

Gene Ontology biological process terms enriched in the SCDgset^a

GO biological process	Terms^b	No. of genes^c	P value^d	FDR^e
GO:0045944	Positive regulation of transcription from RNA polymerase II promoter	31	1.08E-04	0.1893675
GO:0060048	Cardiac muscle contraction	30	6.22E-43	1.09E-39
GO:0086091	Regulation of heart rate by cardiac conduction	28	1.48E-43	2.59E-40
GO:0000122	Negative regulation of transcription from RNA polymerase II promoter	28	7.50E-06	0.013141
GO:0007507	Heart development	23	3.05E-14	5.35E-11
GO:0045893	Positive regulation of transcription, DNA-templated	23	7.49E-06	0.0131182
GO:0006936	Muscle contraction	21	6.95E-17	2.00E-13
GO:0001666	Response to hypoxia	21	8.87E-13	1.55E-09
GO:0010628	Positive regulation of gene expression	21	1.87E-09	3.28E-06
GO:0002027	Regulation of heart rate	19	4.35E-25	7.62E-22

GO:0030049	Muscle filament sliding	18	8.14E-22	1.43E-18
GO:0008284	Positive regulation of cell proliferation	18	5.35E-04	0.9321757
GO:1903779	Regulation of cardiac conduction	17	6.60E-17	2.00E-13
GO:0043066	Negative regulation of apoptotic process	17	0.0011368	1.9722978
GO:0007155	Cell adhesion	17	0.0012493	2.1653837
GO:0060307	Regulation of ventricular cardiac muscle cell membrane repolarization	16	2.65E-26	4.63E-23
GO:0002576	Platelet degranulation	16	2.60E-11	4.56E-08
GO:0045892	Negative regulation of transcription, DNA-templated	16	0.0069142	11.441523
GO:0043547	Positive regulation of GTPase activity	16	0.0197228	29.450069
GO:0086005	Ventricular cardiac muscle cell action potential	14	1.06E-22	1.86E-19
GO:0030308	Negative regulation of cell growth	14	2.52E-08	4.41E-05
GO:0006468	Protein phosphorylation	14	0.0172613	26.282524
GO:0061337	Cardiac conduction	13	1.40E-12	2.45E-09

GO:0042060	Wound healing	13	1.87E-09	3.27E-06
GO:0071805	Potassium ion transmembrane transport	13	2.13E-07	3.74E-04
GO:0001701	In utero embryonic development	13	2.07E-05	0.0363012
GO:0001525	Angiogenesis	13	1.15E-04	0.2003972
GO:0007267	Cell-cell signaling	13	3.78E-04	0.6601007
GO:0086002	Cardiac muscle cell action potential involved in contraction	12	2.17E-17	3.80E-14
GO:0045214	Sarcomere organization	12	1.46E-13	2.56E-10
GO:0010629	Negative regulation of gene expression	12	5.57E-06	0.009753
GO:0000165	MAPK cascade	12	0.0017214	2.9721193
GO:0007399	Nervous system development	12	0.0034789	5.9204999
GO:0043065	Positive regulation of apoptotic process	12	0.0048486	8.1596353
GO:0042493	Response to drug	12	0.0053109	8.9039203
GO:0008285	Negative regulation of cell proliferation	12	0.0320628	43.48719

GO:0055117	Regulation of cardiac muscle contraction	11	1.16E-13	2.03E-10
GO:0055010	Ventricular cardiac muscle tissue morphogenesis	11	1.02E-12	1.79E-09
GO:0007568	Aging	11	1.63E-04	0.2848647
GO:0034220	Ion transmembrane transport	11	0.0010895	1.8908644
GO:0008283	Cell proliferation	11	0.0439472	54.481637
GO:0086012	Membrane depolarization during cardiac muscle cell action potential	10	1.83E-14	3.19E-11
GO:0035725	Sodium ion transmembrane transport	10	1.15E-06	0.0020184
GO:0007517	Muscle organ development	10	6.16E-06	0.0107829
GO:0030335	Positive regulation of cell migration	10	0.0015936	2.7543445
GO:0010881	Regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	9	1.25E-10	2.18E-07
GO:0060412	Ventricular septum morphogenesis	9	6.23E-09	1.09E-05
GO:0007519	Skeletal muscle tissue development	9	7.00E-07	0.0012259

