

Deciphering the Genomic Architecture of Intramuscular and Subcutaneous Fat Composition in Iberian Pigs

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Introduction

The Iberian Pig

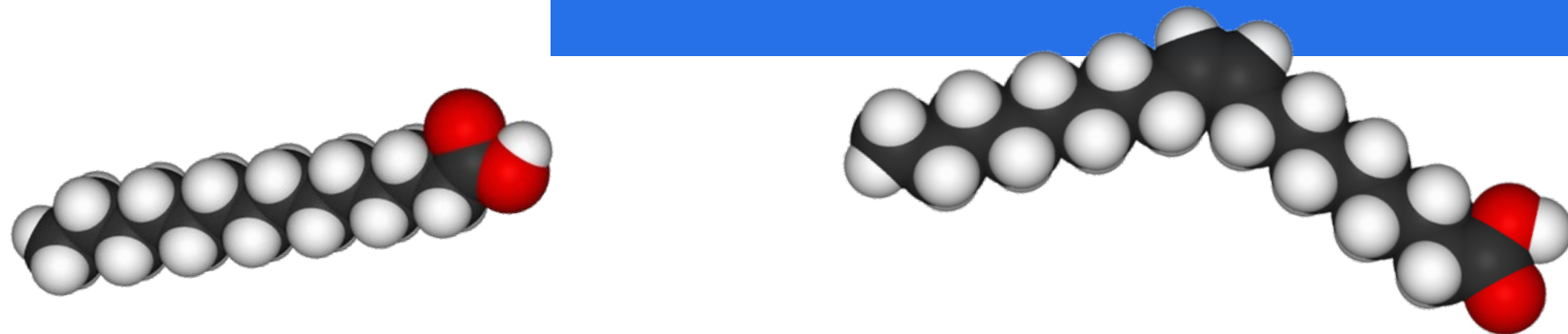
- Native breed of the Iberian Peninsula, especially in the Dehesa
- Different varieties: Retinto (RR), Entrepelado (EE), and Torbiscal (TT)
- High meat quality , due to the presence of specific volatile compounds formed through the oxidation of fatty acids



Introduction

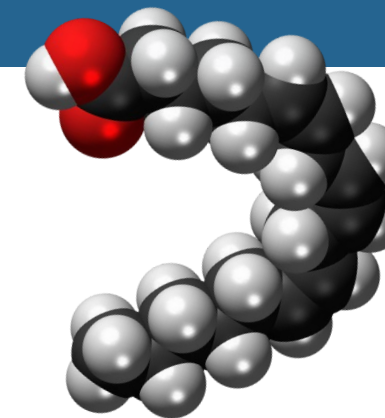
Importance of FA Composition

- Crucial for meat quality
- Influences the firmness of the fat and the cohesion between lean and fat tissues
- Different melting points affect these properties



In Swine

- Proportions of specific fatty acids (stearic and linoleic) correlate with fat firmness
- Intramuscular fat (“marbling”) affects the tenderness and juiciness of the meat
- An optimal balance in composition is necessary to achieve high -quality meat



Material



Geneseek GGP
PorcineHD 70 K

EE	RE	RR	RT	TE	TT
96	127	128	209	42	101

	SCF				IMF			
	Mean	SD	Max	Min	Mean	SD	Max	Min
C14:0	1,42	0,15	2,25	1,05	1,48	0,11	2,05	1,09
C16:0	23,12	1,57	29,30	18,64	25,61	1,45	30,70	19,50
C16:1	2,44	0,36	4,35	1,65	4,32	0,62	7,06	3,09
C17:0	0,26	0,05	0,52	0,15	0,13	0,03	0,31	0,06
C17:1	0,29	0,07	0,65	0,16	0,17	0,05	0,62	0,09
C18:0	10,91	1,56	16,10	6,55	11,38	1,43	14,94	6,90
C18:1 (n-9)	48,15	2,31	55,36	40,60	49,19	2,63	58,36	41,57
C18:2 (n-6)	10,10	1,05	15,08	8,08	5,32	1,10	9,65	2,96
C18:3 (n-3)	0,53	0,06	0,80	0,34	0,21	0,04	0,44	0,12
C20:0	0,21	0,04	0,38	0,10	0,19	0,04	0,31	0,12
C20:1 (n-9)	1,45	0,20	2,10	0,87	0,91	0,11	1,27	0,66
C20:2(n-9)	0,69	0,11	1,10	0,41	0,22	0,04	0,42	0,13
C20:3(n-6)	0,09	0,02	0,18	0,05	0,12	0,04	0,31	0,04
C20:4(n-6)	0,14	0,04	0,29	0,07	0,64	0,21	1,52	0,22
SFA	36,00	2,93	45,69	27,09	38,84	2,74	47,58	28,69
MUFA	52,43	2,59	60,48	43,95	54,65	3,03	65,11	45,97
PUFA	11,57	1,17	17,00	9,18	6,52	1,35	12,09	3,67

Methods

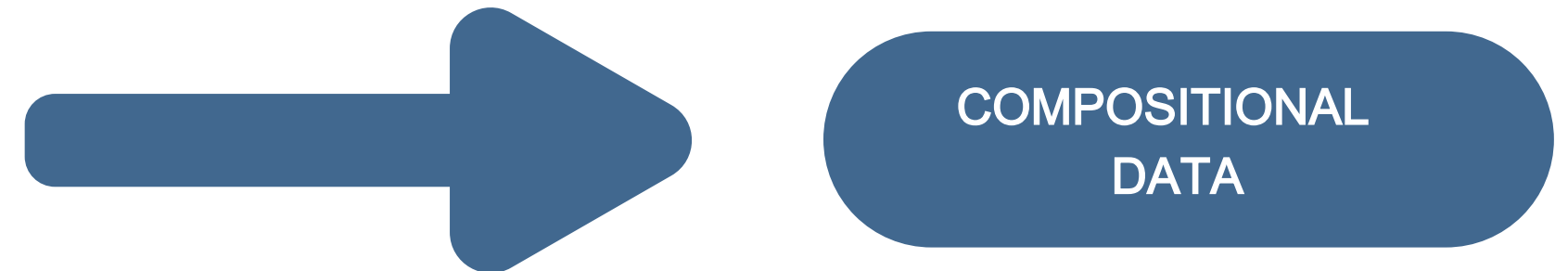
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COMPOSITIONAL
DATA

Methods

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Compositional Data Analysis of Microbiome and Any-Omics Datasets: A Validation of the Additive Logratio Transformation

