Table 5. Ten genes in the qRT-PCR experiments did not have sufficient statistical power to determine a significant pattern of gene action.

GenBank accession no.	BLAST results (*e* value)*	Fold-change[†]	Sector[‡]	Significant pattern[§]	qRT-PCR *P* value
	No significant differences detected in qRT-PCR experiment				
CB815723	Putative cystatin (5e-46)	2.99	2	B < M ≈ F	0.7942
DV489577	Phospholipase-like protein (9e-39)	4.56	4	F ≈ B < M	0.6929
DV493407	Cytochrome *c* oxidase subunit 2 (3e-26)	1.97	5	F ≈ B < M	0.1122
BM348600	ns	3.87	8	F < B	0.1746
DV489676	Expressed protein (1e-25)	6.36	10	M < B ≈ F	0.098
CD484517	H3 histone, family 2 isoform (1e-28)	2.35	11	M < B ≈ F	0.3528
DV493472	Expressed protein (2e-61)	2.27	11	M < F	0.4008
BM351629	ns	3.91	7	F < B ≈ M	0.6863
DV489785	Multidrug resistance protein (6e-19)	1.78	7	F < B ≈ M	0.3865
DV493742	Zein (2e-67)	4.66	7	F < B ≈ M	0.8502

*Individual ESTs or the corresponding EST contigs (if available) were screened against a copy of the NCBI nr database downloaded Feb 8, 2006 by using Blastx. ns indicates no significant BLAST hits using an *E*-value cutoff of 1e-5.

[†] Fold changes were calculated between highest and lowest expressing genotypes.

[‡] Sector location in Fig. 2.

[§] Significant pattern determined in microarray analysis. ≈ indicates a failure to reject the null hypothesis that the values of the indicated genotypes are identical at $p<0.05$. B, B73; M, Mo17; F, F_1.