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Plasma metabolomics profiling of two rabbit lines divergently selected for intramuscular fat

Zubiri-Gaitán, A., Blasco, A., **Hernández, P.**



phernan@dca.upv.es

INTRAMUSCULAR FAT (IMF)



Meat quality



Juiciness

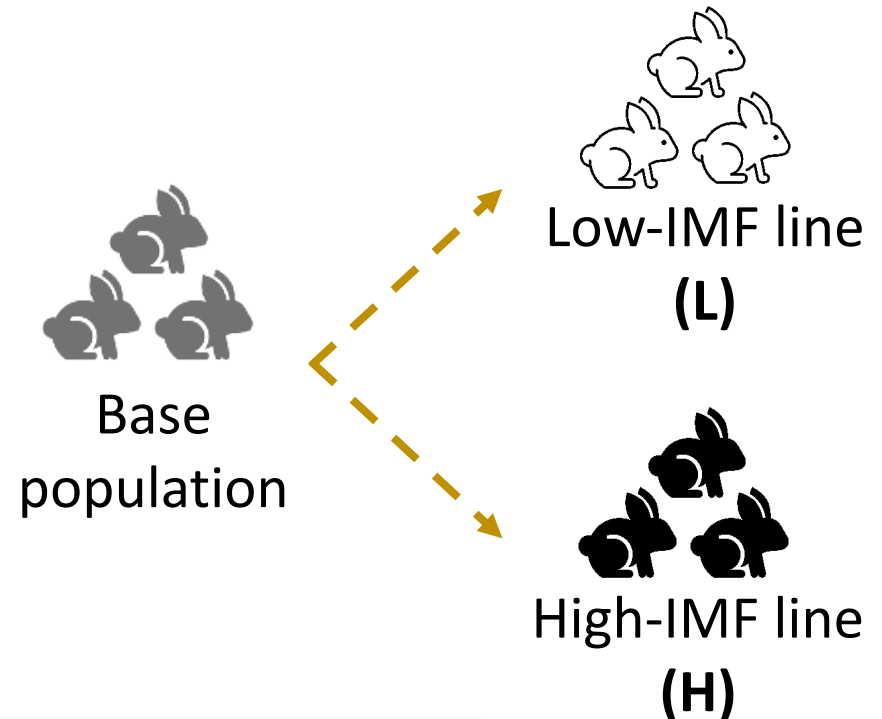


Tenderness



Flavour

Divergent selection for IMF in
Longissimus thoracis et lumborum (LTL)



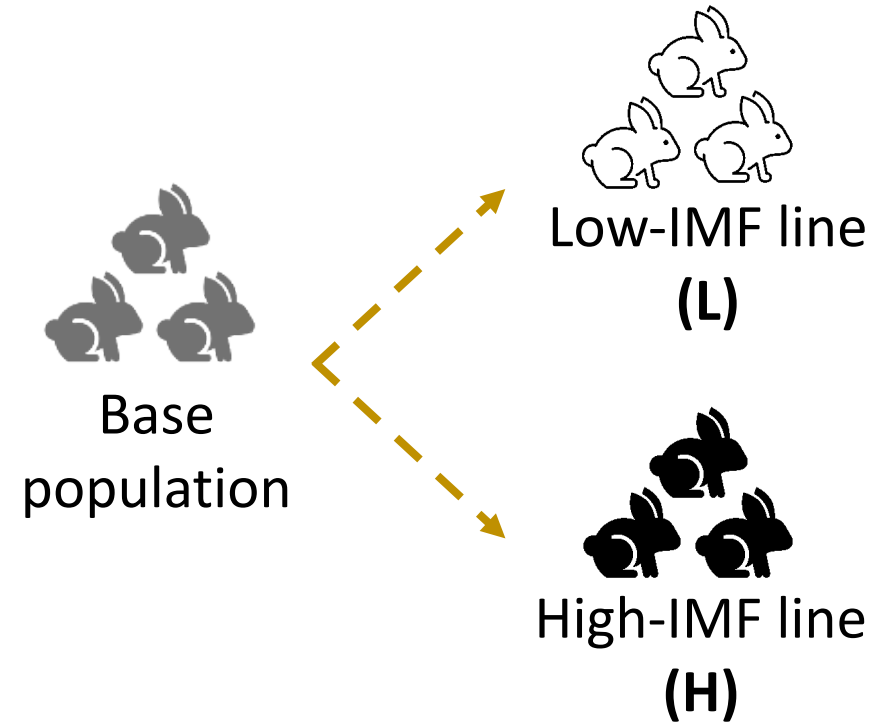
Response H-L = 3.1 SD

- Contemporaneous
- Same environmental conditions
- Same diet



DIFFERENCES ARE DUE TO GENETICS

Divergent selection for IMF in *Longissimus thoracis et lumborum* (LTL)



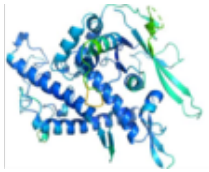
Selection led to a correlated response in the overall adiposity, making these lines a valuable animal material to study also the genetics of obesity



Genotype

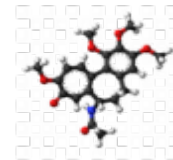


Transcriptome



Proteome

Metabolome

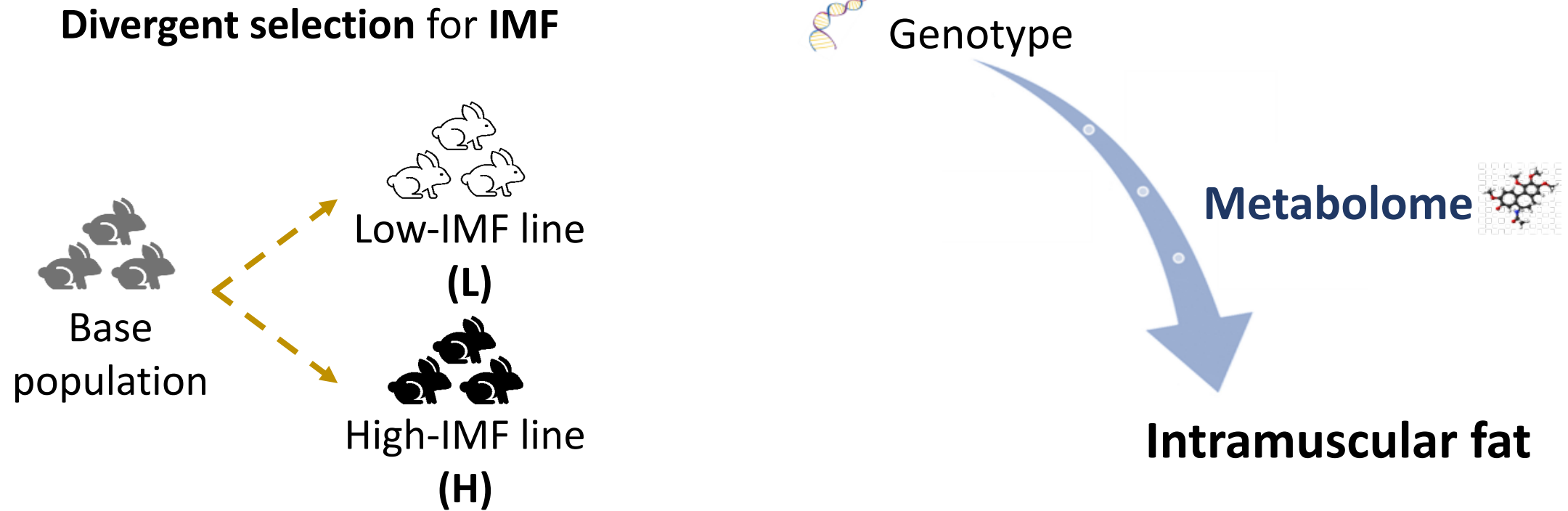


Organic molecules of small molecular mass
found in a biological sample

Phenotype

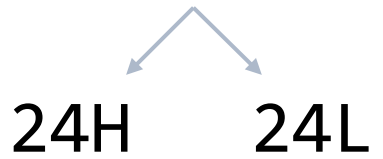


To identify genetically induced changes in plasma metabolomic profile of two divergent rabbit lines selected for IMF





