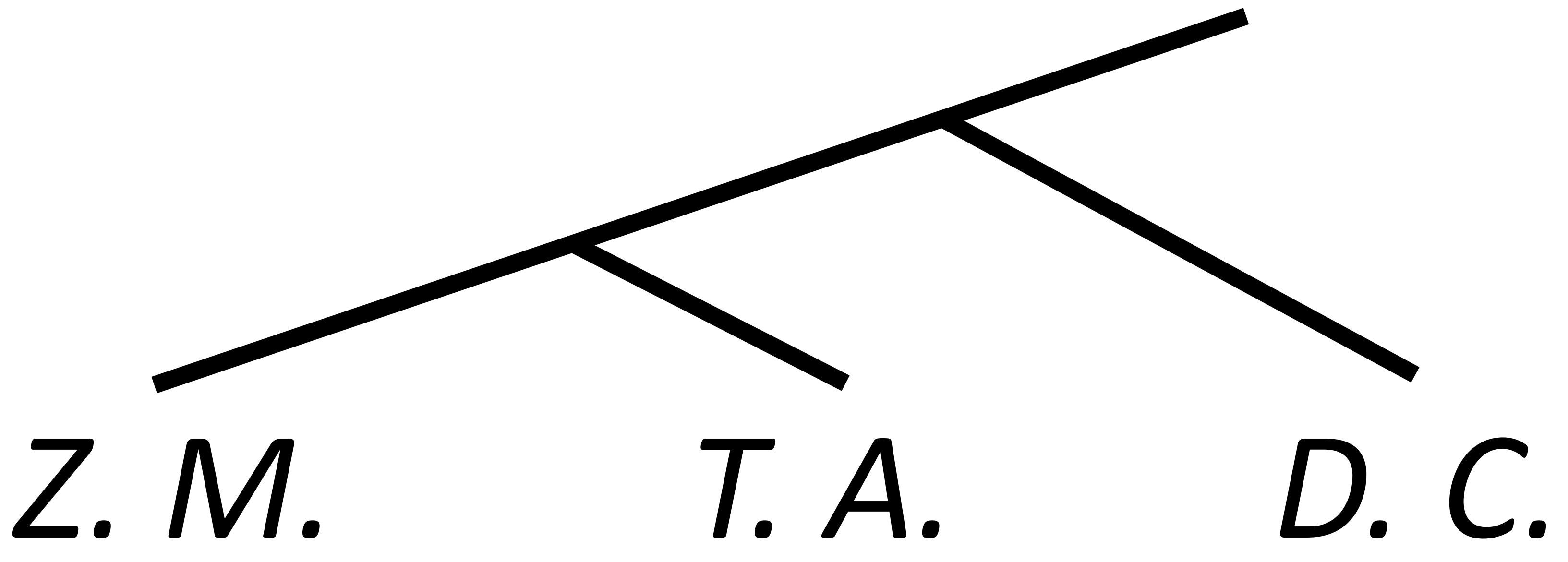


Z.M. : Zea mays.

T.A. : Triticum aestivum.

D.C. : Daucus carota.

ref.	**RNA-seq**			Mutation type in *Z.M.*
C	**C,A**	**C**	**C**	polymorphic
C	**C,T**	**C**	**C**	
C	**C**	**A**	**A**	fixed
C	**C**	**T**	**T**	
C	**C,A**	**A**	**C**	discarded
C	**C**	**T**	**C**	
C	**C,A**	**NA**	**C**	
C	**C**	**C**	**NA**	

NA = not available (indel/gap or unaligned)

Figure S1

Species	CDS sequence	RNA-seq data
Zea mays	ftp://ftp.ensemblgenomes.org/pub/release-43/plants/fasta/zea_mays/cds/	SRR7403478-SRR7403480, SRR7403485-SRR7403487
Triticum aestivum	ftp://ftp.ensemblgenomes.org/pub/release-43/plants/fasta/triticum_aestivum/cds/	SRR8767835, SRR8767837
Daucus carota	ftp://ftp.ensemblgenomes.org/pub/release-43/plants/fasta/daucus_carota/cds/	SRR7641984-SRR7641993

