

Table S1.

Characteristics	PUTATIVE EXPANSINS							
	Expansin A4 (HaEXPN4)	Expansin A7 (HaEXPN7)	Expansin 10 (HaEXPN10)	Expansin 11 (HaEXPN11)	Expansin 1 (HaEXPN1)	Expansin A1 (HaEXPN1.2)	Expansin 3 (HaEXPN3)	Expansin A15 (HaEXPN15)
Accession HaT13I	HaT131004607_1_AA	HaT131007346_1_AA	HaT131009575_1_AA	HaT131018566_1_AA	HaT131014971_1_AA	HaT131009552_1_AA	HaT131005436_1_AA	HaT131025136_1_AA
Locus Tag (gene) accession XRQ	HanXRQChr01g0009521	HanXRQChr06g0178721	HanXRQChr08g0210821	HanXRQChr13g0386941	HanXRQChr16g0503121	HanXRQChr17g0570851	HanXRQChr08g0236981	HanXRQChr09g0270611
Chromosome	HanXRQChr01	HanXRQChr06	HanXRQChr08	HanXRQChr13	HanXRQChr16	HanXRQChr17	HanXRQChr08	HanXRQChr09
Start	64064838	51216670	9589958	2469795	21219190	214553944	151037735	189762140
End	64068076	51219551	9592439	2471756	21222064	214555988	151039716	189763612
Strand	(- strand)	(- strand)	(+ strand)	(- strand)	(- strand)	(- strand)	(- strand)	(+ strand)
ORF Length (bp)	3239	2882	2482	1962	2875	2045	1982	1473
Protein sequence length(aa)	257	273	258	254	274	311	257	265
Blast2GO	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region	Cell Wall, membrane, plant-type cell wall organization, extracellular region
Orthologous Arabidopsis	AT2G39700.1	AT2G39700.1	AT1G26770.2	AT1G20190.1	AT1G69530.3	AT1G69530.2	AT2G37640.1	AT2G03090.1
Identity	80.54%	82.49%	76.40%	75.21%	80.00%	83.13%	80.93%	79.18%
Orthologous Soybean	Glyma.12G062700.1	Glyma.02G248500.1	Glyma.01G050100.1	Glyma.17G260400.1	Glyma.17G101400.4	Glyma.01G050100.1	Glyma.02G248500.1	Glyma.04G167800.1
Identity	84.23%	86.85%	81.20%	76.86%	83.70%	86.61%	85.77%	78.73%
Orthologous B. dystachyon	Bradi1g03640.1	Bradi1g03640.1	Bradi2g22290.1	Bradi5g04120.1	Bradi1g61190.1	Bradi2g22290.1	Bradi1g03640.1	Bradi2g53580.1
Identity	79.34%	81.82%	72.13%	69.08%	70.24%	75.82%	80.33%	76.09%