70 ± 0.35
GIG_EF (13)	27.7 ± 1.8	81.62 ± 11.76	11.30 ± 1.12	5.88 ± 0.76	21.72 ± 2.00	18.18 ± 1.71	6.92 ± 0.41	6.39 ± 0.36	48.03 ± 3.36	54.00 ± 2.95	31.47 ± 4.02	58.39 ± 7.47	26.92 ± 4.25	0.78 ± 0.06	1.25 ± 0.08	4.27 ± 1.57
GIT_GC (5)	33.1 ± 1.3	89.97 ± 6.97	12.27 ± 0.99	8.90 ± 1.21	24.12 ± 1.49	21.43 ± 1.73	6.6 ± 0.19	6.34 ± 0.12	27.70 ± 4.83	32.67 ± 3.77	20.83 ± 1.86	64.15 ± 6.29	43.32 ± 6.07	0.73 ± 0.10	0.95 ± 0.012	2.56 ± 0.70
HAZ_FE (6)	19.4 ± 1.3	81.38 ± 8.00	11.90 ± 0.82	6.46 ± 0.46	22.24 ± 1.28	18.35 ± 1.83	6.96 ± 0.18	6.34 ± 0.16	44.77 ± 1.67	49.49 ± 3.69	31.51 ± 2.38	63.85 ± 5.47	32.34 ± 4.68	0.68 ± 0.08	1.02 ± 0.015	3.41 ± 0.73
JUNIOR_GB (6)	23.2 ± 3.4	86.80 ± 11.59	9.67 ± 1.16	5.76 ± 0.90	20.41 ± 1.82	17.21 ± 1.66	7.30 ± 0.47	6.69 ± 0.46	40.52 ± 5.77	47.22 ± 5.54	25.10 ± 3.09	53.53 ± 7.35	28.44 ± 5.95	0.84 ± 0.11	1.20 ± 0.16	2.24 ± 0.52
LUZ_FH (5)	23.1 ± 1.6	89.68 ± 7.61	11.32 ± 0.99	5.79 ± 0.55	23.27 ± 1.35	20.05 ± 1.27	6.50 ± 0.10	5.76 ± 0.13	48.72 ± 4.59	57.17 ± 3.56	27.82 ± 1.60	48.71 ± 2.21	20.89 ± 2.37	0.76 ± 0.04	1.05 ± 0.07	3.15 ± 0.52
MERCURI_HF (5)	28.0 ± 3.5	92.71 ± 10.26	11.86 ± 0.96	7.16 ± 0.78	23.56 ± 1.33	20.50 ± 0.75	7.00 ± 0.34	6.53 ± 0.44	39.68 ± 4.86	45.14 ± 4.59	27.44 ± 3.41	60.89 ± 5.63	33.45 ± 4.56	0.73 ± 0.04	1.02 ± 0.07	2.08 ± 0.45
NUK_AC (11)	32.4 ± 2.5	113.42 ± 7.98	12.58 ± 1.46	7.38 ± 1.15	26.32 ± 1.87	23.39 ± 1.86	7.22 ± 0.42	6.75 ± 0.39	38.19 ± 6.87	46.22 ± 6.25	30.64 ± 5.85	66.27 ± 8.74	35.62 ± 6.05	0.87 ± 0.11	1.31 ± 0.14	1.86 ± 0.72
PAT_CD (6)	25.5 ± 1.2	102.58 ± 7.53	13.93 ± 0.97	8.30 ± 1.34	26.12 ± 1.12	22.21 ± 1.15	7.42 ± 0.19	6.81 ± 0.21	40.58 ± 7.09	46.82 ± 7.41	34.83 ± 6.06	74.38 ± 6.47	39.55 ± 6.80	0.79 ± 0.12	1.15 ± 0.17	2.47 ± 0.74
PEF_EC (11)	30.3 ± 1.8	83.56 ± 6.40	9.77 ± 0.78	4.81 ± 0.26	21.49 ± 0.58	18.54 ± 1.00	6.17 ± 0.30	5.54 ± 0.32	50.68 ± 2.51	59.37 ± 1.45	25.45 ± 2.03	42.88 ± 3.46	17.44 ± 1.65	0.92 ± 0.12	1.38 ± 0.16	2.83 ± 0.48
POH_DC (5)	27.5 ± 1.3	90.31 ± 10.86	9.75 ± 0.56	5.05 ± 0.14	21.45 ± 1.50	17.65 ± 1.25	6.80 ± 0.26	6.41 ± 0.14	48.01 ± 4.35	52.52 ± 4.85	26.26 ± 5.66	49.65 ± 6.71	23.40 ± 2.18	0.75 ± 0.05	1.22 ± 0.12	2.66 ± 0.84
PUB_CD (6)	23.0 ± 2.2	64.39 ± 5.82	9.09 ± 0.90	5.47 ± 0.92	18.60 ± 1.44	15.68 ± 1.65	5.92 ± 0.25	5.54 ± 0.26	40.04 ± 6.79	46.63 ± 6.37	16.86 ± 1.90	36.42 ± 3.96	19.56 ± 4.01	0.65 ± 0.07	0.95 ± 0.10	2.09 ± 0.73
SAT_GA (9)	28.7 ± 2.2	16.61 ± 4.08	11.06 ± 0.25	7.77 ± 0.64	23.23 ± 0.89	20.95 ± 0.61	36.60 ± 5.66	6.84 ± 0.46	36.86 ± 5.47	36.73 ± 5.56	19.20 ± 3.49	52.38 ± 6.72	33.18 ± 5.68	6.38 ± 0.24	0.82 ± 0.07	2.04 ± 0.33
TAS_FE (7)	18.7 ± 1.5	53.58 ± 5.75	8.98 ± 0.82	6.16 ± 0.65	16.42 ± 0.84	14.20 ± 0.79	6.44 ± 0.26	6.01 ± 0.20	31.15 ± 6.30	38.36 ± 4.98	15.89 ± 3.05	41.96 ± 5.02	26.23 ± 2.91	0.56 ± 0.07	0.82 ± 0.10	1.34 ± 0.23
TOFU_FB (13)	25.4 ± 1.6	81.15 ± 4.97	9.03 ± 3.25	5.30 ± 0.74	20.07 ± 1.39	17.38 ± 1.26	6.69 ± 0.13	6.33 ± 0.17	41.53 ± 4.41	47.44 ± 5.69	21.71 ± 1.32	46.16 ± 4.51	24.45 ± 4.86	0.85 ± 0.12	1.26 ± 0.20	3.14 ± 0.74
TOP_DA (8)	26.0 ± 1.9	98.73 ± 11.23	12.76 ± 0.86	7.20 ± 0.67	24.83 ± 2.00	21.17 ± 1.54	7.02 ± 0.30	6.45 ± 0.27	43.55 ± 3.86	50.20 ± 4.61	32.69 ± 3.33	66.83 ± 4.48	33.25 ± 3.71	0.82 ± 0.11	1.22 ± 0.14	2.61 ± 0.64
WAB2_DH (8)	24.0 ± 1.0	81.70 ± 5.94	10.05 ± 0.54	6.34 ± 0.48	20.66 ± 0.87	17.80 ± 0.89	6.82 ± 0.17	6.29 ± 0.18	36.89 ± 4.10	43.93 ± 3.07	22.16 ± 3.12	50.37 ± 5.15	28.22 ± 2.99	0.87 ± 0.06	1.18 ± 0.08	1.76 ± 0.45
YOX_DE (6)	26.4 ± 1.3	78.64 ± 4.63	12.91 ± 0.62	8.18 ± 0.55	23.09 ± 0.56	19.83 ± 0.69	6.79 ± 0.19	6.14 ± 0.18	36.73 ± 1.96	44.23 ± 3.11	29.19 ± 2.60	65.94 ± 2.58	36.76 ± 2.26	0.67 ± 0.04	0.94 ± 0.06	2.92 ± 0.39

\* Data is presented as mean value ± standard deviation (SD). Number of biological replicates is indicated in brackets next to the strain name. Parameter definitions are provided below in “Ultrasound measurements and calculations” section.