GO:0001947	Heart looping	9	2.85E-06	0.0049973
GO:0071260	Cellular response to mechanical stimulus	9	9.09E-06	0.0159162
GO:0006874	Cellular calcium ion homeostasis	9	6.60E-05	0.1154875
GO:0007204	Positive regulation of cytosolic calcium ion concentration	9	8.08E-04	1.4058744
GO:0007050	Cell cycle arrest	9	0.0011251	1.9520984
GO:0086014	Atrial cardiac muscle cell action potential	8	4.67E-12	8.18E-09
GO:0098911	Regulation of ventricular cardiac muscle cell action potential	8	4.18E-11	7.31E-08
GO:0060306	Regulation of membrane repolarization	8	9.90E-11	1.73E-07
GO:0035994	Response to muscle stretch	8	1.36E-09	2.38E-06
GO:2000649	Regulation of sodium ion transmembrane transporter activity	8	1.36E-09	2.38E-06
GO:0002026	Regulation of the force of heart contraction	8	5.77E-09	1.01E-05
GO:0010765	Positive regulation of sodium ion transport	8	5.77E-09	1.01E-05
GO:0008016	Regulation of heart contraction	8	2.59E-07	4.54E-04

GO:0045429	Positive regulation of nitric oxide biosynthetic process	8	2.73E-06	0.0047863
GO:0032147	Activation of protein kinase activity	8	3.75E-06	0.0065743
GO:0003151	Outflow tract morphogenesis	8	4.37E-06	0.0076582
GO:0010595	Positive regulation of endothelial cell migration	8	4.37E-06	0.0076582
GO:0072659	Protein localization to plasma membrane	8	3.66E-05	0.0640517
GO:0030512	Negative regulation of transforming growth factor beta receptor signaling pathway	8	4.06E-05	0.0710275
GO:0008217	Regulation of blood pressure	8	4.49E-05	0.0786143
GO:0006813	Potassium ion transport	8	1.99E-04	0.3472583
GO:0001822	Kidney development	8	2.67E-04	0.466827
GO:0007179	Transforming growth factor beta receptor signaling pathway	8	4.04E-04	0.7059014
GO:0032496	Response to lipopolysaccharide	8	0.0106183	17.051294
GO:0051260	Protein homooligomerization	8	0.0156175	24.093

GO:0007596	Blood coagulation	8	0.0189112	28.420137
GO:0042127	Regulation of cell proliferation	8	0.0193974	29.038792
GO:0030198	Extracellular matrix organization	8	0.0256382	36.545575
GO:0098915	Membrane repolarization during ventricular cardiac muscle cell action potential	7	2.54E-10	4.45E-07
GO:0098909	Regulation of cardiac muscle cell action potential involved in regulation of contraction	7	2.54E-10	4.45E-07
GO:0060371	Regulation of atrial cardiac muscle cell membrane depolarization	7	2.54E-10	4.45E-07
GO:0071435	Potassium ion export	7	7.53E-10	1.32E-06
GO:0086013	Membrane repolarization during cardiac muscle cell action potential	7	1.86E-09	3.26E-06
GO:0055008	Cardiac muscle tissue morphogenesis	7	7.98E-09	1.40E-05
GO:0086064	Cell communication by electrical coupling involved in cardiac conduction	7	1.46E-08	2.57E-05

GO:0060047	Heart contraction	7	1.46E-08	2.57E-05
GO:1901381	Positive regulation of potassium ion transmembrane transport	7	4.17E-08	7.30E-05
GO:0019229	Regulation of vasoconstriction	7	3.04E-07	5.32E-04
GO:0060078	Regulation of postsynaptic membrane potential	7	5.70E-07	9.98E-04
GO:0010107	Potassium ion import	7	2.67E-06	0.0046831
GO:0003007	Heart morphogenesis	7	6.12E-06	0.0107248
GO:0001570	Vasculogenesis	7	1.64E-04	0.286156
GO:0050729	Positive regulation of inflammatory response	7	6.98E-04	1.2145895
GO:0042391	Regulation of membrane potential	7	8.05E-04	1.4009907
GO:0060021	Palate development	7	8.64E-04	1.5020065
GO:0046718	Viral entry into host cell	7	0.0011311	1.9624902
GO:0006814	Sodium ion transport	7	0.0012069	2.0926543
GO:0050731	Positive regulation of peptidyl-tyrosine phosphorylation	7	0.0012865	2.229214

