

Supplemental Table 1. Bile acids (n=58) for detection and applied for constructing standard curves for exact quantity determinations in this study.

		Analyte	Abbreviation	[MW] ⁱⁱ	Neutral Formula
F r e e	1°	Cholic Acid	CA	407.2797	C ₂₄ H ₄₀ O ₅
	2° and 3°	Chenodeoxycholic Acid	CDCA	391.2848	C ₂₄ H ₄₀ O ₄
Inflammation Modulating BA	Intermediate BA	Deoxycholic Acid	DCA	391.2848	C ₂₄ H ₄₀ O ₄
		Lithocholic Acid	LCA	375.2899	C ₂₄ H ₄₀ O ₃
		Ursodeoxycholic acid	UDCA	391.2848	C ₂₄ H ₄₀ O ₄
		Hyodeoxycholic Acid	HDCA	391.2848	C ₂₄ H ₄₀ O ₄
		Dehydrocholic Acid	DHCA	401.2328	C ₂₄ H ₃₈ O ₅
		3,7-Diketocholanic acid	3,7DKCnA	387.2535	C ₂₄ H ₃₆ O ₄
		3,6-Diketocholanic acid	3,6DKCnA	387.2535	C ₂₄ H ₃₆ O ₄
		Murocholic Acid	MurCA	391.2848	C ₂₄ H ₄₀ O ₄
		β-Hyodeoxycholic Acid	β-HDCA	391.2848	C ₂₄ H ₄₀ O ₄
		β-Deoxycholic Acid	β-DCA	391.2848	C ₂₄ H ₄₀ O ₄
		Isodeoxycholic Acid	IsoDCA	391.2848	C ₂₄ H ₄₀ O ₄
		Ursocholic Acid	UCA	407.2797	C ₂₄ H ₄₀ O ₅
		α-Muricholic Acid	α-MCA	407.2797	C ₂₄ H ₄₀ O ₅
		ω-Muricholic Acid	ω-MCA	407.2797	C ₂₄ H ₄₀ O ₅
		β-Muricholic Acid	β-MCA	407.2797	C ₂₄ H ₄₀ O ₅
		Hyocholic Acid	HCA	407.2797	C ₂₄ H ₄₀ O ₅
		Allocholic Acid	AlloCA	407.2797	C ₂₄ H ₄₀ O ₅
		Urocholanic Acid	UCnA	359.2950	C ₂₄ H ₄₀ O ₂
		7-Ketolithocholic Acid	7KLCA	389.2692	C ₂₄ H ₃₈ O ₄
		12-Ketolithocholic Acid	12KLCA	389.2692	C ₂₄ H ₃₈ O ₄
		3-Oxchenodeoxycholic Acid	3OCDCA	389.2692	C ₂₄ H ₃₈ O ₄
		3-Oxodeoxycholic Acid	3ODCA	389.2692	C ₂₄ H ₃₈ O ₄
		Norursodeoxycholic Acid	NorUDCA	377.2692	C ₂₃ H ₃₈ O ₄
		Nordeoxycholic Acid	NorDCA	377.2692	C ₂₃ H ₃₈ O ₄
		Norcholic Acid	NorCA	393.2641	C ₂₃ H ₃₈ O ₅
		7,12-Diketolithocholic acid	7,12DKLCA	403.2484	C ₂₄ H ₃₆ O ₅
		6,7-Diketolithocholic acid	6,7DKLCA	403.2484	C ₂₄ H ₃₆ O ₅
		12-Dehydrocholic Acid	12DHCA	405.2641	C ₂₄ H ₃₈ O ₅
		7-Dehydrocholic Acid	7DHCA	405.2641	C ₂₄ H ₃₈ O ₅
		β-Glycomuricholic Acid	β-GMCA	464.3012	C ₂₆ H ₄₃ NO ₆
		7-Oxohyocholic acid (Takeda ketol)	7OHCA	405.2641	C ₂₄ H ₃₈ O ₅
		3-Dehydrocholic Acid	3DHCA	405.2641	C ₂₄ H ₃₈ O ₅
		IsoAllolithocholic Acid	IsoAlloLCA	375.2899	C ₂₄ H ₄₀ O ₃
		Allolithocholic Acid	AlloLCA	375.2899	C ₂₄ H ₄₀ O ₃
		Dehydrolithocholic (3-Ketolithocholic acid)	3KLCA	373.2743	C ₂₄ H ₃₈ O ₃
		Isolithocholic Acid	IsoLCA	375.2899	C ₂₄ H ₄₀ O ₃
Tauro-Conjugated	Glyco-Conjugated	Taurolithocholic Acid	TLCA	482.2940	C ₂₆ H ₄₅ NO ₅
		Tauroursodeoxycholic Acid	TUDCA	498.2889	C ₂₆ H ₄₅ NO ₆
		Taurohyodeoxycholic Acid	THDCA	498.2889	C ₂₆ H ₄₅ NO ₆
		Taurochenodeoxycholic Acid	TCDCa	498.2889	C ₂₆ H ₄₅ NO ₆
		Taurodeoxycholic Acid	TDCA	498.2889	C ₂₆ H ₄₅ NO ₆
		Tauro α-Muricholic Acid	α-TMCA	514.2838	C ₂₆ H ₄₅ NO ₅
		Tauro β-Muricholic Acid	β-TMCA	514.2838	C ₂₆ H ₄₅ NO ₅
		Tauro ω-Muricholic Acid	ω-TMCA	514.2838	C ₂₆ H ₄₅ NO ₅
		Taurohyocholic Acid	THCA	514.2838	C ₂₆ H ₄₅ NO ₅
		Taurocholic Acid	TCA	514.2838	C ₂₆ H ₄₅ NO ₅
Internal Standards	Glyco-Conjugated	Taurodehydrocholic acid	TDHCA	508.2369	C ₂₆ H ₃₉ NO ₅
		Taurourscholanic Acid	TUGHa	466.2991	C ₂₆ H ₄₅ NO ₄
		Glycoursoodeoxycholic Acid	GUDCA	448.3063	C ₂₆ H ₄₃ NO ₅
		Glycohyodeoxycholic Acid	GHDCA	448.3063	C ₂₆ H ₄₃ NO ₅
		Glycochenodeoxycholic Acid	GCDCA	448.3063	C ₂₆ H ₄₃ NO ₅
		Glycodeoxycholic Acid	GDCA	448.3063	C ₂₆ H ₄₃ NO ₅
		Glycohyocholic Acid	GHCA	464.3012	C ₂₆ H ₄₃ NO ₆
		Glycocholic Acid	GCA	464.3012	C ₂₆ H ₄₃ NO ₆
		Glycolithocholic Acid	GLCA	432.3114	C ₂₆ H ₄₃ NO ₄
		Glycodehydrocholic acid	GDHCA	458.2543	C ₂₆ H ₃₇ NO ₆
	Internal Standards	Cholic Acid d4	CA d4	411.3049	C ₂₄ H ₃₆ D ₄ O ₅
		Chenodeoxycholic Acid d4	CDCA d4	395.3099	C ₂₄ H ₃₆ D ₄ O ₄
		Deoxycholic Acid d4	DCA d4	395.3099	C ₂₄ H ₃₆ D ₄ O ₄

