

Supplementary Table 1 List of all SNPs that were genotyped in the pilot study candidate gene approach

SNP No.	SNP Location	Chromosome band	RefSNP ID	SNP No.	SNP Location	Chromosome band	RefSNP ID
1	CD14 upstream	5q31.3	rs2569193	41	IL10RB intron	21q22.11	rs2285020
2	TLR4 upstream	9q33.1	rs2737191	42	IL10RB intron	21q22.11	rs2834171
3	TLR4 downstream	9q33.1	rs1554973	43	IL10RB intron	21q22.11	rs2244305
4	TLR2 downstream / RNF175 I315M	4q31.3	rs1339	44	IL10RB intron	21q22.11	rs2243498
5	IL1RL1 A78E	2q11.2	rs1041973	45	ECE1 intron	1p36.12	rs212526
6	IL1RL1 intron	2q11.2	rs1861246	46	ECE1 intron	1p36.12	rs2282714
7	IL1RL1 downstream / IL18R1 upstream	2q11.2	rs12999364	47	ECE1 intron	1p36.12	rs2236847
8	CTF1 3' UTR	16p11.2	rs1046276	48	ECE1 intron	1p36.12	rs212534
9	CTF1 downstream	16p11.2	rs11649653	49	EDN1 intron	6p24.1	rs1476046
10	IL6 upstream	7p15.3	rs1880243	50	EDN1 intron	6p24.1	rs1626492
11	IL6 intron	7p15.3	rs1554606	51	EDN1 K198N	6p24.1	rs5370
12	IL6 intron	7p15.3	rs2069845	52	EDNRA 5' UTR	4q31.22	rs1801708
13	IL6R intron	1q21.3	rs6427641	53	EDNRA intron	4q31.22	rs1400554
14	IL6R intron	1q21.3	rs6687726	54	EDNRA H323H	4q31.23	rs5333
15	IL6R intron	1q21.3	rs4845623	55	EDNRA E335E	4q31.23	rs5334
16	IL6R intron	1q21.3	rs6690230	56	EDNRA 3' UTR	4q31.23	rs5342
17	IL6ST upstream	5q11.2	rs715180	57	EDNRB intron	13q22.3	rs7997107
18	IL6ST intron	5q11.2	rs7719246	58	EDNRB intron	13q22.3	rs7319342
19	IL8 intron	4q13.3	rs2227307	59	ACE intron	17q23.3	rs4295
20	IL8RA downstream	2q35	rs1008562	60	ACE intron	17q23.3	rs4311
21	TRAF3 intron	14q32.32	rs12880641	61	ACE intron	17q23.3	rs4329
22	TRAF3 intron	14q32.32	rs12147254	62	ACE intron	17q23.3	rs4353
23	TRAF3 intron	14q32.32	rs8006649	63	BDKRB1 P41P	14q32.2	rs2071084
24	TRAF3 M129T	14q32.32	rs1131877	64	BDKRB2 upstream	14q32.2	rs1799722
25	TNFRSF1A intron	12p13.31	rs1860545	65	BDKRB2 intron	14q32.2	rs8008168
26	TNFRSF1A intron	12p13.31	rs4149577	66	BDKRB2 intron	14q32.2	rs871547
27	TNFRSF1A intron	12p13.31	rs4149576	67	AGER upstream / PBX2 downstream	6p21.32	rs1800624
28	TNFRSF1B upstream	1p36.22	rs590368	68	AGER intron	6p21.32	rs1035798
29	TNFRSF1B intron	1p36.22	rs496888	69	S100A9 upstream	1q21.3	rs3014866
30	TNFRSF1B intron	1p36.22	rs653667	70	S100A9 downstream	1q21.3	rs724781