48 anim
9th gen



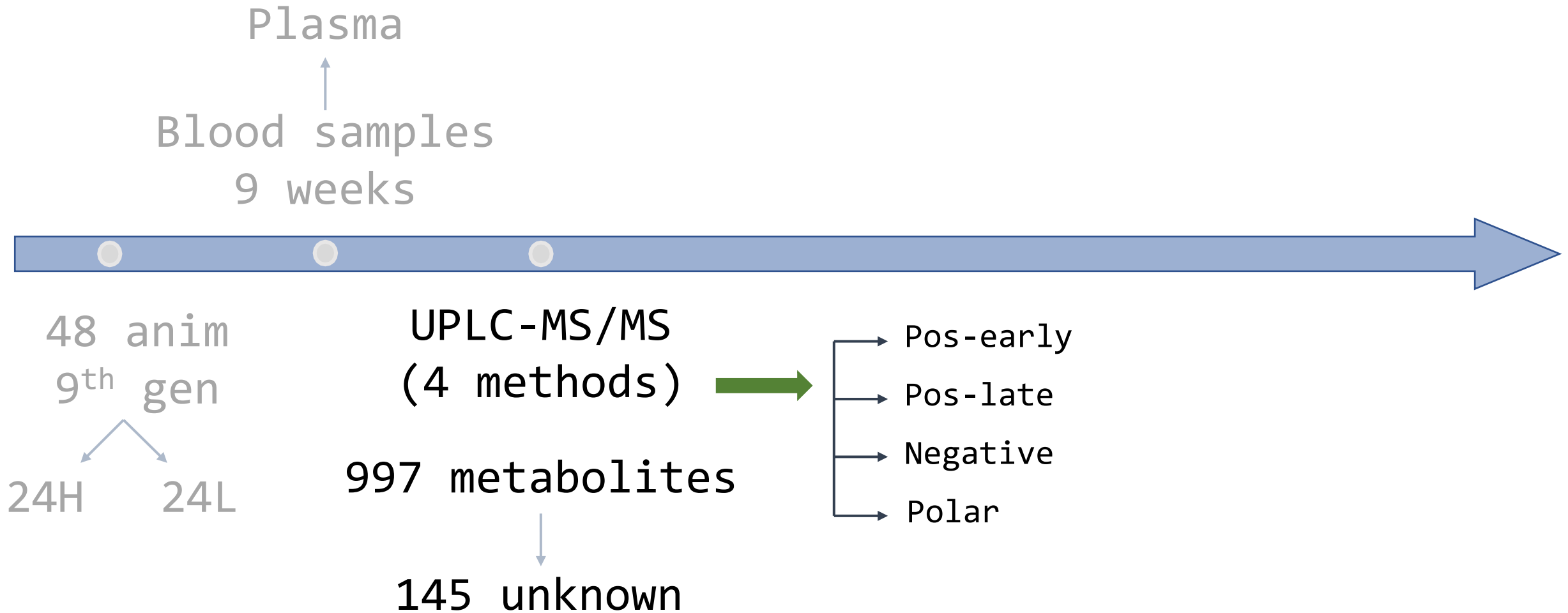
Plasma

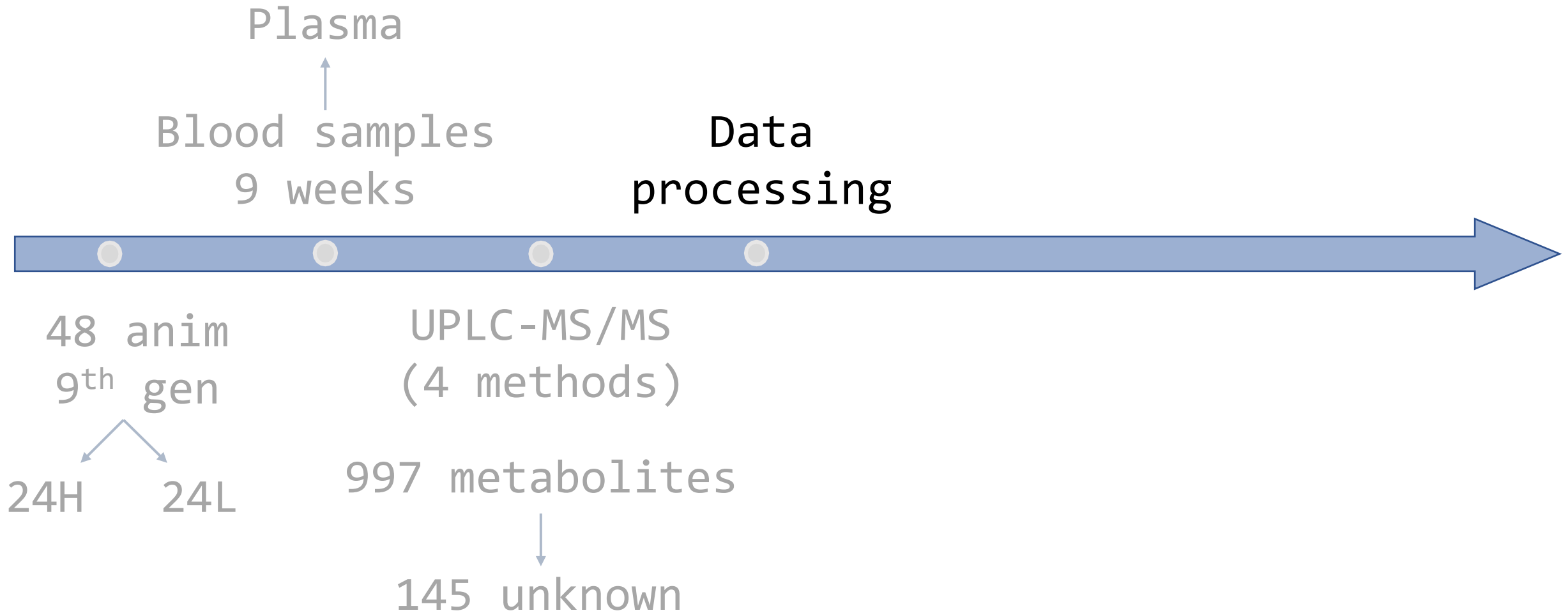
Blood samples
9 weeks



48 anim
9th gen

24H 24L

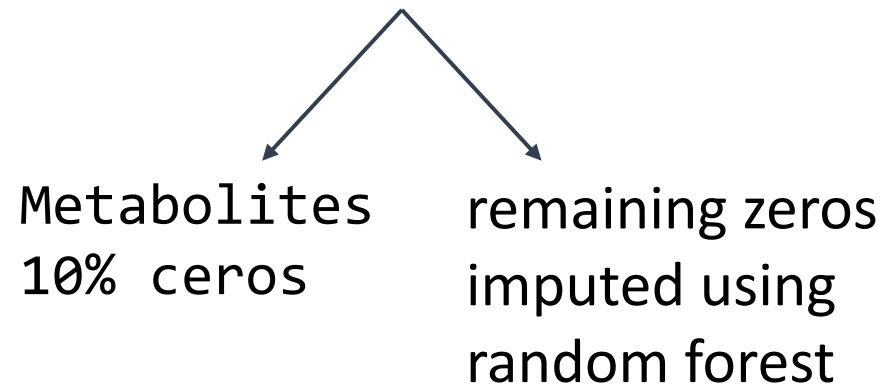




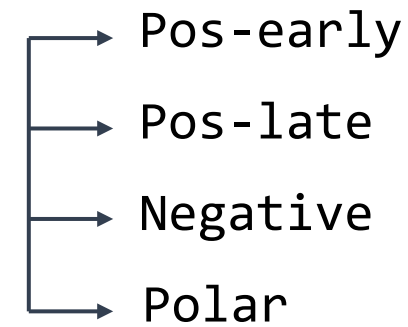