Supplemental Table 2. Long-chain fatty acids (n=12) and short-chain fatty acids (n=12) for detection and applied for constructing standard curves for exact quantity determinations in this study.

Family	Subfamily	Analyte	Abbreviation	[MW] ^H	Neutral Formula	
Saturated		Myristic Acid	MyrA	227.2011	C ₁₄ H ₂₈ O ₂	
		Palmitic Acid	PalA	255.2324	C ₁₆ H ₃₂ O ₂	
		Stearic Acid	SteA	283.2637	C ₁₈ H ₃₆ O ₂	
Unsaturated		Palmitoleic Acid	PalmitoA	253.2168	C ₁₆ H ₃₀ O ₂	
		cis-5,8,11,14,17-Eicosapentaenoic acid	EPA	301.2168	C ₂₀ H ₃₀ O ₂	
	Omega3	Cis-4,7,10,13,16,19-Docosahexaenoic acid	DHA	327.2324	C ₂₂ H ₃₂ O ₂	
		γ-Linolenic Acid	γ-LinoA	277.2168	C ₁₈ H ₃₀ O ₂	
		α-Linolenic acid	α-LinoA	277.2168	C ₁₈ H ₃₀ O ₂	
		Linoleic Acid	LinA	279.2324	C ₁₈ H ₃₂ O ₂	
		Arachidonic Acid	AA	303.2324	C ₂₀ H ₃₂ O ₂	
		Oleic Acid	OIA	281.2481	C ₁₈ H ₃₄ O ₂	
		Cis-11-Eicosenoic acid	EA	309.2794	C ₂₀ H ₃₈ O ₂	
		Cholic Acid d4	CA d4	411.3049	C ₂₄ H ₃₆ D ₄ O ₅	
Internal Standards		Chenodeoxycholic Acid d4	CDCA d4	395.3099	C ₂₄ H ₃₆ D ₄ O ₄	
		Deoxycholic Acid d4	DCA d4	395.3099	C ₂₄ H ₃₆ D ₄ O ₄	
Family		Analyte	Abbreviation	[MW] ^H	Neutral Formula	
SCFA		Acetic acid	AcA	194.0566	C ₂ H ₄ O ₂	
		Lactic acid	LacA	224.0671	C ₃ H ₆ O ₃	
		Propionic Acid	ProA	208.0722	C ₃ H ₆ O ₂	
		IsoButyric Acid	IsobutA	222.0879	C ₄ H ₈ O ₂	
		Butyric Acid	ButA	222.0879	C ₄ H ₈ O ₂	
Branched SCFA		2-Methylbutyric acid	2MeButA	236.1035	C ₅ H ₁₀ O ₂	
		Pivalic acid	PivA	236.1035	C ₅ H ₁₀ O ₂	
		IsoValeric acid	IsoValA	236.1035	C ₅ H ₁₀ O ₂	
		Valeric acid	ValA	236.1035	C ₅ H ₁₀ O ₂	
MCFA		Hexanoic acid acid	HexA	250.1192	C ₆ H ₁₂ O ₂	
		Heptanoic acid acid	HepA	264.1348	C ₇ H ₁₄ O ₂	
		Octanoic acid acid	OctA	278.1505	C ₈ H ₁₆ O ₂	
Internal Standards		Acetic Acid-2-13C-2,2,2-d3	13C-AcA-d3	198.0788	C ₇ D ₃ H ₆ O ₃ N ₃	
		Lactic Acid-13C3	13C3-LacA	227.0772	C ₃ C ₆ H ₁₁ O ₄ N ₃	
		Propionic Acid-d5	ProA-d5	213.1036	C ₃ D ₅ HO ₂	C ₉ D ₅ H ₆ O ₃ N ₃
		Isobutyric-d7	IsobutA-d7	229.1318	C ₄ D ₇ HO ₂	C ₁₀ D ₇ H ₆ O ₃ N ₃
		Butyric Acid-d7	ButA-d7	229.1318	C ₄ D ₇ HO ₂	C ₁₀ D ₇ H ₆ O ₃ N ₃
		Trimethyl-d9-acetic (Pivalic d9)	PivA-d9	245.16	C ₅ D ₉ HO ₂	C ₁₁ D ₉ H ₆ O ₃ N ₃
		Isovaleric-d9	IsoValA-d9	245.16	C ₅ D ₉ HO ₂	C ₁₁ D ₉ H ₆ O ₃ N ₃
		Valeric-d9	ValA-d9	245.16	C ₅ D ₉ HO ₂	C ₁₁ D ₉ H ₆ O ₃ N ₃
		Hexanoic-d5	HexA-d5	255.1506	C ₆ D ₅ H ₇ O ₂	C ₁₂ D ₅ H ₁₂ O ₃ N ₃
		Heptanoic d7	HepA-d7	271.1788	C ₇ D ₇ H ₇ O ₂	C ₁₃ D ₇ H ₁₂ O ₃ N ₃
		Octanoic-d15	OctA-d15	293.2446	C ₈ D ₅ HO ₂	C ₁₄ D ₁₅ H ₆ O ₃ N ₃

Supplemental Table 3. Comparison of bacterial species relative abundance (%) pre- and post-race.

