

# Fine mapping of a QTL region for androstenone level on pig chromosome 6

André Marubayashi Hidalgo

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John Bastiaansen  
Barbara Harlizius  
Hendrik-Jan Megens  
Martien Groenen



# Introduction

- Androstenone is a main compound causing boar taint
- Boar taint: Unpleasant flavor and odor of pork
- $> 2\mu\text{g/g}$  of fat influences acceptability
- Piglets are castrated to prevent boar taint
  - Find alternative method



# Introduction

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- SSC 6 is related to androstenone level (Duijvesteijn et al., 2010)
- 31 significant SNPs on SSC 6 (36.9 – 44.9 Mb)
- 987 Duroc boars

# Objective

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- Narrow down a QTL region on SSC 6, previously reported by Duijvesteijn et al. (2010).

# Material

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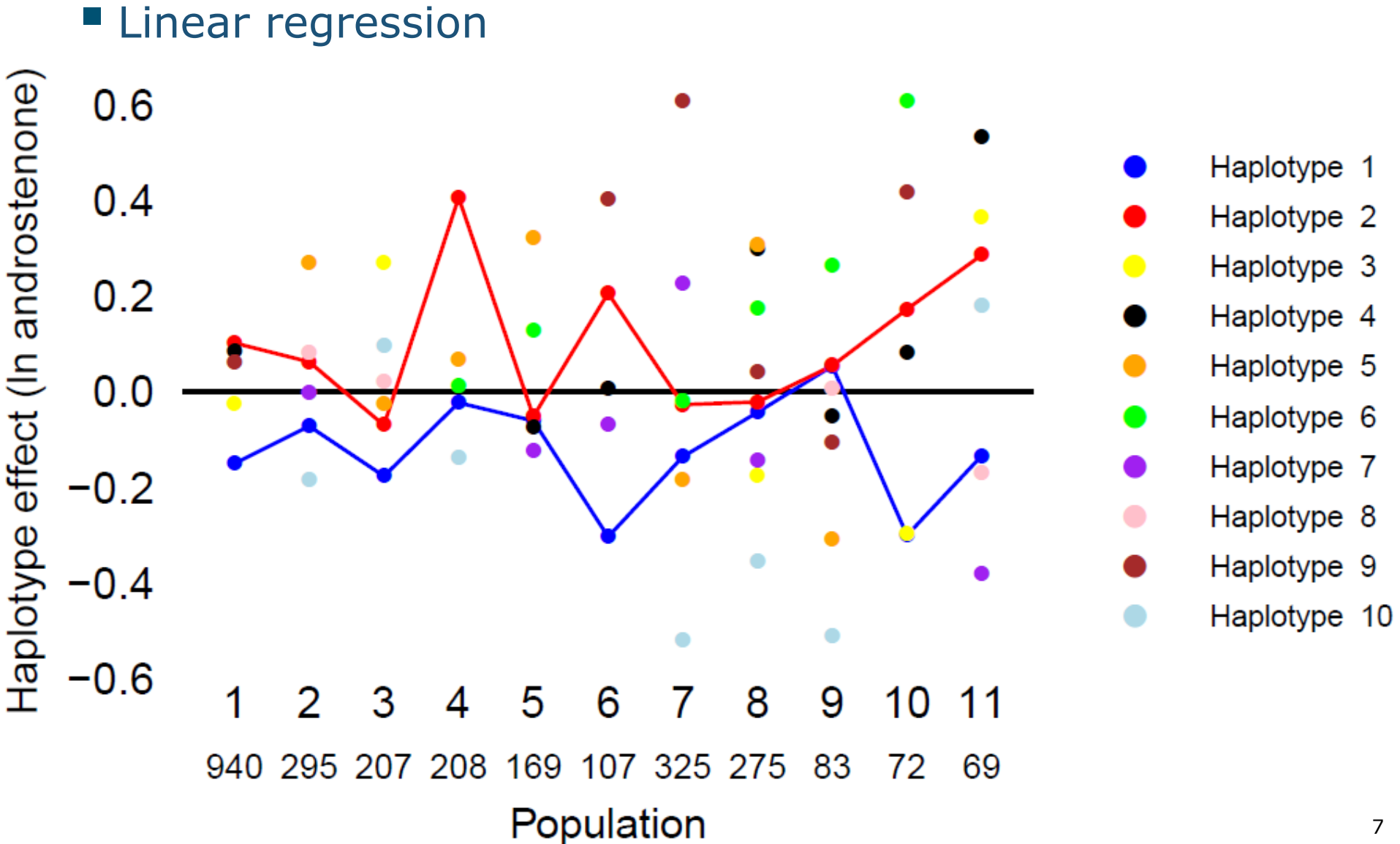
- 2750 animals from 6 pure lines + 5 crosses
- 3025 SNP markers
- Ln-androstenone

