Test A: Strict consensus ontogram of *Tylosaurus proriger* including only specimens that were studied first-hand.

**Strict consensus of 18 trees (28 taxa excluded)**

- Embryo
  - Tp_FHSM_VP_14845
    - Tp_AMNH_1592
    - Tp_AMNH_2160
    - Tp_FMNH_UR902
    - Tp_KUVP_66129
      - Tp_KUVP_28705
      - Tp_KUVP_1033
      - Tp_KUVP_50090
      - Tp_KUVP_1032
      - Tp_AMNH_1555
      - Tp_AMNH_221
      - Tp_FMNH_P15144
      - Tp_FHSM_VP_3
Test B: Ontogram (only one tree recovered) of *Tylosaurus kansasensis/nepaeolicus* including only specimens that were studied first-hand.
Test C: Strict (top) and 50% majority rule (bottom) ontograms of all three taxa including only specimens that were studied first-hand.

**Strict consensus of 9 trees (56 taxa excluded)**

![Strict consensus tree diagram](image_url)

**Majority rule tree (from 9 trees, cut 50)**

![Majority rule tree diagram](image_url)
Test D: Strict (top) and 50% majority rule (bottom) ontograms of *Tylosaurus proriger* with size characters (TSL and QH) excluded.

**Strict consensus of 97 trees (19 taxa excluded)**

```
Embryo
   Tsp_FHSM_VP_14845
      Ip_AMNH_1592
      Ip_AMNH_2160
      Ip_FMNH_US902
      Ip_KUVP_66129
      Ip_CMN_8162
      Ip_CMN_51258_63
      Ip_RMM_5610
         Ip_KUVP_28705
         Ip_KUVP_50090
         Ip_KUVP_1033
         Ip_ROM_7906
         Ip_GSM_1
         Ip_TMP_1982.050.0010
         Ip_FFH_M_1997.10
         Ip_KUVP_1032
         Ip_USNM_8898
         Ip_USNM_6086
         Ip_AMNH_1555
         Ip_AMNH_4909
         Ip_AMNH_221
         Ip_FMNH_P15144
         Ip_FHSM_VP_3
```

**Majority rule tree (from 97 trees, cut 50)**

```
Embryo
   100
      Tsp_FHSM_VP_14845
         100
            Ip_AMNH_1592
            Ip_FMNH_US902
            Ip_CMN_51258_63
            Ip_AMNH_2160
               68
                  Ip_CMN_8162
                  Ip_RMM_5610
                     55
                        Ip_KUVP_28705
                        Ip_KUVP_1033
                        Ip_KUVP_50090
                        Ip_KUVP_1032
                        Ip_USNM_8898
                        Ip_USNM_6086
                        Ip_AMNH_1555
                        Ip_AMNH_4909
                        Ip_AMNH_221
                        Ip_FMNH_P15144
                        Ip_FHSM_VP_3
```


Test E: Strict (top) and 50% majority rule (bottom) ontograms of *Tylosaurus proriger* with size characters (TSL and QH) excluded, including the artificial adult. The artificial adult is recovered as sister to FHSM VP-3 just as it is in the analysis including the size characters.
Test F: Strict (top) and 50% majority rule (bottom) ontograms of *Tylosaurus kansasensis/nepaeolicus* with size characters (TSL and QH) excluded.

**Strict consensus of 7 trees (23 taxa excluded)**

![Strict consensus tree diagram]

**Majority rule tree (from 7 trees, cut 50)**

![Majority rule tree diagram]
Test G: Strict (top) and 50% majority rule (bottom) ontograms of *Tylosaurus kansasensis/nepaeolicus* with size characters (TSL and QH) excluded, including the artificial adult. The artificial adult is recovered as sister to FHSM VP-2209 and YPM 3970 just as it is in the analysis including the size characters.
Test H: Strict (top) and 50% majority rule (bottom) ontograms of all three taxa with size characters (TSL and QH) excluded.

Strict consensus of 5 trees (51 taxa excluded)

Majority rule tree (from 5 trees, cut 50)
Test I: Strict (top) and 50% majority rule (bottom) ontograms of all three taxa with size characters (TSL and QH) excluded, including the artificial adult. The artificial adult is recovered as sister to the group of relatively mature *T. proriger* (specifically, KUVP 5033 and FHSM VP-3), just as it is in the analysis including the size characters.

