(a)

Os_KS AAQ72559
At_KS NP_178064
100
Bn_KS XP_013650279
99.7
Bn_KS XP_013726965
66.5
Sl_KS XP_004243964
61.9
Mt_KS–like XP_003600343
100
Gm_KS XP_006585394
100
Pv_KS XP_007149183
67.9
Ca_KS XP_004488548
99.8
Mt_KS_XP_013464190
Os_CPS NP_001046550
Bn_CPS XP_013740793
100
At_CPS NP_192187
89.6
Bn_CPS XP_013688526
89
Sl_CPS AEP82766
Ca_CPS XP_004491851
99.8
55.8
Mt_CPS XP_013447551
77
Ps_CPS AAB58822
100
Pv_CPS XP_007162437
100
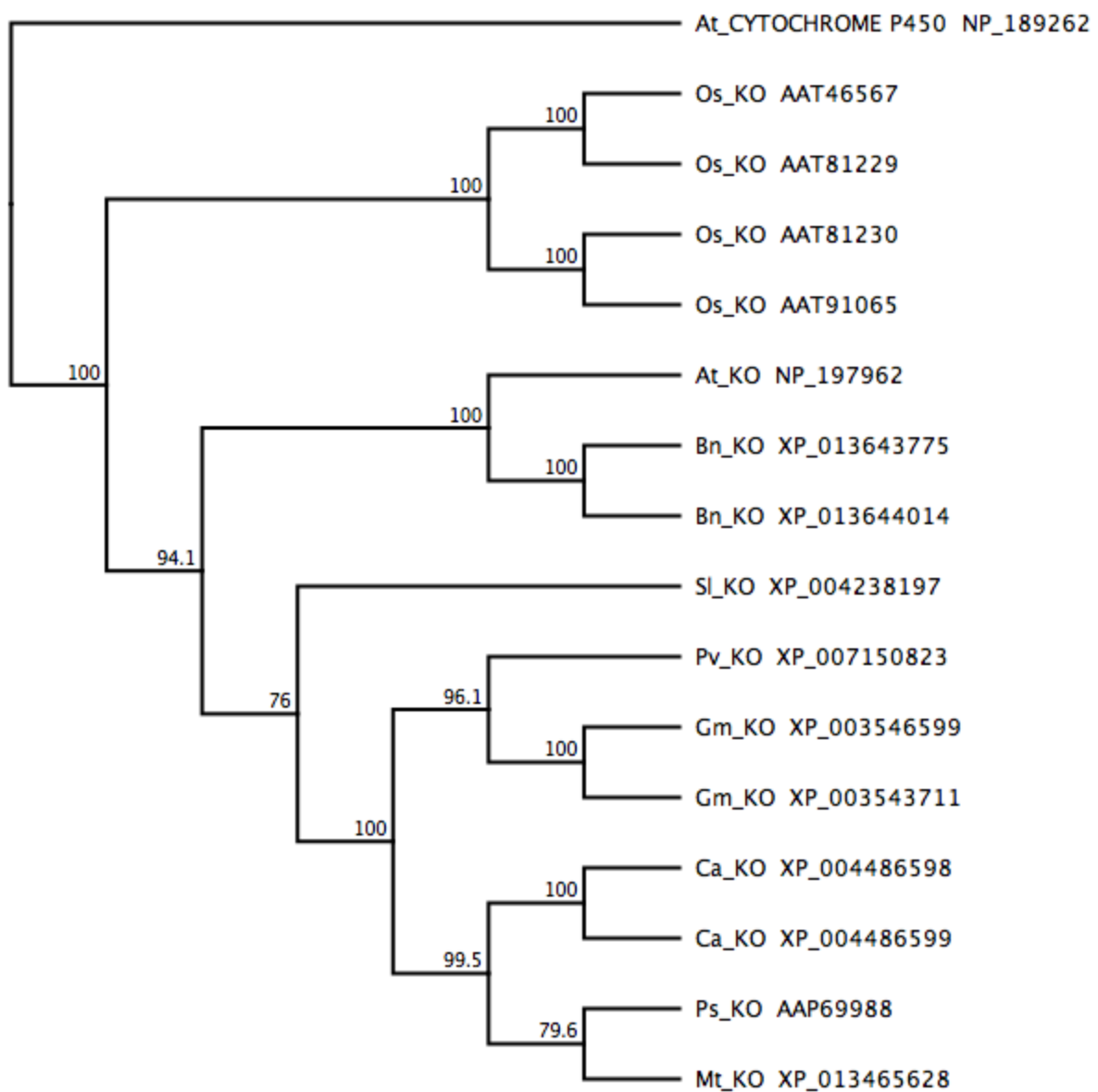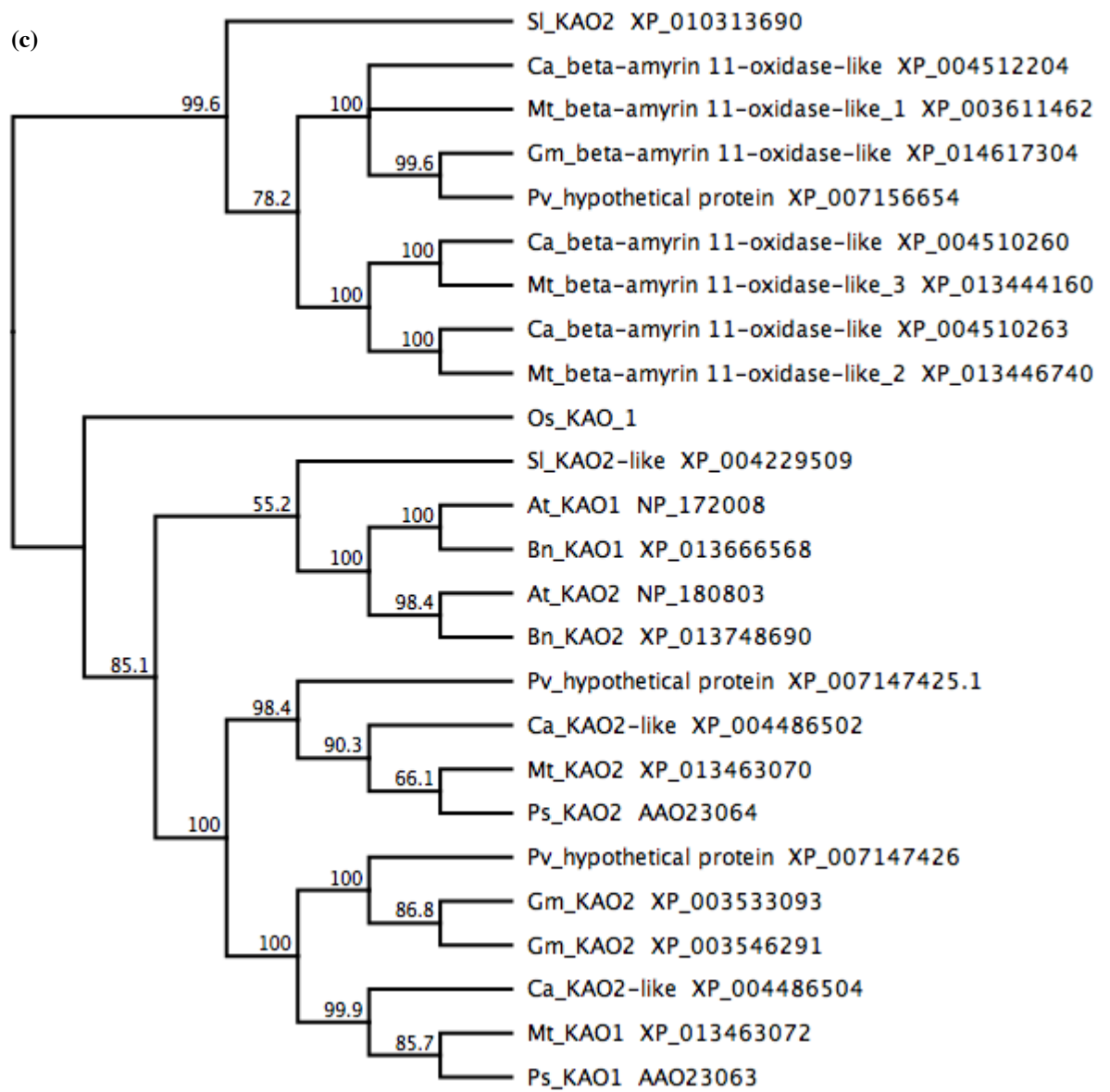Gm_CPS XP_006576898
100
Gm_CPS XP_006604439
100

