

Table S2. Transmission data for initial screening of the six hotspots

Hotspot E		E6.8A/G																	
		CO			NCO														
man	molecules screened	A	G	% G	A	G	% G												
17	14720	20	16	44	9	12	57												
56	22080	17	14	45	3	10	77												
	TOTAL	37	30	45 (ns)	12	22	65 (ns)												
Hotspot F		F5.9T/C						F6.0T/A						F6.1A/G					
		CO			NCO			CO			NCO			CO			NCO		
man	molecules screened	T	C	% C	T	C	% C	A	T	% T	A	T	% T	A	G	% G	A	G	% G
28	16660	n/a	n/a	n/a	n/a	n/a	n/a	81	67	45	8	6	43	83	65	44	0	11	100
11	16560	24	20	45	0	3	100	18	26	59	3	1	25	18	26	59	3	6	67
	TOTAL	24	20	45 (ns)	0	3	100 (ns)	99	93	48 (ns)	11	7	61 (ns)	101	91	47 (ns)	3	17	85 (**)
Hotspot H		H7.5A/G						H7.6A/G											
		CO			NCO			CO			NCO								
man	molecules screened	A	G	% G	A	G	% G	A	G	% G	A	G	% G						
25	24840	13	18	58	3	7	70	9	22	71	4	6	60						
52	22080	28	21	43	3	5	63	23	26	53	2	4	67						
	TOTAL	41	39	49(ns)	6	12	67 (ns)	34	41	60 (ns)	6	10	63 (ns)						

Hotspot K		K7.4T/C						K7.5C/G					
		CO			NCO			CO			NCO		
man	molecules screened	T	C	% C	T	C	% C	C	G	% G	C	G	% G
28	13800	14	6	30	8	12	60	12	8	40	7	10	59
90	29440	26	35	57	12	28	70	31	27	47	28	12	30
	TOTAL	40	41	51 (ns)	20	40	67 (*)	43	35	45 (ns)	35	22	39 (ns)
Hotspot T		T7.9A/G											
		CO			NCO								
man	molecules screened	A	G	% G	A	G	% G						
25	6992	11	20	65	5	10	67						
60	9200	0	2	100	0	1	100						
	TOTAL	11	22	67 (ns)	5	11	69 (ns)						
Hotspot 5A		5A7.1T/C						5A7.2A/G					
		CO			NCO			CO			NCO		
man	molecules screened	T	C	% C	T	C	% C	A	G	% G	A	G	% G
243	16560	20	30	60	2	2	50	n/a	n/a	n/a	n/a	n/a	n/a
253	15180	n/a	n/a	n/a	n/a	n/a	n/a	39	78	67	6	28	82
	TOTAL	20	30	60 (ns)	2	2	50 (ns)	39	78	67 (***)	6	28	82 (***)

Deviation from expected 50:50 ratio of alleles determined by 2-tailed exact binomial test; (ns) = P>0.05, (*) = P<0.05, (**) = P <0.005, (***) = P<0.0005

n/a, not applicable