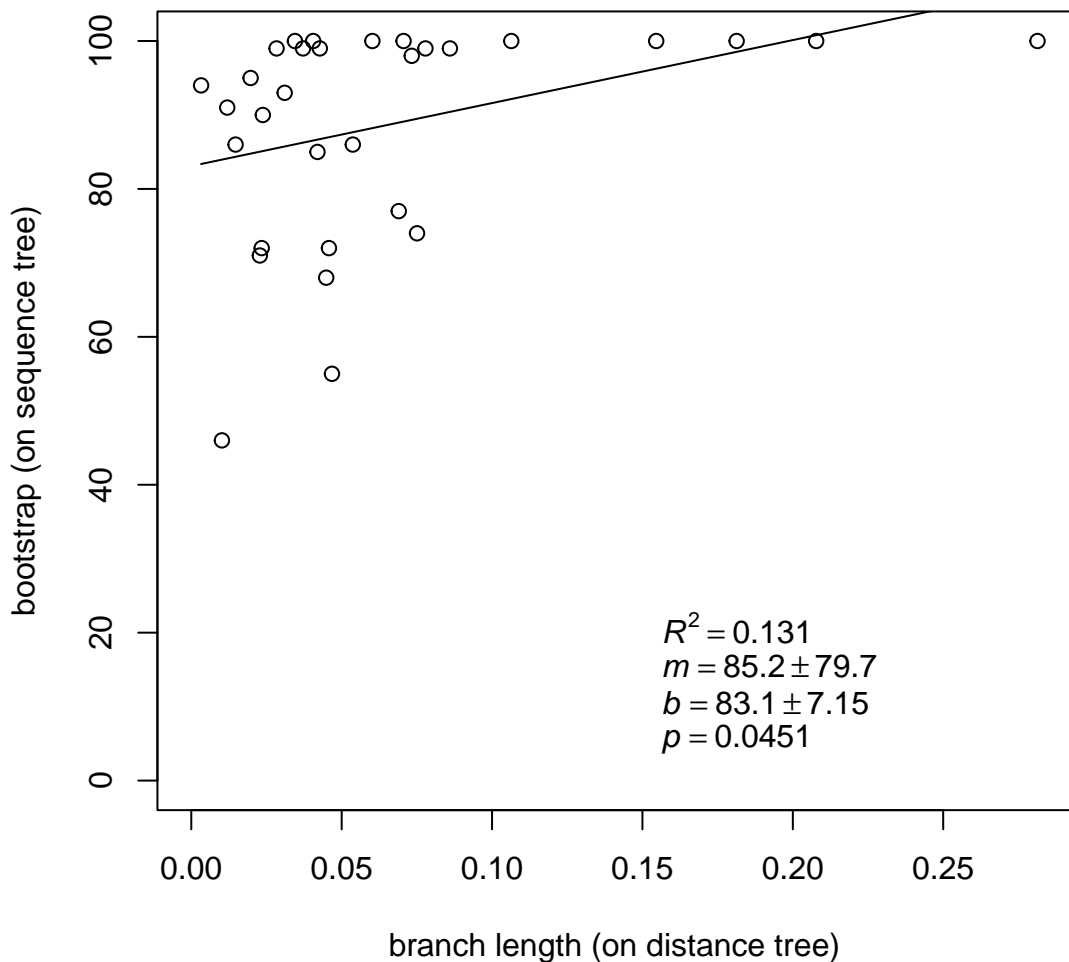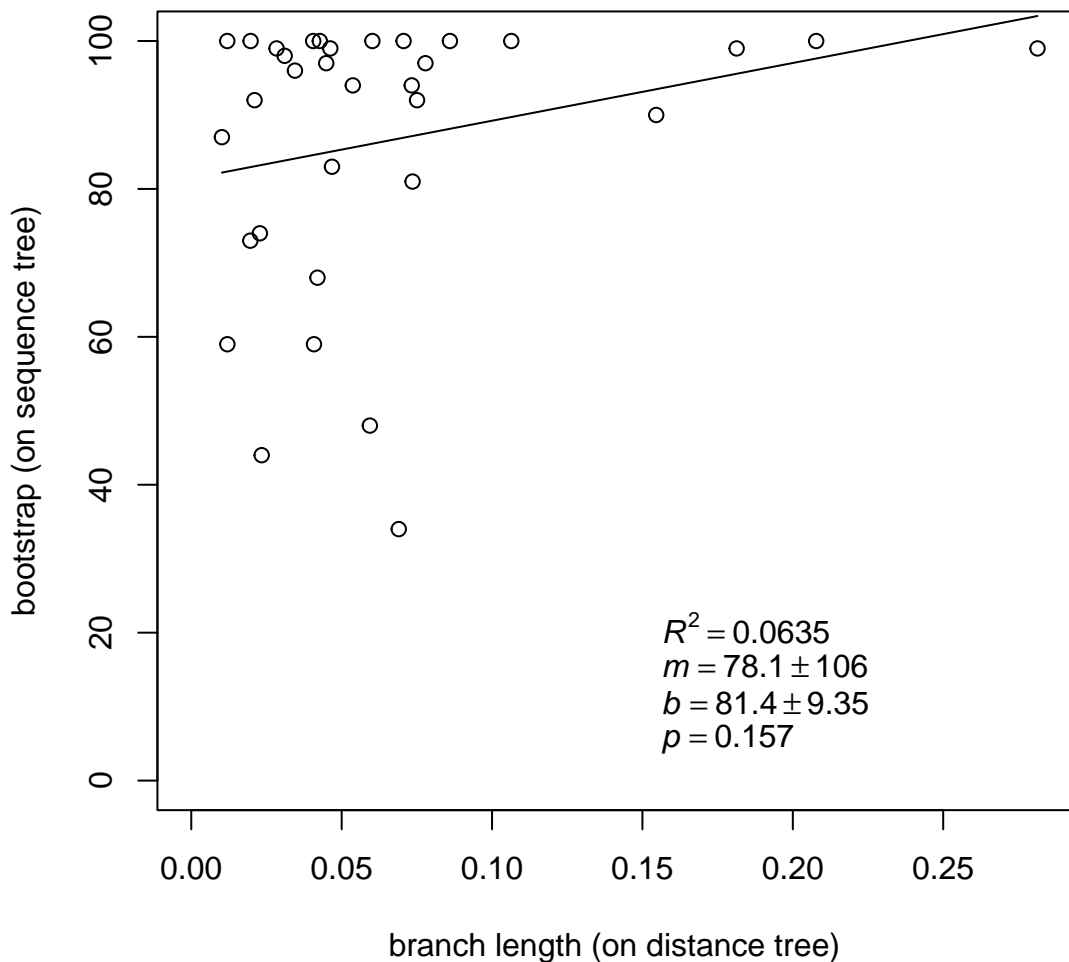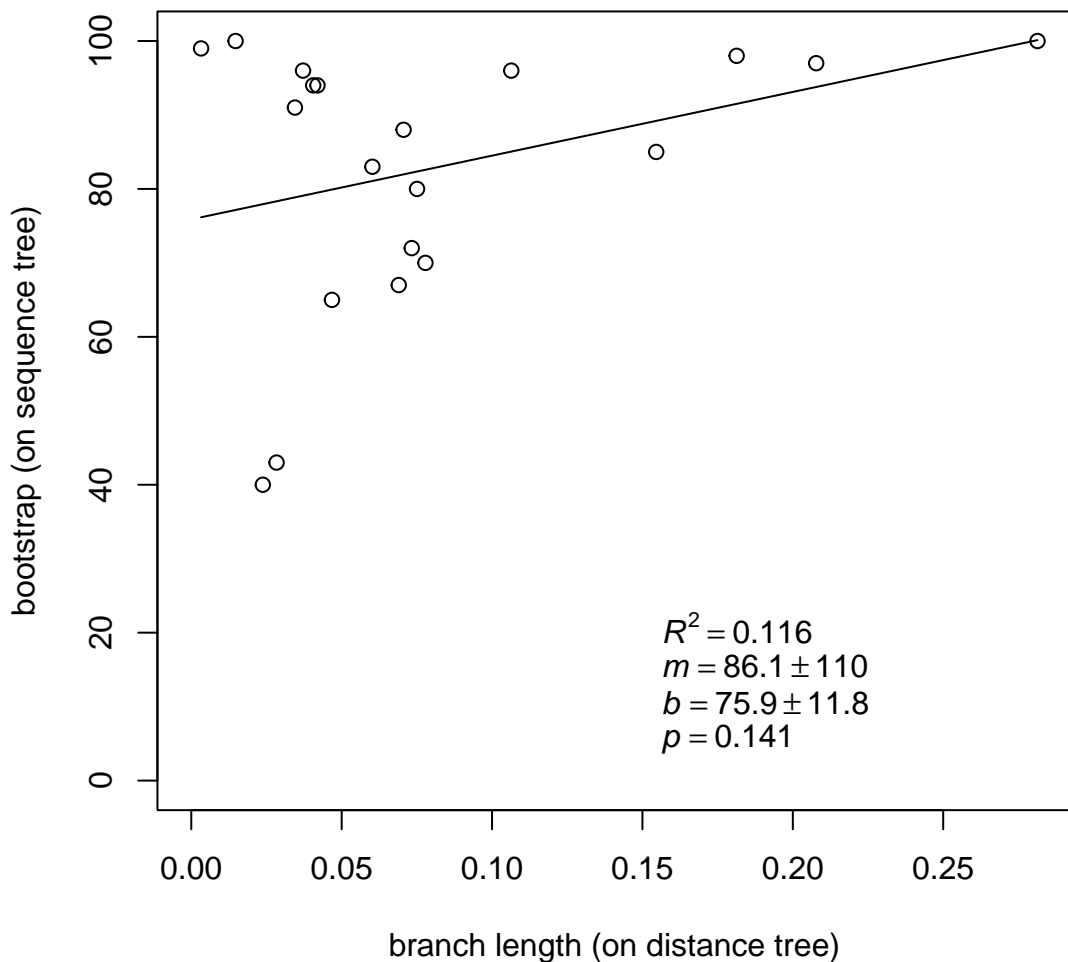**Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (31/52 matches for #1: iqtree_USaln_AA_cut)**