31	IL2RA intron	10p15.1	rs2476491
32	IL2RA upstream	10p15.1	rs1887027
33	IL2RB G250G	22q12.3	rs228953
34	IL2RB intron	22q13.1	rs228966
35	IL2RB upstream	22q13.1	rs743779
36	IL2RB upstream	22q13.1	rs229489
37	IL10 intron	1q32.1	rs1518111
38	IL10RA downstream	11q23.3	rs2512147
39	IL10RA downstream	11q23.3	rs2508446
40	IL10RA downstream	11q23.3	rs4936415

71	S100A9 downstream	1q21.3	rs3014875
72	S100A8 downstream	1q21.3	rs3006485
73	S100A1 intron /S100A13 intron	1q21.3	rs3790411
74	ABCB1 intron	7q21.12	rs12539098
75	ABCB1 intron	7q21.12	rs2235033
76	ABCB1 intron	7q21.12	rs1922242
77	ABCB1 I1145I	7q21.12	rs1045642

Supplementary Table 2 Proinflammatory genetic background in DCM and ICM. Significant associations of SNPs genotyped in the pilot study candidate gene approach and replication results (for study samples see Table S1). ORs with 95% CI were determined by a logistic regression model with the disease status (affected versus not affected) as outcome variable. The predictor variable indicates the presence (dominant model: 1 or 2 minor alleles; recessive model: 2 minor alleles) or absence (dominant model: 0 minor alleles; recessive model: 1 or 0 minor alleles) of the polymorphism. The ORs are adjusted for gender and age. n.s.=not significant

SNP Location	Chr. band	SNP name	Pheno-type	Genetic model	Allele major/minor	Study Sample	Genotypes 0/1/2 Alleles	Logistic regression		P-value
AGER intron	6p21.32	rs1035798	DCM	dominant	C/T	A	Case:149/173/43 Ctrl:254/202/46	1,545	1,12 – 2,13	0,008
						B	Case:347/329/80 Ctrl:889/715/164	1,215	0,99 – 1,49	0,063
						C	Case:89/77/14 Ctrl:262/226/39	0,983	0,69 – 1,40	n.s.
CD14 upstream	5q31.3	rs2569193	DCM	dominant	G/A	A	Case:173/105/33 Ctrl:350/324/52	0,73	0,55 – 0,96	0,024
						B	Case:407/286/63 Ctrl:974/812/151	0,807	0,66 – 0,99	0,039
						C	Case:97/67/16 Ctrl:249/242/45	0,635	0,45 – 0,91	0,012
IL1RL1 A78E	2q12.1	rs1041973	DCM	recessive	C/A	A	Case:210/142/28 Ctrl:305/180/20	2,009	0,97 – 4,15	0,059
						B	Case:438/268/50 Ctrl:1130/689/105	1,447	0,94 – 2,23	0,092
						C	Case:105/67/10 Ctrl:296/203/26	1,222	0,56 – 2,66	n.s.
IL2RA upstream	10p15.1	rs1887027	DCM	dominant	C/T	A	Case:231/131/14 Ctrl:339/145/19	1,371	0,99 – 1,91	0,061
						B	Case:486/262/33 Ctrl:1199/653/84	1,104	0,90 – 1,36	n.s.
						C	Case:102/74/5 Ctrl:336/173/29	1,397	0,98 – 2,00	0,067
IL6R intron	1q21.3	rs6427641	DCM	recessive	A/G	A	Case:119/209/56 Ctrl:156/236/114	0,617	0,41 – 0,93	0,020
						B	Case:237/393/133 Ctrl:643/916/373	0,777	0,60 – 1,01	0,061
						C	Case:61/93/29 Ctrl:175/264/93	0,833	0,52 – 1,33	n.s.
IL6ST upstream	5q11.2	rs715180	DCM	dominant	A/C	A	Case:335/48/2 Ctrl:459/45/3	1,627	0,99 – 2,68	0,056
						B	Case:653/107/3 Ctrl:1716/225/5	1,332	0,99 – 1,79	0,059
						C	Case:165/15/1 Ctrl:471/63/3	0,683	0,38 – 1,23	n.s.
IL8 intron	4q13.3	rs2227307	ICM	dominant	T/G	A	Case:111/135/55 Ctrl:127/257/118	0,515	0,33 – 0,81	0,004
						B				
						C				
IL8RA downstream	2q35	rs1008562	ICM	recessive	G/C	A	Case:66/146/54 Ctrl:123/250/131	0,519	0,31 – 0,87	0,013
						B				
						C				

