

				Full		Glyph								
						7w		12w		7w		12w		
						Female	Male	Female	Male	Female	Male	Female	Male	
GO:ID		Int	Dnn	Definition										
GO:0032092	BP	17	D05	positive regulation of protein binding	X.X..X.X	CSF3	–	CSF3	–	–	WNT3A	–	WNT3A,	
GO:0031647	BP	4	D03	regulation of protein stabilityX.	–	–	–	–	–	–	FAM107A	–	
GO:0010468	BP	1029	D05	regulation of gene expressionX..	–	–	–	–	–	TCF15	–	–	
GO:0010628	BP	193	D06	positive regulation of gene expression	..X..X.X	–	–	NKX2-5	–	–	WNT3A	–	WNT3A,	
GO:0033673	BP	33	D09	negative regulation of kinase activityX..	–	–	–	–	–	NPRL2	–	–	
GO:0035195	BP	26	D10	gene silencing by miRNA	.X.....	–	TNRC6A	–	–	–	–	–	–	
GO:0043280	BP	6	D12	positive regulation of cysteine-type endopeptidase activity involved in apoptotic processX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0006509	BP	4	D07	membrane protein ectodomain proteolysis	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0001819	BP	92	D07	positive regulation of cytokine productionX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0097205	BP	7	D04	renal filtration	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0003016	BP	5	D03	respiratory system processX..	–	–	–	–	–	TCF15	–	–	
GO:0019827	BP	31	D03	stem cell population maintenanceX..	–	–	–	–	–	TCF15	–	–	
GO:0007275	BP	5256	D03	multicellular organism developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0072359	BP	641	D04	circulatory system development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0007507	BP	448	D04	heart development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0072006	BP	323	D03	nephron development	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0003007	BP	197	D04	heart morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0009952	BP	121	D04	anterior/posterior pattern specificationX.X	–	–	–	–	–	TCF15,WNT3A	–	WNT3A,	
GO:0007498	BP	104	D04	mesoderm developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0007517	BP	87	D04	muscle organ developmentX..	–	–	–	–	–	TCF15	–	–	
GO:0048738	BP	84	D06	cardiac muscle tissue development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0030324	BP	80	D04	lung development	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0030879	BP	72	D05	mammary gland developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0043583	BP	65	D05	ear developmentX..	–	–	–	–	–	TCF15	–	–	
GO:0048705	BP	59	D04	skeletal system morphogenesisX..	–	–	–	–	–	TCF15	–	–	
GO:0043588	BP	53	D04	skin development	..X..X..	–	–	ITGA3	–	–	TCF15	–	–	
GO:0048593	BP	47	D06	camera-type eye morphogenesis	..X.....	–	–	–	COL8A2	–	–	–	–	
GO:0007368	BP	39	D05	determination of left/right symmetryX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0048644	BP	21	D04	muscle organ morphogenesisX..	–	–	–	–	–	TCF15	–	–	
GO:0030901	BP	21	D03	midbrain developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0003151	BP	20	D03	outflow tract morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003208	BP	19	D04	cardiac ventricle morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003161	BP	16	D07	cardiac conduction system development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0055008	BP	16	D05	cardiac muscle tissue morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0048339	BP	13	D05	paraxial mesoderm developmentX..	–	–	–	–	–	TCF15	–	–	
GO:0060412	BP	6	D04	ventricular septum morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003211	BP	5	D04	cardiac ventricle formation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0030878	BP	4	D05	thyroid gland development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0048643	BP	4	D07	positive regulation of skeletal muscle tissue developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0062009	BP	3	D04	secondary palate developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0003162	BP	3	D07	atrioventricular node development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0060413	BP	3	D04	atrial septum morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0021766	BP	3	D03	hippocampus developmentX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0003222	BP	2	D07	ventricular trabecula myocardium morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003221	BP	2	D07	right ventricular cardiac muscle tissue morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003228	BP	1	D03	atrial cardiac muscle tissue development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003166	BP	1	D08	bundle of His development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003285	BP	1	D05	septum secundum development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0036342	BP	0	D03	post-anal tail morphogenesisX.X	–	–	–	–	–	TCF15,WNT3A	–	WNT3A,	