Data
processing

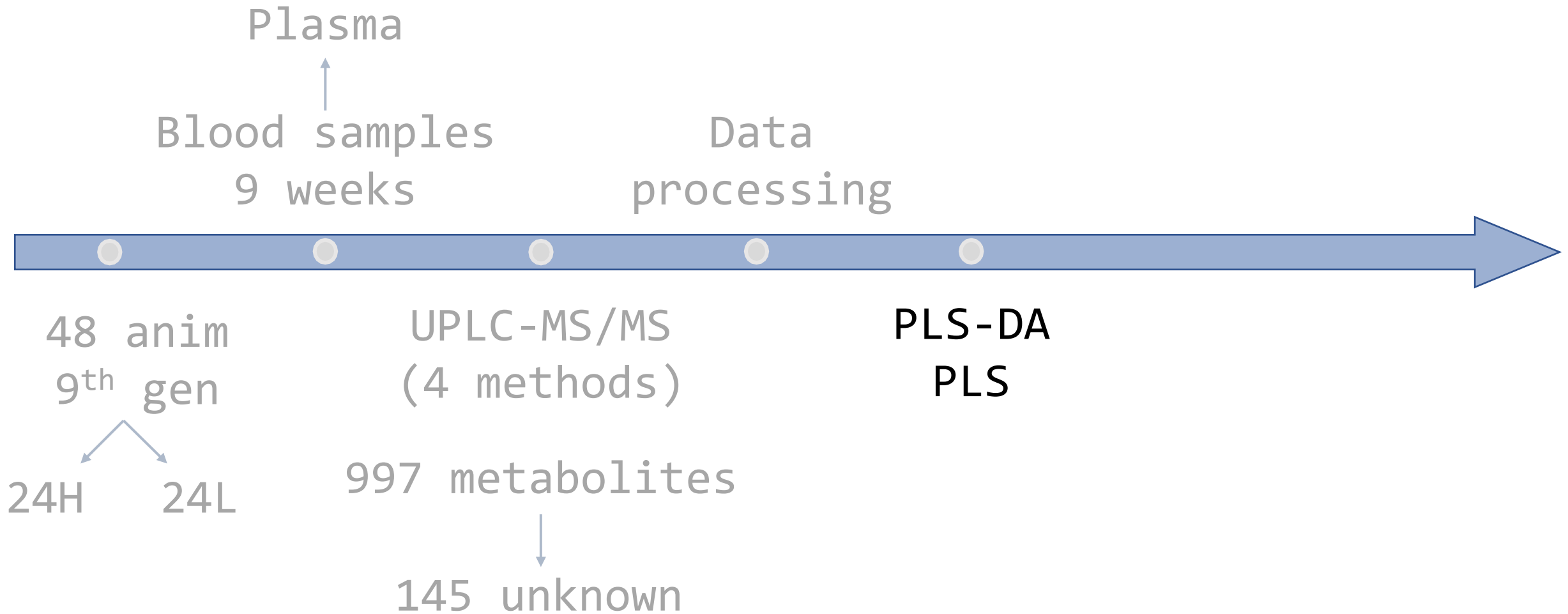


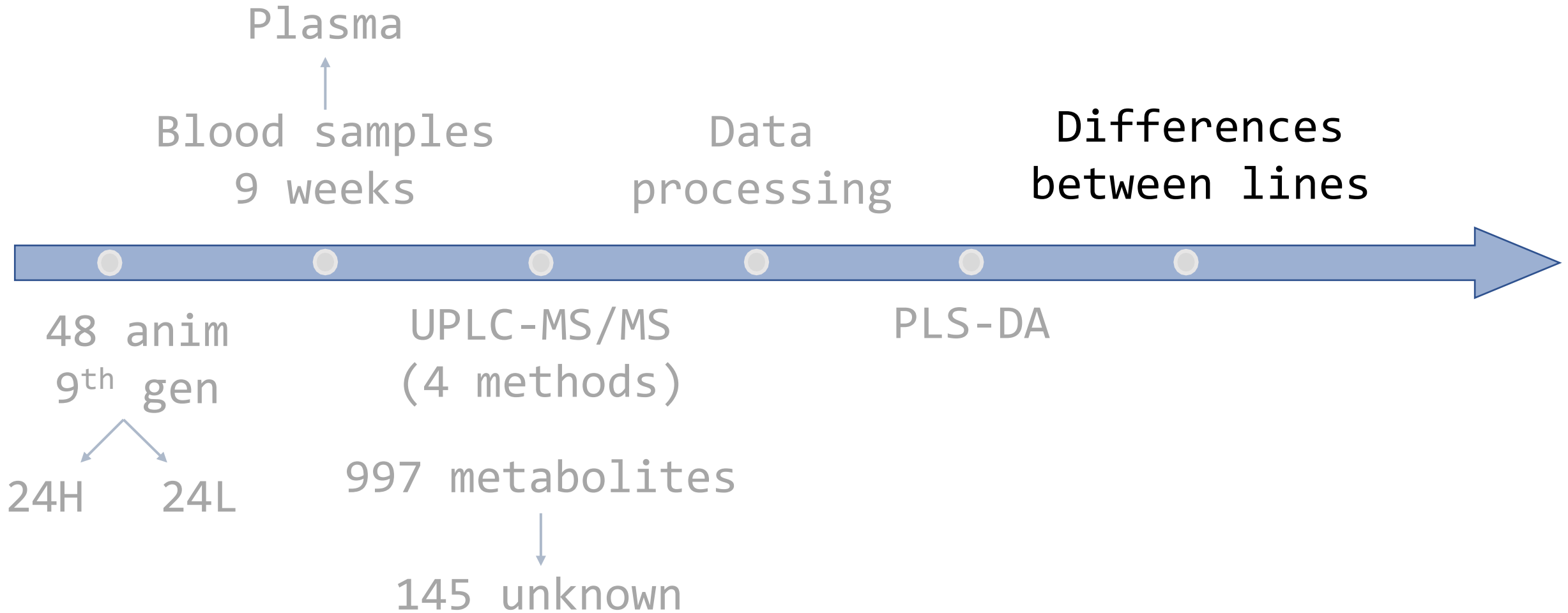
ZEROS

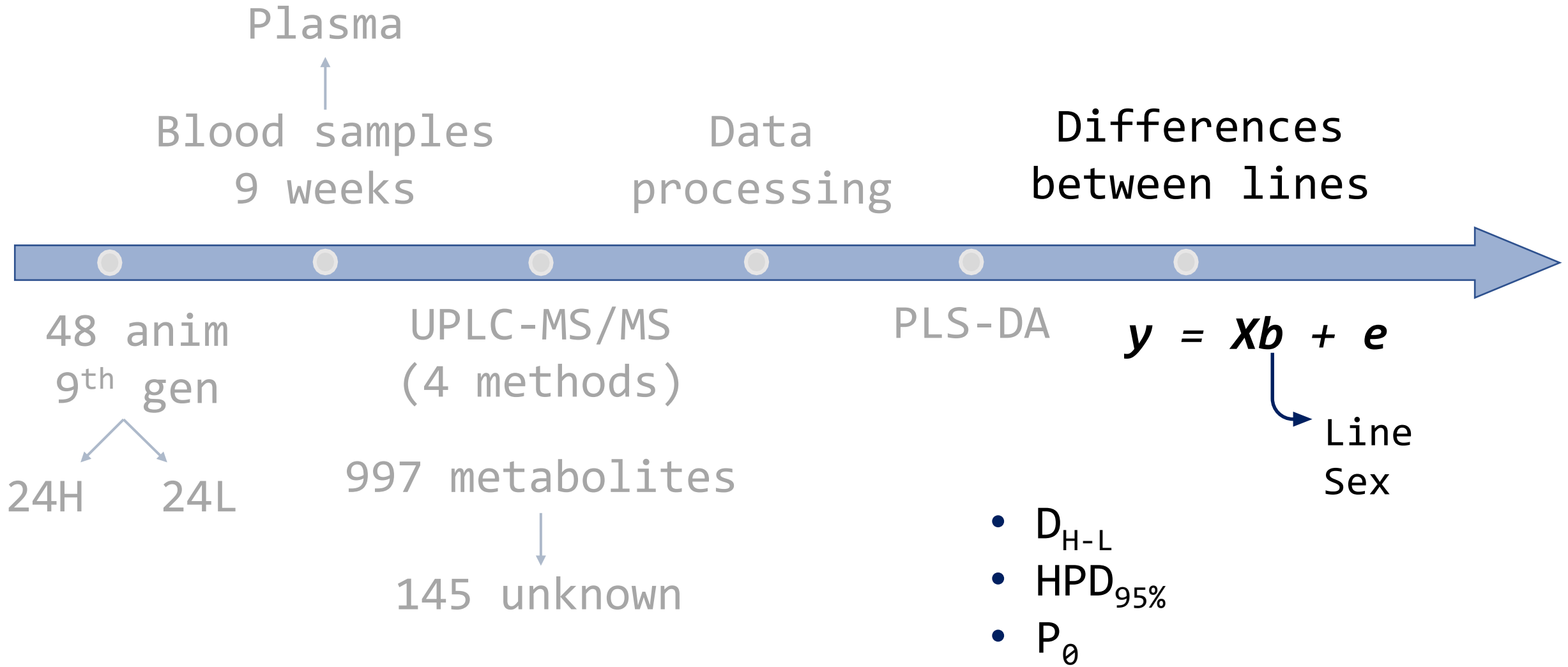


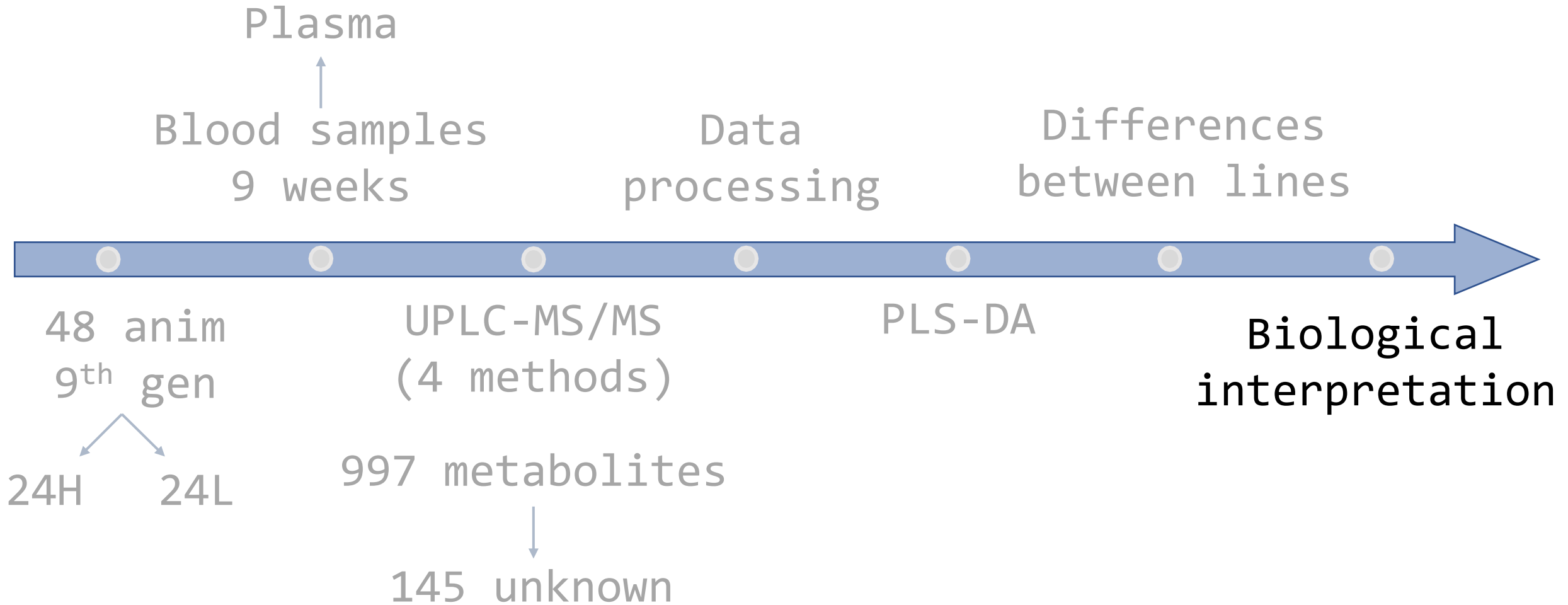
Alr Transformation

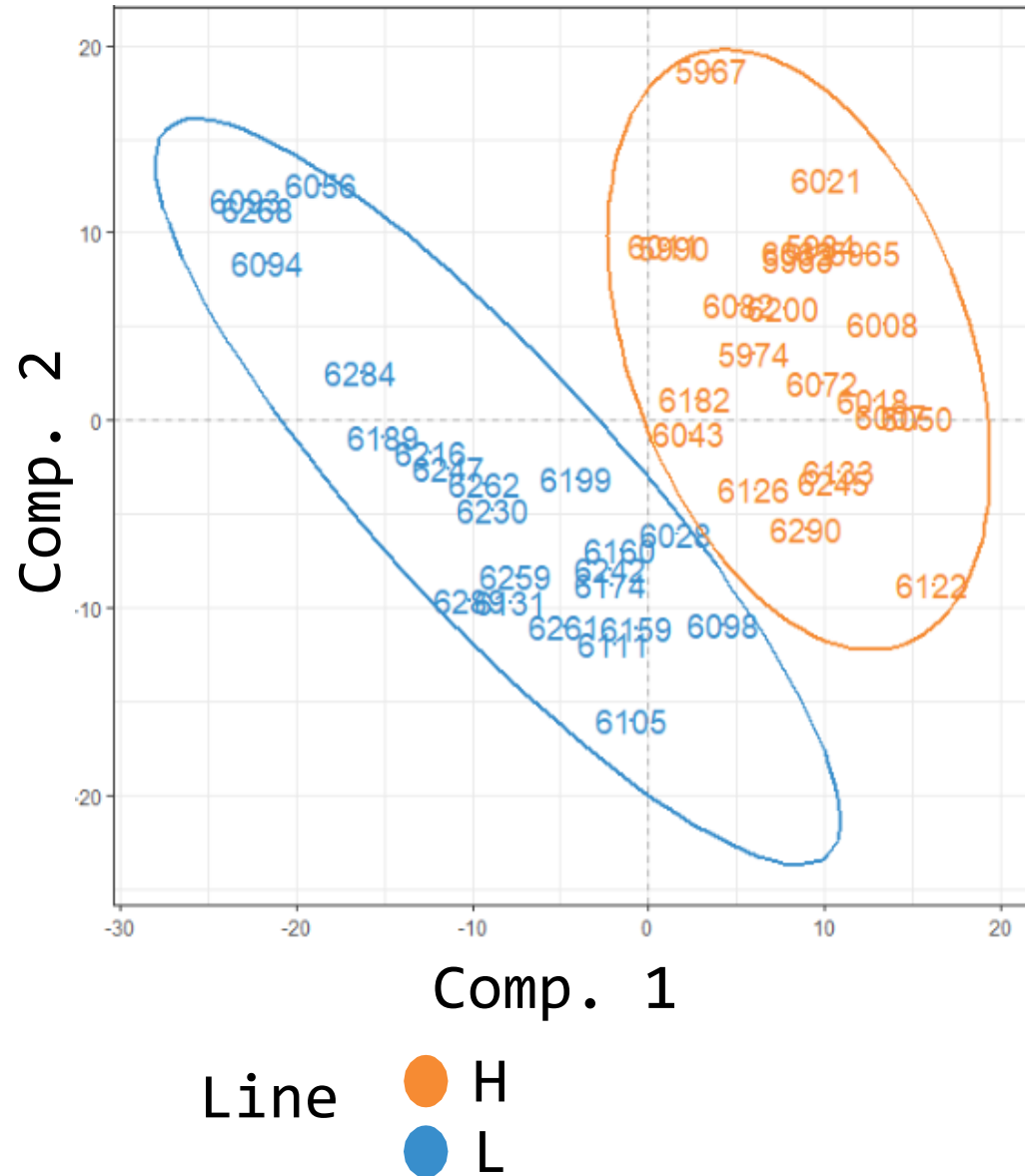










