

Table S4. The significant biological processes related to Energy Metabolism, Protein turnover, and Redox homeostasis and immune system, in Genetic group 1 in the most efficient group.

Go Term	Number of genes	LOR*	p-value	padj	Biological process
GO:0006490	19	-0.866	2.3 x10 ⁻⁰⁴	1.3x10 ⁻⁰²	oligosaccharide-lipid intermediate biosynthetic process
GO:0042158	93	-0.497	2.4 x10 ⁻⁰⁶	2.6x10 ⁻⁰⁴	lipoprotein biosynthetic process
GO:0042157	121	-0.390	2.1 x10 ⁻⁰⁵	1.3x10 ⁻⁰⁴	lipoprotein metabolic process
GO:0015980	271	-0.377	1.0 x10 ⁻⁰⁹	2.5 x10 ⁻⁰⁷	energy derivation by oxidation of organic compounds
GO:0006488	18	-0.928	1.4 x10 ⁻⁰⁴	8.7 x10 ⁻⁰³	dolichol-linked oligosaccharide biosynthetic process
GO:0010517	68	0.384	1.6 x10 ⁻⁰³	6.7 x10 ⁻⁰²	regulation of phospholipase activity
GO:0043550	63	0.429	7.5 x10 ⁻⁰⁴	3.6 x10 ⁻⁰²	regulation of lipid kinase activity
GO:0090218	37	0.560	7.5 x10 ⁻⁰⁴	3.6 x10 ⁻⁰²	positive regulation of lipid kinase activity
GO:0032981	58	-1.082	2.0 x10 ⁻²²	3.6 x10 ⁻¹⁹	mitochondrial respiratory chain complex I assembly
GO:0033108	87	-1.039	3.5 x10 ⁻²⁸	1.8 x10 ⁻²⁴	mitochondrial respiratory chain complex assembly
GO:0042776	19	-0.938	7.0 x10 ⁻⁰⁶	6.6 x10 ⁻⁰⁴	mitochondrial ATP synthesis coupled proton transport
GO:0008535	21	-0.895	9.4 x10 ⁻⁰⁶	8.5 x10 ⁻⁰⁴	respiratory chain complex IV assembly
GO:0042773	81	-0.833	1.2 x10 ⁻¹²	5.1 x10 ⁻¹⁰	ATP synthesis coupled electron transport
GO:0022904	100	-0.772	8.9 x10 ⁻¹⁴	4.4 x10 ⁻¹¹	respiratory electron transport chain
GO:0007260	75	0.380	1.1 x10 ⁻⁰³	4.8 x10 ⁻⁰²	tyrosine phosphorylation of STAT protein
GO:0071900	492	0.369	1.6 x10 ⁻¹⁵	9.7 x10 ⁻¹³	regulation of protein serine/threonine kinase activity
GO:0046777	236	0.474	4.5 x10 ⁻¹³	2.1 x10 ⁻¹⁰	protein autophosphorylation
GO:0032147	324	0.387	6.8 x10 ⁻¹²	2.6 x10 ⁻⁰⁹	activation of protein kinase activity
GO:0031334	234	0.440	4.0 x10 ⁻¹¹	1.4 x10 ⁻⁰⁸	positive regulation of protein-containing complex assembly
GO:190382	321	0.317	2.3 x10 ⁻⁰⁸	4.2 x10 ⁻⁰⁶	positive regulation of cellular protein localization

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GO:004339 3	209	0.265	1.4×10^{-04}	8.8×10^{-03}	regulation of protein binding
GO:007163 4	35	0.721	1.2×10^{-05}	1.1×10^{-03}	regulation of transforming growth factor beta production
GO:001810 7	114	0.385	5.4×10^{-05}	3.8×10^{-03}	peptidyl-threonine phosphorylation
GO:000722 3	37	0.561	1.0×10^{-04}	2.8×10^{-02}	Wnt signaling pathway, calcium modulating pathway
GO:190122 4	75	0.493	6.4×10^{-05}	2.0×10^{-03}	positive regulation of NIK/NF-kappaB signaling
GO:000018 6	55	-0.572	4.2×10^{-05}	9.8×10^{-03}	activation of MAPKK activity
GO:007037 1	284	0.378	4.2×10^{-10}	1.1×10^{-07}	ERK1 and ERK2 cascade
GO:000276 4	353	0.569	8.0×10^{-25}	2.6×10^{-21}	immune response-regulating signaling pathway
GO:000225 3	402	0.471	7.6×10^{-25}	7.8×10^{-17}	activation of immune response
GO:004578 5	386	0.568	1.9×10^{-27}	8.6×10^{-24}	positive regulation of cell adhesion
GO:000181 9	356	0.534	2.1×10^{-22}	3.6×10^{-19}	positive regulation of cytokine production
GO:004578 7	359	0.288	7.4×10^{-08}	1.2×10^{-05}	positive regulation of cell cycle
GO:009769 6	139	0.325	1.5×10^{-04}	9.3×10^{-03}	receptor signaling pathway via STAT

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