GO:0007512	BP	0	D05	adult heart development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003342	BP	0	D05	proepicardium development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0060347	BP	0	D04	heart trabecula formation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003350	BP	0	D06	pulmonary myocardium development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0003148	BP	0	D04	outflow tract septum morphogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0071345	BP	145	D05	cellular response to cytokine stimulus	X.X.....	CSF3	–	CSF3	–	–	–	–	–	
GO:0009749	BP	16	D07	response to glucose	X.X.X.XX	SARM1	–	SARM1	–	SARM1	–	SARM1,SARM1,	–	
GO:0034613	BP	611	D04	cellular protein localizationX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:1903078	BP	4	D08	positive regulation of protein localization to plasma membrane	..X..X.X	–	–	ITGA3	–	–	WNT3A	–	WNT3A,	
GO:0006351	BP	392	D09	transcription. DNA-templated	..X.....	–	–	POLRMT	–	–	–	–	–	
GO:2001141	BP	342	D07	regulation of RNA biosynthetic processX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0006355	BP	308	D09	regulation of transcription. DNA-templated	.X.X....	–	TLX1	–	TLX1	–	–	–	–	
GO:0006357	BP	161	D10	regulation of transcription by RNA polymerase II	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0045892	BP	113	D10	negative regulation of transcription. DNA-templated	...XX..	–	–	–	–	ID1,ID1	–	–	–	
GO:0045893	BP	101	D10	positive regulation of transcription. DNA-templated	..XX..X.X	–	QRICH1,NKX2-5	–	–	WNT3A	–	WNT3A,	–	
GO:0045944	BP	65	D11	positive regulation of transcription by RNA polymerase II	X.X..X.X	CSF3	–	CSF3,NKX2-5	–	–	TCF15,WNT3A	–	WNT3A,	
GO:0000122	BP	33	D11	negative regulation of transcription by RNA polymerase II	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0006390	BP	6	D10	mitochondrial transcription	..X.....	–	–	POLRMT	–	–	–	–	–	
GO:0051091	BP	4	D11	positive regulation of DNA-binding transcription factor activity	X.X..X.X	CSF3	–	CSF3	–	–	WNT3A	–	WNT3A,	
GO:0035278	BP	3	D10	miRNA mediated inhibition of translation	.X.....	–	TNRC6A	–	–	–	–	–	–	
GO:0060261	BP	1	D12	positive regulation of transcription initiation from RNA polymerase II promoter	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0010735	BP	0	D12	positive regulation of transcription via serum response element binding	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0006811	BP	2012	D04	ion transport	..X....	–	–	–	GABRA3	–	–	–	–	
GO:0006821	BP	11	D07	chloride transport	..X....	–	–	–	GABRA3	–	–	–	–	
GO:0010765	BP	10	D07	positive regulation of sodium ion transport	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0030154	BP	2410	D03	cell differentiation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0045595	BP	752	D04	regulation of cell differentiationX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0022008	BP	696	D04	neurogenesisX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0055007	BP	47	D06	cardiac muscle cell differentiation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0050768	BP	24	D07	negative regulation of neurogenesisX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0055013	BP	22	D05	cardiac muscle cell development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0010717	BP	22	D05	regulation of epithelial to mesenchymal transition	..X.....	–	–	DAG1	–	–	–	–	–	

GO:0045666	BP	20	D06	positive regulation of neuron differentiation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0035914	BP	17	D04	skeletal muscle cell differentiationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0010977	BP	15	D08	negative regulation of neuron projection developmentXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0060231	BP	11	D05	mesenchymal to epithelial transitionX.	–	–	–	–	–	TCF15	–	–	
GO:0048709	BP	11	D05	oligodendrocyte differentiation	X.X.X.XX	VTN	–	VTN	–	VTN	–	VTN,VTN,		
GO:0060923	BP	10	D05	cardiac muscle cell fate commitmentXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0001649	BP	9	D04	osteoblast differentiationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:2000738	BP	7	D06	positive regulation of stem cell differentiationX.	–	–	–	–	–	TCF15	–	–	
