

Fig. S4. Information on the polymorphic site YE3 - Pos 10594

(a) Sequence alignment (HT1,2,4,5,6, HTPPrz1,2; HT3; Reference from BAC clone E; homologous sequence on EcaX) with primer positions underlined. Positions identical to the sequence in the first row are represented with a hyphen. The variant leading to HT3 is marked. b) PCR products amplified from male (m) and female (f) genomic DNA and a no-template-control (-) when placing the reverse primer in a Y-exclusive region (underlined.) (c) PCR products amplified from the same samples as in (B) with the reverse primer shifted downstream, leading to an amplification in females also. (d) Capillary sequence traces of the confirmed mutations in HT1,2,3,5,6 and HT3, respectively.

A

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YE3_HT1/2/4/5/6/HTPrz CCCTAATCCA TTTCAGTAAC TTCCCTCTGC TGAGCATCTA GGATTCCAGA AATGAAATCT 10504
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 -----c-----

YE3_HT1/2/4/5/6/HTPrz GGGTCCAAGA TAAGTCTTTT GAAACATGTT GCCAAACTAC TCACCAGAAA AGCTGTCAGA 10564
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 -----c--c-----t--

YE3_HT1/2/4/5/6/HTPrz TTCGTAGTCT AATCAGCATT AGAACAAGTT AAGTGTCTAT TTCTCACAGT CTCACCCACA 10624
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 ---cc-----

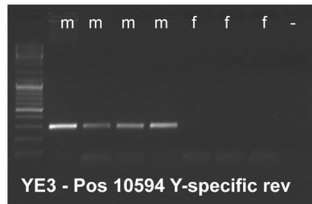
YE3_HT1/2/4/5/6/HTPrz ATGGGCACTG CTCTTCTATT AGATCTCTGT CAACTTGACA GT.AAAACCT AGTGTCTCAC 10683
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 -----t--c-----c-----

YE3_HT1/2/4/5/6/HTPrz TTTTAAA... .CTTGTAGGT CCTAGTTAAA CTCTTTTT... .ATATGC TTGTTTCTTA 10733
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 -----taa g---c---c--- -aTC--g-Tt aaca-----

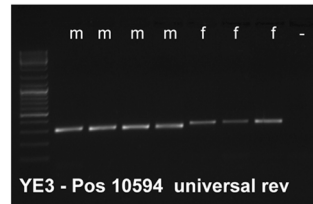
YE3_HT1/2/4/5/6/HTPrz TATGTACTTC TCA..... CTGTCCCTTT CATCCAACTG CCTACTGGGG 10776
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 -t--c----- -ttttagg aactgcctat t--g-----t t-----

YE3_HT1/2/4/5/6/HTPrz TATAAATTC TTTCTTTACA TCAGCTACTG CTAACCAGC TTTGTTACTA TACACCTGCT 10836
YE3_HT3 -----
YE3_BAC -----
ecaX:6050390- 6047628 --c----- c--c----- -t-t----- -t-t-----
    
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B



C



D

