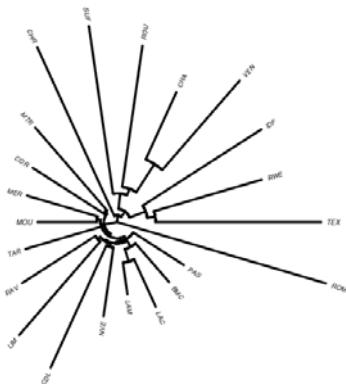


Supporting information: FLK results by region: SNP frequencies, local trees and haplotype cluster frequencies

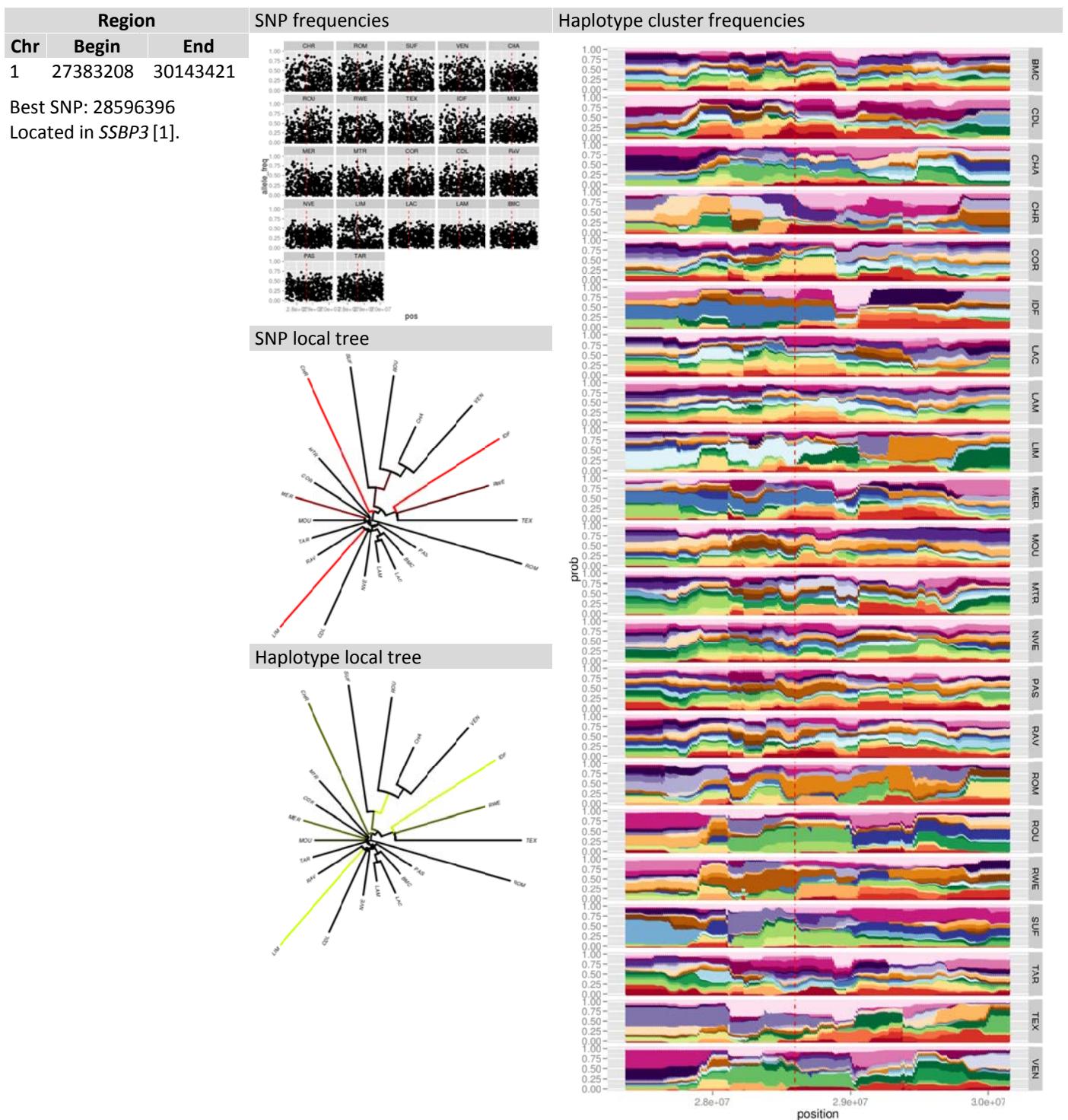
Breeds:

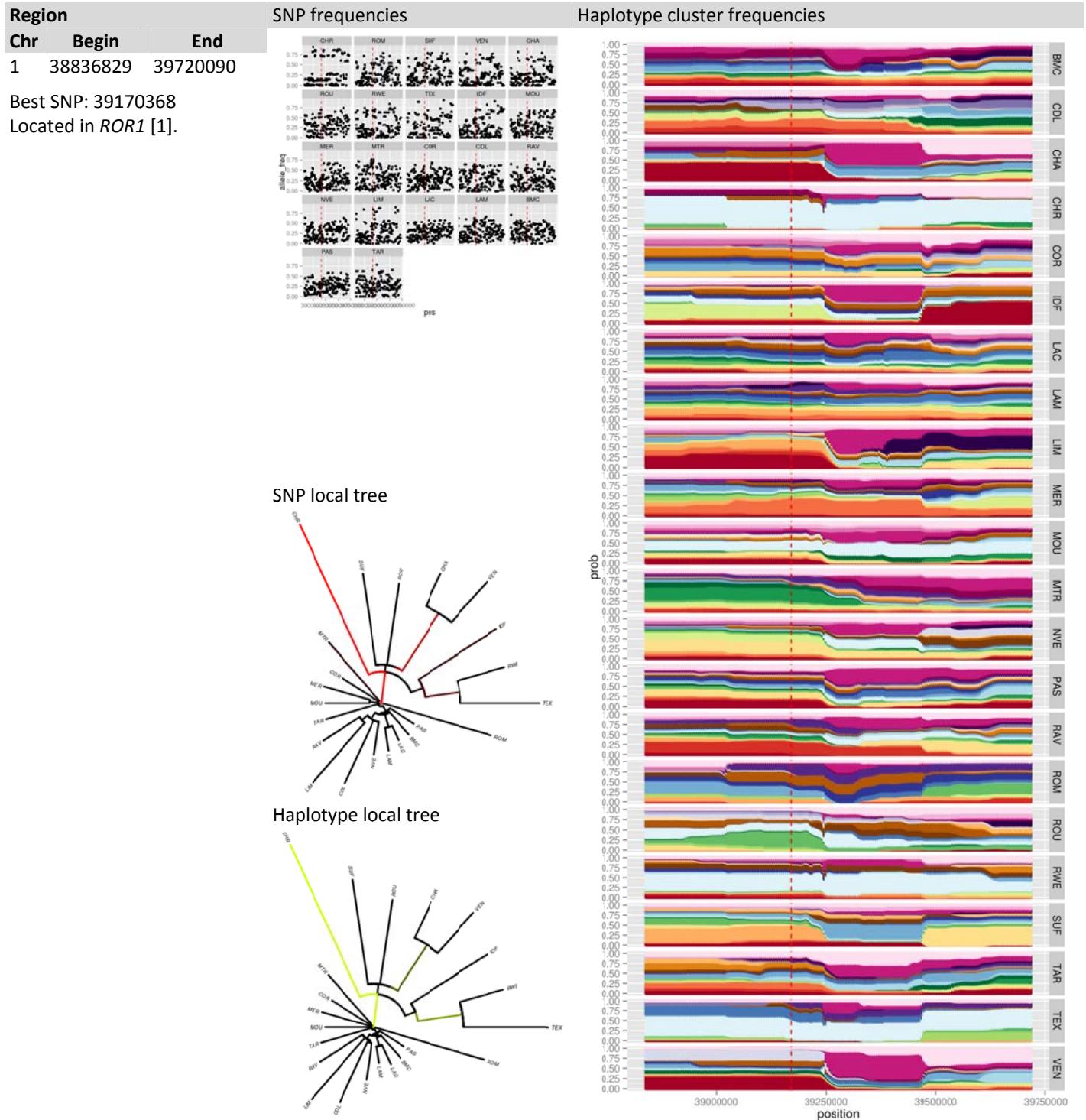
Breed	Abbreviation
Berrichon du Cher	BER
Blanche du Massif Central	BMC
Causse du Lot	CDL
Charollais	CHA
Charmoise	CHR
Corse	COR
European Mouflon	EUR
Île de France	IDF
Asian Mouflon	IRN
Lacaune (dairy)	LAC
Lacaune (meat)	LAM
Limousine	LIM
Mérinos d'Arles	MER
Mourerous	MOU
Manech tête rousse	MTR
Noire du Velay	NVE
Ouessant	OUE
Préalpes du Sud	PAS
Mérinos de Rambouillet	RAM
Rava	RAV
Romane / INRA 401	RMN
Romanov	ROM
Roussin de la Hague	ROU
Rouge de l'Ouest	RWE
Suffolk	SUF
Tarasconnaise	TAR
Texel	TEX
Vendéen	VEN

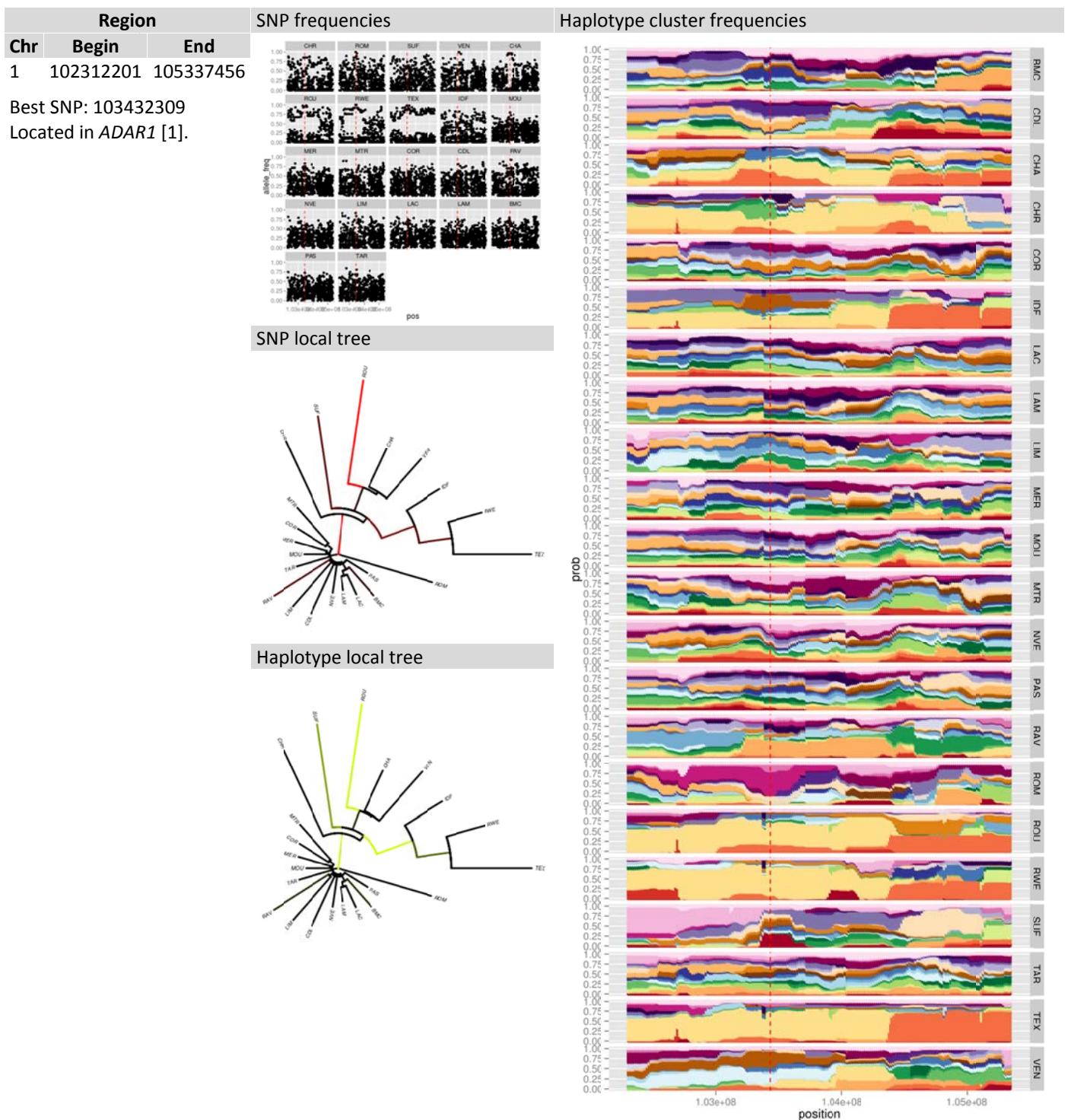
Population tree estimated from all SNPs

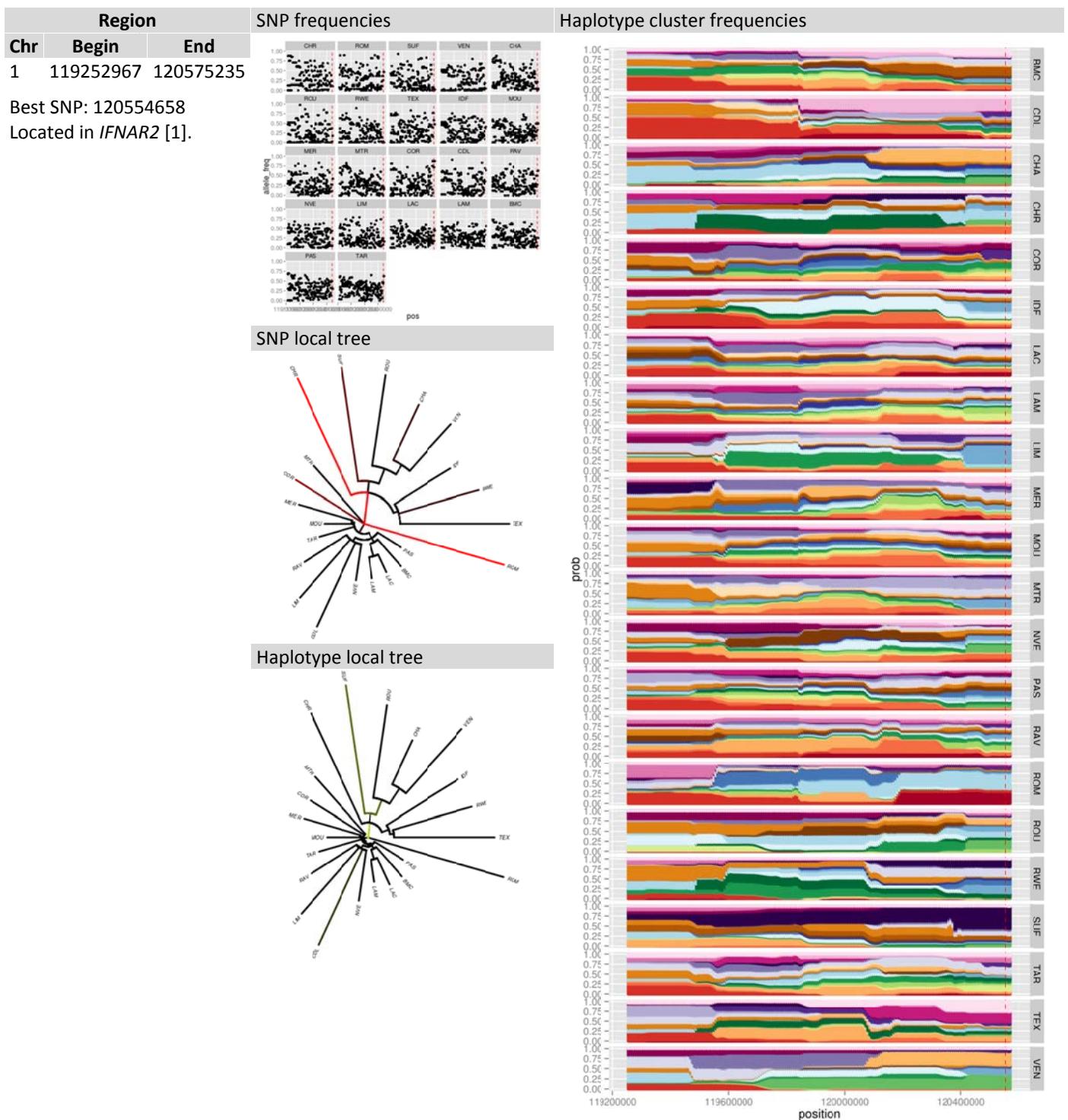


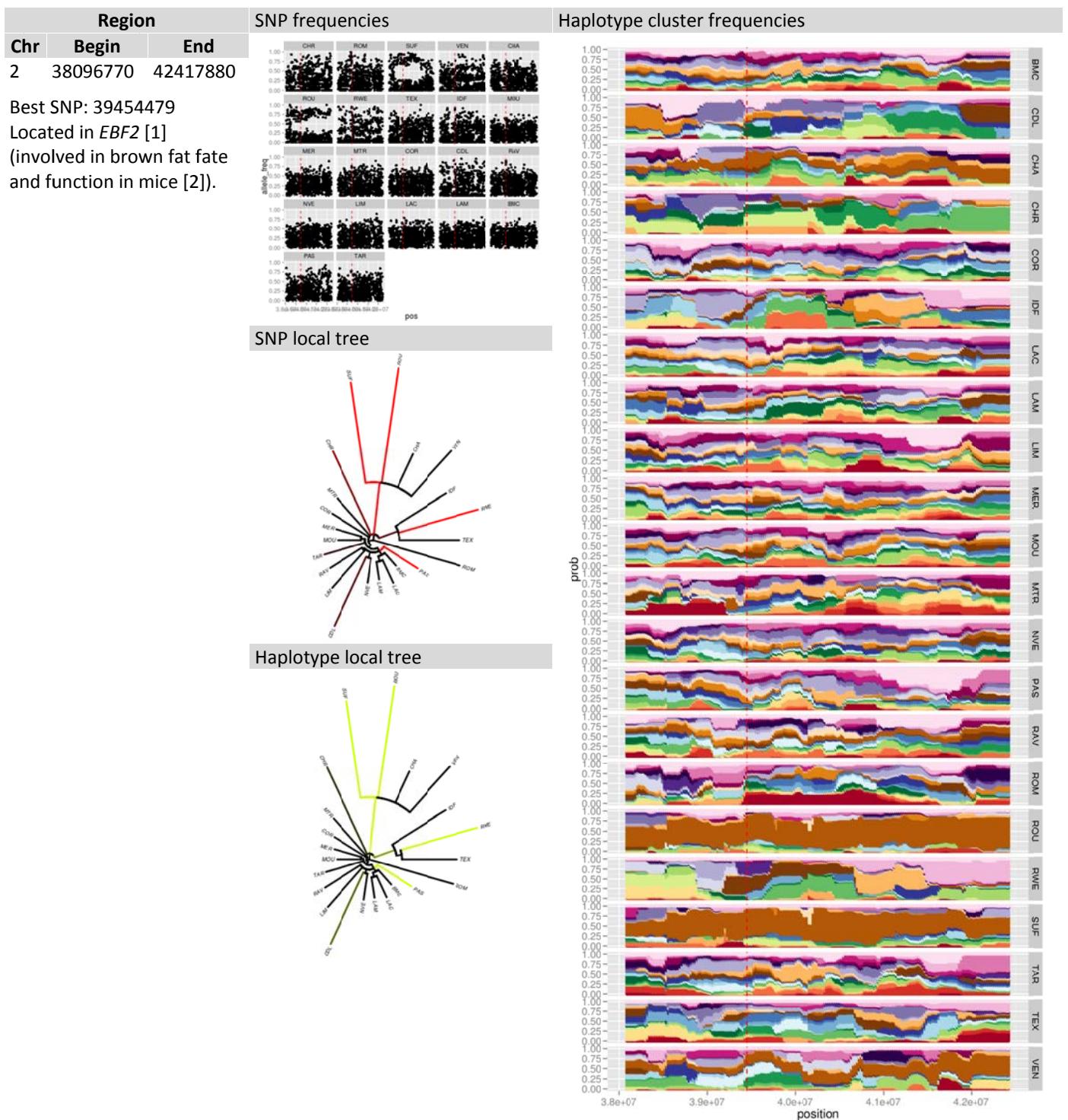
*In SNP frequency and haplotype cluster frequency plots the red dotted line is the SNP with the smallest p value and the two black lines are the beginning and end of candidate genes.