GO:0001570	BP	7	D04	vasculogenesis	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0021527	BP	6	D06	spinal cord association neuron differentiationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0010832	BP	2	D08	negative regulation of myotube differentiation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0045198	BP	2	D06	establishment of epithelial cell apical/basal polarityX.	–	–	–	–	–	TCF15	–	–	
GO:0045599	BP	1	D06	negative regulation of fat cell differentiationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:2000727	BP	1	D08	positive regulation of cardiac muscle cell differentiationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0051891	BP	1	D07	positive regulation of cardioblast differentiation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:1904339	BP	1	D07	negative regulation of dopaminergic neuron differentiationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0003168	BP	0	D08	Purkinje myocyte differentiation	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0060928	BP	0	D07	atrioventricular node cell development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0060929	BP	0	D07	atrioventricular node cell fate commitment	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0023052	BP	2216	D01	signaling	..X.....	–	–	DLGAP3	–	–	–	–	–	
GO:0007165	BP	1646	D04	signal transduction	X.X.X.XX	SARM1	–	GNAI2,SA	–	PLEKHH	–	SARM1,SARM1,		
GO:0007186	BP	175	D05	G protein-coupled receptor signaling pathway	..X.....	–	–	GNAI2	–	–	–	–	–	
GO:0007188	BP	40	D06	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	..X.....	–	–	GNAI2	–	–	–	–	–	
GO:0043409	BP	16	D08	negative regulation of MAPK cascade	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0030510	BP	9	D07	regulation of BMP signaling pathway	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0017015	BP	6	D07	regulation of transforming growth factor beta receptor signaling pathway	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0032007	BP	2	D08	negative regulation of TOR signalingX.	–	–	–	–	–	NPRL2	–	–	
GO:0007214	BP	0	D06	gamma-aminobutyric acid signaling pathwayX...	–	–	–	GABRA3	–	–	–	–	
GO:0051898	BP	0	D08	negative regulation of protein kinase B signaling	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0051897	BP	0	D08	positive regulation of protein kinase B signaling	X.X.....	CSF3	–	CSF3	–	–	–	–	–	
GO:0034128	BP	0	D09	negative regulation of MyD88-independent toll-like receptor signaling pathway	X.X.X.XX	SARM1	–	SARM1	–	SARM1	–	SARM1,SARM1,		
GO:0014068	BP	0	D08	positive regulation of phosphatidylinositol 3-kinase signaling	X.X.....	CSF3	–	CSF3	–	–	–	–	–	
GO:0035024	BP	0	D10	negative regulation of Rho protein signal transduction	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0006511	BP	40	D08	ubiquitin-dependent protein catabolic processX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0032436	BP	5	D11	positive regulation of proteasomal ubiquitin-dependent protein catabolic processX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0006955	BP	653	D02	immune response	X.X.X.XX	CSF3	VTN	–	CSF3,VTN	–	VTN	–	VTN,VTN,	
GO:0030097	BP	333	D05	hemopoiesis	..X..X.X	–	–	NKX2-5	–	–	WNT3A	–	WNT3A,	
GO:0045639	BP	14	D07	positive regulation of myeloid cell differentiation	X.X.....	CSF3	–	CSF3	–	–	–	–	–	
GO:0048536	BP	1	D05	spleen development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:1902037	BP	0	D07	negative regulation of hematopoietic stem cell differentiationX.	–	–	–	–	–	TCF15	–	–	
GO:0034976	BP	64	D04	response to endoplasmic reticulum stress	..X.....	–	QRICH1	–	–	–	–	–	–	
GO:0009267	BP	54	D06	cellular response to starvation	..X.....	–	TNRC6A	–	–	–	–	–	–	
GO:0048678	BP	38	D04	response to axon injury	X.X.X.XX	SARM1	–	SARM1	–	SARM1	–	SARM1,SARM1,		
GO:0034620	BP	19	D06	cellular response to unfolded protein	..X.....	–	–	HSPB8	–	–	–	–	–	
GO:0030968	BP	16	D05	endoplasmic reticulum unfolded protein response	..X.....	–	QRICH1	–	–	–	–	–	–	
GO:0030168	BP	10	D03	platelet activationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0140467	BP	7	D04	integrated stress response signaling	..X.....	–	QRICH1	–	–	–	–	–	–	
GO:0034198	BP	5	D07	cellular response to amino acid starvationX.	–	–	–	–	–	NPRL2	–	–	
GO:0036499	BP	3	D06	PERK-mediated unfolded protein response	..X.....	–	QRICH1	–	–	–	–	–	–	