branch length (on distance tree)

bootstrap (on sequence tree)
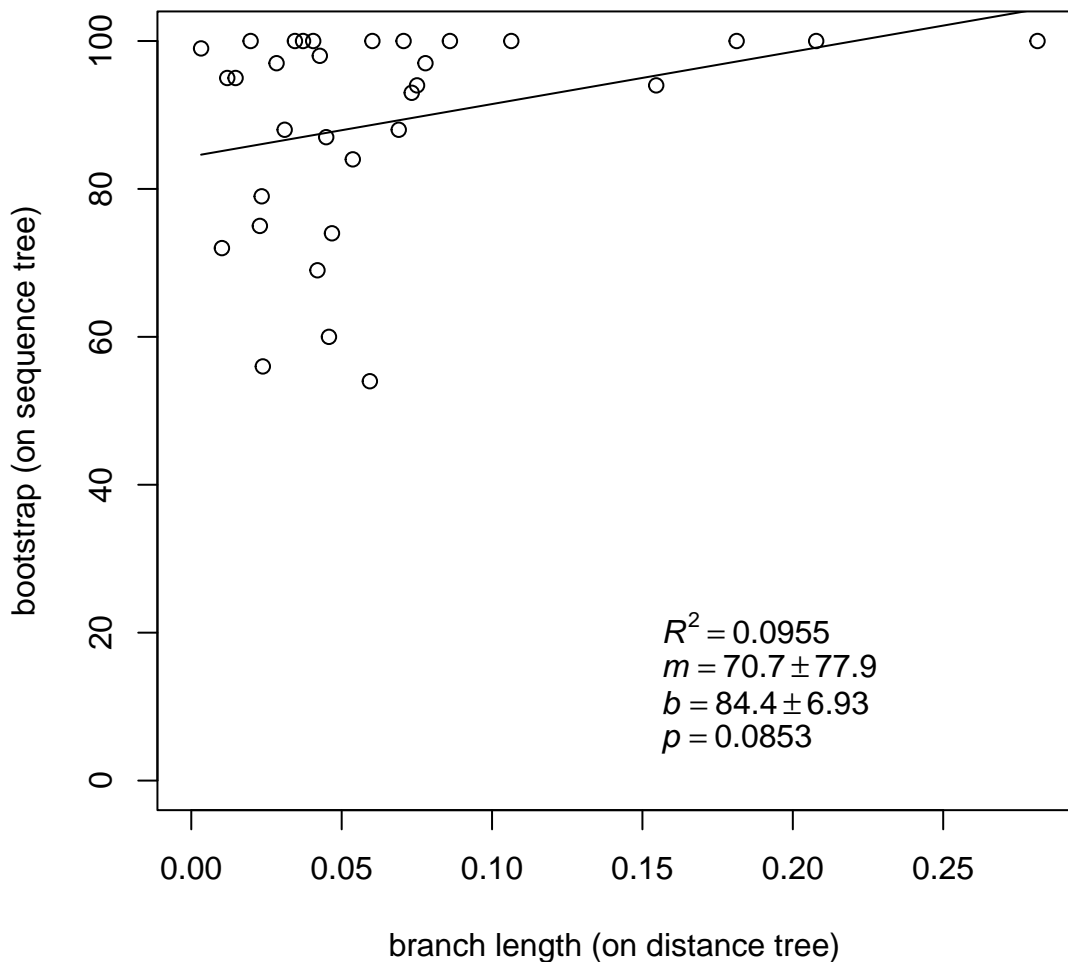
$R^2 = 0.131$
$m = 85.2 \pm 79.7$
$b = 83.1 \pm 7.15$
$p = 0.0451$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (33/52 matches for #2: iqtree_USaln_3di_cut)

bootstrap (on sequence tree)

branch length (on distance tree)