Methods

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CLR
TRANSFORMATION

$$\text{CLR}(j) = \log \left(\frac{X_j}{g(X)} \right), \quad j = 1, \dots, J$$

Methods

SNPs Imputation



Flmpute

1

PLINK

MAF -> 0.05

MIND -> 0.25

GENO-> 0.1

2

BLUPF90+

Estimation of
variance
components
using the
REML method

STATISTICAL MODEL

$$y_{IMF} = cp + X_{IMF}b_{IMF} + T_{IMF}u_{IMF} + e_{IMF}$$

$$y_{SUB} = X_{SUB}b_{SUB} + T_{SUB}u_{SUB} + e_{SUB}$$

y -> Phenotypic data after CLR transformation
(IMF) (SUB)

p -> % IMF

b -> vector of systematic effects (sex, HYS and
population)

u -> vector of additive genetic random effects

e -> vector residual effects

X, T -> incidence matrices for single-step

3

POSTGSF90

Multitrait
Backsolving
Using
moving
average of the
variance for
the 25
adjacent SNPs

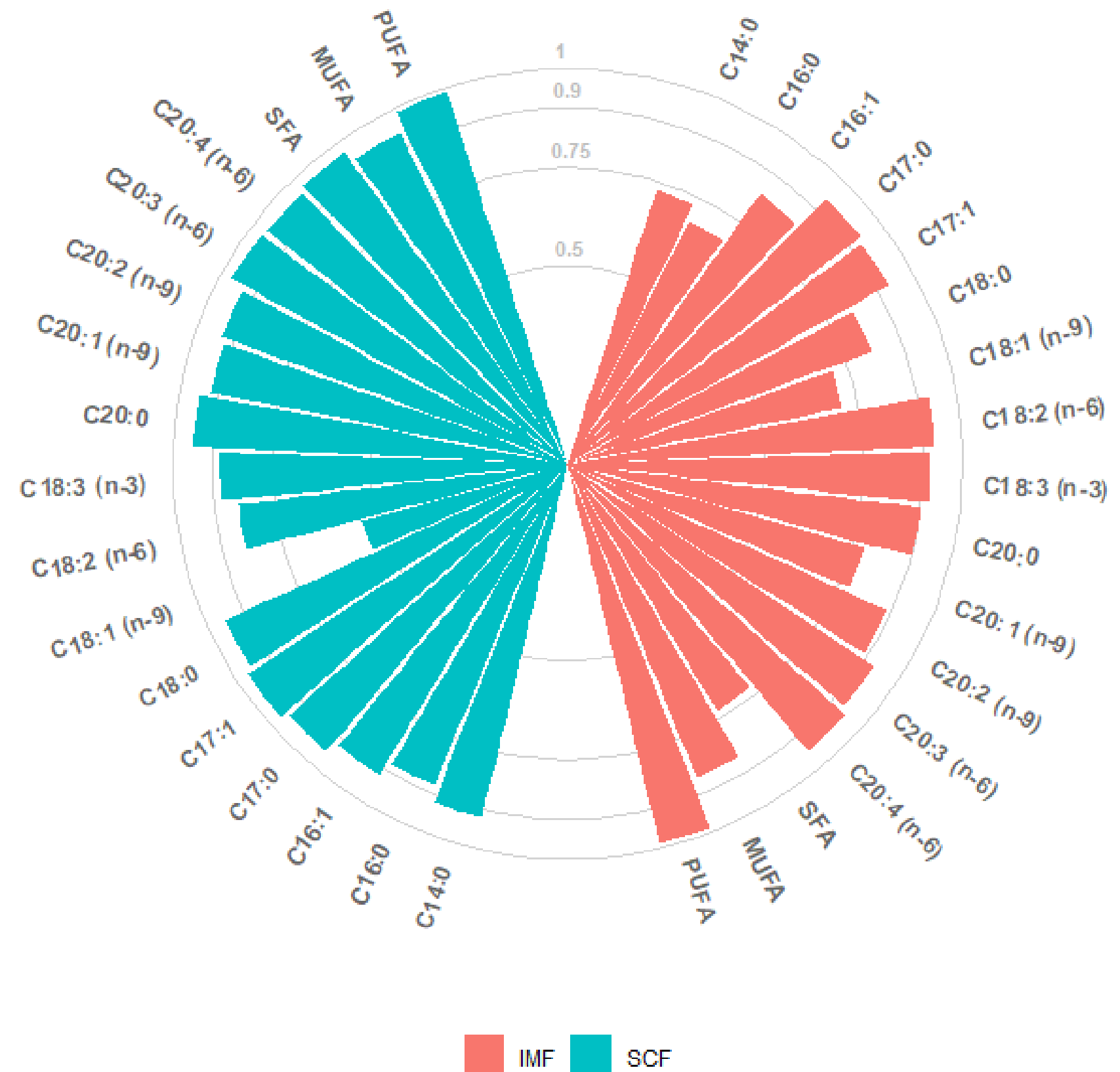
4

Relevance
level 1.5%

Results

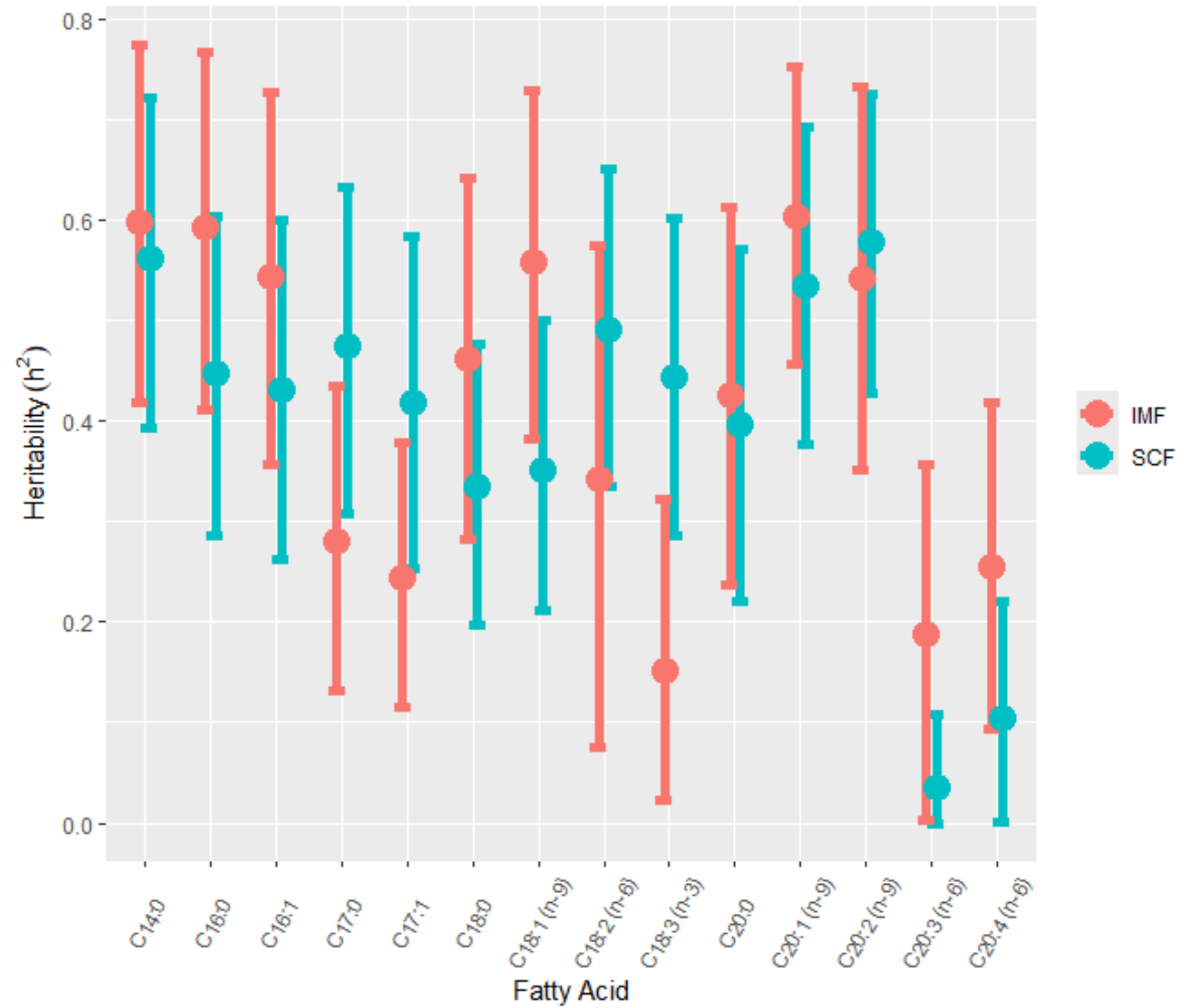
Correlation
before -after CLR

$$\text{CLR}(j) = \log \left(\frac{X_j}{g(X)} \right), \quad j = 1, \dots, J$$