	Pre-Race		Post-Race		P-value
	Mean	SD	Mean	SD	
Methanobrevibacter_smithii	0.22	0.71	0.11	0.34	0.58
Bifidobacterium_adolescentis	0.47	0.89	0.86	1.57	0.69
Bifidobacterium_longum	0.18	0.29	0.45	0.67	0.98
Bifidobacterium_pseudocatenulatum	0.30	0.67	0.43	0.90	0.69
Collinsella_aerofaciens	1.24	1.40	1.05	1.32	0.60
Adlercreutzia_equolifaciens	0.04	0.05	0.02	0.04	0.53
Asaccharobacter_celatus	0.09	0.12	0.04	0.09	0.53
Bacteroides_caccae	1.19	1.54	1.17	1.56	0.98
Bacteroides_cellulosilyticus	0.62	1.41	1.45	3.09	0.58
Bacteroides_dorei	2.30	4.59	2.08	4.03	0.98
Bacteroides_finegoldii	1.69	2.49	3.38	8.57	0.98
Bacteroides_fragilis	0.18	0.44	0.35	0.97	0.90
Bacteroides_massiliensis	0.37	0.64	0.43	0.89	0.98
Bacteroides s_Bacteroides_ovatus	0.86	1.18	1.37	1.80	0.59
Bacteroides_plebeius	0.39	0.78	0.48	1.03	0.98
Bacteroides_stercoris	1.97	4.01	1.55	2.82	1.00
Bacteroides_thetaiotaomicron	0.67	0.75	0.98	1.20	0.70
Bacteroides_uniformis	7.98	10.57	9.43	12.61	0.98
Bacteroides_vulgatus	11.28	8.24	14.42	11.90	0.86
Bacteroides_xylosoxylolyticus	0.17	0.26	0.66	1.57	0.98
Barnesiella_intestinihominis	0.98	1.37	1.03	1.74	1.00
Coprobacter_fastidiosus	0.03	0.06	0.05	0.12	0.98
Butyricimonas_virosa	0.02	0.06	0.02	0.07	1.00
Odoribacter_splanchnicus	0.33	0.43	0.22	0.30	0.86
Prevotella s_Prevotella_copri	7.05	18.84	5.04	12.45	1.00
Alistipes_finegoldii	0.33	0.39	0.45	0.75	0.98
Alistipes_putredinis	3.39	2.80	3.59	3.43	0.98
Alistipes_shahii	0.13	0.16	0.17	0.21	0.94
Parabacteroides_distasonis	1.60	1.64	1.66	1.81	1.00
Parabacteroides_merdeae	0.47	0.60	0.70	1.41	1.00
Streptococcus_parasanguinis	0.03	0.06	0.08	0.18	0.58
Streptococcus_salivarius	0.16	0.19	0.91	2.20	0.53
Streptococcus_thermophilus	0.15	0.32	0.05	0.12	0.98
Clostridium_sp_CAG_58	0.13	0.19	0.09	0.16	0.53
Lawsonibacter_asaccharolyticus	0.03	0.04	0.02	0.06	0.98
Monoglobus_pectinilyticus	0.21	0.40	0.11	0.24	0.86
Eubacterium_eligens	0.30	0.36	0.21	0.28	0.58
Eubacterium_hallii	1.31	1.05	0.92	0.77	0.74
Eubacterium_ramulus	0.11	0.16	0.07	0.17	0.79
Eubacterium_sp_CAG_38	0.35	0.60	0.21	0.48	0.53
Eubacterium_ventriosum	0.06	0.12	0.10	0.31	0.98
Anaerostipes_hadrus	2.68	2.71	1.25	1.05	0.53
Blautia_obeum	1.21	1.46	1.13	1.98	0.98
Blautia_wexlerae	0.71	1.00	0.53	0.61	0.98
Ruminococcus_gnavus	0.09	0.16	0.43	1.34	1.00
Ruminococcus_torques	1.55	1.34	1.20	1.03	0.53
Coprococcus_catus	0.16	0.23	0.11	0.17	0.74
Coprococcus_comes	0.46	0.52	0.36	0.44	0.98
Dorea_formicigenerans	0.43	0.31	0.39	0.53	0.98
Dorea_longicatena	1.09	1.16	0.86	0.98	0.58
Dorea_sp_CAG_317	0.12	0.23	0.06	0.15	0.90
Fusicatenibacter_saccharivorans	4.63	4.85	3.77	4.33	0.98
Eubacterium_rectale	4.25	6.46	3.65	5.17	0.90
Lachnospira_pectinoschiza	0.59	1.12	0.36	0.60	0.69
Roseburia_faecis	1.00	1.82	0.62	1.71	0.58
Roseburia_hominis	0.60	1.09	0.55	1.10	0.97
Roseburia_intestinalis	1.12	2.27	0.34	0.59	0.53
Roseburia_inulinivorans	0.37	0.47	0.18	0.25	0.53
Roseburia_sp_CAG_303	0.98	2.40	0.09	0.24	0.69

Oscillibacter_sp_57_20	0.55	0.97	0.54	0.96	1.00
Agathobaculum_butyriciproducens	0.36	0.34	0.44	0.47	0.98
Faecalibacterium_prausnitzii	7.72	5.22	7.94	5.11	0.98
Flavonifractor_plautii	0.10	0.12	0.13	0.11	0.70
Gemmiger_formicilis	0.11	0.17	0.08	0.13	1.00
Eubacterium_siraeum	2.56	6.84	3.22	7.84	0.98
Ruminococcus_bicirculans	2.20	2.99	2.15	3.41	0.69
Ruminococcus_bromii	2.40	3.55	1.86	2.23	0.98
Ruminococcus_lactaris	0.51	0.97	0.31	0.53	0.90
Ruthenibacterium_lactatiformans	0.02	0.04	0.04	0.06	0.69
Holdemanella_biformis	0.07	0.20	0.06	0.16	0.69
Firmicutes_bacterium_CAG_110	0.20	0.39	0.41	0.92	0.98
Firmicutes_bacterium_CAG_83	0.18	0.44	0.30	0.95	0.98
Phascolarctobacterium_faecium	0.15	0.31	0.22	0.48	0.98
Dialister_invisus	0.04	0.11	0.02	0.03	1.00
Parasutterella_excrementihominis	0.40	0.52	0.79	1.51	0.70
Turicimonas_muris	0.01	0.02	0.01	0.03	0.98
Haemophilus_parainfluenzae	0.11	0.32	0.19	0.39	0.98
Proteobacteria_bacterium_CAG_139	0.18	0.58	0.12	0.27	0.98
Akkermansia_muciniphila	0.70	1.62	0.50	1.08	0.98

Comparisons made using Wilcoxon signed-rank test and p-values corrected for false discovery rate using the Benjamini-Hochberg method.