$R^2 = 0.0635$
$m = 78.1 \pm 106$
$b = 81.4 \pm 9.35$
$p = 0.157$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (20/52 matches for #3: iqtree_USaln_AA3di_cut_wPartitions)

$R^2 = 0.116$
$m = 86.1 \pm 110$
$b = 75.9 \pm 11.8$
$p = 0.141$

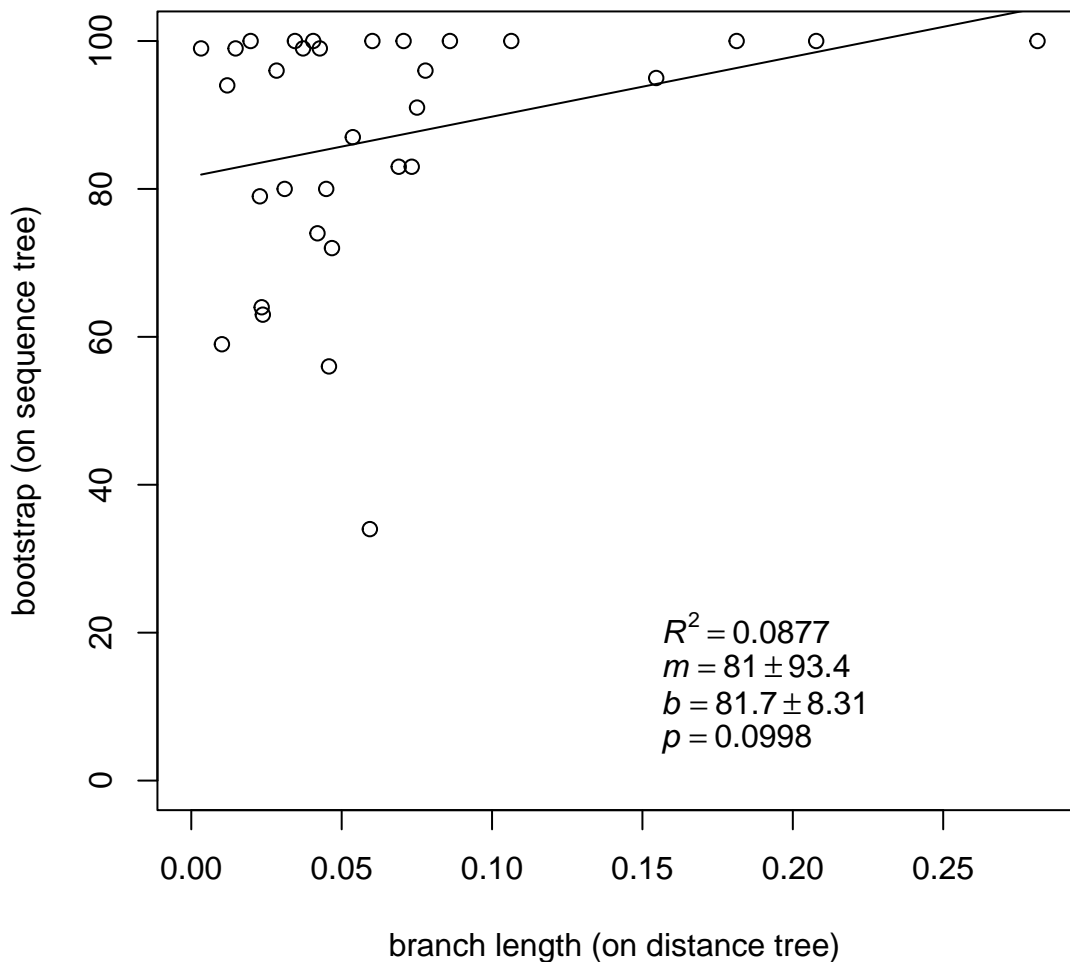bootstrap (on sequence tree)

branch length (on distance tree)

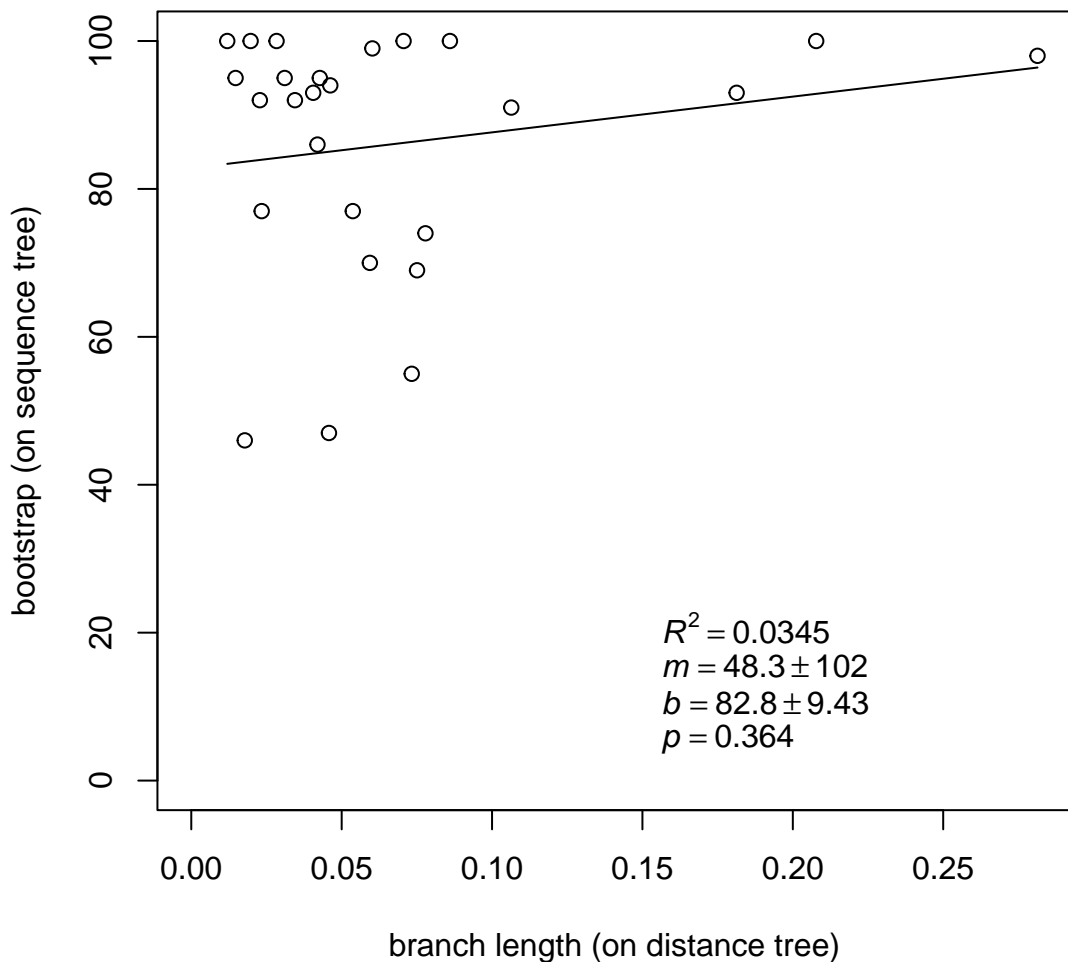**Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (32/52 matches for #4: iqtree_USaln_AA3di_cut_wAllPartitions)**