Supplementary Table 3 List of all SNPs that were genotyped in 5q31.2-3 genomic region in the fine-mapping approach and their association to DCM

SNP #	rs Number	Position	Location	Major/minor	Genotypes (AA/AB/BB)		Allele frequency		OR	p-value	model
				allele (A/B)	DCM	Controls	DCM	Controls			
1	rs2916092	139394936	NRG2 intron	A/G	174/117/20	406/283/38	25,2	24,7	1,265178	0,427	2 v 01
2	rs2436389	139396449	NRG2 intron	T/G	109/156/44	279/343/99	39,5	37,5	1,155304	0,321	12 v 0
3	rs17286578	139412077		T/C	241/61/2	595/118/11	10,7	9,7	1,158046	0,407	12 v 0
4	rs1347142	139425284		T/C	205/93/7	500/201/27	17,5	17,5	0,6418413	0,311	2 v 01
5	rs1614557	139425349		C/G	240/61/2	597/125/10	10,7	9,9	1,131803	0,481	12 v 0
6	rs1623177	139440420		A/C	127/139/39	322/317/81	35,6	33,3	1,216898	0,36	2 v 01
7	rs2974421	139450424		A/G	203/89/10	504/195/26	18,0	17,0	1,144346	0,372	12 v 0
8	rs13156549	139495148		T/C	180/113/17	439/239/43	23,7	22,5	0,8043146	0,472	2 v 01
9	rs269783	139495578		A/G	211/79/13	492/207/29	17,3	18,2	0,9497207	0,735	12 v 0
10	rs156095	139497232		A/G	129/136/42	299/322/95	35,8	35,8	0,9713736	0,838	12 v 0
11	rs185123	139497381		C/T	89/144/69	209/363/147	46,7	45,7	1,202274	0,279	2 v 01
12	rs156094	139497745		C/A	126/127/42	297/329/95	35,8	36,0	0,928195	0,604	12 v 0
13	rs156090	139501868		C/T	89/144/66	212/360/148	46,2	45,6	1,1344	0,464	2 v 01
14	rs156089	139502512		T/C	123/127/42	306/319/95	36,1	35,3	1,042367	0,84	2 v 01
15	rs2291878	139519698		T/C	178/94/21	*440/235/50	23,2	23,1	1,065052	0,821	2 v 01
16	rs156085	139522621		G/A	249/43/0	618/95/5	7,4	7,3	1,111754	0,602	12 v 0
17	rs4913069	139525294		G/A	237/56/4	537/174/15	10,8	14,0	0,7486167	0,093	12 v 0
18	rs4463213	139525932		A/G	80/146/64	195/377/155	47,2	47,2	0,9236825	0,621	12 v 0
19	rs1432874	139591464	ORF1-FL49	A/G	159/112/26	372/298/52	27,6	27,8	0,8794769	0,366	12 v 0
20	rs4913079	139663213		A/G	81/151/73	190/366/162	48,7	48,1	1,117915	0,502	2 v 01
21	rs2337138	139671848		A/G	80/156/76	191/369/161	49,4	47,9	1,154302	0,382	2 v 01
22	rs4913080	139676687		G/A	178/92/21	449/233/41	23,0	21,8	1,353263	0,289	2 v 01
23	rs739954	139682104		T/C	88/150/70	207/362/163	47,1	47,0	0,9664523	0,826	12 v 0
24	rs17118812	139683470		T/C	151/124/32	*371/271/85	30,6	30,3	1,061181	0,672	12 v 0
25	rs11168036	139687623		T/G	82/146/72	200/342/172	48,3	48,0	1,019167	0,909	2 v 01
26	rs7268	139692734		G/T	96/144/74	204/358/167	46,5	47,5	0,8866731	0,429	12 v 0
27	rs13385	139693062	HBEGF 3' UTR	C/T	*185/99/25	417/261/55	24,1	25,3	0,9066701	0,49	12 v 0
28	rs11465458	139694441	HBEGF 3' UTR	C/A	313/1/0	726/6/0	0,2	0,4	0,2778121	0,239	12 v 0
29	rs2074613	139694748	HBEGF intron	A/G	95/134/72	202/350/170	46,2	47,8	0,8450142	0,272	12 v 0