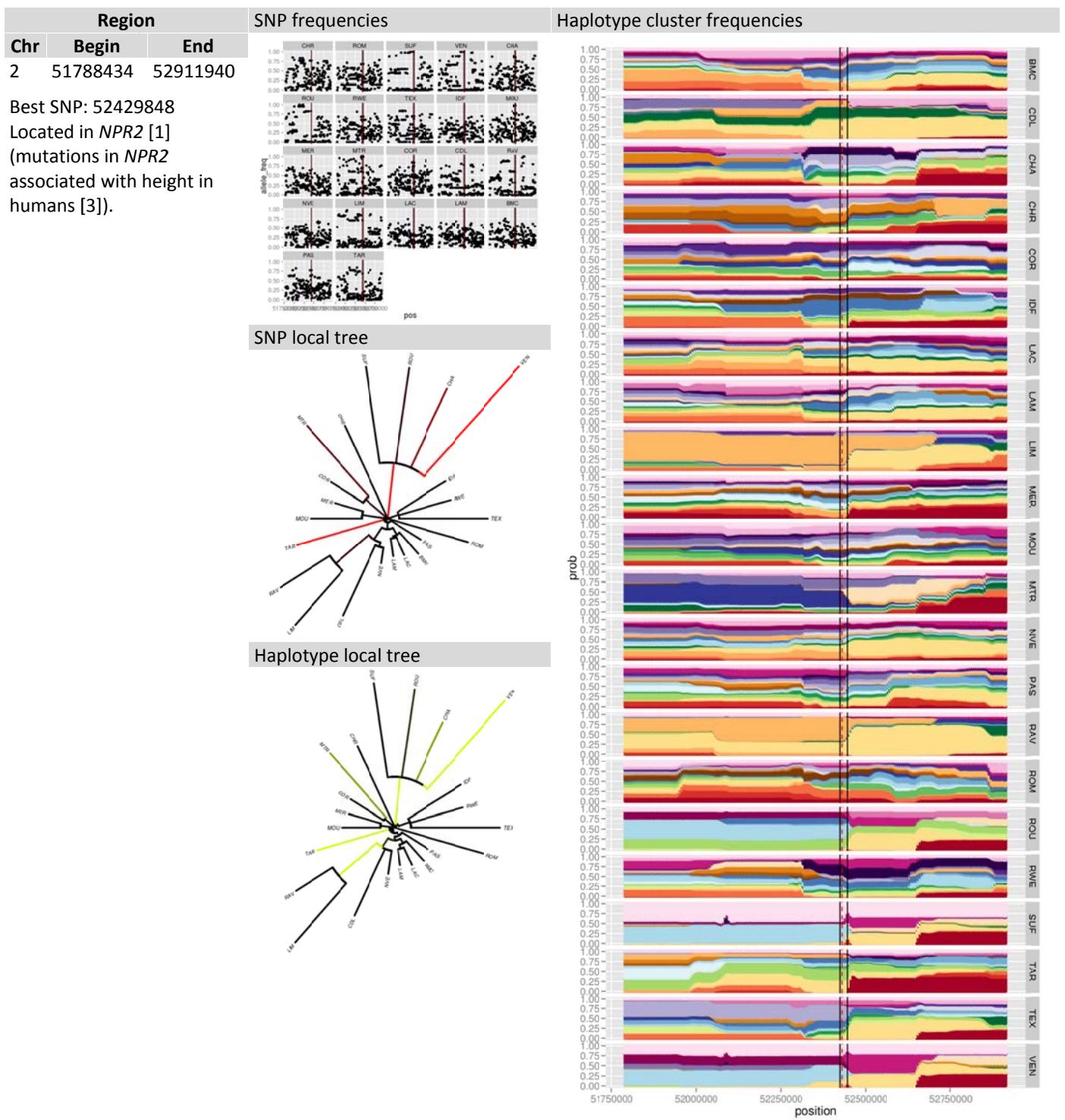


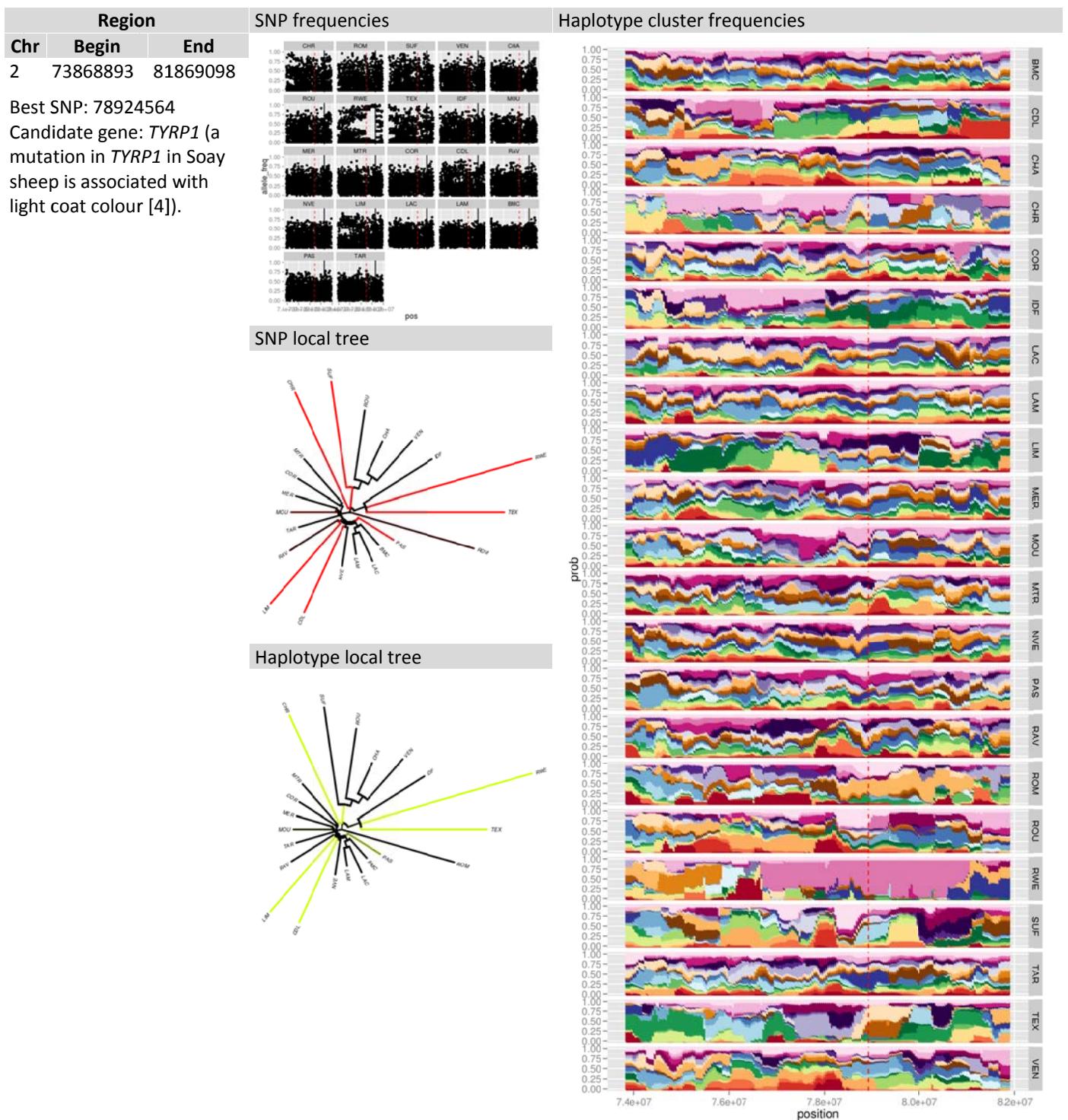


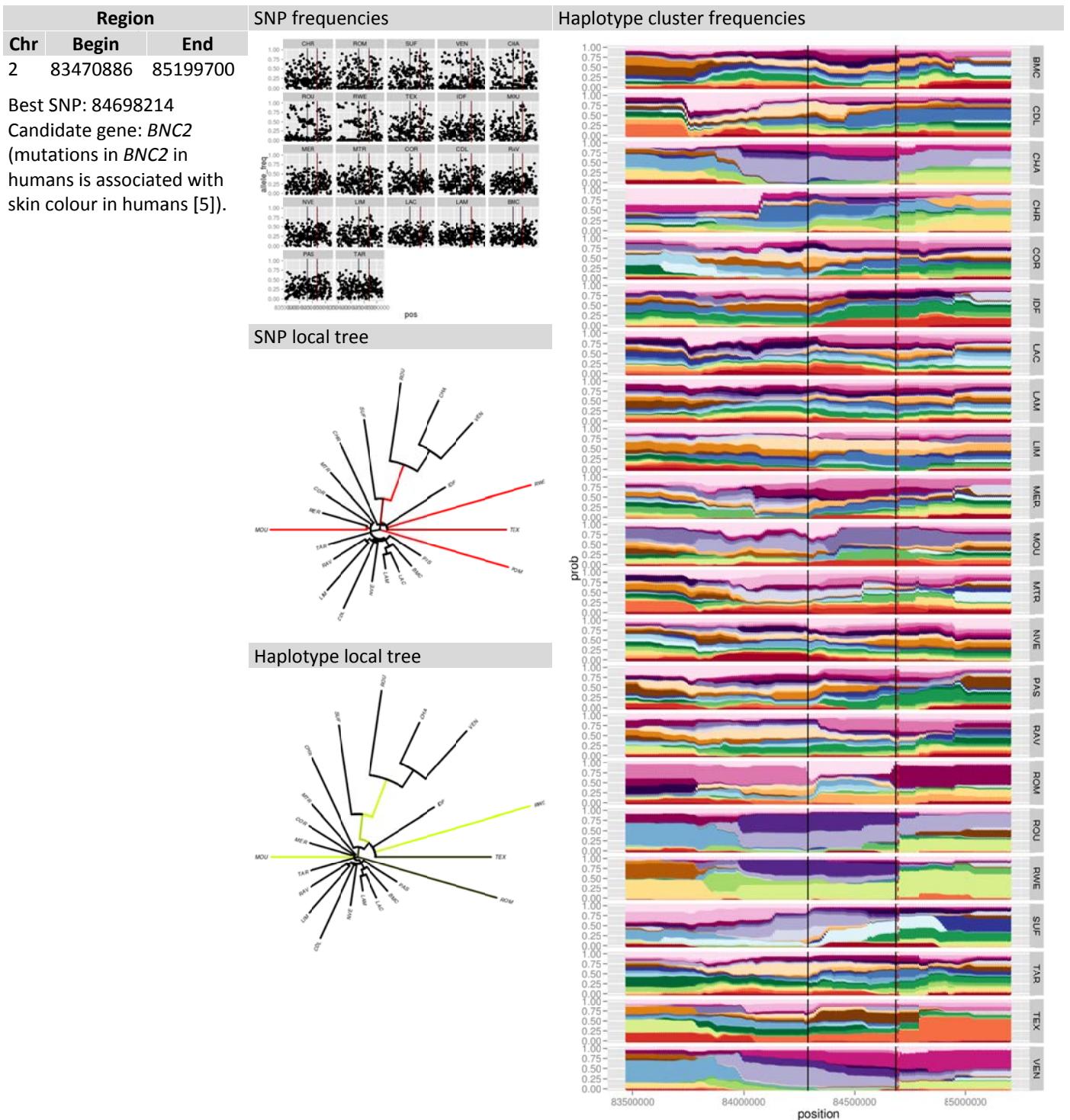


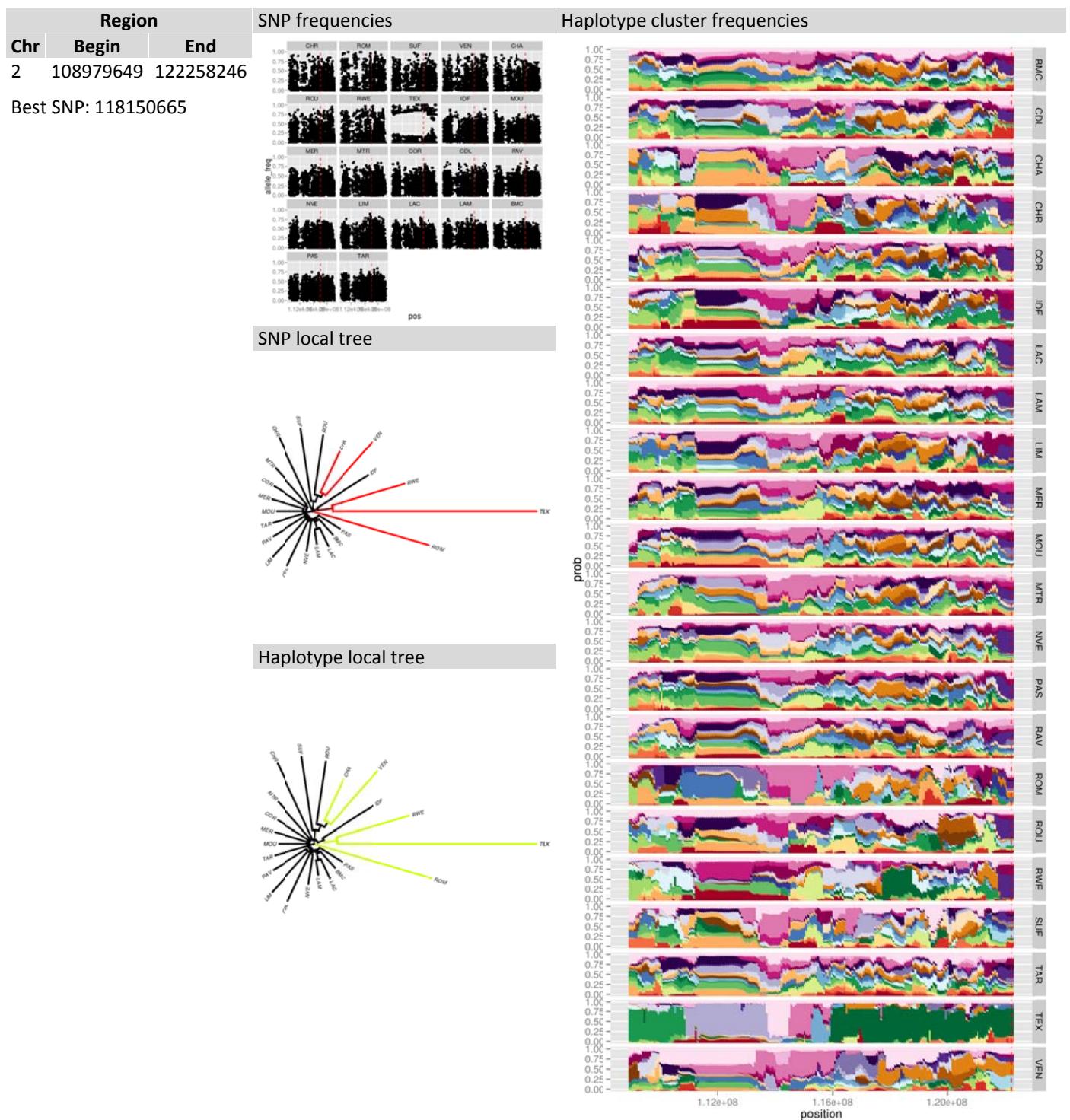


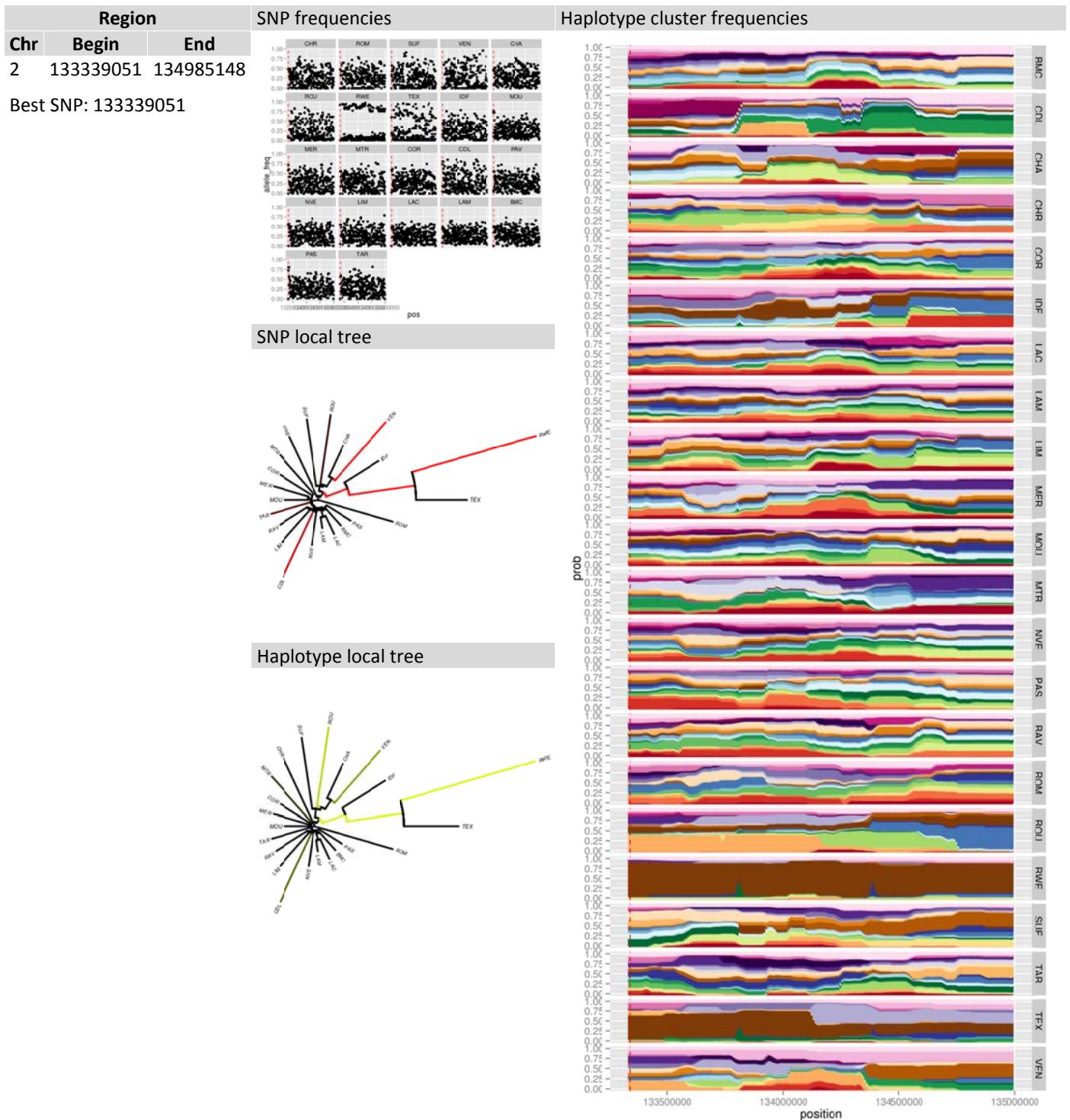