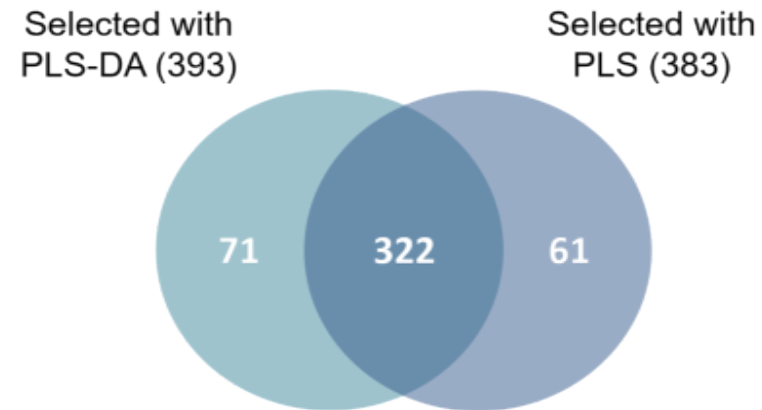


PLS-DA results

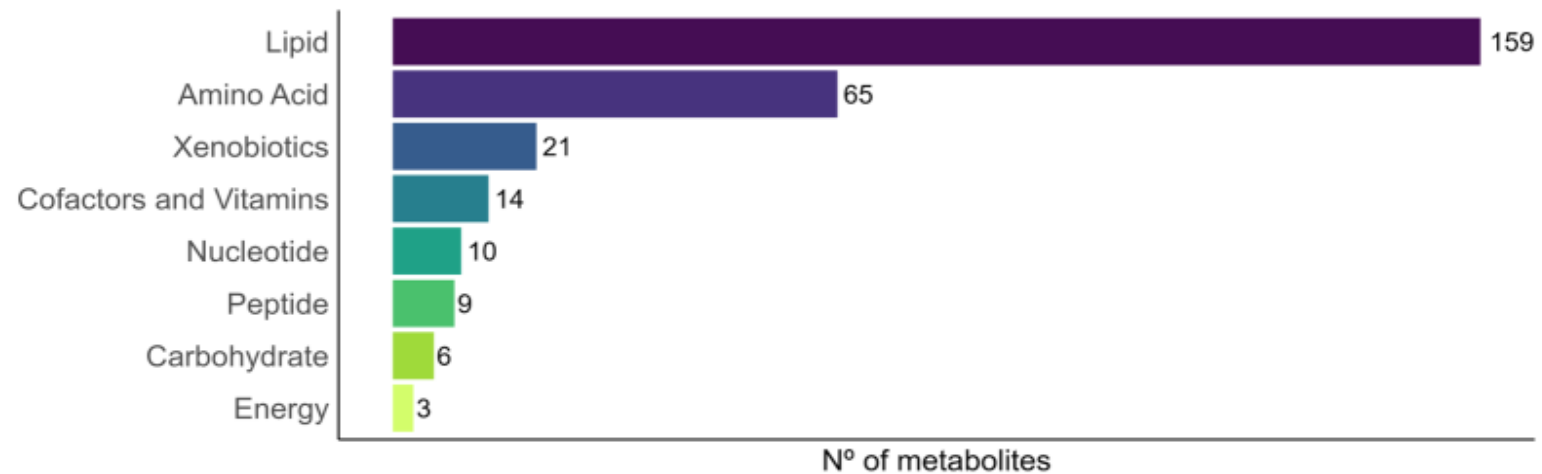
Data misclassification

	H	L
H	96.7%	3.3%
L	5.4%	94.6%

Relevant metabolites obtained with the PLS and PLS-DA models