GO:0001934	BP	56	D09	positive regulation of protein phosphorylationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0045860	BP	40	D10	positive regulation of protein kinase activityXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0016579	BP	27	D09	protein deubiquitinationX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0031398	BP	12	D10	positive regulation of protein ubiquitinationX.	–	–	–	–	–	–	FAM107A	–	
GO:0050731	BP	7	D10	positive regulation of peptidyl-tyrosine phosphorylation	X.X.....	CSF3	–	CSF3	–	–	–	–	–	
GO:0061098	BP	3	D11	positive regulation of protein tyrosine kinase activityXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0071108	BP	2	D10	protein K48-linked deubiquitinationX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0033138	BP	1	D10	positive regulation of peptidyl-serine phosphorylation	X.X..X.X	CSF3	–	CSF3	–	–	WNT3A	–	WNT3A,	
GO:0006699	BP	3	D08	bile acid biosynthetic process	..X.....	–	LOC107312474	–	–	–	–	–	–	
GO:0006707	BP	0	D07	cholesterol catabolic process	..X.....	–	LOC107312474	–	–	–	–	–	–	
GO:0019048	BP	138	D05	modulation by virus of host process	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0034220	BP	721	D05	ion transmembrane transportX....	–	–	–	GABRA3	–	–	–	–	
GO:0090676	BP	0	D09	calcium ion transmembrane transport via low voltage-gated calcium channelXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0030336	BP	71	D07	negative regulation of cell migration	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0030335	BP	71	D07	positive regulation of cell migrationX.	–	–	–	–	–	–	FAM107A	–	
GO:0001764	BP	22	D05	neuron migration	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0016055	BP	138	D07	Wnt signaling pathwayXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0050804	BP	112	D06	modulation of chemical synaptic transmissionXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0030111	BP	69	D06	regulation of Wnt signaling pathway	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0060070	BP	53	D08	canonical Wnt signaling pathwayXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0090090	BP	8	D08	negative regulation of canonical Wnt signaling pathway	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0090263	BP	5	D08	positive regulation of canonical Wnt signaling pathwayXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0061317	BP	3	D10	canonical Wnt signaling pathway involved in cardiac muscle cell fate commitmentXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0099527	BP	1	D06	postsynapse to nucleus signaling pathwayXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0003136	BP	0	D10	negative regulation of heart induction by canonical Wnt signaling pathwayXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0048333	BP	56	D04	mesodermal cell differentiation	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0001701	BP	42	D07	in utero embryonic developmentXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0035050	BP	26	D05	embryonic heart tube development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0042472	BP	25	D04	inner ear morphogenesisXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0001756	BP	16	D05	somitogenesisXX	–	–	–	–	–	TCF15,WNT3A	–	WNT3A,	
GO:0048343	BP	8	D06	paraxial mesodermal cell fate commitmentXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0010470	BP	4	D06	regulation of gastrulation	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0021904	BP	4	D05	dorsal/ventral neural tube patterningXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0048337	BP	4	D08	positive regulation of mesodermal cell fate specificationXX	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0001947	BP	3	D07	heart looping	..X..X.X	–	–	NKX2-5	–	–	WNT3A	–	WNT3A,	
GO:0060037	BP	1	D04	pharyngeal system development	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0061184	BP	0	D07	positive regulation of dermatome developmentXX	–	–	–	–	–	WNT3A	–	WNT3A,	

GO:0060971	BP	0	D05	embryonic heart tube left/right pattern formation	..X.....	_	_		NKX2-5	_	_	_	_	_	
GO:0042981	BP	252	D06	regulation of apoptotic process	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_		SARM1,SARM1,	
GO:0043066	BP	91	D07	negative regulation of apoptotic process	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0043065	BP	80	D07	positive regulation of apoptotic process	.X.....	_	QRICH1		_	_	_	_		_	
GO:1901214	BP	27	D05	regulation of neuron death	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_		SARM1,SARM1,	
GO:1901215	BP	10	D06	negative regulation of neuron deathX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0003278	BP	7	D07	apoptotic process involved in heart morphogenesis	..X.....	_	_		NKX2-5	_	_	_		_	