GO:0060070	Canonical Wnt signaling pathway	7	0.00137	2.3723592
GO:0045766	Positive regulation of angiogenesis	7	0.006944	11.487996
GO:0030168	Platelet activation	7	0.006944	11.487996
GO:0007219	Notch signaling pathway	7	0.006944	11.487996
GO:0050900	Leukocyte migration	7	0.0091726	14.902889
GO:0043524	Negative regulation of neuron apoptotic process	7	0.0131829	20.737319
GO:0050821	Protein stabilization	7	0.0150858	23.371737
GO:0006367	Transcription initiation from RNA polymerase II promoter	7	0.0245996	35.350596
GO:0046777	Protein autophosphorylation	7	0.0412629	52.190876
GO:0060373	Regulation of ventricular cardiac muscle cell membrane depolarization	6	1.33E-08	2.33E-05
GO:0048739	Cardiac muscle fiber development	6	3.50E-08	6.13E-05
GO:0003222	Ventricular trabecula myocardium morphogenesis	6	2.48E-06	0.0043438
GO:0010460	Positive regulation of heart rate	6	3.47E-06	0.0060803

GO:0051000	Positive regulation of nitric-oxide synthase activity	6	1.39E-05	0.0243686
GO:0003148	Outflow tract septum morphogenesis	6	1.76E-05	0.0307662
GO:0010718	Positive regulation of epithelial to mesenchymal transition	6	1.10E-04	0.1924085
GO:0090002	Establishment of protein localization to plasma membrane	6	3.54E-04	0.6182603
GO:0045785	Positive regulation of cell adhesion	6	3.96E-04	0.6910984
GO:0019722	Calcium-mediated signaling	6	8.79E-04	1.527541
GO:0051592	Response to calcium ion	6	0.0015774	2.7267769
GO:0009612	Response to mechanical stimulus	6	0.0017032	2.9411723
GO:0043627	Response to estrogen	6	0.0026177	4.4865959
GO:0014068	Positive regulation of phosphatidylinositol 3-kinase signaling	6	0.0026177	4.4865959
GO:0007015	Actin filament organization	6	0.004083	6.9144149
GO:0006816	Calcium ion transport	6	0.0051435	8.6351254
GO:0007565	Female pregnancy	6	0.0099221	16.023252

GO:0009887	Organ morphogenesis	6	0.0113504	18.119649
GO:0030336	Negative regulation of cell migration	6	0.0129127	20.356319
GO:0071456	Cellular response to hypoxia	6	0.0134642	21.131994
GO:0006469	Negative regulation of protein kinase activity	6	0.0152134	23.545435
GO:0016337	Single organismal cell-cell adhesion	6	0.0164603	25.223113
GO:0034765	Regulation of ion transmembrane transport	6	0.0237127	34.313359
GO:0071222	Cellular response to lipopolysaccharide	6	0.025375	36.244656
GO:0070588	Calcium ion transmembrane transport	6	0.030803	42.185164
GO:0086011	Membrane repolarization during action potential	5	2.22E-07	3.89E-04
GO:0086073	Bundle of His cell-Purkinje myocyte adhesion involved in cell communication	5	6.59E-07	0.001154
GO:0060372	Regulation of atrial cardiac muscle cell membrane repolarization	5	6.59E-07	0.001154
GO:0086015	SA node cell action potential	5	6.59E-07	0.001154

GO:0010882	Regulation of cardiac muscle contraction by calcium ion signaling	5	1.52E-06	0.0026616
GO:1902305	Regulation of sodium ion transmembrane transport	5	3.00E-06	0.0052619
GO:0055003	Cardiac myofibril assembly	5	2.03E-05	0.0355213
GO:0030195	Negative regulation of blood coagulation	5	2.03E-05	0.0355213
GO:0055119	Relaxation of cardiac muscle	5	2.03E-05	0.0355213
GO:0007512	Adult heart development	5	2.90E-05	0.0507154
GO:0006941	Striated muscle contraction	5	2.90E-05	0.0507154
GO:0060402	Calcium ion transport into cytosol	5	4.01E-05	0.0701795
GO:0014898	Cardiac muscle hypertrophy in response to stress	5	5.40E-05	0.0945897
GO:1901379	Regulation of potassium ion transmembrane transport	5	5.40E-05	0.0945897
GO:0010880	Regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	5	1.17E-04	0.2047273
GO:0060314	Regulation of ryanodine-sensitive calcium-release channel activity	5	1.47E-04	0.2562869