SNP #	rs Number	Position	Location	Major/minor	Genotypes (AA/AB/BB)		Allele frequency		OR	p-value	model
				allele (A/B)	DCM	Controls	DCM	Controls			
30	rs4150196	139706825	HBEGF promotor region	G/A	82/153/69	180/357/181	47,9	50,1	0,891102	0,487	2 v 01
31	rs1862176	139710628		A/G	159/121/34	326/337/68	30,1	32,4	0,7838339	0,08	12 v 0
32	rs6879217	139711416		T/C	90/145/71	244/355/128	[‡] 46,9	42,0	1,427691	0,038	2 v 01
33	rs11168051	139728098	SLC4A9 intron	G/A	159/122/32	333/339/62	29,7	31,5	0,7953304	0,1	12 v 0
34	rs17286676	139729212	SLC4A9 intron	G/A	190/99/22	392/294/43	23 [†]	26,1	0,7523705	0,045	12 v 0
35	rs6872579	139756023		A/G	207/91/14	488/217/23	19,1	18,1	1,283885	0,481	2 v 01
36	rs10042299	139785795	MASK-BP3 intron / ANKHD1 intron	A/G	88/148/71	244/358/128	[‡] 47,2	42,1	1,407453	0,046	2 v 01
37	rs11746609	139858207	MASK-BP3 intron / ANKHD1 intron	C/T	291/13/3	699/32/0	3,1	2,2	1,333534	0,376	12 v 0
38	rs12516113	139862830	MASK-BP3 intron / ANKHD1 intron	A/G	279/39/0	681/52/1	[†] 6,1	3,7	1,825447	0,009	12 v 0
39	rs7712617	139868774	MASK-BP3 intron / ANKHD1 intron	A/C	*72/242/0	*132/586/17	38,5	42,2	0,7429955	0,08	12 v 0
40	rs1051309	139886028	MASK-BP3 G1586S / ANKHD1 G1586S	G/A	303/9/0	689/34/0	[†] 1,4	2,4	0,4709071	0,053	12 v 0
41	rs187505	139907249	MASK-BP3 intron / EIF4E-BP3 promotor region	G/C	274/21/3	664/52/3	4,5	4,0	1,068492	0,801	12 v 0
42	rs10463297	139916423	SRA1 intron	T/C	118/146/46	310/327/94	38,4	35,2	1,142253	0,352	12 v 0
43	rs250426	139916944	SRA1 S105T	T/G	154/111/29	328/326/65	[†] 28,7	31,7	0,7570864	0,051	12 v 0
44	rs250427	139917164	SRA1 C32R	C/T	131/104/25	318/330/61	29,6	31,9	0,798868	0,132	12 v 0
45	rs250430	139921412	APBB3 C238R	C/T	*243/55/10	517/189/15	[†] 12,2	15,2	0,7033648	0,035	12 v 0
46	rs250429	139925010	APBB3 promotor region / SLC35A4 intron	G/A	159/125/31	331/334/61	29,7	31,4	0,8133944	0,137	12 v 0
47	rs2569163	139955650		G/A	89/150/73	238/356/140	47,4	43,3	1,281165	0,14	2 v 01
48	rs11167532	139968081		G/A	110/149/54	285/346/103	41,1	37,6	1,252183	0,234	2 v 01
49	rs7711117	139968937		C/T	180/101/18	413/270/44	22,9	24,6	0,8865368	0,403	12 v 0
50	rs778584	139985396		C/T	74/154/84	141/363/224	51,6	55,7	1,254587	0,175	2 v 01
51	rs7721577	139985970		T/C	174/106/19	400/275/46	24,1	25,5	0,9175644	0,548	12 v 0
52	rs778587	139986614		C/T	*160/107/35	343/319/57	29,3	30,1	1,472628	0,096	2 v 01
53	rs778588	139987195		T/C	*166/113/33	345/321/56	28,7	30,0	0,7917228	0,095	12 v 0
54	rs2563298	139991499		C/A	*173/109/30	357/325/51	[†] 27,1	29,1	0,7495128	0,039	12 v 0
55	rs4914	139991652	CD14 L367L	C/G	238/64/4	576/137/13	11,8	11,2	1,028964	0,867	12 v 0
56	rs2569190	139993100	CD14 promotor region	G/A	88/150/70	224/369/135	47,1	43,9	1,255775	0,183	2 v 01
57	rs5744455	139993491	CD14 promotor region	C/T	182/100/19	406/273/46	22,9	25,2	0,8546846	0,274	12 v 0
58	rs2569191	139994087	CD14 promotor region	T/C	87/152/72	219/366/136	47,6	44,2	1,252185	0,185	2 v 01
59	rs2569193	139995679		G/A	*173/105/33	350/324/52	[†] 27,5	29,5	0,7292738	0,024	12 v 0
60	rs5744441	139997031		C/T	184/107/20	404/277/48	23,6	25,6	0,8876233	0,399	12 v 0
61	rs5744431	139998877	promotor regionO1518 promotor region	A/G	301/6/0	720/12/0	^{1,0}	0,8	1,144081	0,796	12 v 0

