

ANT (AT4g37750): global tree  
File name:ANT.njtree0.svg  
122 aa residues 80 OTU included.  
Results of 19 partial trees included.  
Assemble Job Id: MZu87A selectNalign jobid: CD3gUz  
Tree job id: YKALcX  
BP values out of 100  
Analyzed by nonodera@nibb.ac.jp  
Date: Thu Aug 31 17:59:22 JST 2006

Short fragmental sequences  
**Smo\_At4g37750\_6\_1(Pt11)**  
**Smo\_At4g37750\_4\_1(Pt14)**  
**Smo\_At4g37750\_42\_1(Pt14)**  
**AAG52255(Pt14)**



→ Smo\_At4g37750\_2\_1(Pt1)

→ Smo\_At4g37750\_73\_1(Pt18) Smo\_At4g37750\_63\_1(Pt15)

→ BAD33427 Oryza sativa (japonica cultivar-group) WRINKLED1-like protein(Pt10)  
(Nipponbare)chromosome9

→ Smo\_At4g37750\_3\_1  
→ Smo\_At4g37750\_1\_1(Pt2)

(cultivar=?)chromosome8

→ Smo\_At4g37750\_18\_1 → Smo\_At4g37750\_62\_1(Pt17)

→ AAW78368 Oryza sativa (japonica cultivar-group) transcription factor AP2D8 (Dongjin)chromosome2

→ Ppa\_At4g37750\_26\_1 → Ppa\_At4g37750\_75\_1 → Ppa\_At4g37750\_4\_1 → AT2G41710 = NP\_565957 NP\_850355 AAC02777 AAM65663 BAC43380 DNA binding/transcription factor /DNA binding /transcription factor /putative AP2 domain transcription factor /putative AP2 domain transcription factor /putative AP2 domain transcription fac (pt 19) ← Possibly 1 domain possessing

→ Smo\_At4g37750\_31\_1 → Smo\_At4g37750890721677\_1(Pt16) 98% similar to Smo\_At4g37750\_31\_1(High quality mismatch=7)  
(Nipponbare)chromosome6

→ BAD68417 Oryza sativa (japonica cultivar-group) transcription factor AP2D4 (Dongjin)chromosome5  
→ AAW78366 Oryza sativa (japonica cultivar-group) transcription factor AP2D4 (Dongjin)chromosome5

→ XP\_482634 Oryza sativa (japonica cultivar-group) BAD10030 AP2/EREBP transcription factor-like protein /AP2/EREBP transcription factor-like protein (Nipponbare)chromosome8

→ AAF68121 Arabidopsis thaliana F20B17.12  
→ NP\_915953 Oryza sativa (japonica cultivar-group) BAB90395 BAD68218 AP2 DNA-binding domain protein-like/AP2 DNA-binding domain protein-like (Nipponbare)chromosome1

→ CAE00853 Oryza sativa (japonica cultivar-group) ABA96351 AP2-1 protein/AP2 domain, putative /aintegumenta, putative /aintegumenta-like protein (Zhonghua 11)chromosome11  
→ NP\_915953 Oryza sativa (japonica cultivar-group) BAB90395 BAD68218 AP2 DNA-binding domain protein-like/AP2 DNA-binding domain protein-like (Nipponbare)chromosome1  
→ AAW78371 Oryza sativa (japonica cultivar-group) transcription factor AP2D23-like (cultivar=?)chromosome1

→ AT3G54320 = NP\_191000 NP\_001030857 AAF80382 AAX11223 WR11 (WRINKLED 1); DNA binding/transcription factor /WR11 (WRINKLED 1); DNA binding /transcription factor /WRINKLED1 /activator of sporamin LUC 1  
→ NP\_915953 Oryza sativa (japonica cultivar-group) BAB90395 BAD68218 AP2 DNA-binding domain protein-like/AP2 DNA-binding domain protein-like (Nipponbare)chromosome1  
→ AAW78371 Oryza sativa (japonica cultivar-group) transcription factor AP2D23-like (cultivar=?)chromosome1

→ Ppa\_At4g37750\_98\_1  
→ Ppa\_At4g37750\_19\_1  
→ Ppa\_At4g37750\_62\_1  
(Nipponbare) chromosome11  
(Nipponbare) chromosome12  
→ CRE2 CRE1 2 domain-possesing CRE2, CRE1 (Chlamydomonas sequence found from the genomic sequence)

→ 10382\_Cre 5992\_Cre(Pt13) ← Possibly 1 domain possessing

→ BAD37532 Oryza sativa (japonica cultivar-group) BAD37484 putative LIPLESS2/putative LIPLESS2  
→ AAC49567 Zea mays AP2 DNA-binding domain protein  
→ AAV83488 Zea mays GLOSSY15  
→ Smo\_At4g37750\_9\_1 Smo\_At4g37750\_92\_1

→ AT5G67180 = NP\_201519 BAB10952 AAM65779 BAD43908 DNA binding/transcription factor /floral homeotic protein apetal2-like /floral homeotic protein apetal2-like /floral homeotic protein apetal2-like  
→ AT4G36920 = NP\_195410 P47927 AAC13770 CAB16765 CAB80358 AP2 (APETALA 2); transcription factor/AP2\_ARATH Floral homeotic protein APETALA2/APETALA2 protein /APETALA2 protein /APETALA2 protein

→ AAL57045 Malus x domestica transcription factor AHAP2  
→ AAK14326 Pisum sativum APETAL2-like protein  
→ AAD39439 Petunia x hybrida PHAP2A protein  
→ AAO52746 Antirrhinum majus LIPLESS1  
→ AAO52747 Antirrhinum majus LIPLESS2

→ XP\_474122 Oryza sativa (japonica cultivar-group) CAE01667 OSJNBa0010D21.13/OSJNBa0010D21.13  
→ AAG32659 Picea abies APETALA2-related transcription factor 2  
→ AAD39440 Petunia x hybrida PHAP2B protein

→ AAW78371 Oryza sativa (japonica cultivar-group) transcription factor AP2D23-like  
→ BAE48516 Gnetum parvifolium APETALA2-like protein  
→ AAG32658 Picea abies APETALA2-related transcription factor 1  
→ BAD16603 Pinus thunbergii APETALA2-like protein 1  
→ BAE48514 Ginkgo biloba APETALA2-like protein  
→ Smo\_At4g37750\_75\_1 Smo\_At4g37750\_8\_1  
→ BAE48512 Cycas revoluta APETALA2-like protein 1

→ NP\_911602 Oryza sativa (japonica cultivar-group) BAC21448 ABD24033 putative indeterminate spikelet 1/putative indeterminate spikelet 1 /supernumerary bract  
→ AAU94925 Triticum turgidum subsp. carthlicum floral homeotic protein  
→ AAU88192 Triticum aestivum AAU93919 Triticum monococcum AAU94916 Triticum turgidum subsp. polonicum AAU94917 Triticum aestivum subsp. spelta AAU94918 Triticum aestivum subsp. macha AAU94920 Triticum turgidum subsp. dicoccum AAU94921

→ AAL50205 Hordeum vulgare subsp. vulgare APETALA2-like protein  
→ AAC05206 Zea mays indeterminate spikelet 1  
→ XP\_470121 Oryza sativa (japonica cultivar-group) AAO60032 AAO65862 AAW78367 APETALA2-like protein/putative transcription factor AP2 family protein, 3'-partial /APETALA2-like protein /transcription factor AP2D2