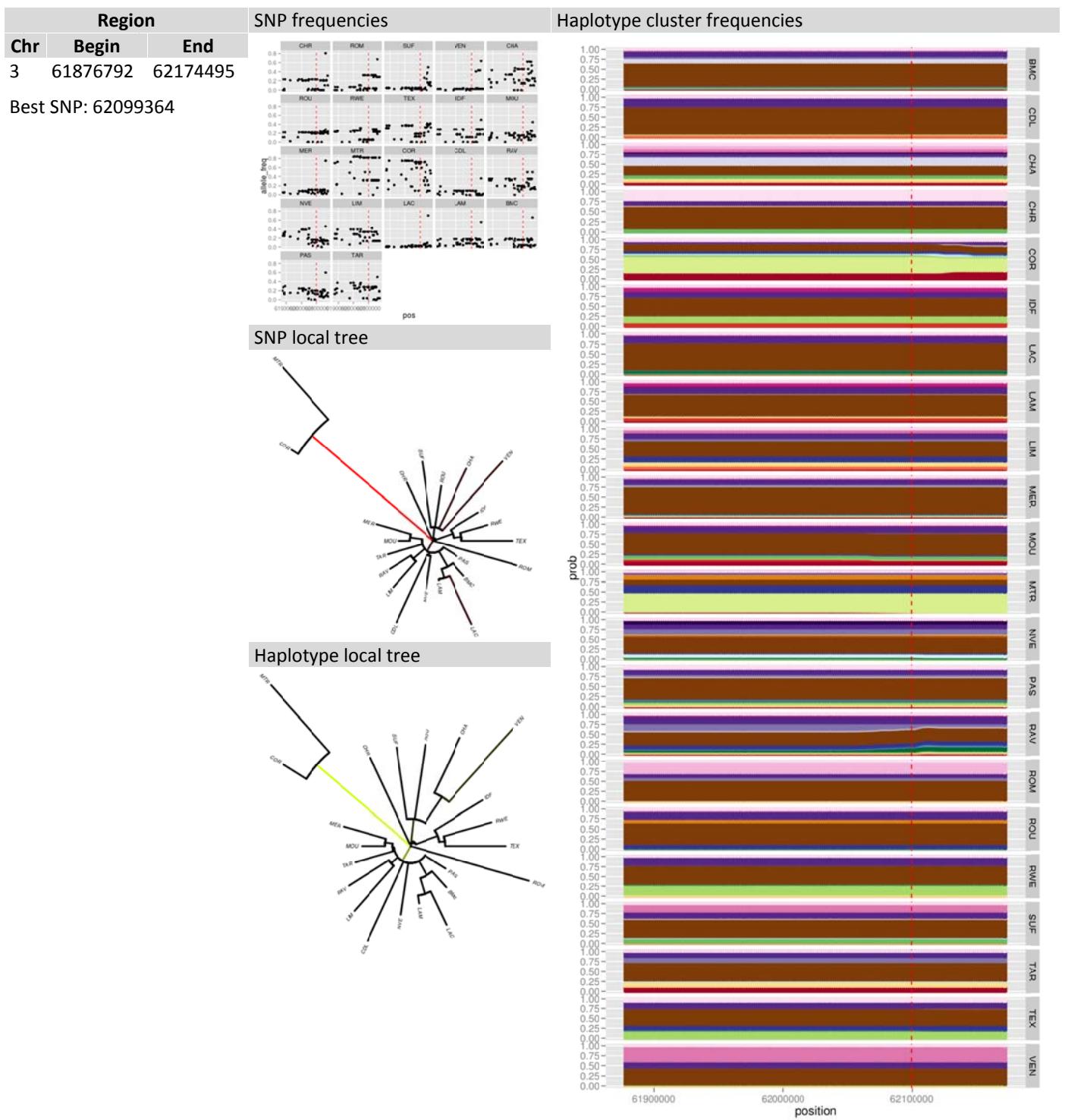


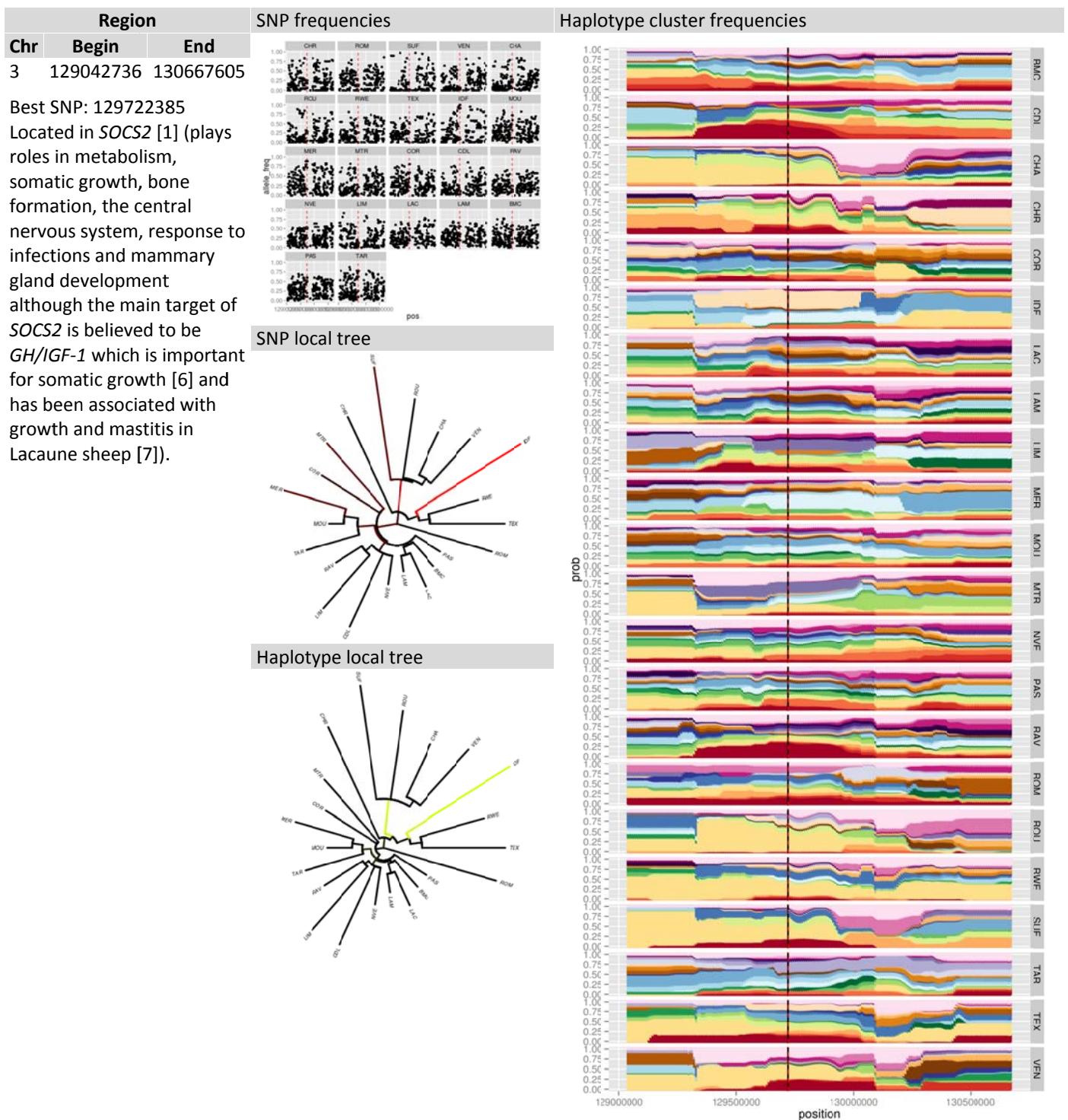


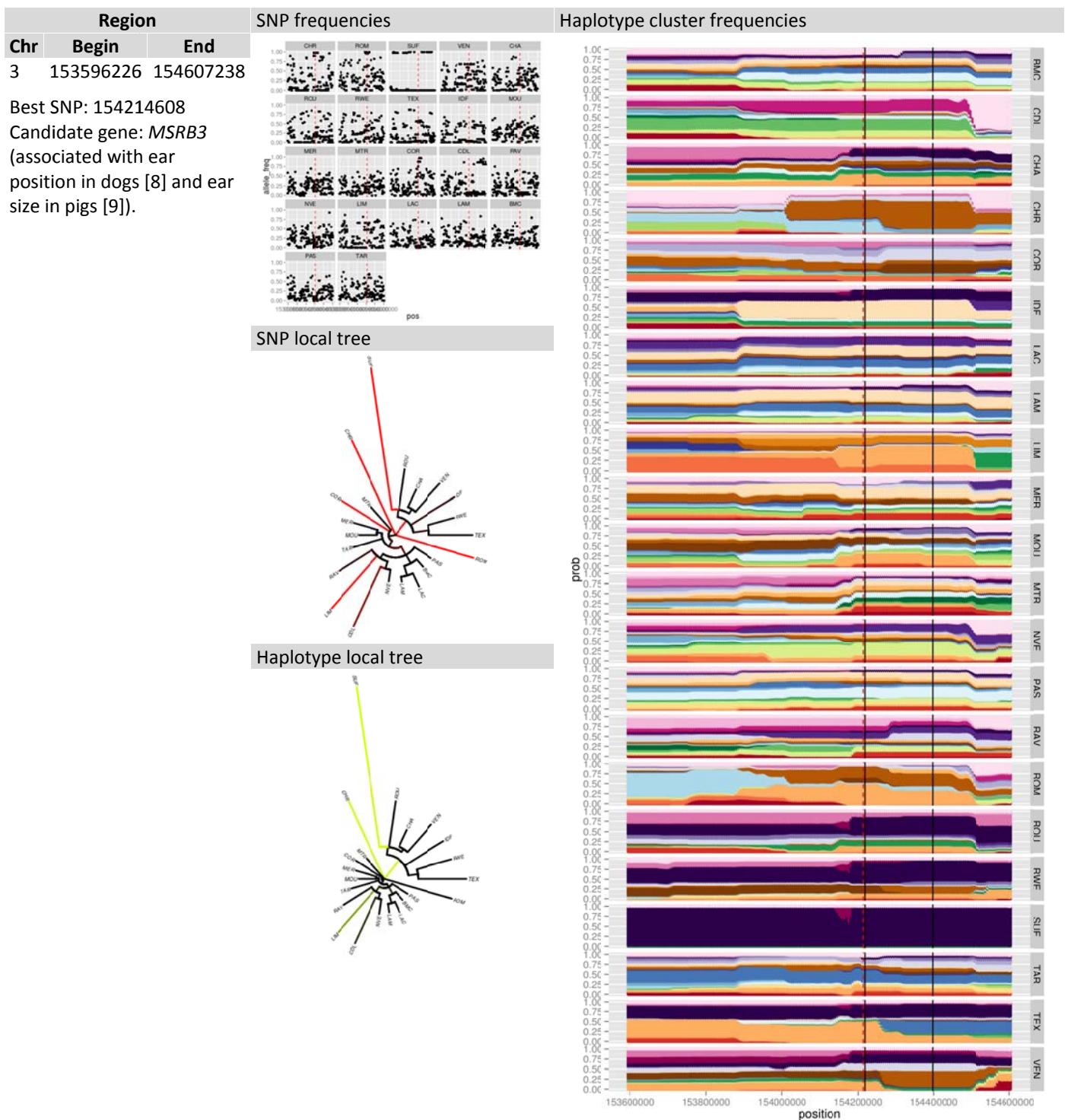


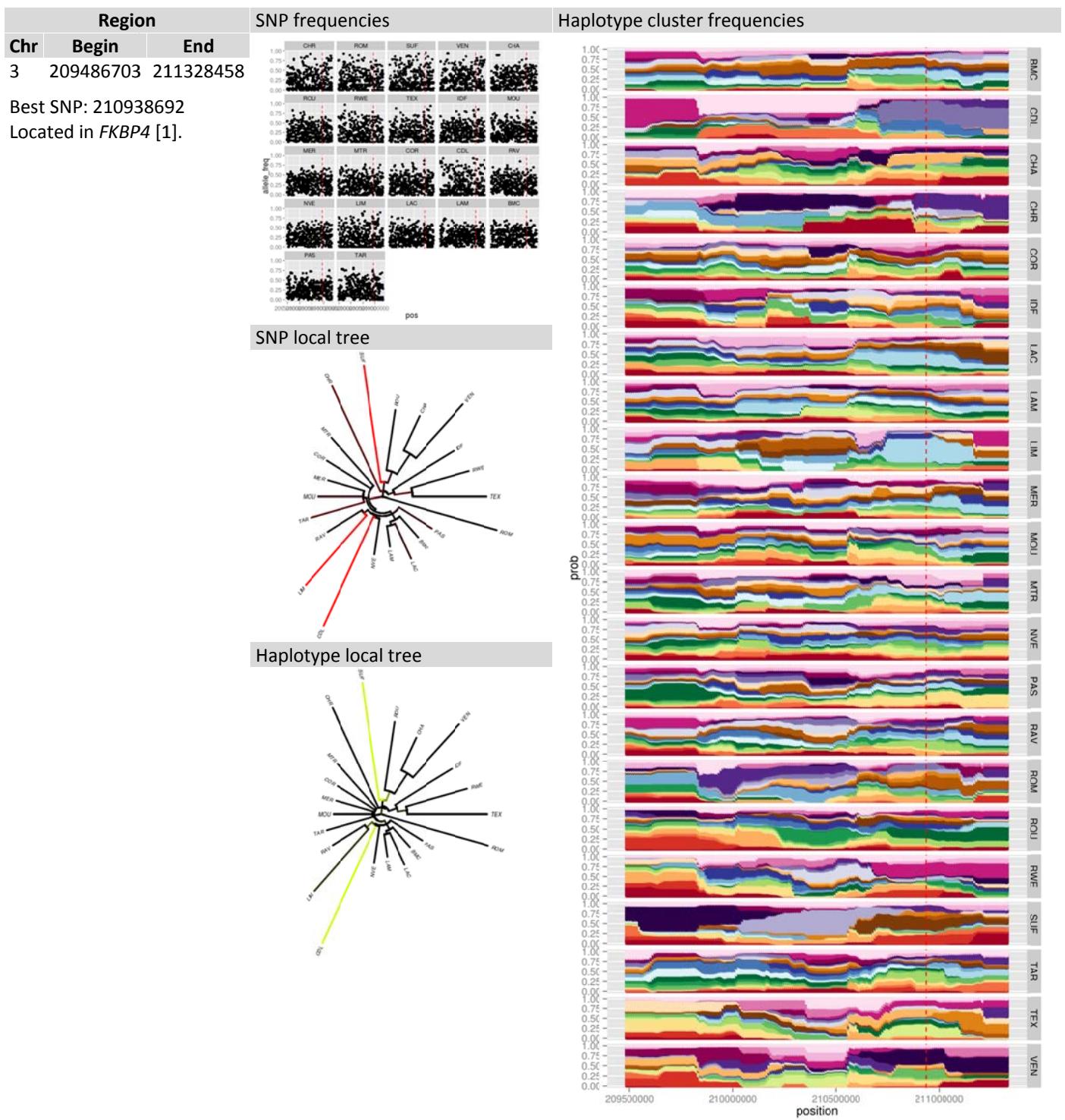


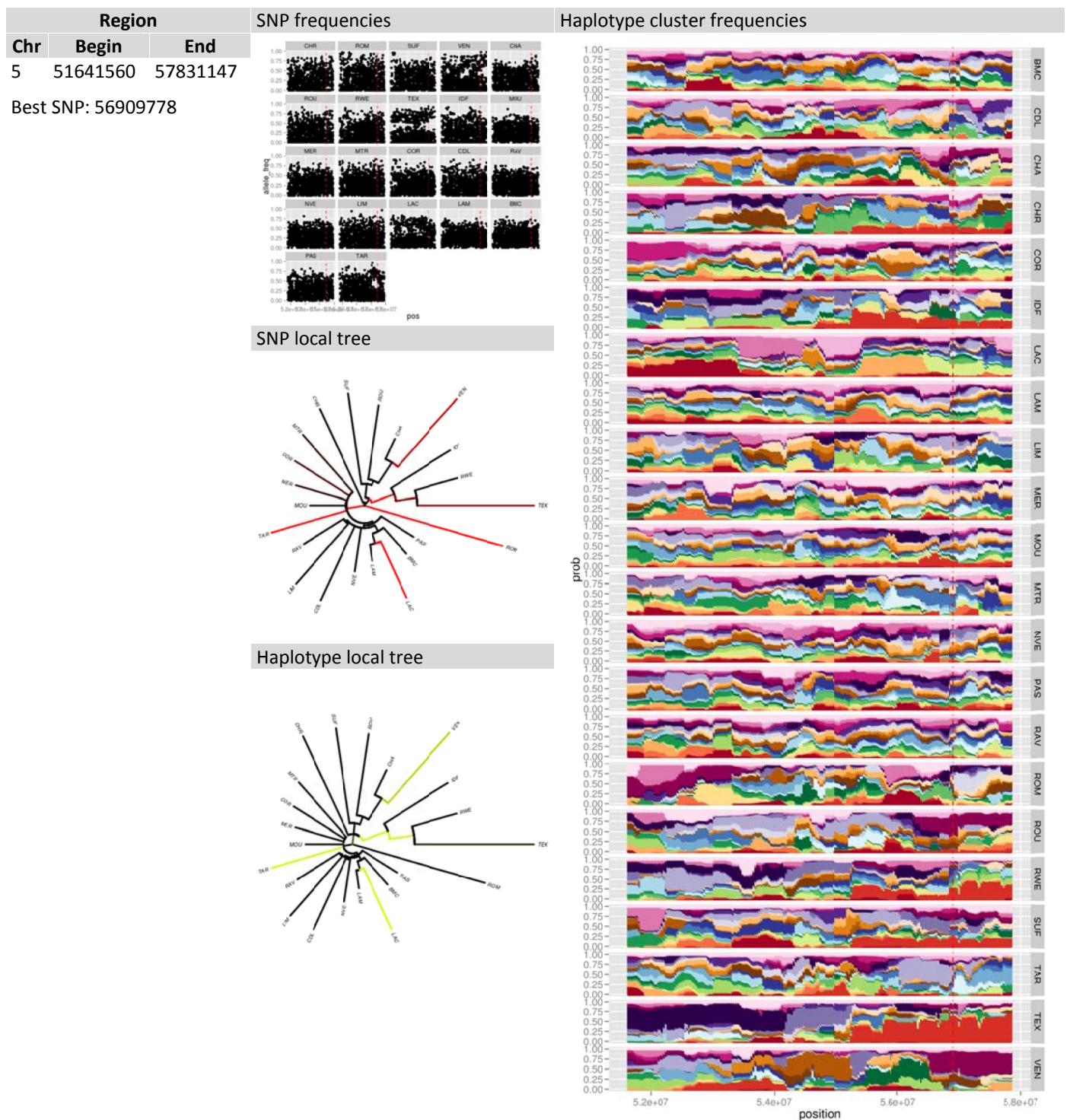


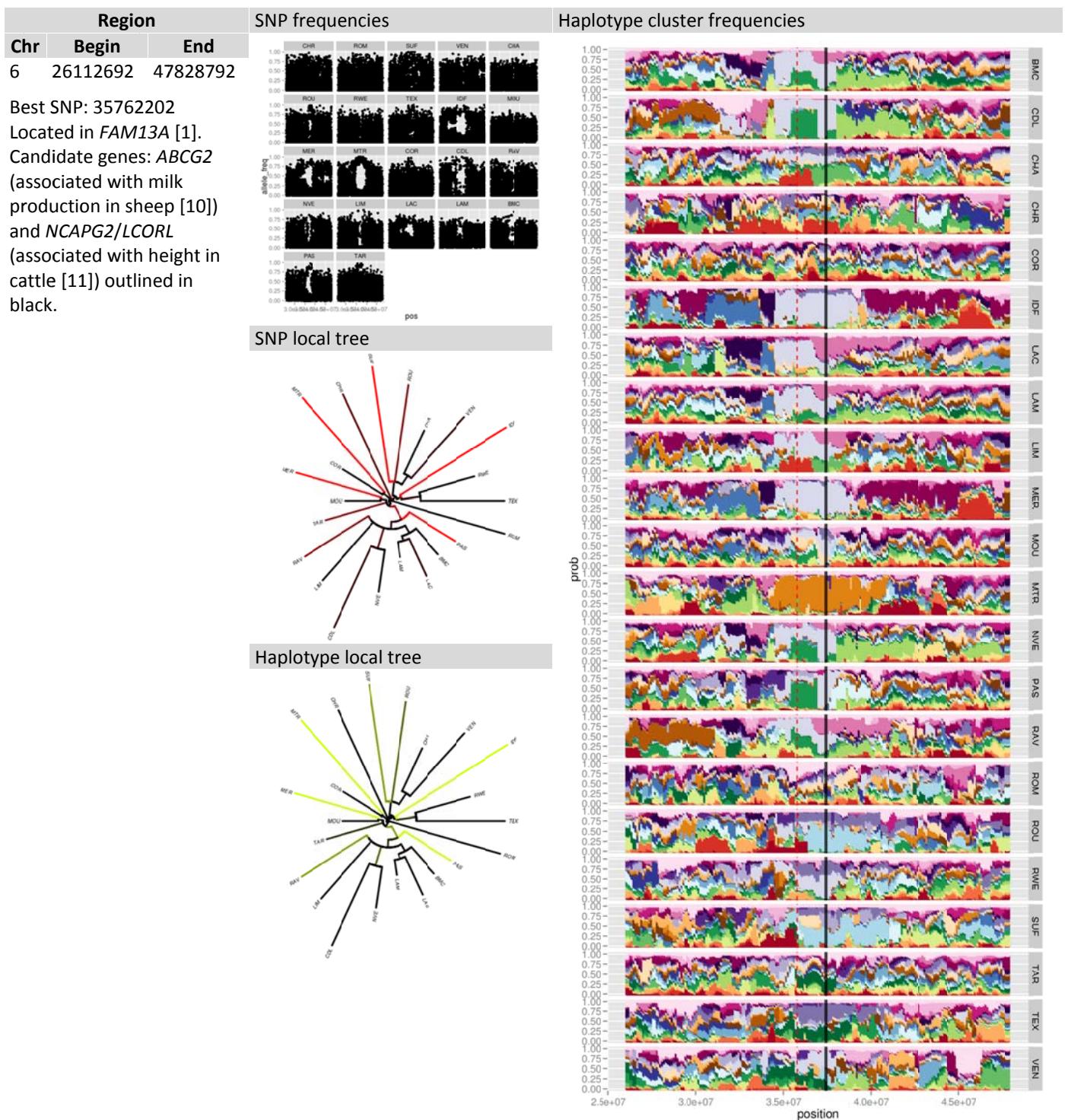