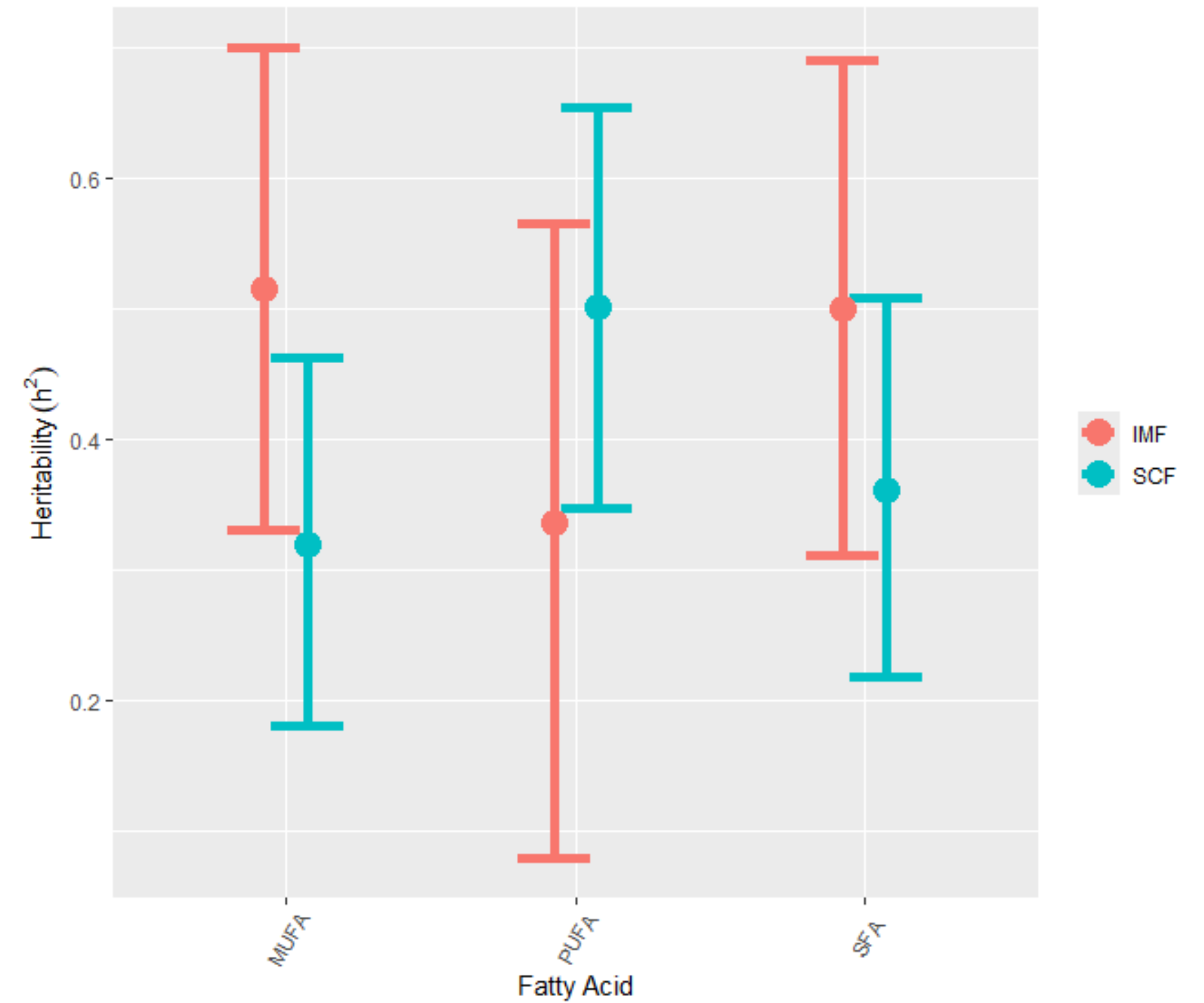
Results

Fatty acid heritabilities



Results

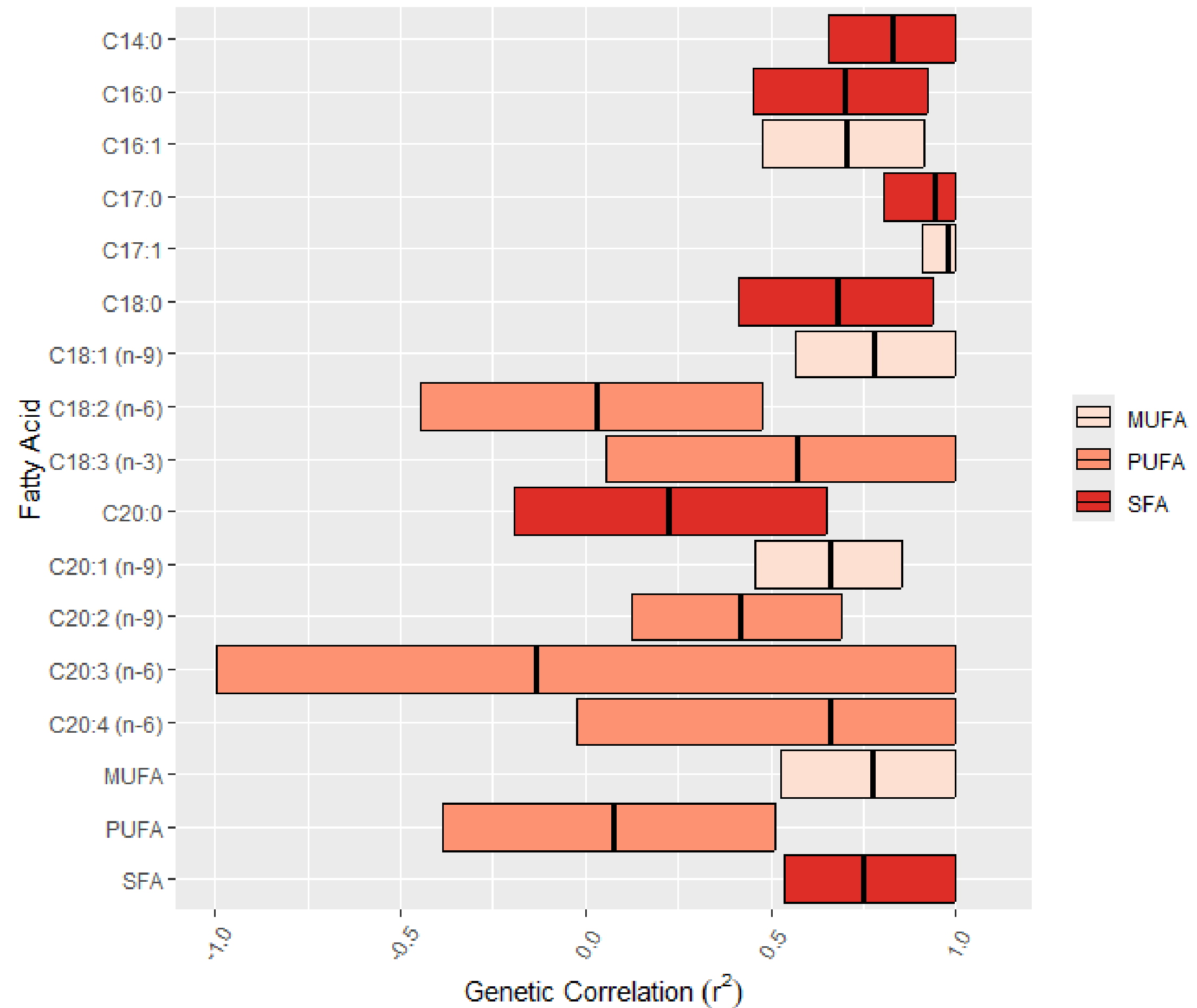
Fatty acid heritabilities by groups



Genetic correlation IMF and SCF



Results

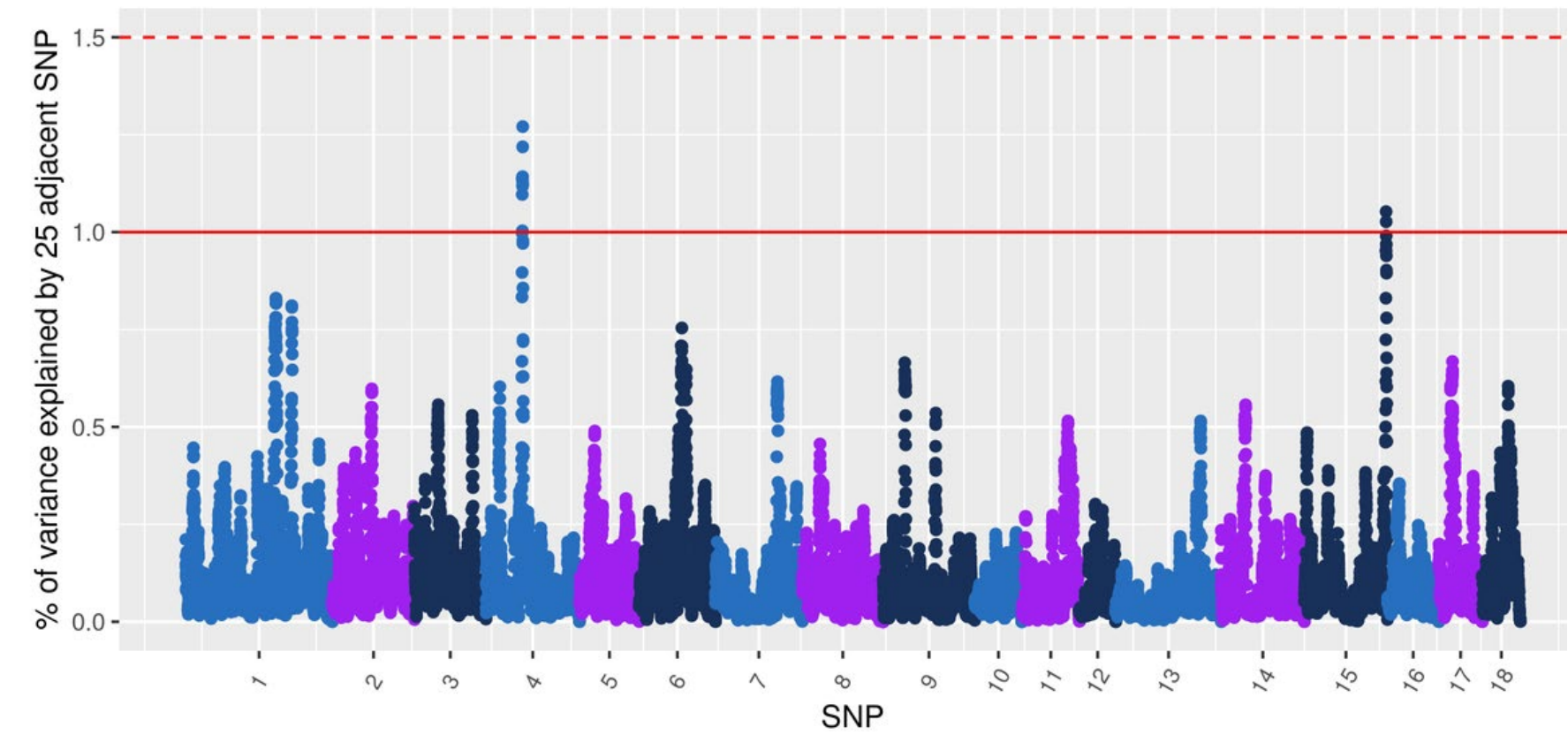
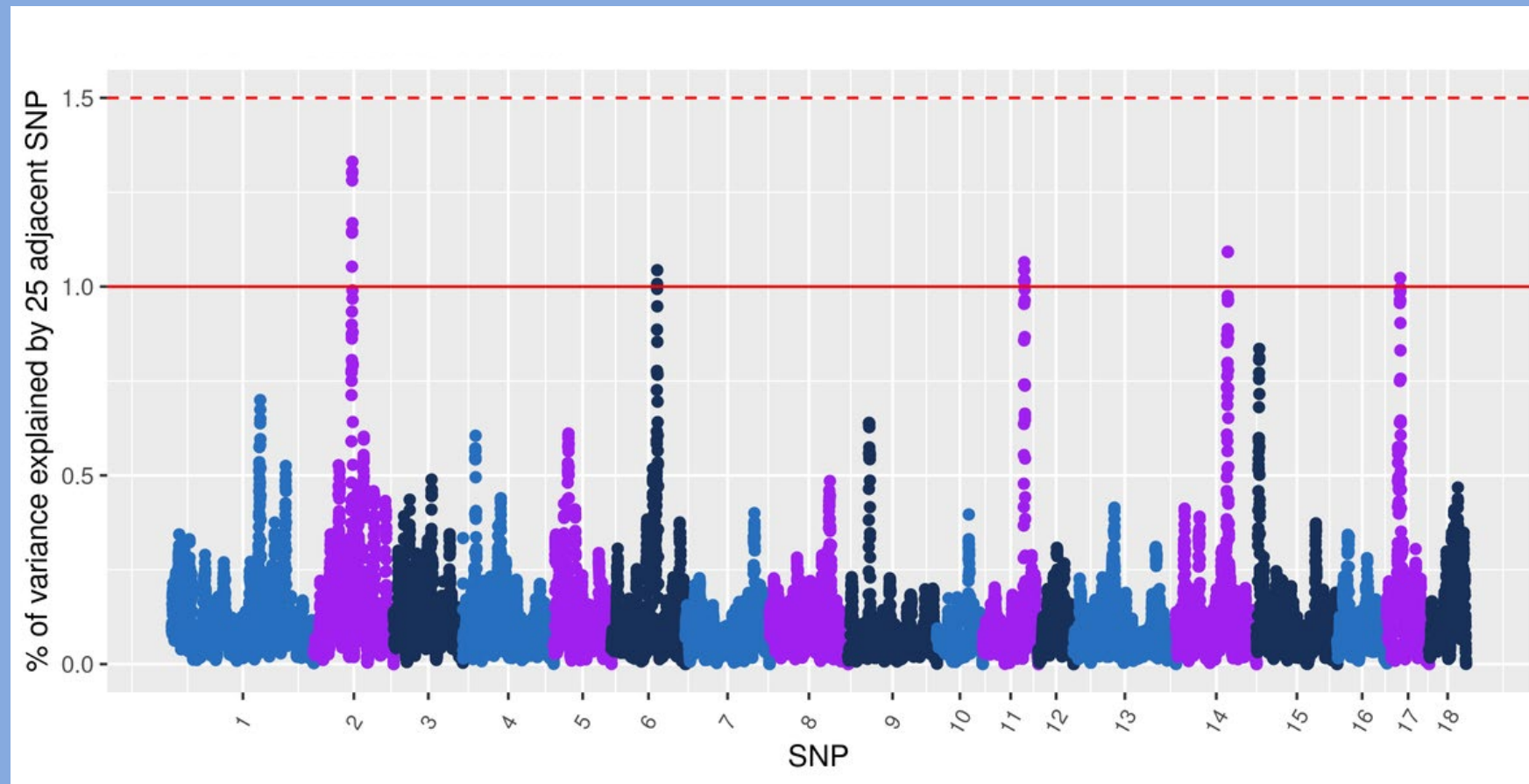