# Step 1: Haplotypes

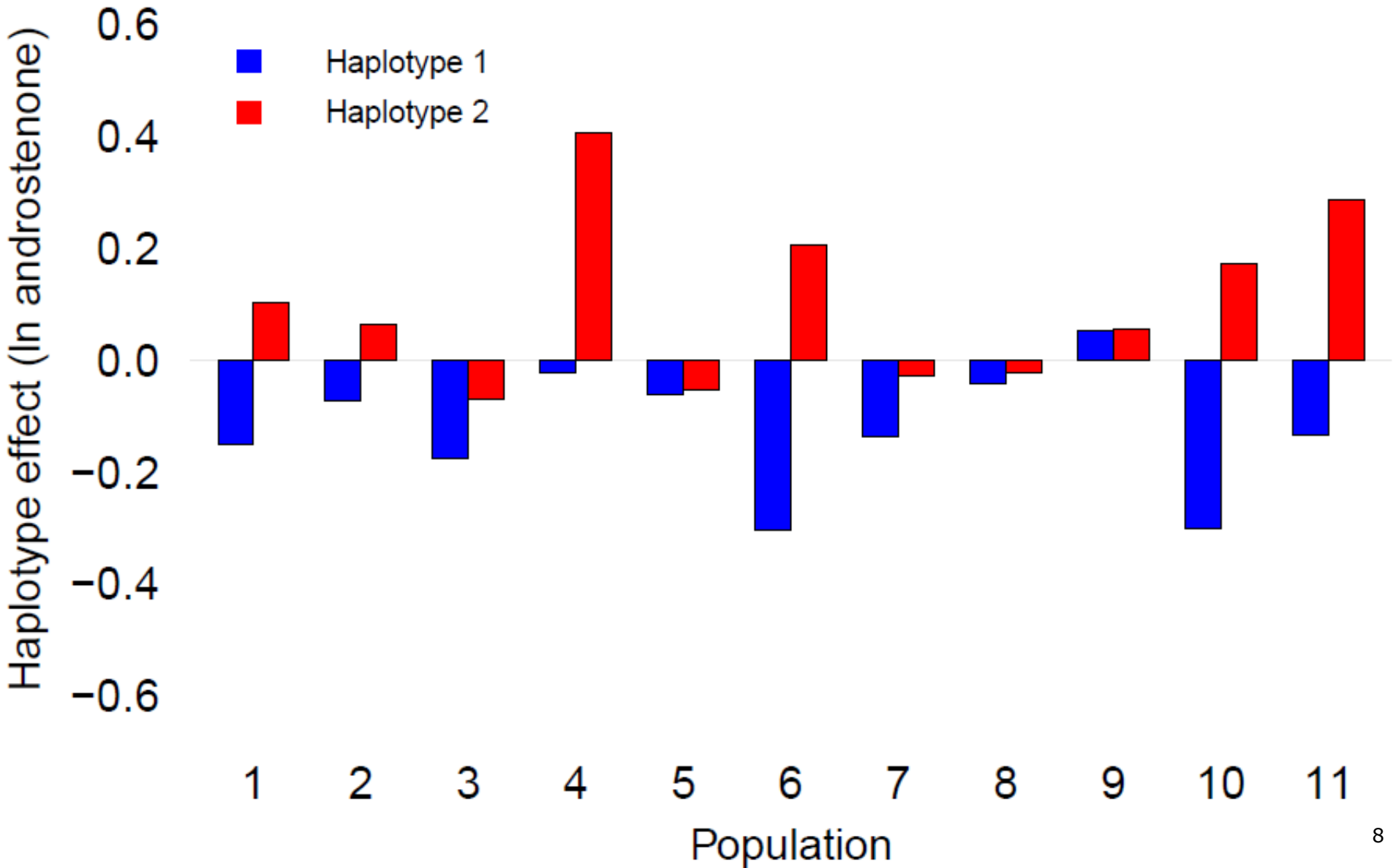
- Haploview 4.2
- 10 most frequent haplotypes
- 46 markers (3.75 Mb)

