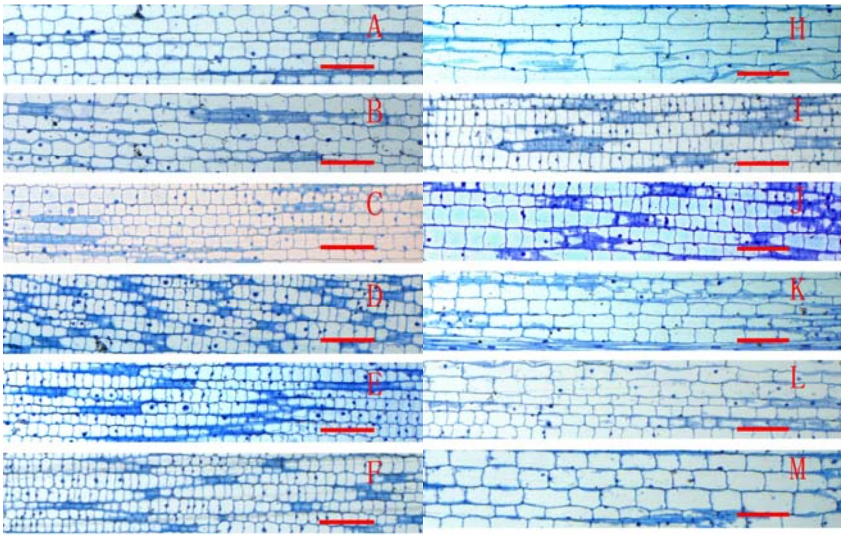
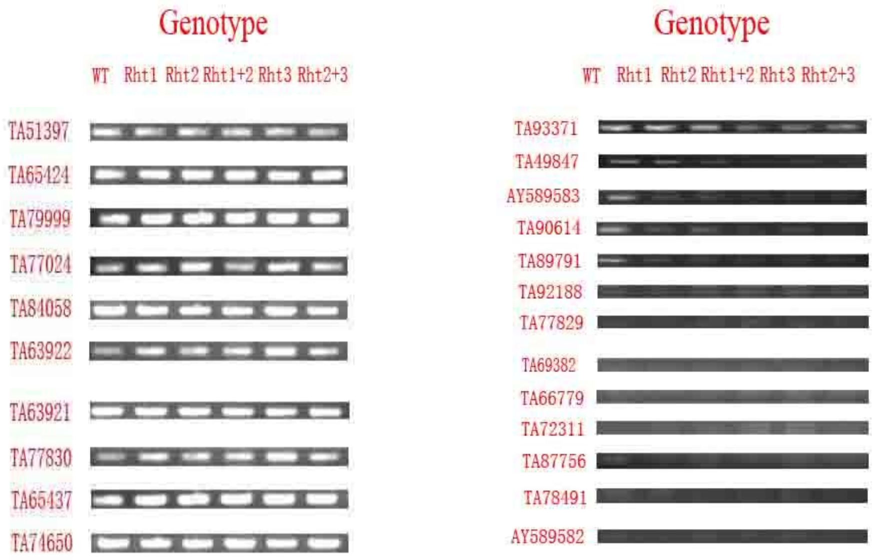
Appendix A Mean plant height and Peduncle length in six NILs

	WT	*Rht-B1b*	*Rht-D1b*	*Rht-B1c*	*Rht-B1b+ Rht-D1b*	*Rht-D1b+ Rht-B1c*
Peduncle length(mm)	331	264	270	148	135	115
Plant height(mm)	847	677	682	357	347	277
Ratio（%）	0.39	0.39	0.40	0.41	0.39	0.42



Appendix B Resin sections of peduncle in six NILs. 0-5mm regions from peduncle base of A , WT; B, *Rht-B1b* line; C, *Rht-D1b* line; D, *Rht-B1c* line; E, *Rht-B1b+Rht-D1c* line; F, *Rht-D1b+Rht-B1c* line and 5-10mm regions from peduncle base of H, WT; I, *Rht-B1b* line; J, *Rht-D1b* line; K, *Rht-B1c* line; L, *Rht-B1b+Rht-D1c* line; M, *Rht-D1b+Rht-B1c* line. Peduncles were taken in 21 May 2008. Sections were observed directly on a light microscope. Bar in A-M, 83 μm.