GO:0048844	Artery morphogenesis	5	2.21E-04	0.386487
GO:0030879	Mammary gland development	5	2.21E-04	0.386487
GO:0045662	Negative regulation of myoblast differentiation	5	3.20E-04	0.5583552
GO:0051924	Regulation of calcium ion transport	5	3.79E-04	0.66204
GO:0003009	Skeletal muscle contraction	5	3.79E-04	0.66204
GO:0051899	Membrane depolarization	5	4.46E-04	0.7787047
GO:2000379	Positive regulation of reactive oxygen species metabolic process	5	9.13E-04	1.586782
GO:0032781	Positive regulation of ATPase activity	5	0.0010362	1.7992698
GO:0042177	Negative regulation of protein catabolic process	5	0.0011708	2.030634
GO:0001837	Epithelial to mesenchymal transition	5	0.0014757	2.5531215
GO:0050714	Positive regulation of protein secretion	5	0.001832	3.160265
GO:0032570	Response to progesterone	5	0.0024719	4.241759
GO:0030326	Embryonic limb morphogenesis	5	0.0027154	4.6502814

GO:0051496	Positive regulation of stress fiber assembly	5	0.0032507	5.5426211
GO:0030155	Regulation of cell adhesion	5	0.0035435	6.0273737
GO:0071560	Cellular response to transforming growth factor beta stimulus	5	0.0056824	9.4978631
GO:0042542	Response to hydrogen peroxide	5	0.0065517	10.873613
GO:0019233	Sensory perception of pain	5	0.0070176	11.602812
GO:0071320	Cellular response to camp	5	0.0070176	11.602812
GO:0016049	Cell growth	5	0.009099	14.792095
GO:0043406	Positive regulation of MAP kinase activity	5	0.0108989	17.462372
GO:0048661	Positive regulation of smooth muscle cell proliferation	5	0.0115462	18.40328
GO:0050679	Positive regulation of epithelial cell proliferation	5	0.0115462	18.40328
GO:0050727	Regulation of inflammatory response	5	0.0136347	21.370456
GO:0042632	Cholesterol homeostasis	5	0.0143807	22.405396
GO:0001938	Positive regulation of endothelial cell proliferation	5	0.0184961	27.887853

GO:0035690	Cellular response to drug	5	0.0184961	27.887853
GO:0048010	Vascular endothelial growth factor receptor signaling pathway	5	0.021282	31.389575
GO:0030334	Regulation of cell migration	5	0.0232744	33.795027
GO:0030509	BMP signaling pathway	5	0.0253767	36.246619
GO:0030324	Lung development	5	0.0253767	36.246619
GO:0001558	Regulation of cell growth	5	0.0299146	41.249949
GO:0043085	Positive regulation of catalytic activity	5	0.0311192	42.514504
GO:0051897	Positive regulation of protein kinase B signaling	5	0.0349024	46.321342
GO:0030307	Positive regulation of cell growth	5	0.0349024	46.321342
GO:0007160	Cell-matrix adhesion	5	0.0432361	53.885043
GO:1900825	Regulation of membrane depolarization during cardiac muscle cell action potential	4	1.23E-05	0.0215223
GO:0035995	Detection of muscle stretch	4	1.23E-05	0.0215223

GO:1905007	Positive regulation of epithelial to mesenchymal transition involved in endocardial cushion formation	4	3.04E-05	0.053214
GO:0003081	Regulation of systemic arterial blood pressure by renin-angiotensin	4	6.01E-05	0.1052485
GO:1901018	Positive regulation of potassium ion transmembrane transporter activity	4	6.01E-05	0.1052485
GO:2001259	Positive regulation of cation channel activity	4	1.04E-04	0.1821235
GO:1901841	Regulation of high voltage-gated calcium channel activity	4	1.04E-04	0.1821235
GO:1901380	Negative regulation of potassium ion transmembrane transport	4	1.65E-04	0.2880989
GO:0003300	Cardiac muscle hypertrophy	4	1.65E-04	0.2880989
GO:0071313	Cellular response to caffeine	4	1.65E-04	0.2880989
GO:0051001	Negative regulation of nitric-oxide synthase activity	4	1.65E-04	0.2880989
GO:1902260	Negative regulation of delayed rectifier potassium channel activity	4	1.65E-04	0.2880989
GO:0086009	Membrane repolarization	4	2.44E-04	0.4271923

