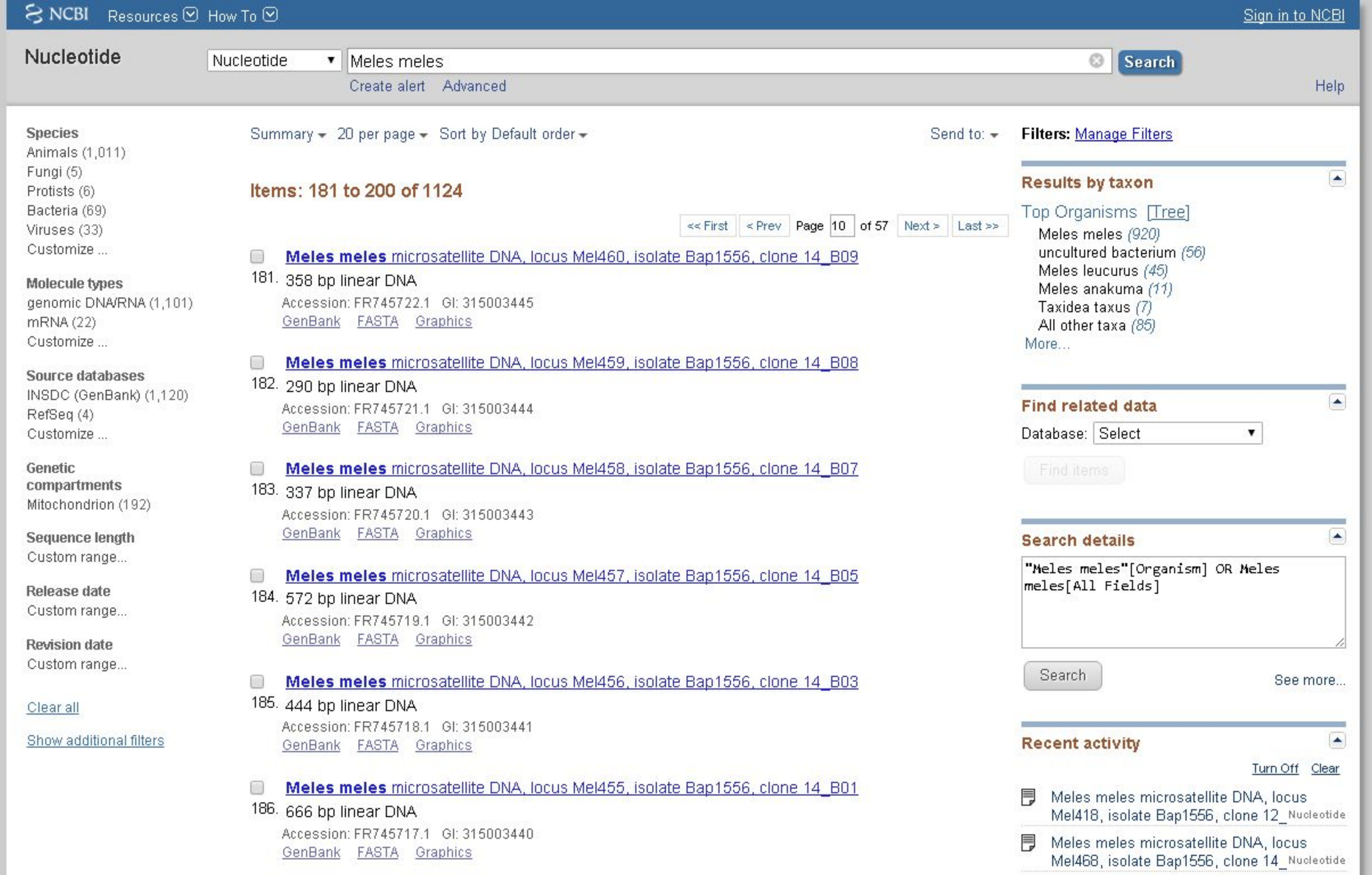

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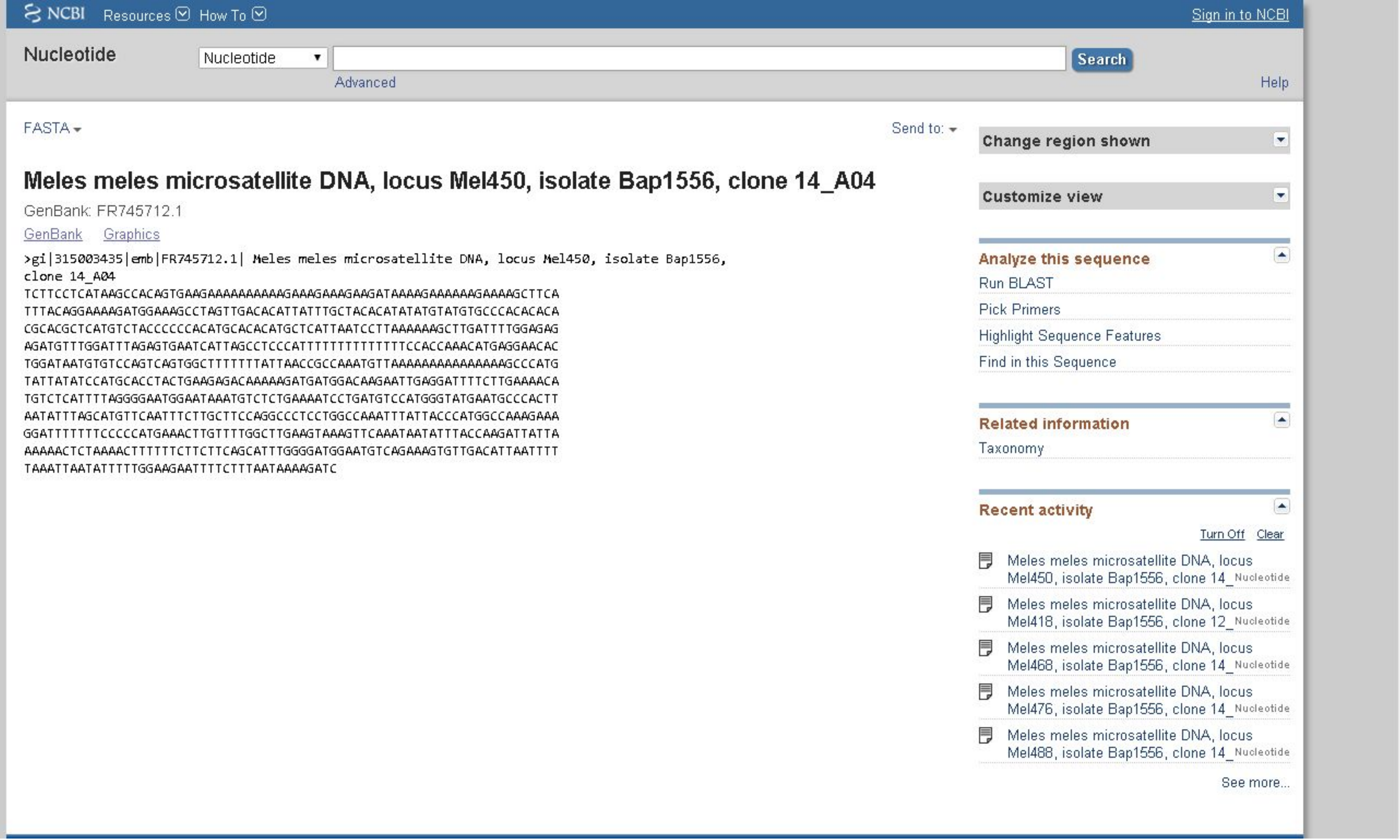

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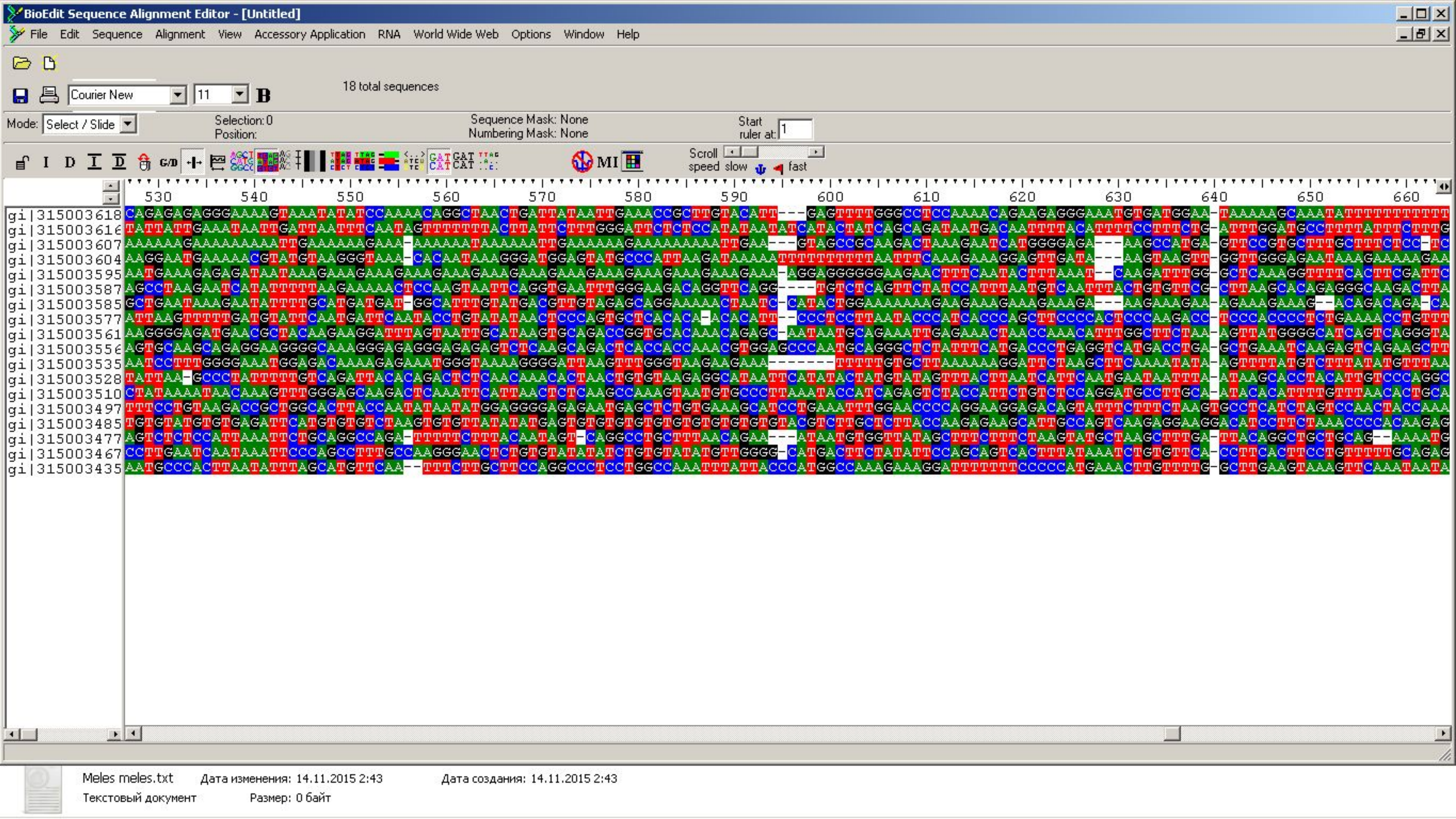

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