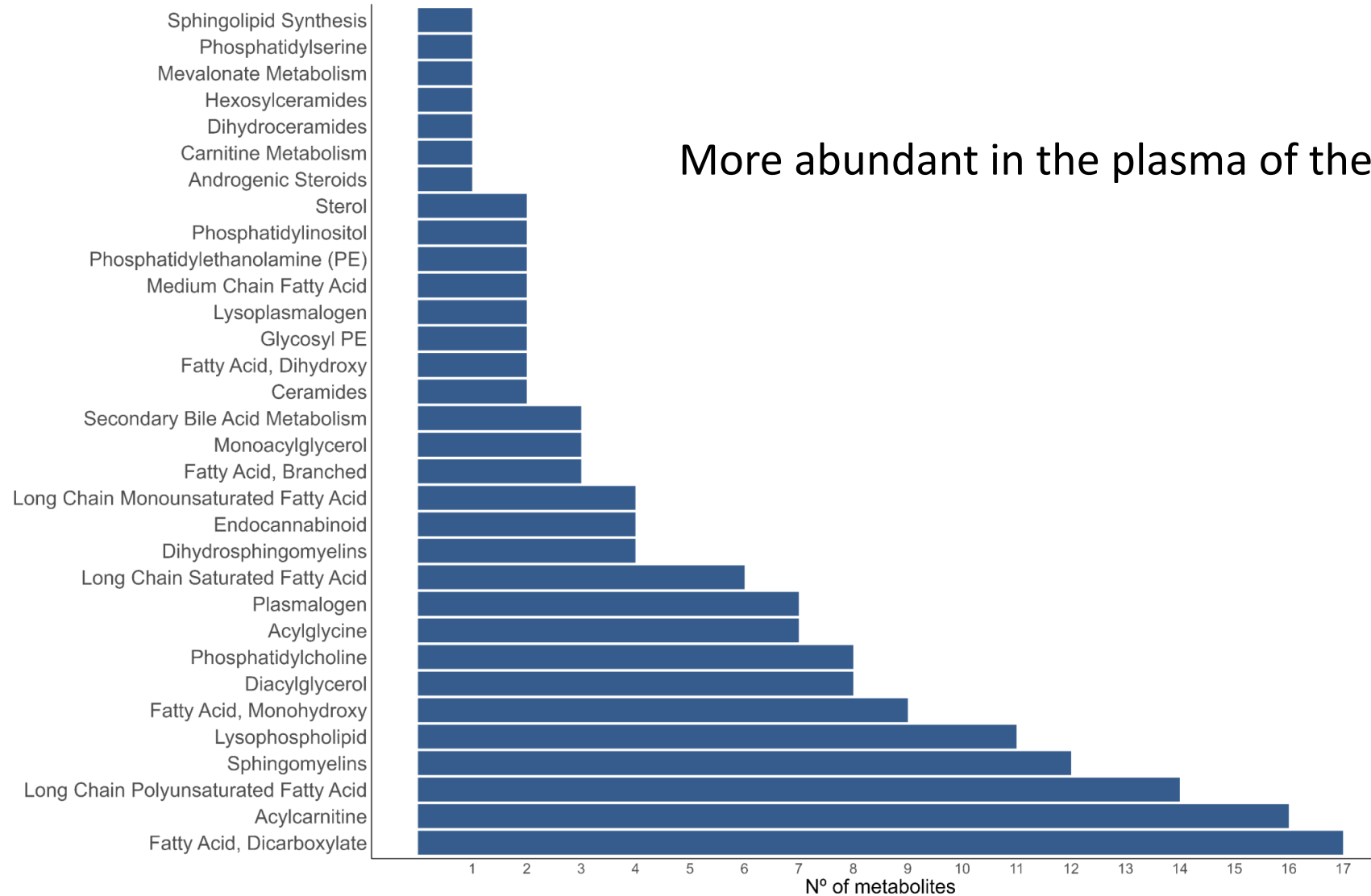
a

Large and varied response to selection in the plasma metabolome. The most affected pathways found were those of lipids and amino acids

b

LIPID METABOLISM

More abundant in the plasma of the L line (127 out of 159)

