Supplementary table 4. Analysis of expression for genes found at Hga locus at chromosome arm 3DS and at homoeologous region of chromosome 3B.[‡]

Non-collinear genes				
3DS	**3DS_matching_ESTs**	**3B**	**3B_matching_ESTs**	**P-values of two-tailed binomial test**
Taa3DS_ctg1484.00020.1				
Taa3DS_ctg1484.00040.1	1			
Taa3DS_ctg1484.00050.1*				
Taa3DS_ctg447.00010.1	3	TAA_ctg0954b.00180.1	1	0,63
Taa3DS_ctg447.00020.1	26	TAA_ctg0954b.00200.1	9	**0,006**
		TAA_ctg0954b.00210.1		
Taa3DS_ctg447.00030.1	3	TAA_ctg0954b.00215.1	3	
Taa3DS_ctg447.00040.1		TAA_ctg0954b.00216.1*		
Taa3DS_ctg447.00050.1	1	TAA_ctg0954b.00220.1	1	
Taa3DS_ctg447.00070.1	2	TAA_ctg0954b.00240.1	0	0,5
Taa3DS_ctg447.00090.1	3	TAA_ctg0954b.00260.1	0	0,25
		TAA_ctg0954b.00270.1		
Taa3DS_ctg447.00100.1		TAA_ctg0954b.00280.1		
Taa3DS_ctg447.00120.1		TAA_ctg0954b.00300.1		
Taa3DS_ctg447.00140.1	0	TAA_ctg0954b.00320.1	2	0,5
Taa3DS_ctg447.00160.1		TAA_ctg0954b.00340.1		
		TAA_ctg0954b.00350.1*		
Taa3DS_ctg447.00170.1	0	TAA_ctg0954b.00360.1	1	0,5
Taa3DS_ctg447.00190.1	1			
Taa3DS_ctg447.00200.1		TAA_ctg0954b.00380.1		
Taa3DS_ctg447.00220.1		TAA_ctg0954b.00400.1*		
Taa3DS_ctg447.00230.1		TAA_ctg0954b.00410.1*		
Taa3DS_ctg447.00240.1	2			
Taa3DS_ctg447.00250.1				
Taa3DS_ctg447.00260.1	1			
Taa3DS_ctg447.00270.1	2	TAA_ctg0954b.00415.1*	0	0,5
Taa3DS_ctg447.00320.1		TAA_ctg0954b.00460.1		
		TAA_ctg0954b.00470.1		
		TAA_ctg0954b.00480.1		

Collinear genes

3DS	3DS_matching_ESTs	3B	3B_matching_ESTs	P-values of two-tailed binomial test
Taa3DS_ctg1484.00010.1	1	TAA_ctg0954b.00140.1	1	
Taa3DS_ctg1484.00030.1*		TAA_ctg0954b.00150.1*		
Taa3DS_ctg1484.00060.1	9	TAA_ctg0954b.00160.1	1	**0,02**
Taa3DS_ctg447.00060.1		TAA_ctg0954b.00230.1		
Taa3DS_ctg447.00080.1	2	TAA_ctg0954b.00250.1	1	1
Taa3DS_ctg447.00110.1	0	TAA_ctg0954b.00290.1	3	0,25
Taa3DS_ctg447.00130.1		TAA_ctg0954b.00310.1		
Taa3DS_ctg447.00150.1		TAA_ctg0954b.00330.1		
Taa3DS_ctg447.00180.1		TAA_ctg0954b.00370.1		
Taa3DS_ctg447.00210.1	24	TAA_ctg0954b.00390.1	28	0,58
Taa3DS_ctg447.00280.1	24	TAA_ctg0954b.00420.1	20	0,65
Taa3DS_ctg447.00290.1		TAA_ctg0954b.00430.1		
Taa3DS_ctg447.00300.1	4	TAA_ctg0954b.00440.1	0	0,13
Taa3DS_ctg447.00310.1	1	TAA_ctg0954b.00450.1	0	0,5
Taa3DS_ctg447.00330.1	5	TAA_ctg0954b.00490.1	0	0,06

[‡] 1,071,335 ESTs publicly available in GenBank were used for expression analysis of CDS. Standalone Blastn programme was used to perform a similarity search with following parameters: reward for a nucleotide match 2; expectation value $1e^{-10}$; and default settings for all other parameters. Only blast hits with 100% identity and minimal length of 100 bp were considered. The number of unique ESTs for each is gene is given in the table. Non-collinear genes specific for one genome are labelled red and genes shared between the homoeologous chromosomes 3D and 3B are labelled in blue. Pseudogenes and gene fragments are marked by an asterisk. P-values of two-tailed binomial test were calculated for each pair of genes with differential expression. Significant differences are labelled in red.