SNP #	rs Number	Position	Location	Major/minor	Genotypes (AA/AB/BB)		Allele frequency		OR	p-value	model
				allele (A/B)	DCM	Controls	DCM	Controls			
62	rs753279	140004002	promotor regionO1518 intron	C/T	101/144/60	261/344/120	43,3	40,3	1,197888	0,316	2 v 01
63	rs1583005	140011721	IK intron	C/T	109/143/59	216/355/162	42,0	46,3	0,7827389	0,098	12 v 0
64	rs2563335	140024476	WDR55 promotor region	C/A	91/142/56	197/345/175	43,9	48,5	0,7309218	0,076	2 v 01
65	rs2286394	140028728	WDR55 S210F	G/A	167/112/12	409/266/44	23,4	24,6	0,6318428	0,178	2 v 01
66	rs11954514	140036959	HARS intron	A/C	237/73/4	555/159/16	12,9	13,1	1,032016	0,846	12 v 0
67	rs811382	140037400	HARS intron	C/T	208/88/18	*426/276/26	†19,7	22,5	0,7108424	0,019	12 v 0
68	rs10515510	140053929	HARSL intron	G/C	284/27/3	669/61/2	5,3	4,4	1,085131	0,733	12 v 0
69	rs2878996	140100917		G/A	115/131/39	310/319/89	36,7	34,6	1,093677	0,541	12 v 0
70	rs3756342	140145808		T/C	85/144/72	183/344/194	47,8	50,8	0,8383552	0,281	2 v 01
71	rs3733712	140147404	PCDHA1 N449H	T/G	292/4/0	709/12/0	0,7	0,8	0,9160923	0,883	12 v 0
72	rs2240695	140148335	PCDHA1 intron	A/C	87/142/66	186/343/192	46,4	50,4	0,7674683	0,115	2 v 01
73	rs6871155	140160343	PCDHA1-2 intron / PCDHA3 promotor region	A/G	313/0/0	732/2/0	0,0	0,1	---	---	2 v 01
74	rs4151679	140160755	PCDHA1-2 intron / PCDHA3 promotor region	C/G	306/0/0	727/2/0	0,0	0,1	---	---	2 v 01
75	rs3733709	140161832	PCDHA1-2 intron / PCDHA3 I289T	A/G	234/63/5	540/172/7	12,1	12,9	0,8898351	0,484	12 v 0
76	rs3733708	140161918	PCDHA1-2 intron / PCDHA3 I318V	C/T	85/147/72	186/343/194	47,9	50,6	0,8306183	0,257	2 v 01
77	rs2240694	140163242	PCDHA1-2 intron / PCDHA3 C759Y	T/C	87/143/73	181/345/195	47,7	51,0	0,8374789	0,26	12 v 0
78	rs17286787	140165409	PCDHA1-3 intron	T/C	271/34/2	618/105/4	6,2	7,8	0,7003921	0,092	12 v 0
79	rs4151680	140166841	PCDHA1-3 intron / PCDHA4 promotor region	G/A	88/148/72	184/341/193	47,4	50,6	0,8085434	0,193	2 v 01
80	rs3822346	140167506	PCDHA1-3 intron / PCDHA4 P184S	A/G	88/151/72	188/342/190	47,4	50,1	0,8138249	0,208	2 v 01
81	rs4151681	140181403	PCDHA1-4 intron / PCDHA5 promotor region	G/A	294/13/0	685/44/1	2,1	3,2	0,5470175	0,068	12 v 0
82	rs4141841	140183616	PCDHA1-4 intron / PCDHA5 A691V	A/G	84/147/74	182/346/190	48,4	50,6	0,8625764	0,363	2 v 01
83	rs3756334	140193980	PCDHA1-6 intron / PCDHA7 promotor region	T/C	75/141/70	182/338/195	49,1	50,9	0,8407352	0,295	2 v 01
84	rs628871	140211436	PCDHA1-9 intron	A/G	*169/102/32	*376/224/110	27,4	31,3	0,6735695	0,071	2 v 01
85	rs17119246	140212530	PCDHA1-9 intron	C/T	*275/26/5	*651/54/7	5,9	4,8	1,261222	0,329	12 v 0
86	rs251368	140221211	PCDHA1-10 intron	C/A	83/149/78	182/337/198	49,2	51,1	0,8561868	0,331	2 v 01
87	rs251371	140227538	PCDHA1-10 intron	C/G	146/129/32	352/291/78	31,4	31,0	1,03162	0,824	12 v 0
88	rs3776121	140254494	PCDHA1-13 intron	C/T	123/136/41	308/318/101	36,3	35,8	1,020556	0,887	12 v 0
89	rs4912732	140285118	PCDHA1-13 intron	A/G	284/28/0	641/85/3	4,5	6,2	0,7668362	0,256	12 v 0
90	rs246074	140288153	PCDHA1-13 intron / PCDHAC1 L498V	C/G	84/144/72	182/336/200	48,0	51,3	0,790292	0,149	2 v 01
91	rs3756325	140349043	PCDHA1-13, PCDHAC1 and PCDHAC2 intron	C/T	151/132/28	360/291/64	30,2	29,3	1,040409	0,777	12 v 0
92	rs31874	140349502	PCDHA1-13, PCDHAC1 and PCDHAC2 intron	T/C	151/124/30	351/292/79	30,2	31,2	0,8597524	0,514	12 v 0
93	rs31872	140352406	PCDHA1-13, PCDHAC1 and PCDHAC2 intron	T/C	102/145/47	257/327/136	40,6	41,6	0,7972555	0,234	2 v 01