GO:1901216	BP	6	D06	positive regulation of neuron death	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_		SARM1,SARM1,	
GO:0070059	BP	6	D07	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	.X.....	_	QRICH1		_	_	_	_		_	
GO:0010667	BP	0	D10	negative regulation of cardiac muscle cell apoptotic process	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0008283	BP	486	D02	cell population proliferationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0008284	BP	97	D05	positive regulation of cell population proliferation	X.X.XX.X	HPSE2	_		GNAI2,NK	_	HPSE2,V	_		WNT3A,	
GO:0050673	BP	80	D03	epithelial cell proliferation	..X....	_	_		_	COL8A2	_	_		_	
GO:0021846	BP	17	D04	cell proliferation in forebrainX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:2000179	BP	7	D06	positive regulation of neural precursor cell proliferationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0033278	BP	3	D04	cell proliferation in midbrainX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0030890	BP	0	D09	positive regulation of B cell proliferationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:2000347	BP	0	D07	positive regulation of hepatocyte proliferationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:2000081	BP	0	D09	positive regulation of canonical Wnt signaling pathway involved in controlling type B pancreX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0002092	BP	1	D09	positive regulation of receptor internalizationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0010387	BP	0	D07	COP9 signalosome assemblyX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0001558	BP	69	D05	regulation of cell growthX.	_	_		_	_	_	_		FAM107A	_
GO:0090245	BP	6	D05	axis elongation involved in somitogenesisX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0060038	BP	4	D05	cardiac muscle cell proliferation	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0060043	BP	3	D08	regulation of cardiac muscle cell proliferation	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0000226	BP	182	D06	microtubule cytoskeleton organization	..X.....	_	_		MAP6D1	_	_	_		_	
GO:0032956	BP	79	D07	regulation of actin cytoskeleton organizationX.	_	_		_	_	_	_		FAM107A	_
GO:0070507	BP	36	D07	regulation of microtubule cytoskeleton organizationXXX	_	_		_	_	_	WNT3A,FAM107A,WNT3A,			
GO:0045104	BP	15	D06	intermediate filament cytoskeleton organizationX.	_	_		_	_	_	MACF1	_		_
GO:0030838	BP	12	D11	positive regulation of actin filament polymerization	X.X.....	CSF3	_		CSF3	_	_	_		_	
GO:0034453	BP	7	D07	microtubule anchoring	..X.....	_	_		DAG1	_	_	_		_	
GO:0045214	BP	3	D08	sarcomere organization	..X.....	_	_		NKX2-5	_	_	_		_	
GO:2000251	BP	0	D09	positive regulation of actin cytoskeleton reorganization	X.X.....	CSF3	_		CSF3	_	_	_		_	
GO:0055005	BP	0	D10	ventricular cardiac myofibril assembly	..X.....	_	_		NKX2-5	_	_	_		_	
GO:2000134	BP	9	D09	negative regulation of G1/S transition of mitotic cell cycleX.	_	_		_	_	_	_		FAM107A	_
GO:0060047	BP	133	D05	heart contraction	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0060048	BP	32	D06	cardiac muscle contraction	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0045823	BP	23	D07	positive regulation of heart contraction	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0055117	BP	15	D08	regulation of cardiac muscle contraction	..X.....	_	_		NKX2-5	_	_	_		_	
GO:1903779	BP	5	D07	regulation of cardiac conduction	..X.....	_	_		NKX2-5	_	_	_		_	
GO:0043488	BP	13	D09	regulation of mRNA stability	..X.....	_	_		PCBP4	_	_	_		_	
GO:0019677	BP	0	D10	NAD catabolic process	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_		SARM1,SARM1,	
GO:0007155	BP	308	D02	cell adhesion	..X.....	_	_		ITGA3	_	_	_		_	
GO:0007160	BP	22	D04	cell-matrix adhesion	X.X.X.XX	VTN	_		VTN	_	VTN	_		VTN,VTN,	
GO:0010811	BP	7	D06	positive regulation of cell-substrate adhesion	X.X.X.XX	VTN	_		VTN	_	VTN	_		VTN,VTN,	
GO:0070527	BP	6	D05	platelet aggregationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:2000049	BP	0	D07	positive regulation of cell-cell adhesion mediated by cadherinX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0007409	BP	124	D09	axonogenesisX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0007411	BP	70	D04	axon guidanceX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0050770	BP	21	D08	regulation of axonogenesisX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0048814	BP	3	D09	regulation of dendrite morphogenesis	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_		SARM1,SARM1,	