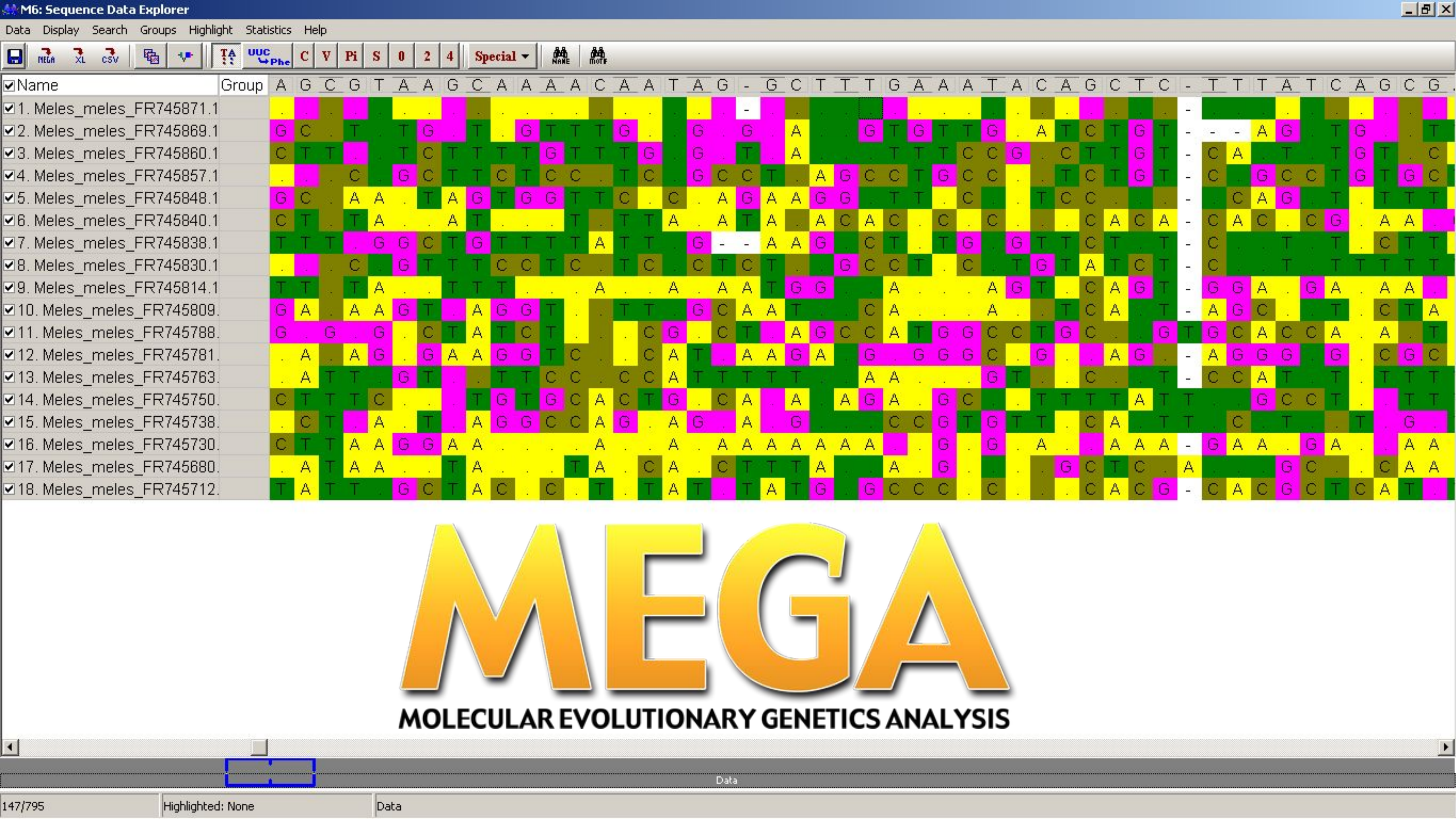

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MEGA

MOLECULAR EVOLUTIONARY GENETICS ANALYSIS

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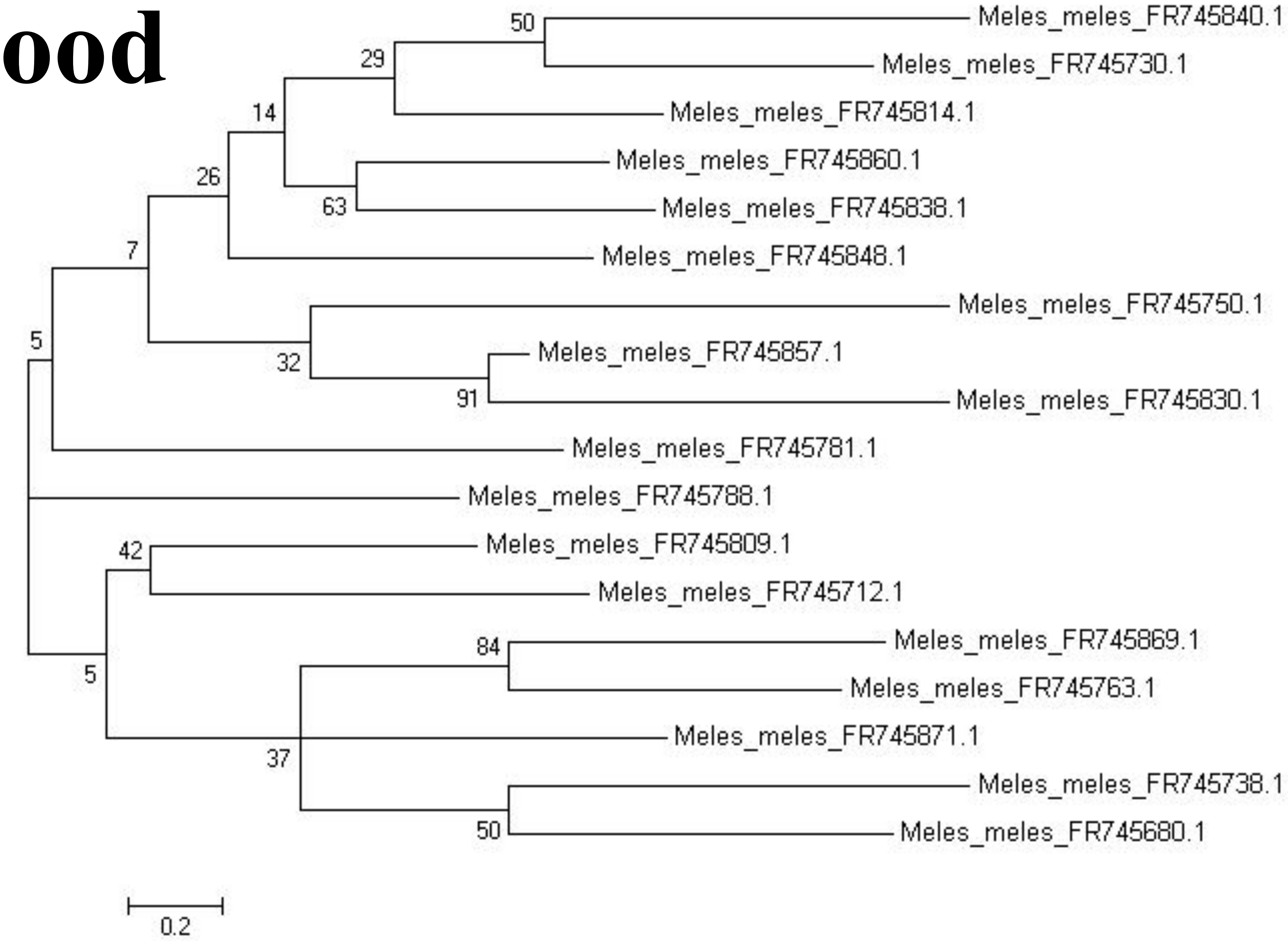

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