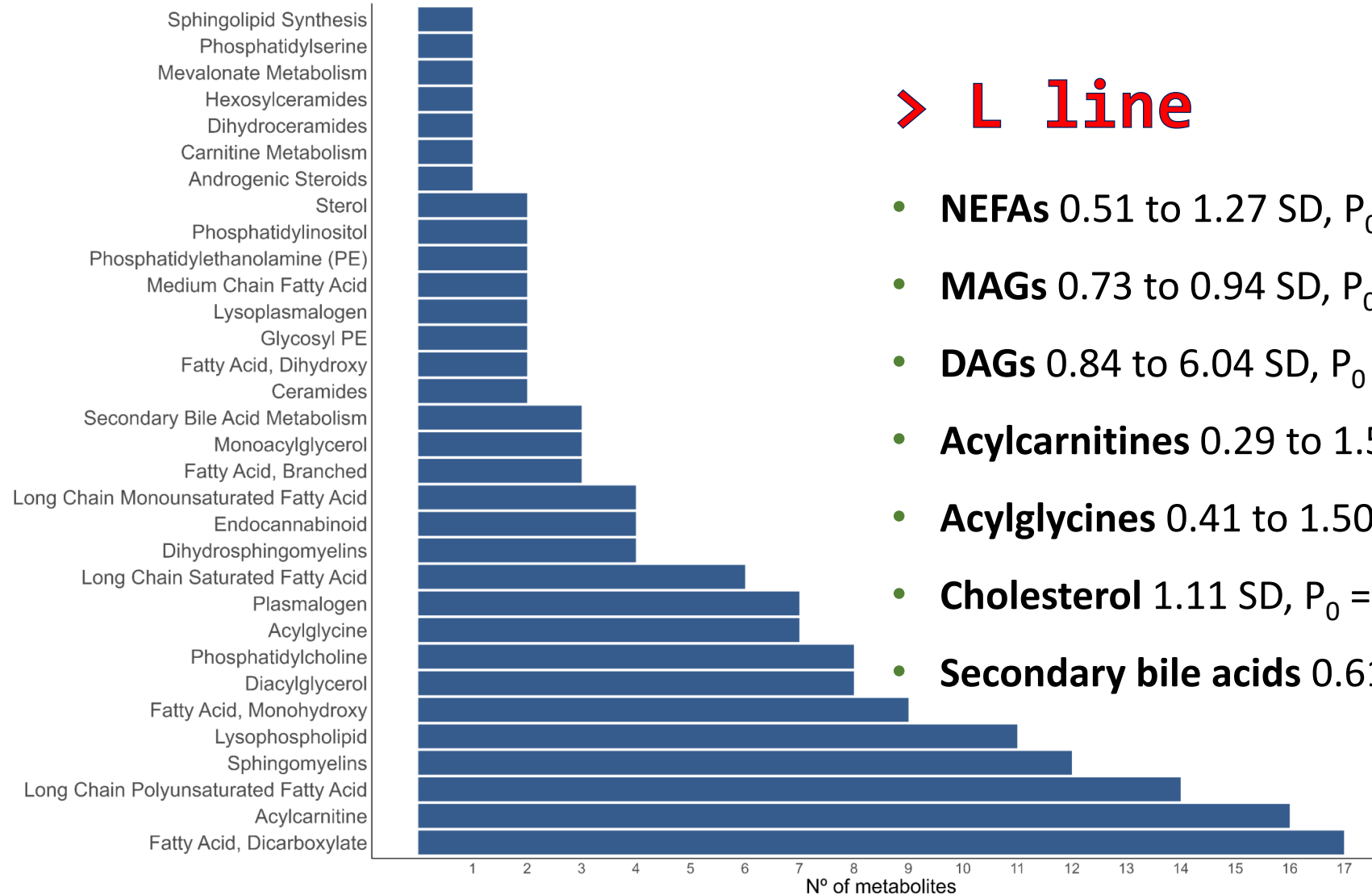


Number of differentially abundant metabolites found for each lipid sub-pathway

LIPID METABOLISM

> **L line**

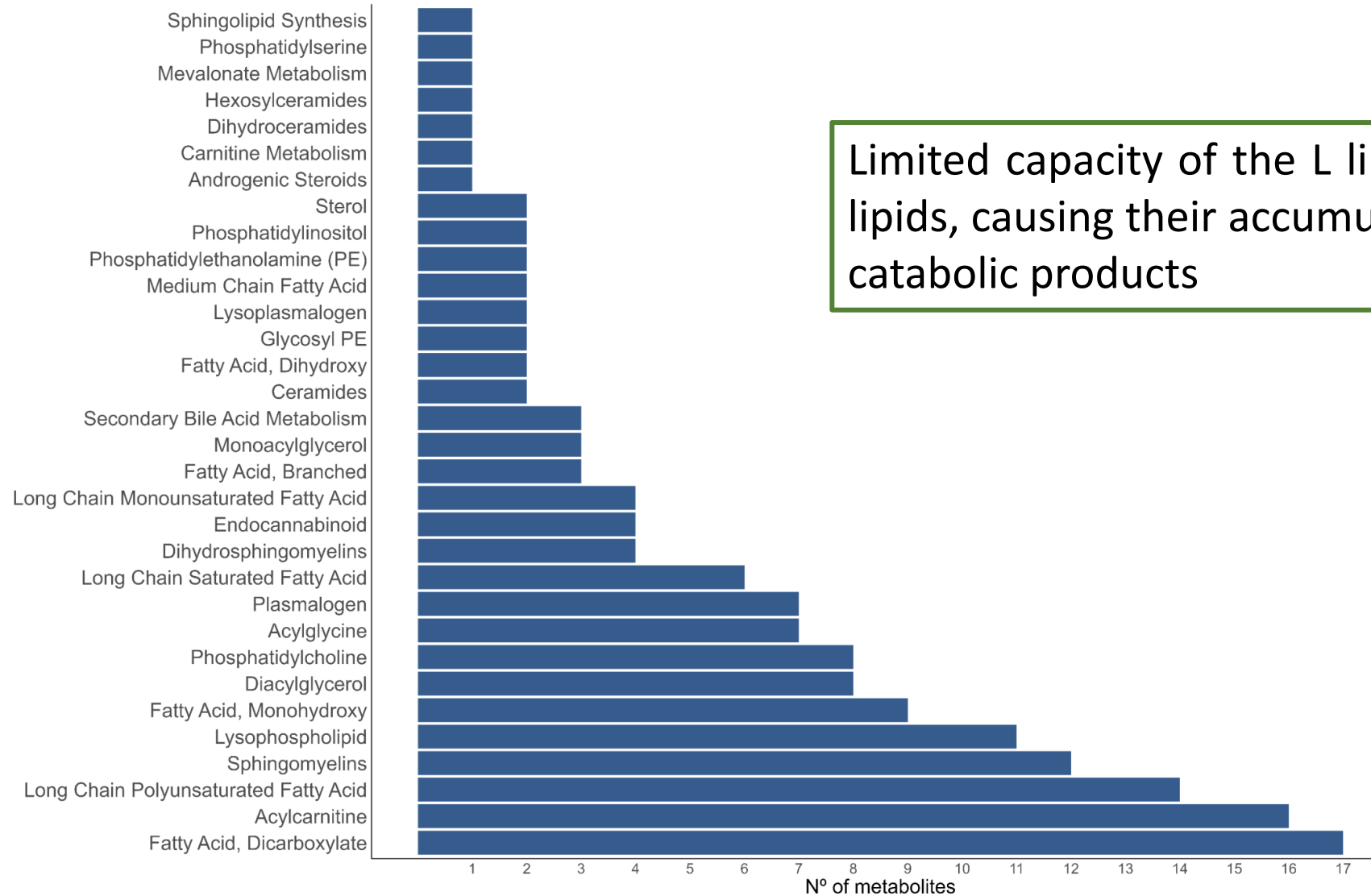
- **NEFAs** 0.51 to 1.27 SD, $P_0 \geq 0.96$
- **MAGs** 0.73 to 0.94 SD, $P_0 \geq 0.99$
- **DAGs** 0.84 to 6.04 SD, $P_0 = 1$
- **Acylcarnitines** 0.29 to 1.56 SD, $P_0 \geq 0.84$
- **Acylglycines** 0.41 to 1.50 SD, $P_0 \geq 0.92$
- **Cholesterol** 1.11 SD, $P_0 = 1$
- **Secondary bile acids** 0.61 to 1.01 SD, $P_0 \geq 0.98$



Number of differentially abundant metabolites found for each lipid sub-pathway

LIPID METABOLISM

Limited capacity of the L line to obtain energy from lipids, causing their accumulation together with their catabolic products