**Table S2 Summary of morphological and functional parameters of selected CC strains based on echocardiographic images  
16-week-old male mice one month after MI**

Strain / Parameter*	BWT (g)	AreaDist;d (mm <sup>2</sup> )	AreaDist;s (mm <sup>2</sup> )	AreaMid;d (mm <sup>2</sup> )	AreaMid;s (mm <sup>2</sup> )	AreaProx;d (mm <sup>2</sup> )	AreaProx;s (mm <sup>2</sup> )	Heart Length;d (mm)	Heart Length;s (mm)	EF (%)	LV Volume;d (μL)	LV Volume;s (μL)	Stroke Volume (μL)	PA Peak Pressure (mm Hg)	LVD (%)	DEF (%)
<b>129x1/SvJArc (3)</b>	31.3 ± 0.5	26.84 ± 5.81	24.76 ± 5.57	24.04 ± 4.13	21.03 ± 5.08	17.92 ± 1.22	13.57 ± 1.98	8.77 ± 0.89	8.15 ± 0.90	20.73 ± 6.98	188.38 ± 53.11	153.07 ± 53.99	35.31 ± 3.43	1.95 ± 0.70	175.23 ± 75.32	60.12 ± 8.90
<b>A/Jarc (8)</b>	26.4 ± 1.4	17.54 ± 4.74	16.13 ± 4.91	17.47 ± 4.67	14.38 ± 4.85	15.65 ± 3.15	10.80 ± 3.03	7.20 ± 0.47	6.75 ± 0.51	24.55 ± 5.99	112.73 ± 31.78	86.48 ± 29.46	26.25 ± 3.74	1.93 ± 0.28	134.05 ± 57.14	54.08 ± 9.27
<b>C57BL/6JArc (5)</b>	28.2 ± 2.2	30.16 ± 5.30	27.69 ± 4.78	30.22 ± 3.09	27.66 ± 3.04	25.93 ± 3.10	21.10 ± 2.65	8.10 ± 0.31	7.84 ± 0.39	14.34 ± 2.05	218.14 ± 33.60	186.87 ± 29.24	31.27 ± 6.84	1.59 ± 0.57	225.01 ± 50.18	70.17 ± 6.77
<b>NOD/ShiLtJArc (6)</b>	28.8 ± 1.0	14.51 ± 3.51	12.70 ± 4.15	18.20 ± 4.10	14.66 ± 4.78	18.04 ± 2.86	12.35 ± 3.31	7.72 ± 0.16	7.31 ± 0.25	27.50 ± 8.81	116.59 ± 21.35	86.08 ± 24.88	30.51 ± 4.91	2.26 ± 0.49	112.31 ± 43.62	51.99 ± 16.80
<b>BEM_AG (4)</b>	35.1 ± 5.0	11.71 ± 1.94	9.34 ± 2.18	15.35 ± 1.46	11.93 ± 1.48	14.41 ± 1.34	9.99 ± 1.83	6.94 ± 0.12	6.40 ± 0.21	30.51 ± 6.29	85.08 ± 10.04	59.37 ± 10.58	25.72 ± 3.99	1.76 ± 0.47	75.30 ± 39.27	42.2 ± 19.63
<b>BOM_GB (12)</b>	24.4 ± 1.5	13.39 ± 3.95	11.10 ± 4.02	15.34 ± 3.20	11.96 ± 3.26	15.80 ± 2.96	10.75 ± 2.97	6.54 ± 0.41	6.03 ± 0.48	31.28 ± 9.41	86.48 ± 21.56	60.84 ± 21.13	25.64 ± 4.25	2.05 ± 0.72	48.37 ± 27.10	34.96 ± 16.92
<b>BOON_HF (4)</b>	31.4 ± 5.1	28.58 ± 8.70	25.60 ± 9.83	29.17 ± 13.01	27.01 ± 14.49	20.44 ± 4.30	16.55 ± 5.99	8.37 ± 0.63	7.98 ± 0.36	17.95 ± 8.55	195.62 ± 86.27	165.26 ± 86.10	30.36 ± 4.88	1.88 ± 0.94	190.4 ± 123.11	64.13 ± 14.55
<b>DAVIS_BA (3)</b>	25.6 ± 0.14	27.92 ± 8.35	26.87 ± 8.39	30.63 ± 8.81	27.84 ± 10.20	25.50 ± 4.61	20.63 ± 4.68	8.00 ± 0.66	7.68 ± 0.92	14.62 ± 7.42	215.61 ± 74.38	186.86 ± 79.52	28.75 ± 5.14	3.09 ± 1.65	206.45 ± 103.76	68.16 ± 16.26
<b>DOD_AH (6)</b>	30.7 ± 2.7	17.89 ± 4.17	16.15 ± 4.53	18.67 ± 3.50	15.71 ± 3.35	16.68 ± 2.31	12.31 ± 1.70	7.95 ± 0.57	7.54 ± 0.38	21.48 ± 2.47	132.22 ± 32.44	104.02 ± 26.67	28.20 ± 6.67	1.76 ± 0.41	116.12 ± 55.65	58.76 ± 5.14
<b>DONNELL_HA (5)</b>	26.8 ± 2.6	10.90 ± 4.09	9.63 ± 4.92	12.71 ± 4.19	10.38 ± 4.19	11.82 ± 2.62	8.30 ± 2.03	6.68 ± 0.54	6.23 ± 0.61	26.62 ± 10.75	76.44 ± 29.75	57.95 ± 29.04	18.49 ± 4.21	1.03 ± 0.45	70.35 ± 58.89	40.79 ± 20.39
<b>FEW_FD (5)</b>	25.0 ± 2.7	21.02 ± 3.41	19.39 ± 3.37	21.08 ± 3.11	18.07 ± 3.65	18.73 ± 3.14	13.81 ± 3.67	8.03 ± 0.47	7.24 ± 0.58	24.21 ± 6.32	151.10 ± 24.33	115.65 ± 27.67	35.45 ± 4.64	2.55 ± 1.11	145.81 ± 63.82	54.50 ± 15.74
<b>FIM_DF (4)</b>	23.5 ± 2.0	9.62 ± 0.77	7.30 ± 1.58	12.31 ± 1.71	8.91 ± 2.20	13.42 ± 0.75	8.60 ± 1.52	6.86 ± 0.19	6.31 ± 0.23	35.79 ± 10.84	74.07 ± 5.31	47.37 ± 6.80	26.70 ± 9.14	2.63 ± 1.36	35.66 ± 19.76	28.84 ± 19.87
<b>FIV_AC (6)</b>	26.1 ± 1.8	12.47 ± 5.66	10.28 ± 5.58	12.96 ± 3.98	9.55 ± 4.24	12.94 ± 1.73	8.10 ± 1.85	7.25 ± 0.62	6.80 ± 0.59	32.74 ± 9.01	82.86 ± 24.25	57.18 ± 23.13	25.68 ± 3.93	1.64 ± 0.29	84.44 ± 42.59	50.56 ± 13.49
<b>GALASUPREME_CE (3)</b>	20.8 ± 2.7	28.00 ± 10.26	25.78 ± 11.95	22.63 ± 6.73	20.15 ± 9.12	19.12 ± 3.97	13.99 ± 3.84	8.71 ± 0.99	8.38 ± 1.14	19.35 ± 13.64	199.08 ± 78.37	167.26 ± 85.65	31.82 ± 8.20	1.86 ± 0.75	301.54 ± 186.79	54.31 ± 31.02
<b>GIG_EF (3)</b>	27.6 ± 2.3	13.98 ± 3.78	12.29 ± 4.19	13.86 ± 2.78	10.67 ± 3.48	14.33 ± 1.18	8.51 ± 1.15	7.27 ± 0.36	6.79 ± 0.62	30.75 ± 5.51	96.42 ± 14.56	67.25 ± 15.03	29.17 ± 1.54	2.96 ± 1.00	61.91 ± 16.42	42.27 ± 9.42
<b>GIT_GC (3)</b>	33.0 ± 1.5	14.80 ± 0.83	13.14 ± 1.74	18.05 ± 3.24	15.08 ± 3.25	18.01 ± 1.59	12.29 ± 1.15	7.21 ± 0.32	6.81 ± 0.12	25.19 ± 3.19	113.04 ± 6.52	84.70 ± 8.00	28.35 ± 2.50	3.40 ± 0.94	79.23 ± 37.83	21.30 ± 14.98
<b>HAZ_EF (3)</b>	19.8 ± 1.2	15.59 ± 0.83	12.91 ± 1.83	18.07 ± 1.28	14.15 ± 1.65	18.48 ± 1.85	12.33 ± 1.92	7.51 ± 0.02	6.71 ± 0.27	32.41 ± 8.18	113.67 ± 6.80	76.87 ± 10.79	36.80 ± 8.85	3.27 ± 0.60	76.39 ± 14.86	35.69 ± 14.52
<b>JUNIOR_GB (3)</b>	24.8 ± 3.2	10.25 ± 0.83	8.42 ± 3.11	13.11 ± 4.21	10.56 ± 3.40	13.58 ± 1.83	9.50 ± 1.36	7.38 ± 0.09	7.07 ± 0.07	25.94 ± 3.94	87.37 ± 27.82	64.32 ± 18.97	23.05 ± 9.84	1.58 ± 0.30	57.63 ± 29.20	43.13 ± 16.38
<b>LUZ_FH (4)</b>	23.2 ± 0.5	18.65 ± 4.07	17.45 ± 4.53	19.22 ± 2.07	15.70 ± 2.20	17.40 ± 1.68	12.22 ± 1.49	7.08 ± 0.27	6.57 ± 0.27	23.74 ± 4.07	113.78 ± 12.21	86.87 ± 12.22	26.91 ± 4.77	2.00 ± 0.35	134.04 ± 23.99	44.86 ± 7.33
<b>NUK_AC (5)</b>	27.3 ± 4.1	12.87 ± 2.11	10.03 ± 2.66	15.37 ± 2.38	11.12 ± 2.55	14.94 ± 2.04	10.24 ± 1.81	7.12 ± 0.61	6.56 ± 0.58	35.15 ± 4.06	91.07 ± 14.44	66.77 ± 20.80	31.95 ± 6.80	2.42 ± 1.59	58.89 ± 33.18	22.02 ± 2.14
<b>PAT_CD (3)</b>	32.1 ± 4.1	15.73 ± 8.84	14.80 ± 8.60	18.76 ± 4.07	15.90 ± 2.42	16.97 ± 3.99	11.13 ± 1.93	7.65 ± 1.19	7.06 ± 1.03	24.25 ± 4.10	123.99 ± 50.22	92.73 ± 35.00	31.26 ± 15.61	2.41 ± 0.52	81.38 ± 68.42	48.17 ± 0.89
<b>PEF_EC (6)</b>	27.2 ± 1.0	12.99 ± 4.07	11.21 ± 4.17	16.02 ± 3.69	11.82 ± 3.64	17.63 ± 3.46	10.57 ± 2.75	7.50 ± 0.42	7.02 ± 0.37	32.91 ± 8.81	102.85 ± 26.97	69.65 ± 22.75	33.19 ± 9.68	2.31 ± 0.42	41.61 ± 32.77	28.48 ± 18.97
<b>POH_DC (3)</b>	32.1 ± 2.4	8.01 ± 0.87	5.28 ± 0.71	10.97 ± 0.80	7.52 ± 0.33	11.77 ± 0.81	6.84 ± 0.35	6.05 ± 0.19	5.67 ± 0.15	40.24 ± 2.37	53.97 ± 6.71	32.23 ± 3.52	21.74 ± 3.58	1.64 ± 0.37	22.44 ± 17.68	31.18 ± 3.50
<b>SAT_GA (5)</b>	24.5 ± 2.5	10.47 ± 2.34	9.33 ± 2.66	12.31 ± 2.44	9.91 ± 2.65	12.95 ± 2.18	8.50 ± 1.42	6.35 ± 0.57	6.01 ± 0.61	28.73 ± 5.73	60.20 ± 10.62	49.34 ± 13.88	17.47 ± 3.21	2.34 ± 1.47	61.47 ± 34.68	37.75 ± 17.11
<b>TOFU_FB (10)</b>	19.8 ± 1.5	20.66 ± 2.44	19.63 ± 2.78	18.95 ± 2.85	17.53 ± 2.98	17.82 ± 1.95	12.98 ± 2.22	7.59 ± 0.35	7.28 ± 0.20	16.05 ± 5.12	134.51 ± 19.60	112.66 ± 16.38	21.85 ± 8.04	1.53 ± 0.39	217.55 ± 41.76	56.47 ± 17.69
<b>TOP_DA (4)</b>	27.5 ± 0.9	15.03 ± 6.30	12.71 ± 6.39	16.37 ± 4.19	13.78 ± 5.09	13.75 ± 5.25	9.58 ± 4.71	7.23 ± 0.68	6.77 ± 0.75	26.68 ± 8.31	99.07 ± 42.10	75.03 ± 41.26	24.04 ± 5.12	n/a**	112.18 ± 81.45	45.80 ± 16.95
<b>WAB2_DH (3)</b>	25.9 ± 2.2	14.42 ± 0.96	11.86 ± 1.07	18.13 ± 1.92	14.50 ± 2.42	17.30 ± 0.34	13.66 ± 1.95	7.28 ± 0.63	6.70 ± 0.64	25.96 ± 4.85	106.03 ± 11.25	78.52 ± 10.56	27.51 ± 5.14	2.21 ± 0.39	65.00 ± 23.99	44.52 ± 13.30

