

Table S5. The significant biological processes related to Energy Metabolism. Protein turnover, and Redox homeostasis and immune system in genetic group 2 in the most efficient group.

Go Term	Number of genes	LOR*	p-value	padj	Biological process
GO:1901570	88	0.397	2.2×10^{-04}	3.7×10^{-02}	fatty acid derivative biosynthetic process
GO:0031663	54	0.570	5.9×10^{-05}	1.3×10^{-02}	lipopolysaccharide-mediated signaling pathway
GO:0005978	49	-0.549	1.5×10^{-04}	2.7×10^{-02}	glycogen biosynthetic process
GO:0009250	49	-0.549	1.5×10^{-04}	2.7×10^{-02}	glucan biosynthetic process
GO:0006110	72	-0.524	1.5×10^{-05}	4.7×10^{-03}	regulation of glycolytic process
GO:0002718	63	0.474	3.3×10^{-04}	5.1×10^{-03}	regulation of cytokine production involved in immune response
GO:0042149	40	-0.697	8.7×10^{-06}	2.9×10^{-02}	cellular response to glucose starvation
GO:0006120	46	1.141	2.9×10^{-12}	6.8×10^{-09}	mitochondrial electron transport, NADH to ubiquinone
GO:0042773	81	-1.199	2.5×10^{-07}	1.7×10^{-03}	ATP synthesis coupled electron transport
GO:1901685	19	1.047	1.3×10^{-07}	1.0×10^{-04}	glutathione derivative metabolic process
GO:1901687	19	1.047	1.3×10^{-07}	1.0×10^{-04}	glutathione derivative biosynthetic process
GO:1990748	102	0.362	2.6×10^{-04}	4.2×10^{-02}	cellular detoxification
GO:0097237	110	0.357	1.9×10^{-04}	3.2×10^{-02}	cellular response to toxic substance
GO:0006614	94	1.139	6.3×10^{-18}	1.2×10^{-13}	SRP-dependent cotranslational protein targeting to membrane
GO:2001056	135	0.408	2.9×10^{-06}	1.3×10^{-03}	positive regulation of cysteine-type endopeptidase activity
GO:0010952	172	0.350	6.4×10^{-06}	2.4×10^{-03}	positive regulation of peptidase activity
GO:0006577	17	-0.736	1.2×10^{-03}	1.4×10^{-01}	amino-acid betaine metabolic process
GO:0052548	358	0.225	2.6×10^{-05}	6.6×10^{-03}	regulation of endopeptidase activity
GO:2001056	135	0.408	2.9×10^{-06}	1.3×10^{-03}	positive regulation of cysteine-type endopeptidase activity
GO:0043280	118	0.408	1.2×10^{-05}	3.8×10^{-03}	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0007249	253	0.222	4.7×10^{-04}	6.5×10^{-02}	I-kappaB kinase/NF-kappaB signaling
GO:0043123	176	0.276	2.9×10^{-04}	4.5×10^{-02}	positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0000186	55	-0.572	4.2×10^{-05}	9.8×10^{-03}	activation of MAPKK activity
GO:0032963	98	0.594	7.8×10^{-09}	8.8×10^{-06}	collagen metabolic process
GO:0030574	42	0.619	5.2×10^{-05}	1.1×10^{-03}	collagen catabolic process
GO:2000251	19	0.827	2.1×10^{-04}	3.5×10^{-02}	positive regulation of actin cytoskeleton reorganization

GO:0001516	24	0.794	1.6×10^{-04}	2.8×10^{-02}	prostaglandin biosynthetic process
GO:0018107	114	-0.364	1.4×10^{-04}	2.5×10^{-02}	peptidyl-threonine phosphorylation
GO:0052547	383	0.238	4.6×10^{-06}	1.9×10^{-03}	regulation of peptidase activity
GO:0002283	449	0.328	1.3×10^{-06}	2.6×10^{-08}	neutrophil activation involved in immune response
GO:0002446	460	0.329	6.4×10^{-12}	1.4×10^{-08}	neutrophil mediated immunity
GO:0002694	476	0.283	1.6×10^{-09}	2.1×10^{-06}	regulation of leukocyte activation
GO:0050867	306	0.349	2.3×10^{-09}	3.0×10^{-08}	positive regulation of cell activation
GO:0002250	352	0.279	2.8×10^{-07}	1.9×10^{-04}	adaptive immune response
GO:0042110	431	0.226	3.8×10^{-06}	1.6×10^{-03}	T cell activation
GO:0033006	30	0.863	7.5×10^{-06}	2.6×10^{-03}	regulation of mast cell activation involved in immune response
GO:0002697	351	0.241	8.7×10^{-07}	2.9×10^{-03}	regulation of immune effector process

*The LOR (Logarithm Of Ratio) refer to LRFI group, this value positions each biological process in a classification in relation to the rest (total), being able to identify biological processes, molecular mechanisms and significant cellular components and their regulation within the groups.