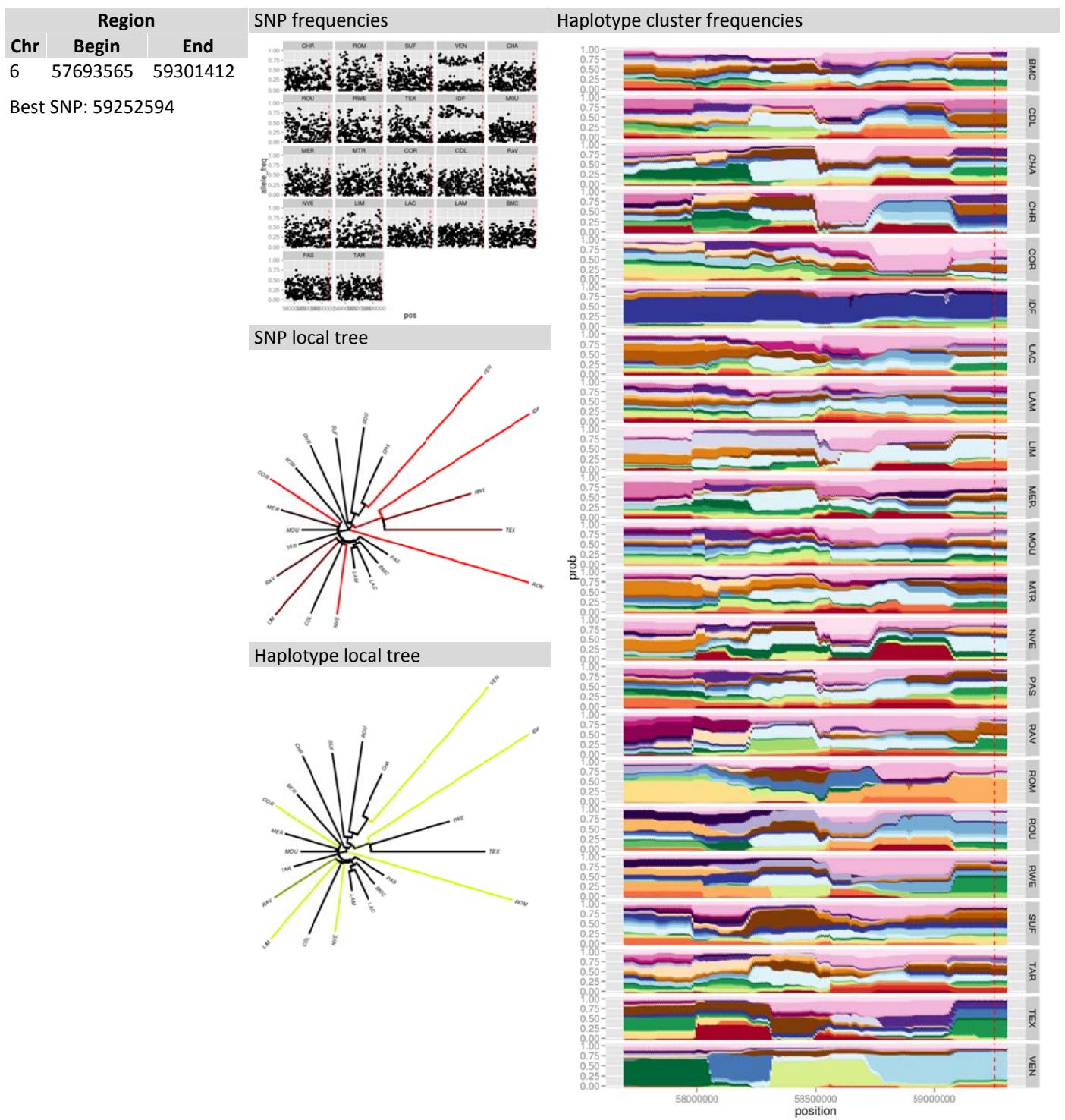


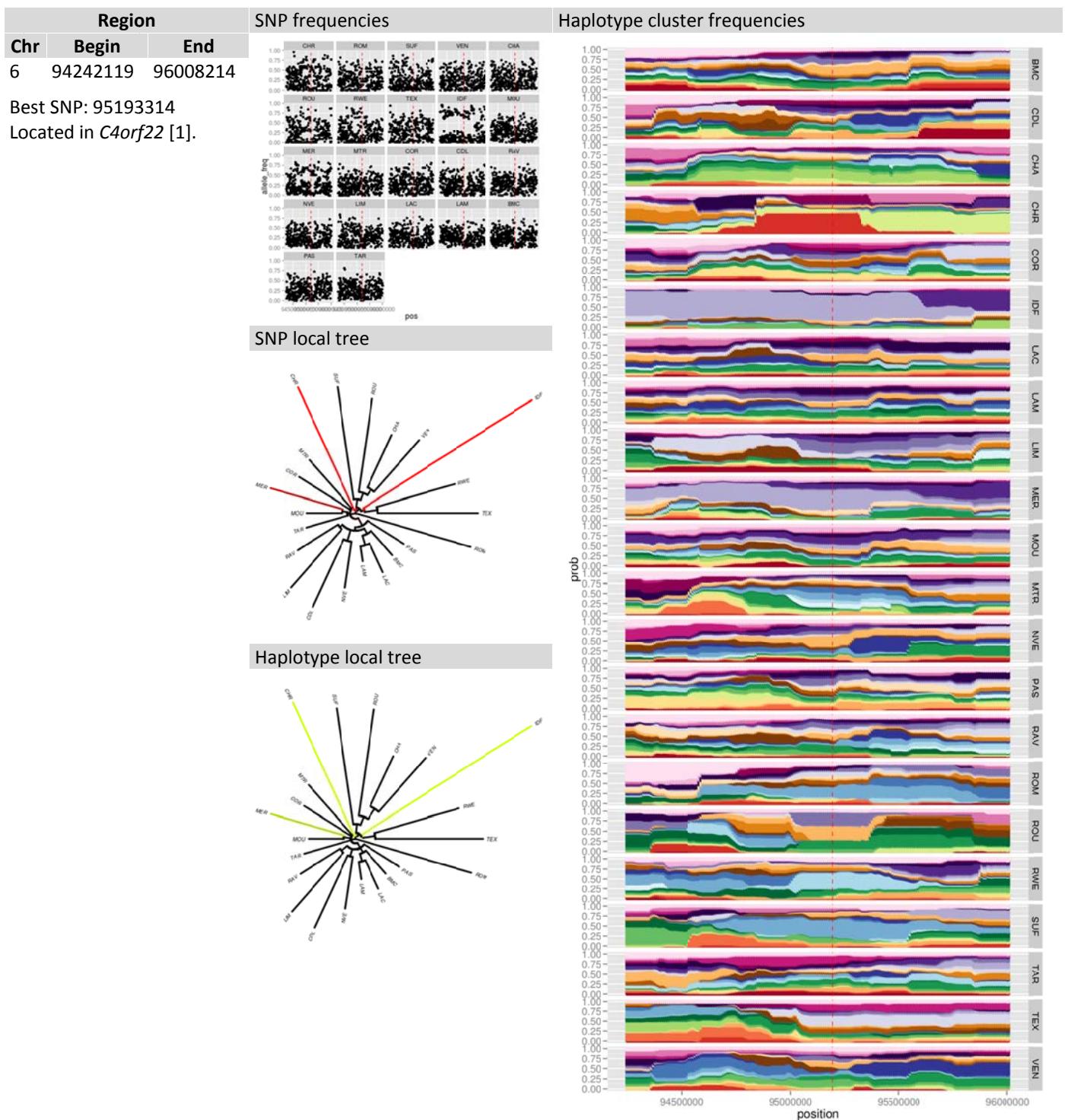


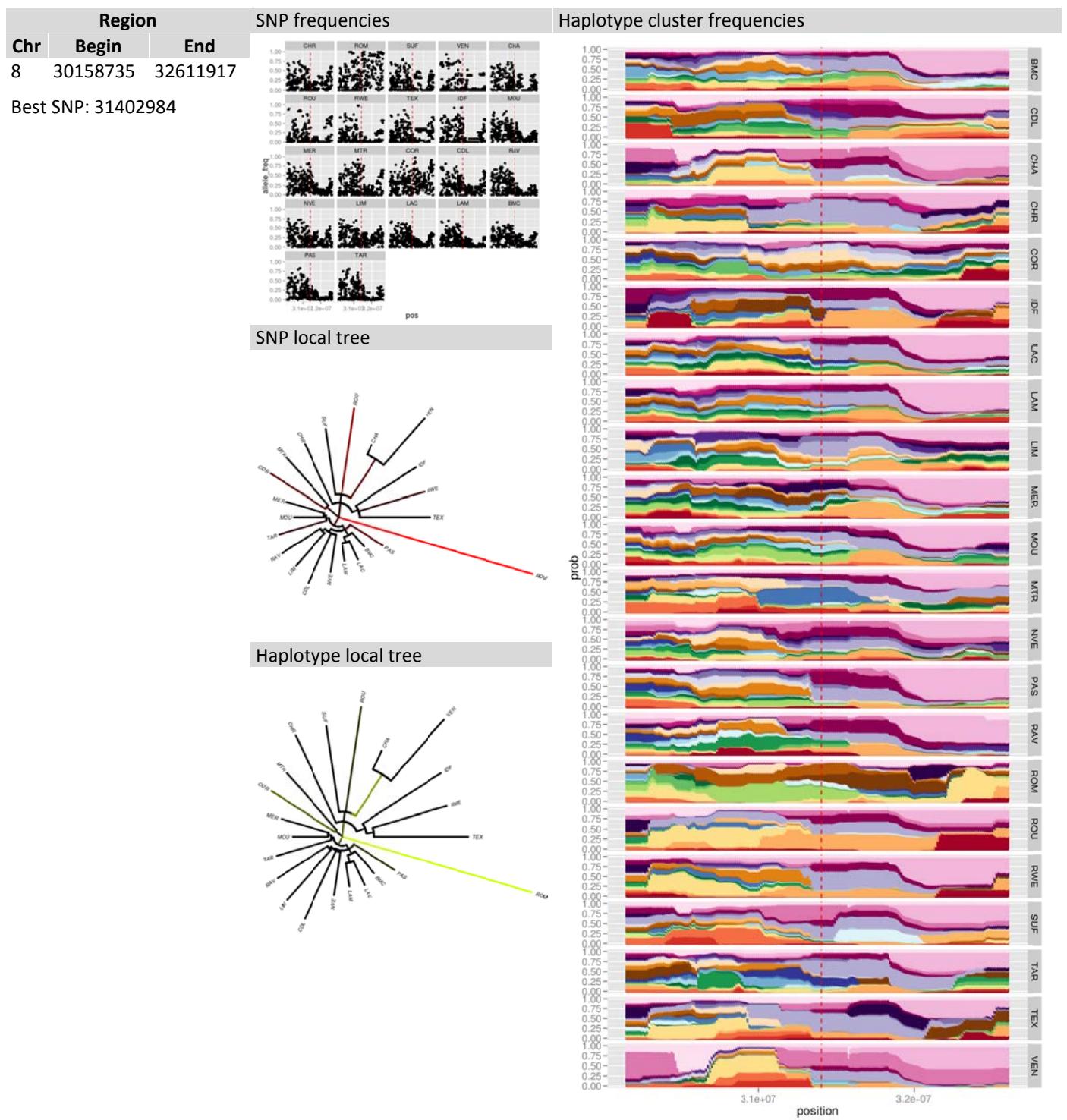


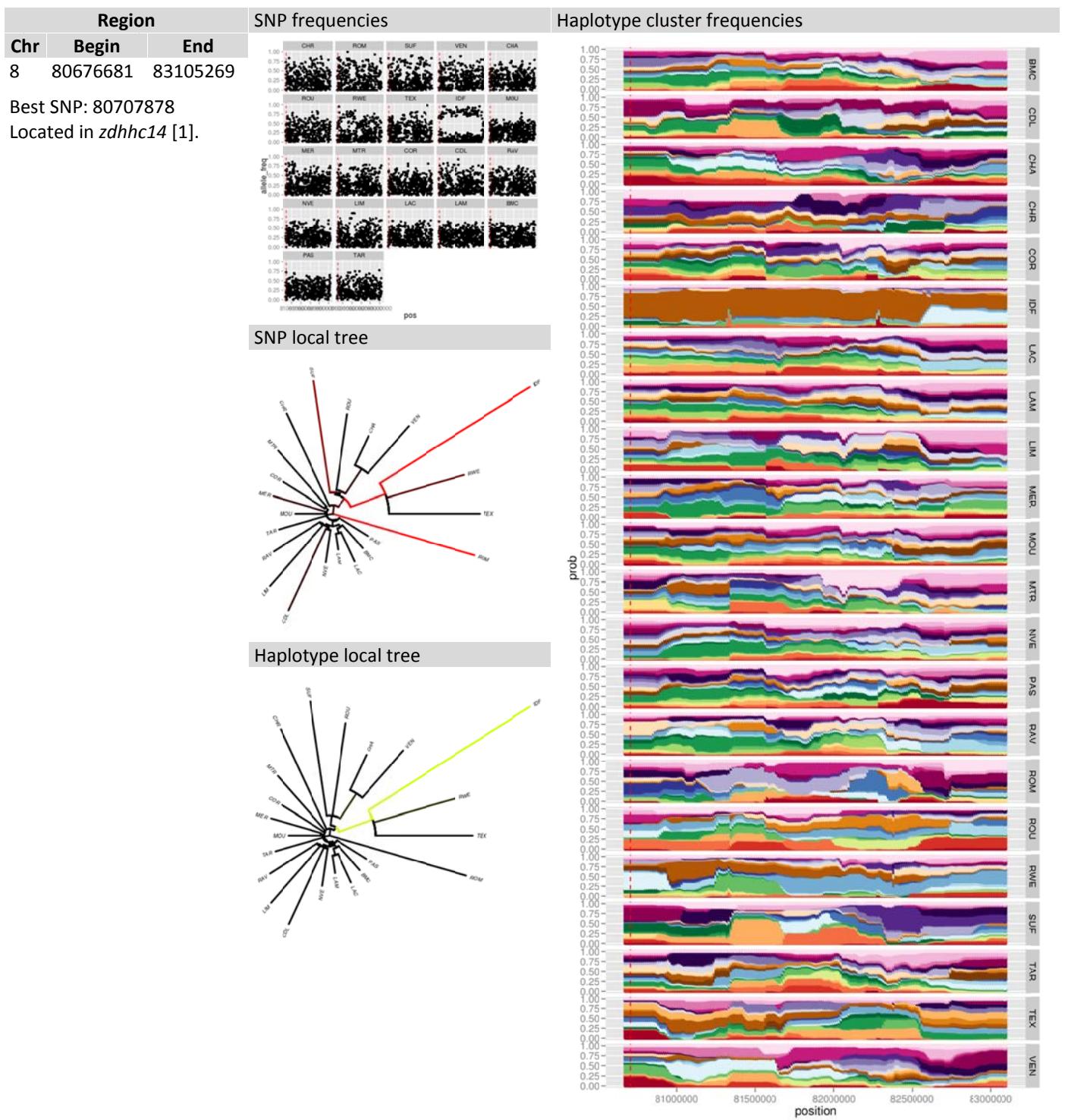


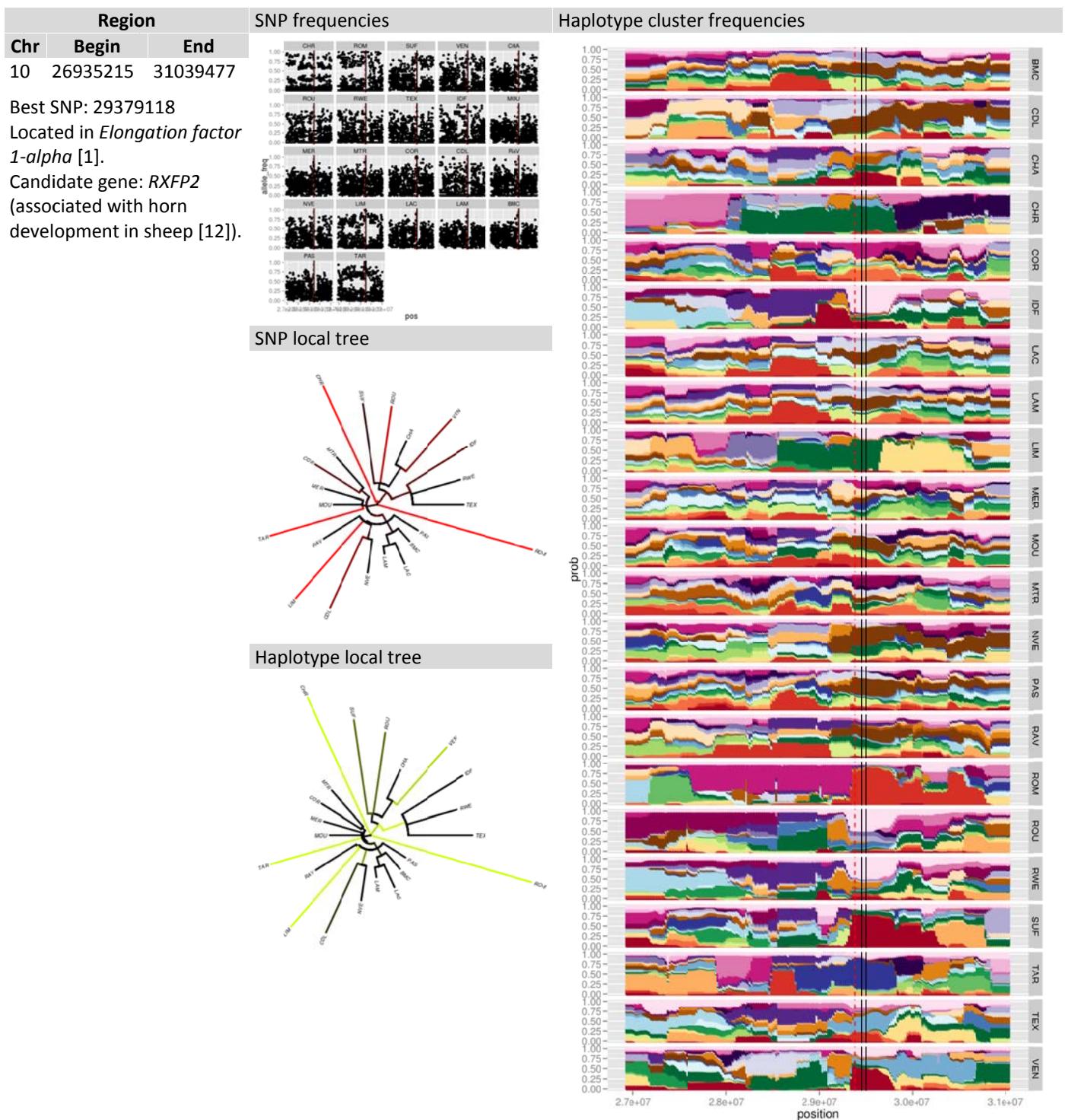