Supplemental Table 4. Comparison of pre-race fecal metabolites in athletes with shorter and longer duration lifetime training histories.

	≤12 Years Training (n=5)	>12 Years Training (n=6)	P-value
Bile Acids (ng/mg)			
Taurine	25.1±25.5	33.9±63.6	0.784
DHCA	<LOD	<LOD	<LOD
3KLCA	8.2±13.9	13.3±20.8	0.083
3,6DKCnA/3,7DKCnA	1.5±2.8	2.3±3.8	0.235
AlloLCA/IsoAlloLCA	2.9±4.4	3.1±4.7	0.523
IsoLCA	10.2±8.7	24.4±18.5	0.121
LCA	145.8±90.1	300±169	0.121
MurCA	2.8±4.5	0.70±0.65	0.235
UDCA	59.3±73.4	61.5±130.3	1.000
β-HDCA	26.5±30.2	59.6±92.3	0.523
HDCA	98.3±52.8	225±144	0.055
β-DCA	70.7±24.1	140±68	0.036
CDCA	199±174	105±185	0.927
*DCA	810±443	1217±602	0.231
IsoDCA	<LOD	<LOD	<LOD
UCA	33.6±50.0	64.1±137	0.927
αω-MCA	43.0±47.5	20.0±23.8	0.523
β-MCA	1.3±1.0	0.7±0.6	0.235
HCA	18.2±18.7	10.9±15.9	0.927
CA	356±364	175±336	0.648
AlloCA	7.8±8.7	6.7±12.1	0.927
UCnA	<LOD	<LOD	<LOD
7KLCA	9.1±10.3	15.0±27.4	0.784
12KLCA	80.1±135.3	140±218	0.171
3OCDCA	1.3±0.7	1.1±1.5	0.523
3ODCA	14.2±20.3	36.8±55.5	0.083
*NorUDCA	0.20±0.07	0.18±0.06	0.505
NorDCA	0.13±0.05	0.28±0.43	0.927
NorCA	0.86±0.47	0.79±0.43	0.784
7,12DKLCA/6,7DKLCnA	2.7±1.6	3.0±2.2	1.000
6,7DKLCA	<LOD	<LOD	<LOD
12DHCA	<LOD	<LOD	<LOD
7DHCA	12.3±17.6	15.5±31.6	0.927
7OHCA	4.3±3.1	3.5±5.2	0.235
3DHCA	1.9±1.1	1.5±2.0	0.171
TUDCA	4.1±4.9	1.3±1.9	0.523
THDCA	<LOD	<LOD	<LOD

TCDCA	84.7±164.7	19.7±22.6	0.927
TDCA	102±196	22.1±33.2	0.927
TMCA	<LOD	<LOD	<LOD
THCA	1.11±1.14	0.40±0.28	0.315
TCA	112±213	13.8±21.0	0.648
TLCA	3.2±4.3	2.1±3.4	0.927
*TDHCA	2.7±1.3	2.9±1.01	0.738
TUCnA	1.4±0.8	1.3±0.9	1.000
GUDCA	4.2±5.3	2.4±3.0	0.927
GHDCA	<LOD	<LOD	<LOD
GCDCA	46.2±72.4	41.7±44.3	1.000
GDCA	60.2±121	29.3±44.7	0.411
β-GMCA	1.5±1.9	0.4±0.4	0.315
GHCA	<LOD	<LOD	<LOD
GCA	71.4±139	26.0±28.1	1.000
GLCA	0.1±0.1	0.1±0.04	0.523
*GDHCA	7.6±4.4	7.6±3.0	0.996
Total BA	2550±1845	2852±1951	0.523
Primary BA	869±973	381±607	0.784
*Secondary BA	1189±817	1635±853	0.401
Free BA	1669±1030	2083±1465	0.648
Intermediate BA	354±181	564±504	0.784
Conjugated BA	502±924	171±174	0.927
Inflammation Modulating BA	24.4±25.1	42.8±42.8	0.171