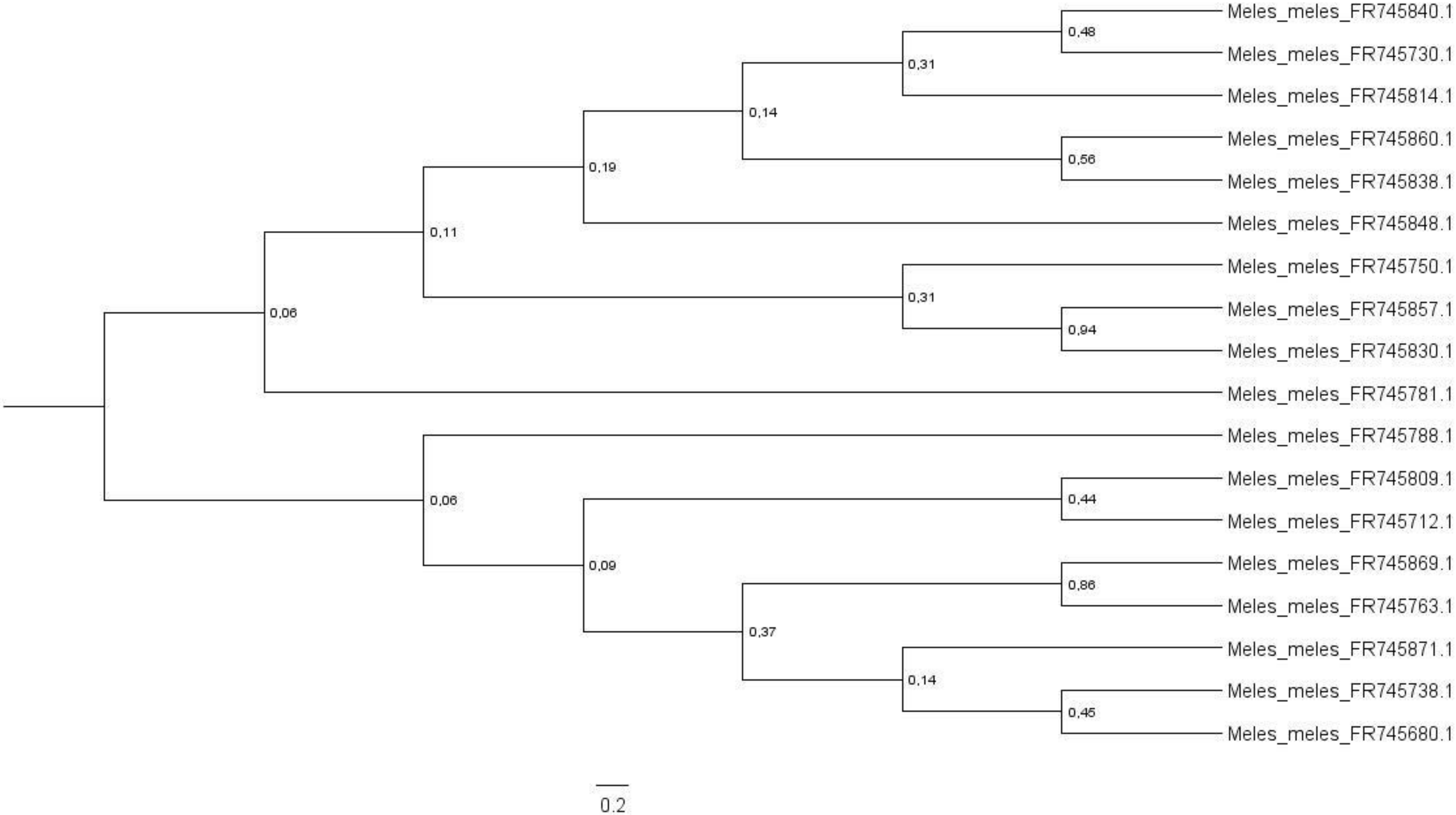
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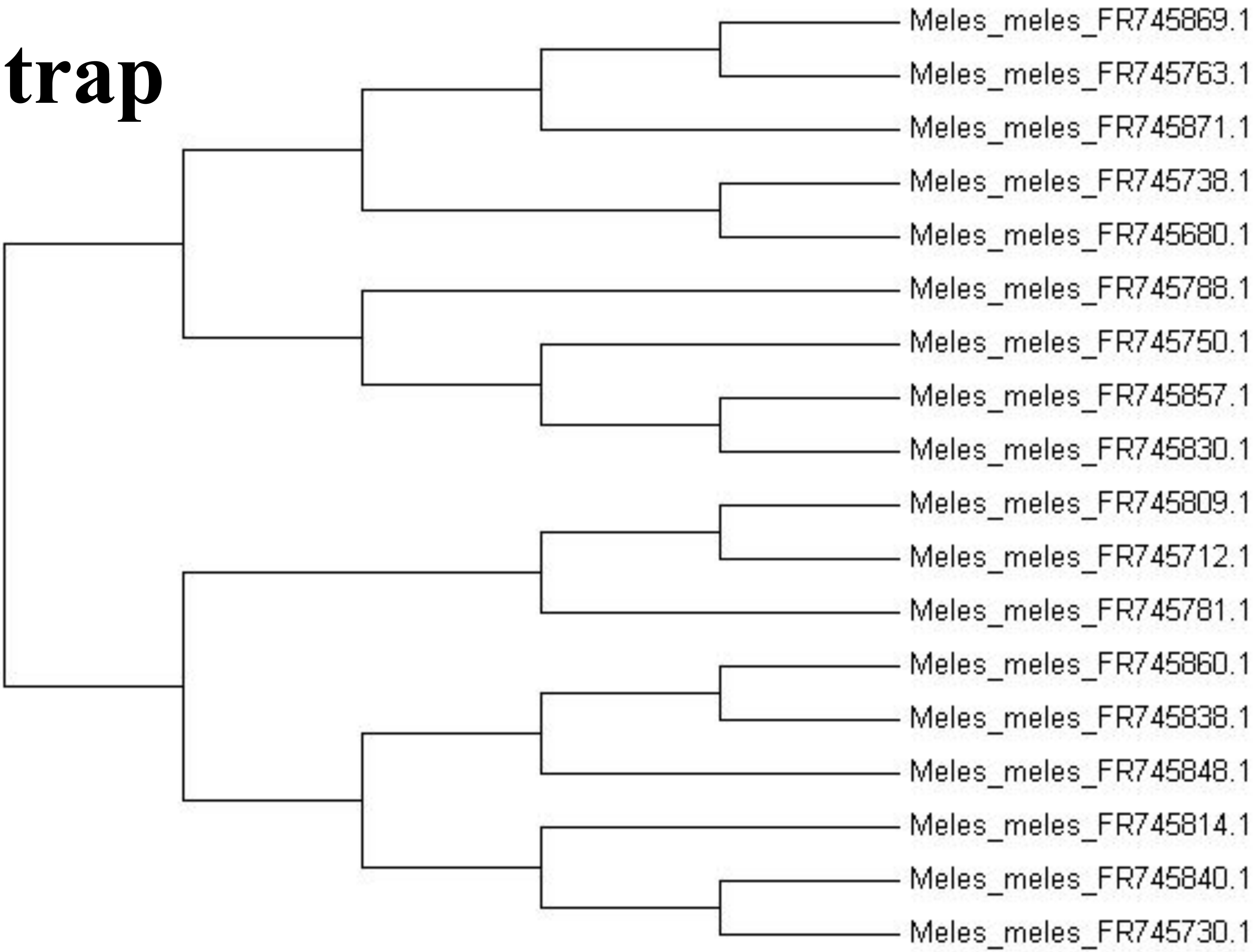
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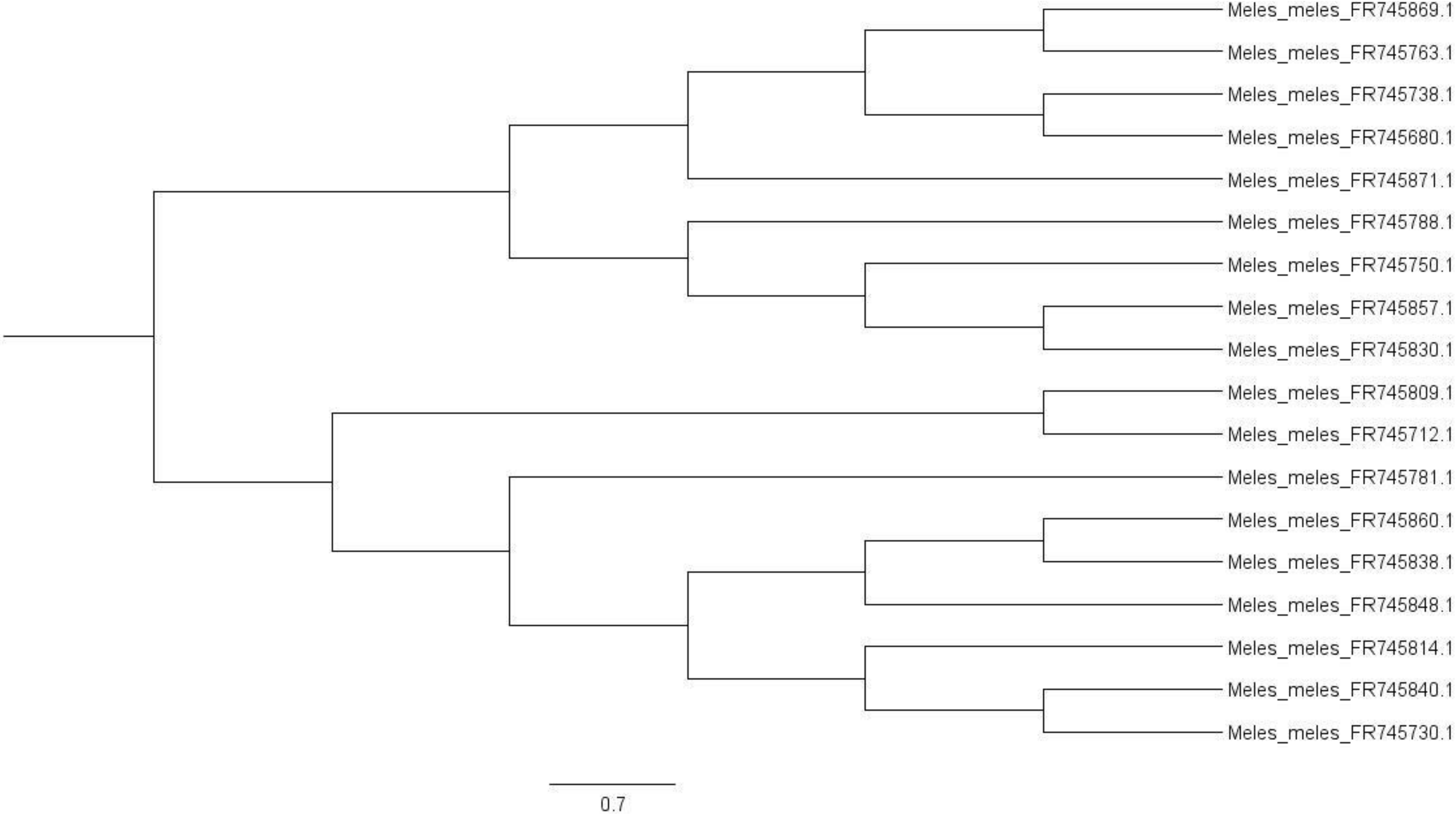
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