

Supplementary Table S4. Biological processes of DEGs (FC > 2, p < 0.05) that positively correlated (r > 0.5, p < 0.05) with Temperature loss.

Category	Term	Count	%	Pathways	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR	Term
GOTERM_BP	GO:0002455~humoral immune	3	1.93548387	humoral imm	0.00253854	IGHG2B, IGH	116	12	18082	38.9698276	0.88414523	1	1	1 GO:0002455 humoral immune response mediated by circulating immunoglobulin
GOTERM_BP	GO:0043401~steroid hormone r	4	2.58064516	steroid horm	0.00465868	RARG, NR1H	116	53	18082	11.7644763	0.98093289	1	1	1 GO:0043401 steroid hormone mediated signaling pathway
GOTERM_BP	GO:0006954~inflammatory resp	8	5.16129032	inflammatory	0.00644661	NAIP6, P1P1,	116	344	18082	3.62510024	0.99584908	1	1	1 GO:0006954 inflammatory response
GOTERM_BP	GO:0016064~immunoglobulin n	3	1.93548387	immunoglobi	0.00852406	IGHG2B, IGH	116	22	18082	21.2562696	0.99929646	1	1	1 GO:0016064 immunoglobulin mediated immune response
GOTERM_BP	GO:0001570~vasculogenesis	4	2.58064516	vasculogenes	0.00930432	ANGPT1, SOX	116	68	18082	9.1693712	0.99963913	1	1	1 GO:0001570 vasculogenesis
GOTERM_BP	GO:0002376~immune system pi	8	5.16129032	immune syst	0.01125768	CR2, KLRK1, I	116	383	18082	3.25596471	0.99993232	1	1	1 GO:0002376 immune system process
GOTERM_BP	GO:0045087~innate immune re	8	5.16129032	innate immu	0.01401583	IGHG2B, IGH	116	400	18082	3.11758621	0.99999367	1	1	1 GO:0045087 innate immune response
GOTERM_BP	GO:0042113~B cell activation	3	1.93548387	B cell activati	0.01455491	CR2, BANK1,	116	29	18082	16.1254459	0.99999602	1	1	1 GO:0042113 B cell activation
GOTERM_BP	GO:2001240~negative regulatio	3	1.93548387	negative regu	0.01861939	CX3CR1, EYA,	116	33	18082	14.1708464	0.99999988	1	1	1 GO:2001240 negative regulation of extrinsic apoptotic signaling pathway in absence of ligand
GOTERM_BP	GO:0030154~cell differentiation	11	7.09677419	cell differenti	0.02693384	PAQR8, TTL:	116	780	18082	2.19829797	1	1	1	1 GO:0030154 cell differentiation
GOTERM_BP	GO:0007165~signal transductio	15	9.67741935	signal transd	0.02810257	CX3CR1, GPR	116	1255	18082	1.86309933	1	1	1	1 GO:0007165 signal transduction
GOTERM_BP	GO:0010466~negative regulatio	4	2.58064516	negative regu	0.03866427	ITIH4, SERPIN	116	117	18082	5.32920719	1	1	1	1 GO:0010466 negative regulation of peptidase activity
GOTERM_BP	GO:0060291~long-term synapti	3	1.93548387	long-term syr	0.03883968	SNAP47, SERI	116	49	18082	9.54363125	1	1	1	1 GO:0060291 long-term synaptic potentiation
GOTERM_BP	GO:0006935~chemotaxis	4	2.58064516	chemotaxis	0.03949465	CX3CR1, ROB	116	118	18082	5.28404442	1	1	1	1 GO:0006935 chemotaxis
GOTERM_BP	GO:0032729~positive regulatio	3	1.93548387	positive regu	0.04326146	KLRK1, FLT3,	116	52	18082	8.99303714	1	1	1	1 GO:0032729 positive regulation of interferon-gamma production
GOTERM_BP	GO:0006958~complement activ	3	1.93548387	complement	0.04786098	IGHG2B, IGH	116	55	18082	8.50250784	1	1	1	1 GO:0006958 complement activation, classical pathway