GO:1990573	Potassium ion import across plasma membrane	4	2.44E-04	0.4271923
GO:0060316	Positive regulation of ryanodine-sensitive calcium-release channel activity	4	2.44E-04	0.4271923
GO:0043267	Negative regulation of potassium ion transport	4	3.45E-04	0.6031745
GO:0003181	Atrioventricular valve morphogenesis	4	4.70E-04	0.819564
GO:0060315	Negative regulation of ryanodine-sensitive calcium-release channel activity	4	6.20E-04	1.0796205
GO:0086004	Regulation of cardiac muscle cell contraction	4	6.20E-04	1.0796205
GO:0060413	Atrial septum morphogenesis	4	7.97E-04	1.3863392
GO:0005513	Detection of calcium ion	4	0.0010032	1.7424449
GO:0006937	Regulation of muscle contraction	4	0.0010032	1.7424449
GO:0048738	Cardiac muscle tissue development	4	0.0018143	3.1301535
GO:0045216	Cell–cell junction organization	4	0.0021538	3.705451

GO:0006883	Cellular sodium ion homeostasis	4	0.0025301	4.3395183
GO:1902895	Positive regulation of pri-miRNA transcription from RNA polymerase II promoter	4	0.0029446	5.0333581
GO:0071375	Cellular response to peptide hormone stimulus	4	0.0029446	5.0333581
GO:0045663	Positive regulation of myoblast differentiation	4	0.0033986	5.7876775
GO:0060045	Positive regulation of cardiac muscle cell proliferation	4	0.003893	6.6028892
GO:0033137	Negative regulation of peptidyl-serine phosphorylation	4	0.004429	7.4791128
GO:0048709	Oligodendrocyte differentiation	4	0.0056295	9.4136323
GO:0050999	Regulation of nitric-oxide synthase activity	4	0.0062958	10.470741
GO:0055007	Cardiac muscle cell differentiation	4	0.0070072	11.586499
GO:0001569	Patterning of blood vessels	4	0.0077643	12.759642
GO:0086010	Membrane depolarization during action potential	4	0.0077643	12.759642
GO:0045909	Positive regulation of vasodilation	4	0.0085678	13.98865

GO:0001937	Negative regulation of endothelial cell proliferation	4	0.0085678	13.98865
GO:0060325	Face morphogenesis	4	0.0094183	15.271764
GO:0001974	Blood vessel remodeling	4	0.0112625	17.992149
GO:0051480	Regulation of cytosolic calcium ion concentration	4	0.0112625	17.992149
GO:0002088	Lens development in camera-type eye	4	0.0122571	19.424818
GO:0001756	Somitogenesis	4	0.019259	28.86322
GO:0046426	Negative regulation of JAK-STAT cascade	4	0.0206004	30.547998
GO:0007190	Activation of adenylate cyclase activity	4	0.0206004	30.547998
GO:0048839	Inner ear development	4	0.0219919	32.255923
GO:0070527	Platelet aggregation	4	0.0219919	32.255923
GO:0023014	Signal transduction by protein phosphorylation	4	0.0264671	37.48425
GO:0007077	Mitotic nuclear envelope disassembly	4	0.0264671	37.48425
GO:0030514	Negative regulation of BMP signaling pathway	4	0.0280589	39.250392

GO:0008015	Blood circulation	4	0.0280589	39.250392
GO:0009267	Cellular response to starvation	4	0.0313919	42.797254
GO:0051781	Positive regulation of cell division	4	0.0313919	42.797254
GO:0031100	Organ regeneration	4	0.0313919	42.797254
GO:0010862	Positive regulation of pathway-restricted SMAD protein phosphorylation	4	0.0331328	44.571305
GO:0048812	Neuron projection morphogenesis	4	0.0331328	44.571305
GO:0035914	Skeletal muscle cell differentiation	4	0.0349231	46.341437
GO:0045727	Positive regulation of translation	4	0.0425722	53.3215
GO:0098910	Regulation of atrial cardiac muscle cell action potential	3	6.35E-04	1.1063454
GO:0033292	T-tubule organization	3	6.35E-04	1.1063454
GO:1903598	Positive regulation of gap junction assembly	3	6.35E-04	1.1063454
GO:0098912	Membrane depolarization during atrial cardiac muscle cell action	3	6.35E-04	1.1063454