Species	Number of unique genes	Number of unique codons
Zea mays	39254	13958446

Number of mutations detected in the whole CDS regions

Type	Total	Synonymous	Non-synonymous	Nonsense
Fixed	843285	437056	400943	5286
Polymorphic	12041	4865	6875	301

Figure S2

Fixed/polymorphic ratio of mutations detected in the whole CDS regions

Type	**Synonymous**		**Non-synonymous**	**Nonsense**
	tAI up	**tAI down**		
Highly expressed genes	127.2	60.3	52.9	14.5
Lowly expressed genes	101.6	72.8	61.4	19.3

Figure S3

Frequency spectrum of the polymorphic mutations

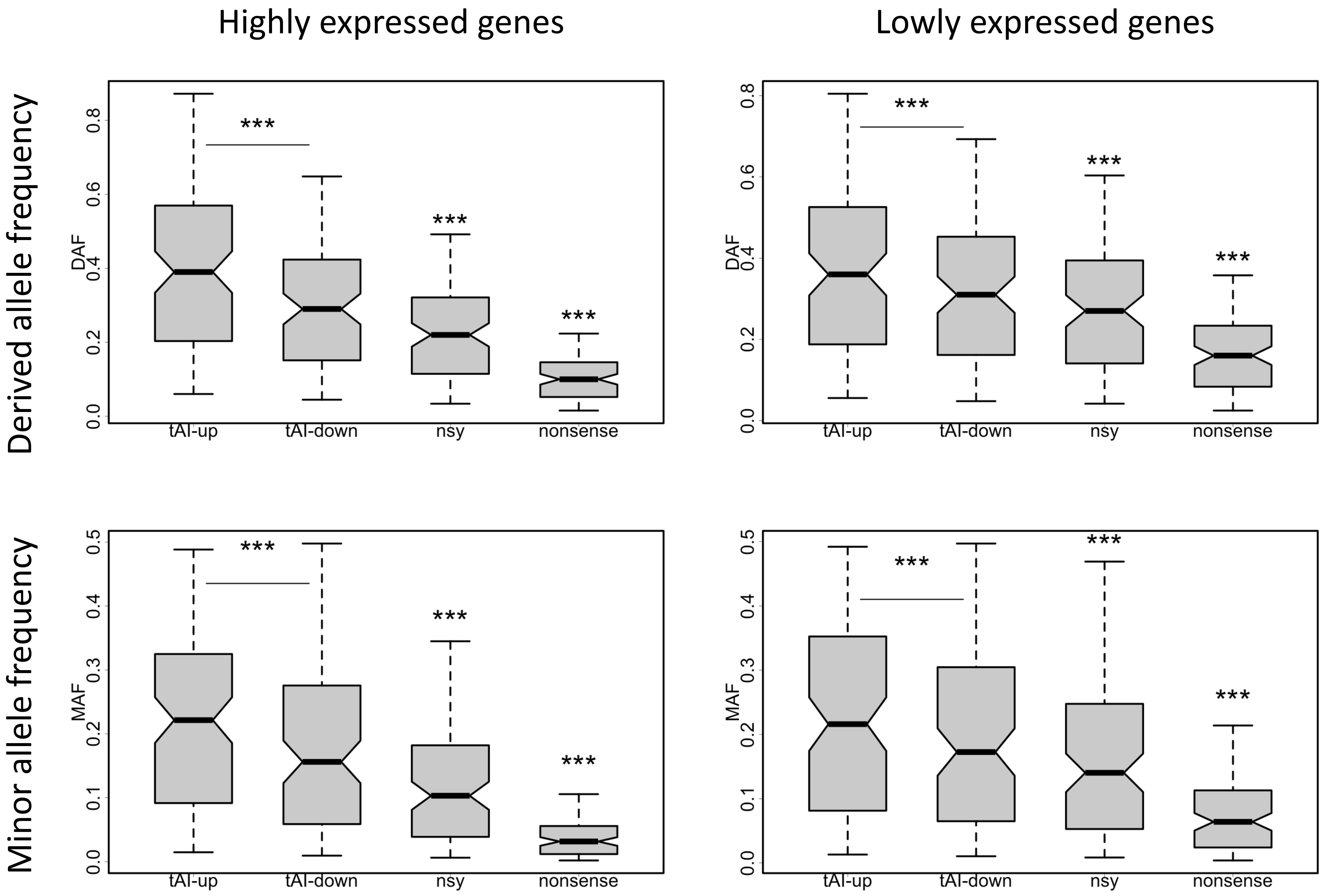


Figure S4

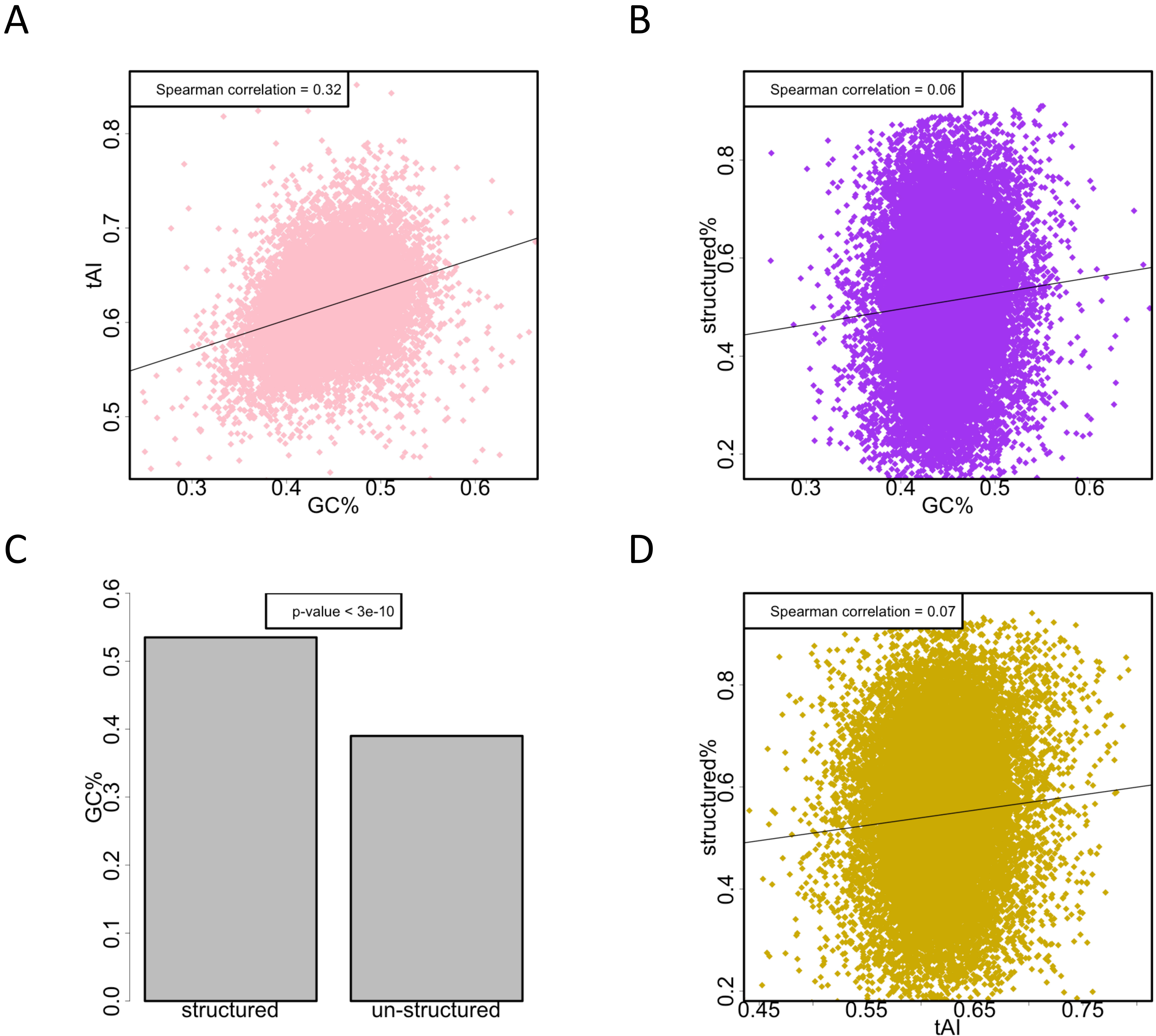

A
Spearman correlation = 0.32
tAI
0.5
0.6
0.7
0.8
0.3
0.4
0.5
0.6
GC%
B
Spearman correlation = 0.06
structured%
0.2
0.4
0.6
0.8
0.3
0.4
0.5
0.6
GC%
C
p-value < 3e-10
GC%
0.0
0.1
0.2
0.3
0.4
0.5
0.6
structured
un-structured
D
Spearman correlation = 0.07
structured%
0.2
0.4
0.6
0.8
0.45
0.55
0.65
0.75
tAI