\* Data is presented as mean value ± standard deviation (SD). Number of biological replicates is indicated in brackets next to the strain name.

Parameter definitions are provided below in “Ultrasound measurements and calculations” section.

\*\* Not assessed

# Ultrasound Measurement and Calculation definitions

Vevo2100 (FUJIFILM/VisualSonics)

## Measurement definitions

Label	Description	Units	Generic type	Mode
Endocardial Area; d	Endocardial area in diastole	mm <sup>2</sup>	Area	B-Mode
Endocardial Major; d	Endocardial major in diastole	mm	Length	B-Mode
Endocardial Area; s	Endocardial area in systole	mm <sup>2</sup>	Area	B-Mode
Endocardial Major; s	Endocardial major in systole	mm	Length	B-Mode
Epicardial Area; d	Epicardial area in diastole	mm <sup>2</sup>	Area	B-Mode
Epicardial Major; d	Epicardial major in diastole	mm	Length	B-Mode
Epicardial Area; s	Epicardial area in systole	mm <sup>2</sup>	Area	B-Mode
Epicardial Major; s	Epicardial major in systole	mm	Length	B-Mode
LVPW;d	Left ventricular posterior wall (diastole)	mm	Depth	M-Mode
LVPW;s	Left ventricular posterior wall (systole)	mm	Depth	M-Mode

## Calculations

Name	Description	Units	Formula
Endocardial Volume; d	Endocardial volume in diastole	μL	$\frac{4\pi}{2} \times \frac{End\ Major; d}{2} \times \left( \frac{End\ Area; d}{\pi \left( \frac{End\ Area; d}{2} \right)} \right)^2$
Endocardial Volume; s	Endocardial volume in systole	μL	$\frac{4\pi}{2} \times \frac{End\ Major; s}{2} \times \left( \frac{End\ Area; s}{\pi \left( \frac{End\ Area; s}{2} \right)} \right)^2$
Endocardial Stroke Volume (SV)	Stroke volume (SV)	μL	<i>Endocardial Volume; d - Endocardial Volume; s</i>
Endocardial %EF	Percent ejection fraction	%	$\frac{Endocardial\ SV}{Endocardial\ Vol; d} \times 100$
Endocardial %FAC	Percent fractional area change	%	$\frac{Endocardial\ area; d - Endocardial\ area; s}{Endocardial\ area; d} \times 100$
LV Mass	LV Mass	mg	$1.05 \times (5/6 \times Epicardial\ Area; d \times (Epicardial\ Major; d + T; d)) - (5/6 \times Endocardial\ Area; d \times (Endocardial\ Major; d))$
Simp Volume; d	Simpson's volume calculation in diastole	μL	$(AreaProx; d + AreaMid; d) \times h + AreaDist; d \times \frac{h}{2} + \frac{\pi}{6} \times h^3$ h = Simpson Length in diastole
Simp Volume; s	Simpson's volume calculation in systole	μL	$(AreaProx; s + AreaMid; s) \times h + AreaDist; s \times \frac{h}{2} + \frac{\pi}{6} \times h^3$ h = Simpson Length in diastole
Simp SV	Stroke volume	μL	<i>Simp Volume; d - Simp Volume; s</i>
Simp %EF	Ejection fraction	%	$100 * Simp\ SV / Simp\ Volume; d$

