

Additional file 6 – Multiple alignments of non-coding DNA within each of 9 tandemly duplicated blocks in the *F3'5'H* locus on chr6

On top of each page, coloured bars indicate annotated TEs in the PN40024 genome; sequence gaps (Ns) in the genome assembly are indicated by dotted red lines. Plots of sequence identity range from 50 to 100% on the y-axis in the LAGAN multi-panels. The number of base pairs shared by each duplicated block with the reference block (on top) is given on the right-hand side, with the average nucleotide identity.

















