

Species	CDS sequence	RNA-seq data
<i>Zea mays</i>	ftp://ftp.ensemblgenomes.org/pub/release-43/plants/fasta/zea_mays/cds/	SRR8560815- SRR8560819

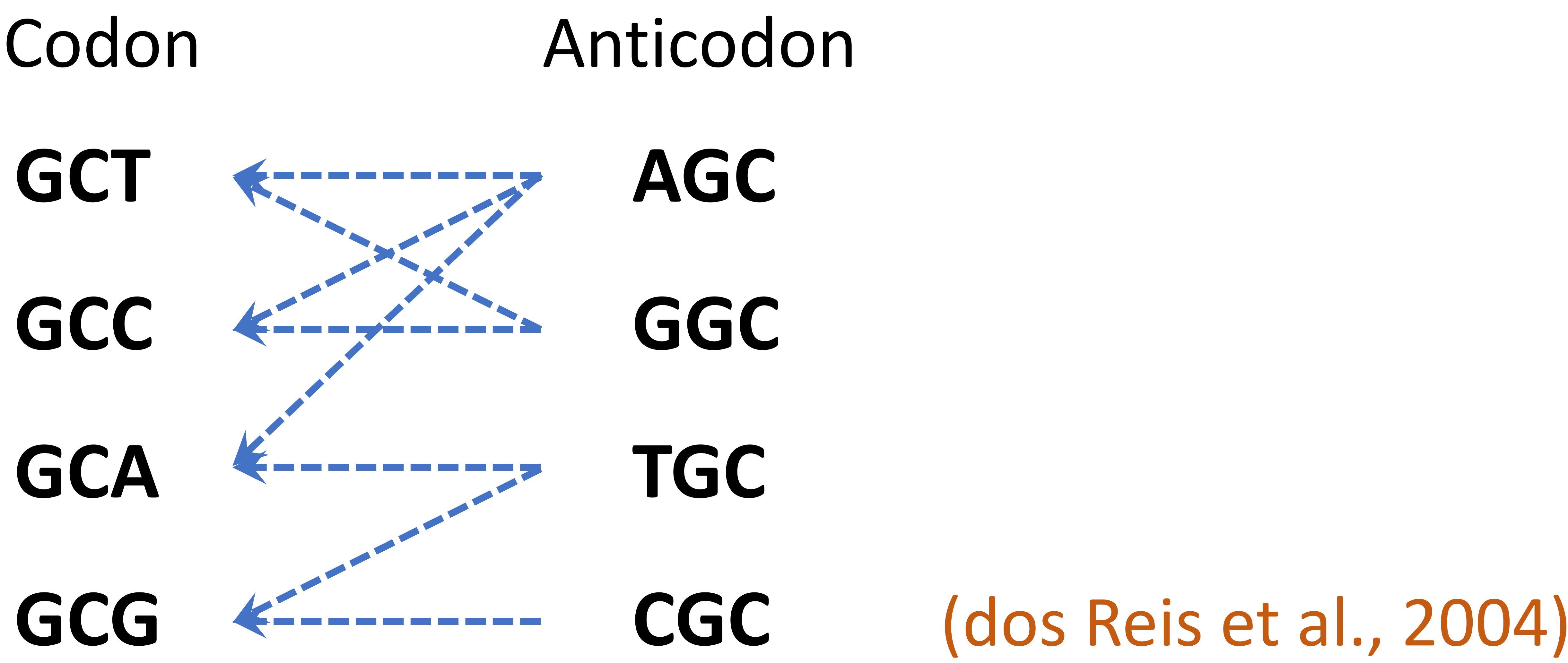
Number of mutations detected in the whole CDS regions

Type	Total	Isoaccepting	Non-isoaccepting	Non-synonymous	Nonsense
Polymorphic	24323	6964	2459	14511	389

Species	Number of unique genes	Number of unique codons
<i>Zea mays</i>	39254	13958446

Relationship between the focal codon and the front codon

Start codon	Isoaccepting	Non-isoaccepting	Nonsynonymous
39254	334757	903994	12680441



