

#### UNITED KINGDOM · CHINA · MALAYSIA

# **Dietary and genetic regulation of B12 metabolism in Sheep**

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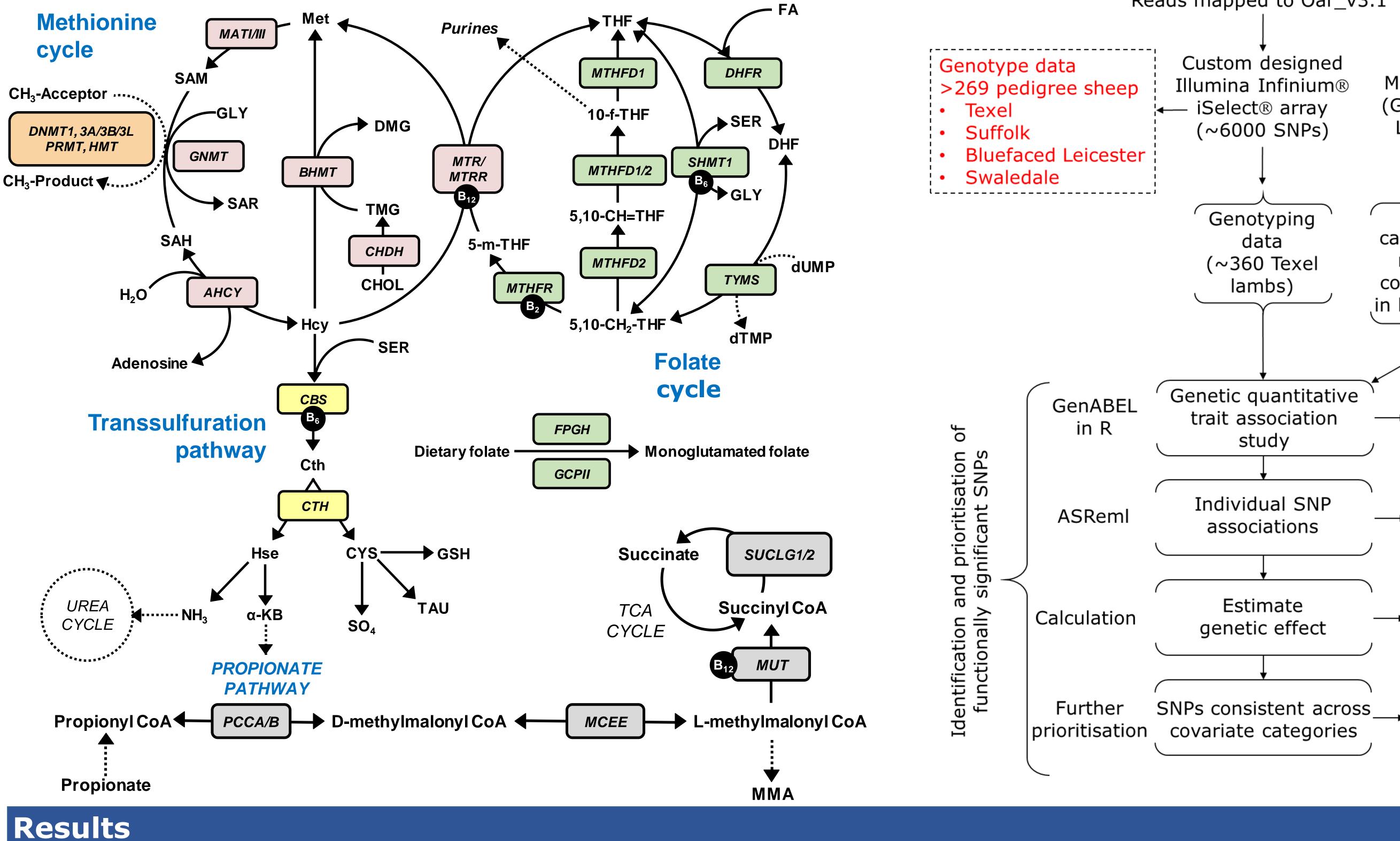