$R^2 = 0.0955$
$m = 70.7 \pm 77.9$
$b = 84.4 \pm 6.93$
$p = 0.0853$

bootstrap (on sequence tree)

branch length (on distance tree)

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (32/52 matches for #5: iqtree_FAMSA_AA_cut)

bootstrap (on sequence tree)

branch length (on distance tree)
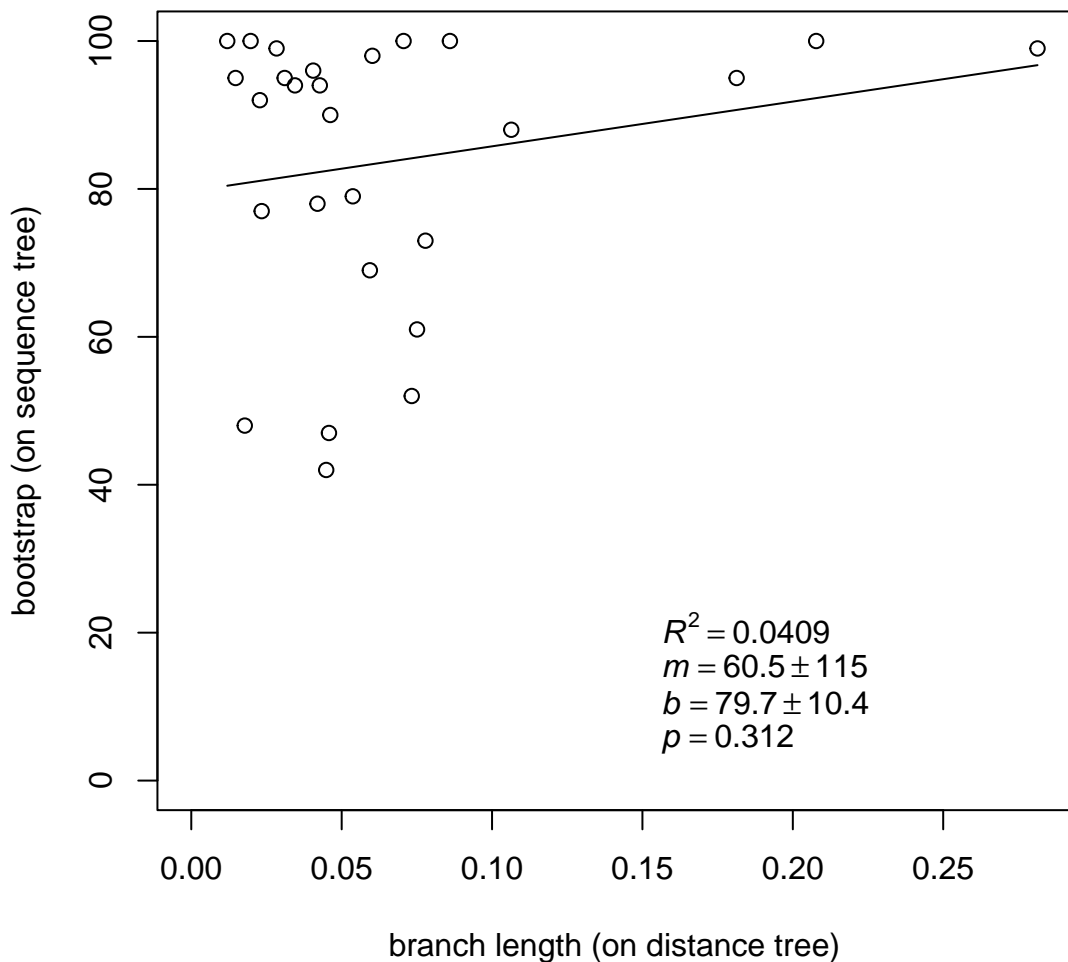
$R^2 = 0.0877$
$m = 81 \pm 93.4$
$b = 81.7 \pm 8.31$
$p = 0.0998$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (26/52 matches for #6: iqtree_FAMSA_AA_cut_v1a)

$R^2 = 0.0345$
$m = 48.3 \pm 102$
$b = 82.8 \pm 9.43$
$p = 0.364$

branch length (on distance tree)

bootstrap (on sequence tree)

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (27/52 matches for #7: iqtree_FAMSA_3di_cut)

bootstrap (on sequence tree)

branch length (on distance tree)