GOTERM_BP	GO:0007275~multicellular orgar	12	7.74193548	multicellular	0.0629818	PAQR8, TTL:	116	1029	18082	1.81783452	1	1	1	1 GO:0007275 multicellular organism development
GOTERM_BP	GO:0071300~cellular response t	3	1.93548387	cellular resp	0.064373	RARG, NTRK3	116	65	18082	7.19442971	1	1	1	1 GO:0071300 cellular response to retinoic acid
GOTERM_BP	GO:0007179~transforming grow	3	1.93548387	transforming	0.08248634	HPGD, LTBP4	116	75	18082	6.23517241	1	1	1	1 GO:0007179 transforming growth factor beta receptor signaling pathway
GOTERM_BP	GO:0007399~nervous system de	6	3.87096774	nervous syste	0.09281204	TTL7, ROBO:	116	377	18082	2.48083783	1	1	1	1 GO:0007399 nervous system development
GOTERM_BP	GO:0001933~negative regulatio	3	1.93548387	negative regu	0.09994422	WWTR1, ANG	116	84	18082	5.56711823	1	1	1	1 GO:0001933 negative regulation of protein phosphorylation
GOTERM_BP	GO:0001934~positive regulatio	4	2.58064516	positive regu	0.11264437	FLT3, AKAP5,	116	184	18082	3.38868066	1	1	1	1 GO:0001934 positive regulation of protein phosphorylation
GOTERM_BP	GO:0042742~defense response	4	2.58064516	defense resp	0.12225059	IGHG2B, IGH	116	191	18082	3.26448817	1	1	1	1 GO:0042742 defense response to bacterium
GOTERM_BP	GO:0007169~transmembrane re	3	1.93548387	transmembr	0.13314803	ANGPT1, FLT:	116	100	18082	4.67637931	1	1	1	1 GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway
GOTERM_BP	GO:0030336~negative regulatio	3	1.93548387	negative regu	0.14617407	CX3CR1, TIE1	116	106	18082	4.41167859	1	1	1	1 GO:0030336 negative regulation of cell migration
GOTERM_BP	GO:0007166~cell surface recept	4	2.58064516	cell surface r	0.16339366	TSPAN17, MS	116	219	18082	2.84711069	1	1	1	1 GO:0007166 cell surface receptor signaling pathway
GOTERM_BP	GO:0043065~positive regulatio	3	1.93548387	positive regu	0.16505815	RARG, KLRK1	116	335	18082	2.32655687	1	1	1	1 GO:0043065 positive regulation of apoptotic process
GOTERM_BP	GO:0006629~lipid metabolic pro	6	3.87096774	lipid metabol	0.16847624	SULT1A1, CEF	116	459	18082	2.03763804	1	1	1	1 GO:0006629 lipid metabolic process
GOTERM_BP	GO:0035264~multicellular orgar	3	1.93548387	multicellular	0.17747985	WWTR1, RAR	116	120	18082	3.89698276	1	1	1	1 GO:0035264 multicellular organism growth
GOTERM_BP	GO:0045766~positive regulatio	3	1.93548387	positive regu	0.17975615	CX3CR1, CEL:	116	121	18082	3.86477629	1	1	1	1 GO:0045766 positive regulation of angiogenesis
GOTERM_BP	GO:0001525~angiogenesis	4	2.58064516	angiogenesis	0.19498022	ANGPT1, SOX	116	239	18082	2.60885875	1	1	1	1 GO:0001525 angiogenesis
GOTERM_BP	GO:0007155~cell adhesion	6	3.87096774	cell adhesion	0.19644342	CX3CR1, TRO	116	485	18082	1.92840384	1	1	1	1 GO:0007155 cell adhesion
GOTERM_BP	GO:0055085~transmembrane tr	5	3.22580645	transmembr	0.20181014	TRPC6, TRPC:	116	364	18082	2.14119932	1	1	1	1 GO:0055085 transmembrane transport