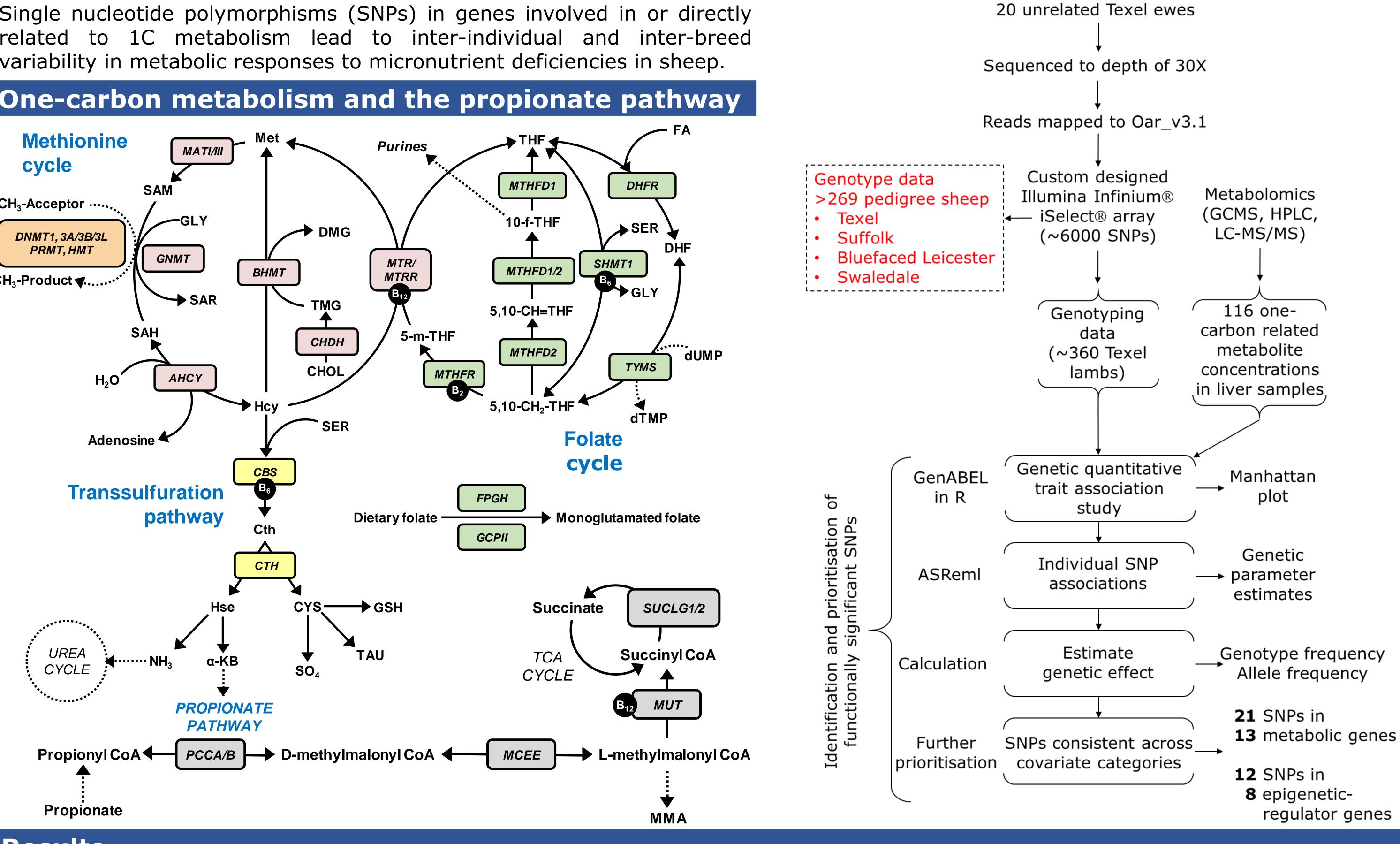
## Hypothesis

Single nucleotide polymorphisms (SNPs) in genes involved in or directly related to 1C metabolism lead to inter-individual and inter-breed variability in metabolic responses to micronutrient deficiencies in sheep.