$R^2 = 0.0409$
$m = 60.5 \pm 115$
$b = 79.7 \pm 10.4$
$p = 0.312$

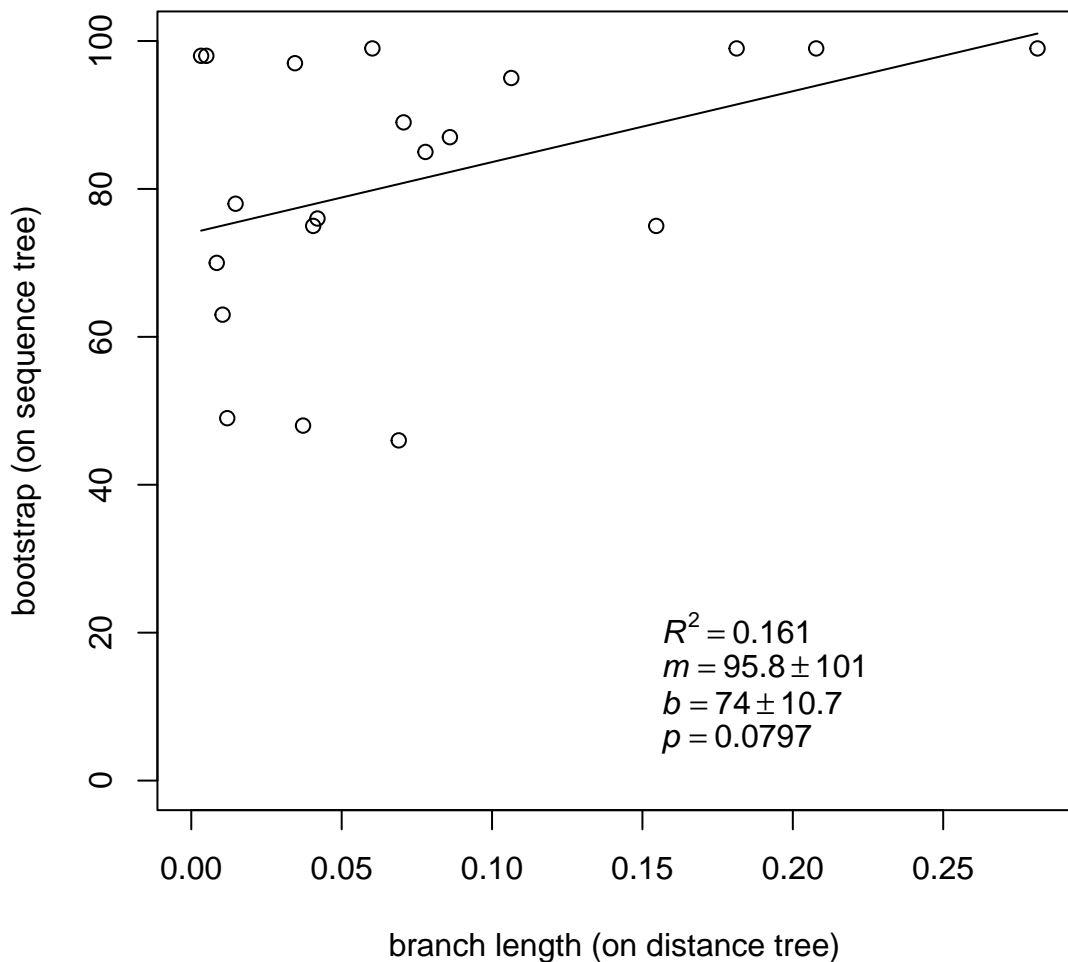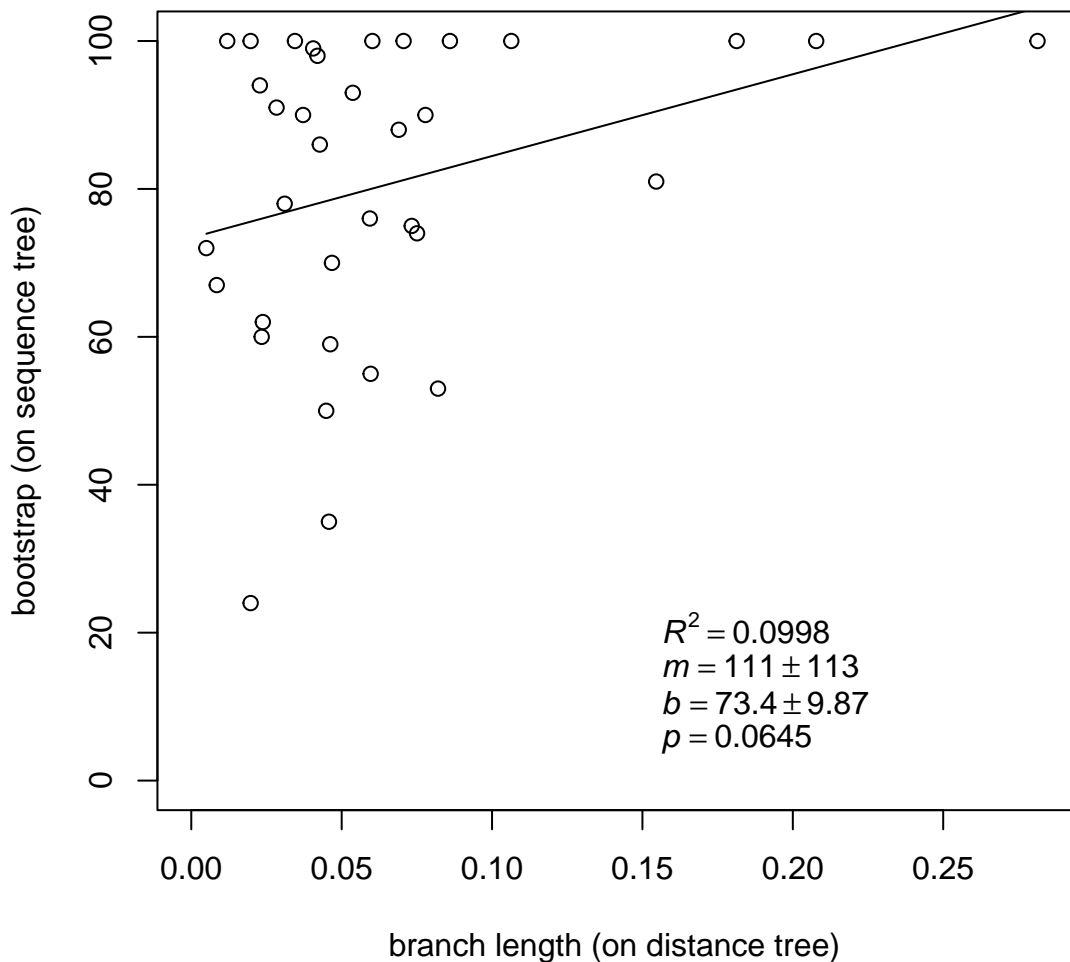**Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (20/52 matches for #8: iqtree_FAMSA_AA3di_cut_wPartitions)**

branch length (on distance tree)

bootstrap (on sequence tree)