Figure S5

Frequency spectrum of the polymorphic mutations

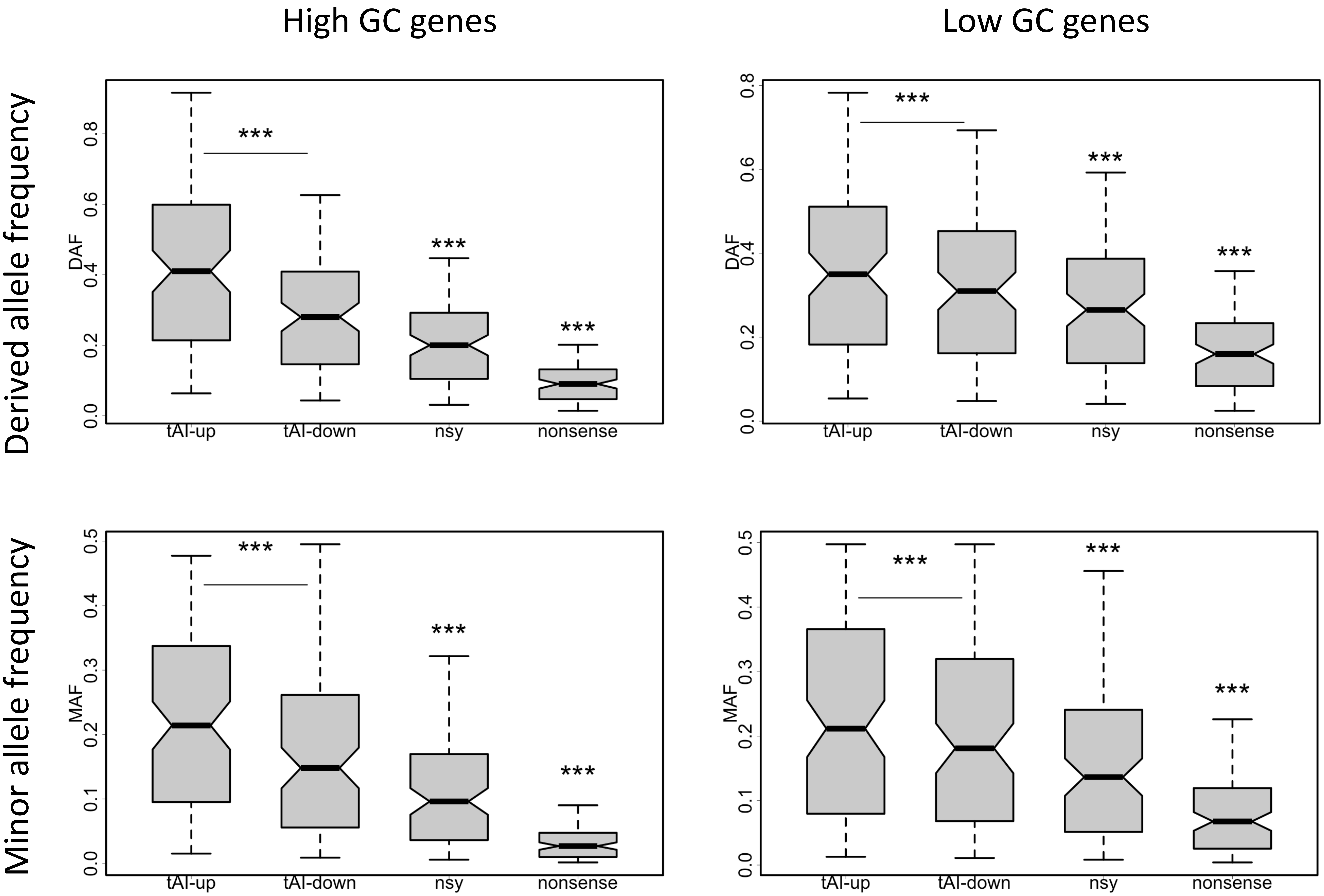


Figure S6

