# Phylogram (no calibrations): MrBayes Allcompat consensus of 10k trees

## Plot #1 – Node support: black if PP >= 0.95; red if PP < 0.95 – Tips: red if ancient DNA

*197 total tips (176 Microdipodops), 20 Dipodomys, 1 Perognathus outgroup*



0.02    expected substitutions per site
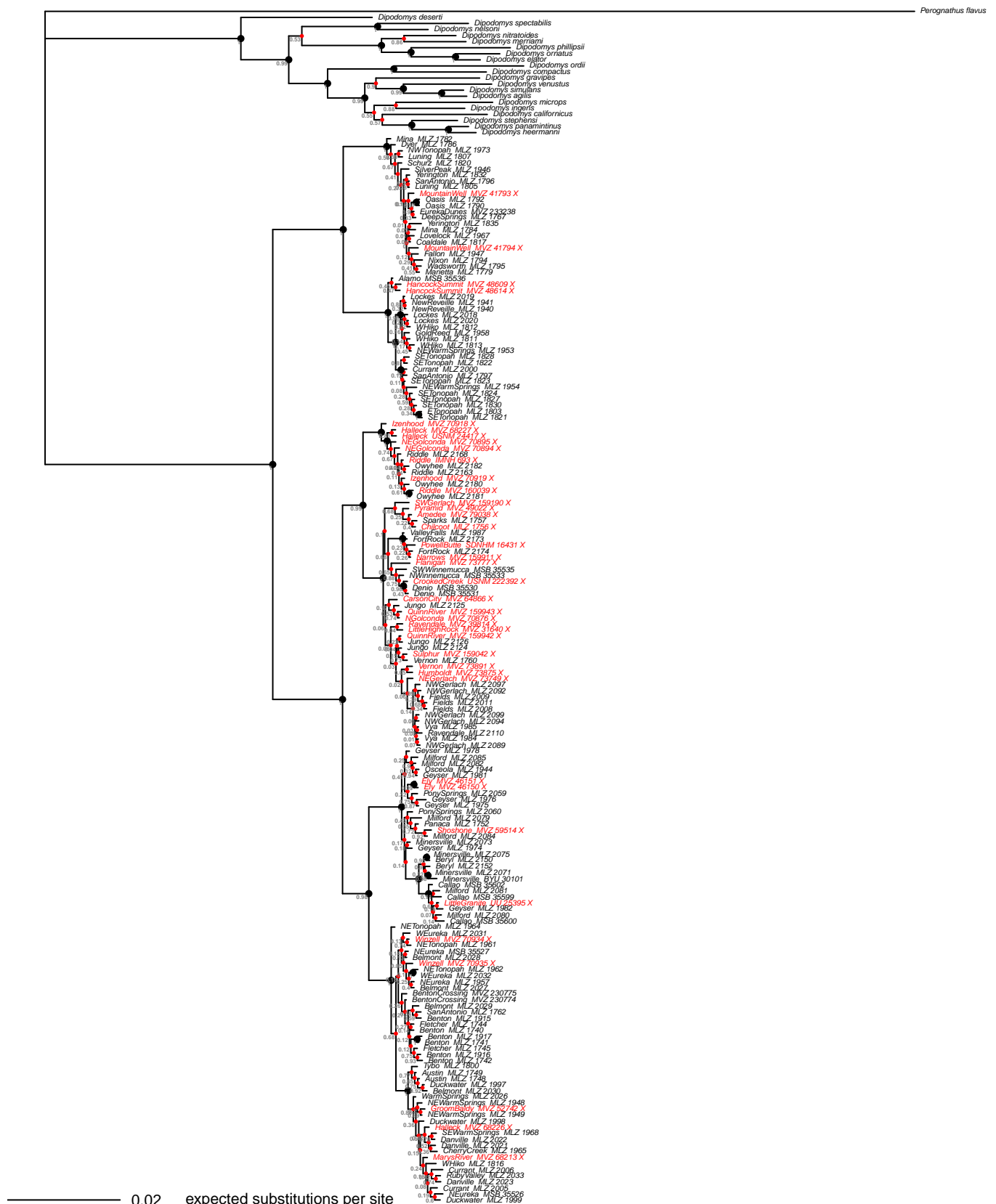
**Phylogram (no calibrations): MrBayes Allcompat consensus of 10k trees**