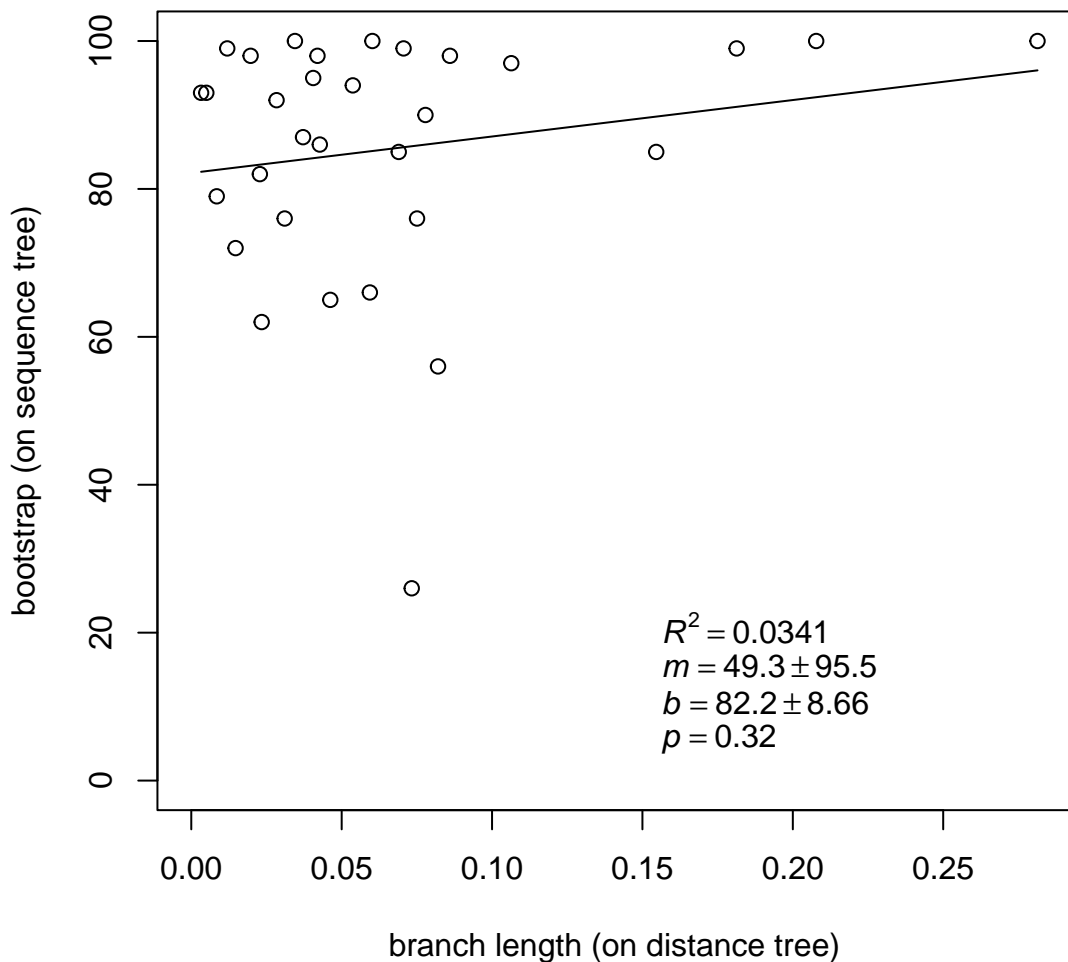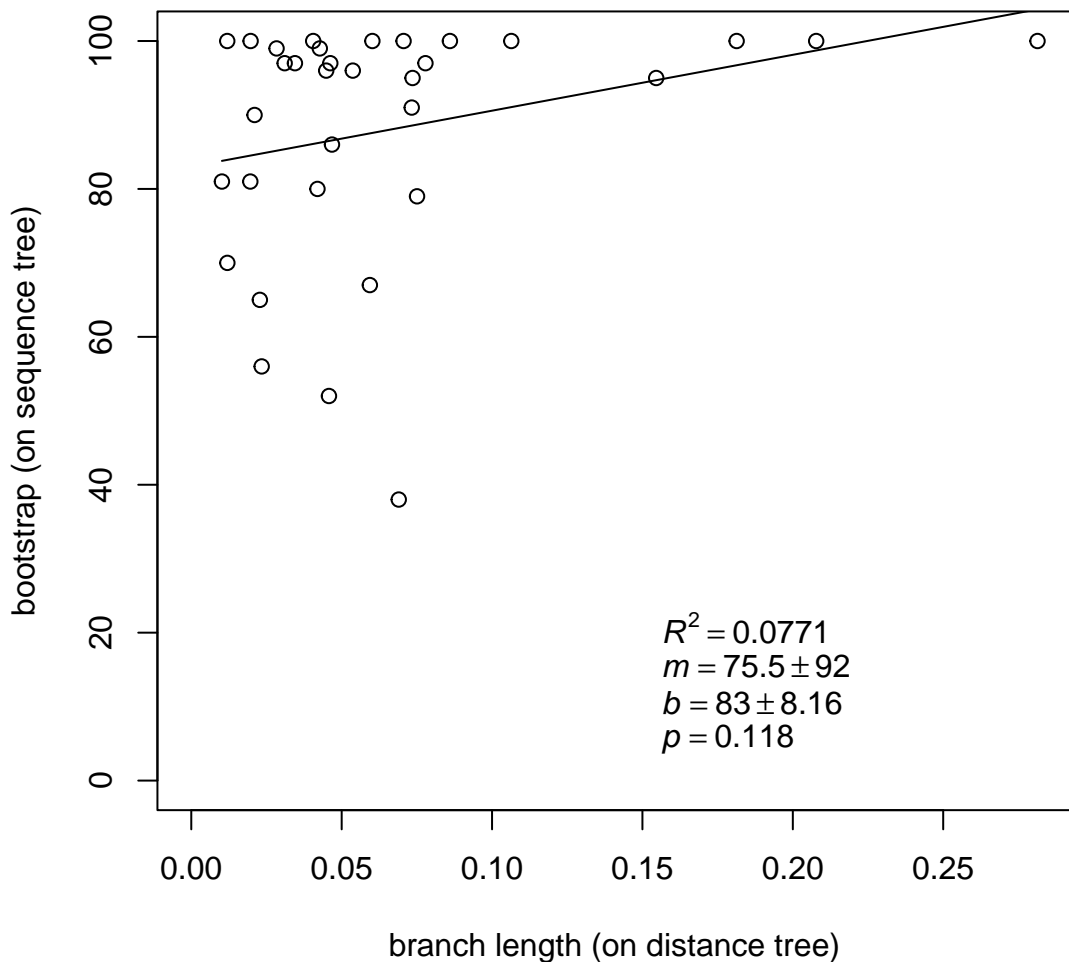$R^2 = 0.161$
$m = 95.8 \pm 101$
$b = 74 \pm 10.7$
$p = 0.0797$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (35/52 matches for #9: iqtree_FAMSA_AA3di_cut_wAllPartitions)

bootstrap (on sequence tree)

branch length (on distance tree)

$R^2 = 0.0998$
$m = 111 \pm 113$
$b = 73.4 \pm 9.87$
$p = 0.0645$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (31/52 matches for #10: iqtree_USaln_AA_all)

branch length (on distance tree)

bootstrap (on sequence tree)

$R^2 = 0.0341$
$m = 49.3 \pm 95.5$
$b = 82.2 \pm 8.66$
$p = 0.32$

**Ferritin superfamily: Branch lengths (structural distance tree)
vs. bootstraps (33/52 matches for #11: iqtree_USaln_3di_all)**

branch length (on distance tree)

bootstrap (on sequence tree)

$R^2 = 0.0771$
$m = 75.5 \pm 92$
$b = 83 \pm 8.16$
$p = 0.118$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (21/52 matches for #12: iqtree_USaln_AA3di_all_wAllPartitions)