SNP #	rs Number	Position	Location	Major/minor	Genotypes (AA/AB/BB)		Allele frequency		OR	p-value	model
				allele (A/B)	DCM	Controls	DCM	Controls			
94	rs13167551	140375729		A/G	253/43/2	621/100/7	7,9	7,8	0,9286557	0,709	12 v 0
95	rs246592	140388357		G/A	135/138/32	347/312/68	33,1	30,8	1,102629	0,488	12 v 0
96	rs702390	140422393		C/T	89/155/56	*229/327/167	44,5	45,7	0,7688365	0,138	2 v 01
97	rs31801	140434685		T/C	72/155/73	*197/331/193	50,2	49,7	0,8297272	0,253	2 v 01
98	rs3822339	140484616	PCDHB4 3'UTR	T/G	256/44/2	605/104/9	7,9	8,5	0,9158148	0,653	12 v 0
99	rs246723	140499350		C/T	102/162/41	270/326/128	40,0	40,2	0,7239802	0,105	2 v 01
100	rs246711	140507433		C/T	110/149/45	266/330/119	39,3	39,7	0,9088806	0,626	2 v 01
101	rs3776096	140510713	PCDHB6 V231I	C/T	172/110/17	435/254/37	24,1	22,6	1,217735	0,529	2 v 01
102	rs17629216	140512593	PCDHB6 3'UTR	G/A	276/37/1	653/73/1	6,2	5,2	1,264866	0,283	12 v 0
103	rs246688	140526378		C/A	92/150/61	218/354/148	44,9	45,1	0,9885179	0,947	2 v 01
104	rs10477144	140527381		T/C	182/84/9	*536/166/23	†18,5	14,6	1,487179	0,012	12 v 0
105	rs17286891	140532958	PCDHB7 E120K	G/A	247/47/2	609/113/7	8,6	8,7	1,013443	0,944	12 v 0
106	rs2910326	140568557	PCDHB12 5' UTR	C/T	137/137/32	318/320/88	32,8	34,2	0,8411553	0,443	2 v 01
107	rs2910002	140586298		T/C	138/141/33	318/321/86	33,2	34,0	0,8661894	0,52	2 v 01
108	rs10516156	140609874		G/T	180/99/17	445/253/34	22,5	21,9	1,364618	0,327	2 v 01
109	rs1638537	140619766		G/C	93/158/60	221/357/142	44,7	44,5	1,072341	0,647	12 v 0