**Plot #2 – Node support: black if PP >= 0.95; red if PP < 0.95 – Tips: red if ancient DNA**

*196 total tips (176 Microdipodops), 20 Dipodomys, excluding outgroup*



0.02    expected substitutions per site
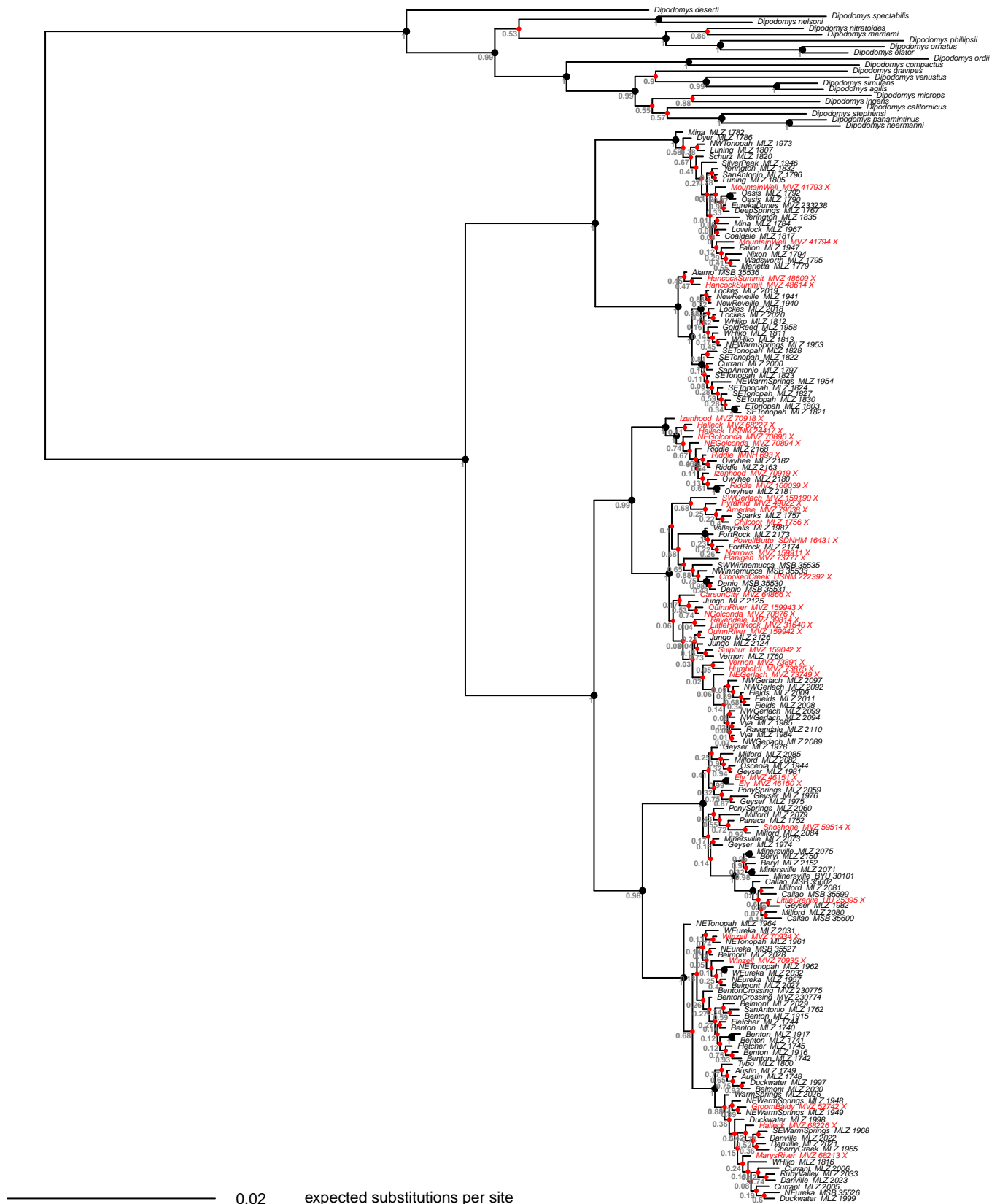
**Phylogram (no calibrations): MrBayes Allcompat consensus of 10k trees**