Strict consensus of 5 trees (50 taxa excluded)

Majority rule tree (from 5 trees, cut 50)
Test J: Strict (top) and 50% majority rule (bottom) ontograms of *Tylosaurus proriger* after TSL states were changed to equal (400 mm) bins. For this analysis, TSL was coded as follows: < 400 mm (0), 400–799 mm (1), 800–1199 mm (2), 1200–1599 mm (3), ≥ 1600 mm (4). Notes: in the original analysis, TSL was coded as follows: < 400 mm (0), 400–799 mm (1), 800–999 mm (2), 1000–1399 mm (3), ≥ 1400 mm (4); the ontogram of *T. kansasensis/nepaeolicus* was not affected by this change, since the largest TSL in that dataset is 890 mm.

Strict consensus of 7 trees (18 taxa excluded)

Majority rule tree (from 7 trees, cut 50)
Test K: Strict (top) and 50% majority rule (bottom) ontograms of all three taxa after TSL states were changed to equal (400 mm) bins. For this analysis, TSL was coded as follows: < 400 mm (0), 400–799 mm (1), 800–1199 mm (2), 1200–1599 mm (3), ≥ 1600 mm (4). Note: in the original analysis, TSL was coded as follows: < 400 mm (0), 400–799 mm (1), 800–999 mm (2), 1000–1399 mm (3), ≥ 1400 mm (4).
Test L: Strict (top) and 50% majority rule (bottom) ontograms including all specimens of *Tylosaurus proriger* that are scored for five or more characters. Note: an analysis including all specimens resulted in a complete polytomy (not figured).

**Strict consensus of 41 trees (14 taxa excluded)**

```
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**Majority rule tree (from 41 trees, cut 50)**

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Test M: Strict (top) and 50% majority rule (bottom) ontograms including all specimens of *Tylosaurus kansasensis/nepaeolicus*. Note: TMM 31051-64 is mislabeled in the diagram as TMM 81051-64.
Test N: Strict (top) and 50% majority rule (bottom) ontograms including all specimens of *Tylosaurus kansasensis/nepaeolicus* that are scored for five or more characters.

**Strict consensus of 61 trees (19 taxa excluded)**

```
Embryo
  - Tk_FHSM_VP_18520
  - Tk_FMNH_PR2103_Bob
  - Tk_IPB_R322
  - Tk_FSM_VP_43
  - Tk_FHSM_VP_15632
  - Tk_FHSM_VP_15631
  - Tk_FHSM_VP_14848
  - Tk_FHSM_VP_14845
  - Tk_FHSM_VP_9350
  - Tk_FHSM_VP_2495
  - Tk_FHSM_VP_78
  - Tk_FHSM_VP_2295*
  - In_AMNH_2167
  - In_YPM_3976
  - In_FHSM_VP_2209
  - In_FHSM_VP_7262
  - In_AMNH_1561
  - In_YPM_3974
  - In_YPM_3970
  - In_AMNH_124_134
  - Tsp_FHSM_VP_14845
```

**Majority rule tree (from 61 trees, cut 50)**

```
Embryo
  - Tk_IPB_R322
  - Tsp_FHSM_VP_14845
  - Tk_FHSM_VP_14845
  - Tk_FHSM_VP_9350
  - Tk_FHSM_VP_2495
  - Tk_FHSM_VP_14848
    - Tk_FHSM_VP_15632
    - Tk_FHSM_VP_15631
    - Tk_FHSM_VP_2295*
    - In_AMNH_1565*
      - Tk_FHSM_VP_18520
      - Tk_FMNH_PR2103_Bob
      - Tk_FHSM_VP_13742
      - In_YPM_3976
      - In_FHSM_VP_7262
        - Tk_FGM_V_43
        - In_AMNH_2167
        - In_YPM_3970
        - Tn_FHSM_VP_2209
        - In_YPM_3974
        - In_AMNH_1561
          - Tn_FHSM_VP_3974
            - In_AMNH_124_134
```
Test O: Strict (left) and 50% majority rule (right) onograms including all specimens of all three taxa that are scored for five or more characters. Note: an analysis including all specimens resulted in a complete polytomy (not figured). Note: TMM 31051-64 is mislabeled in the diagram as TMM 81051-64.