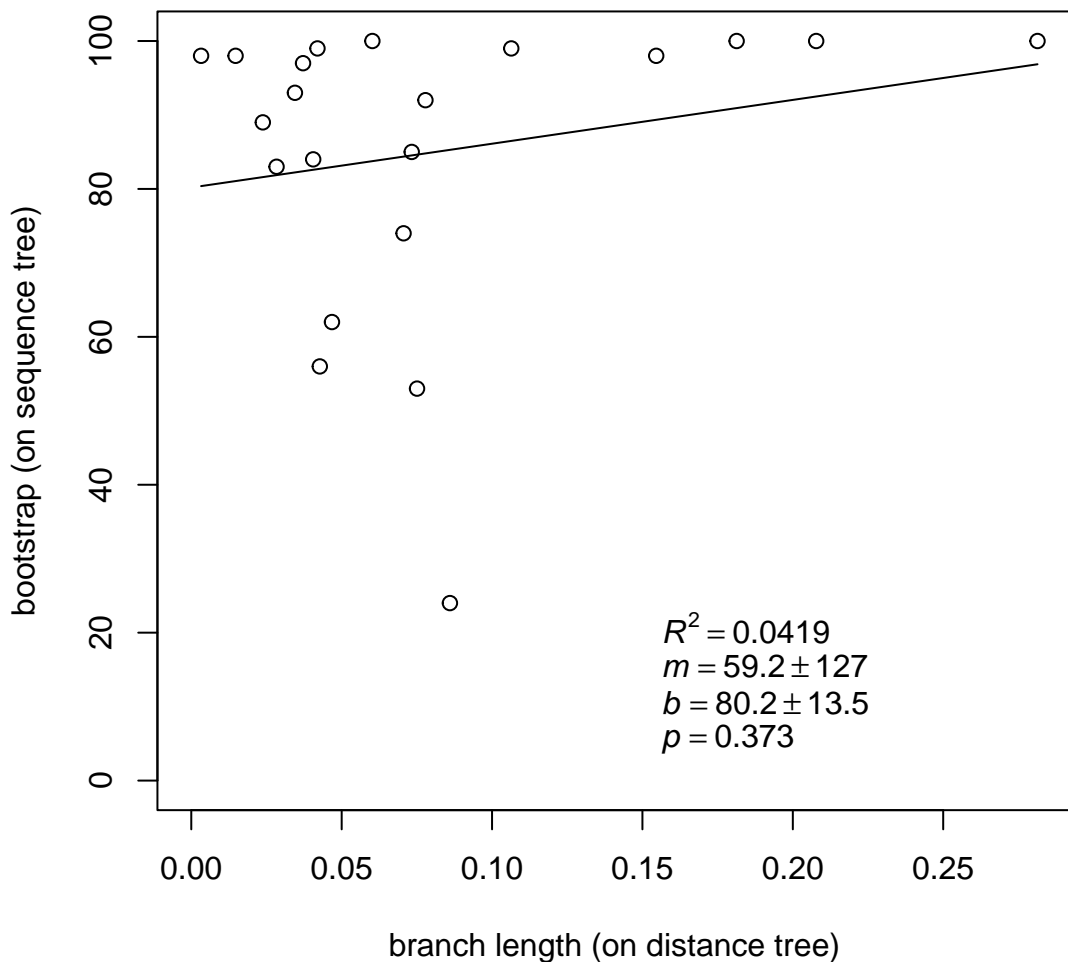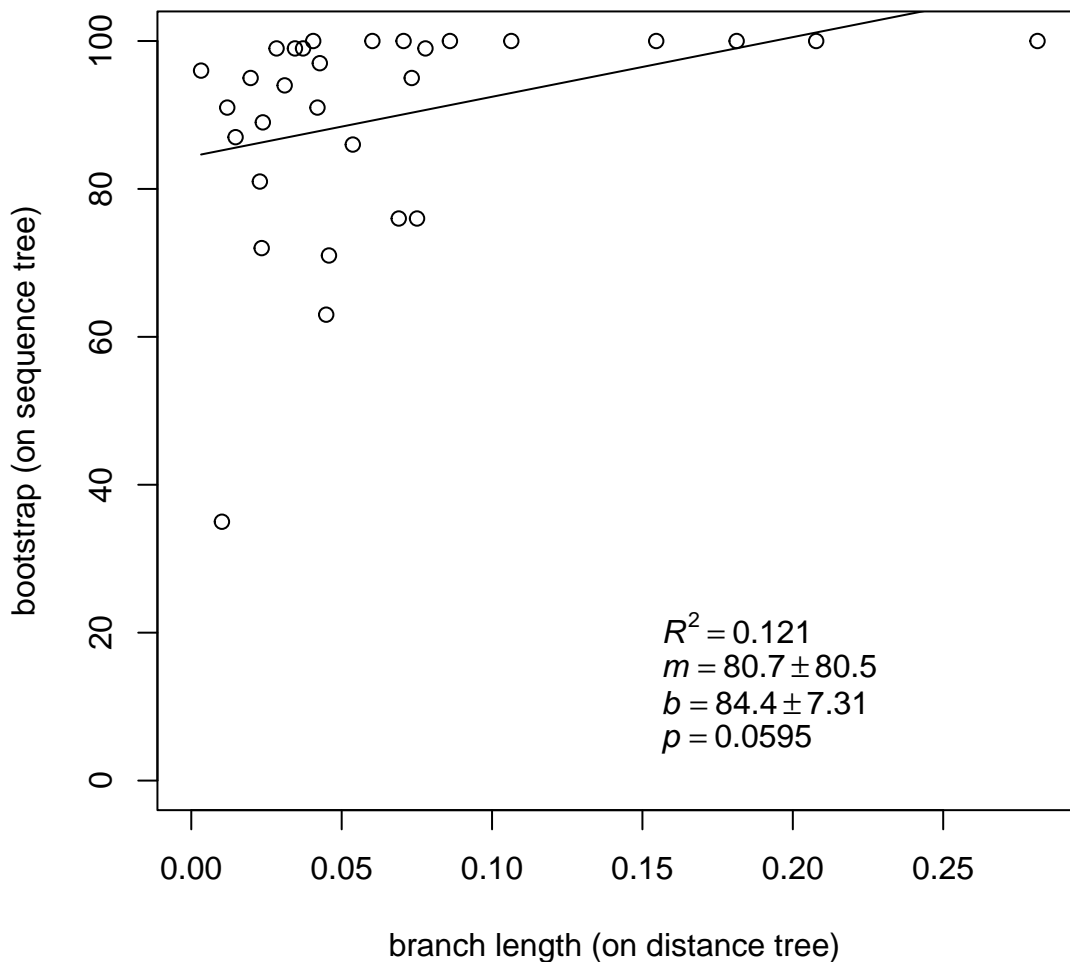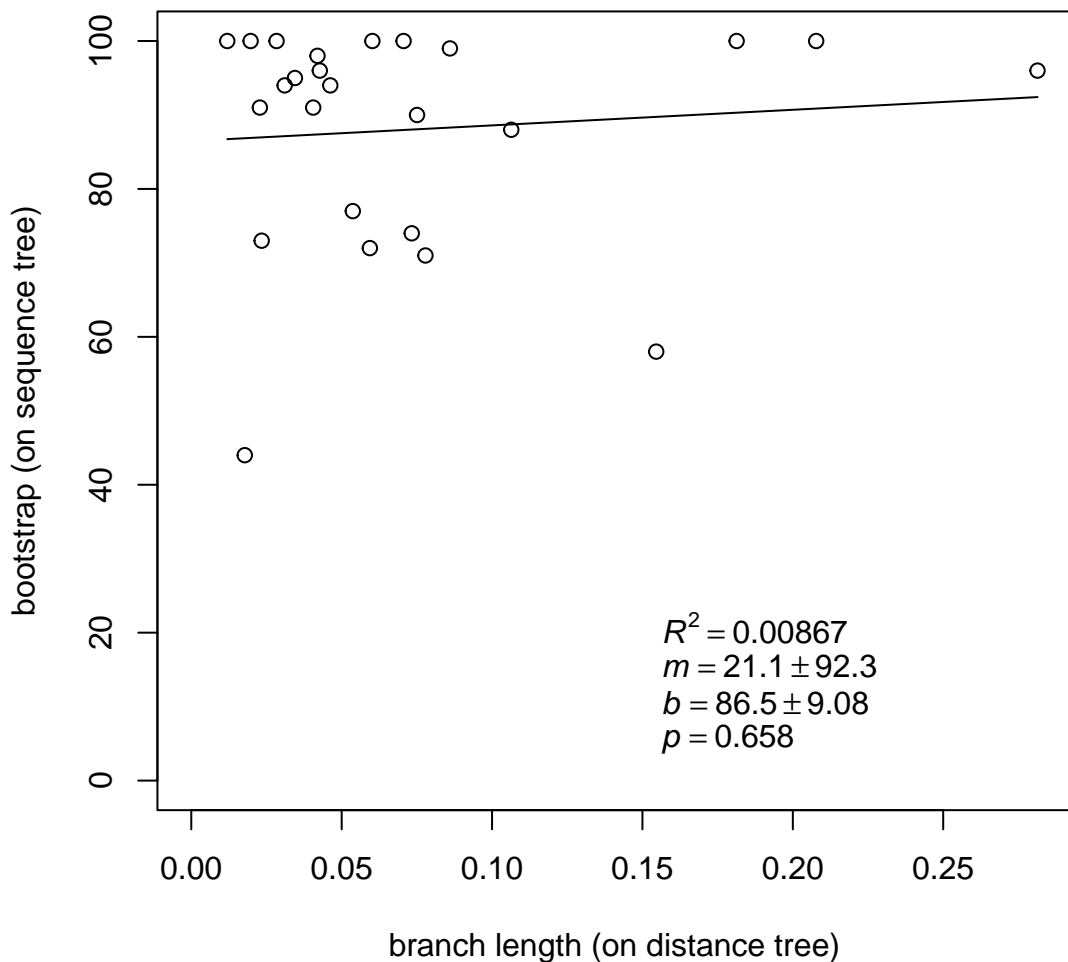$R^2 = 0.0419$
$m = 59.2 \pm 127$
$b = 80.2 \pm 13.5$
$p = 0.373$