## Supplementary Table S3

### GeneNetwork/WebQTL correlation analysis of cardiac gene expression vs LVSD/HF-related traits

	Record ID	Gene Symbol	Description	Mean Expression	LVD		D%EF	
					Correlation	p-Value	Correlation	p-Value
1	ILMN_2856568	<b>Gppb1</b>	Mus musculus GC-rich promoter binding protein 1	9.063	0.897	1.22E-05	0.888	2.29E-05
2	ILMN_1219002	<b>Usmg5</b>	Upregulated during skeletal muscle growth 5	8.049	0.924	1.21E-06	0.857	1.20E-04
3	ILMN_2712634	<b>Nab1</b>	Mus musculus Ngfi-A binding protein 1	7.026	-0.843	2.20E-04	-0.901	9.26E-06
4	ILMN_2924601	<b>Klhl17</b>	Mus musculus kelch-like 17 (Drosophila)	8.672	-0.891	1.92E-05	-0.815	6.20E-04
5	ILMN_1254837	<b>Rab7</b>	Mus musculus RAB7, member RAS oncogene family	7.031	-0.857	1.20E-04	-0.844	2.10E-04
6	ILMN_1250201	<b>Fndc10</b>	Fibronectin type III domain containing 10 (B930041F14Rik)	7.574	-0.817	5.90E-04	-0.938	2.44E-07
7	ILMN_3163159	<b>Gng5</b>	Mus musculus guanine nucleotide binding protein (G protein), gamma 5 subunit	7.813	0.858	1.20E-04	0.815	6.20E-04
8	ILMN_2748205	<b>Hspb3</b>	Mus musculus heat shock protein 3	8.589	0.843	2.20E-04	0.813	6.60E-04
9	ILMN_2724570	<b>Mapk12</b>	Mus musculus mitogen-activated protein kinase 12	8.106	-0.816	6.10E-04	-0.875	4.96E-05
10	ILMN_2821501	<b>Zfand6</b>	Mus musculus zinc finger, AN1-type domain 6	7.536	0.859	1.10E-04	0.803	8.90E-04
11	ILMN_1227012	<b>Ndufb4</b>	Mus musculus NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	8.2	0.837	2.80E-04	0.815	6.10E-04
12	ILMN_1235230	<b>Pdlim3</b>	Mus musculus PDZ and LIM domain 3	8.734	-0.842	2.30E-04	-0.806	8.10E-04
13	ILMN_3144289	<b>Traf3</b>	Mus musculus Tnf receptor-associated factor 3	8.463	0.832	3.40E-04	-0.821	5.00E-04
14	ILMN_2776899	<b>Atp5k</b>	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1F0 complex, subunit E	7.113	0.860	1.10E-04	0.795	1.13E-03
15	ILMN_2670230	<b>Tbrg4</b>	Mus musculus transforming growth factor beta regulated gene 4	7.428	-0.884	2.87E-05	-0.787	1.43E-03
16	ILMN_2723881	<b>Hcfc1</b>	Host cell factor C1	8.766	0.804	8.70E-04	0.832	3.40E-04
17	ILMN_2756008	<b>Nasp</b>	Nuclear autoantigenic sperm protein (histone-binding)	7.439	-0.864	8.65E-05	-0.786	1.47E-03
18	ILMN_3133522	<b>Ppm1d</b>	Mus musculus protein phosphatase 1D magnesium-dependent, delta isoform	8.126	-0.841	2.40E-04	-0.802	9.40E-04
19	ILMN_2671689	<b>Cox7b</b>	Cytochrome c oxidase subunit VIIb	8.63	0.819	5.30E-04	0.810	7.30E-04
20	ILMN_2718416	<b>Eif3k</b>	Mus musculus eukaryotic translation initiation factor 3	9.583	0.794	1.17E-03	0.824	4.50E-04
21	ILMN_2680262	<b>Polr2g</b>	Mus musculus polymerase (RNA) II (DNA directed) polypeptide G	9.393	0.831	3.50E-04	0.786	1.44E-03
22	ILMN_1242391	<b>Tmem8</b>	Mus musculus transmembrane protein 8 (five membrane-spanning domains)	7.027	0.793	1.19E-03	0.805	8.60E-04
23	ILMN_2684279	<b>Edem2</b>	ER degradation enhancer, mannosidase alpha-like 2 (9530090G24Rik)	8.636	-0.801	9.50E-04	-0.792	1.23E-03
24	ILMN_2896492	<b>Jmjd8</b>	Jumonji domain containing 8 (2610003J06Rik)	8.918	-0.777	1.84E-03	-0.821	5.00E-04
25	ILMN_2868981	<b>Ehbp1</b>	Mus musculus EH domain binding protein 1	8.526	0.827	4.10E-04	0.764	2.57E-03
26	ILMN_2972645	<b>Pdzd11</b>	Mus musculus PDZ domain containing 11	8.285	-0.765	2.49E-03	-0.854	1.40E-04
27	ILMN_2655429	<b>C530015C18</b>	Hypothetical protein C530015C18	7.95	-0.838	2.70E-04	-0.748	3.68E-03
28	ILMN_2966826	<b>Ttl1</b>	Mus musculus tubulin tyrosine ligase-like 1	9.286	0.787	1.41E-03	0.783	1.56E-03
29	ILMN_1257503	<b>Tm9sf2</b>	Mus musculus transmembrane 9 superfamily member 2	7.024	0.786	1.45E-03	0.777	1.87E-03
30	ILMN_2698606	<b>Tmed4</b>	Transmembrane p24 trafficking protein 4 (1110014L17Rik)	8.147	-0.779	1.78E-03	-0.786	1.46E-03
31	ILMN_1221702	<b>Plaa</b>	phospholipase A2, activating protein	9.027	0.803	9.00E-04	0.755	3.14E-03
32	ILMN_2692615	<b>Tgm2</b>	Transglutaminase 2, C polypeptide	11.845	-0.763	2.59E-03	-0.802	9.30E-04
33	ILMN_2687032	<b>Fbxo31</b>	Mus musculus F-box protein 31	8.462	-0.784	1.54E-03	-0.761	2.72E-03
34	ILMN_2591917	<b>Akr1b3</b>	Aldo-keto reductase family 1, member B3 (aldose reductase)	9.977	0.828	3.90E-04	0.7179	6.73E-03
35	ILMN_1215862	<b>Cxcl9</b>	Chemokine (C-X-C motif) ligand 9	7.752	0.771	2.16E-03	0.771	2.14E-03
36	ILMN_1223614	<b>Rbpms</b>	RNA binding protein gene with multiple splicing	10.15	-0.769	2.27E-03	-0.773	2.05E-03
37	ILMN_2771219	<b>Pdlim5</b>	PDZ and LIM domain 5 (1110001A05Rik)	11.826	-0.785	1.51E-03	-0.757	3.00E-03
38	ILMN_2666406	<b>Prrc1</b>	proline-rich coiled-coil 1 (1190002C06Rik)	9.173	-0.788	1.37E-03	-0.748	3.69E-03
39	ILMN_2605004	<b>Ndufb9</b>	Mus musculus NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	11.241	0.768	2.34E-03	0.768	2.33E-03
40	ILMN_3126933	<b>Tacc1</b>	Mus musculus transforming, acidic coiled-coil containing protein 1	8.472	-0.754	3.23E-03	-0.796	1.12E-03
41	ILMN_1249116	<b>Cpsf3l</b>	Mus musculus cleavage and polyadenylation specific factor 3-like	7.78	-0.762	2.71E-03	-0.760	2.81E-03
42	ILMN_2702197	<b>Pcbp1</b>	Poly(rC) binding protein 1	10.336	-0.781	1.69E-03	-0.731	5.19E-03
43	ILMN_1230271	<b>Anp32a</b>	Mus musculus acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	7.812	0.774	1.99E-03	0.744	4.00E-03
44	ILMN_1252302	<b>Taf6</b>	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	7.257	0.759	2.87E-03	0.762	2.65E-03
45	ILMN_2510364	<b>Trip12</b>	Thyroid hormone receptor interactor 12	7.455	0.805	8.50E-04	0.705	8.50E-03
46	ILMN_2928573	<b>Rev1</b>	Mus musculus REV1 homolog (S. cerevisiae)	7.205	-0.747	3.75E-03	-0.795	1.13E-03
47	ILMN_2973097	<b>Coq3</b>	Mus musculus coenzyme Q3 homolog, methyltransferase (yeast)	7.495	0.774	2.02E-03	0.742	4.17E-03
48	ILMN_2859978	<b>Papss1</b>	Mus musculus 3'-phosphoadenosine 5'-phosphosulfate synthase 1	8.581	-0.761	2.73E-03	-0.758	2.91E-03
49	ILMN_2883952	<b>YdjC</b>	YdjC homolog (bacterial) (1810015A11Rik)	7.148	-0.756	3.08E-03	-0.761	2.71E-03
50	ILMN_3008361	<b>Bmper</b>	Mus musculus BMP-binding endothelial regulator	7.414	-0.744	4.01E-03	-0.785	1.49E-03

The 50 top correlates common for the LVD and  $\Delta$ EF traits (correlation coefficient  $\geq 0.74$ ) for normalized gene expression level  $> 7$ .