* not in HW equilibrium as assessed with the exact test that is implemented in the program Haploview at a significance level of 0.05

‡ association for the recessive inheritance model (two copies of minor allele versus zero or one copy)

† association for the dominant inheritance model (one or two copies of minor allele versus zero copy)

Supplementary Table 4 Symbols and names of genes located in the CM-cluster

Official symbol	Official full name	MIM number
HBEGF	Heparin-binding EGF-like growth factor	126150
SLC4A9	Solute carrier family 4, sodium bicarbonate cotransporter, member 9	610207
ANKHD1	Ankyrin repeat and KH domain containing 1	610500
EIF4EBP3	Eukaryotic translation initiation factor 4E binding protein 3	603483
ANKHD1-EIF4EBP3	ANKHD1-EIF4EBP3 readthrough transcript	610500
SRA1	Steroid receptor RNA activator 1	603819
APBB3	Amyloid beta (A4) precursor protein-binding, family B, member 3	602711
SLC35A4	Solute carrier family 35, member A4	-
CD14	CD14 molecule	158120
TMCO6	Transmembrane and coiled-coil domains 6	-
NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	602137
IK	IK cytokine, down-regulator of HLA II	600549
WDR55	WD repeat domain 55	-
DND1	Dead end homolog 1 (zebrafish)	609385
HARS	Histidyl-tRNA synthetase	142810
HARS2	Histidyl-tRNA synthetase 2, mitochondrial (putative)	600783
ZMAT2	Zinc finger, matrin type 2	-
PCDHA1-13	Protocadherin alpha 1-13	604966
PCDHAC1 and 2	Protocadherin alpha subfamily C, 1 and 2	604966

Supplementary Table 5 Functional evaluation of 5q31 CM-cluster genes in zebrafish using morpholino-modified antisense oligonucleotides

A Morpholinos (MO)

