Supplementary Information (SI) for Food & Function.
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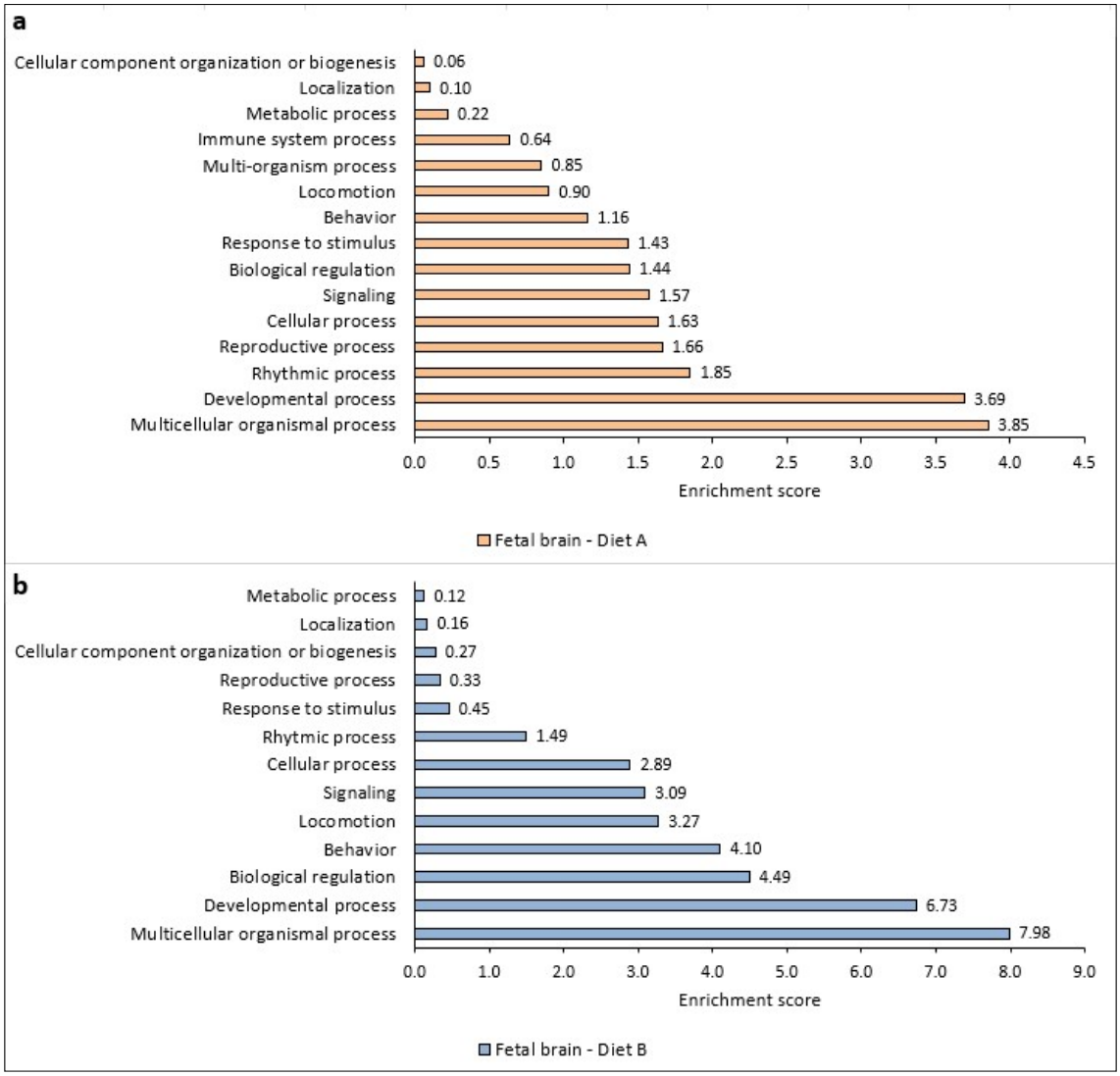
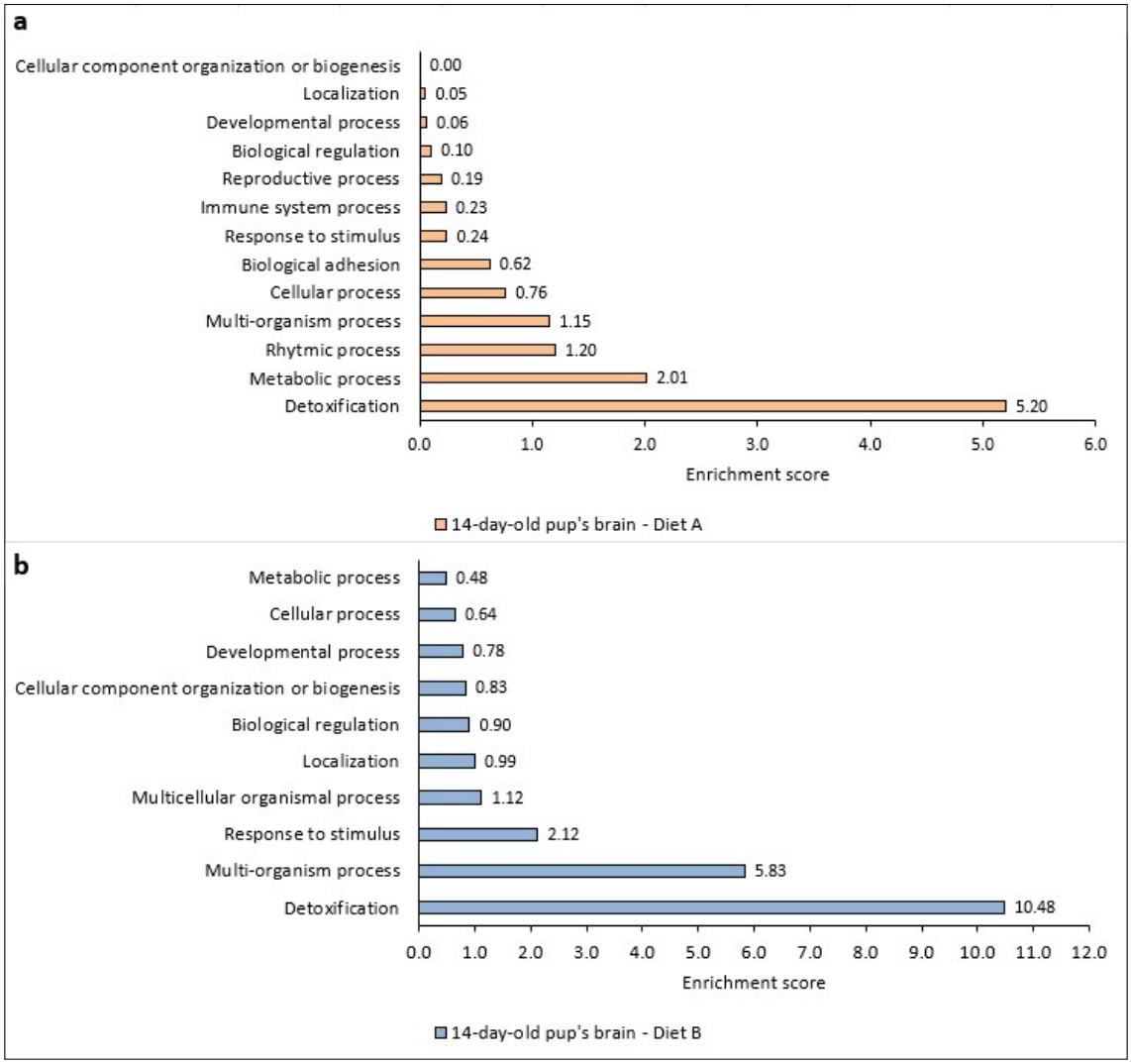
Annex 1. GO processes affected in fetal brain from groups A (a) and B (b) compared to control, classified by enrichment score. GO, gene ontology.