Results

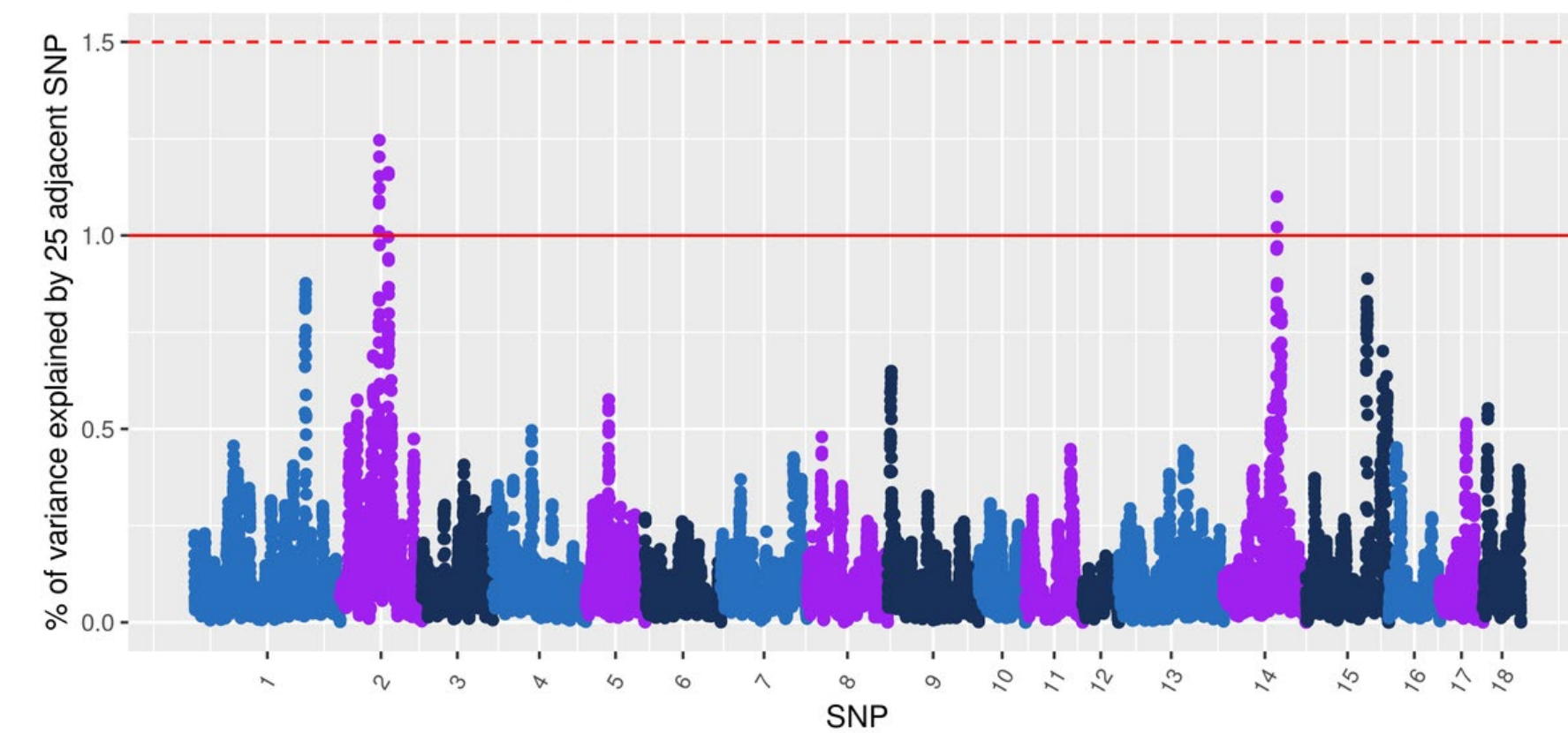
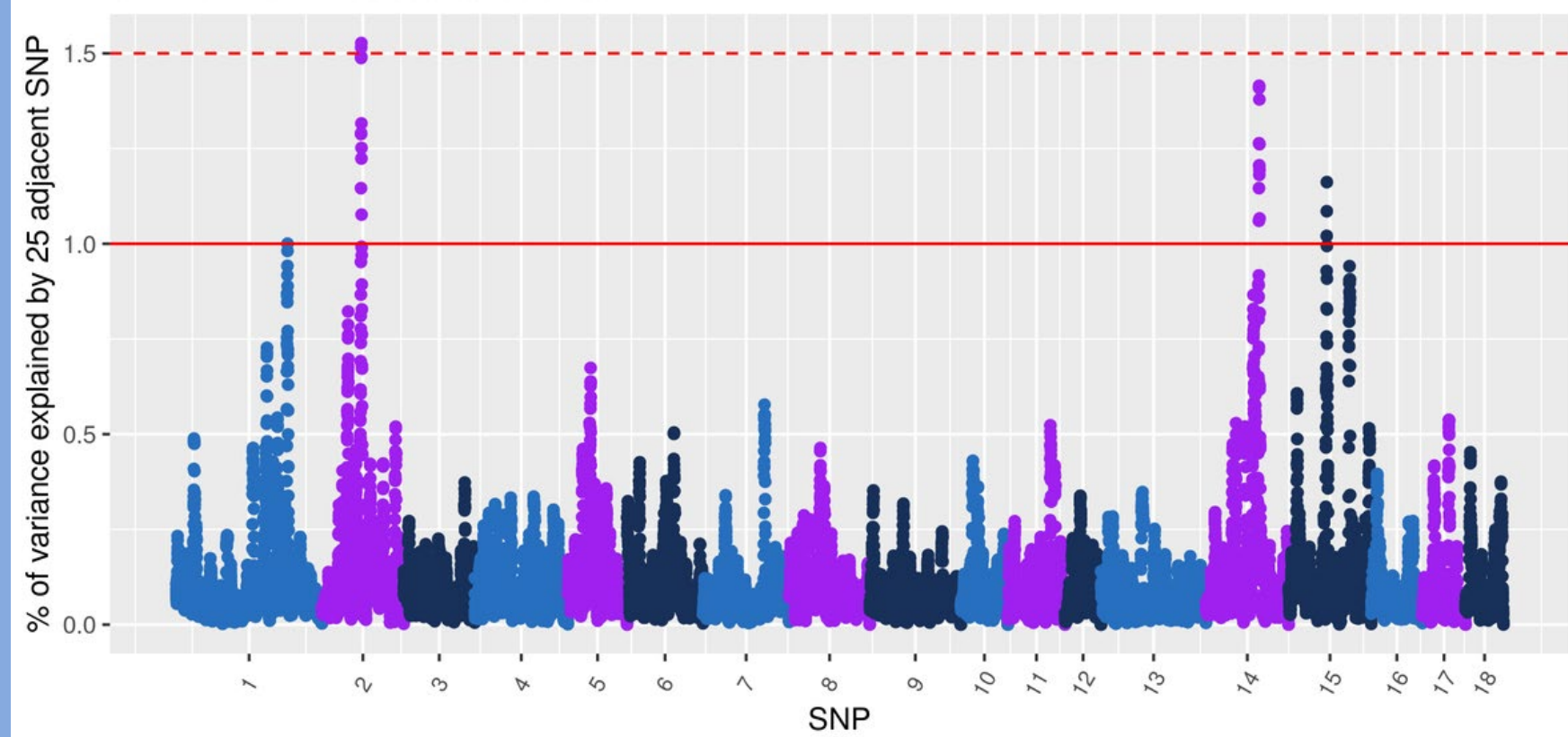
SUBCUTANEOUS FAT