Appendix C Check the specific of 23 expansin gene primers in the peduncle of six near iso-genetic lines. The repeatability of the patterns was verified by comparing results from three independent experiments.



Appendix D The expression data for all detected expansin genes

TA63921		
	0-5mm	5-10mm
WT	0.008	0.0073
Rht-B1b	NA	0.001
Rht-D1b	0.05	0.0015
Rht-D1b+Rht-B1b	0.0085	0.008
Rht-B1c	0.005	0.001
Rht-D1b+Rht-B1c	NA	0.008
TA90614	0-5mm	5-10mm
WT	0.008	0
Rht-B1b	0.0082	0.0075
Rht-D1b	0.0075	0.004
Rht-D1b+Rht-B1b	0.009	NA
Rht-B1c	0.005	0.003
Rht-D1b+Rht-B1c	NA	NA
TA89791		
WT	NA	0.001
Rht-B1b	0.001	0.0025
Rht-D1b	NA	NA

Rht-D1b+Rht-B1b	NA	0.007
Rht-B1c	NA	NA
Rht-D1b+Rht-B1c	0.007	0.254
TA93371		
WT	0.006	0.007
Rht-B1b	NA	0.001
Rht-D1b	NA	0.002
Rht-D1b+Rht-B1b	0.001	0.0023
Rht-B1c	0.0025	0.007
Rht-D1b+Rht-B1c	NA	0.263
TA49847		
WT	0.007	NA
Rht-B1b	0.0015	NA
Rht-D1b	0.14	0.006
Rht-D1b+Rht-B1b	0.0027	0.007
Rht-B1c	0.08	NA
Rht-D1b+Rht-B1c	0.0021	NA
TA77829		
WT	0.008	0.0073
Rht-B1b	NA	0.001
Rht-D1b	0.05	0.0015
Rht-D1b+Rht-B1b	0.0085	0.008
Rht-B1c	0.005	0.001
Rht-D1b+Rht-B1c	NA	0.008
TA77830		
WT	0.008	0
Rht-B1b	0.0082	0.0075
Rht-D1b	0.0075	0.004
Rht-D1b+Rht-B1b	0.009	NA
Rht-B1c	0.005	0.003
Rht-D1b+Rht-B1c	NA	NA
TA74650		
WT	0.5975	0.4269
Rht-B1b	0.001	NA
Rht-D1b	0.799	NA
Rht-D1b+Rht-B1b	NA	0.007
Rht-B1c	0.007	0.001
Rht-D1b+Rht-B1c	NA	0.002
AY589583		
WT	0.001	NA
Rht-B1b	0.006	NA
Rht-D1b	0.007	0.001
Rht-D1b+Rht-B1b	NA	0.006
Rht-B1c	0.0022	NA

Rht-D1b+Rht-B1c	0.001	0.002
TA69382		
WT	0.4085	0.212
Rht-B1b	0.001	NA
Rht-D1b	0.004	0.0025
Rht-D1b+Rht-B1b	0.007	0.001
Rht-B1c	0.0019	0.0021
Rht-D1b+Rht-B1c	0.006	NA
TA63922		
WT	0.6085	0.3124
Rht-B1b	0.006	NA
Rht-D1b	0.0017	0.0015
Rht-D1b+Rht-B1b	0.006	0.001
Rht-B1c	NA	NA
Rht-D1b+Rht-B1c	0.001	0.263
TA65437		
WT	0.008	0
Rht-B1b	NA	NA
Rht-D1b	0.0014	0.006
Rht-D1b+Rht-B1b	NA	NA
Rht-B1c	0.008	0.001
Rht-D1b+Rht-B1c	NA	NA
ExpB2		
WT	0.8	1.189
Rht-B1b	0.93	1.013
Rht-D1b	0.9505	1.0015
Rht-D1b+Rht-B1b	1.0485	1.2885
Rht-B1c	0.5535	0.991
Rht-D1b+Rht-B1c	1.069	0.928
ExpB9		
WT	0.4965	1.003
Rht-B1b	0.1165	0.7315
Rht-D1b	0.075	0.455
Rht-D1b+Rht-B1b	0.365	0.6
Rht-B1c	0.2755	0.3035
Rht-D1b+Rht-B1c	0.5315	0.379
ExpA7		
WT	0.5925	1.13
Rht-B1b	0.6095	0.8325
Rht-D1b	0.799	0.8775
Rht-D1b+Rht-B1b	0.6665	0.627
Rht-B1c	0.4535	0.497
Rht-D1b+Rht-B1c	0.349	0.254
ExpA3		