GOTERM_BP	GO:0007507~heart developmen	4	2.58064516	heart develop	0.23128572	SOX18, NTRK	116	261	18082	2.38895495	1	1	1	1 GO:0007507 heart development
GOTERM_BP	GO:0019221~cytokine-mediate	3	1.93548387	cytokine-mec	0.23777493	CX3CR1, POD	116	146	18082	3.20299953	1	1	1	1 GO:0019221 cytokine-mediated signaling pathway
GOTERM_BP	GO:0010628~positive regulatio	5	3.22580645	positive regu	0.24902798	RARG, NTRK3	116	399	18082	1.95337482	1	1	1	1 GO:0010628 positive regulation of gene expression
GOTERM_BP	GO:0006955~immune response	4	2.58064516	immune resp	0.24989382	IL7, CCR6, MS	116	272	18082	2.2923428	1	1	1	1 GO:0006955 immune response
GOTERM_BP	GO:0006631~fatty acid metabol	3	1.93548387	fatty acid me	0.26131659	HACD1, HPGI	116	156	18082	2.99767905	1	1	1	1 GO:0006631 fatty acid metabolic process
GOTERM_BP	GO:0008284~positive regulatio	6	3.87096774	positive regu	0.26264345	WWTR1, RAR	116	542	18082	1.72560122	1	1	1	1 GO:0008284 positive regulation of cell proliferation
GOTERM_BP	GO:0001701~in utero embryoni	4	2.58064516	in utero emb	0.29638579	ANGPT1, SOX	116	299	18082	2.08534194	1	1	1	1 GO:0001701 in utero embryonic development
GOTERM_BP	GO:0051260~protein homoolig	3	1.93548387	protein hom	0.35717537	ANGPT1, NAC	116	197	18082	2.37379636	1	1	1	1 GO:0051260 protein homooligomerization
GOTERM_BP	GO:0030335~positive regulatio	3	1.93548387	positive regu	0.37090764	WNF5B, NTR	116	203	18082	2.30363513	1	1	1	1 GO:0030335 positive regulation of cell migration
GOTERM_BP	GO:0071222~cellular response t	3	1.93548387	cellular resp	0.38452495	CX3CR1, KLR	116	209	18082	2.23750206	1	1	1	1 GO:0071222 cellular response to lipopolysaccharide
GOTERM_BP	GO:0042127~regulation of cell p	3	1.93548387	regulation of	0.42458451	CELA1, CXCL	116	227	18082	2.06007899	1	1	1	1 GO:0042127 regulation of cell proliferation
GOTERM_BP	GO:0008285~negative regulatio	4	2.58064516	negative regu	0.44285966	RARG, SERPI	116	384	18082	1.62374282	1	1	1	1 GO:0008285 negative regulation of cell proliferation
GOTERM_BP	GO:0045944~positive regulatio	8	5.16129032	positive regu	0.44784861	WWTR1, RAR	116	995	18082	1.25330099	1	1	1	1 GO:0045944 positive regulation of transcription from RNA polymerase II promoter
GOTERM_BP	GO:0045944~positive regulatio	8	5.16129032	positive regu	0.44784861	WWTR1, RAR	116	995	18082	1.25330099	1	1	1	1 GO:0045944 positive regulation of transcription from RNA polymerase II promoter
GOTERM_BP	GO:0043066~negative regulatio	5	3.22580645	negative regu	0.48713961	RARG, SERPI	116	566	18082	1.37702571	1	1	1	1 GO:0043066 negative regulation of apoptotic process
GOTERM_BP	GO:0006468~protein phosphor	3	1.93548387	protein phosph	0.50084983	FLT3, NTRK3,	116	576	18082	1.35311901	1	1	1	1 GO:0006468 protein phosphorylation
GOTERM_BP	GO:0006811~ion transport	5	3.22580645	ion transport	0.51170677	TRPC6, TRPC:	116	584	18082	1.33458314	1	1	1	1 GO:0006811 ion transport
GOTERM_BP	GO:0016310~phosphorylation	5	3.22580645	phosphorylat	0.54884702	FLT3, NTRK3,	116	612	18082	1.27352378	1	1	1	1 GO:0016310 phosphorylation
