Table 1: Ontological analysis of genome-wide bioinformatics analysis using KLF16 and BTE consensus sequences as probes.

GOID	Term	Matches	Total	p
GO:0008152	metabolic process	105	6961	8.62E-03
GO:0044238	primary metabolic process	97	6295	8.99E-03
GO:0044237	cellular metabolic process	93	6043	1.44E-02
GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	57	3356	2.96E-02
GO:0051171	regulation of nitrogen compound metabolic process	57	3435	4.31E-02
GO:0009889	regulation of biosynthetic process	56	3323	3.38E-02
GO:0031326	regulation of cellular biosynthetic process	55	3296	4.62E-02
GO:0009058	biosynthetic process	53	2424	8.06E-05
GO:0010556	regulation of macromolecule biosynthetic process	53	3129	4.25E-02
GO:0051252	regulation of RNA metabolic process	52	2914	1.96E-02
GO:2000112	regulation of cellular macromolecule biosynthetic process	52	3068	4.60E-02
GO:0048856	anatomical structure development	52	3087	4.85E-02
GO:0044249	cellular biosynthetic process	50	2328	3.09E-04
GO:0006355	regulation of transcription, DNA-dependent	50	2854	2.96E-02
GO:0048731	system development	48	2769	4.60E-02
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	47	2633	2.96E-02
GO:0048522	positive regulation of cellular process	44	2443	3.62E-02
GO:0034645	cellular macromolecule biosynthetic process	37	1600	1.46E-03
GO:0009059	macromolecule biosynthetic process	37	1620	1.93E-03
GO:0010467	gene expression	37	1760	1.05E-02
GO:0032774	RNA biosynthetic process	27	931	3.85E-04
GO:0006351	transcription, DNA-dependent	26	844	1.89E-04
GO:0006357	regulation of transcription from RNA polymerase II promoter	22	921	2.87E-02
GO:0051173	positive regulation of nitrogen compound metabolic process	21	840	2.17E-02
GO:0009888	tissue development	21	889	3.34E-02
GO:0031328	positive regulation of cellular biosynthetic process	21	899	3.80E-02
GO:0009891	positive regulation of biosynthetic process	21	915	4.60E-02
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	20	816	2.96E-02
GO:0051254	positive regulation of RNA metabolic process	19	733	2.38E-02
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	16	482	6.04E-03
GO:0031667	response to nutrient levels	12	289	4.63E-03
GO:0009991	response to extracellular stimulus	12	311	9.03E-03
GO:0001501	skeletal system development	11	312	2.30E-02
GO:0006366	transcription from RNA polymerase II promoter	10	289	3.34E-02
GO:0007423	sensory organ development	10	302	4.57E-02
GO:0007584	response to nutrient	9	198	1.32E-02
GO:0046039	GTP metabolic process	7	153	2.96E-02
GO:0045598	regulation of fat cell differentiation	6	42	7.05E-05
GO:0007565	female pregnancy	6	126	4.05E-02
GO:0033273	response to vitamin	6	129	4.55E-02