WT	0.6085	0.912
Rht-B1b	0.226	0.227
Rht-D1b	0.148	0.242
Rht-D1b+Rht-B1b	0.2005	0.136
Rht-B1c	0.3415	0.7085
Rht-D1b+Rht-B1c	0.135	0.263
ExpB1		
WT	0.3785	0.7265
Rht-B1b	0.116	0.125
Rht-D1b	0.14	0.137
Rht-D1b+Rht-B1b	0.0905	0.1285
Rht-B1c	0.08	0.321
Rht-D1b+Rht-B1c	0.479	0.3285

The gene expression data obtained from multiplex RT-PCR were normalized by dividing the peak area for each gene by the peak area of the internal control genes α-tubulin (DQ435660) and Tubb4 (U76895).

Appendix E The expression of five expansin genes along the first 25 mm of the peduncle from the base in six NILs.

	0-5mm	5-10mm	10-15mm	15-20mm	20-25mm
ExpB2					
WT	0.8	1.189	0.626	0.546	0.53
Rht-B1b	0.93	1.013	1.093	0.81	0.39
Rht-D1b	0.9505	1.0015	1.056	0.835	0.435
Rht-D1b+Rht-B1b	1.0485	1.2885	1.079	0.8	0.425
Rht-B1c	0.5535	0.991	0.6755	0.489	0.0575
Rht-D1b+Rht-B1c	1.069	0.928	0.5975	0.468	0.2585
ExpB9					
WT	0.4965	1.003	0.4215	0.3245	0.2365
Rht-B1b	0.1165	0.7315	0.9095	0.485	0.215
Rht-D1b	0.075	0.455	0.767	0.44	0.175
Rht-D1b+Rht-B1b	0.365	0.6	0.775	0.52	0.35
Rht-B1c	0.2755	0.3035	0.311	0.315	0.274
Rht-D1b+Rht-B1c	0.5315	0.379	0.5205	0.408	0.23
ExpA7					
WT	0.5925	1.13	0.539	0.5275	0.4034
Rht-B1b	0.6095	0.8325	0.899	0.635	0.435
Rht-D1b	0.799	0.8775	0.718	0.625	0.615
Rht-D1b+Rht-B1b	0.6665	0.627	0.9065	0.695	0.395
Rht-B1c	0.4535	0.497	0.5095	0.4175	0.307
Rht-D1b+Rht-B1c	0.349	0.254	0.4155	0.2285	0.1675

ExpA3					
WT	0.6085	0.912	0.475	0.3185	0.383
Rht-B1b	0.226	0.227	0.2485	0.245	0.205
Rht-D1b	0.148	0.242	0.185	0.085	0.145
Rht-D1b+Rht-B1b	0.2005	0.136	0.1405	0.1215	0.11
Rht-B1c	0.3415	0.7085	0.4025	0.4035	0.1975
Rht-D1b+Rht-B1c	0.135	0.263	0.0585	0.071	0.0445
ExpB1					
WT	0.3785	0.7265	0.322	0.1355	0.1175
Rht-B1b	0.116	0.125	0.108	0.095	0.09
Rht-D1b	0.14	0.137	0.1385	0.11	0.1
Rht-D1b+Rht-B1b	0.0905	0.1285	0.1575	0.145	0.045
Rht-B1c	0.08	0.321	0.1515	0.1245	0.109
Rht-D1b+Rht-B1c	0.479	0.3285	0.558	0.455	0.2985

The gene expression data obtained from multiplex RT-PCR were normalized by dividing the peak area for each gene by the peak area of the internal control genes α-tubulin (DQ435660) and Tubb4 (U76895).