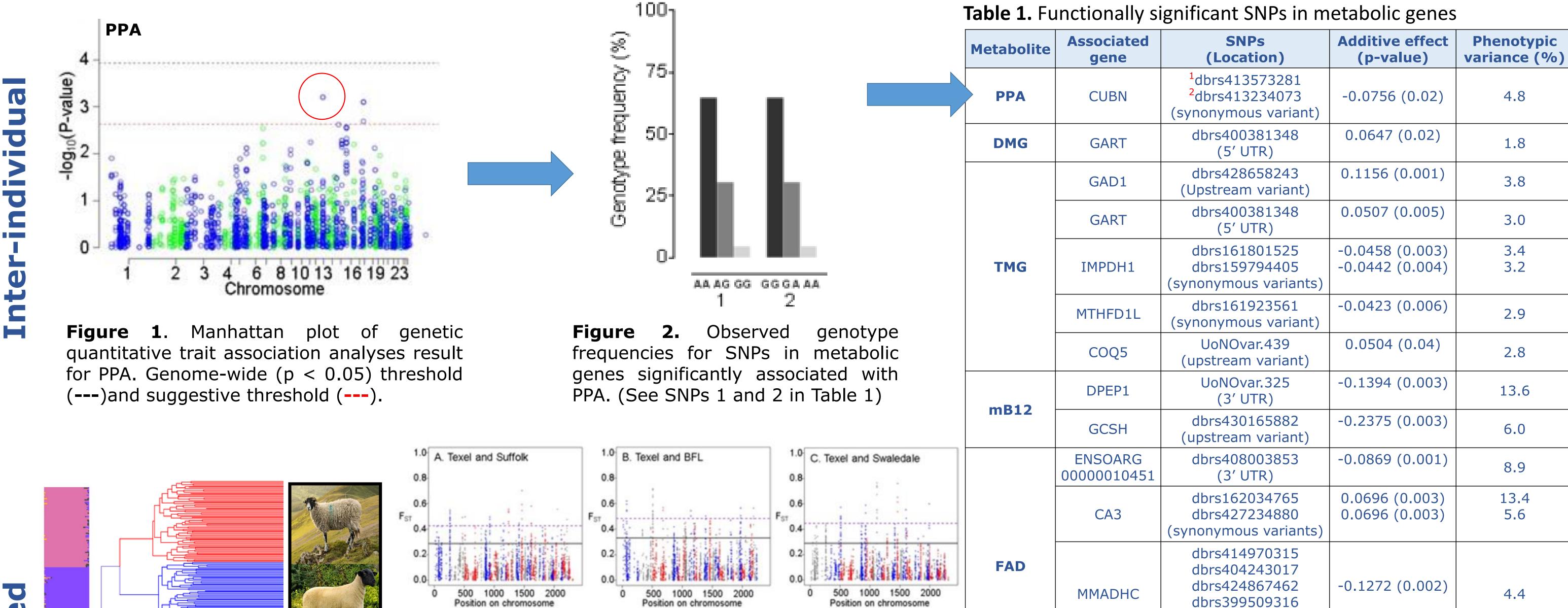
## **One-carbon metabolism and the propionate pathway**