P-value provided according to Pearson's product-moment correlations.

**Table S4 List of functional SNPs corresponding to the QTL located on Chromosome 12 associated with the myocardial rupture trait**

Gene	dbSNP	Genomic Location	Ref	129S1/ SvlmJ	A/J	C57BL/ 6NJ	CAST/EiJ	NOD/ ShiLtJ	NZO/ HILtJ	PWK/PhJ	WSB/EiJ	Consequence Type	Amino acids	Protein position	Impact	SIFT
<b>Nrxn3</b>	rs231902337	12:90283564	G	-	-	-	-	-	-	A	-	Splice region variant			low	
<b>Cep128</b>	rs227456595	12:91159065	C	-	-	-	G	-	-	G	-	Splice donor variant			high	
<b>Cep128</b>	rs249098074	12:91183657	G	-	-	-	-	-	-	T	-	Splice region variant			low	
<b>Cep128</b>	rs261503899	12:91213702	C	-	-	-	-	-	-	T	-	Missense variant	S/N	889	moderate	tolerated (0.57)
<b>Cep128</b>	rs48798187	12:91213755	A	-	-	-	-	-	-	G	-	Splice region variant			low	
<b>Cep128</b>	rs48026157	12:91234161	A	-	-	-	C	-	-	C	-	Missense variant	H/Q	811	moderate	tolerated (1)
<b>Cep128</b>	rs46662645	12:91255722	A	-	-	-	-	-	-	T	-	Missense variant	D/E	742	moderate	tolerated (0.43)
<b>Cep128</b>	rs261762568	12:91260124	G	-	-	-	T	-	-	-	-	Missense variant	D/E	690	moderate	tolerated (0.5)
<b>Cep128</b>	rs51557552	12:91260575	T	-	-	-	C	-	-	C	-	Missense variant	N/S	540	moderate	tolerated (0.52)
<b>Cep128</b>	rs46446778	12:91266888	T	-	-	-	C	-	-	C	-	Missense variant	T/A	469	moderate	tolerated (1)
<b>Cep128</b>	rs262007891	12:91294082	G	-	-	-	-	-	-	C	-	Missense variant	P/A	336	moderate	tolerated (0.08)
<b>Cep128</b>	rs46978148	12:91294173	T	-	-	-	C	-	-	C	-	Splice region variant			low	
<b>Cep128</b>	rs252980304	12:91299035	C	-	-	-	T	-	-	T	-	Missense variant	V/I	268	moderate	tolerated (0.32)
<b>Cep128</b>	rs217950132	12:91320001	T	-	-	-	G	-	-	G	-	Splice region variant			low	
<b>Cep128</b>	rs266165675	12:91366444	C	-	-	-	-	-	-	T	-	Missense variant	G/R	16	moderate	tolerated (0.92)
<b>Cep128</b>	rs49587405	12:91370201	G	-	-	-	A	-	-	A	-	Splice region variant			low	

**Table S5 List of functional SNPs corresponding to the QTL located on Chromosome 5 associated with the LVD trait**

Gene	dbSNP	Genomic Location	Ref	129S1/SvlmJ	A/J	C57BL/6NJ	CAST/EiJ	NOD/ShiLtJ	NZO/HILtJ	PWK/PhJ	WSB/EiJ	Consequence Type	Amino acids	Protein position	Impact	SIFT
<b>Tfip11</b>	rs32109670	5:112333231	G	-	-	-	A	-	-	-	-	Missense variant	E/K	358	moderate	tolerated (0.39)
<b>Tfip11</b>	rs33218387	5:112333336	G	-	-	-	-	-	A	-	A	Missense variant	A/T	393	moderate	tolerated (0.63)
<b>Srrd</b>	rs234879464	5:112339730	T	-	-	-	G	-	-	-	-	Missense variant	S/R	169	moderate	tolerated (0.21)
<b>Gm6583</b>	rs32113318	5:112354764	C	-	-	-	T	-	-	-	-	Missense variant	C/T	358	moderate	tolerated (0.51)
<b>Gm6583</b>	rs264081076	5:112355358	T	-	-	-	C	-	-	C	-	Missense variant	K/R	160	moderate	tolerated (0.8)
<b>Gm6583</b>	rs32113322	5:112355547	G	-	-	-	A	-	-	-	-	Missense variant	A/V	97	moderate	tolerated (0.88)
<b>Gm6583</b>	rs258837611	5:112355749	C	-	-	-	T	-	-	-	-	Missense variant	G/R	30	moderate	tolerated (0.97)
<b>Hps4</b>	rs253490750	5:112349378	C	-	-	-	-	-	-	-	T	Missense variant	R/C	76	moderate	tolerated(0.05)
<b>Hps4</b>	rs239835610	5:112368976	C	-	-	-	T	-	-	-	-	Splice region variant	-	-	low	
<b>Hps4</b>	rs32107636	5:112370143	G	-	-	-	A	-	-	-	-	Missense variant	C/Y	334	moderate	tolerated (0.16)
<b>Hps4</b>	rs228327059	5:112374979	C	-	-	-	-	-	-	-	T	Missense variant	L/F	568	moderate	deleterious (0)
<b>Hps4</b>	rs32112489	5:112377955	A	-	-	-	T	-	-	-	-	Splice region variant	-	-	low	
<b>Sez6l</b>	rs32114817	5:112422009	T	-	-	-	C	-	-	-	-	Stop retained variant	-	-	low	
<b>Sez6l</b>	rs32116976	5:112425616	C	-	-	-	-	-	-	-	T	Splice region variant	-	-	low	
<b>Sez6l</b>	rs32122208	5:112472926	G	-	-	-	-	-	-	-	A	Splice region variant	-	-	low	
<b>Sez6l</b>	rs32118052	5:112475023	G	C	-	-	-	C	-	C	C	Splice region variant	-	-	low	
<b>Sez6l</b>	rs32118955	5:112475412	C	T	-	-	-	T	-	-	T	Missense variant	C/N	91	moderate	tolerated (0.44)
<b>Myo18b</b>	rs212801037	5:112775403	A	-	-	-	T	-	-	-	-	Splice region variant	-	-	low	
<b>Myo18b</b>	rs47968507	5:112802426	G	C	-	-	-	C	C	-	-	Missense variant	L/V	1535	moderate	tolerated (0.18)
<b>Myo18b</b>	rs46076017	5:112809682	T	C	C	-	-	C	C	C	-	Missense variant	T/A	1472	moderate	tolerated (0.87)
<b>Myo18b</b>	rs237692588	5:112837808	T	-	-	-	C	-	-	-	-	Missense variant	T/A	1092	moderate	tolerated (0.6)
<b>Myo18b</b>	rs48666049	5:112837826	G	-	-	-	C	-	-	C	-	Missense variant	Q/E	1086	moderate	tolerated (0.8)
<b>Myo18b</b>	rs234142160	5:112858503	C	-	-	-	T	-	-	-	-	Missense variant	R/Q	847	moderate	tolerated (1)
<b>Myo18b</b>	rs48271099	5:112871438	C	-	-	-	T	-	-	-	-	Missense variant	V/M	658	moderate	tolerated (0.06)
<b>Myo18b</b>	rs260627251	5:112871446	G	-	-	-	T	-	-	-	-	Missense variant	T/K	655	moderate	tolerated (0.12)
<b>Myo18b</b>	rs220128630	5:112871546	C	-	-	-	T	-	-	-	-	Missense variant	V/I	622	moderate	tolerated (0.09)
<b>Myo18b</b>	rs238856395	5:112871552	C	-	-	-	T	-	-	T	-	Missense variant	V/I	620	moderate	tolerated (0.69)
<b>Myo18b</b>	rs51366779	5:112873984	A	-	-	-	C	-	-	C	-	Missense variant	V/G	514	moderate	tolerated-LC (0.44)
<b>Myo18b</b>	rs45640773	5:112874114	C	-	-	-	T	-	-	-	-	Missense variant	A/T	471	moderate	tolerated-LC (0.18)
<b>Myo18b</b>	rs244439177	5:112874302	G	-	-	-	A	-	-	-	-	Missense variant	P/L	408	moderate	tolerated-LC (0.08)
<b>Myo18b</b>	rs582288427	5:112874336	G	-	-	-	A	-	-	-	-	Missense variant	P/S	397	moderate	tolerated-LC (0.41)
<b>Myo18b</b>	rs584773560	5:112874338	C	-	-	-	T	-	-	-	-	Missense variant	G/E	396	moderate	tolerated-LC (0.37)
<b>Myo18b</b>	rs585945270	5:112874344	G	-	-	-	A	-	-	-	-	Missense variant	P/L	394	moderate	tolerated-LC (0.19)
<b>Myo18b</b>	rs580478289	5:112874362	G	-	-	-	A	-	-	-	-	Missense variant	A/V	388	moderate	tolerated-LC (0.22)
<b>Myo18b</b>	rs249974165	5:112874363	C	-	-	-	A	-	-	A	-	Missense variant	A/S	388	moderate	tolerated-LC (0.43)
<b>Myo18b</b>	rs212290244	5:112874384	A	-	-	-	C	-	-	-	-	Missense variant	S/P	1369	moderate	tolerated-LC (0.73)
<b>Myo18b</b>	rs47749211	5:112874531	G	-	-	-	C	-	-	-	-	Missense variant	R/G	332	moderate	tolerated-LC (0.01)
<b>Myo18b</b>	rs51932075	5:112874585	A	-	-	-	G	-	-	G	-	Missense variant	W/R	314	moderate	tolerated-LC (1)
<b>Myo18b</b>	rs581501658	5:112874614	G	-	-	-	A	-	-	-	-	Missense variant	P/L	304	moderate	tolerated-LC (0.23)
<b>Myo18b</b>	rs257889290	5:112874803	A	-	-	-	T	-	-	T	-	Missense variant	I/N	241	moderate	tolerated-LC (0.09)
<b>Myo18b</b>	rs33706581	5:112875024	A	-	-	-	C	-	-	C	-	Missense variant	D/E	167	moderate	tolerated-LC (1)