Ala Codon	Isoaccepting codon(s)
GCA	GCT/GCC/GCG
GCC	GCT/GCA
GCG	GCA
GCT	GCA/GCC

Fraction of nucleotide in CDS

Species	A (%)	C (%)	G (%)	T (%)	CpG (%)	C(%)*G(%)
<i>Zea mays</i>	23.3	26.7	28.4	21.6	13.6	7.6

Non-CpG region in CDS

Minor allele frequency (MAF) of polymorphic synonymous mutations

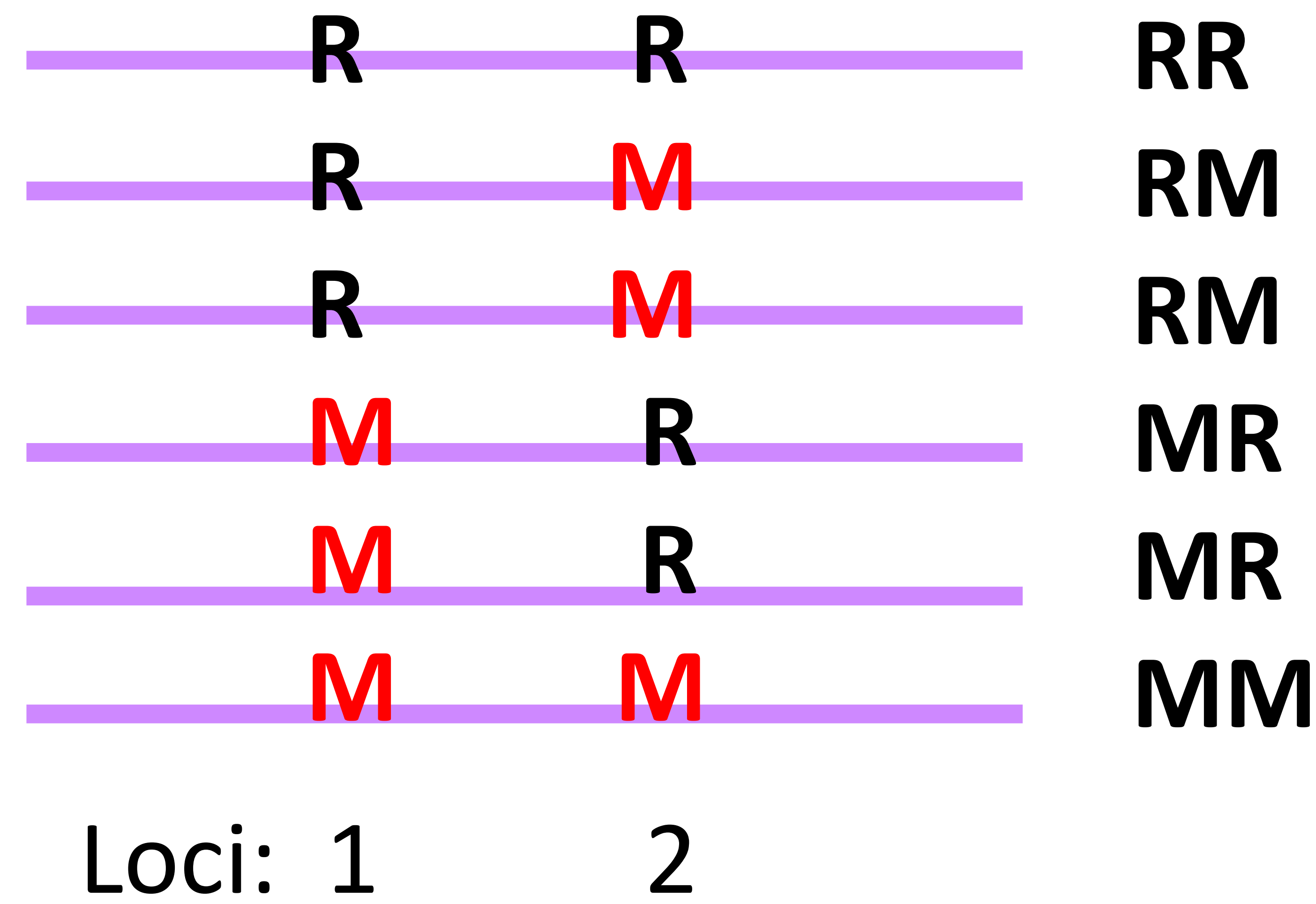
Item	iso context	Non-iso context	nsy context	All syn
iso%	77.5%	61.1%	73.2%	73.6%
MAF iso	0.292	0.253	0.240	0.243
MAF non-iso	0.229	0.275	0.245	0.246