GO:0008589	regulation of smoothened signaling pathway	4	32	4.52E-03
GO:0060021	palate development	4	48	2.00E-02
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	3	17	4.85E-03
GO:0046697	decidualization	3	17	4.85E-03
GO:0009220	pyrimidine ribonucleotide biosynthetic process	3	17	4.85E-03
GO:0009218	pyrimidine ribonucleotide metabolic process	3	18	6.17E-03
GO:0001893	maternal placenta development	3	20	9.32E-03
GO:0045599	negative regulation of fat cell differentiation	3	21	1.12E-02
GO:0006221	pyrimidine nucleotide biosynthetic process	3	24	1.48E-02
GO:0046131	pyrimidine ribonucleoside metabolic process	3	25	1.60E-02
GO:0002053	positive regulation of mesenchymal cell proliferation	3	28	2.35E-02
GO:0010464	regulation of mesenchymal cell proliferation	3	31	2.96E-02
GO:0007416	synapse assembly	3	33	3.38E-02
GO:0072528	pyrimidine-containing compound biosynthetic process	3	35	4.20E-02
GO:0043588	skin development	3	36	4.57E-02
GO:0045161	neuronal ion channel clustering	2	8	8.62E-03
GO:0009396	folic acid-containing compound biosynthetic process	2	8	8.62E-03
GO:0046655	folic acid metabolic process	2	9	1.26E-02
GO:0040015	negative regulation of multicellular organism growth	2	9	1.26E-02
GO:0048194	Golgi vesicle budding	2	10	1.48E-02
GO:0048200	Golgi transport vesicle coating	2	10	1.48E-02
GO:0048205	COPI coating of Golgi vesicle	2	10	1.48E-02
GO:0000768	syncytium formation by plasma membrane fusion	2	10	1.48E-02
GO:0007520	myoblast fusion	2	10	1.48E-02
GO:0006183	GTP biosynthetic process	2	11	1.80E-02
GO:0006228	UTP biosynthetic process	2	11	1.80E-02
GO:0046051	UTP metabolic process	2	11	1.80E-02
GO:0071320	cellular response to cAMP	2	11	1.80E-02
GO:0007213	muscarinic acetylcholine receptor signaling pathway	2	12	2.30E-02
GO:0006949	syncytium formation	2	12	2.30E-02
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	2	12	2.30E-02
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	2	12	2.30E-02
GO:0006241	CTP biosynthetic process	2	12	2.30E-02
GO:0046036	CTP metabolic process	2	12	2.30E-02
GO:0043403	skeletal muscle tissue regeneration	2	12	2.30E-02
GO:0046689	response to mercury ion	2	13	2.91E-02
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	2	13	2.91E-02
GO:0045880	positive regulation of smoothened signaling pathway	2	13	2.91E-02
GO:0043113	receptor clustering	2	14	2.96E-02
GO:0043586	tongue development	2	15	3.60E-02
GO:0014902	myotube differentiation	2	16	4.31E-02
GO:0045600	positive regulation of fat cell differentiation	2	16	4.31E-02
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	2	16	4.31E-02
GO:0002467	germinal center formation	1	5	4.85E-02
GO:0031659	positive regulation of cyclin-dependent protein kinase activity involved in G1/S	1	5	4.85E-02
GO:0032717	negative regulation of interleukin-8 production	1	5	4.85E-02

GO:0051005	negative regulation of lipoprotein lipase activity	1	5	4.85E-02
GO:2000344	positive regulation of acrosome reaction	1	5	4.85E-02
GO:2000018	regulation of male gonad development	1	5	4.85E-02
GO:0030970	retrograde protein transport, ER to cytosol	1	5	4.85E-02
GO:0007386	compartment pattern formation	1	5	4.85E-02
GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	1	5	4.85E-02
GO:0060023	soft palate development	1	5	4.85E-02
GO:0061037	negative regulation of cartilage development	1	5	4.85E-02
GO:0002367	cytokine production involved in immune response	1	5	4.85E-02
GO:0042092	type 2 immune response	1	5	4.85E-02
GO:0048293	regulation of isotype switching to IgE isotypes	1	5	4.85E-02
GO:0043570	maintenance of DNA repeat elements	1	5	4.85E-02
GO:0051096	positive regulation of helicase activity	1	5	4.85E-02
GO:2000278	regulation of DNA biosynthetic process	1	5	4.85E-02
GO:0051387	negative regulation of nerve growth factor receptor signaling pathway	1	5	4.85E-02
GO:0007023	post-chaperonin tubulin folding pathway	1	5	4.85E-02
GO:0006862	nucleotide transport	1	5	4.85E-02
GO:0003032	detection of oxygen	1	5	4.85E-02
GO:0033152	immunoglobulin V(D)J recombination	1	5	4.85E-02
GO:0045898	regulation of RNA polymerase II transcriptional preinitiation complex assembly	1	5	4.85E-02
GO:0051798	positive regulation of hair follicle development	1	5	4.85E-02
GO:0060346	bone trabecula formation	1	5	4.85E-02
GO:0016139	glycoside catabolic process	1	5	4.85E-02
GO:0044245	polysaccharide digestion	1	5	4.85E-02