Annex 2. KEGG pathways affected in fetal brain from groups A and B compared to control, classified by enrichment score. KEGG, Kyoto encyclopedia of genes and genomes.

KEGG Pathway	Enrichment score	*P*	Genes in the pathway
Diet A			
Tyrosine metabolism	4.20	0.015	*Dbh*
Tryptophan metabolism	3.97	0.019	*Tph2*
Amyotrophic lateral sclerosis	3.81	0.022	*Prph*
Serotonergic synapse	2.95	0.052	*Tph2*
Metabolic pathways	2.60	0.074	*Dbh, Tph2*
Diet B			
Tryptophan metabolism	3.97	0.019	*Tph2*
Cholinergic synapse	3.08	0.046	*Chrm1*
Serotonergic synapse	2.95	0.052	*Tph2*
FoxO signaling pathway	2.89	0.056	*Foxg1*
Calcium signaling pathway	2.58	0.075	*Chrm1*
Regulation of actin cytoskeleton	2.43	0.088	*Chrm1*
Neuroactive ligand-receptor interaction	2.16	0.116	*Chrm1*
PI3K-Akt signaling pathway	2.01	0.134	*Chrm1*
Metabolic pathways	0.86	0.422	*Tph2*

Annex 3. GO processes affected in 14-day-old pup's brain from groups A (a) and B (b) compared to control, classified by enrichment score. GO, gene ontology.



Annex 4. KEGG pathways affected in 14-day-old pup's brain from groups A and B compared to control, classified by enrichment score. KEGG, Kyoto encyclopedia of genes and genomes.

KEGG Pathway	Enrichment score	*P*	Genes in the pathway
Diet A			
Ribosome	5.25	0.005	*Rps29*
Mineral absorption	3.25	0.039	*Mt2A*
Long-term depression	3.00	0.050	*Ppp1r17*
Glutamatergic synapse	2.37	0.093	*Slc1a6*
Parkinson's disease	2.20	0.111	*Atp5e*
Oxidative phosphorylation	2.20	0.111	*Atp5e*
Alzheimer's disease	1.97	0.139	*Atp5e*
Huntington's disease	1.93	0.145	*Atp5e*
Metabolic pathways	0.41	0.666	*Atp5e*
Diet B			
African trypanosomiasis	4.60	0.010	*Hba-a1*
Mineral absorption	4.33	0.013	*Mt2A*
Malaria	4.23	0.015	*Hba-a1*