GO:0048843	BP	0	D11	negative regulation of axon extension involved in axon guidanceX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0048697	BP	0	D11	positive regulation of collateral sprouting in absence of injuryX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0051301	BP	226	D02	cell division	..X.....	_	_		GNAI2	_	_	_		_	
GO:0048103	BP	7	D04	somatic stem cell divisionX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0021874	BP	0	D08	Wnt signaling pathway involved in forebrain neuroblast divisionX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0050884	BP	4	D05	neuromuscular process controlling postureX.	_	_		_	_	_	TCF15	_		_
GO:0050807	BP	62	D05	regulation of synapse organizationX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0099563	BP	8	D06	modification of synaptic structure	..X.....	_	_		DLGAP3	_	_	_		_	
GO:1905606	BP	4	D07	regulation of presynapse assemblyX.X	_	_		_	_	_	WNT3A	_		WNT3A,
GO:0097062	BP	3	D08	dendritic spine maintenance	..X.....	_	_		ITGA3	_	_	_		_	
GO:0051895	BP	0	D08	negative regulation of focal adhesion assemblyX.	_	_		_	_	_	_		FAM107A	_
GO:0042755	BP	8	D03	eating behaviorX.	_	_		_	_	_	TCF15	_		_
GO:0007613	BP	4	D06	memory	..X.....	_	_		ITGA3	_	_	_		_	
GO:0035640	BP	1	D02	exploration behavior	..X.....	_	_		ITGA3	_	_	_		_	
GO:0032981	BP	0	D08	mitochondrial respiratory chain complex I assembly	..X...X	_	NDUFAF3		_	NDUFAF3	_	_		_	NDUFAF3,
GO:1905337	BP	0	D09	positive regulation of aggregophagy	..X.....	_	_		HSPB8	_	_	_		_	
GO:0030198	BP	45	D05	extracellular matrix organization	X.X.XXXX	HPSE2	VTN		_	VTN	_	HPSE2,VTN,WNT3A,VTN,VTN,WNT3A,			
GO:1903053	BP	19	D05	regulation of extracellular matrix organizationX.	_	_		_	_	_	TCF15	_		_
GO:1904261	BP	0	D08	positive regulation of basement membrane assembly involved in embryonic body morphog	..X.....	_	_		DAG1	_	_	_		_	
GO:0016020	CC	1044	D02	membrane	X.XXX...	HPSE2	_		DAG1,GAI	_	_	_		_	
GO:0071944	CC	727	D02	cell periphery	..X.....	_	_		ITGA3	_	_	_		_	
GO:0005886	CC	470	D03	plasma membrane	..X.....	_	_		DAG1,GN	_	_	_		_	
GO:0016021	CC	232	D03	integral component of membrane	..XX.....	_	_		DAG1,GAI	_	_	_		_	
GO:0045202	CC	189	D03	synapse	X.X.XXXX	SARM1	_		DLGAP3,I	_	SARM1,WNT3A,SARM1,SARM1,WNT3A,				
GO:0097060	CC	47	D04	synaptic membrane	..X.....	_	_		ITGA3	_	_	_		_	
GO:0030425	CC	41	D05	dendrite	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_		SARM1,SARM1,	
GO:0009986	CC	19	D02	cell surface	..X..X.X	_	_		ITGA3	_	_	WNT3A	_		WNT3A,
GO:0031594	CC	10	D04	neuromuscular junction	..X.....	_	_		DLGAP3	_	_	_		_	
GO:0070938	CC	9	D02	contractile ring	..X.....	_	_		DAG1	_	_	_		_	
GO:0009897	CC	9	D03	external side of plasma membrane	..X.....	_	_		ITGA3	_	_	_		_	
GO:0060076	CC	7	D04	excitatory synapse	..X.....	_	_		ITGA3	_	_	_		_	
GO:0030175	CC	5	D05	filopodium	..X.....	_	_		DAG1	_	_	_		_	
GO:0098978	CC	3	D04	glutamatergic synapse	..X..X.X	_	_		DLGAP3	_	_	WNT3A	_		WNT3A,
GO:0030027	CC	3	D04	lamellipodium	..X.....	_	_		DAG1	_	_	_		_	
GO:0030496	CC	1	D02	midbody	..X.....	_	_		GNAI2	_	_	_		_	

GO:0098981	CC	1	D04	cholinergic synapse	..X.....	_	_		DLGAP3	_	_	_	_	_	
GO:0005925	CC	0	D05	focal adhesion	..X...X.	_	_		DAG1	_	_	_	FAM107A	_	
GO:0032587	CC	0	D05	ruffle membraneX.	_	_		_	_	_	_	FAM107A	_	
GO:0016323	CC	0	D04	basolateral plasma membrane	..X.....	_	_		ITGA3	_	_	_	_	_	
GO:0031527	CC	0	D05	filopodium membrane	..X.....	_	_		ITGA3	_	_	_	_	_	
GO:0005737	CC	1229	D02	cytoplasm	X.X.XXXX	SARM1	_		DAG1,GN	_		ID1,SARM1,ID1,FAM107A,SARM1,SARM1,			
GO:0005829	CC	83	D02	cytosol	..X.....	_	_		GNAI2,HS	_	_	_	_	_	
GO:0032991	CC	2105	D01	protein-containing complex	..X.....	_	_		NKX2-5,Pi	_	_	_	_	_	
GO:0043235	CC	108	D02	receptor complex	..X.....	_	_		ITGA3	_	_	_	_	_	
GO:0005667	CC	83	D02	transcription regulator complex	..X.....	_	_		NKX2-5	_	_	_	_	_	
GO:0032993	CC	51	D02	protein-DNA complex	..X.....	_	_		NKX2-5	_	_	_	_	_	
GO:0008305	CC	24	D05	integrin complex	..X.....	_	_		ITGA3	_	_	_	_	_	
GO:0101031	CC	7	D02	chaperone complex	..X.....	_	_		HSPB8	_	_	_	_	_	
GO:0016010	CC	4	D04	dystrophin-associated glycoprotein complex	..X.....	_	_		DAG1	_	_	_	_	_	
GO:1990130	CC	0	D02	GATOR1 complexX.	_	_		_	_	_	NPRL2	_	_	
GO:0016442	CC	0	D04	RISC complex	.X.....	_	TNRC6A		_	_	_	_	_	_	
GO:1990851	CC	0	D04	Wnt-Frizzled-LRP5/6 complexXX	_	_		_	_	_	WNT3A	_	WNT3A,	