S2 Fig.
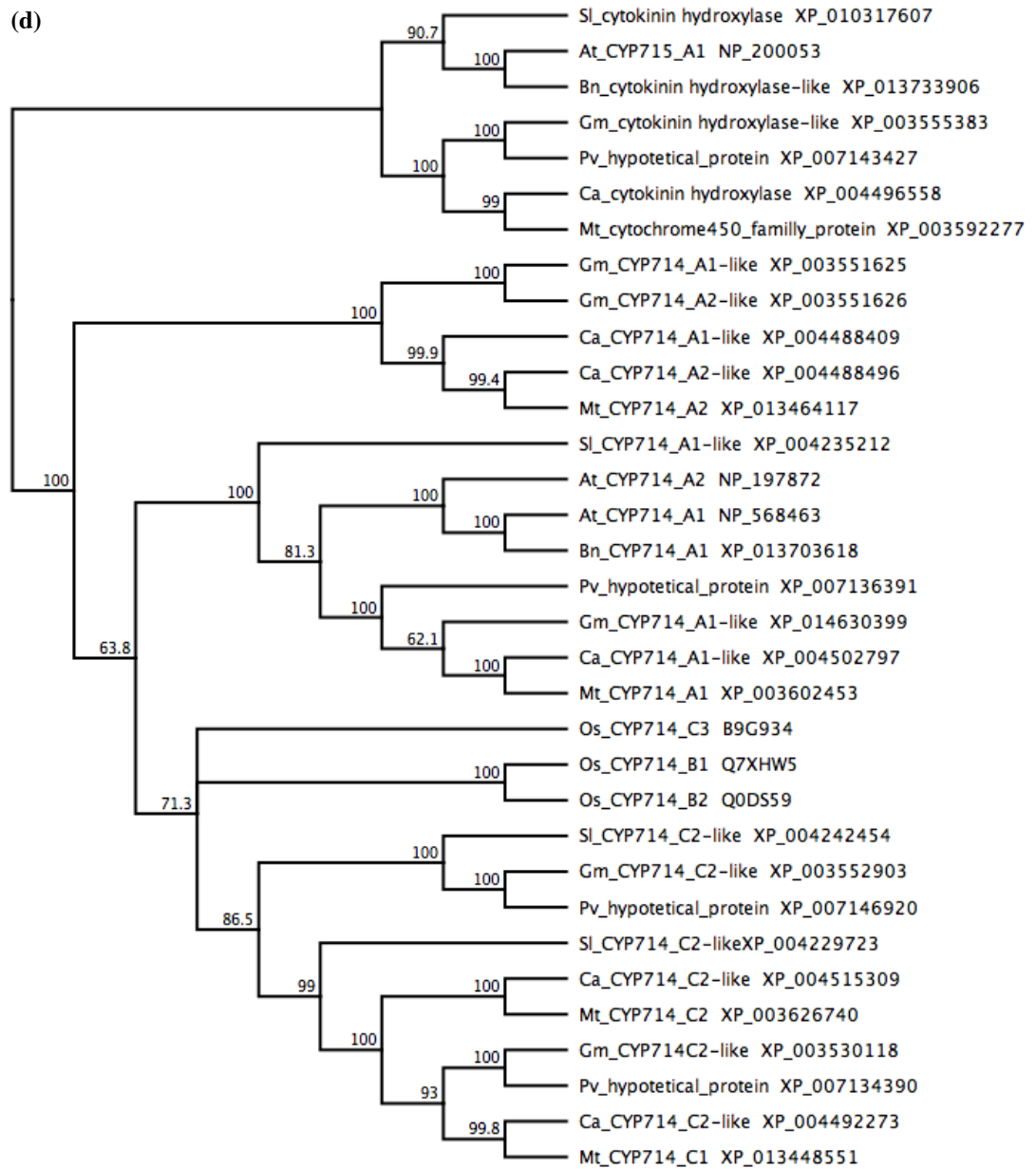**Phylogenetic relationships between amino acid sequences of gibberellin biosynthesis enzymes.**
Phylogenetic tree generated from protein sequences of (a) - CPS (ent-copalyl diphosphate synthase) and KS (ent-kaurene synthase), (b) - KO (ent-kaurene oxidase), (c) - KAO (ent-kaurenoic acid oxidase) and beta-amyrin 11-oxidase, (d) - CYP714 (Cytochrome 450 family, known also as Gibberellin 13-oxidases, GA13ox), (e) - GA20ox (gibberellin 20-oxidase) and GA3ox (gibberellin 3-oxidase), (f) - GA3ox (gibberellin 3-oxidase) representing phylogenetic relationships between plant taxa. Taxa terminologies are abbreviated using the first letter of the genus and first letter of the species name: At – *Arabidopsis thaliana*, Bn – *Brassica napus*, Ca – *Cicer arietinum,* Gm – *Glycine max,* Mt – *Medicago truncatula,* Os - *Oryza sativa*, Ps - *Pisum sativum*, Pv – *Phaseolus vulgaris,* Sl – *Solanum lycopersicum.* Phylogenetic analysis was performed using Geneious 6.1 software with Neighbor-Joining tree building method and Jukes-Cantor genetic distance model. Trees were resampled 1000 times using bootstrap method.

