



Supplemental Fig. 1. Neighbor-Joining phylogenetic tree of EXPANSIN A and B protein sequences. The same tree as shown in Fig. 1 but with bootstrap values (1000 replicates).

AtEXPB1 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KTIIC-KRA-VTIIAIDQSPSGPSAKAKH----- 70
 AtEXPB2 GGACGYGVAVGQPPFSSRIAAGSPYIYDSKGGCCGACVYKCTIS--KSACS-KMH-VTWVITDCECPG--CVKESV----- 68
 AtEXPB3 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CSKTS----- 67
 AtEXPB4 GGACGYGVAVANPPLIYAVSAGSPILFNNKGGCCGACVYKCTIS--HPACS-ESP-VTWVITDCECPG--CPASBP----- 69
 AtEXPB5 GGACGYGVAVAKIIFPKYRCVYSGSPILFKDGKGGCCGACVYKCTIS--HPLCT-KKE-IKVMITDCECPG--CTKES----- 66
 OsEXPB1 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB10 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB11 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB12 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB13 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB14 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB15 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB16 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB17 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB18 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB2 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB3 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB4 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB6 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB8 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB9 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 PteEXPB1 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 Sb04g032820 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 Sb04g032830 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPB5 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 HvEXPB1 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 Sb06g024640 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 Sb06g024660 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 ZmEXPB2 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 VvCA070613 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 ZmEXPB4 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPL1 AGCGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 RdEXPA1 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 RsEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 TaEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 ZmEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 AtEXPA18 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 AtEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 BoEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 CmEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 HvEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 IbEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 MtEXPA7 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 MteXPA8 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPA17 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68
 OsEXPA30 GGACGYGLVDVVPKARVAVSPILFKGEGCGACIKVRCID--KSIIC-RRA-VTWVITDCECPG--CVKESV----- 68

AtEXPB1 -----HFDLSSGAFGAMAI--PCHNGVIRNRGHLNIIYRRTACKYRG---KNIAFHVWEGST--DFFLLSL 129
 AtEXPB2 -----HFDLSSGAFGAMAI--SGODSQRNRVGLQIQYRRVPCVHWG---KTVTFHVDGSGN--ANSFAV 126
 AtEXPB3 -----HFDLSSGAFGAMAI--ACESGPRNRGHLNIIYRRTACKYRG---KNIAFHVWEGST--DFFLLSL 128
 AtEXPB4 -----VHFDLSSGAFGAMAI--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 126
 AtEXPB5 -----VHFDLSSGAFGAMAI--RKGEDQRNRGHLNIIYRRTACKYRG---K-----K-----K-----K----- 123
 OsEXPB1 -----HFDLSSGAFGAMAK--DGKDEBRKAGIIDDQRRVPCVHWG---TKTFHVEEGSN--BFFLAV 115
 OsEXPB10 -----HFDLSSGAFGAMAK--EGKDEBRKAGIIDDQRRVPCVHWG---TKTFHVEEGSN--BFFLAV 125
 OsEXPB11 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 128
 OsEXPB12 CMNRAAHFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 137
 OsEXPB13 -----HFDLSSGAFGAMAK--DGKDEBRKAGIIDDQRRVPCVHWG---TKTFHVEEGSN--BFFLAV 125
 OsEXPB14 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 128
 OsEXPB15 -----HFDLSSGAFGAMAI--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 128
 OsEXPB16 -----HFDLSSGAFGAMAI--AGHGGQQRNRGHLNIIYRRTACKYRG---KNIAFHVWEGST--DFFLLSL 128
 OsEXPB17 -----HFDLSSGAFGAMAI--AGAGHQRNRGHLNIIYRRTACKYRG---KNIAFHVWEGST--DFFLLSL 128
 OsEXPB18 -----HFDLSSGAFGAMAI--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 128
 OsEXPB2 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVEEGSN--BFFLAV 124
 OsEXPB3 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVEEGSN--BFFLAV 124
 OsEXPB4 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVEEGSN--BFFLAV 124
 OsEXPB6 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVEEGSN--BFFLAV 124
 OsEXPB7 -----HFDLSSGAFGAMAK--DNRDDEBRKAGIIDDQRRVPCVHWG---LTVTFHVEEGSN--BFFLAV 124
 OsEXPB8 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVEEGSN--BFFLAV 124
 OsEXPB9 -----HFDLSSGAFGAMAK--PCKETBRKAGIIDDQRRVPCVHWG---QKTVFHWEGSN--BFFLAV 125
 PteEXPB1 -----HFDLSSGAFGAMAI--SGKEDQRNRAGLIIQYRRVPCVHWG---KTVTFHVDGSGN--BFFLAV 130
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 OsEXPB5 -----HFDLSSGAFGAMAI--RGMADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 127
 HvEXPB1 -----HFDLSSGAFGAMAI--RGMADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 127
 Sb06g024640 -----HFDLSSGAFGAMAI--RGMADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 131
 Sb06g024660 -----HFDLSSGAFGAMAI--RGMADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 128
 ZmEXPB2 -----HFDLSSGAFGAMAI--RGMADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 129
 VvCA070613 -----HFDLSSGAFGAMAK--SGODSQRNRVGLQIQYRRVPCVHWG---TSVTFHVDGSGN--BFFLAV 126
 ZmEXPB4 -----HFDLSSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 128
 OsEXPL1 -----LVLSGAFGAMAK--PCCADQRNRAGLIIQYRRVPCVHWG---VNLTFHVDGSGN--BFFLAV 124
 RdEXPA1 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 127
 RsEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 TaEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 126
 ZmEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 AtEXPA18 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 AtEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 127
 BoEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 CmEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 HvEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 126
 IbEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 MtEXPA7 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 MteXPA8 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 128
 OsEXPA17 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 129
 OsEXPA30 CNPFRHFDLSSGAFGAMAK--YRGIVPVYRRVPCVHWG---GVRFTIN--GN--BFFLAV 130