bootstrap (on sequence tree)

branch length (on distance tree)

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (30/52 matches for #13: iqtree_FAMSA_AA_all)

branch length (on distance tree)

bootstrap (on sequence tree)

$R^2 = 0.121$
$m = 80.7 \pm 80.5$
$b = 84.4 \pm 7.31$
$p = 0.0595$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (25/52 matches for #14: iqtree_FAMSA_3di_all)

bootstrap (on sequence tree)

branch length (on distance tree)

$R^2 = 0.00867$
$m = 21.1 \pm 92.3$
$b = 86.5 \pm 9.08$
$p = 0.658$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (22/52 matches for #15: iqtree_FAMSA_AA3di_cut_wPartitions)

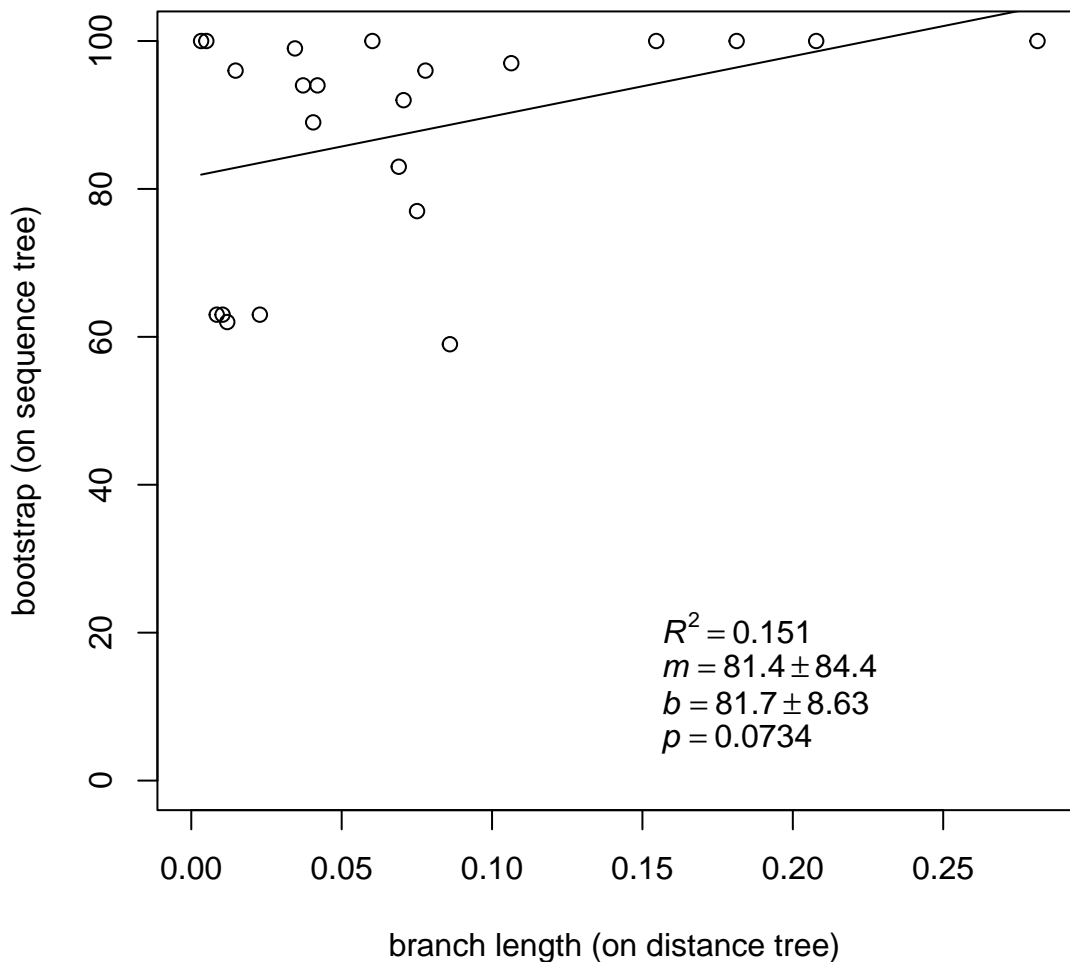bootstrap (on sequence tree)

branch length (on distance tree)

$R^2 = 0.151$
$m = 81.4 \pm 84.4$
$b = 81.7 \pm 8.63$
$p = 0.0734$

Ferritin superfamily: Branch lengths (structural distance tree) vs. bootstraps (34/52 matches for #16: iqtree_FAMSA_AA3di_all_wAllPartitions)

bootstrap (on sequence tree)

branch length (on distance tree)

$R^2 = 0.0524$
$m = 66.1 \pm 97.3$
$b = 83.2 \pm 8.53$
$p = 0.193$