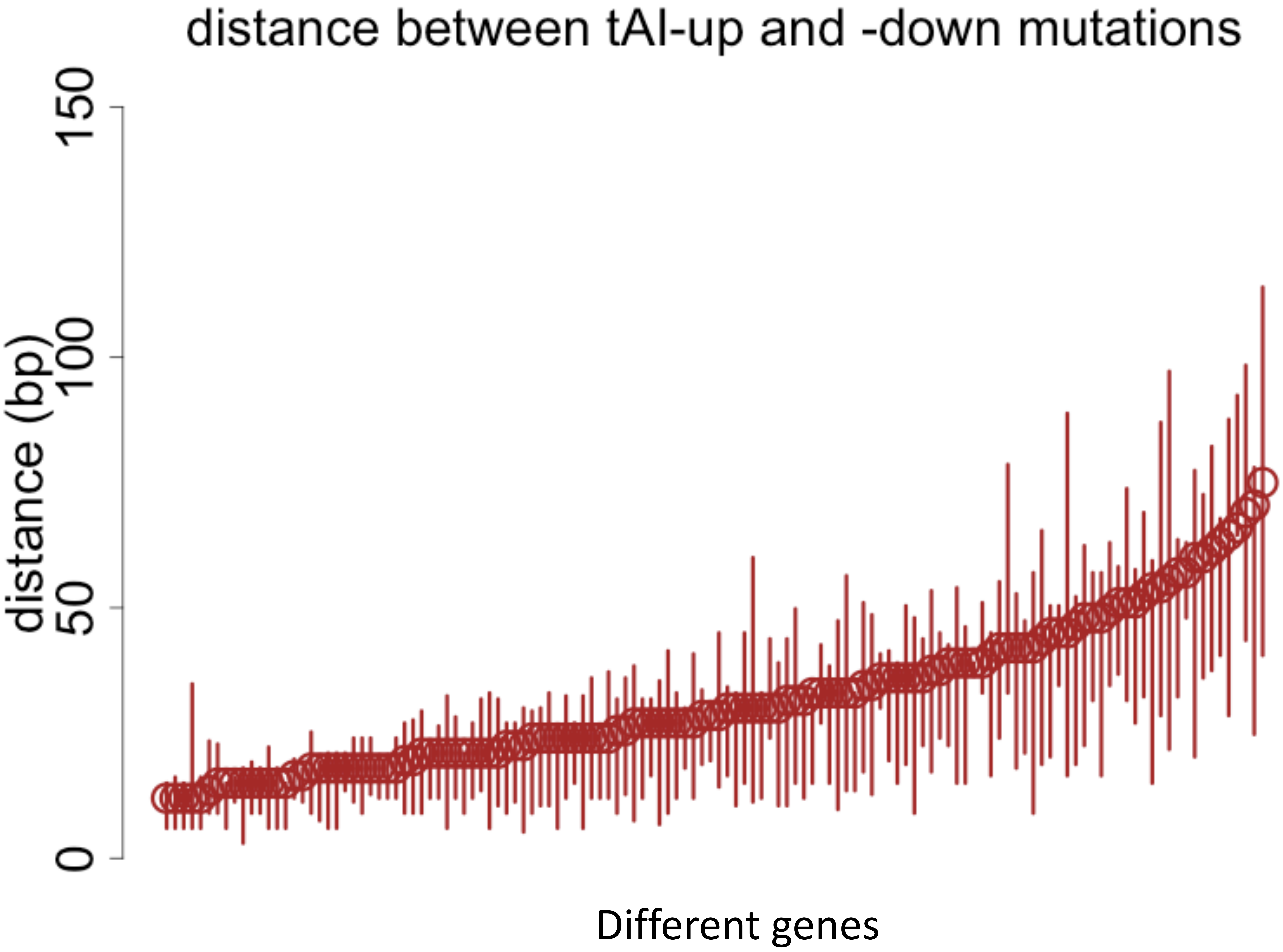
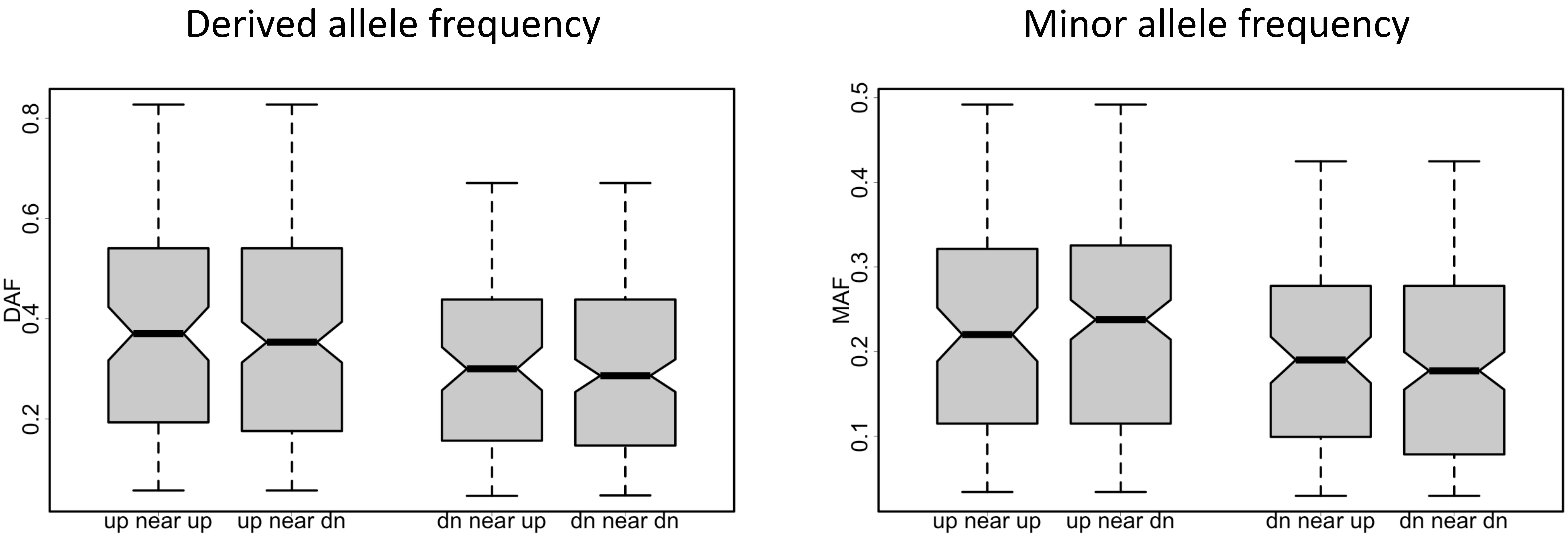

distance between tAI-up and -down mutations
distance (bp)
150
100
50
0
Different genes

Figure S7



Derived allele frequency

Minor allele frequency

Figure S8