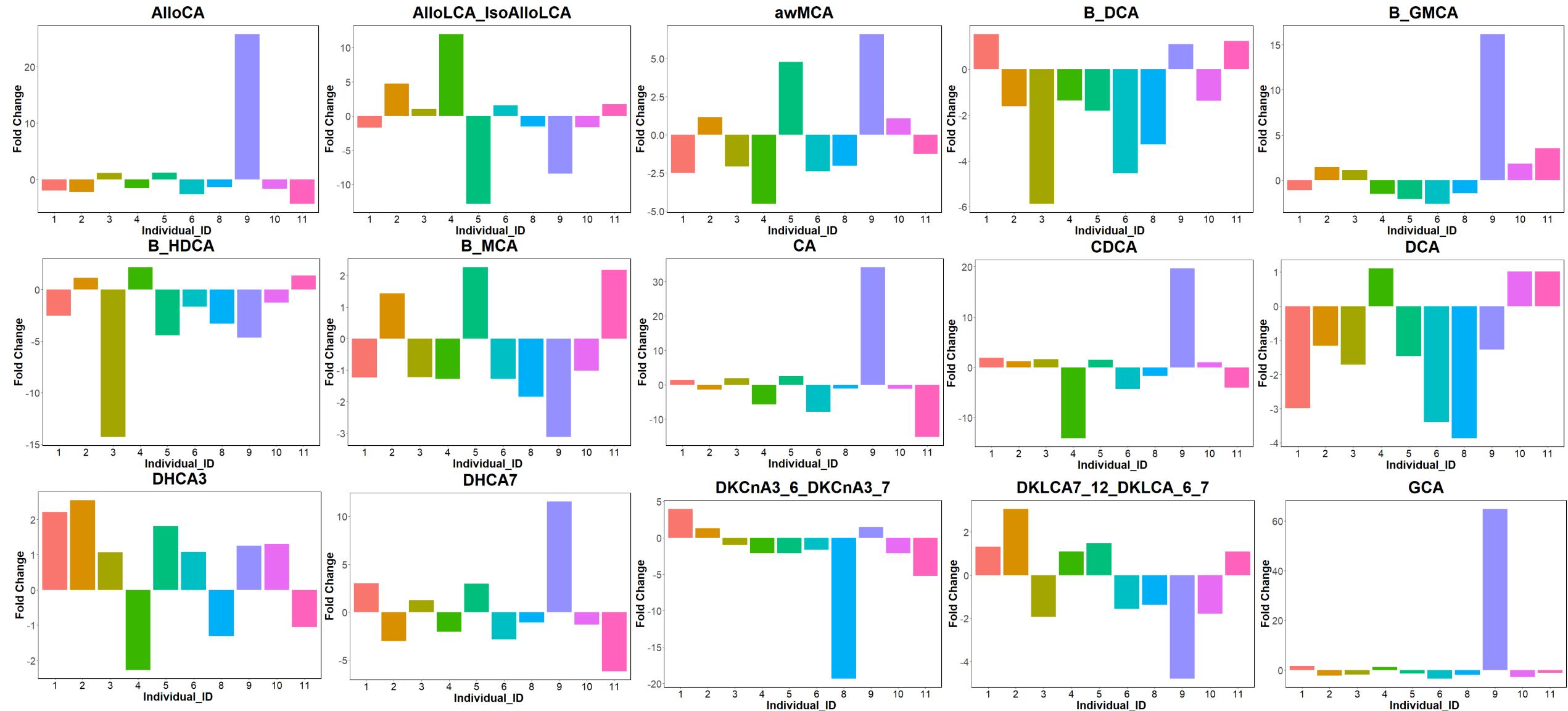
Long Chain Fatty Acids (ng/mg)

MyrA	70.7±26.0	70.2±23.8	0.927
PalmitoA	51.7±26.4	32.9±14.5	<LOD
PalA	422±157	420±123.2	1.000
αγLinoA	306±478	44.8±38.4	0.411
LinA	508±270	334.1±143.8	0.235
OIA	202±131	120.7±40.4	0.235
SteA	325±126	315.6±88.5	1.000
EPA	1.6±0.62	1.1±0.6	0.171
AA	21.5±24.8	10.2±9.6	0.411
EA	1.7±0.63	1.1±0.3	0.121
DHA	23.8±14.7	14.2±7.5	0.171
Saturated	818±290	805.8±215.7	0.927
Unsaturated	1116±482	559±226.1	0.121
Total	1934±633	1364.9±393.6	0.121
Omega3	25±15	15.2±7.9	<LOD
Omega6	857±489	399.2±183.6	0.121

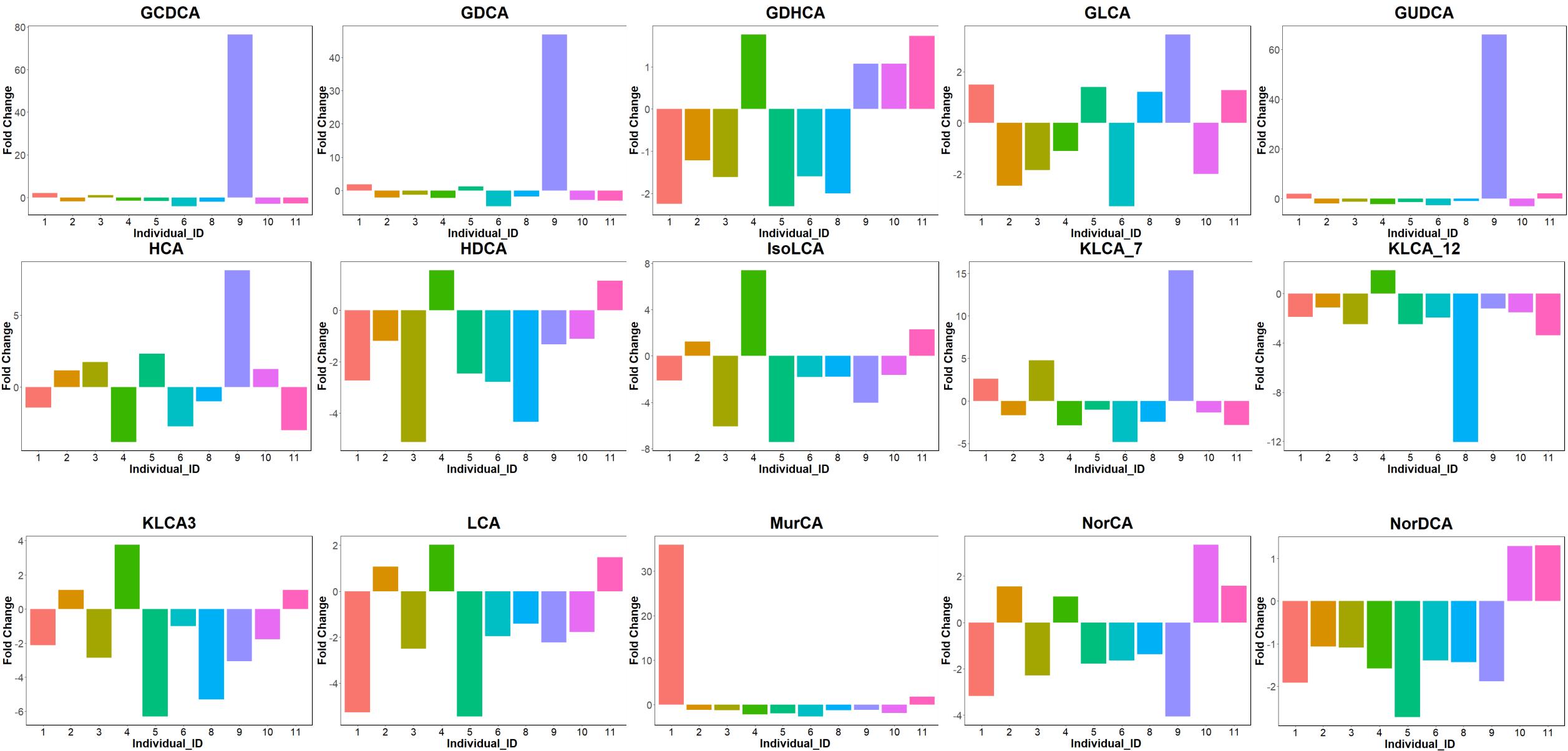
Short Chain and Medium Chain Fatty Acids (μmol/g)