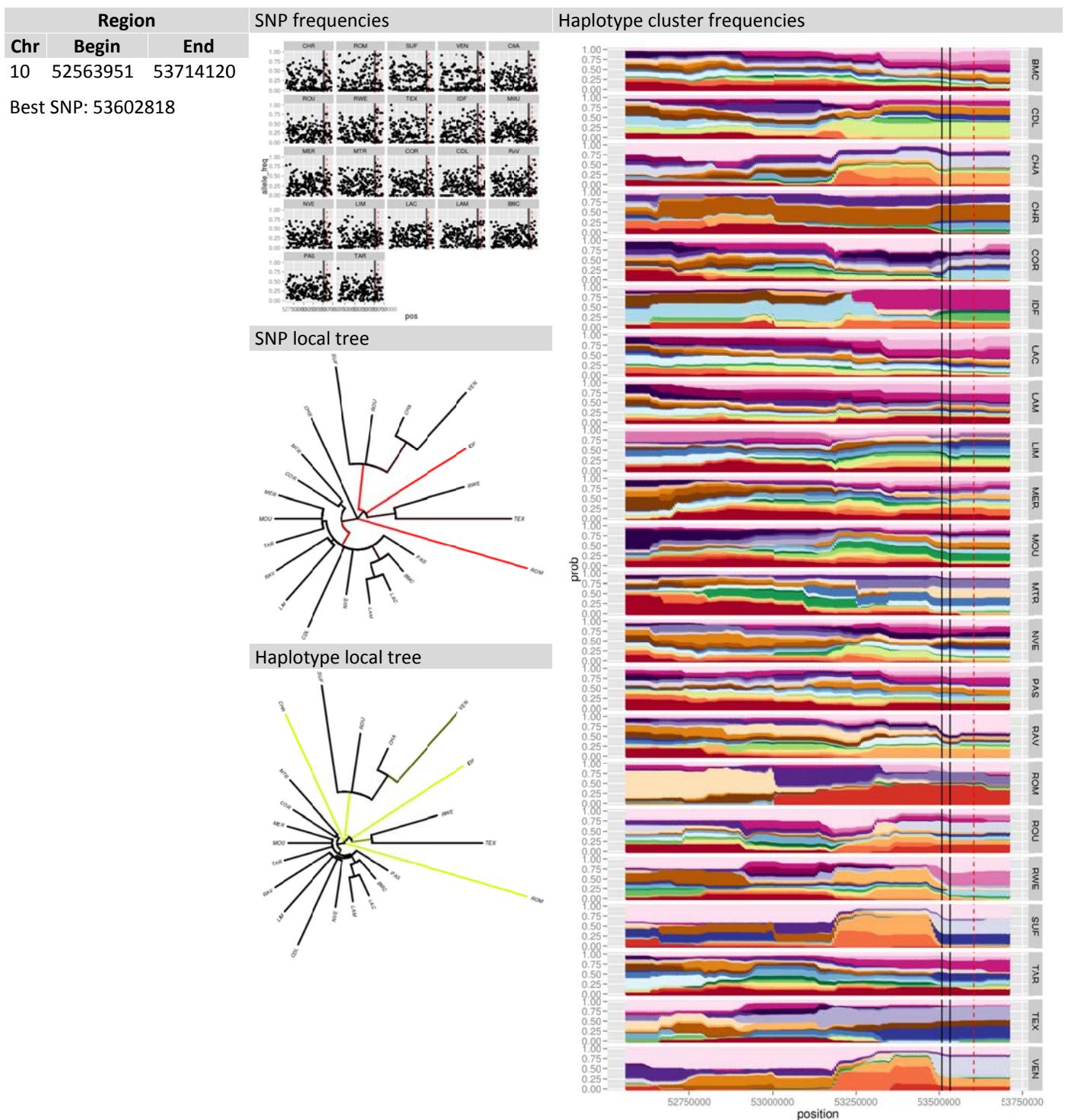


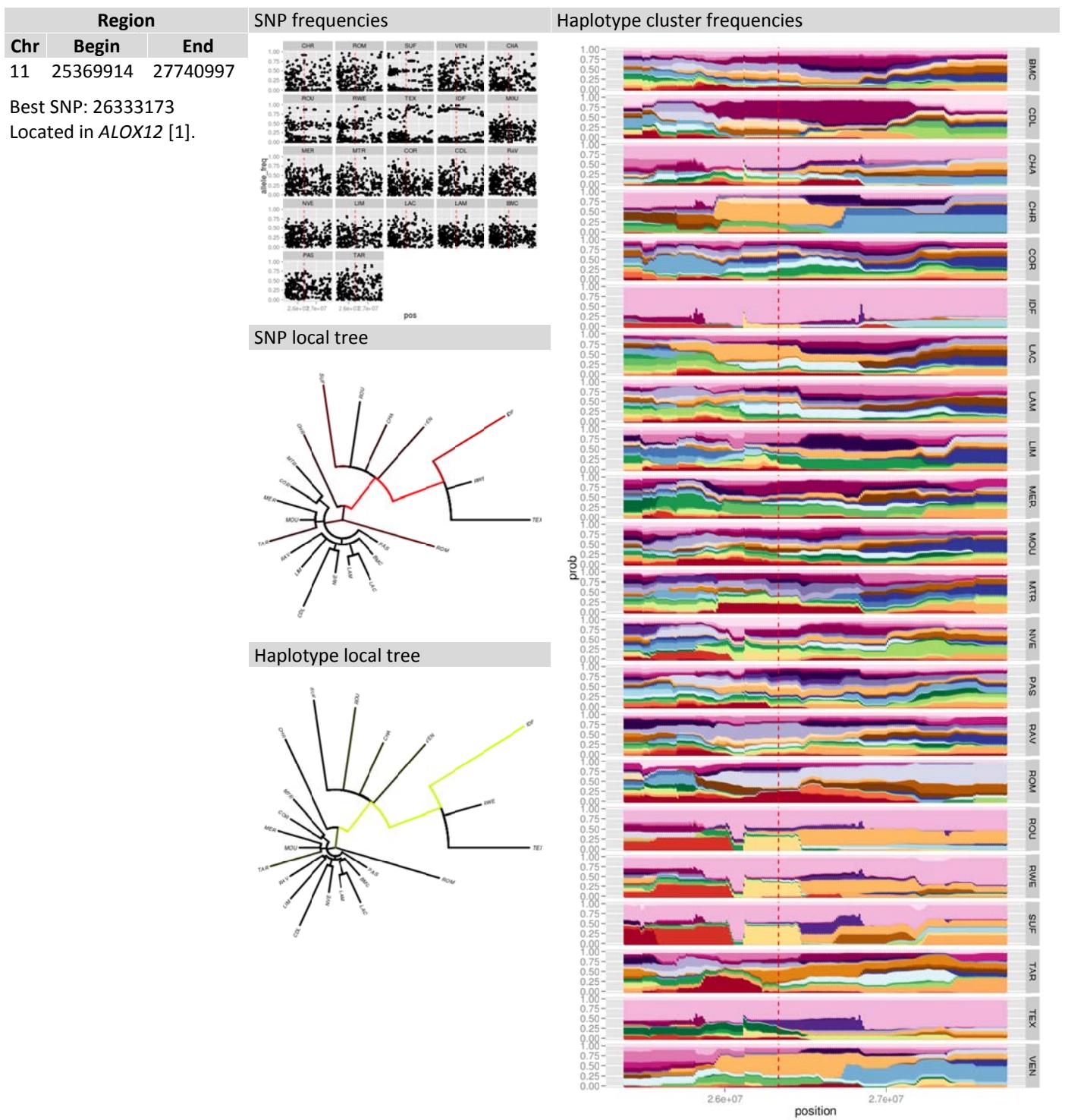


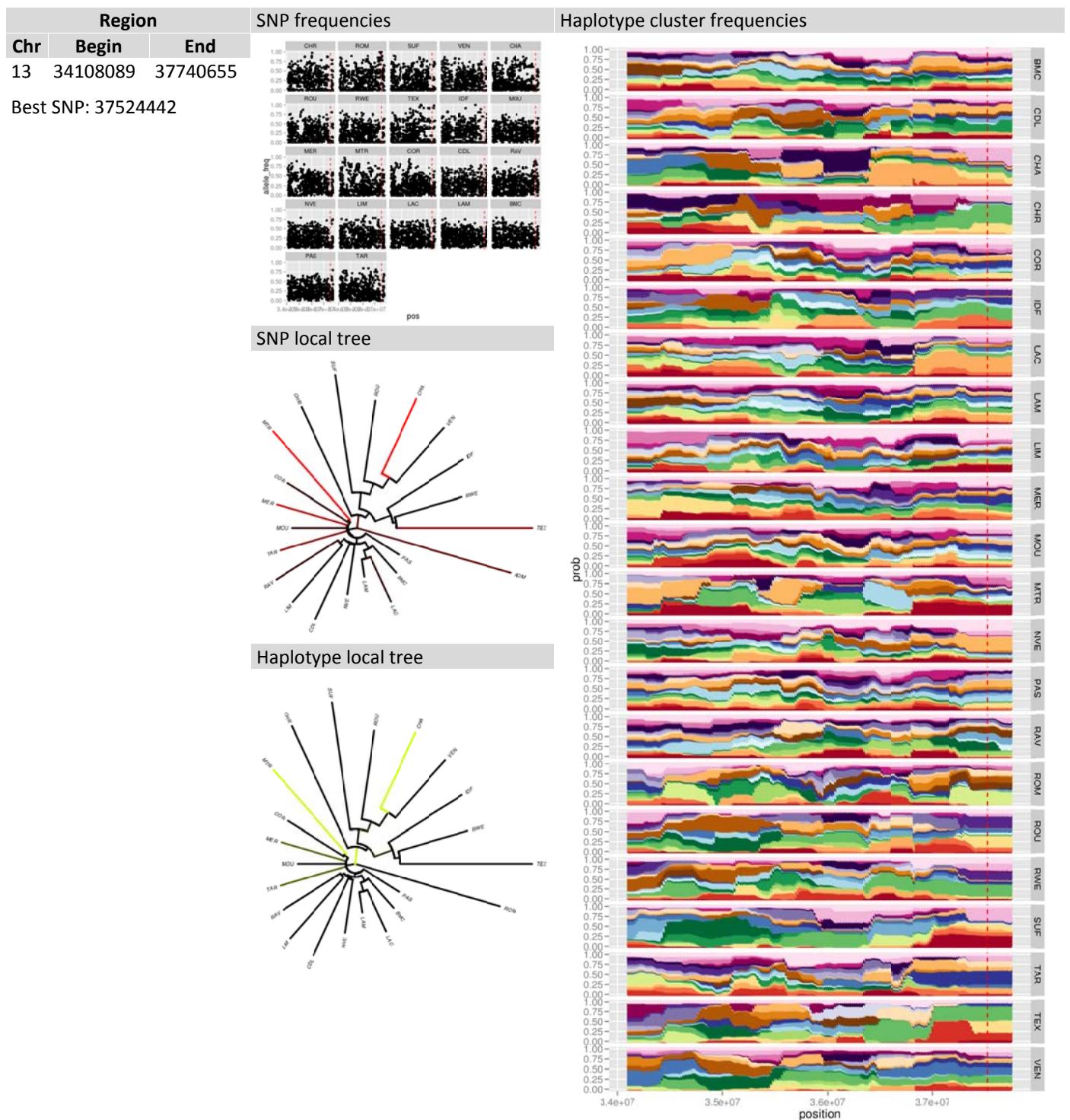


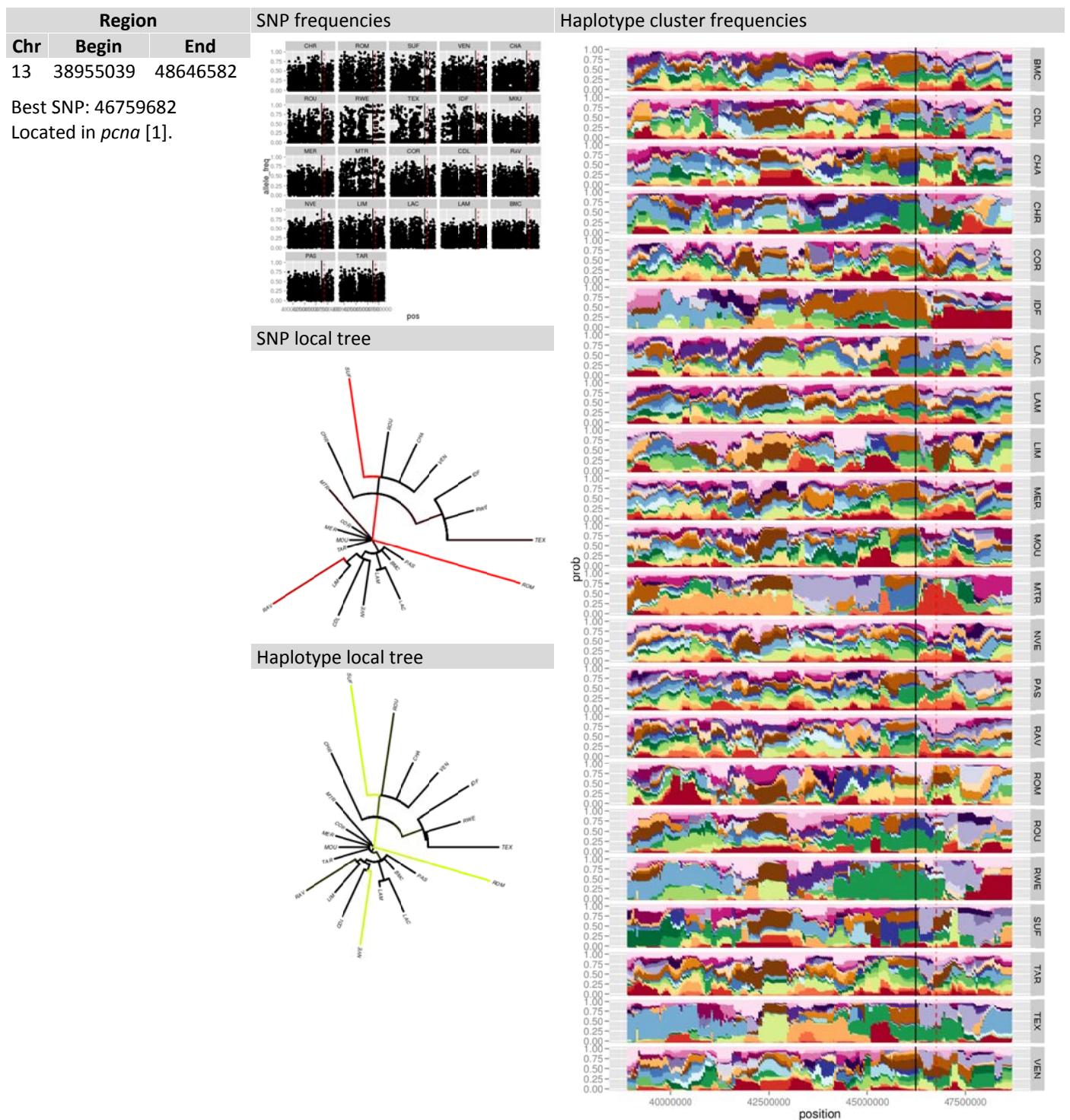


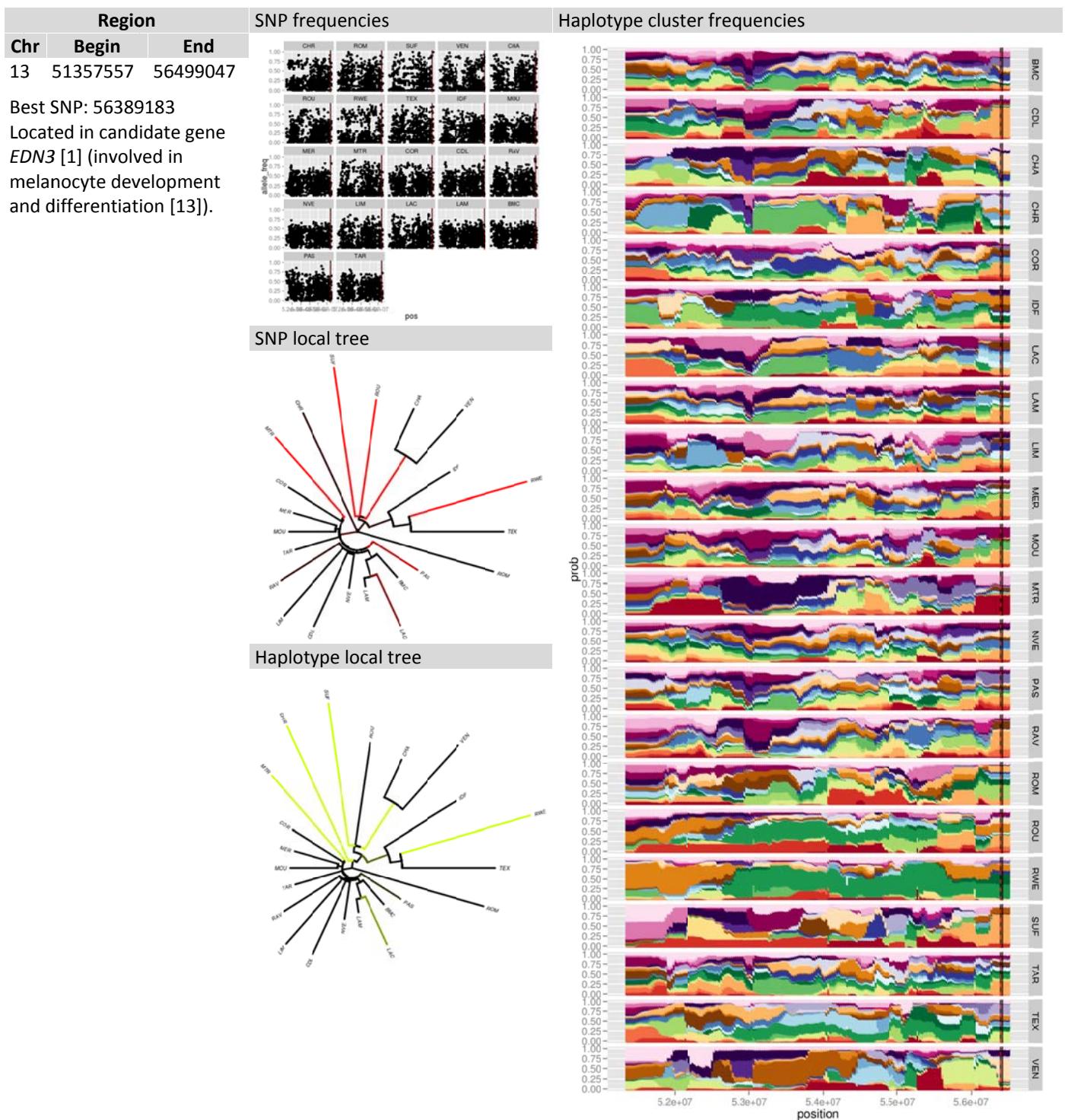


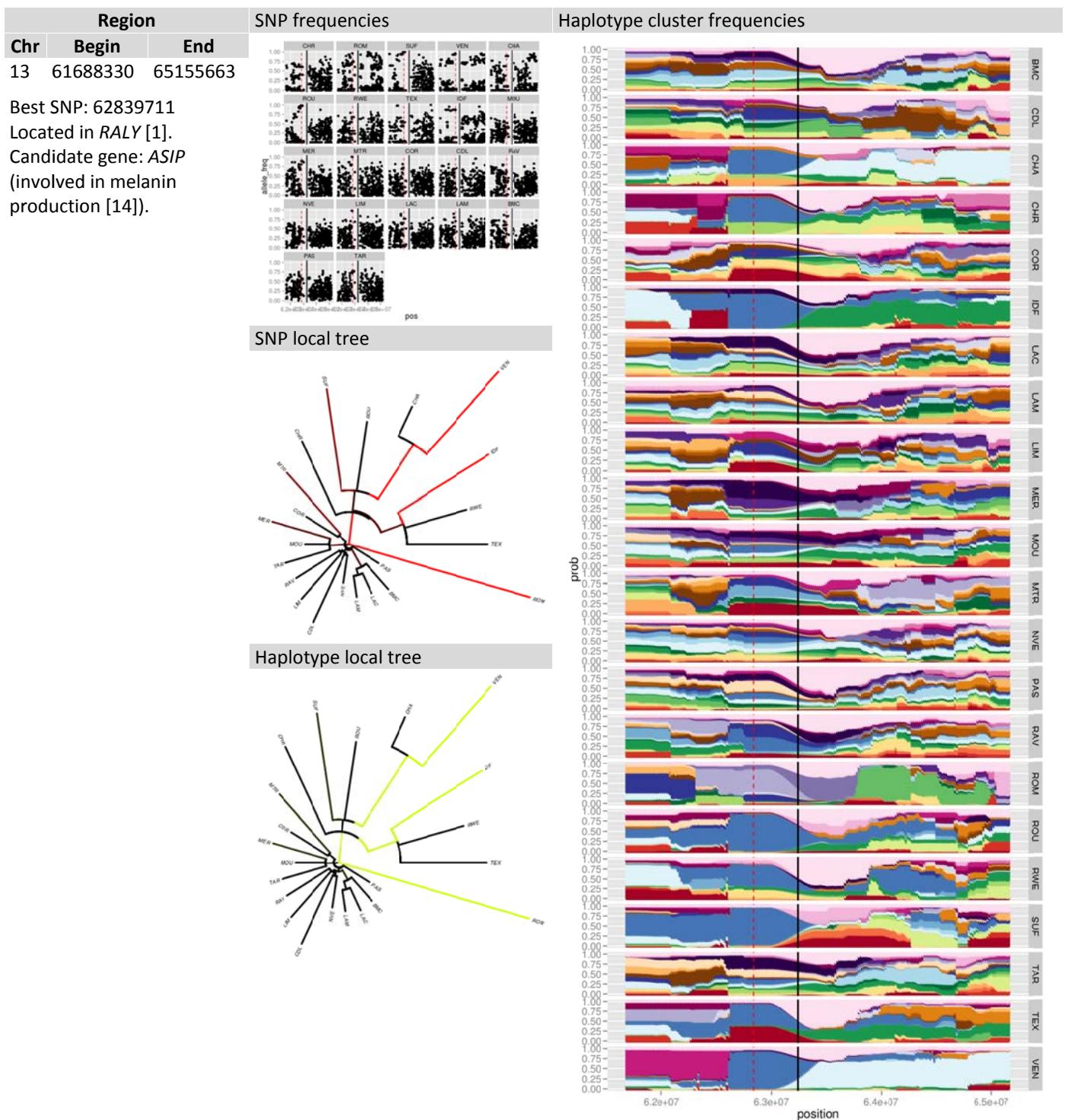


