

Table S2: Metabolite-set Enrichment Pathways analysis results derived from the metabolites selected as relevant in the classification of CTRL vs. CRC serum samples. Total column represents the total number of compounds in the pathway; the Hits column is the number of metabolites from a given pathway that were selected as relevant; the Raw p is the original p value evaluated from the enrichment analysis; the Holm adjust column is the raw p-value adjusted by the Holm-Bonferroni method; the FDR is the p-value adjusted using False Discovery Rate; the Impact is the pathway impact value calculated from pathway topology analysis.

	Total	Expected	Hits	Raw p	-Log ₁₀ (p)	Holm adjust	FDR	Impact
<i>Arginine biosynthesis</i>	14	0.32516	5	8.75E-06	5.0578	0.000735	0.000676	0.11675
<i>Valine, leucine and isoleucine biosynthesis</i>	8	0.18581	4	1.61E-05	4.7932	0.001336	0.000676	0
<i>Aminoacyl-tRNA biosynthesis</i>	48	1.1148	7	7.37E-05	4.1324	0.006045	0.002064	0
<i>D-Glutamine and D-glutamate metabolism</i>	6	0.13935	3	0.00022	3.6583	0.017791	0.004613	0.5
<i>Alanine, aspartate and glutamate metabolism</i>	28	0.65032	5	0.000339	3.4694	0.027145	0.005701	0.58254
<i>Nicotinate and nicotinamide metabolism</i>	15	0.34839	3	0.004324	2.3641	0.34163	0.060542	0
<i>Glyoxylate and dicarboxylate metabolism</i>	32	0.74323	4	0.005547	2.256	0.43265	0.066562	0
<i>Nitrogen metabolism</i>	6	0.13935	2	0.007422	2.1295	0.57148	0.077929	0
<i>Galactose metabolism</i>	27	0.6271	3	0.022957	1.6391	1	0.21427	0.19819
<i>Glycine, serine and threonine metabolism</i>	33	0.76645	3	0.038938	1.4096	1	0.32149	0
<i>Butanoate metabolism</i>	15	0.34839	2	0.045562	1.3414	1	0.32149	0
<i>Neomycin, kanamycin and gentamicin biosynthesis</i>	2	0.046452	1	0.045927	1.3379	1	0.32149	0
<i>Histidine metabolism</i>	16	0.37161	2	0.051323	1.2897	1	0.33163	0
<i>Arginine and proline metabolism</i>	38	0.88258	3	0.055637	1.2546	1	0.33382	0.1638
<i>Pantothenate and CoA biosynthesis</i>	19	0.44129	2	0.070037	1.1547	1	0.39221	0
<i>Citrate cycle (TCA cycle)</i>	20	0.46452	2	0.076707	1.1152	1	0.40271	0.1049
<i>Pyruvate metabolism</i>	22	0.51097	2	0.090621	1.0428	1	0.44778	0.26749
<i>Propanoate metabolism</i>	23	0.53419	2	0.097841	1.0095	1	0.45659	0.04061
<i>Glycolysis / Gluconeogenesis</i>	26	0.60387	2	0.12042	0.91931	1	0.53238	0.1295
<i>Glutathione metabolism</i>	28	0.65032	2	0.13613	0.86604	1	0.57175	0.02675
<i>Cysteine and methionine metabolism</i>	33	0.76645	2	0.17718	0.75157	1	0.70874	0.05983
<i>Purine metabolism</i>	65	1.5097	3	0.18925	0.72297	1	0.72259	0.01281
<i>Amino sugar and nucleotide sugar metabolism</i>	37	0.85935	2	0.21131	0.67508	1	0.77173	0
<i>Valine, leucine and isoleucine degradation</i>	40	0.92903	2	0.23735	0.62461	1	0.83072	0

<i>Tyrosine metabolism</i>	42	0.97548	2	0.25483	0.59375	1	0.85623	0.08872
<i>Fatty acid biosynthesis</i>	47	1.0916	2	0.29865	0.52484	1	0.96486	0.01473
<i>Pentose and glucuronate interconversions</i>	18	0.41806	1	0.34647	0.46034	1	1	0
<i>Starch and sucrose metabolism</i>	18	0.41806	1	0.34647	0.46034	1	1	0.4207
<i>beta-Alanine metabolism</i>	21	0.48774	1	0.39149	0.40728	1	1	0
<i>Porphyrin and chlorophyll metabolism</i>	30	0.69677	1	0.50922	0.2931	1	1	0
<i>Biosynthesis of unsaturated fatty acids</i>	36	0.83613	1	0.57506	0.24029	1	1	0
<i>Steroid hormone biosynthesis</i>	85	1.9742	2	0.59754	0.22363	1	1	0.14685
<i>Fatty acid elongation</i>	39	0.90581	1	0.60468	0.21848	1	1	0
<i>Fatty acid degradation</i>	39	0.90581	1	0.60468	0.21848	1	1	0
<i>Pyrimidine metabolism</i>	39	0.90581	1	0.60468	0.21848	1	1	0