AcA	618 ± 787	374 ± 183	0.784
LacA	122 ± 100	55.2 ± 42.6	0.411
ProA	43.4 ± 28.2	106 ± 78	0.055
IsobutA	3.0 ± 4.1	3.7 ± 2.3	0.747
ButA	35.1 ± 23.8	40.0 ± 20.5	0.731
2MeButA	1.9 ± 2.8	2.3 ± 2.0	0.315
PivA	0.1 ± 0.02	0.04 ± 0.01	0.411
IsoValA	2.6 ± 3.9	2.7 ± 2.1	0.411
ValA	2.9 ± 3.3	5.4 ± 2.2	0.177
HexA	0.45 ± 0.31	2.2 ± 1.8	0.055
HepA	0.12 ± 0.09	0.47 ± 0.64	0.523
OctA	0.18 ± 0.07	0.28 ± 0.21	0.648
Total SCFA_MCFA	830 ± 907	592 ± 237	0.648
SCFA	829 ± 907	589 ± 238	0.648
MCFA	0.8 ± 0.4	2.96 ± 2.5	0.083

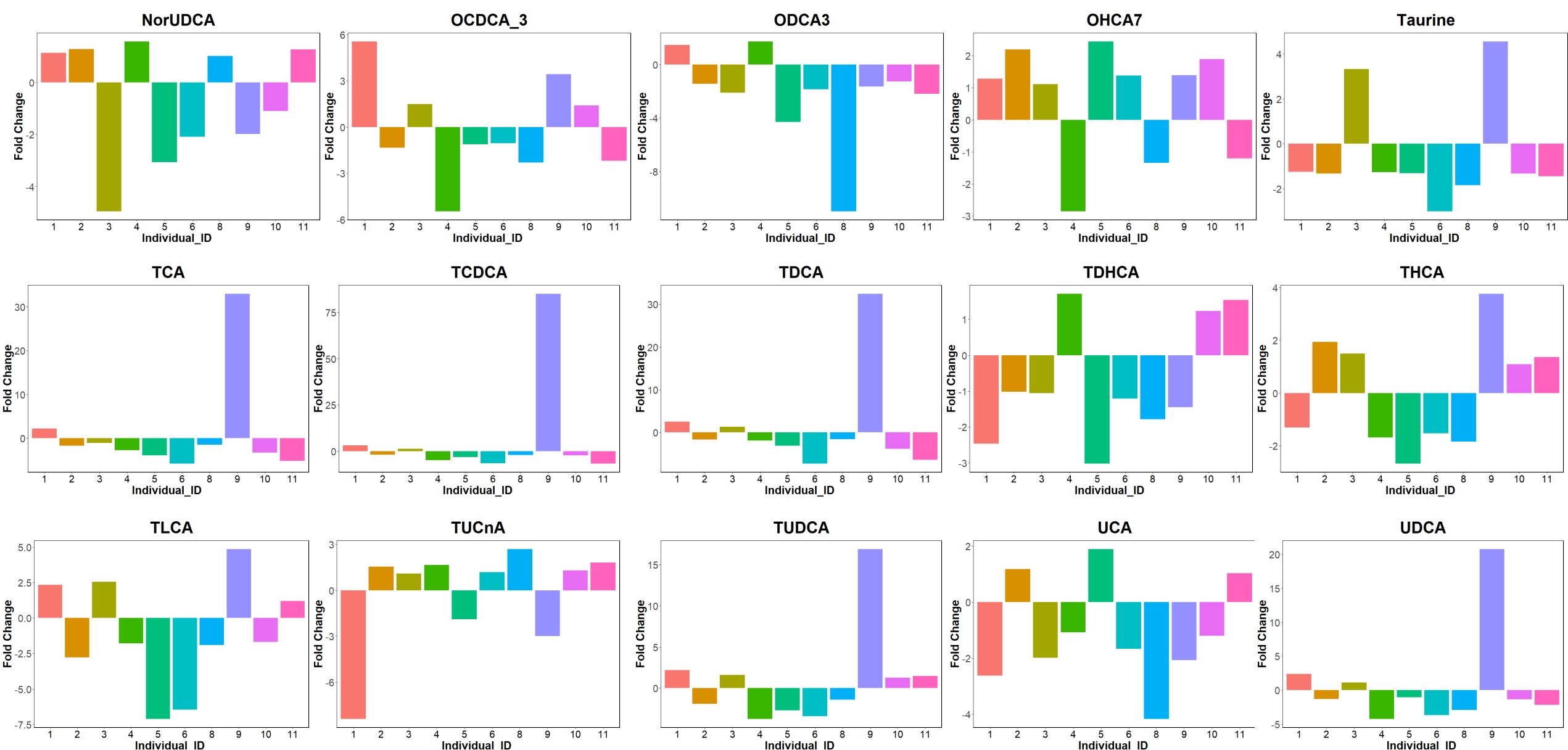
*t-test statistically testing carried out for normally distributed data. All other metabolites testing by Wilcoxon signed-rank test. P-values corrected using false discovery rate using the Benjamini-Hochberg method.