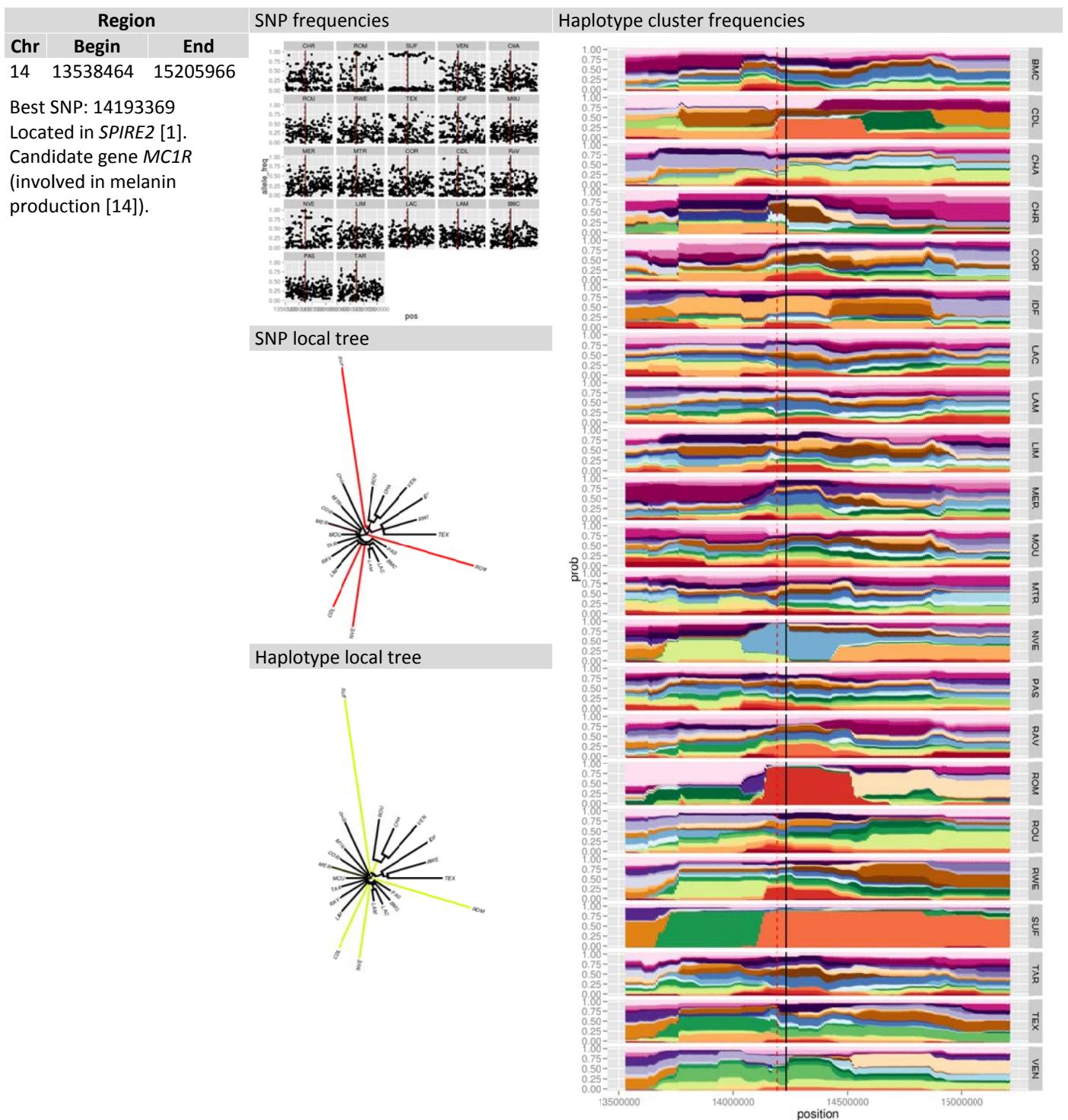


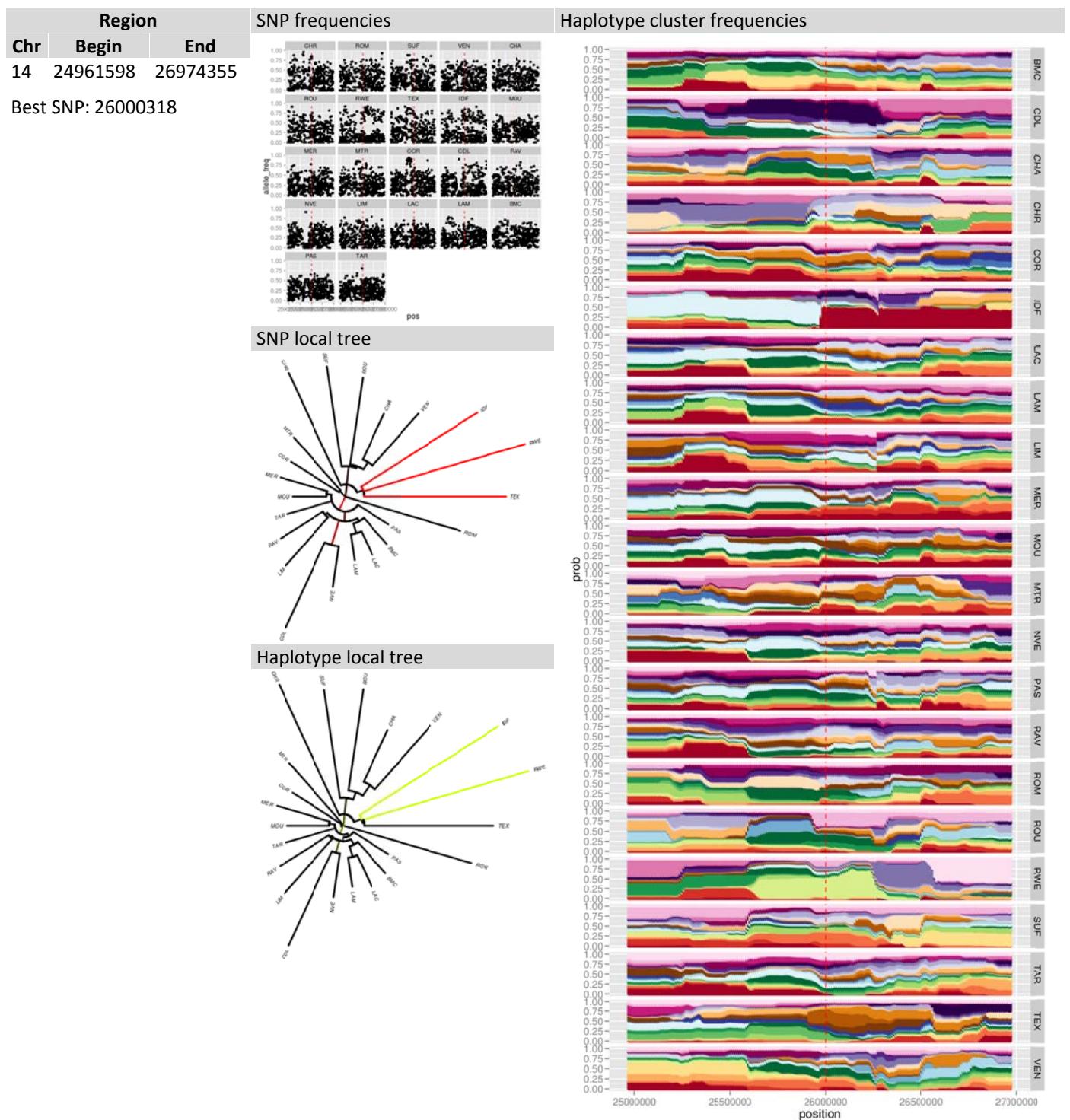


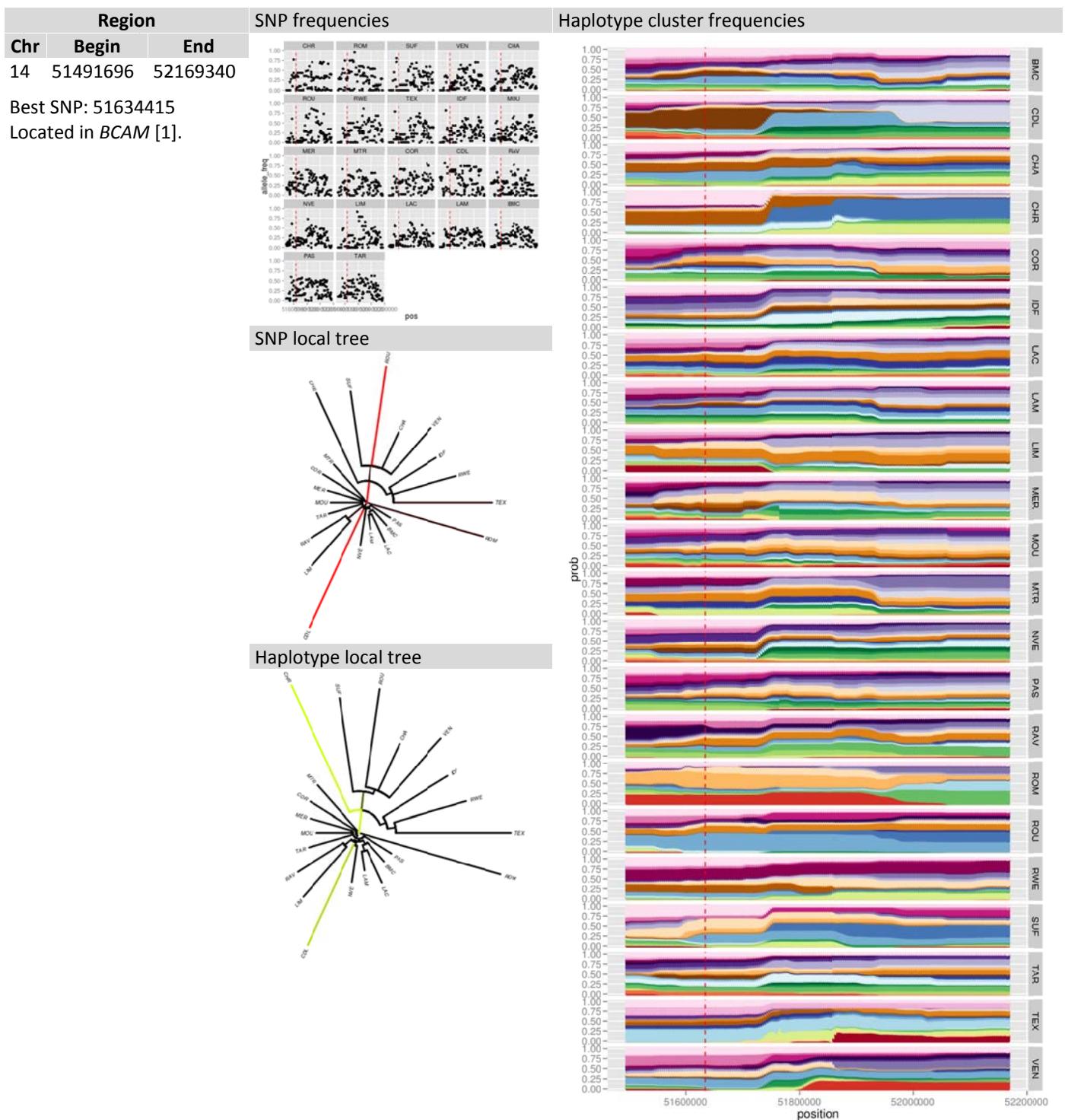


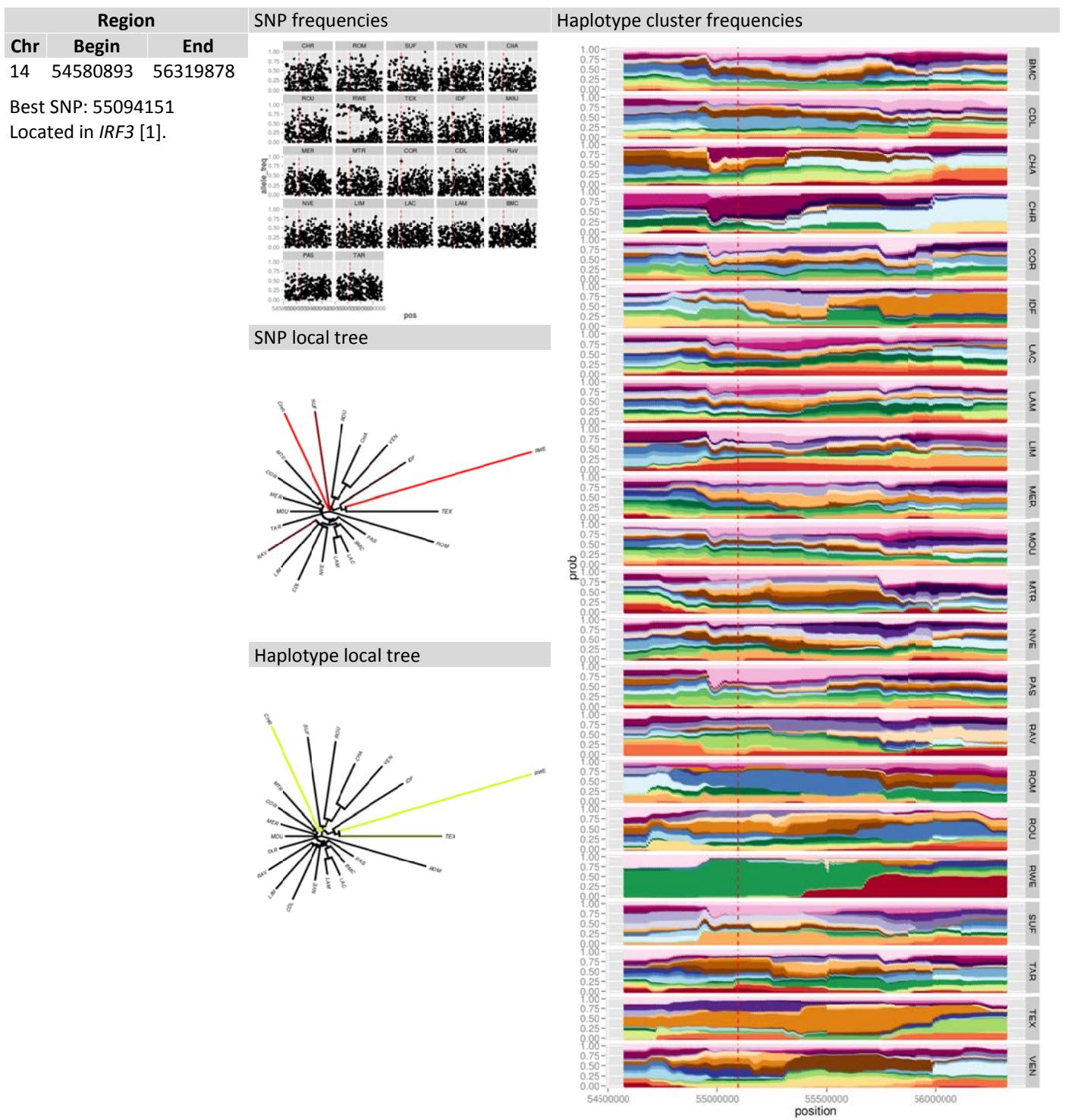


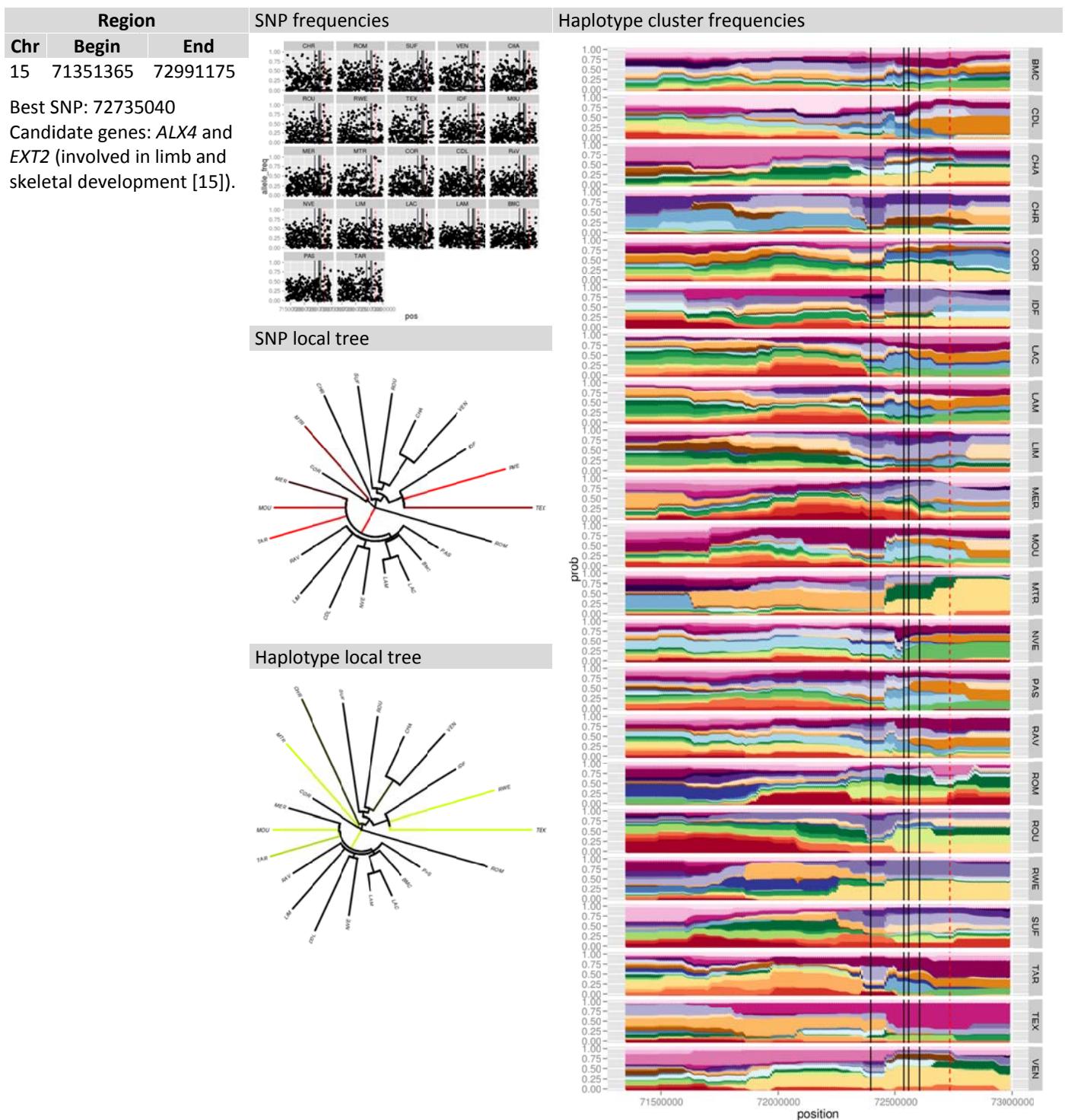


