Understanding the relationship between intrinsic cardiorespiratory fitness and serum and skeletal muscle metabolomics profile

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SUPPORTING INFORMATION

Figure S1. Representation of the serum 1D $_1$H-NMR spectrum region where the main metabolites were quantified for a single participant. (A): Entire Spectrum; (B): Ornithine; (C): Betaine; (D): Proline; (E): Threonine; (F): Glutamine.

Figure S2. Representation of a skeletal muscle 1D $_1$H-NMR spectrum region where the main metabolites were quantified for a single participant. (A): Entire Spectrum; (B): Formate; (C): Fumarate; (D): Lactate; (E): NADP$^+$.

Table S1. Summary of serum and skeletal muscle pathways related to iCRF.
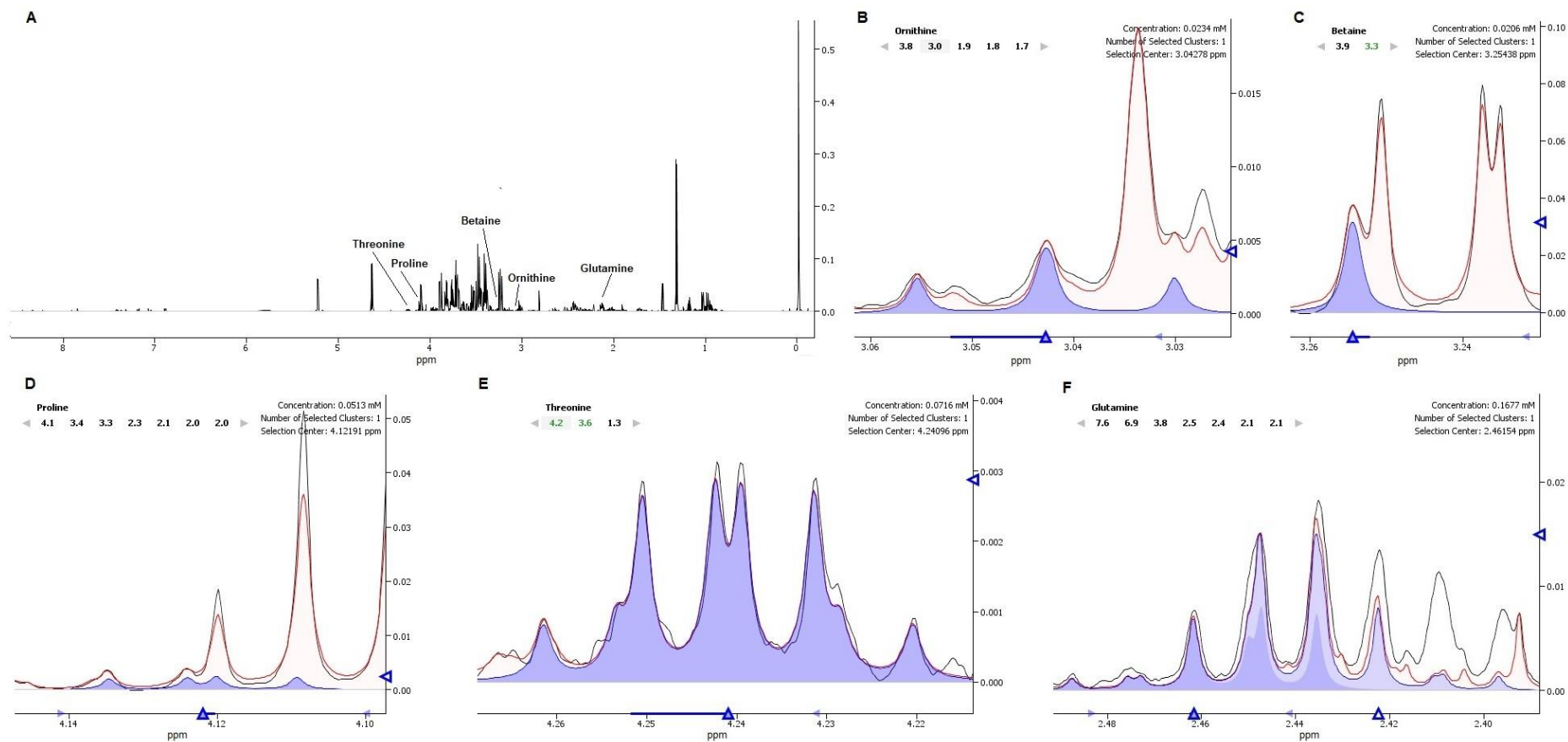
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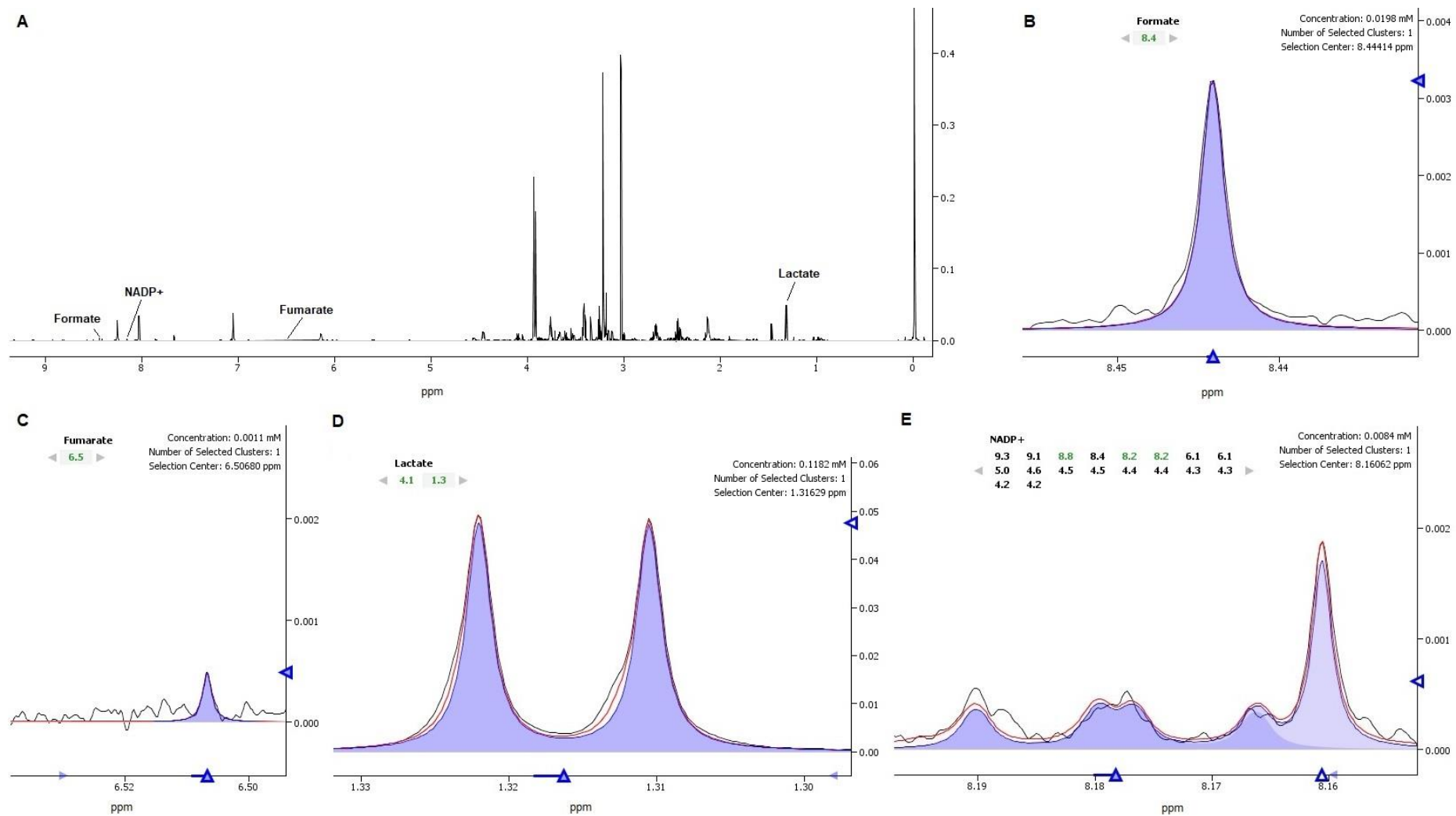
Figure S2. Representation of a skeletal muscle 1D ^{1}H-NMR spectrum region where the main metabolites were quantified for a single participant. (A): Entire Spectrum; (B): Formate; (C): Fumarate; (D): Lactate; (E): NADP$^+$.