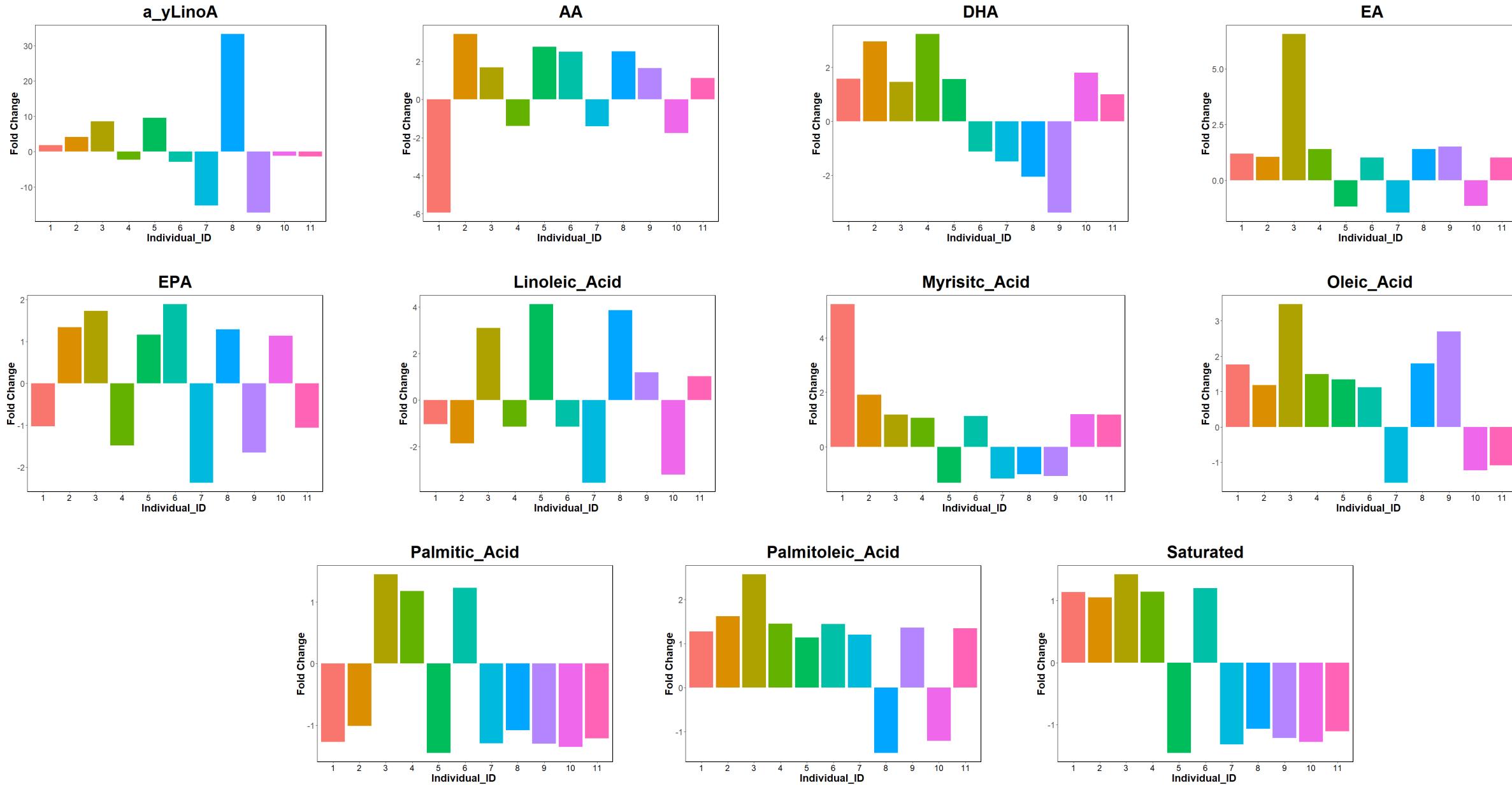
Supplemental Figure 1: Bile acids individual fold change plots. Fold change calculated as post- relative to pre-race, where a positive value indicates an increase.



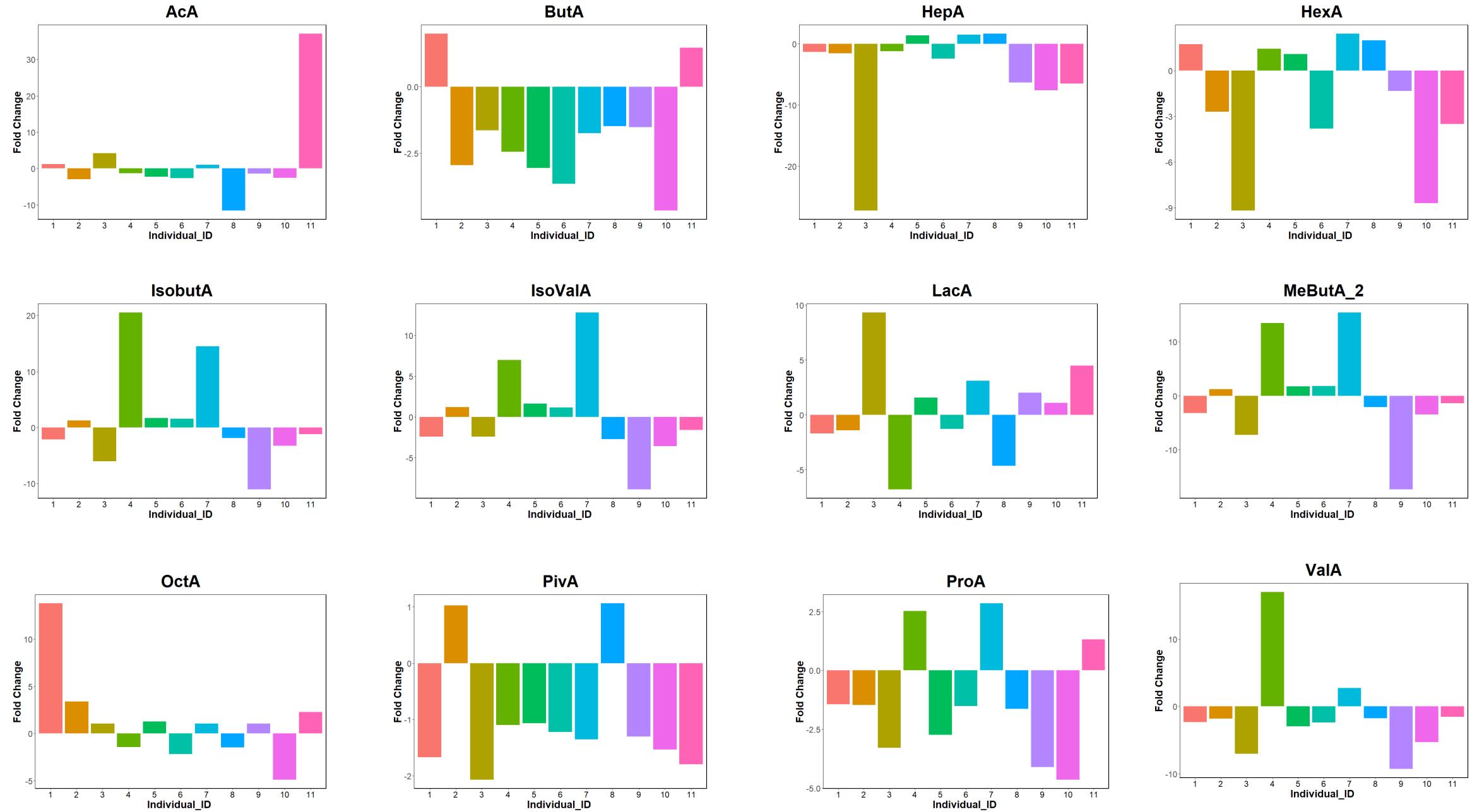
Supplemental Figure 1: Bile acids individual fold change plots. Fold change calculated as post- relative to pre-race, where a positive value indicates an increase.