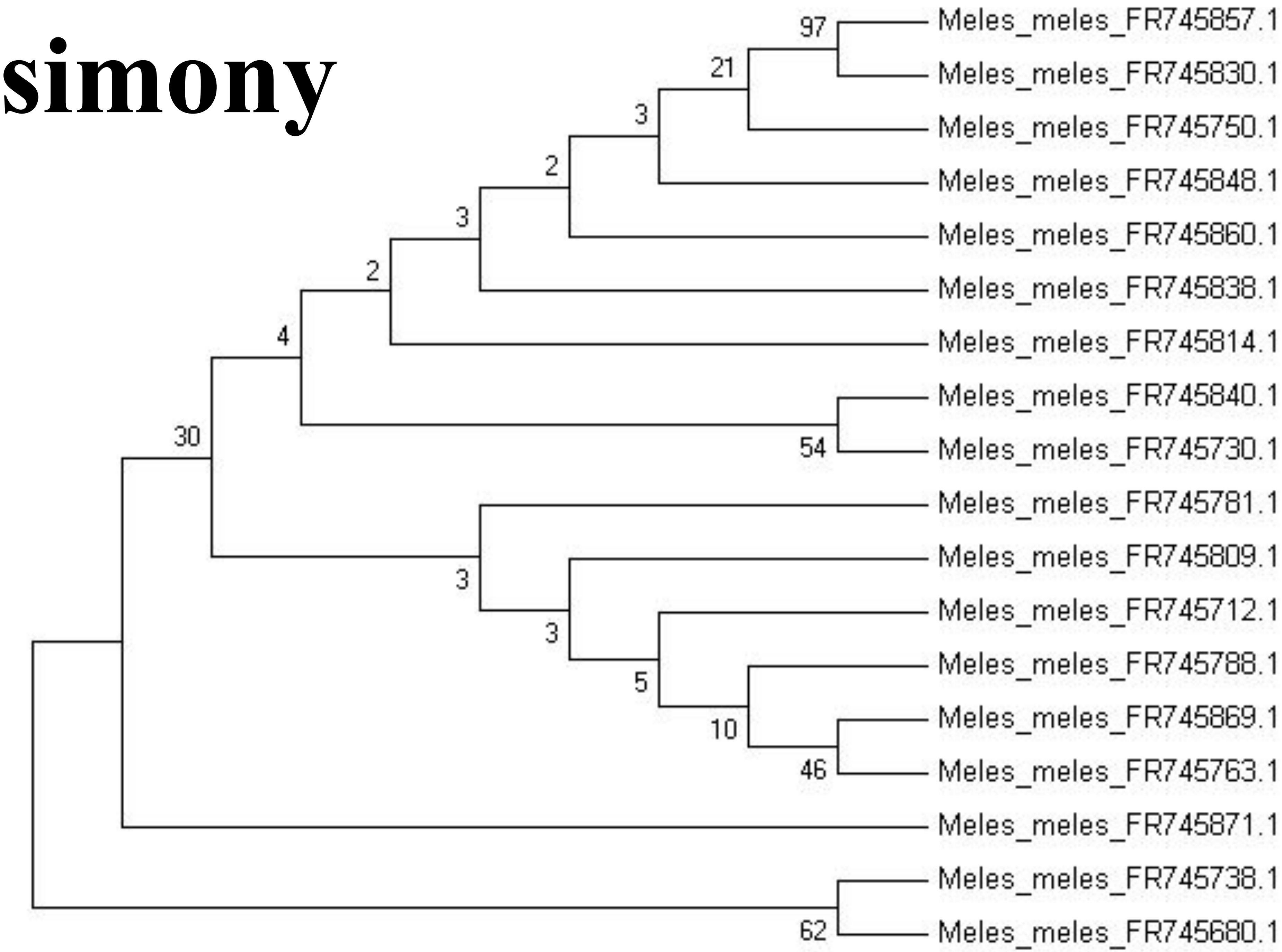
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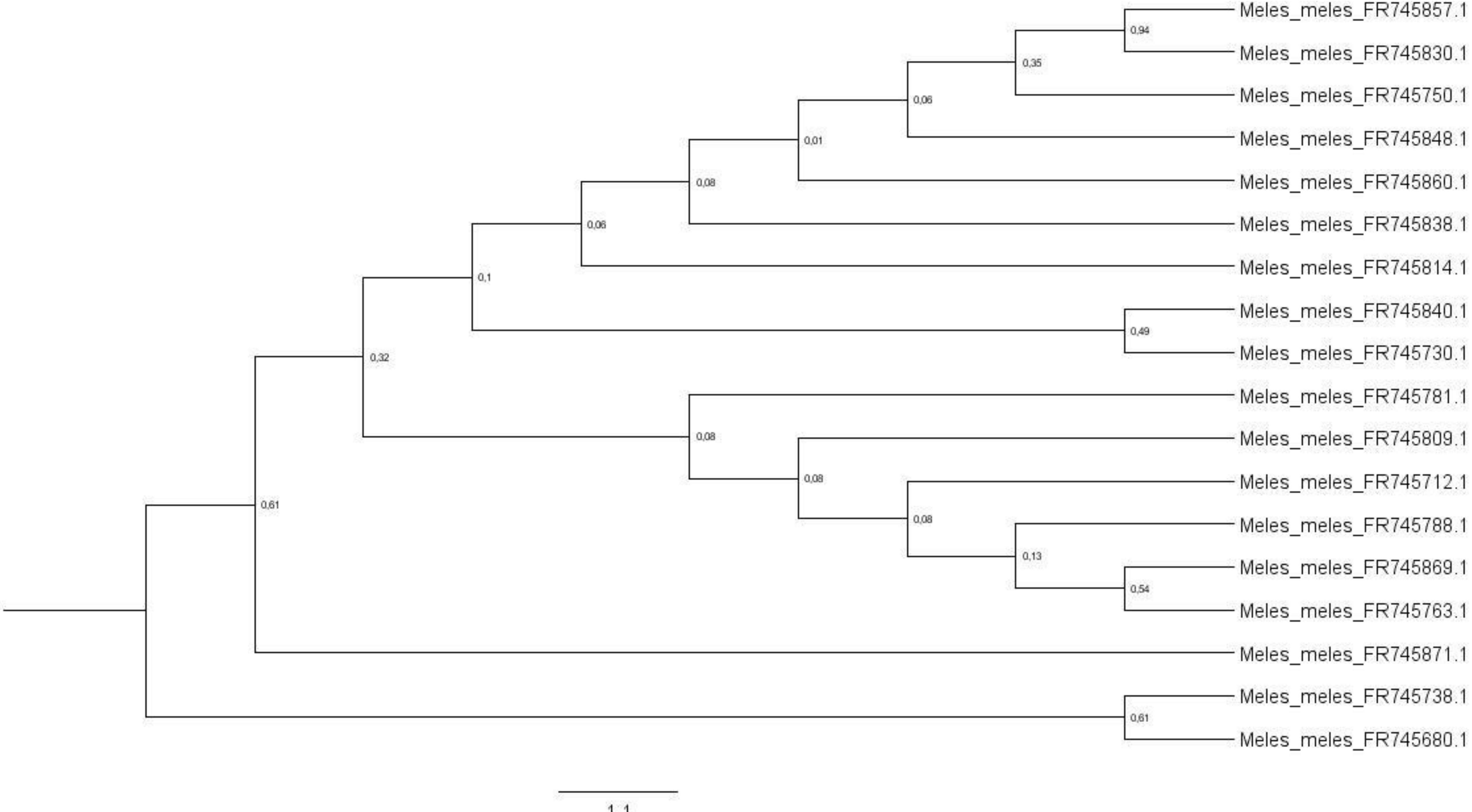
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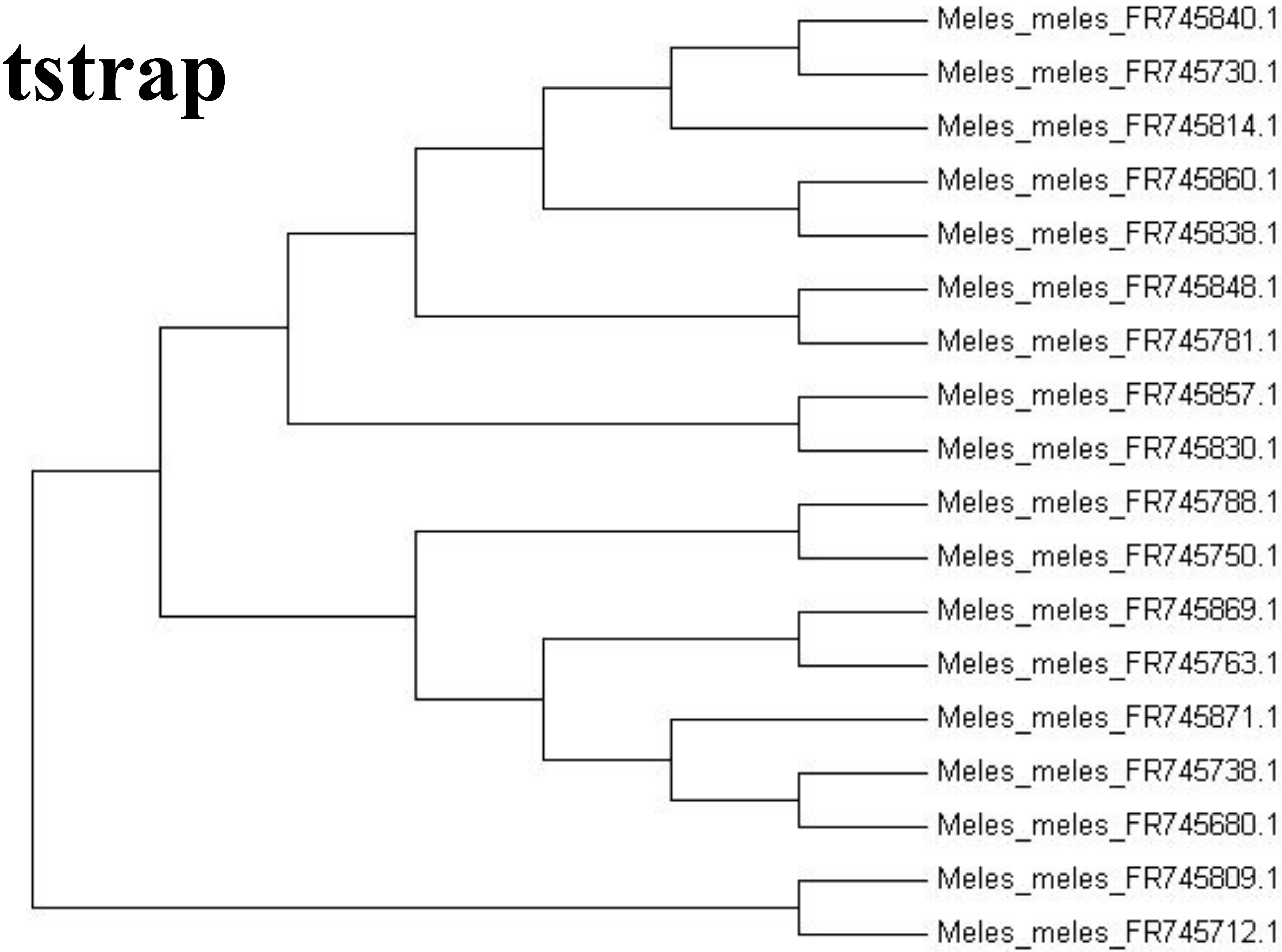
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