

SUPPLEMENTAL MATERIAL

Table S2. Sequence context and positions of re-sequenced SNPs

Each SNP detected in *M. fascicularis* is listed with its chromosomal location, its flanking region and the number of reads observed for each of the SNP containing alleles. The ambiguity character is given in upper- or lower-case to indicate which allele was observed more frequently. In the case of ideal sampling, it is expected to observe maternal and paternal alleles with equal frequencies. Note that some SNPs in this table do not fulfill all criteria as mentioned in the main text (i.e., more than 12 reads present). They were included for quality assessment and verified by re-sequencing. In the draft sequence submitted to the EMBL-EBI database, potential SNPs were indicated by IUPAC ambiguity characters using the following conventions (where n stands for number of reads observed):

R: A/G SNP with $n(A) \geq n(G)$; r: A/G SNP with $n(A) < n(G)$; Y: C/T SNP with $n(C) \geq n(T)$; y: C/T SNP with $n(C) < n(T)$ etc. Lowercase letters a, c, g, t indicate positions that aligned to gap characters in some (but not the majority of) reads. Thus, translating letters using following scheme will replace all ambiguities with their most frequently observed unambiguous character:

R→A, r→G, Y→C, y→T, M→A, m→C, K→G, k→T, W→A, w→T, S→C, s→G, a→A, c→C, g→G, t→T.

SNP ID	flanking region	chr	SNP position	A	C	G	T
1	GGTGGAAACAGGTGCCAAGTGrCCTTCTCACTTAGTCAGCAG	1	42115179	5	0	7	0
2	CAGACATCAGAATCAAAGCyAAACCCTGTCGTTAAAACTG	2	48974723	0	3	0	7
3	GAACAGTCTGGCTCTATCTAKGAGGGCTGAACAATTmCATA	2	153926899	0	0	5	4
4	TCTAKGAGGGCTGAACAATTmCATATCCCATGAACAAGCAA	2	153926915	4	5	0	0
5	CCATTCCCAGCAATATACCCrAAAGAGCCAAGAGAAATTCT	2	153926958	4	0	8	0
6	GTGGCAGGATTATTTTGAGASTCAGCCACAACGGTTTCCCT	3	49253194	0	4	4	0
7	ACACCACTCTATCAGTACCARTTTAAATGGTATTAGTTCAT	4	91567845	4	0	3	0
8	GTGAAGTGTCTGGGTTAGrAGCTCTTCTTCTACGTGTAG	8	14911750	4	0	7	0
9	TGTTTTAAAGGGTTTGCAGrTTAACTTTTCTAAGATGCT	8	73523707	3	0	4	0
10	TGTTGTCCACAATCCTGCTAyACCATCTTCTCTCTCCAGC	8	146241555	0	5	0	6
11	AGGCCCTAGTCAGATCTGAGRGtGTCTGTTTTATCAGTTCT	9	27908614	3	0	2	0
12	TTGAGTCATCTCTGTGTGAYTCAATTTCTTACTGGTAAAA	10	78723700	0	4	0	4

13	TGCTCCTTGACTGACCGTGGRGTTCTATCCCAGCAAAGCCC	10	94243544	5	0	4	0
14	CTCTATTTGGAAGTCAAGGGRATGTTGGCTGTGCCTATCAG	11	53991066	10	0	6	0
15	GTAAGGGAGAAAGGGAAGAGMACCCTCTTTTCCACTCCTGT	12	75693801	5	4	0	0
16	GTCCTCTATAGGATTAGAGrCACCAGGACAAGACAGAATA	13	30435795	4	0	9	0
17	CATTCTGCTAAATAGAGAAGYTAGTCACTAAGAGCATCTGT	15	3318468	0	5	0	2
18	ATGCCCAGGATCAGCAAATCYGTAGAGACAGAAAGGAGATT	15	3318531	0	4	0	2
19	GTCAGGTAAGACCTAGGGGARGTGTGGGATTGGGGAATGAC	15	3318586	5	0	5	0
20	CACCTCTCCAGCCATGCTGCSAACACTTCTACCTTCTTCCC	16	5406756	0	4	4	0
21	TCAGATGATAATACACCCTCYTCTCAAAGAAGGACACAGTT	17	37407553	0	5	0	5
22	CTTATAATCTCCTCTTGCTGsTTTATTTTTACTGTGGCTAC	18	21002152	0	3	4	0
23	AGGATCACTTGAGCCTGGGARTTCGAATGAATGAAGGCCGG	19	6310124	6	0	6	0
24	GTTGGTGATGGGGTAAAATAYTGAAGACCACATGGACGACT	20	9325943	0	5	0	3
25	AGATCAGATAGAAAACCTCCAYATCCCCTTCCCTCCATATC	20	9326004	0	4	0	3
26	GCAGCGGCCTGATGGCTTCKTTAGTGCCCTCCATGGTCAG	20	9326071	0	0	7	3
27	TTGGGAAGCTGAGGTGGGCMGATCACAAGGTCAAGAGTTCG	20	60948392	3	3	0	0
28	ACCACCGCTTACGCAGAAGARAGAAGGCACCGGAGAGCGAT	X	154397246	8	0	3	0