Supplemental Fig. 2. Multiple alignments of expansin protein sequences by CLUSTAL W. The amino acid sequence between 55 (Gly) and 181 (Ile) of AtEXPA7 and the equivalent regions of each protein were aligned.

The 'RH' cluster
 The 'D' cluster

		Percent Identity													
		1	2	3	4	5	6	7	8	9	10	11	12		
Divergence	1	████	65.8	63.1	64.2	63.8	49.3	52.2	51.3	51.4	51.3	45.8	36.9	1	HvEXPB1
	2	40.3	████	67.6	68.7	69.8	50.7	53.3	54.9	53.1	52.0	46.9	42.9	2	OsEXPB5
	3	40.1	38.1	████	69.8	86.9	50.4	55.5	52.4	52.2	52.0	48.0	38.1	3	ZmEXPB2
	4	39.1	36.7	34.8	████	67.7	47.8	52.2	52.7	51.8	51.3	46.5	40.1	4	Sb06g024640
	5	39.1	36.7	13.2	34.4	████	50.7	54.8	53.1	52.2	55.3	48.7	39.7	5	Sb06g024660
	6	75.0	70.8	71.7	77.4	70.9	████	73.9	69.0	69.3	70.7	64.8	44.0	6	PtrEXPB1
	7	66.0	61.8	58.3	66.8	58.7	28.0	████	70.6	69.5	65.4	64.0	46.8	7	RcXP002511649
	8	69.5	65.6	64.8	68.3	64.9	36.9	34.3	████	94.2	70.0	61.2	41.3	8	SIABB83474
	9	70.9	64.4	66.2	69.6	67.1	36.3	35.5	6.1	████	71.8	61.2	41.3	9	StABC47127
	10	68.6	64.6	64.7	69.1	61.6	35.3	39.3	37.3	34.4	████	63.4	45.6	10	WvCA070613
	11	81.4	77.9	75.0	80.9	70.8	44.2	44.8	52.1	50.7	47.0	████	46.0	11	AtEXPB2
	12	100.9	82.1	96.2	98.3	91.6	84.9	76.1	98.5	93.3	82.0	82.6	████	12	AtEXPB5
	1	2	3	4	5	6	7	8	9	10	11	12			

Supplemental Fig. 4. Percent amino acid identity of EXPBs from the 'RH' and 'D' clusters in Fig. 1. Whole amino acid sequences were aligned by CLUSTAL W. Red box indicates the 'RH' cluster, and blue box indicates the 'D' cluster. AtEXPB5 was taken as an outgroup member.