

**DRAFT**

<sup>4</sup>MalariaGEN @@TODO

Mutation			Population allele frequency (%)									LD ( $D'$ )	
Position <sup>1</sup>	<i>Ag</i> <sup>2</sup>	<i>Md</i> <sup>3</sup>	AO <i>Ac</i>	BF <i>Ac</i>	GN <i>Ag</i>	BF <i>Ag</i>	CM <i>Ag</i>	GA <i>Ag</i>	UG <i>Ag</i>	KE	GW	L995S	L995F
2,390,177 G>A	R254K	R261	0	0	0	0	32	21	0	0	0	-0.98	0.96
2,391,228 G>C	V402L	V410	0	7	0	0	0	0	0	0	0	-1	-0.41
2,391,228 G>T	V402L	V410	0	7	0	0	0	0	0	0	0	-1	0.10
2,399,997 G>C	D466H	-	0	0	0	0	7	0	0	0	0	-1	1
2,400,071 G>A	M490I	M508	0	0	0	0	0	0	0	18	0	-0.33	-1
2,400,071 G>T	M490I	M508	0	0	0	0	0	0	0	0	0	-1	-0.01
2,416,980 C>T	T791M	T810	0	1	13	14	0	0	0	0	0	-1	1
2,422,651 T>C	L995S	L1014	0	0	0	0	15	64	100	76	0	1	-1
2,422,652 A>T	L995F	L1014	86	85	100	100	53	36	0	0	0	-1	1
2,424,384 C>T	A1125V	K1133	9	0	0	0	0	0	0	0	0	-1	-1
2,425,077 G>A	V1254I	I1262	0	0	0	0	0	0	0	0	5	-1	-1
2,429,617 T>C	I1527T	I1532	0	14	0	0	0	0	0	0	0	-1	-1
2,429,745 A>T*	N1570Y	N1575	0	26	10	22	6	0	0	0	0	-1	0.98
2,429,897 A>G	E1597G	E1602	0	0	6	4	0	0	0	0	0	-1	1
2,429,915 A>C	K1603T	K1608	0	5	0	0	0	0	0	0	0	-1	1
2,430,424 G>T	A1746S	A1751	0	0	11	13	0	0	0	0	0	-1	1
2,430,817 G>A	V1853I	V1858	0	0	8	5	0	0	0	0	0	-1	1
2,430,863 T>C	I1868T	I1873	0	0	18	25	0	0	0	0	0	-1	1
2,430,880 C>T	P1874S	P1879	0	21	0	0	0	0	0	0	0	-1	1
2,430,881 C>T	P1874L	P1879	0	7	45	26	0	0	0	0	0	-1	1
2,431,061 C>T	A1934V	A1939	0	12	0	0	0	0	0	0	0	-1	1
2,431,079 T>C	I1940T	I1945	0	4	0	0	7	0	0	0	0	-1	1

**Table 1. Non-synonymous mutations in the voltage-gated sodium channel gene.** All mutations are at 5% frequency or above in one or more of the 9 Ag1000G phase 1 populations, with the exception of 2,400,071 G>T which is only found in the CM*Ag* population at 0.4% frequency but is included because another mutation (2,400,071 G>A) is found at the same position causing the same amino acid substitution (M490I). Substitutions marked with an asterisk (\*) failed conservative variant filters applied genome-wide in the Ag1000G phase 1 AR3 callset, but appeared sound on manual inspection of read alignments.

<sup>1</sup>Position relative to AgamP3 reference sequence, chromosome arm 2L.

<sup>2</sup>Codon numbering according to transcript AGAP004707-RA in geneset AgamP4.4.

<sup>3</sup>Codon numbering according to *Musca domestica Vgsc* EMBL accession X96668 [2].



**Figure 1.** Demo figure.

TODO

Foo	Bar	Baz
1	a	True
2	b	False

**Table 2.** This is a table.

## Discussion

TODO

## Methods

TODO

## References

- [1] Nandita R. Garud et al. ‘Recent Selective Sweeps in North American *Drosophila melanogaster* Show Signatures of Soft Sweeps’. In: *PLoS Genetics* 11.2 (2015), pp. 1–32. issn: 15537404. arXiv: 1303.0906.
- [2] Martin S Williamson et al. ‘Identification of mutations in the houseflypara-type sodium channel gene associated with knockdown resistance (kdr) to pyrethroid insecticides’. In: *Molecular and General Genetics MGG* 252.1 (1996), pp. 51–60.