	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
01	---	GGGAAAGGGAGGACGGAAAGCAACAAAAAGGGAAACGGGAAAAGG	.281																																											
02	---	AAAGGGAAAGAAAAAGGCAAGCAGGGGGGAAAGGAAAAACGGGA	.262																																											
03	---	GGGAAAGGGAGGCCGGAAAGCAACAAAAGGGGAGGGCGGGAAAAGG	.107																																											
04	---	AAAGGGGAAGAAAAAGGCAAGCAGGGGGGAAAGGAAAAACGGGA	.089																																											
05	---	AAAGGGAAAGAAAAAGGAGAGCAGGGAGGAAAGGAAGGGGAGGAA	.064																																											
06	---	AAAGGGGAAGAAAAAGGCAAGCAGGGAGGAAAGGAAAAACGGGA	.041																																											
07	---	AAAGGGAAAGAAACGGAAAGCAACAAGAGAGGAGGGCGGGAAAAGG	.036																																											
08	---	GGGAAAGGGAGGACGGAAAGCAACAAAAGGGGAGGGCGGGAAGAGG	.032																																											
09	---	AAAGGGGGAGAAAAAGGAGCGCAGGGAGGAAAGGAAAAACGGGA	.023																																											
10	---	AGGAGGGGGAGGACGGAAAGCAACAAAAAGGAGGGCGGGAAGGGG	.019																																											

## Step 2: Haplotype effects for all haplotypes in 11 populations



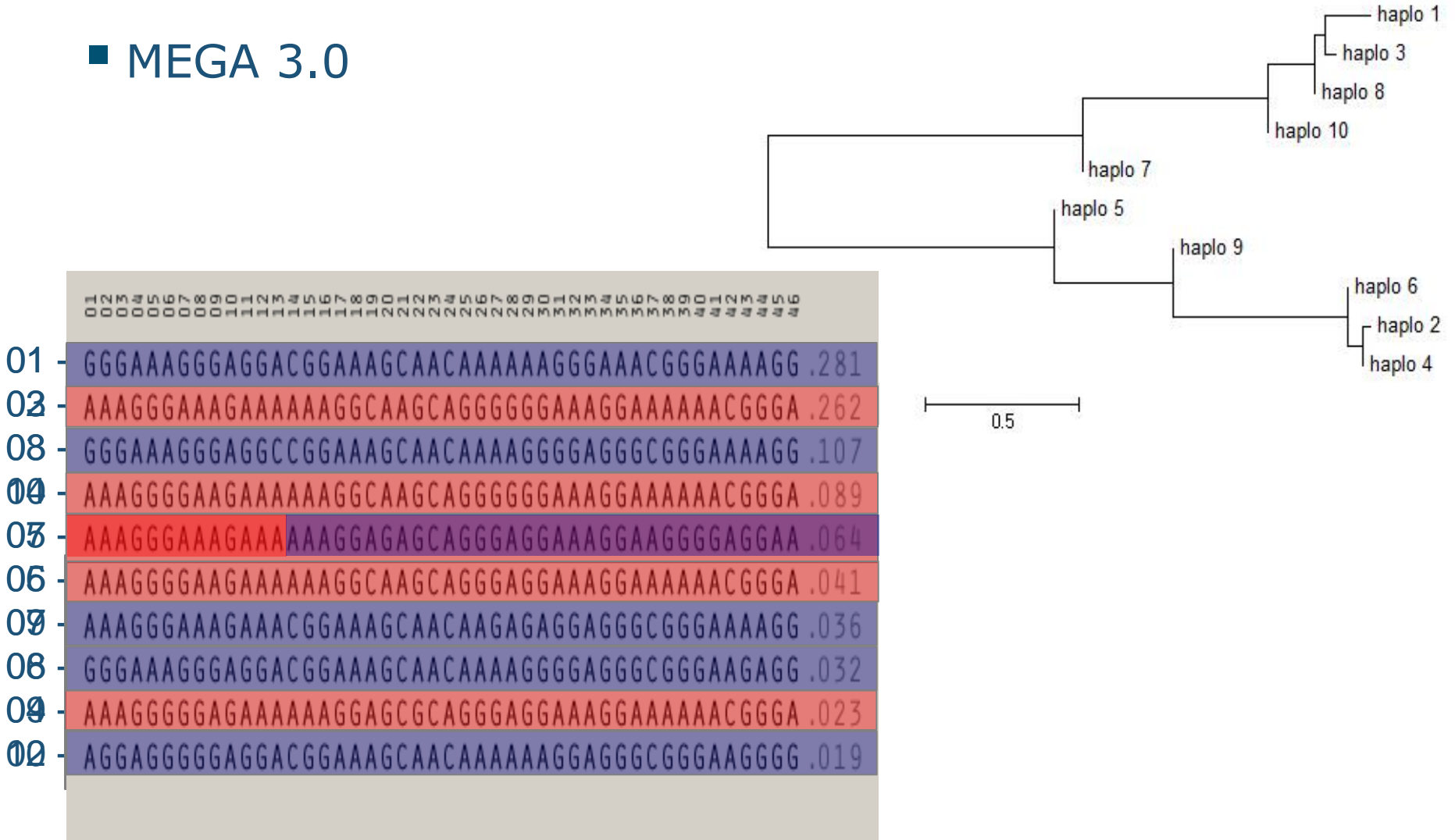
# Haplotype effects for haplotypes 1 and 2 in 11 populations