Table S1. Summary of serum and skeletal muscle pathways related to iCRF.

Biologycal Sample	Pathways	Total	Expected	Hits	Raw p-values	-LOG(p)	P-values Ranking	FDR (q-values)	Impact	Decision
Blood	Aminoacyl-tRNA biosynthesis	48	0.3716	7	0.00000001	7.9093	1	0.0025	0.0000	SIG
Blood	Glycine serine and threonine metabolism	33	0.2555	4	0.00007492	4.1254	2	0.0050	0.2961	SIG
Muscle	Pyruvate metabolism	22	0.1419	3	0.00027962	3.5534	3	0.0075	0.1446	SIG
Muscle	Glyoxylate and dicarboxylate metabolism	32	0.2065	3	0.00087031	3.0603	4	0.0100	0.0000	SIG
Blood	Alanine aspartate and glutamate metabolism	28	0.2168	3	0.00104270	2.9818	5	0.0125	0.1138	SIG
Blood	Valine leucine and isoleucine biosynthesis	8	0.0619	2	0.00150000	2.8239	6	0.0150	0.0000	SIG
Muscle	Arginine biosynthesis	14	0.0903	2	0.00327270	2.4851	7	0.0175	0.1168	SIG
Blood	Arginine biosynthesis	14	0.1084	2	0.00475060	2.3233	8	0.0200	0.0609	SIG
Muscle	Glutathione metabolism	28	0.1807	2	0.01295300	1.8876	9	0.0225	0.0215	SIG
Muscle	Alanine aspartate and glutamate metabolism	28	0.1807	2	0.01295300	1.8876	10	0.0250	0.1995	SIG
Blood	Glutathione metabolism	28	0.2168	2	0.01857800	1.7310	11	0.0275	0.0887	SIG
Blood	Glyoxylate and dicarboxylate metabolism	32	0.2477	2	0.02396100	1.6205	12	0.0300	0.1058	SIG
Blood	Arginine and proline metabolism	38	0.2942	2	0.03309400	1.4802	13	0.0325	0.1884	NS
Muscle	Nitrogen metabolism	6	0.0387	1	0.03815100	1.4185	14	0.0350	0.0000	NS
Muscle	D-Glutamine and D-glutamate metabolism	6	0.0387	1	0.03815100	1.4185	15	0.0375	0.5000	NS
Blood	D-Glutamine and D-glutamate metabolism	6	0.0465	1	0.04563400	1.3407	16	0.0400	0.0000	NS
Blood	Nitrogen metabolism	6	0.0465	1	0.04563400	1.3407	17	0.0425	0.0000	NS
Muscle	Taurine and hypotaurine metabolism	8	0.0516	1	0.05057400	1.2961	18	0.0450	0.4286	NS
Muscle	Butanoate metabolism	15	0.0968	1	0.09292500	1.0319	19	0.0475	0.0000	NS
Muscle	Nicotinate and nicotinamide metabolism	15	0.0968	1	0.09292500	1.0319	20	0.0500	0.0000	NS
Muscle	Histidine metabolism	16	0.1032	1	0.09883400	1.0051	21	0.0525	0.0000	NS
Blood	Butanoate metabolism	15	0.1161	1	0.11052000	0.9566	22	0.0550	0.0000	NS
Blood	Histidine metabolism	16	0.1239	1	0.11747000	0.9301	23	0.0575	0.2213	NS
Muscle	Citrate cycle (TCA cycle)	20	0.1290	1	0.12213000	0.9132	24	0.0600	0.0298	NS
Blood	Pantothenate and CoA biosynthesis	19	0.1471	1	0.13803000	0.8600	25	0.0625	0.0000	NS
Blood	Citrate cycle (TCA cycle)	20	0.1548	1	0.14479000	0.8393	26	0.0650	0.0327	NS

Blood	beta-Alanine metabolism	21	0.1626	1	0.15150000	0.8196	27	0.0675	0.0000	NS
Muscle	Glycolysis/Gluconeogenesis	26	0.1677	1	0.15605000	0.8067	28	0.0700	0.0291	NS
Blood	Propanoate metabolism	23	0.1781	1	0.16477000	0.7831	29	0.0725	0.0000	NS
Muscle	Porphyrin and chlorophyll metabolism	30	0.1936	1	0.17801000	0.7496	30	0.0750	0.0000	NS
Blood	Porphyrin and chlorophyll metabolism	30	0.2323	1	0.20973000	0.6783	31	0.0775	0.0000	NS
Muscle	Arginine and proline metabolism	38	0.2452	1	0.22038000	0.6568	32	0.0800	0.0860	NS
Muscle	Tyrosine metabolism	42	0.2710	1	0.24082000	0.6183	33	0.0825	0.0246	NS
Blood	Glycerophospholipid metabolism	36	0.2787	1	0.24649000	0.6082	34	0.0850	0.0258	NS
Muscle	Primary bile acid biosynthesis	46	0.2968	1	0.26078000	0.5837	35	0.0875	0.0076	NS
Blood	Pyrimidine metabolism	39	0.3019	1	0.26428000	0.5779	36	0.0900	0.0000	NS
Blood	Valine leucine and isoleucine degradation	40	0.3097	1	0.27012000	0.5684	37	0.0925	0.0000	NS
Muscle	Aminoacyl-tRNA biosynthesis	48	0.3097	1	0.27058000	0.5677	38	0.0950	0.0000	NS
Blood	Primary bile acid biosynthesis	46	0.3561	1	0.30429000	0.5167	39	0.0975	0.0076	NS
Blood	Purine metabolism	65	0.5032	1	0.40307000	0.3946	40	0.1000	0.0000	NS

FDR: false discovery rate of 0.1. All identified pathways were ranked based on their p-values from smallest to largest. Then, the FDR values were calculated for each pathway (q), assuming q = (0.1×i)/m, where i denotes the i-th position of the pathway in the ranking of p-values (in the i-th row) and m the total number of ranked pathways. When the p-values of the pathways were less than the q-values, the pathway was declared to be significantly enriched; SIG: Significant pathway at the FDR level; NS: Non-significant pathway at the FRD level.