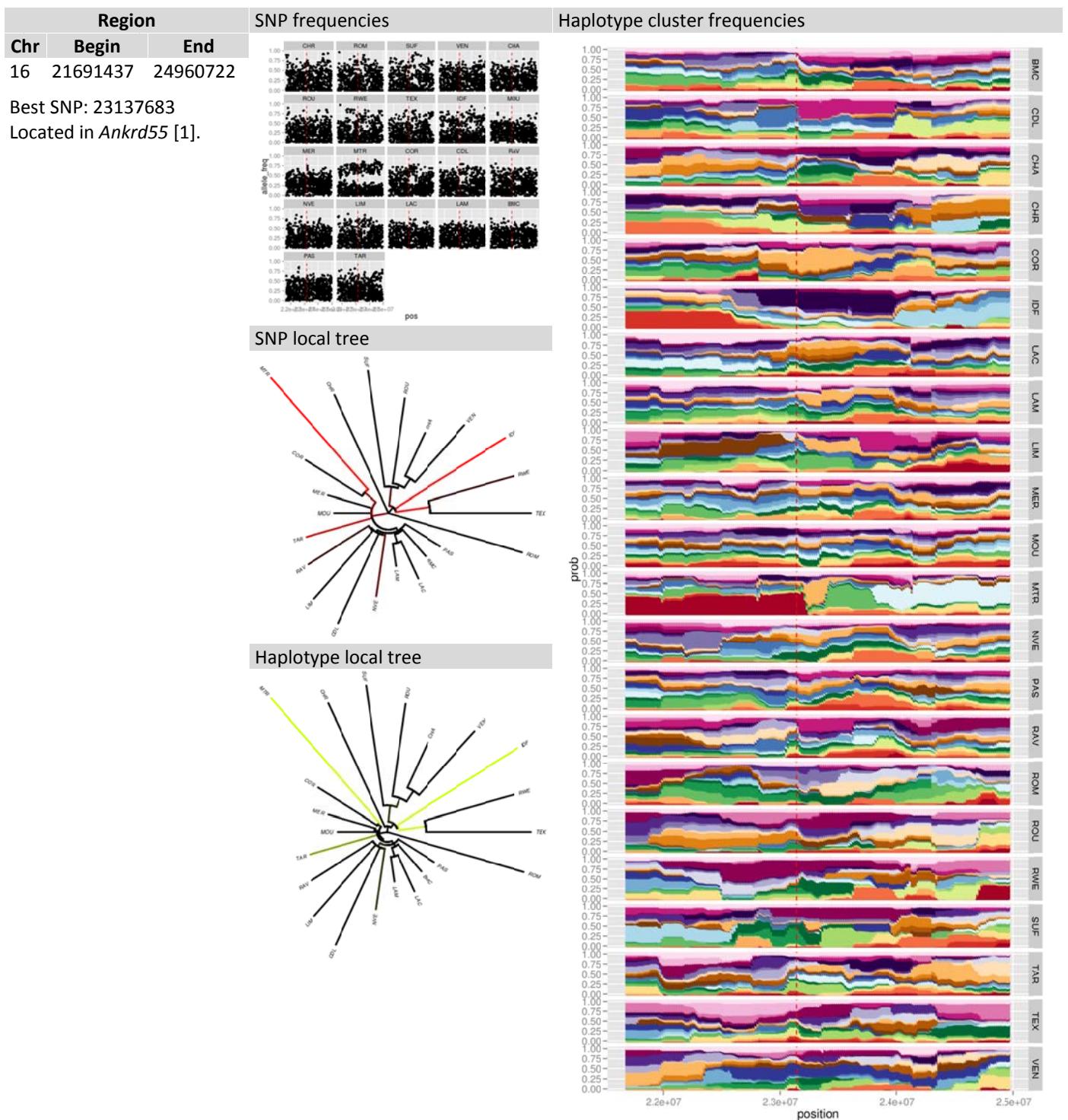


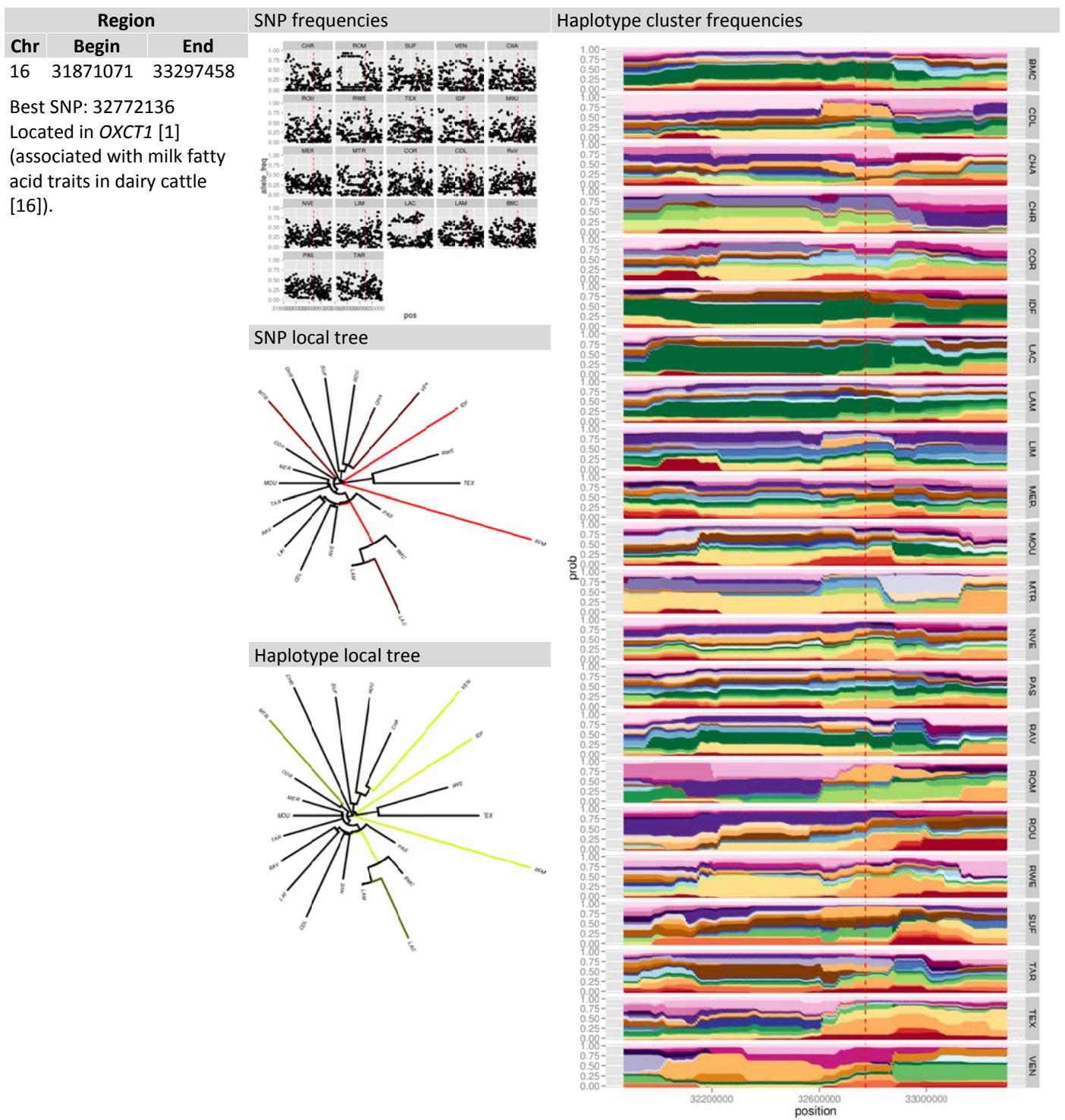


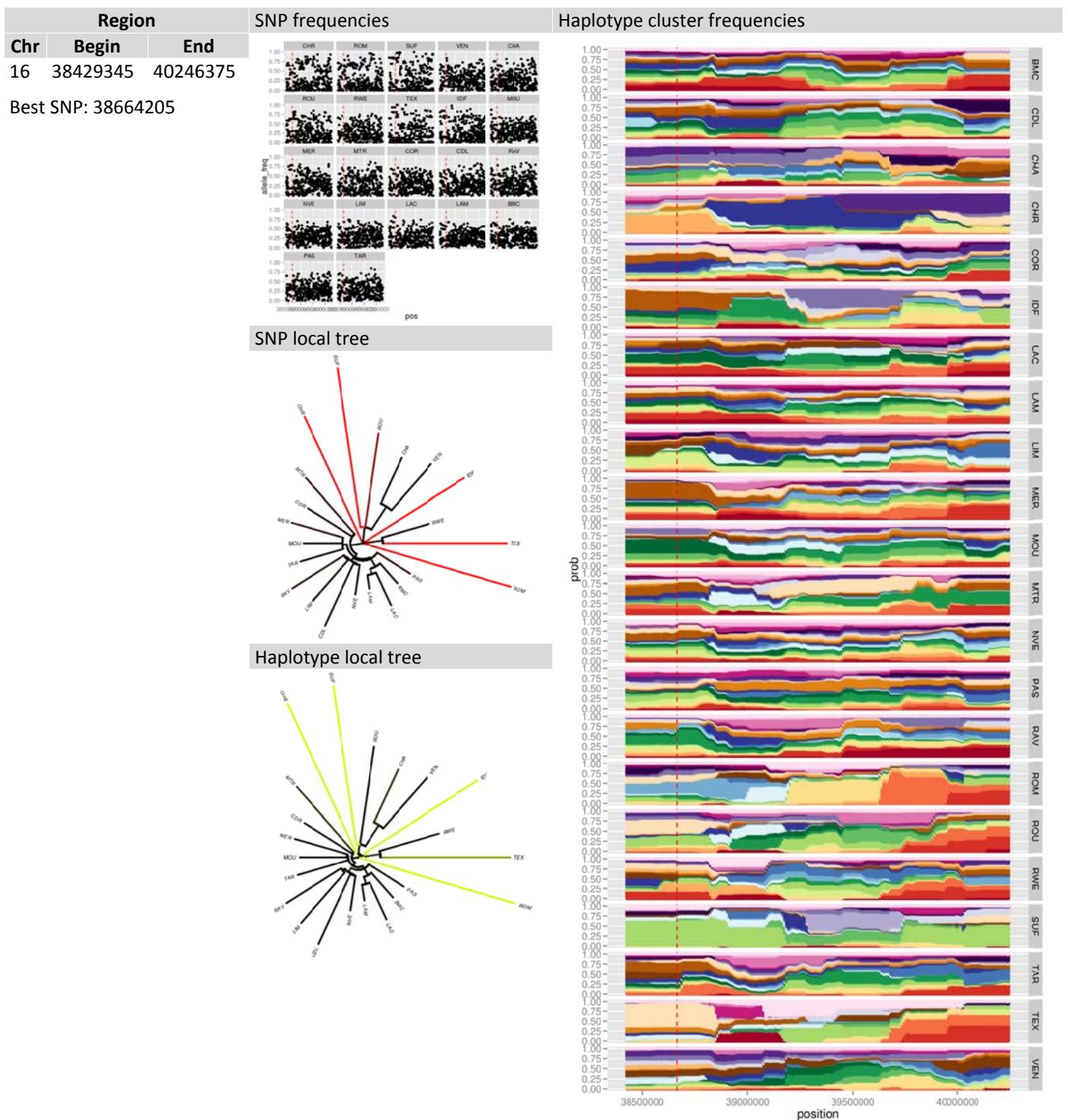


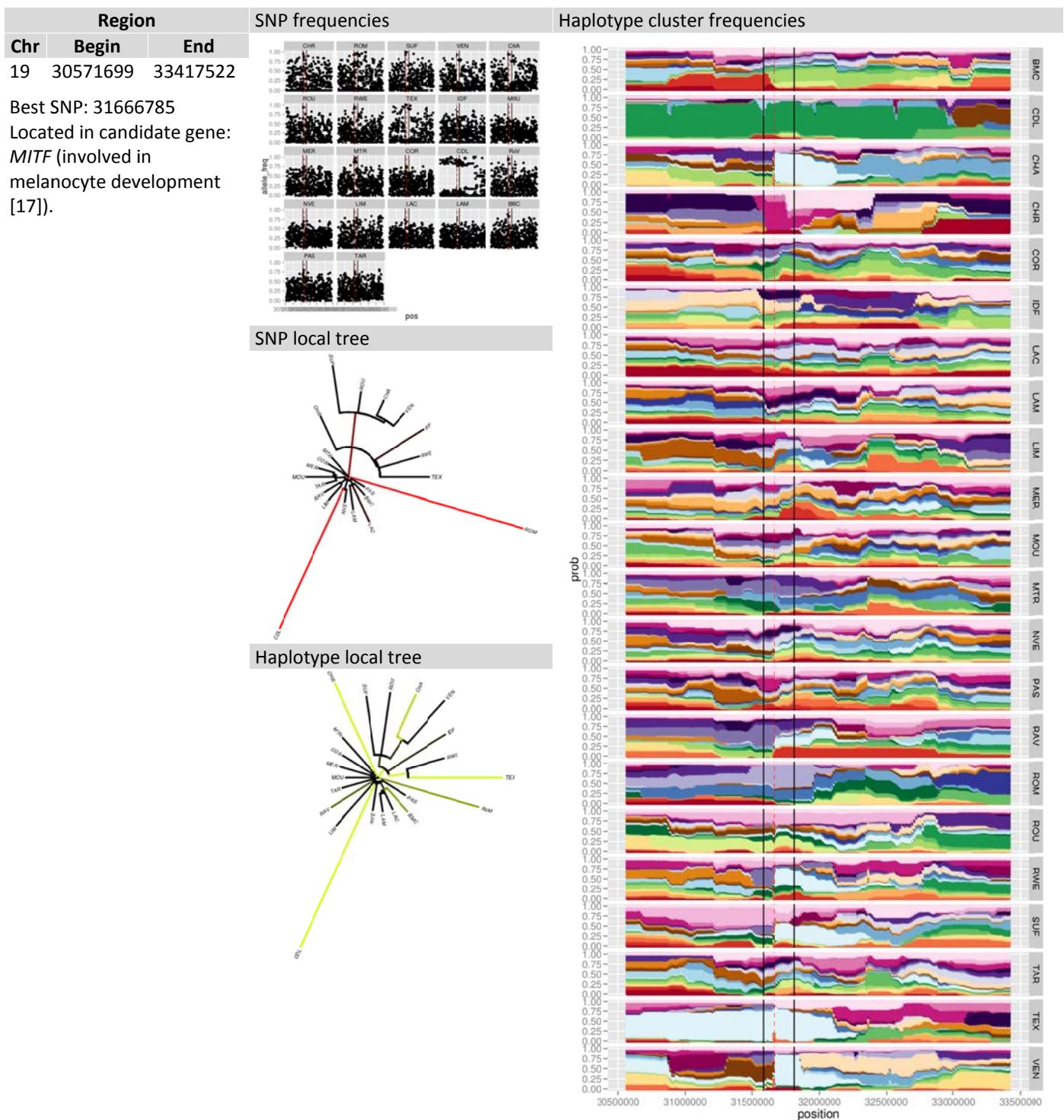


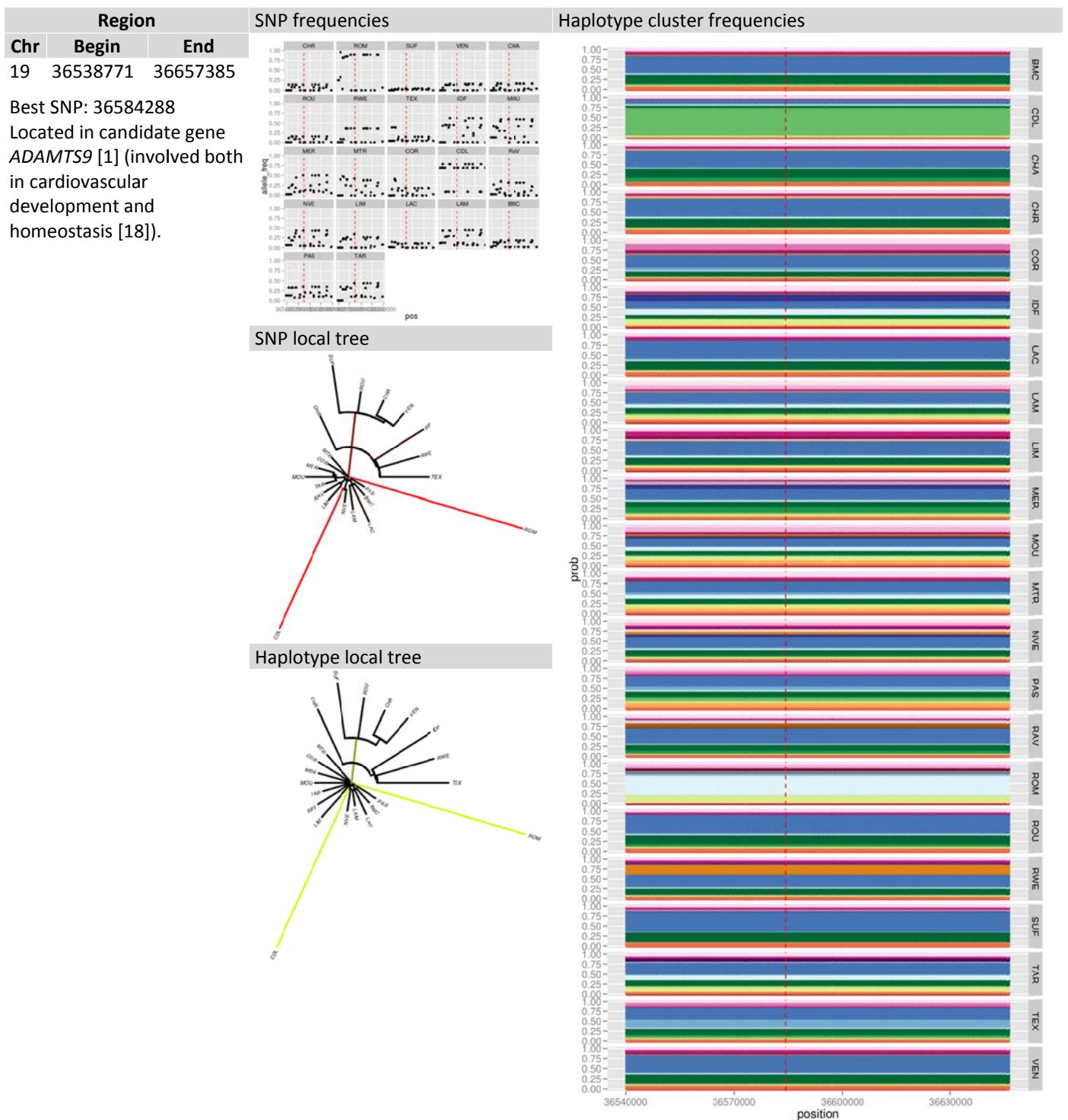


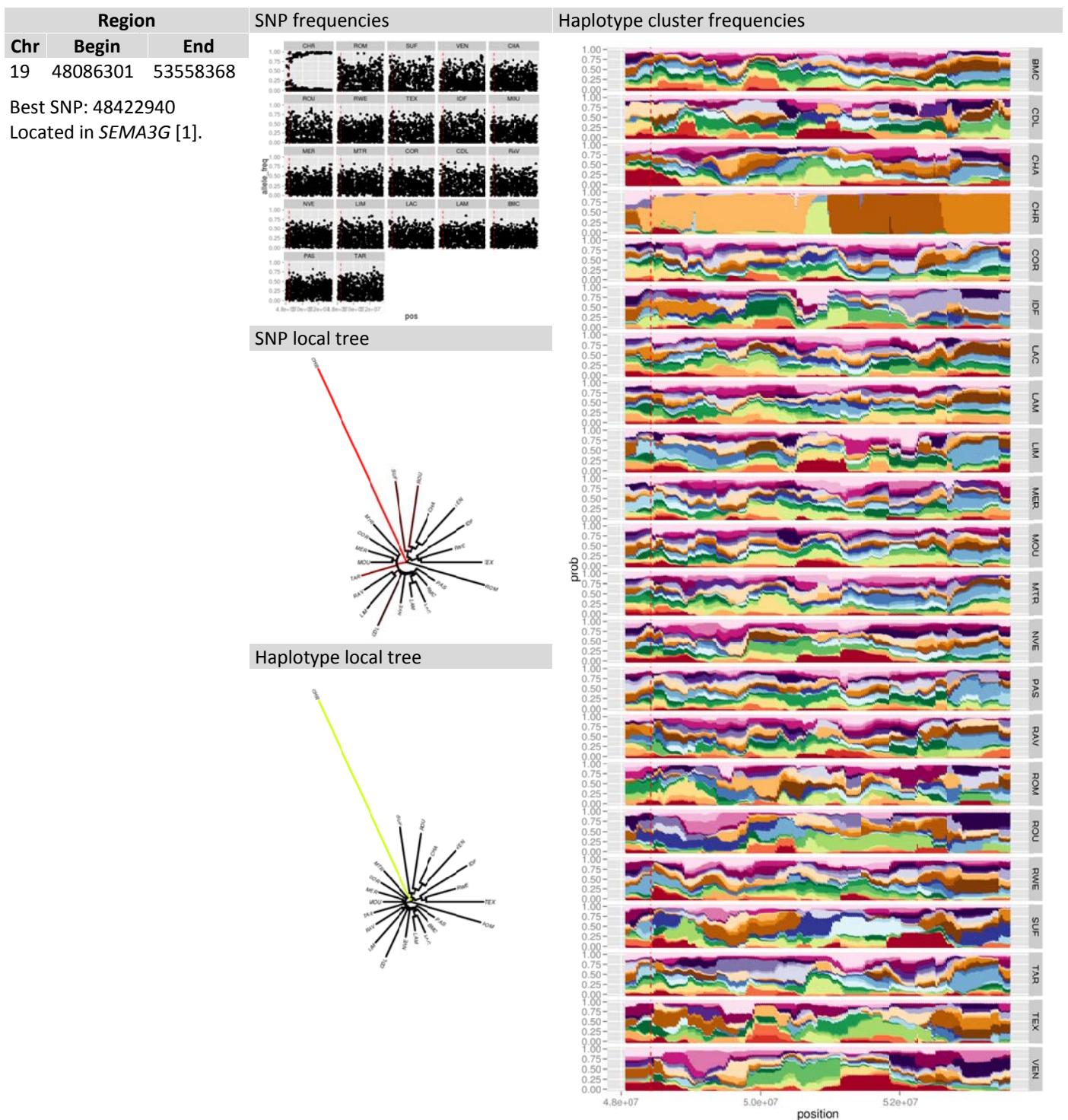