**Plot #3 – Node support: black if PP >= 0.95; red if PP < 0.95 – Tips: red if ancient DNA**

*176 Microdipodops only, excluding Dipodomys and outgroup*

0.005    expected substitutions per site

**Phylogram (no calibrations): MrBayes Allcompat consensus of 10k trees**

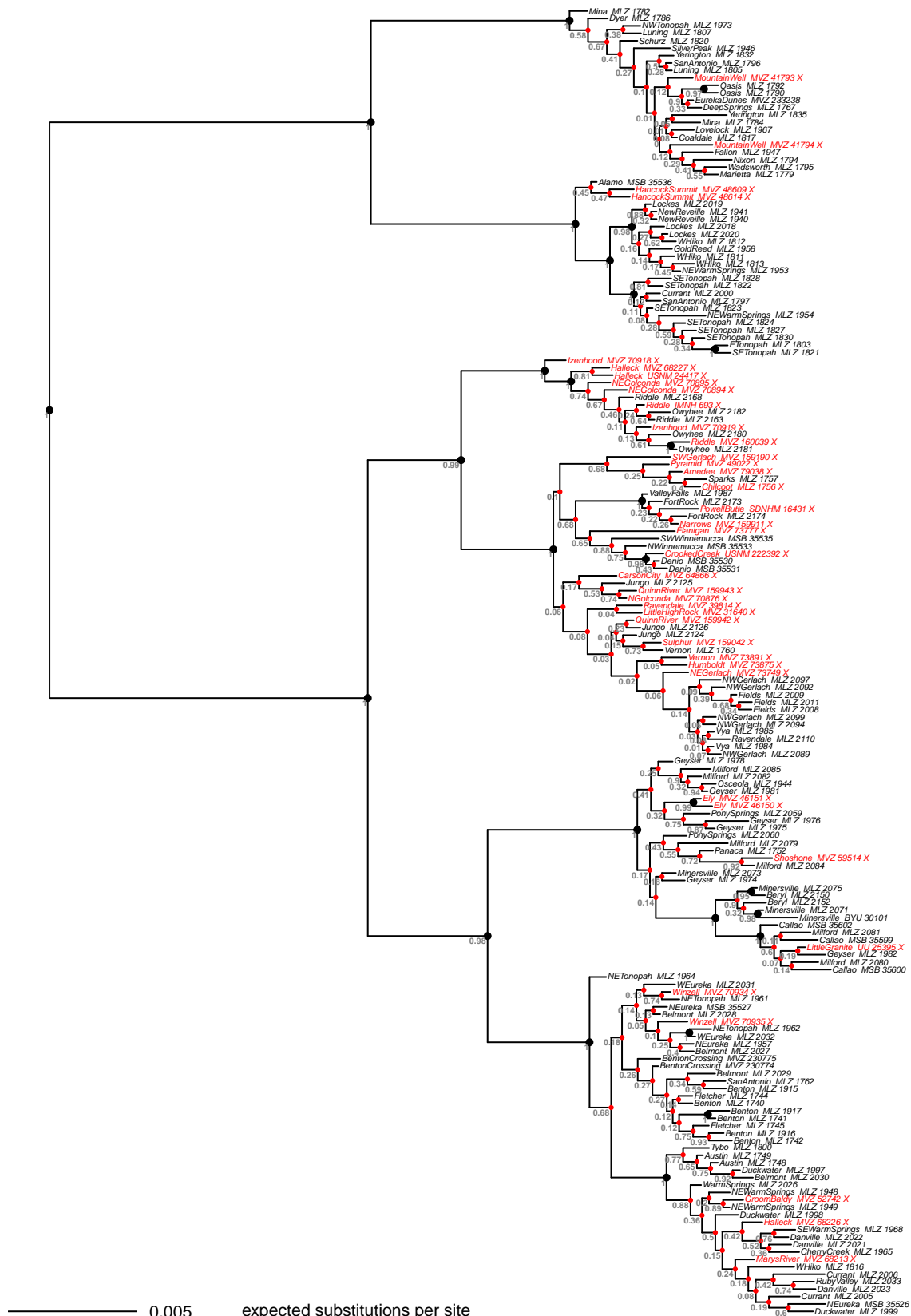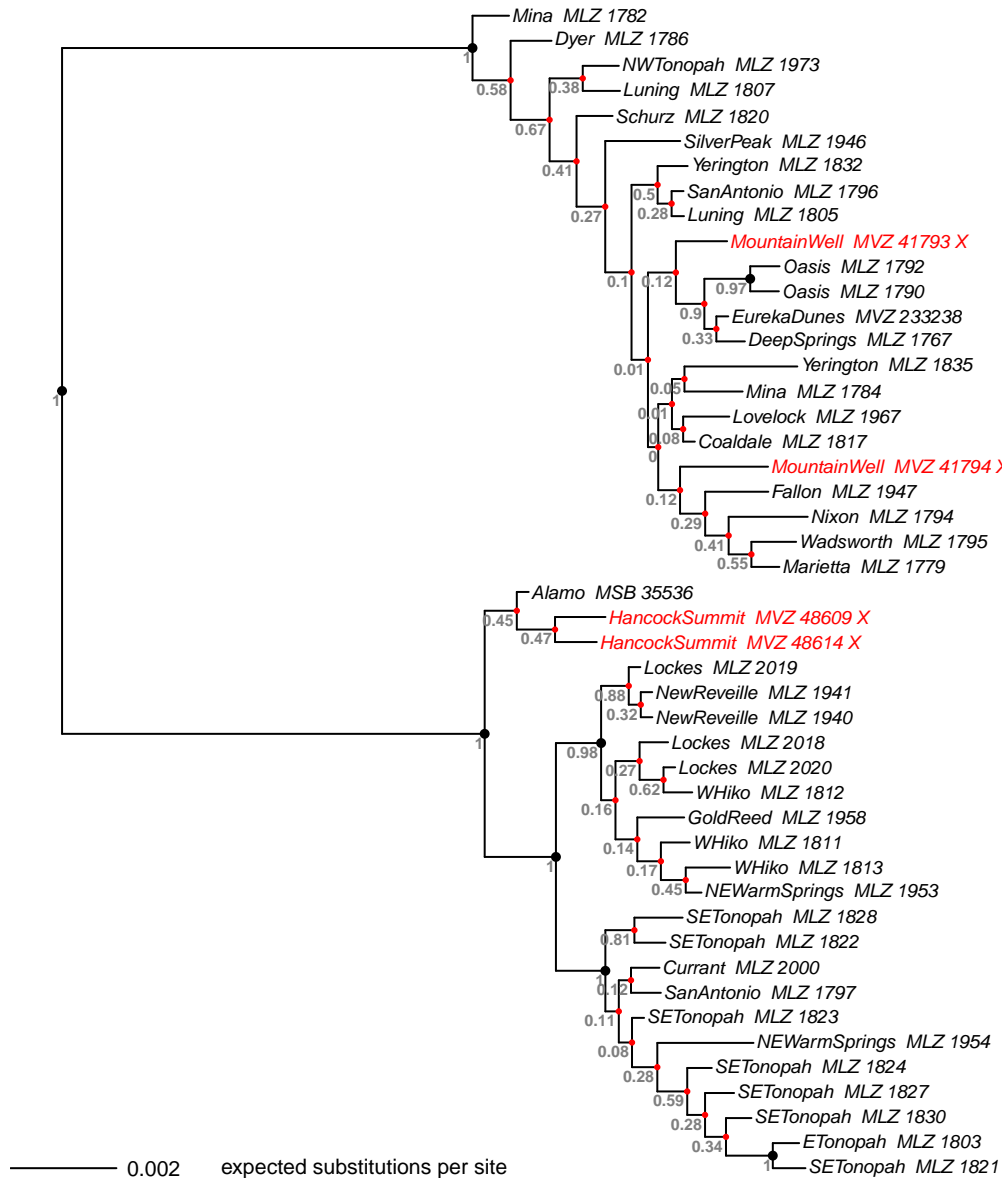**Plot #4 – Node support: black if PP >= 0.95; red if PP < 0.95 – Tips: red if ancient DNA**