INTRAMUSCULAR FAT

SFA



MUFA

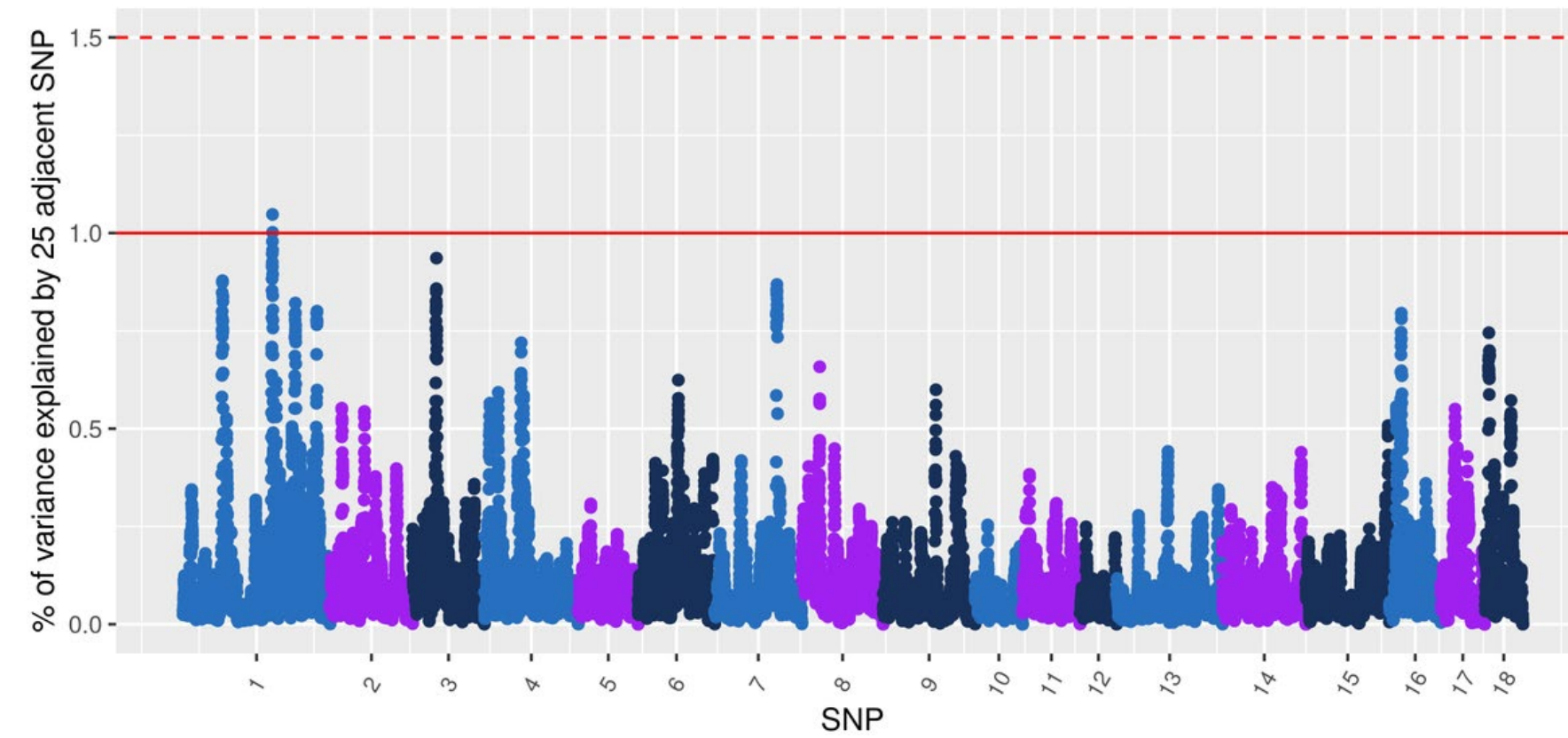
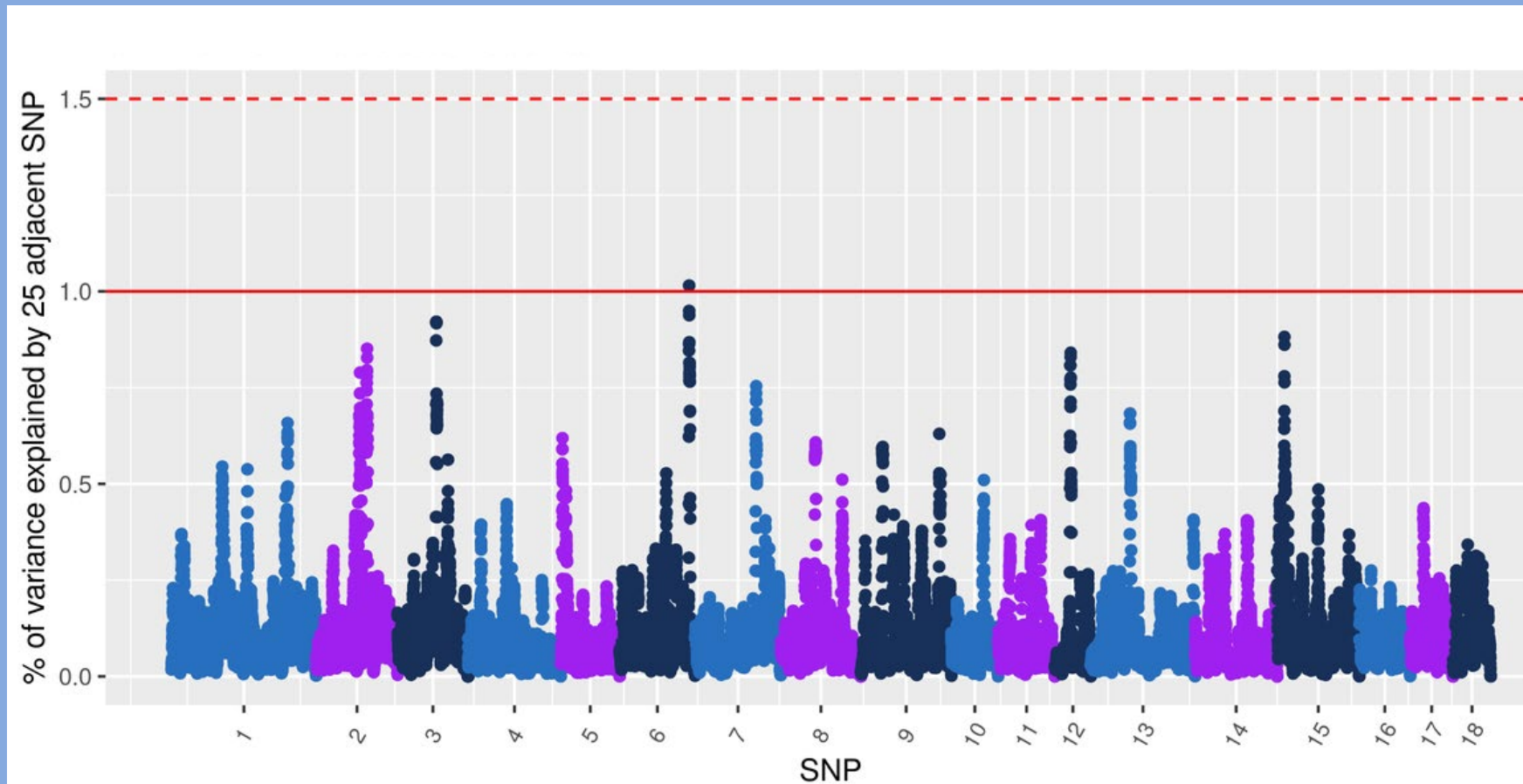