GOTERM_BP	GO:0010468~regulation of gene	3	1.93548387	regulation of	0.58585531	RARG, IL7, AF	116	308	18082	1.51830497	1	1	1	1 GO:0010468 regulation of gene expression
GOTERM_BP	GO:0055114~oxidation-reductio	5	3.22580645	oxidation-re	0.62791536	HSD3B6, HPG	116	676	18082	1.15295348	1	1	1	1 GO:0055114 oxidation-reduction process
GOTERM_BP	GO:0007186~G-protein couple	11	7.09677419	G-protein cou	0.65394242	CX3CR1, GPR	116	1706	18082	1.00508348	1	1	1	1 GO:0007186 G-protein coupled receptor signaling pathway
GOTERM_BP	GO:0000122~negative regulatio	5	3.22580645	negative regu	0.68644432	WWTR1, RAR	116	729	18082	1.06913107	1	1	1	1 GO:0000122 negative regulation of transcription from RNA polymerase II promoter
GOTERM_BP	GO:0035556~intracellular signal	3	1.93548387	intracellular s	0.72602852	ARHGGEF5, RG	116	400	18082	1.16909483	1	1	1	1 GO:0035556 intracellular signal transduction
GOTERM_BP	GO:0006351~transcription, DNA	11	7.09677419	transcription,	0.77183156	WWTR1, RAR	116	1885	18082	0.90964054	1	1	1	1 GO:0006351 transcription, DNA-templated
GOTERM_BP	GO:0008152~metabolic process	3	1.93548387	metabolic pro	0.79727363	HSD3B6, ECH	116	463	18082	1.01001713	1	1	1	1 GO:0008152 metabolic process
GOTERM_BP	GO:0006355~regulation of trans	13	8.38709677	regulation of	0.79794928	WWTR1, RAR	116	2279	18082	0.88917553	1	1	1	1 GO:0006355 regulation of transcription, DNA-templated
GOTERM_BP	GO:0006810~transport	10	6.4516129	transport	0.83101836	TRPC6, CCDC	116	1822	18082	0.85553957	1	1	1	1 GO:0006810 transport
GOTERM_BP	GO:0045893~positive regulatio	3	1.93548387	positive regu	0.88519171	SOX18, RO	116	576	18082	0.81187141	1	1	1	1 GO:0045893 positive regulation of transcription, DNA-templated
GOTERM_BP	GO:0045892~negative regulatio	3	1.93548387	negative regu	0.8869598	SOX18, NACC	116	579	18082	0.80766482	1	1	1	1 GO:0045892 negative regulation of transcription, DNA-templated

**Supplementary Table S4. Biological processes of DEGs (FC > 2, p < 0.05) that negatively correlated (r < -0.5, p < 0.05) with Temperature loss**

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_BP	GO:0071356~cellular response to	3	7.89473684	0.01427647	POSTN, ACOD1, TDGF1	31	110	18082	15.9079179	0.95891931	1	1
GOTERM_BP	GO:0007155~cell adhesion	4	10.5263158	0.04558362	RET, POSTN, ITGB2L, COL6A5	31	485	18082	4.81064184	0.99996825	1	1
GOTERM_BP	GO:0071222~cellular response to	3	7.89473684	0.04679909	TNIP3, ACOD1, CD14	31	209	18082	8.37258836	0.99997607	1	1
GOTERM_BP	GO:0001701~in utero embryonic	3	7.89473684	0.08759786	HBA-A2, HBA-A1, TDGF1	31	299	18082	5.85241126	1	1	1
GOTERM_BP	GO:0006954~inflammatory respo	3	7.89473684	0.11088837	ITGB2L, ACOD1, CD14	31	344	18082	5.08683421	1	1	1
GOTERM_BP	GO:0002376~immune system pro	4	10.5263158	0.02507866	IL4RA, ACOD1, CD14, CLEC4E	31	383	18082	6.09180494	0.99644167	1	1
GOTERM_BP	GO:0045087~innate immune res	3	7.89473684	0.14185407	ACOD1, CD14, CLEC4E	31	400	18082	4.37467742	1	1	1