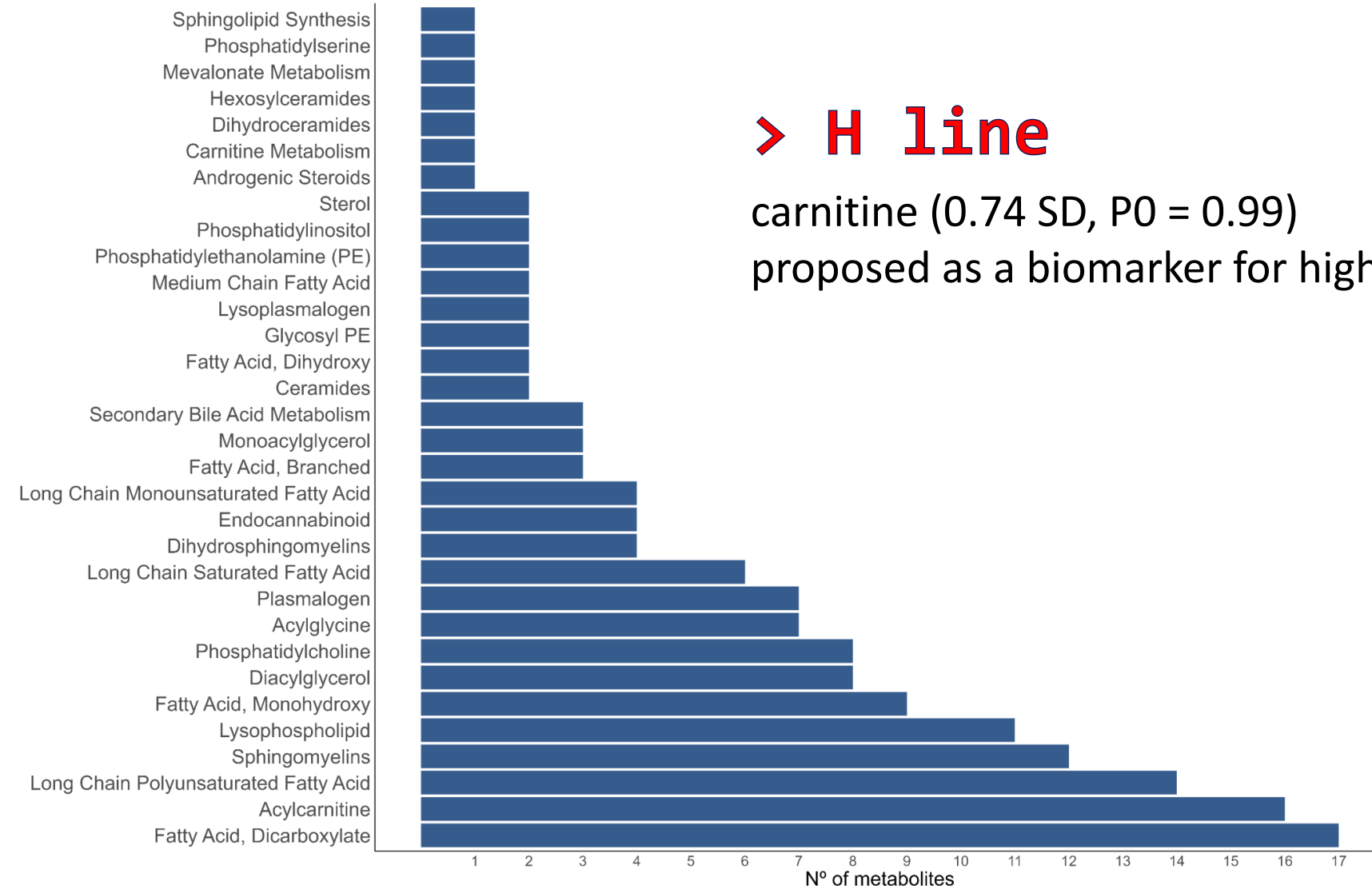
Number of differentially abundant metabolites found for each lipid sub-pathway

LIPID METABOLISM

> **H line**

carnitine (0.74 SD, P0 = 0.99)

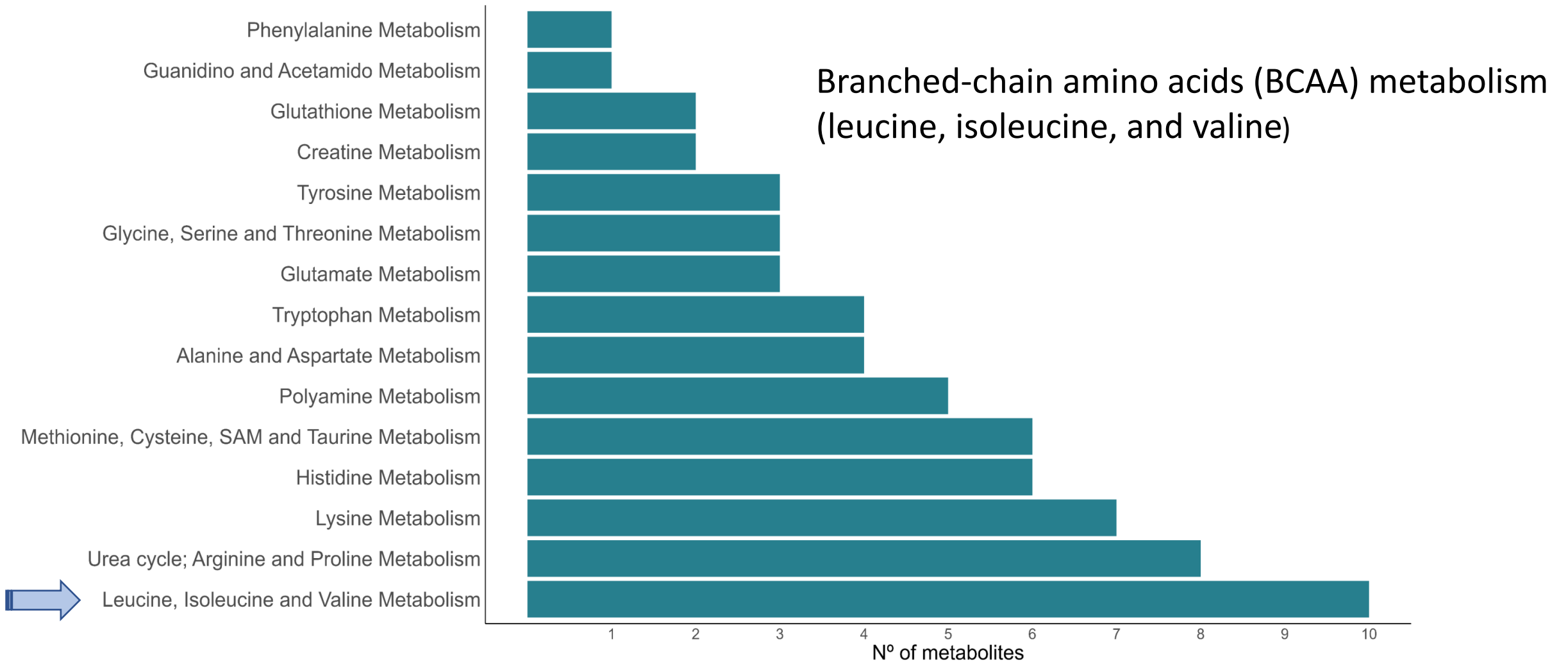
proposed as a biomarker for higher meat quality and IMF



Number of differentially abundant metabolites found for each lipid sub-pathway

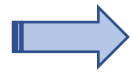


AMINO ACIDS METABOLISM

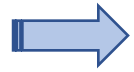


Number of differentially abundant metabolites found for each amino acid sub-pathway

Metabolic pathways related to the microbiome metabolism



Gut microbiota has a large effect on the blood metabolome



Several metabolites found are related to the gut microbiome metabolism, and their differences indicate changes in the microbial activity of the lines

- Secondary bile acids
- Branched-chain and aromatic amino acids
- Metabolites from the arginine and histidine metabolisms

