Fig. S6. Information on the polymorphic site YE17.1 - Pos 1277

(a) Sequence alignment (HT1,4,5,6, HTPrz1,2; HT2,3; Reference from BAC clone E; homologous sequence on EcaX) with primer positions underlined. Positions identical to the sequence in the first raw are represented with a hyphen. The mutation leading to HT2/3 is marked. (b) PCR products amplified from male (m) and female (f) genomic DNA and a no-template-control (-). (c) Capillary sequence traces of the confirmed mutations in HT1,4,5,6 and HT2,3 respectively.

А		
YE17_HT1/4/5/6/HTPrz	TCTGAGGTGG TGAGAGAATC ATACTTGAGA GCACATGTTG CAAAGCCAAG ATGCAGG <u>GCC</u> 1166	
YE17_HT2/3 YE17-BACcontig		
ecaX:6089749-6071249	cccaagtg	
YE17_HT1/4/5/6/HTPrz	TAAGTTGTTC GCAGAGAGCA AGATTACCTC CTGGGACAAC TAGAGCAGGA CCCAGAGGTG 1126	
YE17_HT2/3 YE17-BACcontig		
ecaX:6089749-6071249	tgc-g	
YE17_HT1/4/5/6/HTPrz YE17 HT2/3	CTGCCTTTGC AACAGAGCTA GGCTTCCATG AATGAC TCTCGAGTTC TACATTCACA 1282	
YE17-BACcontig		
ecaX:6089749-6071249	cccagt cagt c	
YE17_HT1/4/5/6/HTPrz YE17 HT2/3	GTTTGAGATT ACTGTTTAGA AAGCACACTT CTGTTGGTTG CAGGCGTGAA TAACAGTGAT 1342	
YE17-BACcontig		
ecaX:6089749-6071249	gggatt cgggtgtgag tcac	
YE17_HT1/4/5/6/HTPrz YE17 HT2/3	TGTATAAAGT GTAGAATCAC TTATTAGAAA TCAGAGACAA TCTATCTGTT GTTCAGCCGG 1402	
YE17-BACcontig		
ecaX:6089749-6071249	gcc ct-	
YE17_HT1/4/5/6/HTPrz YE17 HT2/3	GTGG <u>ACA CTGGACACCA CCAGTCA</u> GG. CTGTCCGATG CTGGAGAACA ACGATGCTAC 1458	
YE17-BACcontig		
ecaX:6089749-6071249	gatgtgg tt	

	Traces from y-50869
B mmmmmmmmf-	1-3 00 ? set-Chrani. NextFrame MaskMatches Help
	HT1, 4, 5, 6
YE17.1 - Pos 1277	HT2, 3

Base 72 of 209 (102 in contig)