	potential			
GO:0098904	Regulation of AV node cell action potential	3	6.35E-04	1.1063454
GO:0086016	AV node cell action potential	3	0.0012578	2.1800627
GO:0097623	Potassium ion export across plasma membrane	3	0.0012578	2.1800627
GO:0002018	Renin-angiotensin regulation of aldosterone production	3	0.0012578	2.1800627
GO:0002159	Desmosome assembly	3	0.0012578	2.1800627
GO:0060043	Regulation of cardiac muscle cell proliferation	3	0.0020761	3.5741748
GO:0086046	Membrane depolarization during SA node cell action potential	3	0.0020761	3.5741748
GO:0070296	Sarcoplasmic reticulum calcium ion transport	3	0.0020761	3.5741748
GO:0098735	Positive regulation of the force of heart contraction	3	0.0020761	3.5741748
GO:1902261	Positive regulation of delayed rectifier potassium channel activity	3	0.0020761	3.5741748
GO:0030240	Skeletal muscle thin filament assembly	3	0.0020761	3.5741748
GO:0051891	Positive regulation of cardioblast differentiation	3	0.0020761	3.5741748

GO:0098914	Membrane repolarization during atrial cardiac muscle cell action potential	3	0.0020761	3.5741748
GO:0003161	Cardiac conduction system development	3	0.0020761	3.5741748
GO:0086045	Membrane depolarization during AV node cell action potential	3	0.0020761	3.5741748
GO:0010649	Regulation of cell communication by electrical coupling	3	0.0030841	5.2657374
GO:0055075	Potassium ion homeostasis	3	0.0030841	5.2657374
GO:0003158	Endothelium development	3	0.0030841	5.2657374
GO:0014883	Transition between fast and slow fiber	3	0.0042761	7.2299963
GO:0060982	Coronary artery morphogenesis	3	0.0042761	7.2299963
GO:1901017	Negative regulation of potassium ion transmembrane transporter activity	3	0.0042761	7.2299963
GO:0014808	Release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	3	0.0042761	7.2299963

GO:0055013	Cardiac muscle cell development	3	0.0042761	7.2299963
GO:1901844	Regulation of cell communication by electrical coupling involved in cardiac conduction	3	0.0056466	9.4408502
GO:0016264	Gap junction assembly	3	0.0056466	9.4408502
GO:0061049	Cell growth involved in cardiac muscle cell development	3	0.0056466	9.4408502
GO:0086036	Regulation of cardiac muscle cell membrane potential	3	0.0056466	9.4408502
GO:0003254	Regulation of membrane depolarization	3	0.0071901	11.871297
GO:0060452	Positive regulation of cardiac muscle contraction	3	0.0071901	11.871297
GO:0043462	Regulation of ATPase activity	3	0.0071901	11.871297
GO:0006942	Regulation of striated muscle contraction	3	0.0071901	11.871297
GO:0003184	Pulmonary valve morphogenesis	3	0.0089012	14.49386
GO:0060044	Negative regulation of cardiac muscle cell proliferation	3	0.0089012	14.49386
GO:0032780	Negative regulation of ATPase activity	3	0.0089012	14.49386

GO:0038166	Angiotensin-activated signaling pathway	3	0.0089012	14.49386
GO:0051481	Negative regulation of cytosolic calcium ion concentration	3	0.0089012	14.49386
GO:0051272	Positive regulation of cellular component movement	3	0.0089012	14.49386
GO:0050927	Positive regulation of positive chemotaxis	3	0.0107749	17.280979
GO:0002003	Angiotensin maturation	3	0.0107749	17.280979
GO:0034374	Low-density lipoprotein particle remodeling	3	0.0107749	17.280979
GO:0051279	Regulation of release of sequestered calcium ion into cytosol	3	0.0107749	17.280979
GO:0061045	Negative regulation of wound healing	3	0.0107749	17.280979
GO:0060394	Negative regulation of pathway-restricted SMAD protein phosphorylation	3	0.012806	20.205373
GO:0034329	Cell junction assembly	3	0.012806	20.205373
GO:0042312	Regulation of vasodilation	3	0.012806	20.205373
GO:0002687	Positive regulation of leukocyte migration	3	0.012806	20.205373