- There was a correlated response to selection in the plasma metabolome. The most affected pathways found were those of lipids and amino acids
- General increase of lipids in the plasma of the L line, suggesting an impaired β -oxidation in this line. Limited capacity of the L line to obtain energy from lipids, reducing their uptake and re-esterification in muscle and adipose tissue
- The most relevant results among the amino acids metabolism were related to the BCAA
- The changes in the secondary bile acids, in branched-chain and aromatic amino acids, and also in the metabolites from the arginine and histidine metabolisms, supported the relevant role of the microbiome activity in the development of the IMF



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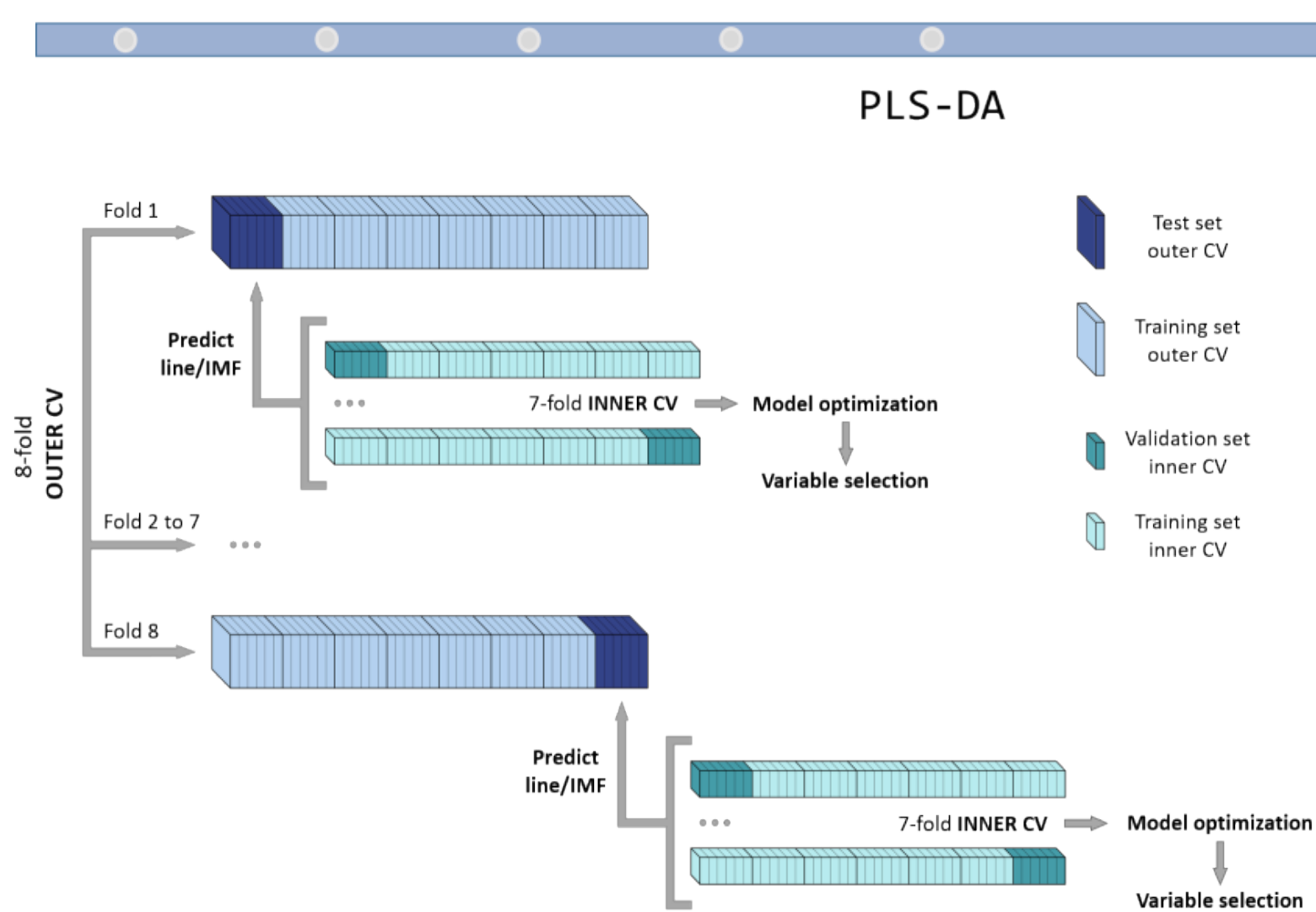
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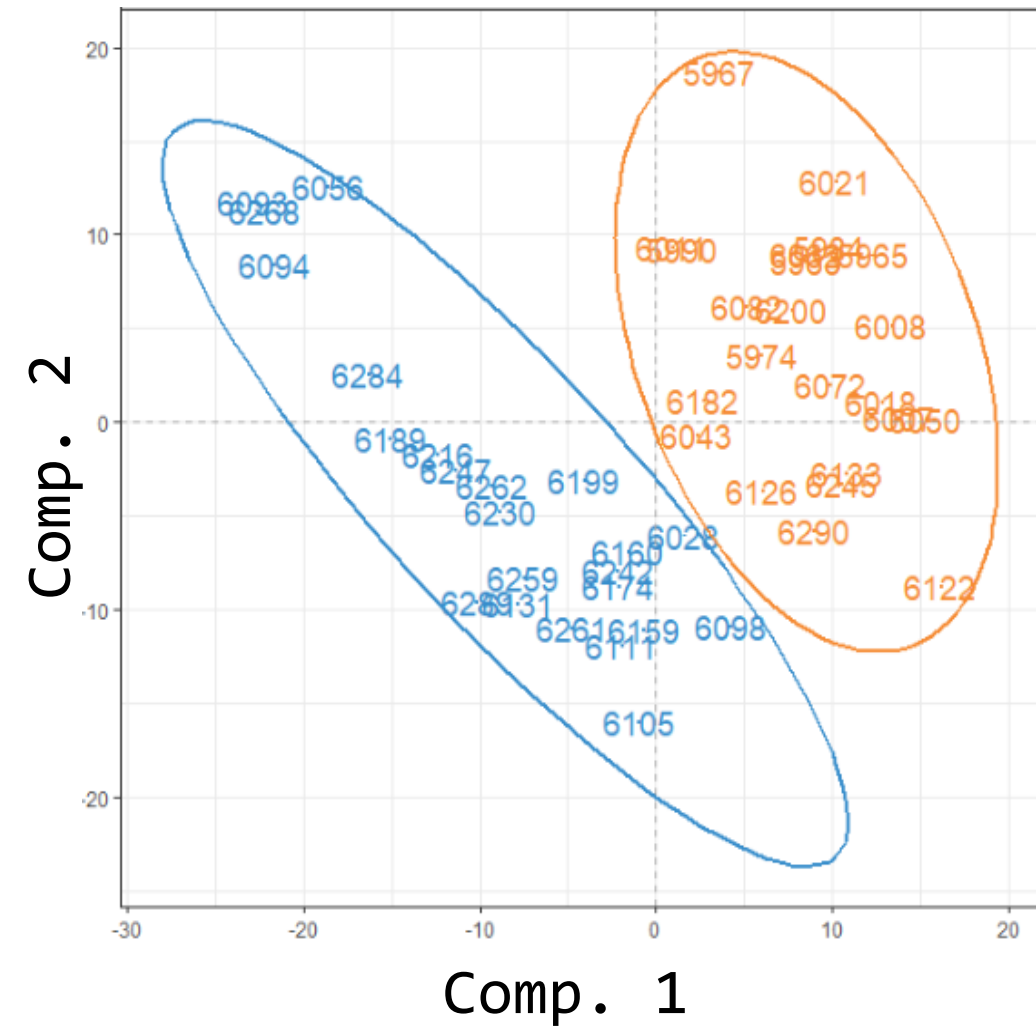
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X20





Adjustment parameters obtained from the predictions of the PLS-DA model during the CMV procedure

Misclassification with true data **Misclassification with permuted data**

	true data		permuted data		
	H	L	H	L	
H	96.7%	3.3%	H	54.8%	45.2%
L	5.4%	94.6%	L	49.2%	50.8%