GO:0034667	CC	0	D06	integrin alpha3-beta1 complex	..X.....	_	_		ITGA3	_	_	_	_	_	
GO:0043231	CC	1025	D04	intracellular membrane-bounded organelle	..XX.....	_	TNRC6A,DAG1		_	_	_	_	_	_	
GO:0005739	CC	95	D05	mitochondrion	XXXXXX.XX	SARM1,S	_		SARM1,SARM1,						
GO:0005794	CC	46	D05	Golgi apparatus	.X.....	_	TNRC6A		_	_	_	_	_	_	
GO:0005743	CC	36	D05	mitochondrial inner membrane	.X.X...X	_	NDUFAF3		_	NDUFAF3	_	_	_	NDUFAF3,	
GO:0099572	CC	22	D03	postsynaptic specialization	..X.....	_	_		DLGAP3	_	_	_	_	_	
GO:0005759	CC	21	D04	mitochondrial matrix	..X.....	_	_		POLRMT	_	_	_	_	_	
GO:0000932	CC	1	D07	P-body	.X.....	_	TNRC6A		_	_	_	_	_	_	
GO:0042645	CC	1	D05	mitochondrial nucleoid	..X.....	_	_		POLRMT	_	_	_	_	_	
GO:0031315	CC	0	D04	extrinsic component of mitochondrial outer membrane	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_	SARM1,SARM1,		
GO:0005634	CC	491	D05	nucleus	..XXXXXX	_	NDUFAF3,QRICH1,HSPB8,NKX2-5,NDUFAF3,ID1,ID1,TCF15,FAM107A,NDUFAF3,								
GO:0005654	CC	86	D02	nucleoplasm	.XX.....	_	QRICH1,TNRC6A		_	_	_	_	_	_	
GO:0090575	CC	45	D03	RNA polymerase II transcription regulator complex	..X..X.	_	_		NKX2-5	_	_	TCF15	_	_	
GO:0016604	CC	14	D02	nuclear body	..X.....	_	_		HSPB8	_	_	_	_	_	
GO:0016607	CC	1	D03	nuclear speckX.	_	_		_	_	_	FAM107A	_	_	
GO:0005856	CC	272	D05	cytoskeletonX.	_	_		_	_	PLEKHH	_	_	_	
GO:0015630	CC	112	D06	microtubule cytoskeleton	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_	SARM1,SARM1,		
GO:0015629	CC	73	D06	actin cytoskeletonX.	_	_		_	_	_	FAM107A	_	_	
GO:0005874	CC	30	D06	microtubule	X.X.X.XX	SARM1	_		MAP6D1,S	_	SARM1	_	SARM1,SARM1,		
GO:0005813	CC	5	D03	centrosome	..X.....	_	_		GNAI2	_	_	_	_	_	
GO:0045095	CC	0	D07	keratin filament	.X.X....	_	LOC107325817		_	LOC1073	_	_	_	_	
GO:0001725	CC	0	D04	stress fiberX.	_	_		_	_	_	FAM107A	_	_	
GO:0005576	CC	93	D02	extracellular region	X.X..X.X	CSF3	_		CSF3	_	_	WNT3A	_	WNT3A,	
GO:0005615	CC	52	D02	extracellular space	..X..X.X	_	_		DAG1	_	_	WNT3A	_	WNT3A,	
GO:0031012	CC	89	D03	extracellular matrix	X.X.X.XX	HPSE2	VTN		_	VTN	_	HPSE2,VTN	_	VTN,VTN,	
GO:0005604	CC	23	D05	basement membrane	..X.....	_	_		DAG1	_	_	_	_	_	
GO:0005765	CC	14	D07	lysosomal membraneX.	_	_		_	_	_	NPRL2	_	_	
GO:0016491	MF	2426	D02	oxidoreductase activity	..X.....	_	_		_	ADHFE1	_	_	_	_	
GO:0016705	MF	707	D03	oxidoreductase activity. acting on paired donors. with incorporation or reduction of molecu	.X.....	_	LOC107312474		_	_	_	_	_	_	
GO:0004497	MF	478	D03	monooxygenase activity	.X.....	_	LOC107312474		_	_	_	_	_	_	
GO:0016616	MF	415	D04	oxidoreductase activity. acting on the CH-OH group of donors. NAD or NADP as acceptor	.X.....	_	LOC107309790		_	_	_	_	_	_	
GO:0008387	MF	0	D05	steroid 7-alpha-hydroxylase activity	.X.....	_	LOC107312474		_	_	_	_	_	_	
GO:0008396	MF	0	D05	oxysterol 7-alpha-hydroxylase activity	.X.....	_	LOC107312474		_	_	_	_	_	_	
GO:0005515	MF	932	D02	protein binding	XXXXXXXX	SARM1,LINGO3,LRRC20,POLRMT,SARM1,COL8A2,SARM1,USP5,LINGO3,MACF1,SARM1,USP5,SARM1,									
GO:0005102	MF	432	D03	signaling receptor bindingXX	_	_		_	_	_	WNT3A	_	WNT3A,	
GO:0003676	MF	312	D03	nucleic acid binding	..XX.....	_	TNRC6A,PCBP4		_	_	_	_	_	_	
GO:0019904	MF	79	D03	protein domain specific bindingXX	_	_		_	_	_	WNT3A	_	WNT3A,	
GO:0030247	MF	21	D03	polysaccharide binding	X.X.X.XX	VTN	_		VTN	_	VTN	_	VTN,VTN,		
GO:0019001	MF	13	D06	guanyl nucleotide binding	..X.....	_	_		GNAI2	_	_	_	_	_	
GO:0003682	MF	8	D02	chromatin binding	..X.....	_	_		NKX2-5	_	_	_	_	_	
GO:0050840	MF	5	D02	extracellular matrix binding	X.X.X.XX	VTN	_		VTN	_	VTN	_	VTN,VTN,		
GO:0046983	MF	2	D03	protein dimerization activityXX.	_	_		_	_	ID1,ID1,	_	_	_	
GO:0051287	MF	2	D05	NAD binding	.X.....	_	LOC107309790		_	_	_	_	_	_	
GO:0042802	MF	1	D03	identical protein binding	..X.....	_	_		HSPB8	_	_	_	_	_	
GO:0001618	MF	0	D03	virus receptor activity	..X.....	_	_		DAG1	_	_	_	_	_	
GO:0005516	MF	0	D03	calmodulin binding	..X.....	_	_		MAP6D1	_	_	_	_	_	
GO:0039706	MF	0	D03	co-receptor bindingXX	_	_		_	_	_	WNT3A	_	WNT3A,	
GO:0031683	MF	0	D03	G-protein beta/gamma-subunit complex binding	..X.....	_	_		GNAI2	_	_	_	_	_	
GO:0042803	MF	0	D04	protein homodimerization activity	..X.....	_	_		HSPB8,NF	_	_	_	_	_	
GO:0046982	MF	0	D04	protein heterodimerization activity	..X.....	_	_		ITGA3	_	_	_	_	_	
GO:0001540	MF	0	D04	amyloid-beta binding	..X.....	_	_		DLGAP3	_	_	_	_	_	
GO:0020037	MF	0	D04	heme binding	.X.....	_	LOC107312474		_	_	_	_	_	_	
GO:0043395	MF	0	D04	heparan sulfate proteoglycan binding	X..X...	HPSE2	_		_	_	HPSE2	_	_	_	