*47 M.(P) only, excluding M(M.), Dipodomys, and outgroup*



Mina  MLZ 1782
Dyer  MLZ 1786
NWTonopah  MLZ 1973
Luning  MLZ 1807
Schurz  MLZ 1820
SilverPeak  MLZ 1946
Yerington  MLZ 1832
SanAntonio  MLZ 1796
Luning  MLZ 1805
*MountainWell  MVZ 41793 X*
Oasis  MLZ 1792
Oasis  MLZ 1790
EurekaDunes  MVZ 233238
DeepSprings  MLZ 1767
Yerington  MLZ 1835
Mina  MLZ 1784
Lovelock  MLZ 1967
Coaldale  MLZ 1817
*MountainWell  MVZ 41794 X*
Fallon  MLZ 1947
Nixon  MLZ 1794
Wadsworth  MLZ 1795
Marietta  MLZ 1779
Alamo  MSB 35536
*HancockSummit  MVZ 48609 X*
*HancockSummit  MVZ 48614 X*
Lockes  MLZ 2019
NewReveille  MLZ 1941
NewReveille  MLZ 1940
Lockes  MLZ 2018
Lockes  MLZ 2020
WHiko  MLZ 1812
GoldReed  MLZ 1958
WHiko  MLZ 1811
WHiko  MLZ 1813
NEWarmSprings  MLZ 1953
SETonopah  MLZ 1828
SETonopah  MLZ 1822
Currant  MLZ 2000
SanAntonio  MLZ 1797
SETonopah  MLZ 1823
NEWarmSprings  MLZ 1954
SETonopah  MLZ 1824
SETonopah  MLZ 1827
SETonopah  MLZ 1830
ETonopah  MLZ 1803
SETonopah  MLZ 1821

0.002    expected substitutions per site

**Phylogram (no calibrations): MrBayes Allcompat consensus of 10k trees**

**Plot #5 – Node support: black if PP >= 0.95; red if PP < 0.95 – Tips: red if ancient DNA**

*129 M.(M) only, excluding M(P.), Dipodomys, and outgroup*

0.005    expected substitutions per site