(b)

(c)

- Sl_KAO2 XP_010313690
- 99.6
  - 78.2
    - 100
      - Ca_beta-amyrin 11-oxidase-like XP_004512204
      - Mt_beta-amyrin 11-oxidase-like_1 XP_003611462
      - 99.6
        - Gm_beta-amyrin 11-oxidase-like XP_014617304
        - Pv_hypothetical protein XP_007156654
    - 100
      - 100
        - Ca_beta-amyrin 11-oxidase-like XP_004510260
        - Mt_beta-amyrin 11-oxidase-like_3 XP_013444160
      - 100
        - Ca_beta-amyrin 11-oxidase-like XP_004510263
        - Mt_beta-amyrin 11-oxidase-like_2 XP_013446740
- Os_KAO_1
- 85.1
  - 100
    - 55.2
      - Sl_KAO2-like XP_004229509
      - 100
        - 100
          - At_KAO1 NP_172008
          - Bn_KAO1 XP_013666568
        - 98.4
          - At_KAO2 NP_180803
          - Bn_KAO2 XP_013748690
    - 100
      - 98.4
        - Pv_hypothetical protein XP_007147425.1
        - 90.3
          - Ca_KAO2-like XP_004486502
          - 66.1
            - Mt_KAO2 XP_013463070
            - Ps_KAO2 AAO23064
      - 100
        - 100
          - Pv_hypothetical protein XP_007147426
          - 86.8
            - Gm_KAO2 XP_003533093
            - Gm_KAO2 XP_003546291
        - 99.9
          - Ca_KAO2-like XP_004486504
          - 85.7
            - Mt_KAO1 XP_013463072
            - Ps_KAO1 AAO23063

(d)

- Sl_cytokinin hydroxylase XP_010317607
- At_CYP715_A1 NP_200053
- Bn_cytokinin hydroxylase-like XP_013733906
- Gm_cytokinin hydroxylase-like XP_003555383
- Pv_hypotetical_protein XP_007143427
- Ca_cytokinin hydroxylase XP_004496558
- Mt_cytochrome450_familly_protein XP_003592277
- Gm_CYP714_A1-like XP_003551625
- Gm_CYP714_A2-like XP_003551626
- Ca_CYP714_A1-like XP_004488409
- Ca_CYP714_A2-like XP_004488496
- Mt_CYP714_A2 XP_013464117
- Sl_CYP714_A1-like XP_004235212
- At_CYP714_A2 NP_197872
- At_CYP714_A1 NP_568463
- Bn_CYP714_A1 XP_013703618
- Pv_hypotetical_protein XP_007136391
- Gm_CYP714_A1-like XP_014630399
- Ca_CYP714_A1-like XP_004502797
- Mt_CYP714_A1 XP_003602453
- Os_CYP714_C3 B9G934
- Os_CYP714_B1 Q7XHW5
- Os_CYP714_B2 Q0DS59
- Sl_CYP714_C2-like XP_004242454
- Gm_CYP714_C2-like XP_003552903
- Pv_hypotetical_protein XP_007146920
- Sl_CYP714_C2-likeXP_004229723
- Ca_CYP714_C2-like XP_004515309
- Mt_CYP714_C2 XP_003626740
- Gm_CYP714C2-like XP_003530118
- Pv_hypotetical_protein XP_007134390
- Ca_CYP714_C2-like XP_004492273
- Mt_CYP714_C1 XP_013448551

(e)

(f)