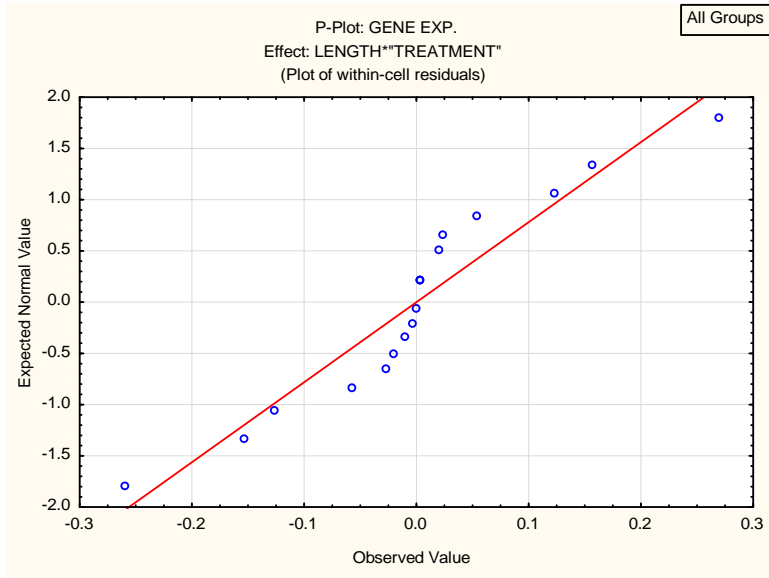
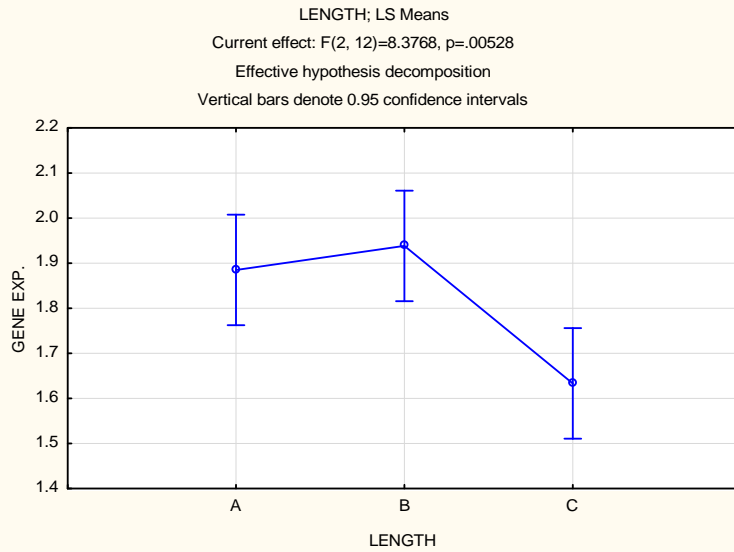


Appendix 7 Two way ANOVA analysis and multi-comparison analysis (Tukey HSD test) to compare expression levels of DhMYB gene between treated buds and untreated control

Univariate Tests of Significance for GENE EXP. (Spreadsheet24)					
Sigma-restricted parameterization					
Effective hypothesis decomposition					
Effect	SS	Degr. of Freedom	MS	F	p
Intercept	59.55042	1	59.55042	3133.317	0.000000
LENGTH	0.31841	2	0.15921	8.377	0.005284
TREATMENT	5.66722	1	5.66722	298.188	0.000000
LENGTH*TREATMENT	0.15148	2	0.07574	3.985	0.047076
Error	0.22807	12	0.01901		



Levene's Test for Homogeneity of Variances (Spreadsheet24)				
Effect: LENGTH*TREATMENT				
Degrees of freedom for all F's: 5, 12				
	MS Effect	MS Error	F	p
GENE EXP.	0.012251	0.005915	2.071084	0.139923



Univariate Tests of Significance for GENE EXP. (Spreadsheet24)					
Sigma-restricted parameterization					
Effective hypothesis decomposition					
Effect	SS	Degr. of Freedom	MS	F	p
Intercept	59.55042	1	59.55042	3133.317	0.000000
LENGTH	0.31841	2	0.15921	8.377	0.005284
TREATMENT	5.66722	1	5.66722	298.188	0.000000
LENGTH*TREATMENT	0.15148	2	0.07574	3.985	0.047076
Error	0.22807	12	0.01901		

Tukey HSD test; variable GENE EXP. (Spreadsheet24)					
Approximate Probabilities for Post Hoc Tests					
Error: Between MS = .01901, df = 12.000					
Cell No.	LENGTH	TREATMENT	{1}	{2}	{3}
			1.2667	2.5033	1.5067
1	A	C		0.000159	0.333947
2	A	T	0.000159		0.000165
3	B	C	0.333947	0.000165	
4	B	T	0.000160	0.836013	0.000208
5	C	C	0.240619	0.000159	0.007400
6	C	T	0.000164	0.347175	0.000357

Tukey HSD test; variable GENE EXP. (Spreadsheet24)						
Homogenous Groups, alpha = .05000						
Error: Between MS = .01901, df = 12.000						
Cell No.	LENGTH	TREATMENT	GENE EXP. Mean	1	2	3
5	C	C	1.000000		****	
1	A	C	1.266667		****	****
3	B	C	1.506667			****
6	C	T	2.266667	****		
4	B	T	2.370000	****		
2	A	T	2.503333	****		