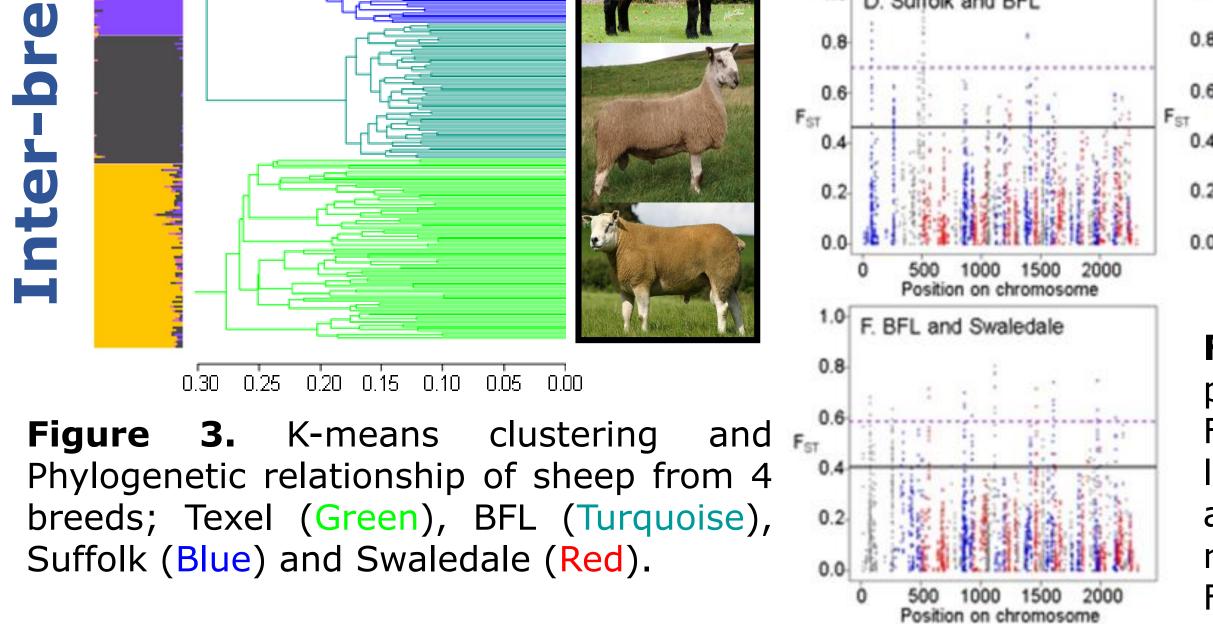
#### Methods



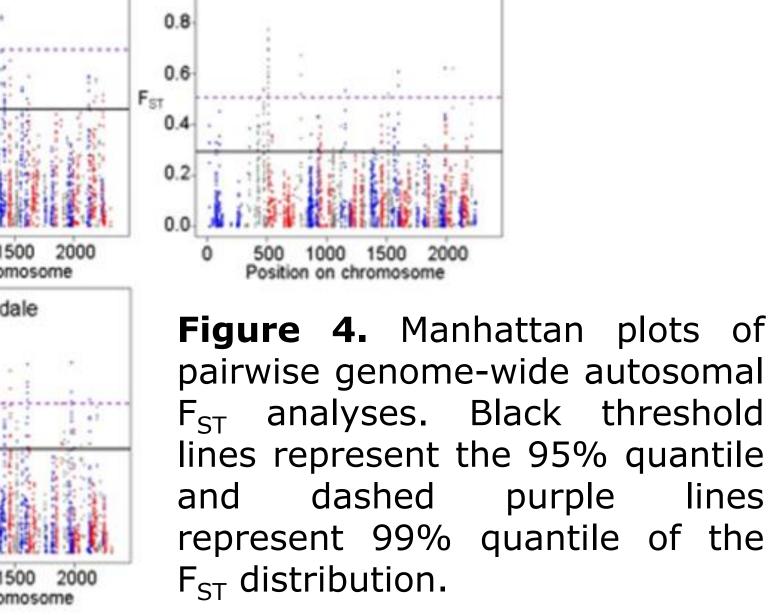
**Table 1.** Functionally significant SNPs in metabolic genes



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1.0 D. Suffolk and BFL



1.0 E. Suffolk and Swaledale

		(upstream variants)		
	NOX4	UoNOvar.764 (upstream variant)	-0.0600 (0.003)	4.4
PL	ENSOARG 00000010451	dbrs408003853 (3' UTR)	-0.0575 (0.01)	2.9

dbrs404706479

## **Key Findings**

#### •33 significant SNPs

• **CUBN** associated with **PPA** concentrations = biologically significant • encodes the protein cubilin, a multi-ligand hydrophobic protein which binds to intrinsic factor-cobalamin (Cbl-IF) complexes with high affinity facilitating **B12 uptake** 

• Swaledales more different from other breeds • Genetic adaptation to natural environment?

#### Summary

Inter-individual and inter-breed variation in 1C metabolism and related pathways results from SNPs in 1C regulatory genes. They therefore support and promote the importance of early identification of susceptible animals to enable effective management of B12 deficiency through targeted supplementation and selection of genetic tolerance in breeding programmes.