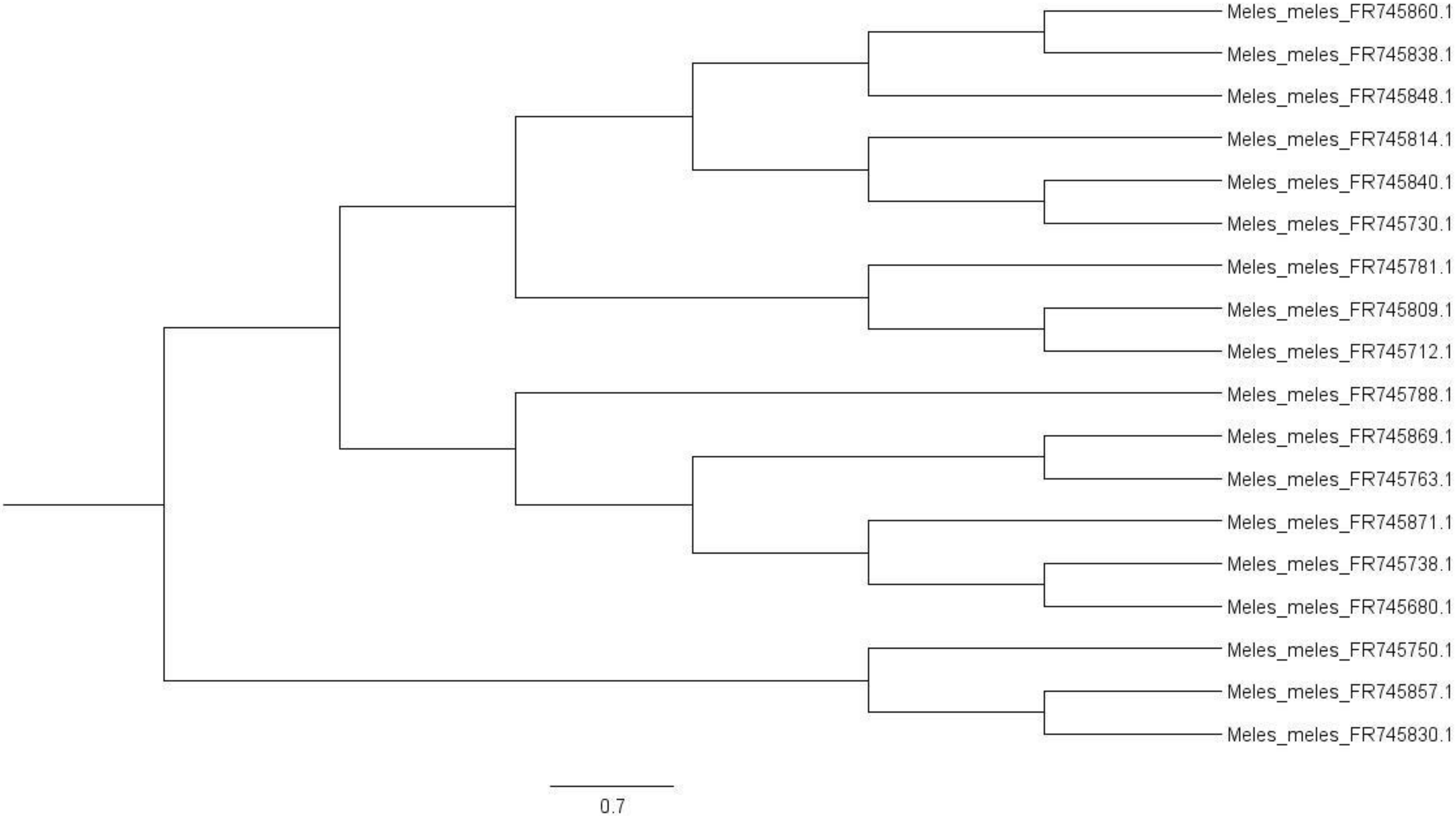
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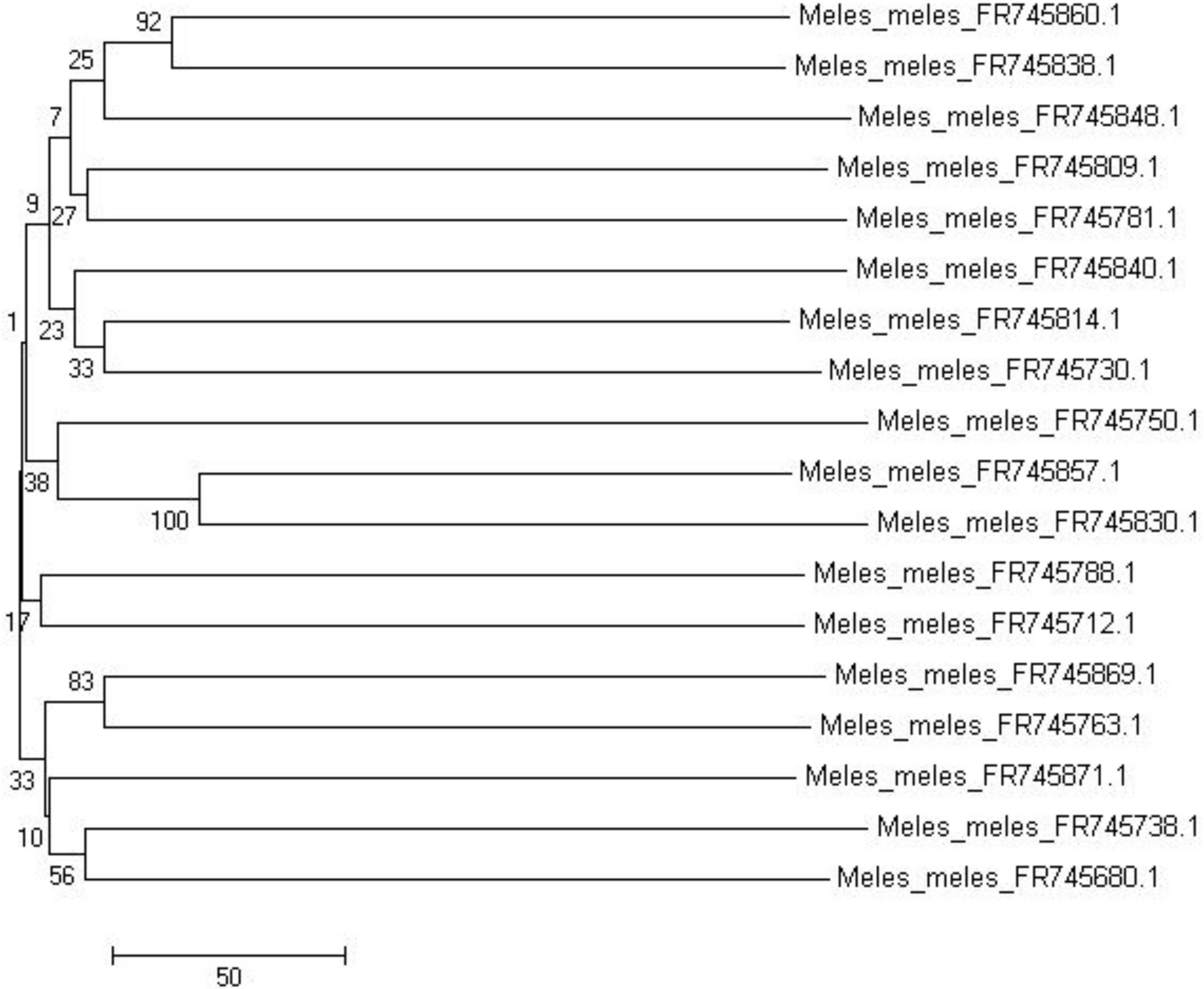
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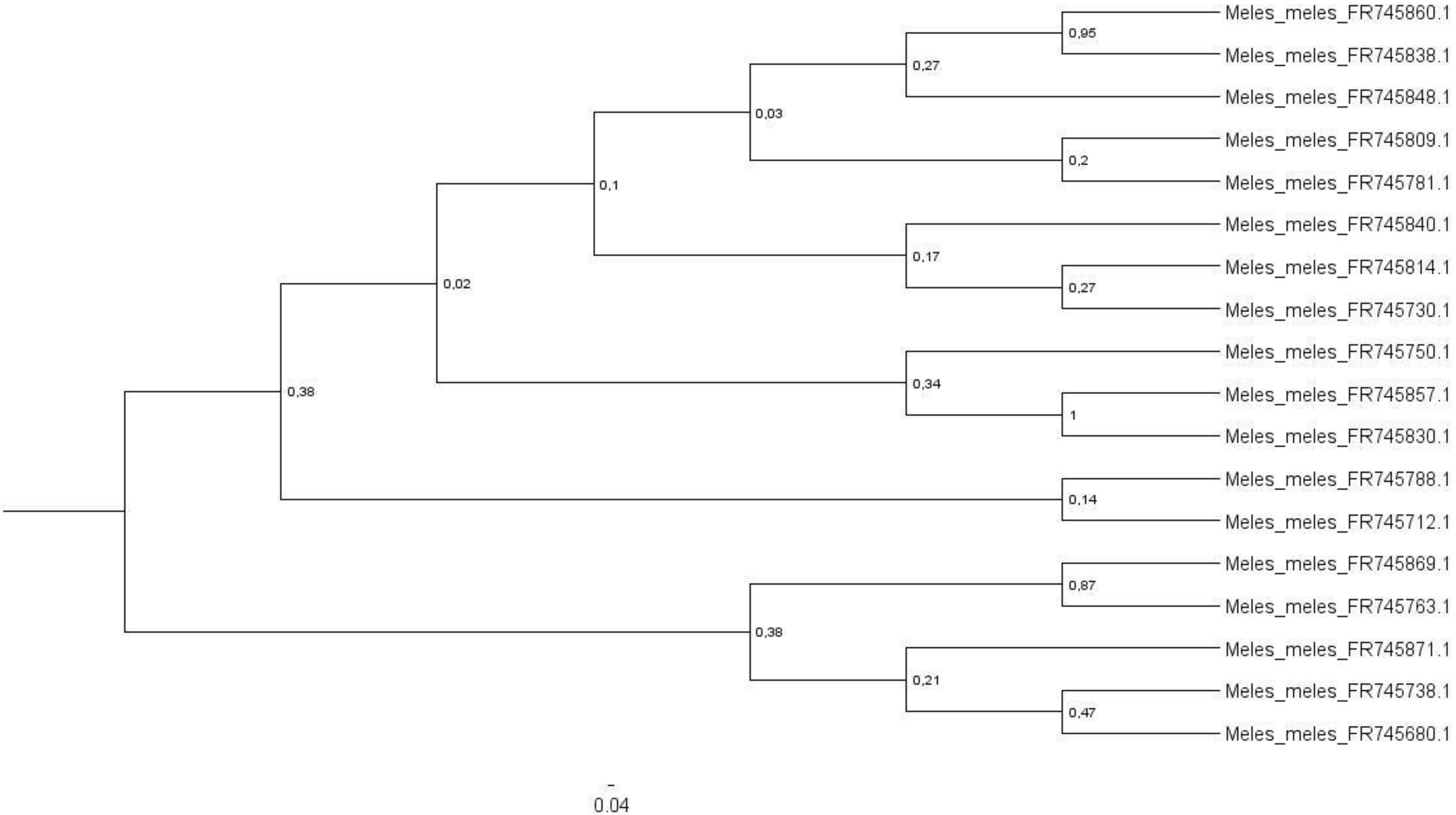
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