**Table S6****The Jackson Laboratory nomenclature of the CC founder and RI strains used in this study**

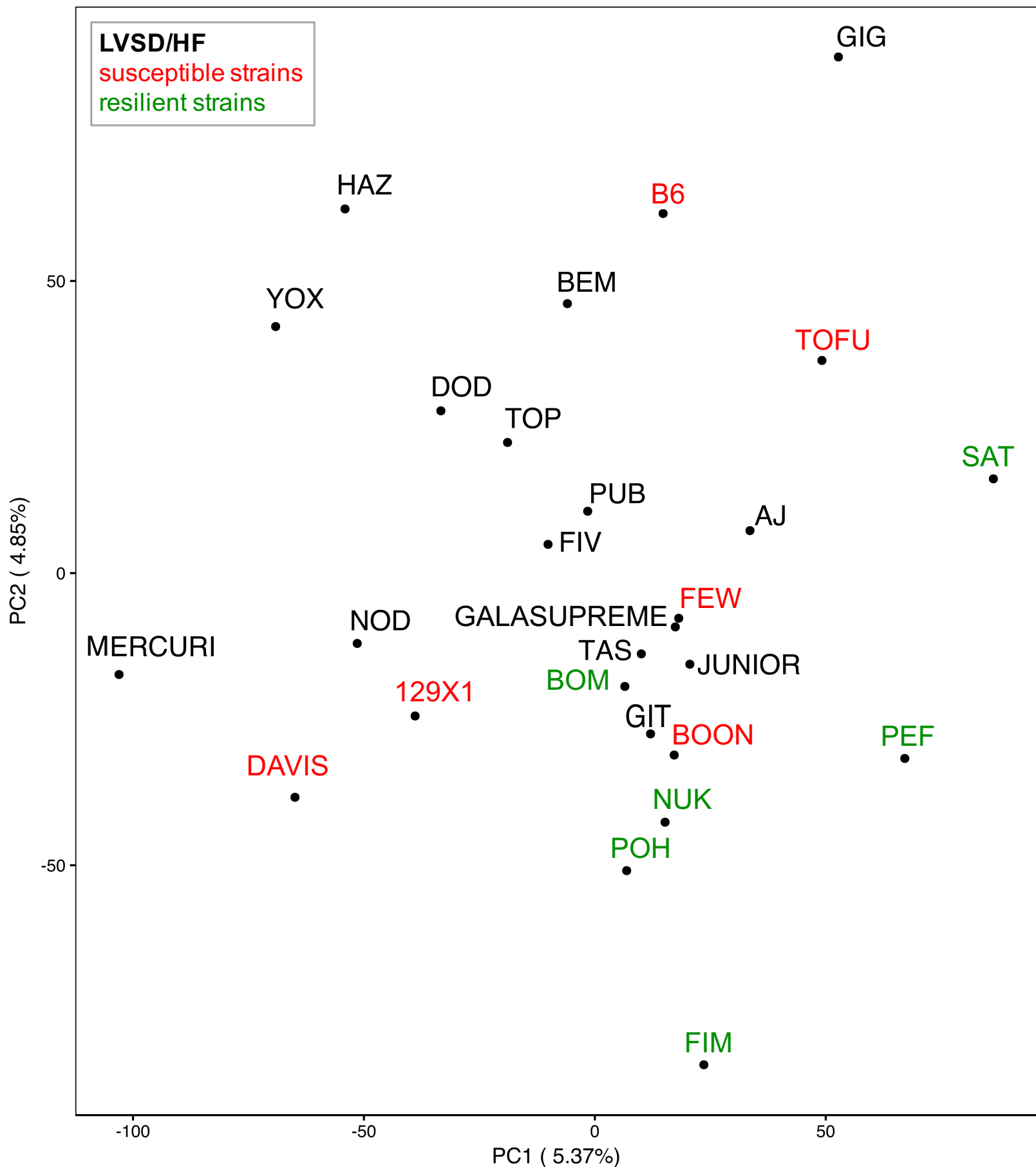
<b>ARC/GENIAD Strain Code</b>	<b>JAX Strain Code</b>
129X1/SvJArc	129S1/SvImJ
A/JArc	A/J
C57BL/6JArc	C57BL/6J
NOD/ShiLtJArc	NOD/ShiLtJ
BEM_AG	CC032
BOM_GB	CC042
BOON_HF	CC008
CIS_AD	CC024
DAVIS_BA	CC012
DOD_AH	N/A
DONNELL_HA	N/A
FEW_FD	CC025
FIM_DF	CC061
FIV_AC	N/A
GALASUPREME_CE	N/A
GIG_EF	CC013
GIT_GC	N/A
HAZ_FE	N/A
JUNIOR_GB	CC020
LUZ_FH	N/A
MERCURI_HF	N/A
NUK_AC	CC010
PAT_CD	N/A
PEF_EC	N/A
POH_DC	N/A
PUB_CD	CC056
SAT_GA	CC016
TAS_FE	CC026
TOFU_FB	CC027
TOP_DA	CC023
WAB2_DH	CC031
YOX_DE	N/A