Results

SUBCUTANEOUS FAT

INTRAMUSCULAR FAT

PUFA



Results

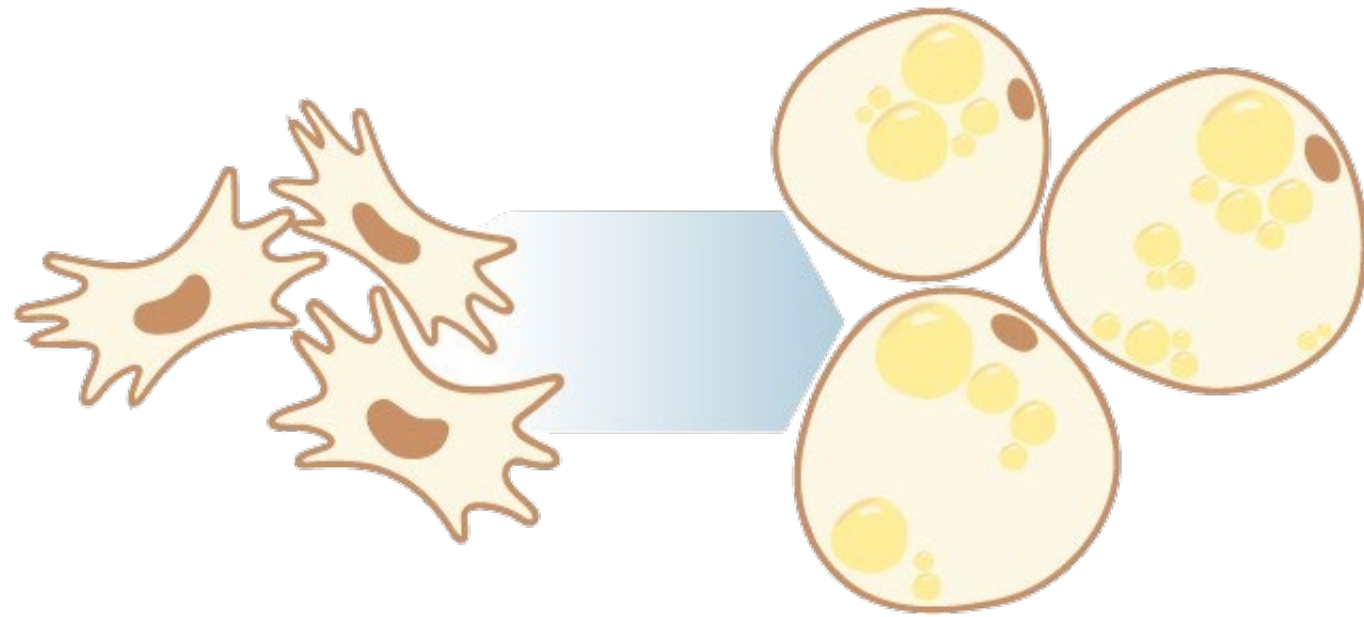
SSC	Start	End	Size (Mb)	Trait	Max %	Candidate Genes
1	171311843	175313955	4.00	Myristic (IMF), <i>PUFA</i>	2.36	
1	222855324	226269523	3.41	Oleic (IMF), <i>MUFA</i>	1.80	
2	80025649	83395466	3.36	MUFA (<i>SCF</i> , IMF), <i>SFA</i>	1.52	<i>B4GALT7</i> <i>FAF2</i>
3	97178250	101479314	4.30	Arachidonic (SCF), <i>DGLA</i>	1.69	<i>ZFP36L2</i> <i>COX7A2L</i> <i>SOS1</i>
4	44704517	49757804	5.05	Gadoleic (IMF)	2.31	<i>SLC26A7</i> <i>TMEM64</i> <i>DECR1</i> <i>RIPK2</i>
7	91928401	94531891	2.60	Arachidonic, Gadoleic (SCF)	2.14	<i>ZFP36L1</i>
8	10249282	11417428	1.16	C20_2n9 , <i>Palmitoleic</i>	1.57	

ZFP36L1

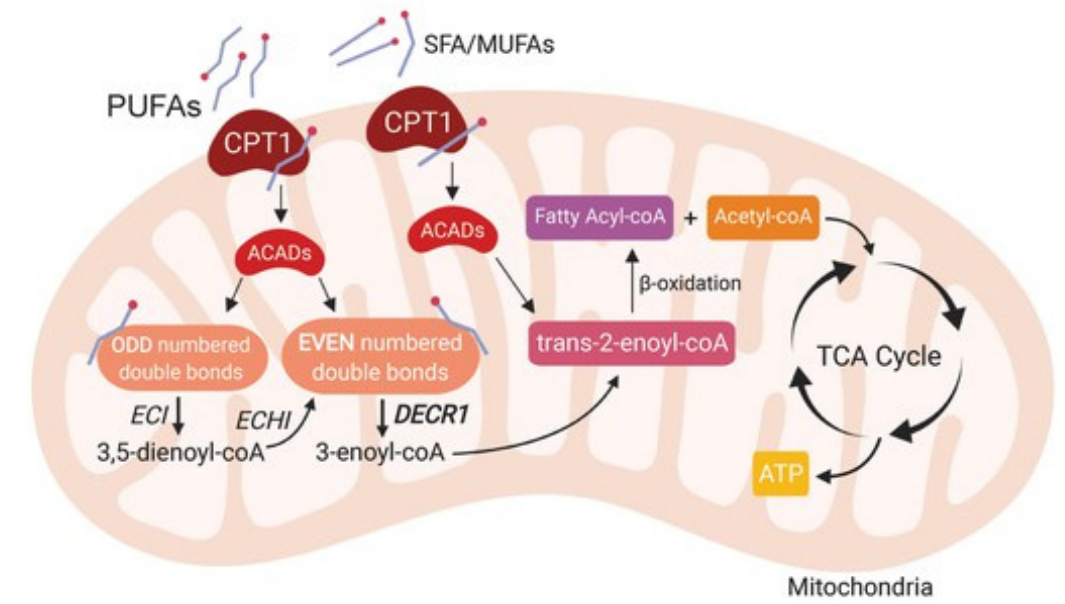
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TMEM64

+



DECR1



Nassar et al., 2020

Conclusion

”

- Heritability estimates were higher in IMF than in SCF, and genetic correlations were predominantly positive
- High correlations between IMF and SCF profiles can predict IMF composition from SCF samples
- Several regions were associated with fatty acid composition in various chromosomes, preliminarily identifying key genes for lipid metabolism

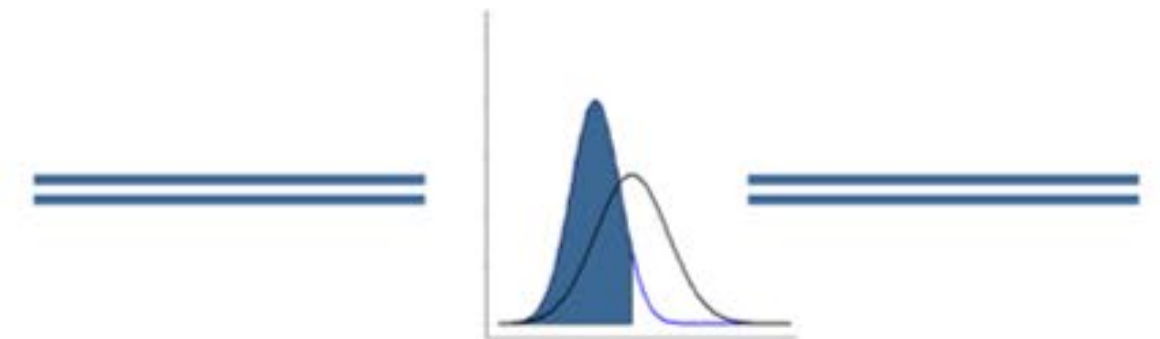
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**QUANTITATIVE
GENETICS LAB**



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