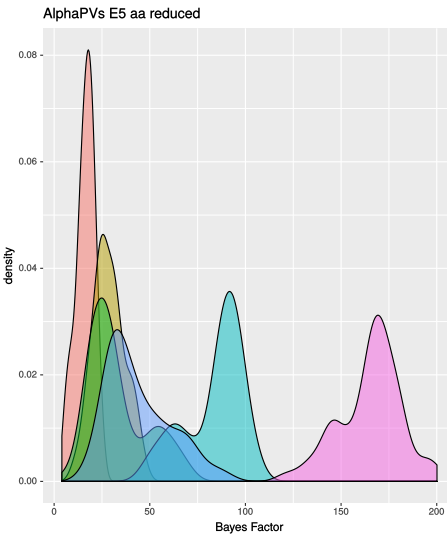
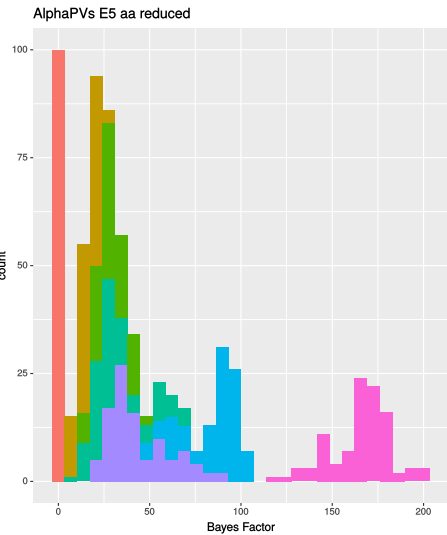
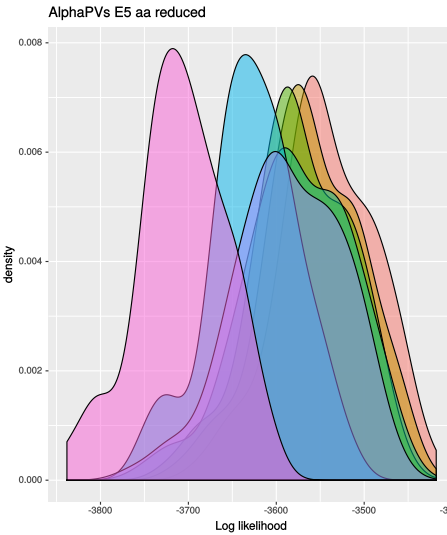
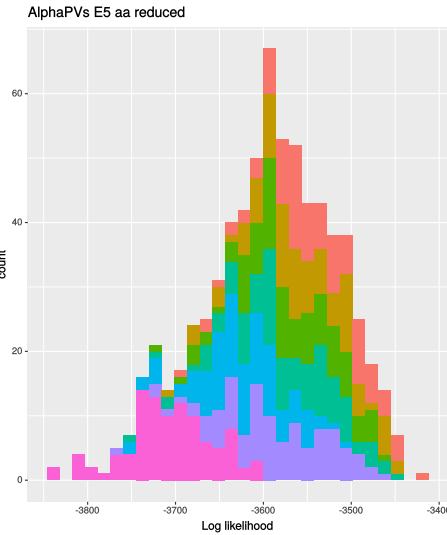
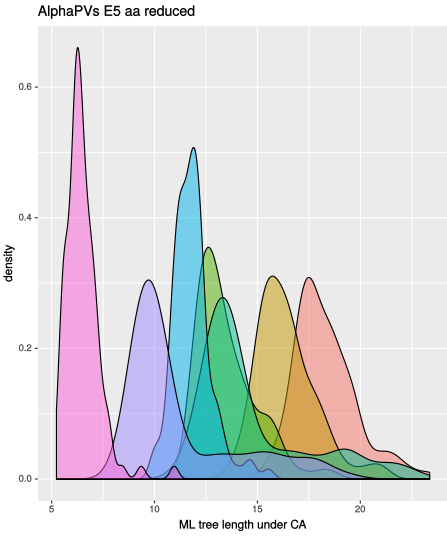
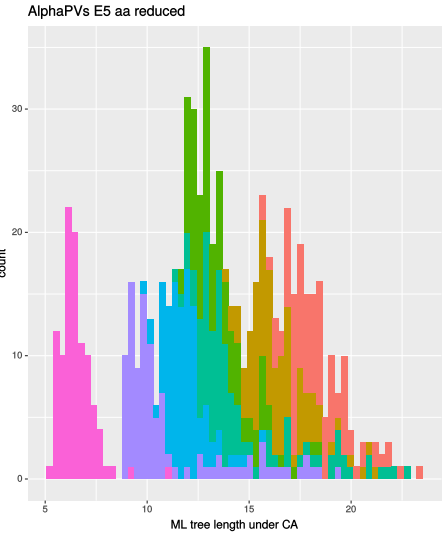


