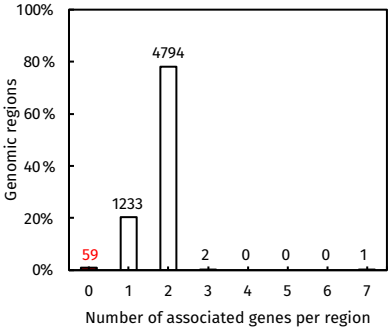
A



B

Biological Process

Term Name	Binom Rank	Binom Raw P-Value	*Binom FDR Q-Val*	Binom Fold Enrichment
mesodermal cell differentiation	129	1.7525e-10	1.1903e-8	2.7512
platelet-derived growth factor receptor signaling pathway	131	1.9466e-10	1.3020e-8	2.4883
regulation of coagulation	166	2.5289e-9	1.3348e-7	2.2263
regulation of blood coagulation	192	1.6212e-8	7.3986e-7	2.2580
metanephric nephron development	206	3.7873e-8	1.6109e-6	2.0854
response to magnesium ion	212	4.6986e-8	1.9419e-6	2.5222
regulation of metanephros development	235	1.2605e-7	4.6996e-6	2.5574
regulation of smooth muscle cell migration	256	1.9799e-7	6.7766e-6	2.2516
embryonic cranial skeleton morphogenesis	271	3.1716e-7	1.0254e-5	2.0937
regulation of stem cell differentiation	352	2.4067e-6	5.9907e-5	2.1140
tight junction assembly	397	7.0028e-6	1.5456e-4	2.0115
regulation of the force of heart contraction	410	8.7805e-6	1.8765e-4	2.3089
mammary gland epithelial cell differentiation	506	3.0842e-5	5.3407e-4	2.2946
nephric duct morphogenesis	619	1.1087e-4	1.5694e-3	2.2352
regulation of smooth muscle cell apoptosis	819	5.8120e-4	6.2179e-3	2.2798
metanephric glomerulus development	918	1.1107e-3	1.0601e-2	2.3250

C

Cellular Component

Term Name	Binom Rank	Binom Raw P-Value	*Binom FDR Q-Val*	Binom Fold Enrichment
focal adhesion	9	7.2141e-16	8.9856e-14	2.0874
caveola	20	9.9148e-11	5.5573e-9	2.0720
stress fiber	29	4.5581e-8	1.7619e-6	2.3657
cytoplasmic membrane-bounded vesicle lumen	31	1.2426e-7	4.4934e-6	2.0059
actin filament bundle	32	1.7350e-7	6.0778e-6	2.2618
spectrin-associated cytoskeleton	137	2.7319e-3	2.2353e-2	3.4459

D

Mouse Phenotype

Term Name	Binom Rank	Binom Raw P-Value	*Binom FDR Q-Val*	Binom Fold Enrichment
decreased dendritic cell number	134	1.2617e-10	6.8678e-9	2.6344
abnormal dendritic cell number	149	2.6198e-10	1.2825e-8	2.2496
abnormal aortic arch and aortic arch branch attachment	150	2.9220e-10	1.4209e-8	2.1231
lymph node hyperplasia	177	1.5728e-9	6.4812e-8	2.4340
abnormal CD4-positive T cell differentiation	192	5.3833e-9	2.0451e-7	2.0191
abnormal B cell apoptosis	198	6.4560e-9	2.3783e-7	2.1200
abnormal secondary ovarian follicle morphology	212	1.6589e-8	5.7074e-7	2.2063
abnormal right subclavian artery morphology	223	2.7501e-8	8.9952e-7	2.0660
decreased B cell apoptosis	230	3.8025e-8	1.2059e-6	2.9511
short nasal bone	234	4.1889e-8	1.3057e-6	2.0796
abnormal T-helper 2 cell differentiation	237	4.5071e-8	1.3871e-6	3.1780
abnormal subclavian artery morphology	239	4.7867e-8	1.4608e-6	2.0024
aberrant origin of the right subclavian artery	241	5.1002e-8	1.5436e-6	2.0684
abnormal visceral yolk sac blood island morphology	286	2.6568e-7	6.7758e-6	2.0904
abnormal circadian phase	292	3.0278e-7	7.5632e-6	2.2189
increased thymocyte number	351	2.0333e-6	4.2253e-5	2.2349
decreased memory T cell number	383	4.1105e-6	7.8281e-5	2.2707
decreased cardiomyocyte apoptosis	515	2.3918e-5	3.3875e-4	2.4978
abnormal induced retinal neovascularization	541	3.4964e-5	4.7140e-4	2.7384
decreased vasoconstriction	557	4.2168e-5	5.5219e-4	2.1912

E

MSigDB Pathway

Term Name	Binom Rank	Binom Raw P-Value	*Binom FDR Q-Val*	Binom Fold Enrichment
NFkB activation by Nontypeable Hemophilus influenzae	3	6.8870e-11	2.0202e-8	2.8600
Genes involved in Smooth Muscle Contraction	10	2.7285e-8	2.4011e-6	3.2520
Circadian rhythm - mammal	32	1.8260e-6	5.0216e-5	3.4446

F