GO:0042169	MF	0	D04	SH2 domain binding	..X.....	_	_		DAG1	_	_	_	_	_	
GO:0005130	MF	0	D05	granulocyte colony-stimulating factor receptor binding	X.X.....	CSF3	_		CSF3	_	_	_	_	_	
GO:0005109	MF	0	D05	frizzled bindingXX	_	_		_	_	_	WNT3A	_	WNT3A,	
GO:0005216	MF	133	D05	ion channel activity	..X.....	_	_		_	GABRA3	_	_	_	_	
GO:0005230	MF	20	D08	extracellular ligand-gated ion channel activity	..X.....	_	_		_	GABRA3	_	_	_	_	
GO:0004888	MF	325	D03	transmembrane signaling receptor activity	..X.....	_	_		_	GABRA3	_	_	_	_	
GO:0004890	MF	0	D05	GABA-A receptor activity	..X.....	_	_		_	GABRA3	_	_	_	_	
GO:0004672	MF	108	D05	protein kinase activityX.	_	_		_	_	_	NPRL2	_	_	
GO:0016798	MF	293	D03	hydrolase activity. acting on glycosyl bonds	X..X...	HPSE2	_		_	_	HPSE2	_	_	_	
GO:0003953	MF	2	D05	NAD+ nucleosidase activity	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_	SARM1,SARM1,		
GO:0061809	MF	0	D06	NAD+ nucleotidase. cyclic ADP-ribose generating	X.X.X.XX	SARM1	_		SARM1	_	SARM1	_	SARM1,SARM1,		
GO:0048018	MF	30	D04	receptor ligand activityXX	_	_		_	_	_	WNT3A	_	WNT3A,	
GO:0005125	MF	1	D05	cytokine activity	X.X.....	CSF3	_		CSF3	_	_	_	_	_	
GO:0046872	MF	33	D04	metal ion binding	..X.....	_	_		_	ADHFE1	_	_	_	_	
GO:0005509	MF	4	D05	calcium ion binding	..X..X.	_	_		DAG1,LOC	_	_	MACF1	_	_	
GO:0005506	MF	3	D06	iron ion binding	.X.....	_	LOC107312474		_	_	_	_	_	_	

GO:0008270	MF	1	D06	zinc ion bindingX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0005525	MF	0	D08	GTP binding	..X.....	–	–	GNAI2	–	–	–	–	–	
GO:0003723	MF	172	D04	RNA binding	..X.....	–	–	PCBP4	–	–	–	–	–	
GO:0005096	MF	0	D05	GTPase activator activityX..	–	–	–	–	–	NPRL2	–	–	
GO:0005085	MF	0	D05	guanylnucleotide exchange factor activity	..X.....	–	–	PLEKHG5	–	–	–	–	–	
GO:0003677	MF	129	D04	DNA binding	..XXX....	–	–	QRICH1,TLX1,NK	–	–	–	–	–	
GO:0043565	MF	62	D05	sequence-specific DNA binding	..X.....	–	–	NKX2-5,Pl	–	–	–	–	–	
GO:1990837	MF	51	D06	sequence-specific double-stranded DNA binding	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0000976	MF	34	D07	transcription regulatory region sequence-specific DNA binding	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0000978	MF	11	D09	RNA polymerase II cis-regulatory region sequence-specific DNA binding	..X..X..	–	–	NKX2-5	–	–	TCF15	–	–	
GO:0070888	MF	0	D10	E-box bindingX..	–	–	–	–	–	TCF15	–	–	
GO:0003899	MF	12	D07	DNA-directed 5'-3' RNA polymerase activity	..X.....	–	–	POLRMT	–	–	–	–	–	
GO:0003730	MF	1	D06	mRNA 3'-UTR binding	..X.....	–	–	PCBP4	–	–	–	–	–	
GO:0004843	MF	0	D05	thiol-dependent ubiquitin-specific protease activityX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0019899	MF	70	D03	enzyme binding	X.X.....	CSF3	–	CSF3	–	–	–	–	–	
GO:0002020	MF	2	D04	protease binding	..X.....	–	–	ITGA3	–	–	–	–	–	
GO:0015631	MF	7	D04	tubulin binding	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0003779	MF	3	D04	actin binding	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0008017	MF	3	D05	microtubule binding	..X..X..	–	–	MAP6D1	–	–	MACF1	–	–	
GO:0051393	MF	1	D05	alpha-actinin binding	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0017166	MF	0	D04	vinculin binding	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0008134	MF	49	D03	transcription factor binding	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0043425	MF	1	D05	bHLH transcription factor bindingX..	–	–	–	–	–	TCF15	–	–	
GO:0005198	MF	42	D01	structural molecule activity	..X...X.	–	–	LOC10732	–	–	–	LOC107325234	–	
GO:0008307	MF	0	D02	structural constituent of muscle	..X.....	–	–	DAG1	–	–	–	–	–	
GO:0035591	MF	5	D03	signaling adaptor activity	X.X.X.XX	SARM1	–	SARM1	–	SARM1	–	SARM1,SARM1,		
GO:0003713	MF	1	D03	transcription coactivator activityX.X	–	–	–	–	–	WNT3A	–	WNT3A,	
GO:0005044	MF	0	D02	scavenger receptor activity	X.X.X.XX	VTN	–	VTN	–	VTN	–	VTN,VTN,		
GO:0003700	MF	10	D02	DNA-binding transcription factor activity	..XXX....	–	TLX1,NKX2-5,TLX	–	–	–	–			
GO:0000981	MF	3	D03	DNA-binding transcription factor activity. RNA polymerase II-specific	..XXX.X..	–	TLX1,NKX2-5,TLX	–	TCF15	–	–			
GO:0001216	MF	1	D03	DNA-binding transcription activator activity	..X.....	–	–	NKX2-5	–	–	–	–	–	
GO:0001228	MF	0	D04	DNA-binding transcription activator activity. RNA polymerase II-specific	..X..X..	–	–	NKX2-5	–	–	TCF15	–	–	
GO:0043130	MF	1	D04	ubiquitin bindingX.X.	–	–	–	–	USP5	–	USP5	–	
GO:0003924	MF	2	D07	GTPase activity	..X.....	–	–	GNAI2	–	–	–	–	–	