A. TNFα upregulated protein-coding genes and adjacent genomic regions

GO Biological Process	**Binom FDR Q-Val**	**Binom Fold Enrichment**
defense response	6.89E-27	3.53
immune response	6.62E-24	3.54
response to stress	5.57E-22	2.02
immune system process	1.32E-20	2.48
inflammatory response	1.15E-15	4.29
response to wounding	3.20E-15	2.49
regulation of programmed cell death	4.82E-13	2.19
response to cytokine stimulus	1.09E-12	3.54
innate immune response	1.03E-12	3.64
regulation of cell death	1.08E-12	2.13
regulation of apoptosis	1.09E-12	2.17
regulation of cytokine production	2.89E-12	3.83
regulation of response to stress	3.44E-11	2.65
regulation of immune system process	2.86E-10	2.36
cellular response to cytokine stimulus	5.25E-10	3.89
positive regulation of response to stimulus	1.01E-09	2.10
cytokine-mediated signaling pathway	1.90E-09	4.44
multi-organism process	3.03E-09	2.21
positive regulation of cellular component movement	5.61E-09	3.29
response to other organism	6.27E-09	2.85

B. TNFα downregulated protein-coding genes and adjacent genomic regions

GO Biological Process	**Binom FDR Q-Val**	**Binom Fold Enrichment**
cofactor metabolic process	2.00E-10	2.37
cofactor biosynthetic process	2.35972E-06	2.55
coenzyme metabolic process	5.39966E-05	2.01

C. TNFα upregulated lncRNA genes and adjacent genomic regions

GO Biological Processes	**Binom FDR Q-Val**	**Binom Fold Enrichment**
regulation of cell proliferation	1.40E-07	2.94
multi-organism process	7.68E-08	3.64
response to mechanical stimulus	6.38E-07	8.79
regulation of apoptosis	2.40742E-06	2.86
response to stress	2.23523E-06	2.18
regulation of cell death	2.02791E-06	2.78
negative regulation of cellular process	1.99749E-06	2.02
regulation of programmed cell death	1.89378E-06	2.83
vasculature development	3.23846E-06	3.88
positive regulation of macromolecule metabolic process	3.14824E-06	2.38
response to lipopolysaccharide	3.52322E-06	6.90

response to wounding	3.59794E-06	3.05
blood vessel development	3.85106E-06	3.93
positive regulation of metabolic process	5.30154E-06	2.28
response to molecule of bacterial origin	4.31218E-06	6.44
regulation of immune system process	4.69096E-06	3.28
positive regulation of cell proliferation	9.04782E-06	3.25
response to peptidoglycan	9.17262E-06	32.4
regulation of response to stress	1.08144E-05	3.55
response to cytokine stimulus	1.27001E-05	4.66

D. TNFα upregulated enhancers and adjacent genomic regions

GO Biological Process	Binom FDR Q-Val	Binom Fold Enrichment
regulation of response to stress	1.47E-08	3.19
multi-organism process	2.91E-08	2.71
regulation of cell proliferation	1.72E-07	2.20
regulation of cellular response to stress	7.31E-07	4.18
response to abiotic stimulus	1.09E-06	2.85
regulation of cytokine-mediated signaling pathway	2.03E-06	7.67
regulation of response to cytokine stimulus	1.89E-06	7.65
regulation of cytokine production	4.87E-06	3.83
negative regulation of transport	1.12E-05	3.79
cytokine-mediated signaling pathway	1.29E-05	4.87
regulation of myeloid cell differentiation	1.46E-05	5.43
positive regulation of cytokine production	1.43E-05	5.09
regulation of type I interferon-mediated signaling pathway	1.41E-05	17.5
regulation of immune system process	1.38E-05	2.42
cellular response to cytokine stimulus	1.66E-05	4.06
JAK-STAT cascade	2.05E-05	12.8
cell proliferation	2.46E-05	2.53
response to other organism	2.61E-05	3.05
response to cytokine stimulus	4.25E-05	3.21
cellular response to stress	5.81E-05	2.27

E. TNFα upregulated antisense RNA genes and adjacent genomic regions

GO Biological Process	Binom FDR Q-Val	Binom Fold Enrichment
regulation of response to stress	1.47E-08	3.20
multi-organism process	2.91E-08	2.71
regulation of cell proliferation	1.72E-07	2.20
regulation of cellular response to stress	7.31E-07	4.18
response to abiotic stimulus	1.09E-06	2.85
regulation of cytokine-mediated signaling pathway	2.03E-06	7.67
regulation of response to cytokine stimulus	1.89E-06	7.65
regulation of cytokine production	4.87E-06	3.83

negative regulation of transport	1.12E-05	3.79
cytokine-mediated signaling pathway	1.29E-05	4.87
regulation of myeloid cell differentiation	1.46E-05	5.43
positive regulation of cytokine production	1.43E-05	5.09
regulation of type I interferon-mediated signaling pathway	1.41E-05	17.5
regulation of immune system process	1.38E-05	2.42
cellular response to cytokine stimulus	1.66E-05	4.06
JAK-STAT cascade	2.05E-05	12.8
cell proliferation	2.46E-05	2.53
response to other organism	2.61E-05	3.05
response to cytokine stimulus	4.25E-05	3.21
cellular response to stress	5.81E-05	2.27