Supplemental Figure 1: Bile acids individual fold change plots. Fold change calculated as post- relative to pre-race, where a positive value indicates an increase.



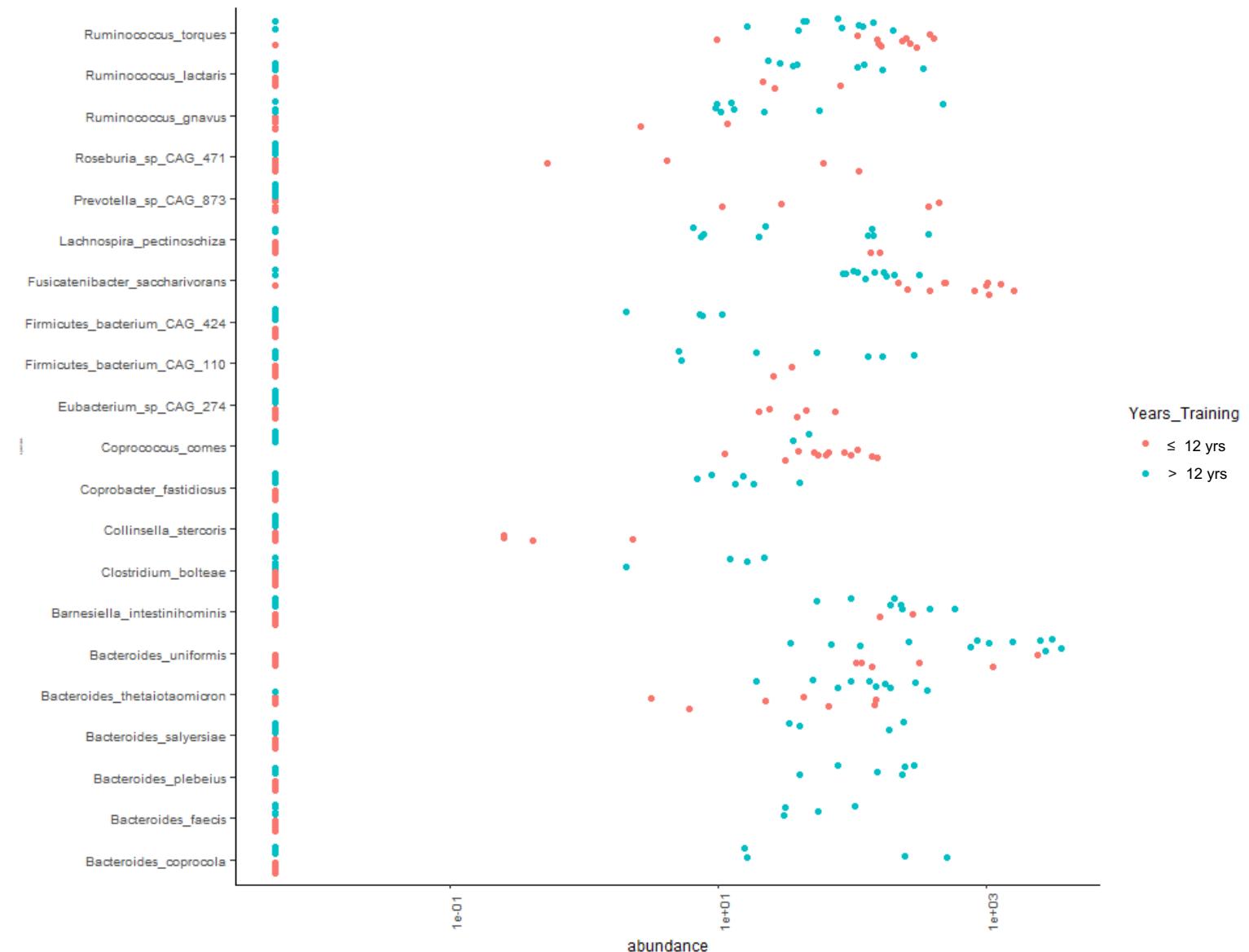
Supplemental Figure 2. Long-chain fatty acids individual fold change plots. Fold change calculated as post- relative to pre-race, where a positive value indicates an increase.



Supplemental Figure 3. Short-chain fatty acids individual fold change plots. Fold change calculated as post- relative to pre-race, where a positive value indicates an increase.



Supplemental Figure 4. Pre-race microbial abundance and race finish time. Kruskal-Wallis test identified microbial species (y-axis) that differed by finish time.



Supplemental Figure 5. Pre-race microbial abundance and years of training. Kruskal-Wallis test identified microbial species (y-axis) that differed with years of training.