GO:2000010	Positive regulation of protein localization to cell surface	3	0.012806	20.205373
GO:0031000	Response to caffeine	3	0.012806	20.205373
GO:0035815	Positive regulation of renal sodium excretion	3	0.012806	20.205373
GO:0060389	Pathway-restricted SMAD protein phosphorylation	3	0.0149894	23.240366
GO:0032516	Positive regulation of phosphoprotein phosphatase activity	3	0.0149894	23.240366
GO:0048747	Muscle fiber development	3	0.0149894	23.240366
GO:0045019	Negative regulation of nitric oxide biosynthetic process	3	0.0149894	23.240366
GO:0060317	Cardiac epithelial to mesenchymal transition	3	0.0149894	23.240366
GO:0060038	Cardiac muscle cell proliferation	3	0.0149894	23.240366
GO:0014912	Negative regulation of smooth muscle cell migration	3	0.0173205	26.360166
GO:0003407	Neural retina development	3	0.0173205	26.360166
GO:0042311	Vasodilation	3	0.0173205	26.360166
GO:0035050	Embryonic heart tube development	3	0.0197943	29.540111

GO:0010667	Negative regulation of cardiac muscle cell apoptotic process	3	0.0197943	29.540111
GO:0003203	Endocardial cushion morphogenesis	3	0.0224063	32.756871
GO:0030949	Positive regulation of vascular endothelial growth factor receptor signaling pathway	3	0.0224063	32.756871
GO:0010613	Positive regulation of cardiac muscle hypertrophy	3	0.0224063	32.756871
GO:0006940	Regulation of smooth muscle contraction	3	0.0224063	32.756871
GO:0010744	Positive regulation of macrophage derived foam cell differentiation	3	0.0224063	32.756871
GO:0048663	Neuron fate commitment	3	0.0251519	35.988612
GO:0031589	Cell-substrate adhesion	3	0.0251519	35.988612
GO:0030224	Monocyte differentiation	3	0.0251519	35.988612
GO:0070266	Necroptotic process	3	0.0280266	39.215118
GO:0051412	Response to corticosterone	3	0.0280266	39.215118
GO:0060037	Pharyngeal system development	3	0.0280266	39.215118

GO:0090190	Positive regulation of branching involved in ureteric bud morphogenesis	3	0.0310262	42.417879
GO:0032332	Positive regulation of chondrocyte differentiation	3	0.0310262	42.417879
GO:0046716	Muscle cell cellular homeostasis	3	0.0310262	42.417879
GO:0017015	Regulation of transforming growth factor beta receptor signaling pathway	3	0.0341464	45.580147
GO:0035902	Response to immobilization stress	3	0.037383	48.686955
GO:0031954	Positive regulation of protein autophosphorylation	3	0.037383	48.686955
GO:0001954	Positive regulation of cell-matrix adhesion	3	0.040732	51.72512
GO:0034394	Protein localization to cell surface	3	0.040732	51.72512
GO:0055074	Calcium ion homeostasis	3	0.040732	51.72512
GO:0010906	Regulation of glucose metabolic process	3	0.040732	51.72512
GO:0032733	Positive regulation of interleukin-10 production	3	0.0441895	54.683207

GO:0032967	Positive regulation of collagen biosynthetic process	3	0.0441895	54.683207
GO:0048870	Cell motility	3	0.0477515	57.551482
GO:0048041	Focal adhesion assembly	3	0.0477515	57.551482
GO:0007422	Peripheral nervous system development	3	0.0477515	57.551482
GO:0003218	Cardiac left ventricle formation	2	0.0290859	40.364841
GO:0098907	Regulation of SA node cell action potential	2	0.0290859	40.364841
GO:0086001	Cardiac muscle cell action potential	2	0.0290859	40.364841
GO:1901979	Regulation of inward rectifier potassium channel activity	2	0.0290859	40.364841
GO:0086019	Cell–cell signaling involved in cardiac conduction	2	0.0290859	40.364841
GO:1903762	Positive regulation of voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization	2	0.0290859	40.364841
GO:1903233	Regulation of calcium ion-dependent exocytosis of neurotransmitter	2	0.0290859	40.364841