N/A – strain not maintained at the Jackson Laboratory depository

**Table S7****Abbreviations of the mouse strains employed in this publication**

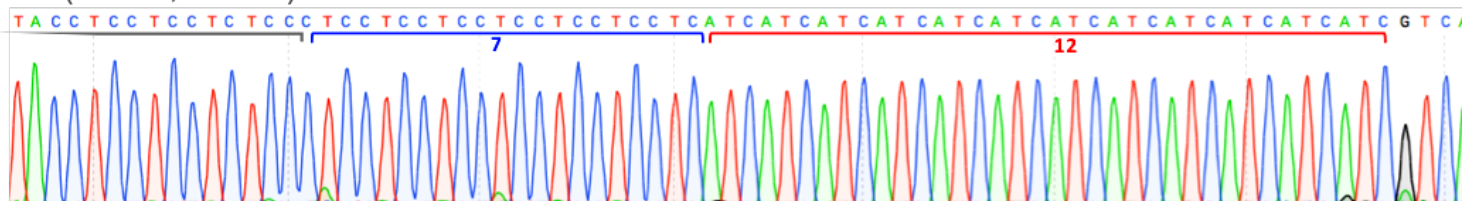
<b>ARC strains</b>	<b>Abbreviation</b>
129X1/SvJArc	129X1
A/JArc	AJ
C57BL/6JArc	B6
NOD/ShiLtJArc	NOD
<b>CC RI strains</b>	
BEM_AG	BEM
BOM_GB	BOM
BOON_HF	BOON
CIS_AD	CIS
DAVIS_BA	DAVIS
DOD_AH	DOD
DONNELL_HA	DONNELL or DON
FEW_FD	FEW
FIM_DF	FIM
FIV_AC	FIV
GALASUPREME_CE	GALASUPREME or GALA
GIG_EF	GIG
GIT_GC	GIT
HAZ_FE	HAZ
JUNIOR_GB	JUNIOR
LUZ_FH	LUZ
MERCURI_HF	MERCURY
NUK_AC	NUK
PAT_CD	PAT
PEF_EC	PEF
POH_DC	POH
PUB_CD	PUB
SAT_GA	SAT
TAS_FE	TAS
TOFU_FB	TOFU
TOP_DA	TOP
WAB2_DH	WAB2
YOX_DE	YOX



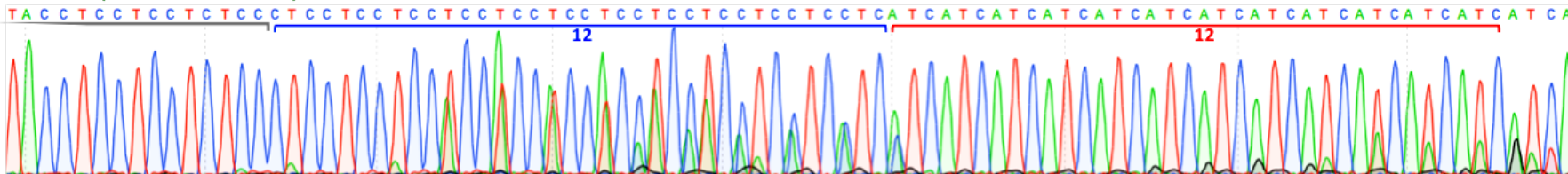


**Supplementary Figure S1. Principal Component Analysis (PCA) on whole-transcriptome profiles of 27 strains employed in this study.** The plot depicts a principal component analysis of the transcriptomes of uninjured hearts across 27 selected RI CC strains. The first principal component (PC1) explains 5.37% of the observed variation across strains while the second principal component (PC2) explains 4.85% of the variation. LVSD/HF resilient strains are highlighted in green, while LVSD/HF susceptible strains are highlighted in red.