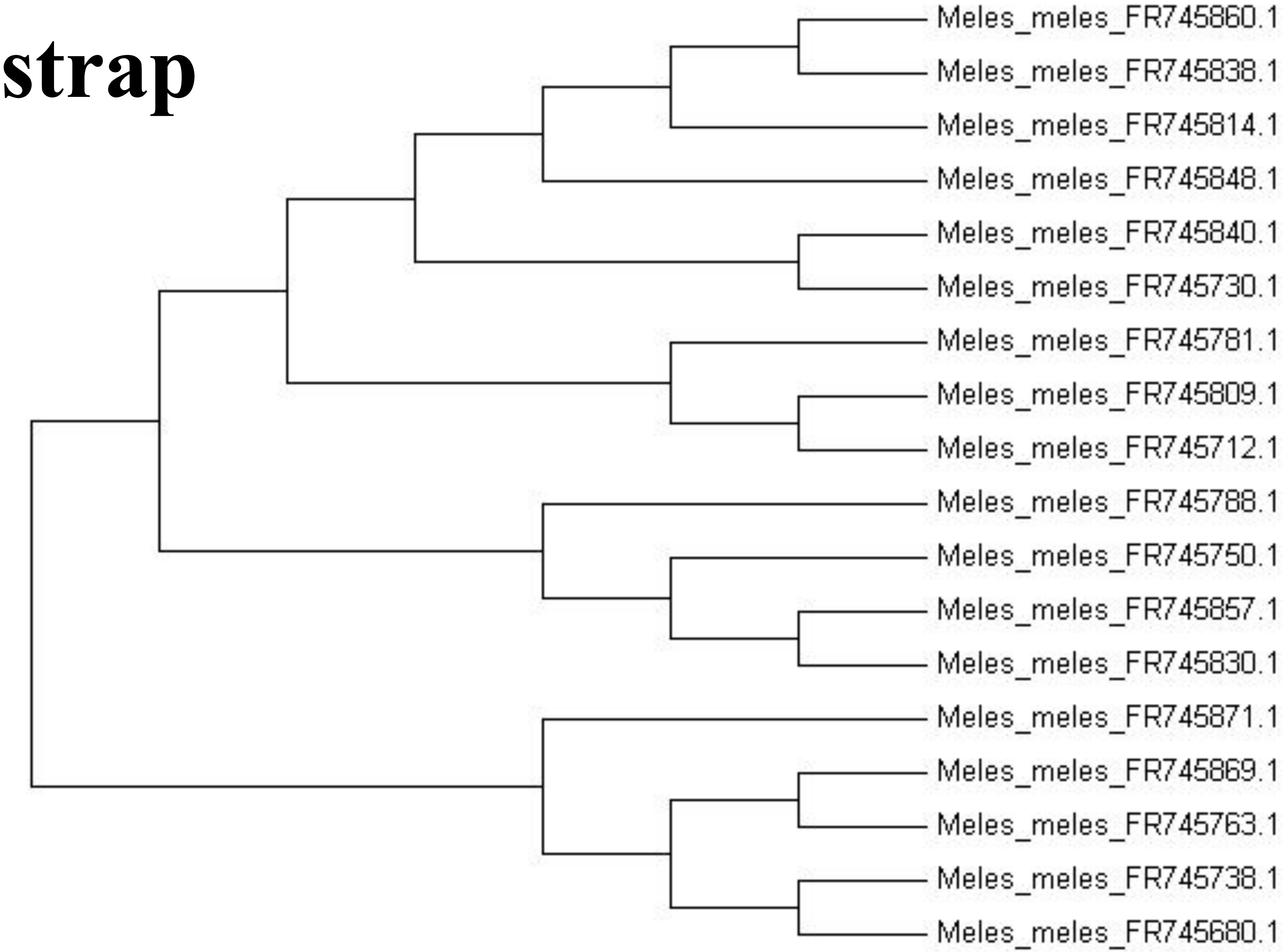
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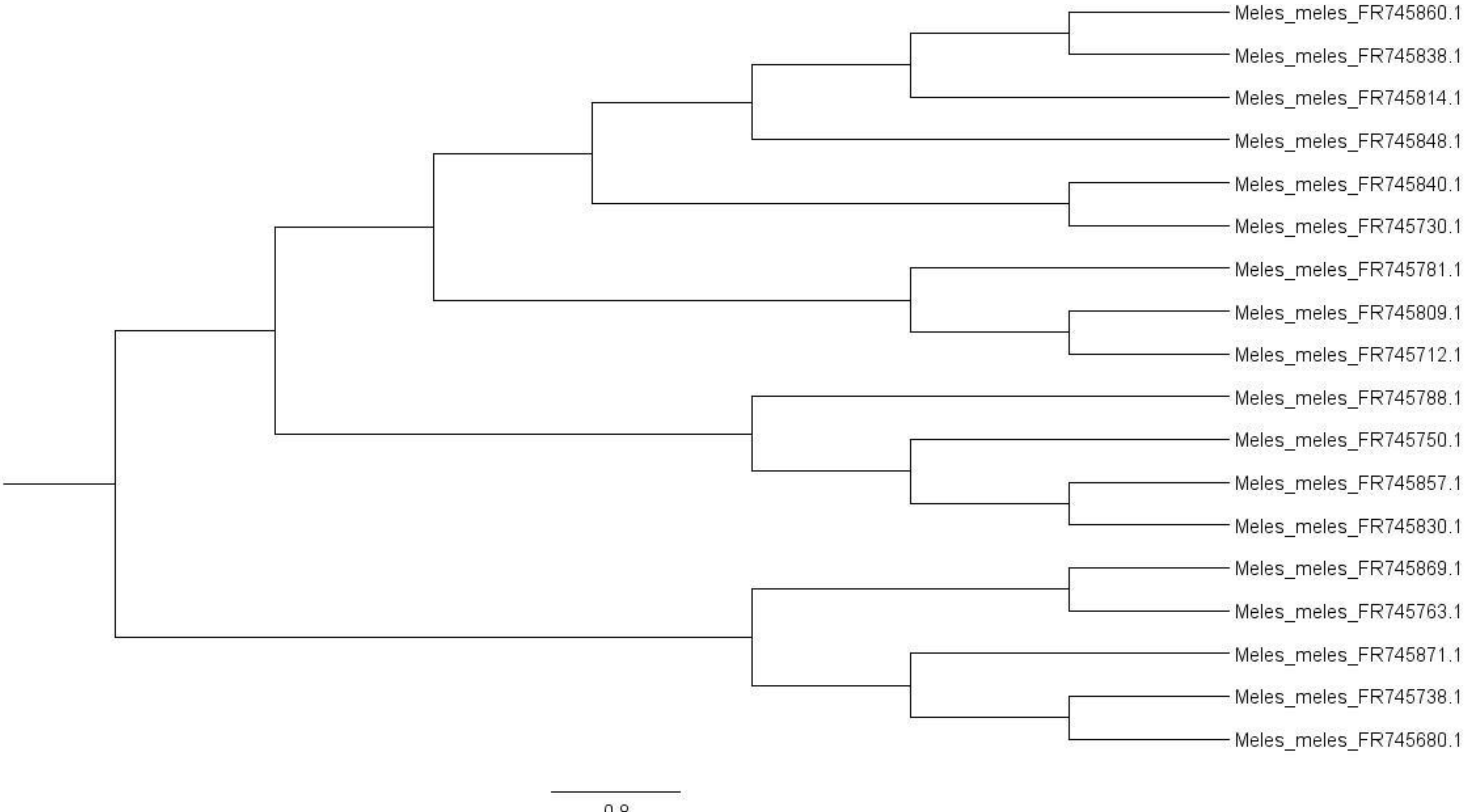
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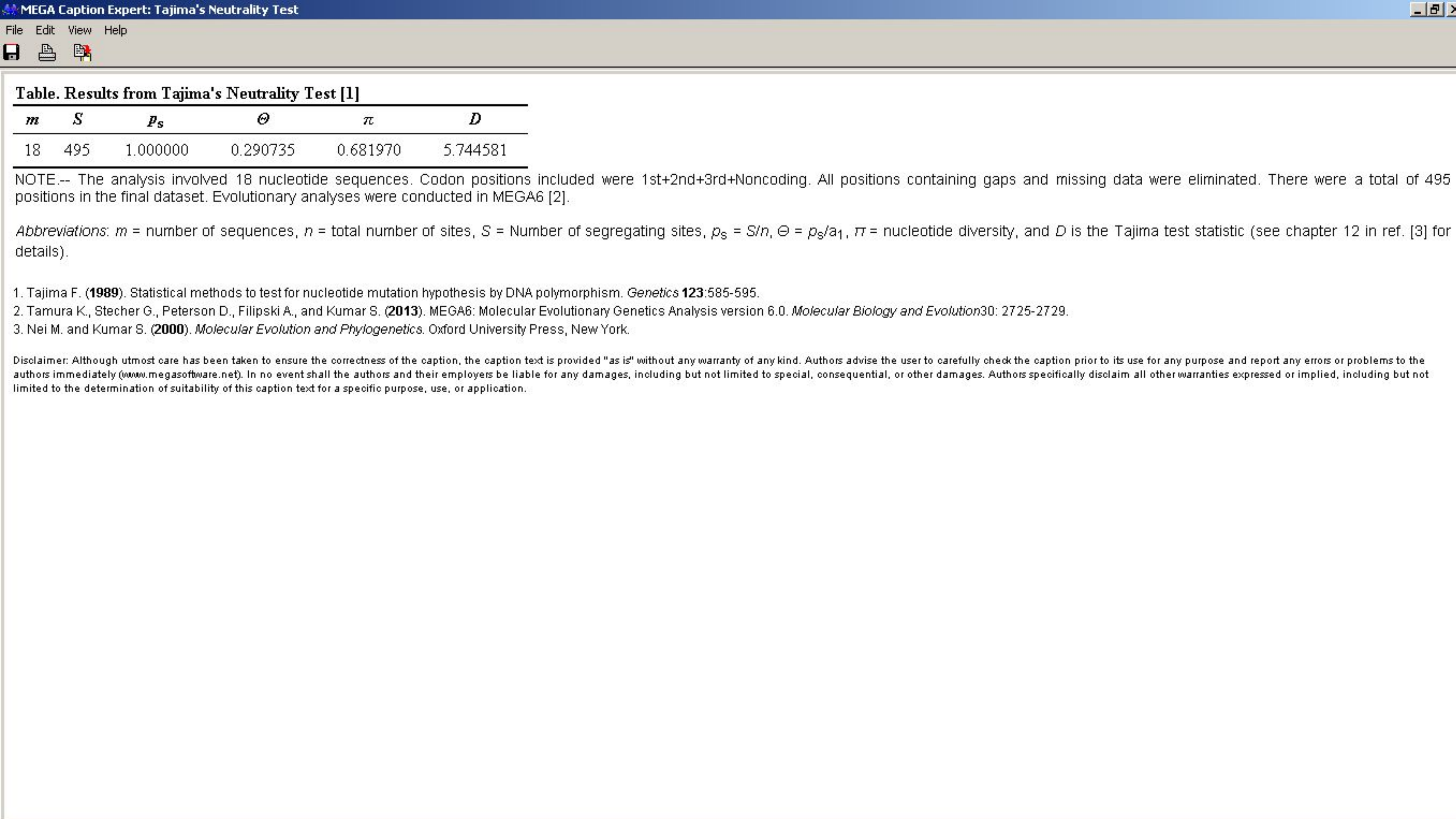

Table. Results from Tajima's Neutrality Test [1]