Genes	Human protein	Zebrafish Ortholog	MO-type	MO-sequence
HBEGF	NP_001936	ENSDART00000010193 (Ensembl Zv6)	splice	AAAAGAAGCAAATTTACCTCTTGGC
ANKHD1	NP_060217.1	ENSDART00000112410 (Ensembl Zv8)	splice	AGGTGTCCCCAGTACCTTGTGCCAA
EIF4EBP3	NP_003723	Zgc:103720	start	AGCTTCACTGTTTGACATGATTTGT
EIF4EBP3l	NP_003723	CF269291/Zgc:56330	start	TGCTCTGCTGCGTGTTTGTGGACAT
SRA1	AAH40043	ENSDART00000075672 (Ensembl Zv6)	splice	TTACATGGCCTGACCTGTGGTTTG
IK	NP_006074	NM_199589	start	GGAGCCAGAGGATTAGAGTACACAT
WDR55	NP_060176	GENSCAN00000030918 (Ensembl Zv6)	start	ACTTTACGACCTCTTTTCATAATGG
DND1	NP_061900	NM_212795	start	GCTGGGCATCCATGTCTCCGACCAT
ZMAT2	NP_653324	NM_212681	splice	TTCTTGGACTIONAGAAACCAGAATATG

B Morpholino injections

Genes	MO amounts injected (ng)	Total number of embryos injected	Embryos showing a heart phenotype in %	CM phenotype at 72 hpf	Control embryos with heart phenotype in %	Other organs affected °
HBEGF	2,4,8	60 (2 ng)	60 (2 ng)	weak contractility (2 ng)	0	Skeletal muscle (2 ng) General necrosis (4,8 ng)
ANKHD1	2,4,8	120	71 (2 ng) 80 (4 ng) 100 (8 ng)	dilated atrium, weak contractility (2 ng)	0	General necrosis (4,8 ng)
EIF4EBP3	2,4,8	43	0	0	0	Skeletal muscle (4 ng)
EIF4EBP3I	2,4,8	50*	0	0	0	No effect
SRA1	2,4,8	87 (4 ng)	49 (4 ng)	silent ventricle (4 ng)	0	Skeletal muscle (4 ng) General necrosis (8 ng)
IK	2,4,8	86 (2 ng)	71 (2 ng)	weak contractility (2 ng)	0	Skeletal muscle General necrosis (4,8 ng)
WDR55	2,4,8	50*	0	0	0	General necrosis (8 ng)
DND1	2,4,8	45 (4 ng)	11 (4 ng)	weak contractility (4 ng)	0	General necrosis (8 ng)
ZMAT2	2,4,8	50*	0	0	0	No effect

(*) Different amounts of morpholinos were injected in approximately 50 eggs. Remaining embryos were not counted if there was no heart defect.

(°) MO injected embryos were screened primarily for a heart phenotype, effects on other organs, except skeletal muscle, are not included in this table.

Supplementary Table 6 KNN analysis of CM-cluster genes across NCBI Gene Expression Omnibus data set. Affymetrix human HG_U133A DNA chip probeset IDs (HBEGF: 203821_at; HBEGF+: 38037_at; ANKHD1: 208772_at; ANKHD1+: 208773_s_at; ANKHD1++: 219081_at; EIF4EBP3: 214919_s_at; APBB3: 204650_s_at; CD14: 201743_at; TMCO6: 221096_s_at; NDUFA2: 209224_s_at; IK: 200066_at; WDR55: 219809_at; DND1: 222070_at; DND1+: 57739_at; HARS: 202042_at; HARS2: 209252_at; PCDHA*: 210674_s_at; PCDHA2: 211365_s_at; PCDHA3: 211870_s_at; PCDHA5: 211838_x_at; PCDHA8: 211811_s_at; PCDHA9: 208205_at; PCDHA10: 211867_s_at) for the CM-cluster genes were used to perform KNN analysis. The significances of two probesets showing expression co-regulation across all GEO experiments performed on HG_U133A chips were represented by the local Z-scores.

[illegible]