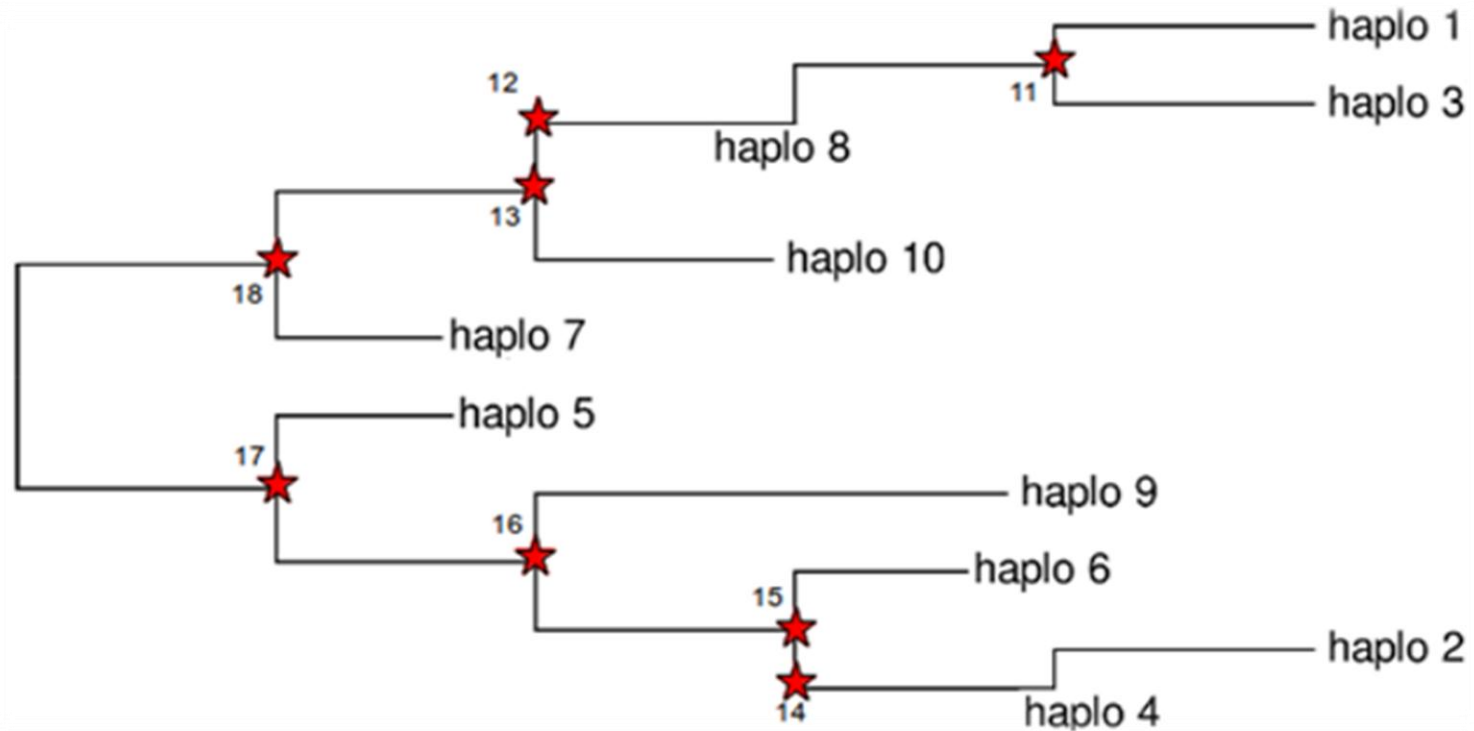


# Step 3: Phylogenetic tree

## MEGA 3.0



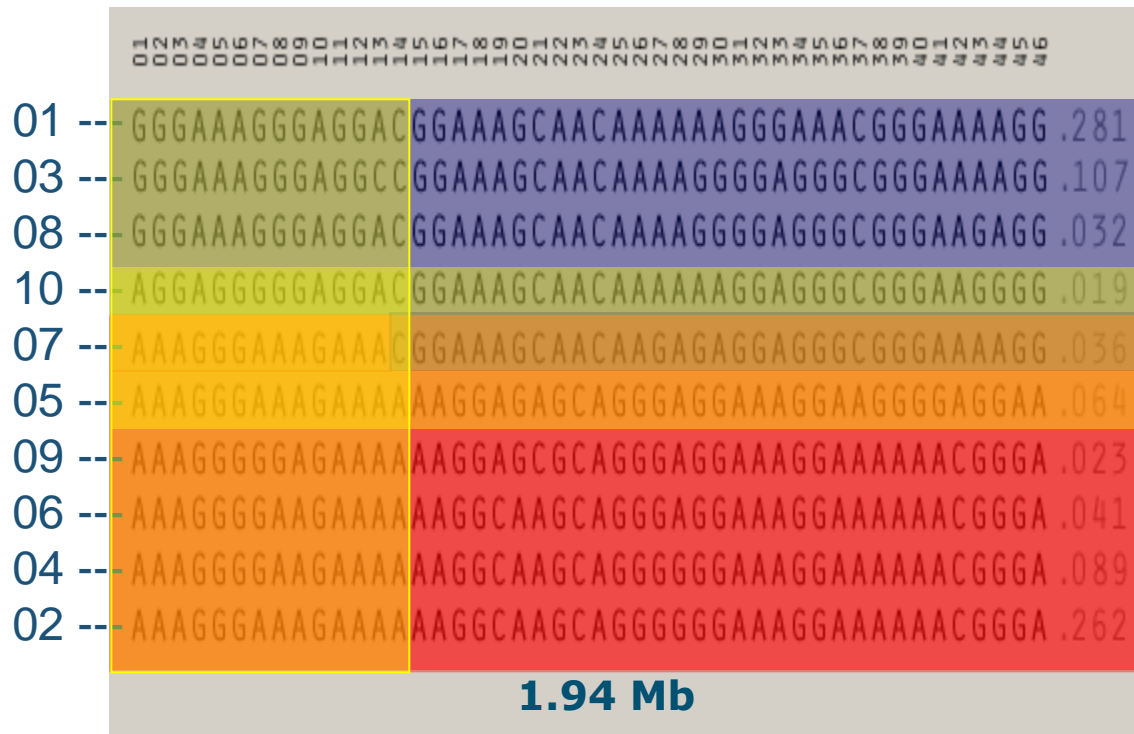
# Step 4: Treescanning



Branch	Location	F	P
1	18-13	64.63	0.000 *

# Step 5: Haplotype effect

Haplotype 7	Estimate	Std. Error
Haplo 1	-0.17	0.04
Haplo 2	-0.02	0.04
Haplo 7	-0.04	0.06



# Conclusion

- Reduced from 3.75 Mb to 1.94 Mb (48%)
- Candidate genes