GO:0003169	Coronary vein morphogenesis	2	0.0290859	40.364841
GO:0003221	Right ventricular cardiac muscle tissue morphogenesis	2	0.0290859	40.364841
GO:0032971	Regulation of muscle filament sliding	2	0.0290859	40.364841
GO:0098905	Regulation of bundle of His cell action potential	2	0.0290859	40.364841
GO:0086043	Bundle of His cell action potential	2	0.0290859	40.364841
GO:1905150	Regulation of voltage-gated sodium channel activity	2	0.0290859	40.364841
GO:0032972	Regulation of muscle filament sliding speed	2	0.0290859	40.364841
GO:1901201	Regulation of extracellular matrix assembly	2	0.0290859	40.364841
GO:0007199	G-protein-coupled receptor signaling pathway coupled to CGMP nucleotide second messenger	2	0.0290859	40.364841
GO:0045844	Positive regulation of striated muscle tissue development	2	0.0290859	40.364841
GO:0003051	Angiotensin-mediated drinking behavior	2	0.0290859	40.364841
GO:0001300	Chronological cell aging	2	0.0290859	40.364841

GO:2000170	Positive regulation of peptidyl-cysteine S-nitrosylation	2	0.0290859	40.364841
GO:0086097	Phospholipase C-activating angiotensin-activated signaling pathway	2	0.0290859	40.364841
GO:0086067	AV node cell to bundle of His cell communication	2	0.0290859	40.364841
GO:0002019	Regulation of renal output by angiotensin	2	0.0290859	40.364841
GO:0003294	Atrial ventricular junction remodeling	2	0.0290859	40.364841
GO:1901019	Regulation of calcium ion transmembrane transporter activity	2	0.0290859	40.364841
GO:0010652	Positive regulation of cell communication by chemical coupling	2	0.0290859	40.364841
GO:0086029	Purkinje myocyte to ventricular cardiac muscle cell signaling	2	0.0290859	40.364841
GO:1905075	Positive regulation of occluding junction disassembly	2	0.0290859	40.364841
GO:0042704	Uterine wall breakdown	2	0.0290859	40.364841
GO:0070483	Detection of hypoxia	2	0.0290859	40.364841
GO:1903817	Negative regulation of voltage-gated potassium channel activity	2	0.0290859	40.364841
GO:0003166	Bundle of His development	2	0.0433113	53.948533

GO:1902083	Negative regulation of peptidyl-cysteine S-nitrosylation	2	0.0433113	53.948533
GO:0003342	Proepicardium development	2	0.0433113	53.948533
GO:0002034	Regulation of blood vessel size by renin-angiotensin	2	0.0433113	53.948533
GO:0010572	Positive regulation of platelet activation	2	0.0433113	53.948533
GO:0086048	Membrane depolarization during bundle of His cell action potential	2	0.0433113	53.948533
GO:0014819	Regulation of skeletal muscle contraction	2	0.0433113	53.948533
GO:1901843	Positive regulation of high voltage-gated calcium channel activity	2	0.0433113	53.948533
GO:0086047	Membrane depolarization during Purkinje myocyte cell action potential	2	0.0433113	53.948533
GO:0060948	Cardiac vascular smooth muscle cell development	2	0.0433113	53.948533
GO:0055098	Response to low-density lipoprotein particle	2	0.0433113	53.948533
GO:0051647	Nucleus localization	2	0.0433113	53.948533
GO:0030801	Positive regulation of cyclic nucleotide metabolic process	2	0.0433113	53.948533

GO:0099625	Ventricular cardiac muscle cell membrane repolarization	2	0.0433113	53.948533
GO:0002005	Angiotensin catabolic process in blood	2	0.0433113	53.948533
GO:0061577	Calcium ion transmembrane transport via high voltage-gated calcium channel	2	0.0433113	53.948533
GO:0003274	Endocardial cushion fusion	2	0.0433113	53.948533
GO:0010643	Cell communication by chemical coupling	2	0.0433113	53.948533
GO:0048769	Sarcomerogenesis	2	0.0433113	53.948533
GO:0098903	Regulation of membrane repolarization during action potential	2	0.0433113	53.948533
GO:0030241	Skeletal muscle myosin thick filament assembly	2	0.0433113	53.948533
GO:0014809	Regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion	2	0.0433113	53.948533
GO:0045213	Neurotransmitter receptor metabolic process	2	0.0433113	53.948533

^a SCD-related gene set

^b Only the leaf GO biological process terms containing 5 or more genes among the SCDgset are shown.

^c Number of genes among the SCDgset.

^d *P* values were calculated with the hypergeometric test.

^e FDRs were adjusted by the Benjamini–Hochberg method.