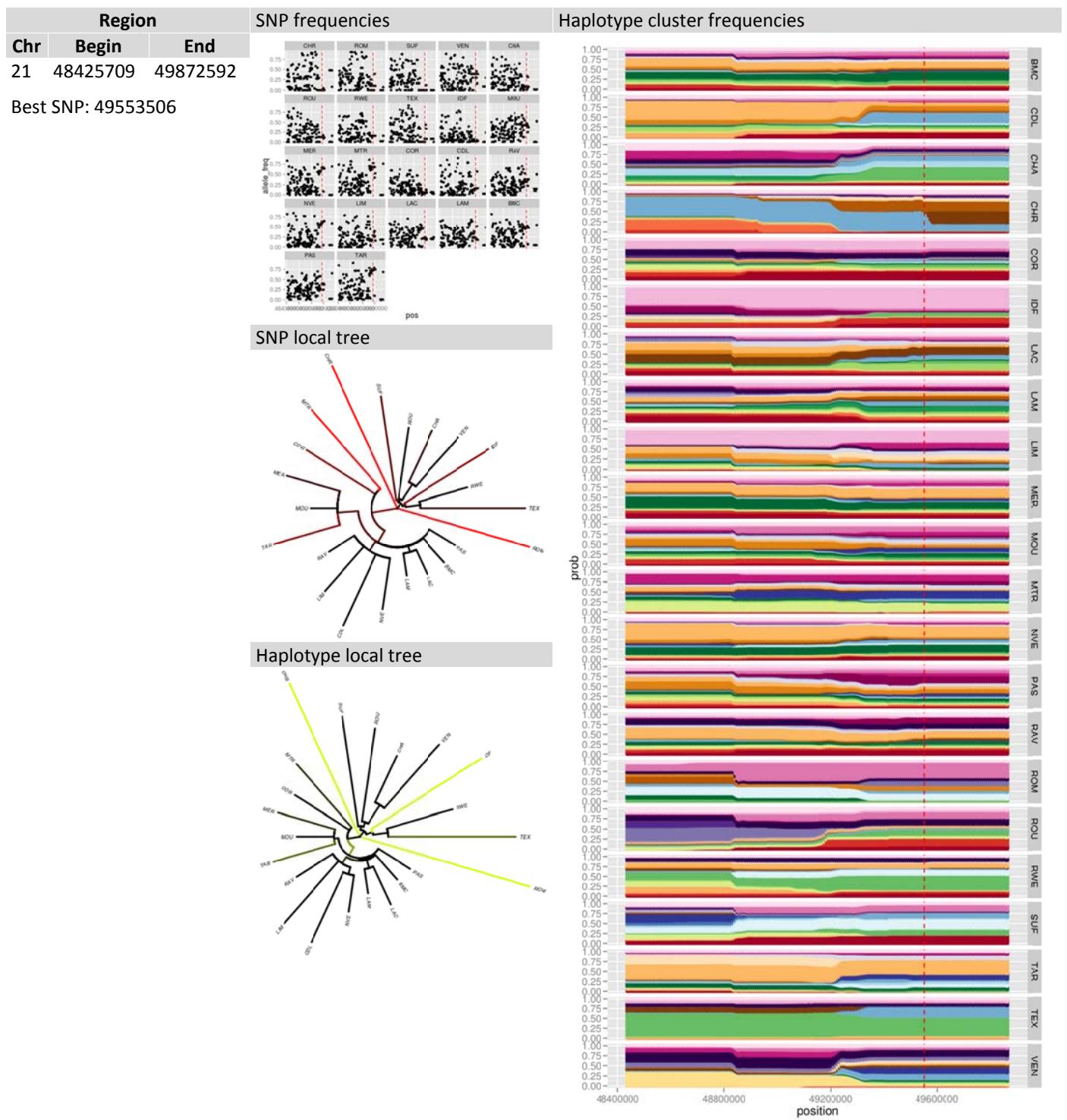


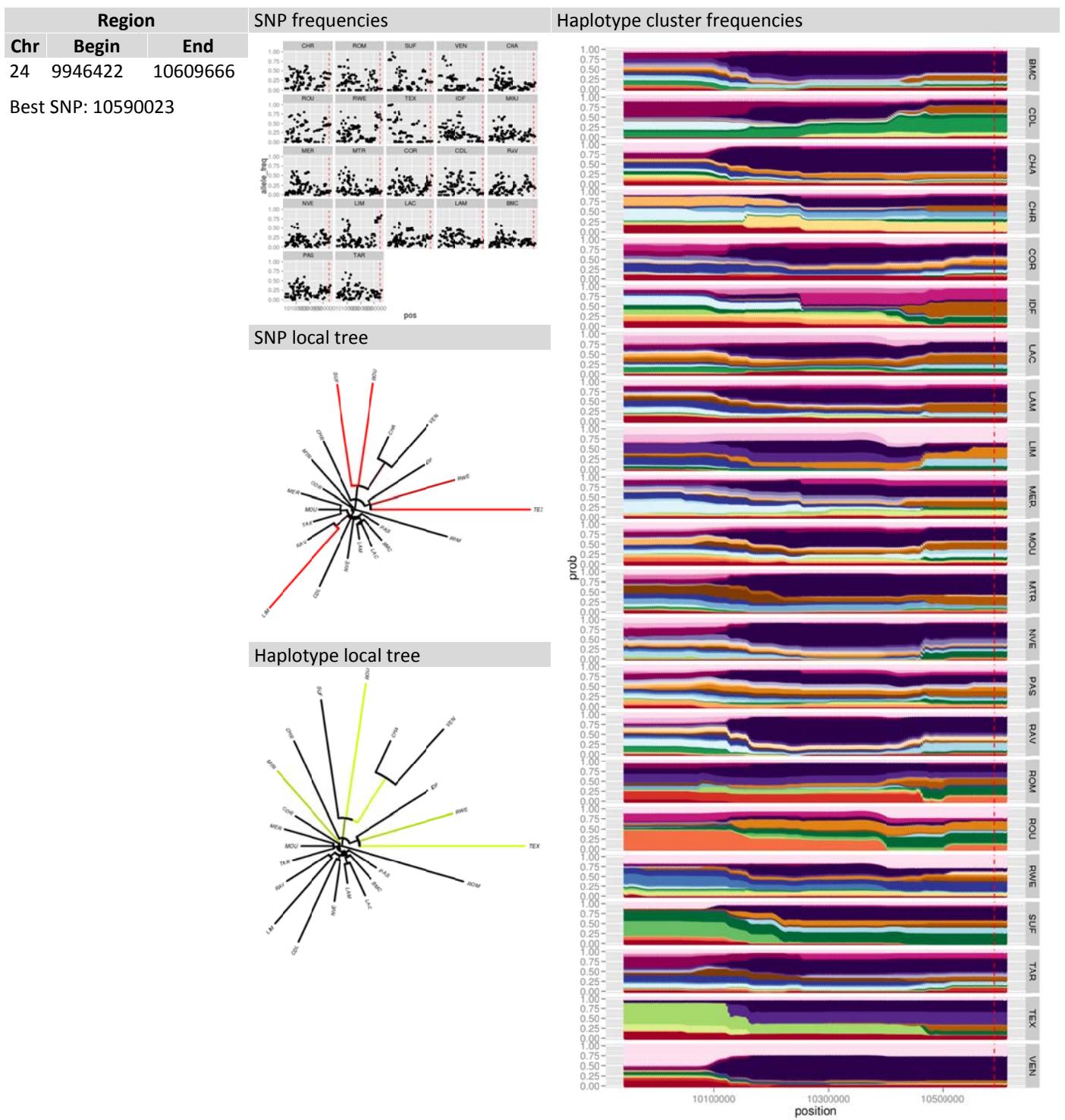


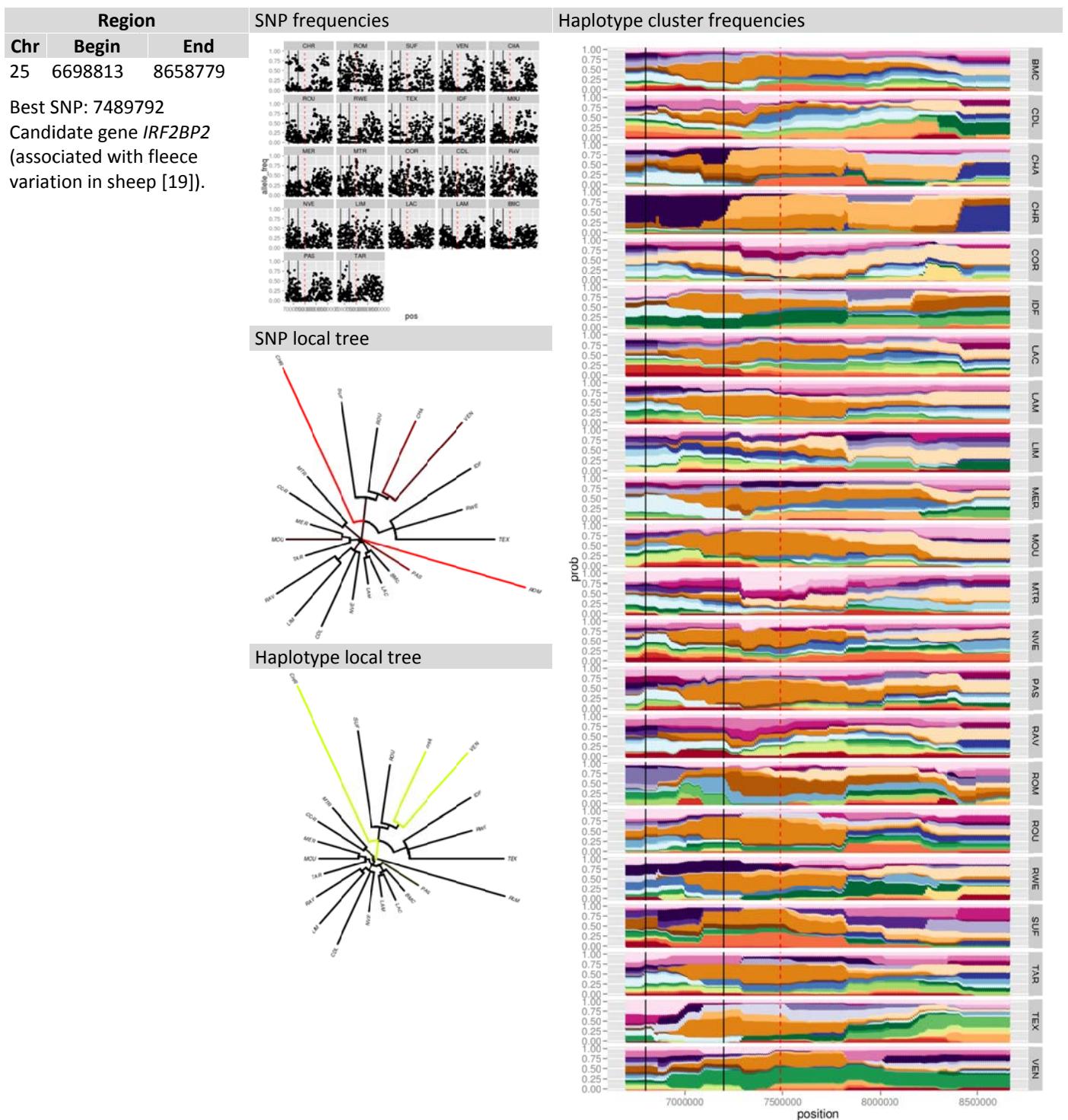


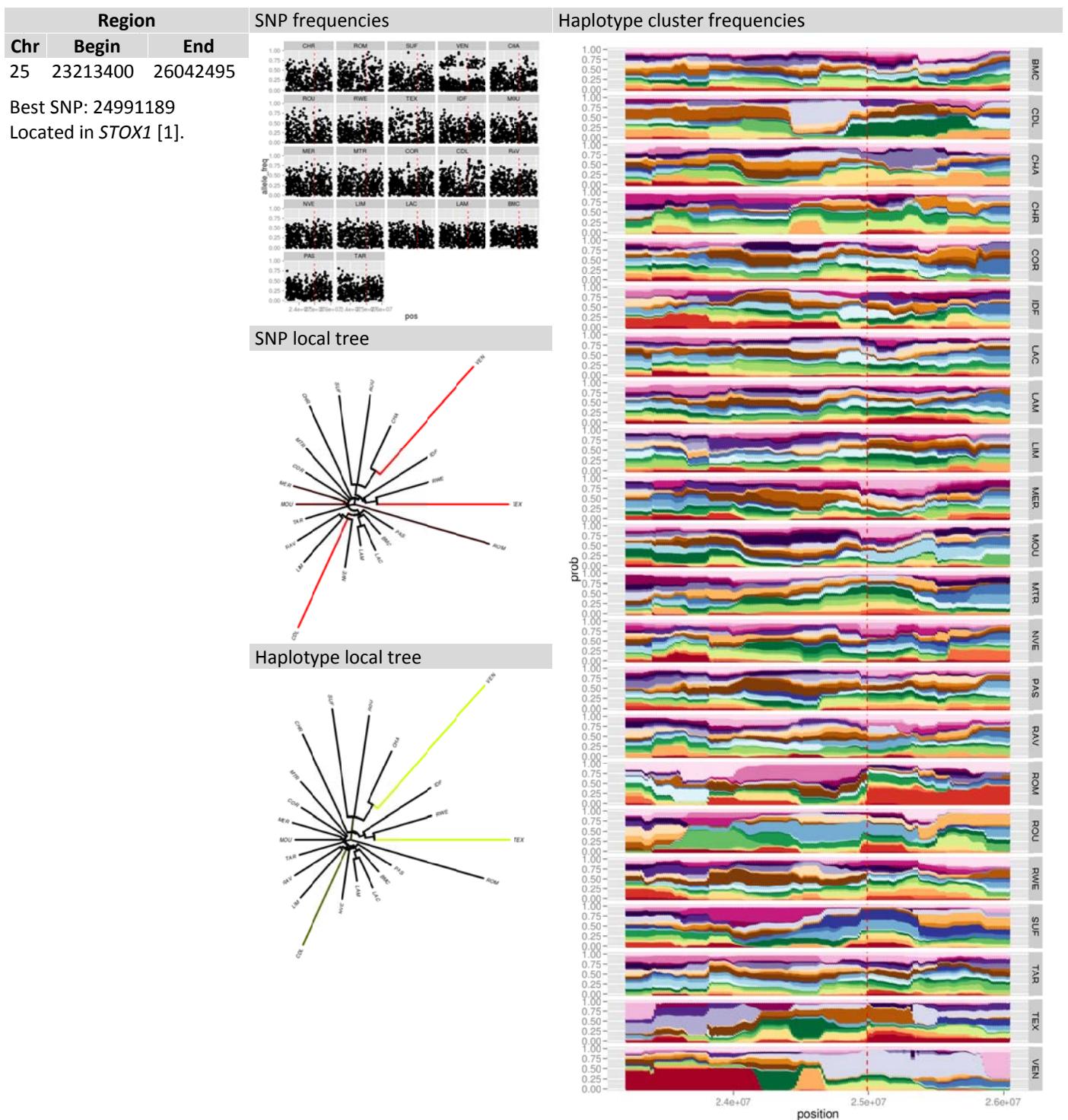












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