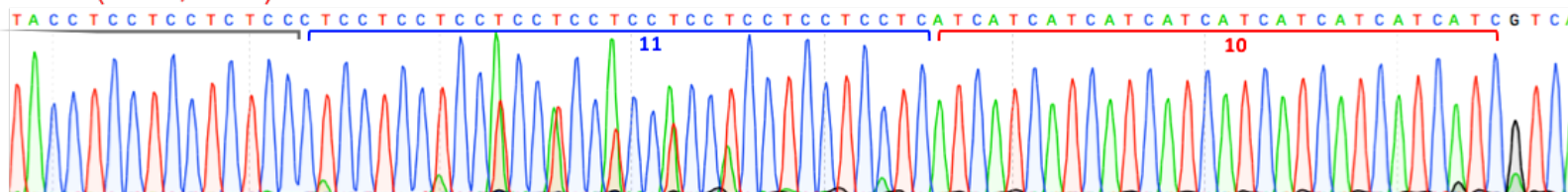
**B6 (TOFU, BOON)**



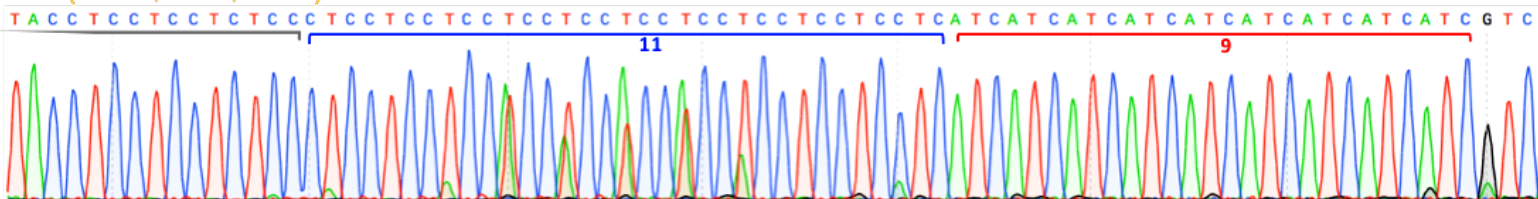
**CAST (GALA, DAVIS)**



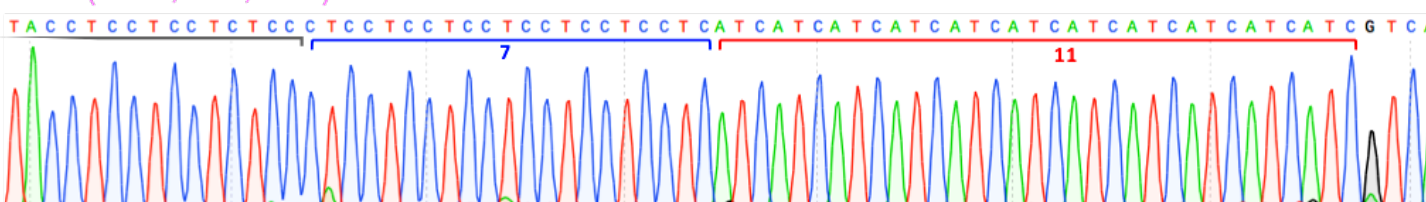
**PWK (FEW, HAZ)**



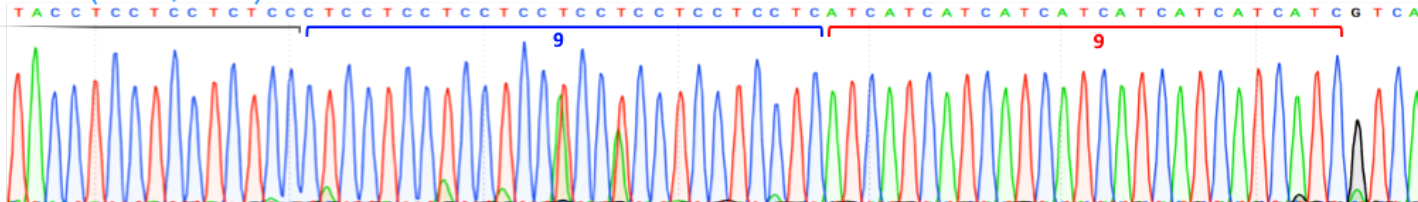
**AJ (DOD, FIM, LUZ)**



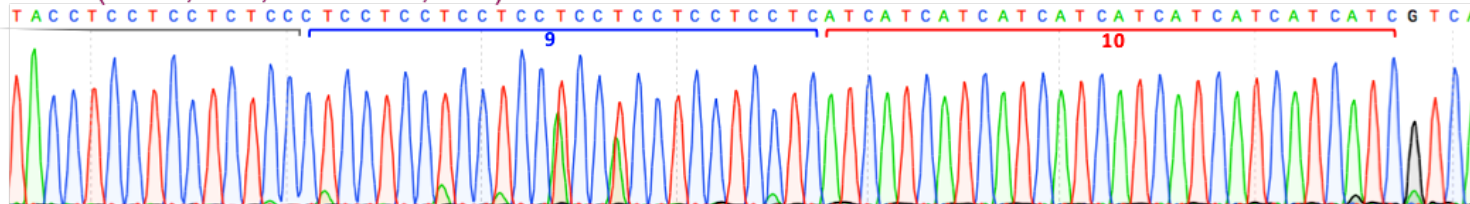
**129s (BEM, GIT, PAT)**



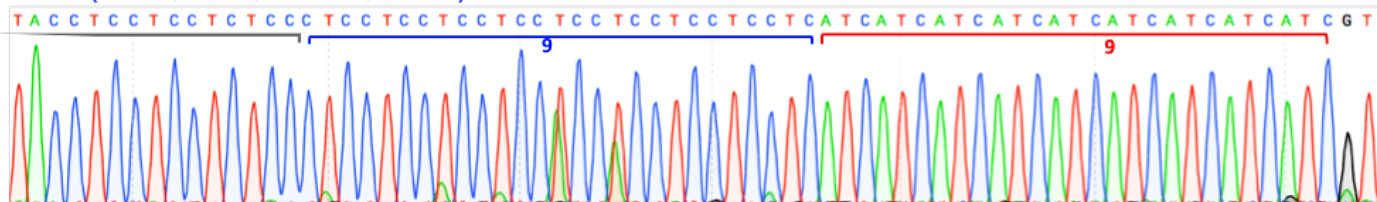
**NZO (NUK, GIG)**



**WSB (BOM, SAT, DONNEL, FIV)**



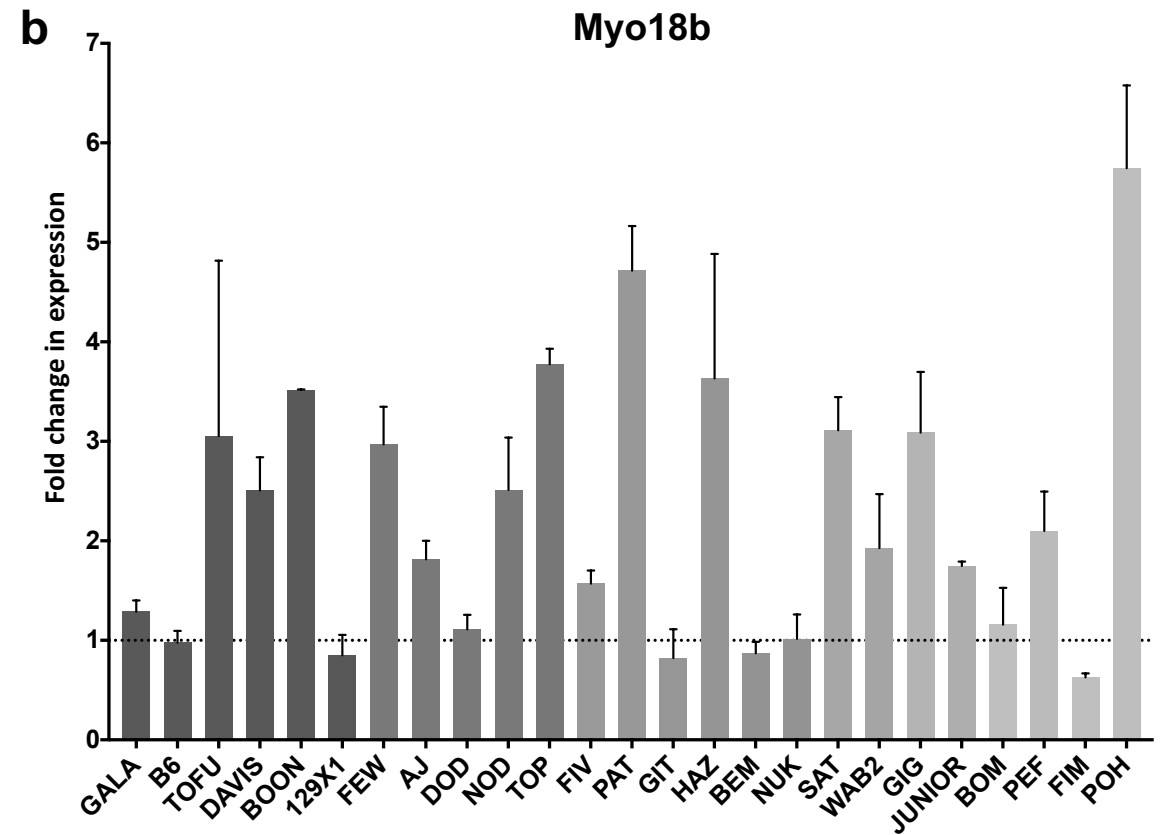
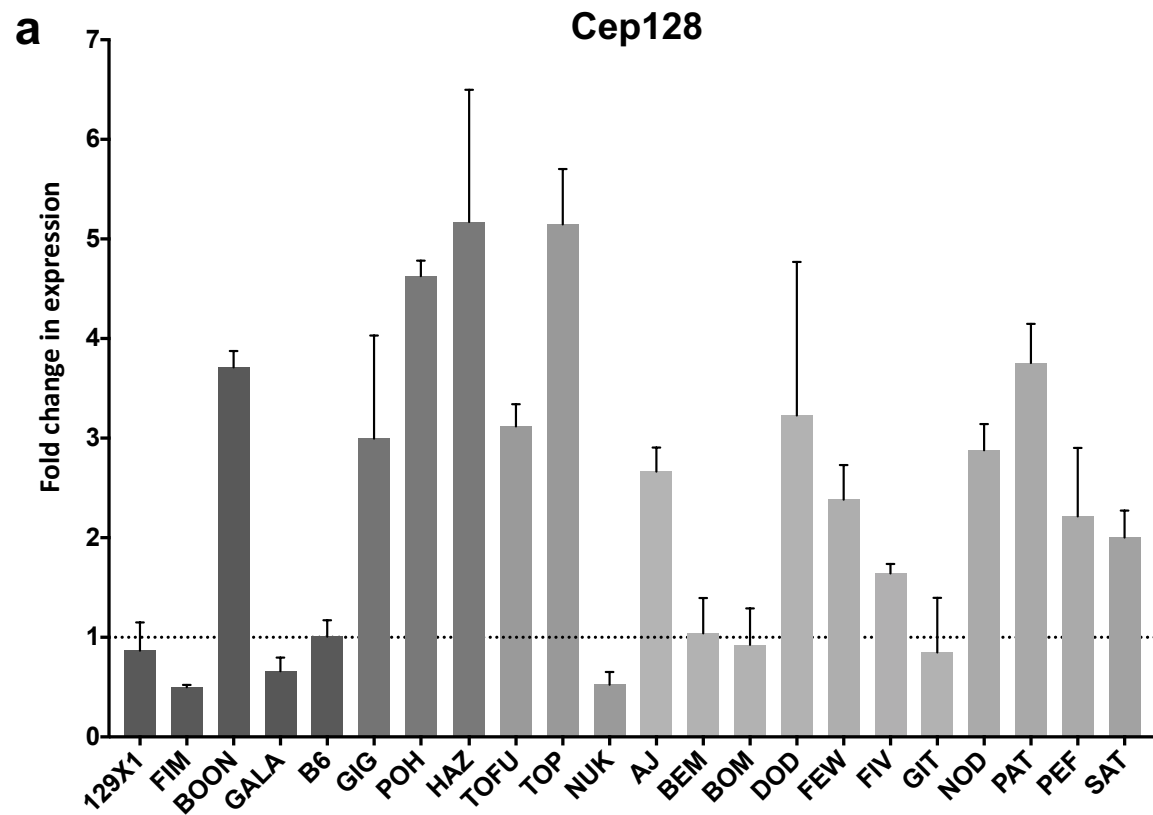
**NOD (POH, PEF, WAB2, TOP)**



**Supplementary Figure S2. Intronic polymorphism in the *Myo18b* region associated with the LVD trait.**

Representative chromatograms of the 8 haplotypes in the intronic region (Chr5: 112856370-112856440) capturing microsatellite variation corresponding to polymorphisms rs578974233, rs582659088, rs585674637 and rs226166519.

Forward primer: 5'-AAGCCCATGAATGCACATTGG; reverse primer: 5'-AGACTTGGTGGGAAGAGGCAA



**Supplementary Figure S3. Expression levels of *Cep128* (a), *Myo18b* (b) and *Tnni3k* (c) genes in selected CC strains determined by RT-qPCR.**

Strains are ordered according to the quantitative expressivity of the trait: LV dilation for *Myo18b* and *Tnni3k*, and survival rate (occurrence of myocardial rupture) for *Cep128*. Expression levels are normalised against *Gapdh* and presented as fold expression change relative to expression in B6 strain, considered as 1. Data is presented as mean value  $\pm$  SD of 2-5 biological replicates.