Different context types

RNA-seq reads

R: reference allele.

M: mutation.



$$N = RR + RM + MR + MM$$

$$P1 = (RR + RM)/N$$

$$Q1 = (MR + MM)/N$$

$$P2 = (RR + MR)/N$$

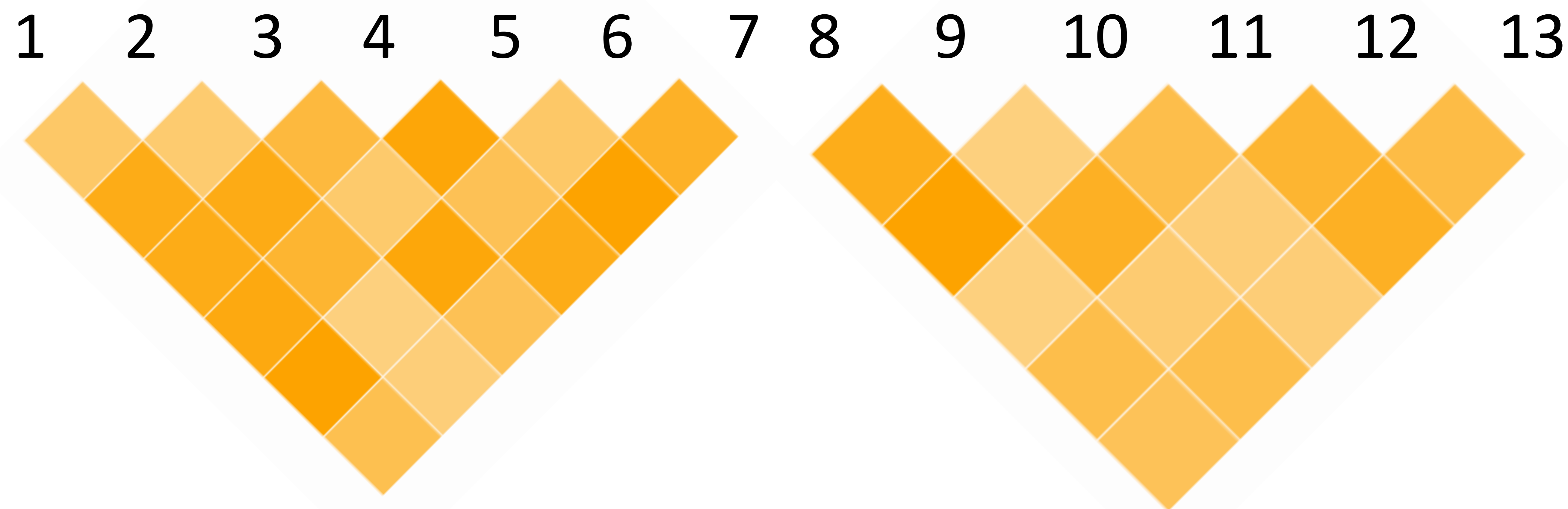
$$Q2 = (RM + MM)/N$$

$$D = (RR*MM - RM*MR)/N^2$$

$$R^2 = D^2/(P1*Q1*P2*Q2)$$

Zm00001d031523_T001

Loci



Loci 1-13: CDS position 240, 248, 254, 255, 256, 271, 287, 291, 299, 308, 315, 319, 326

All detected polymorphic mutations