Random Permutation Test

E5 ORF within AlphaPVs  
amino acids

H0:  $(\alpha_1-\alpha_2-\beta-\gamma\delta-\delta-\varepsilon\zeta)$   
H1:  $(\alpha_1-\alpha_2-\gamma\delta-\delta-\varepsilon\zeta) + \beta$   
H2:  $(\alpha_1-\alpha_2-\gamma\delta-\delta) + \beta + \varepsilon\zeta$   
H3:  $(\alpha_1-\alpha_2-\varepsilon\zeta) + (\gamma\delta-\delta) + \beta$   
H4:  $(\alpha_1-\alpha_2-\varepsilon\zeta) + \beta + \gamma\delta + \delta$   
H5:  $(\alpha_1-\alpha_2) + (\gamma\delta-\delta) + \beta + \varepsilon\zeta$   
H6:  $\alpha_1 + \alpha_2 + \gamma\delta + \delta + \beta + \varepsilon\zeta$



Kruskal-Wallis rank sum test on ML tree length  
chi-squared = 547.73, df = 6, p-value < 2.2e-16

Multiple comparison test after Kruskal-Wallis  
p.value: 0.05

	obs.dif	critical.dif	difference
tlen_H0-tlen_H1	87.33	86.8822	TRUE
tlen_H0-tlen_H2	251.17	86.8822	TRUE
tlen_H0-tlen_H3	186.10	86.8822	TRUE
tlen_H0-tlen_H4	370.89	86.8822	TRUE
tlen_H0-tlen_H5	390.46	86.8822	TRUE
tlen_H0-tlen_H6	563.03	86.8822	TRUE
tlen_H1-tlen_H2	163.84	86.8822	TRUE
tlen_H1-tlen_H3	98.77	86.8822	TRUE
tlen_H1-tlen_H4	283.56	86.8822	TRUE
tlen_H1-tlen_H5	303.13	86.8822	TRUE
tlen_H1-tlen_H6	475.70	86.8822	TRUE
tlen_H2-tlen_H3	65.07	86.8822	FALSE
tlen_H2-tlen_H4	119.72	86.8822	TRUE
tlen_H2-tlen_H5	139.29	86.8822	TRUE
tlen_H2-tlen_H6	311.86	86.8822	TRUE
tlen_H3-tlen_H4	184.79	86.8822	TRUE
tlen_H3-tlen_H5	204.36	86.8822	TRUE
tlen_H3-tlen_H6	376.93	86.8822	TRUE
tlen_H4-tlen_H5	19.57	86.8822	FALSE
tlen_H4-tlen_H6	192.14	86.8822	TRUE
tlen_H5-tlen_H6	172.57	86.8822	TRUE

Kruskal-Wallis rank sum test on the Log likelihood  
chi-squared = 293.34, df = 6, p-value < 2.2e-16

Multiple comparison test after Kruskal-Wallis  
p.value: 0.05

	obs.dif	critical.dif	difference
lnL_H0-lnL_H1	46.26	86.8822	FALSE
lnL_H0-lnL_H2	81.91	86.8822	FALSE
lnL_H0-lnL_H3	93.37	86.8822	TRUE
lnL_H0-lnL_H4	246.96	86.8822	TRUE
lnL_H0-lnL_H5	126.15	86.8822	TRUE
lnL_H0-lnL_H6	412.93	86.8822	TRUE
lnL_H1-lnL_H2	35.65	86.8822	FALSE
lnL_H1-lnL_H3	47.11	86.8822	FALSE
lnL_H1-lnL_H4	200.70	86.8822	TRUE
lnL_H1-lnL_H5	79.89	86.8822	FALSE
lnL_H1-lnL_H6	366.67	86.8822	TRUE
lnL_H2-lnL_H3	11.46	86.8822	FALSE
lnL_H2-lnL_H4	165.05	86.8822	TRUE
lnL_H2-lnL_H5	44.24	86.8822	FALSE
lnL_H2-lnL_H6	331.02	86.8822	TRUE
lnL_H3-lnL_H4	153.59	86.8822	TRUE
lnL_H3-lnL_H5	32.78	86.8822	FALSE
lnL_H3-lnL_H6	319.56	86.8822	TRUE
lnL_H4-lnL_H5	120.81	86.8822	TRUE
lnL_H4-lnL_H6	165.97	86.8822	TRUE
lnL_H5-lnL_H6	286.78	86.8822	TRUE

Kruskal-Wallis rank sum test on the ΔBF  
chi-squared = 498.06, df = 5, p-value < 2.2e-16

Multiple comparison test after Kruskal-Wallis  
p.value: 0.05

	obs.dif	critical.dif	difference
bf_H1-bf_H2	137.24	71.9573	TRUE
bf_H1-bf_H3	152.51	71.9573	TRUE
bf_H1-bf_H4	371.76	71.9573	TRUE
bf_H1-bf_H5	233.99	71.9573	TRUE
bf_H1-bf_H6	479.10	71.9573	TRUE
bf_H2-bf_H3	15.27	71.9573	FALSE
bf_H2-bf_H4	234.52	71.9573	TRUE
bf_H2-bf_H5	96.75	71.9573	TRUE
bf_H2-bf_H6	341.86	71.9573	TRUE
bf_H3-bf_H4	219.25	71.9573	TRUE
bf_H3-bf_H5	81.48	71.9573	TRUE
bf_H3-bf_H6	326.59	71.9573	TRUE
bf_H4-bf_H5	137.77	71.9573	TRUE
bf_H4-bf_H6	107.34	71.9573	TRUE
bf_H5-bf_H6	245.11	71.9573	TRUE