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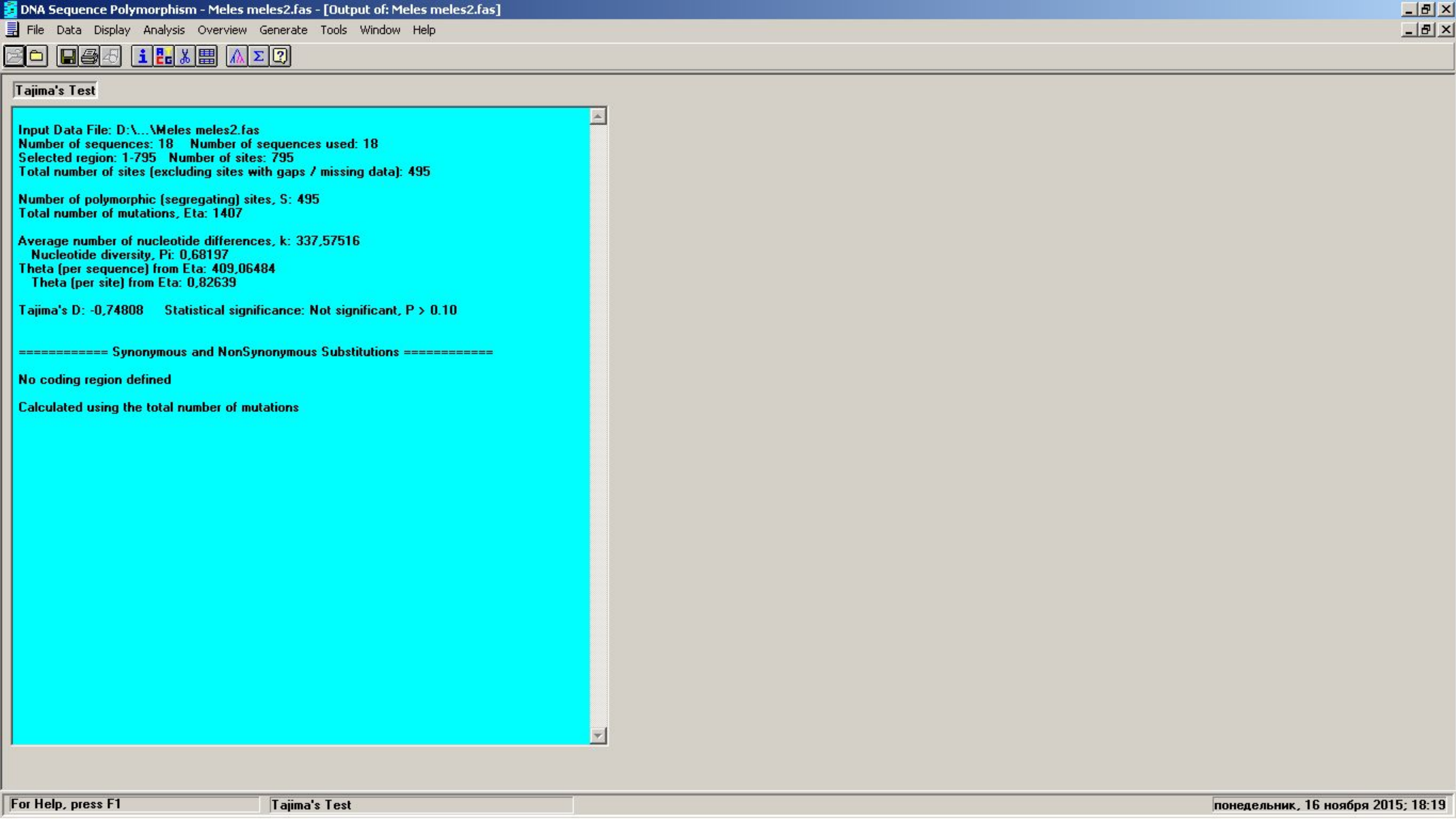
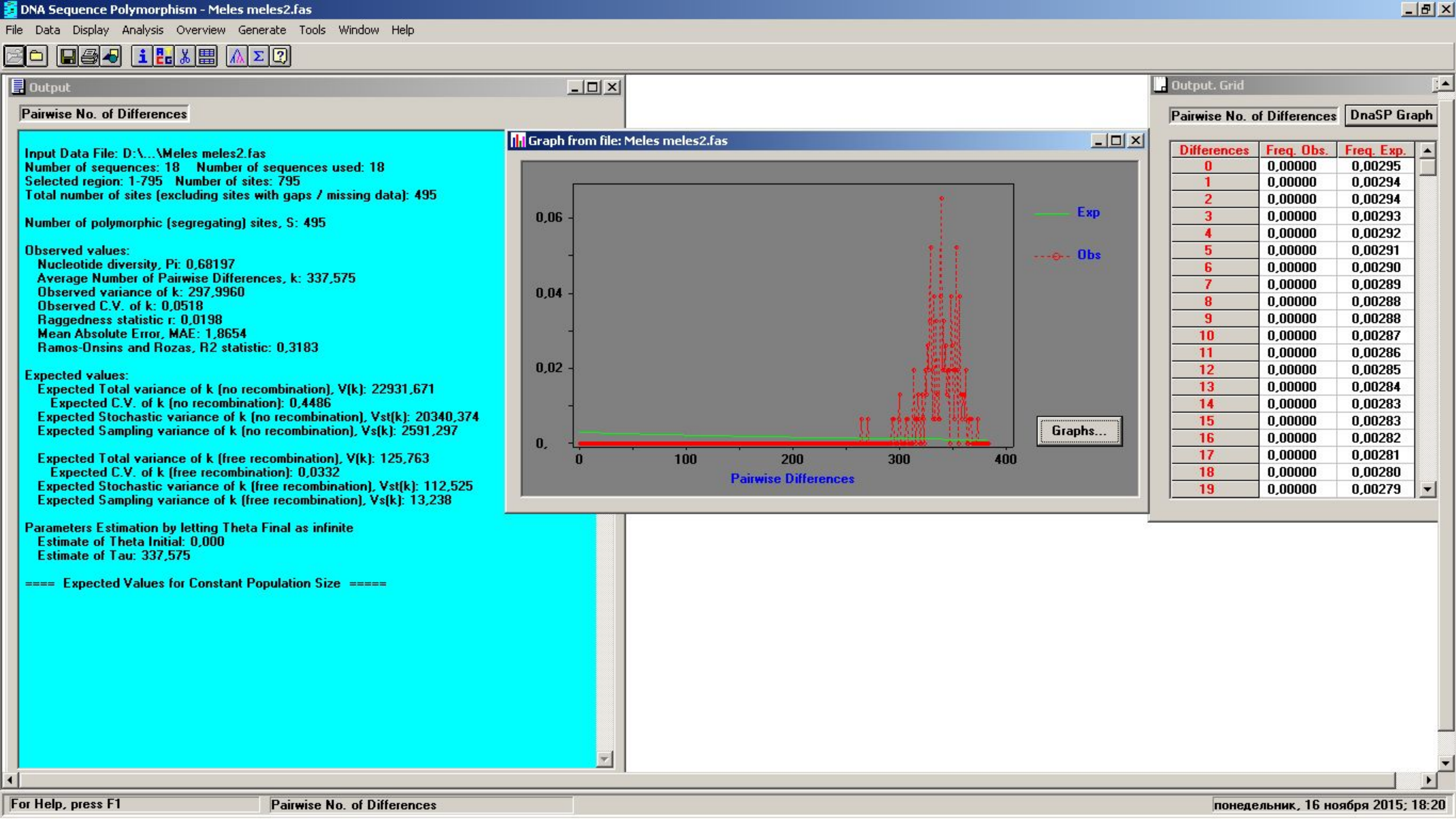
NOTE.-- The analysis involved 18 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 495 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [2].

Abbreviations: m = number of sequences, n = total number of sites, S = Number of segregating sites, $p_S = S/n$, $\Theta = p_S/a_1$, π = nucleotide diversity, and D is the Tajima test statistic (see chapter 12 in ref. [3] for details).

1. Tajima F. (**1989**). Statistical methods to test for nucleotide mutation hypothesis by DNA polymorphism. *Genetics* **123**:585-595.
2. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (**2013**). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution*30: 2725-2729.
3. Nei M. and Kumar S. (**2000**). *Molecular Evolution and Phylogenetics*. Oxford University Press, New York.



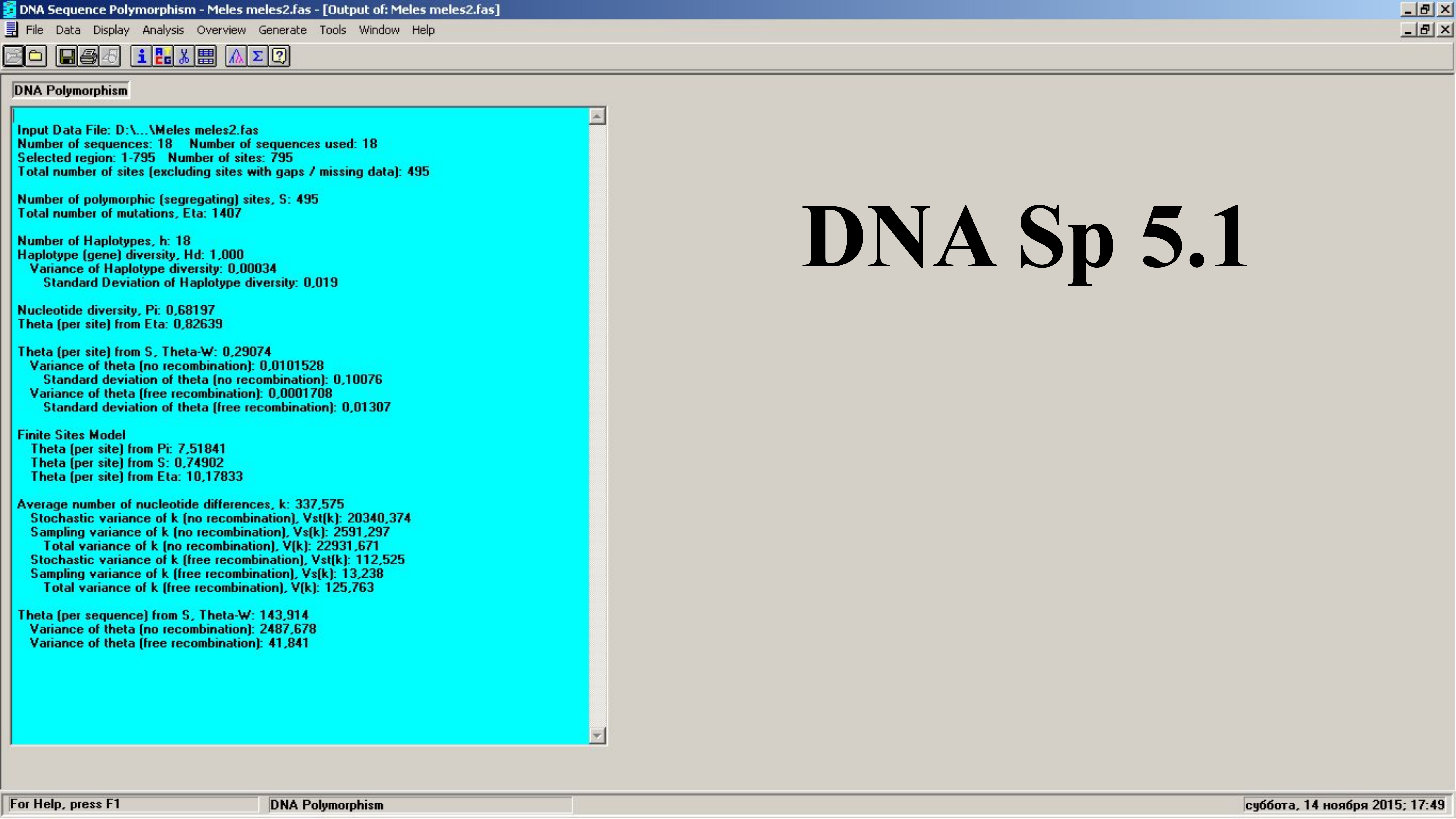
```
Input Data File: D:\...\Meles meles2.fas
Number of sequences: 18    Number of sequences used: 18
Selected region: 1-795   Number of sites: 795
Total number of sites (excluding sites with gaps / missing data): 495

Number of polymorphic (segregating) sites, S: 495
Total number of mutations, Eta: 1407

Average number of nucleotide differences, k: 337,57516
   Nucleotide diversity, Pi: 0,68197
Theta (per sequence) from Eta: 409,06484
   Theta (per site) from Eta: 0,82639

Tajima's D: -0,74808     Statistical significance: Not significant, P > 0.10


=========== Synonymous and NonSynonymous Substitutions ===========

No coding region defined

Calculated using the total number of mutations
```



```
Input Data File: D:\...\Meles meles2.fas
Number of sequences: 18    Number of sequences used: 18
Selected region: 1-795   Number of sites: 795
Total number of sites (excluding sites with gaps / missing data): 495

Number of polymorphic (segregating) sites, S: 495

Observed values:
   Nucleotide diversity, Pi: 0,68197
   Average Number of Pairwise Differences, k: 337,575
   Observed variance of k: 297,9960
   Observed C.V. of k: 0,0518
   Raggedness statistic r: 0,0198
   Mean Absolute Error, MAE: 1,8654
   Ramos-Onsins and Rozas, R2 statistic: 0,3183

Expected values:
   Expected Total variance of k (no recombination), V(k): 22931,671
      Expected C.V. of k (no recombination): 0,4486
   Expected Stochastic variance of k (no recombination), Vst(k): 20340,374
   Expected Sampling variance of k (no recombination), Vs(k): 2591,297

   Expected Total variance of k (free recombination), V(k): 125,763
      Expected C.V. of k (free recombination): 0,0332
   Expected Stochastic variance of k (free recombination), Vst(k): 112,525
   Expected Sampling variance of k (free recombination), Vs(k): 13,238

Parameters Estimation by letting Theta Final as infinite
   Estimate of Theta Initial: 0,000
   Estimate of Tau: 337,575

====  Expected Values for Constant Population Size  =====
```

Differences	Freq. Obs.	Freq. Exp.
0	0,00000	0,00295
1	0,00000	0,00294
2	0,00000	0,00294
3	0,00000	0,00293
4	0,00000	0,00292
5	0,00000	0,00291
6	0,00000	0,00290
7	0,00000	0,00289
8	0,00000	0,00288
9	0,00000	0,00288
10	0,00000	0,00287
11	0,00000	0,00286
12	0,00000	0,00285
13	0,00000	0,00284
14	0,00000	0,00283
15	0,00000	0,00283
16	0,00000	0,00282
17	0,00000	0,00281
18	0,00000	0,00280
19	0,00000	0,00279

DNA Sp 5.1



```
Input Data File: D:\...\Meles meles2.fas
Number of sequences: 18    Number of sequences used: 18
Selected region: 1-795   Number of sites: 795
Total number of sites (excluding sites with gaps / missing data): 495

Number of polymorphic (segregating) sites, S: 495
Total number of mutations, Eta: 1407

Number of Haplotypes, h: 18
Haplotype (gene) diversity, Hd: 1,000
   Variance of Haplotype diversity: 0,00034
      Standard Deviation of Haplotype diversity: 0,019

Nucleotide diversity, Pi: 0,68197
Theta (per site) from Eta: 0,82639

Theta (per site) from S, Theta-W: 0,29074
   Variance of theta (no recombination): 0,0101528
      Standard deviation of theta (no recombination): 0,10076
   Variance of theta (free recombination): 0,0001708
      Standard deviation of theta (free recombination): 0,01307

Finite Sites Model
   Theta (per site) from Pi: 7,51841
   Theta (per site) from S: 0,74902
   Theta (per site) from Eta: 10,17833

Average number of nucleotide differences, k: 337,575
   Stochastic variance of k (no recombination), Vst(k): 20340,374
   Sampling variance of k (no recombination), Vs(k): 2591,297
      Total variance of k (no recombination), V(k): 22931,671
   Stochastic variance of k (free recombination), Vst(k): 112,525
   Sampling variance of k (free recombination), Vs(k): 13,238
      Total variance of k (free recombination), V(k): 125,763

Theta (per sequence) from S, Theta-W: 143,914
   Variance of theta (no recombination): 2487,678
   Variance of theta (free recombination): 41,841
```