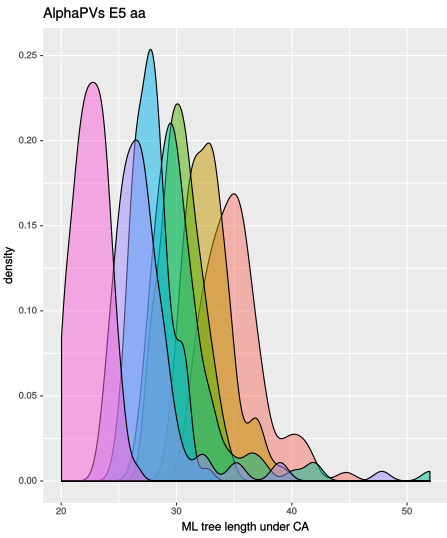
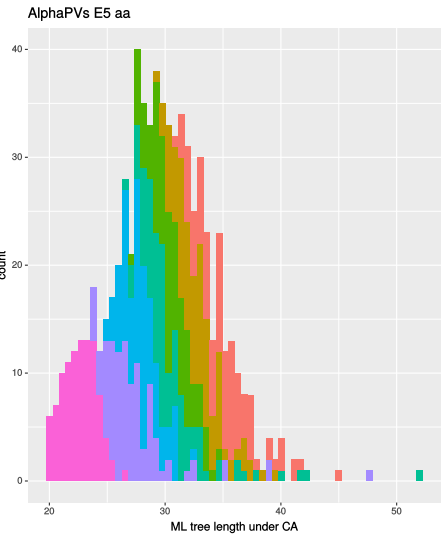


Random Permutation Test

E5 ORF within AlphaPVs
amino acids

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



Kruskal-Wallis rank sum test on ML tree length
chi-squared = 535.38, df = 6, p-value < 2.2e-16

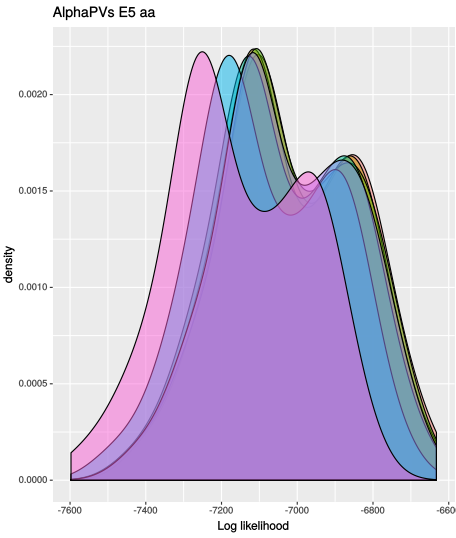
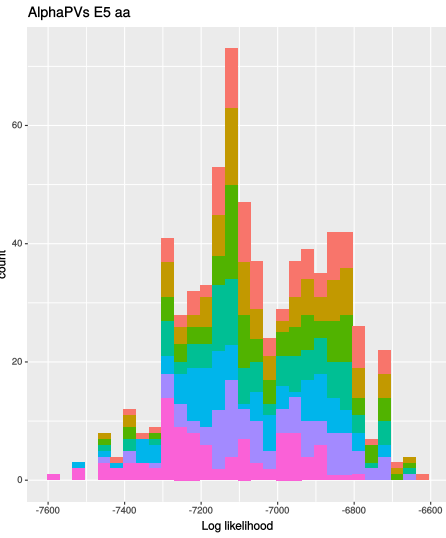
Multiple comparison test after Kruskal-Wallis
p.value: 0.05

	obs.dif	critical.dif	difference
tlen_H0-tlen_H1	78.27	86.8822	FALSE
tlen_H0-tlen_H2	204.16	86.8822	TRUE
tlen_H0-tlen_H3	212.32	86.8822	TRUE
tlen_H0-tlen_H4	359.66	86.8822	TRUE
tlen_H0-tlen_H5	388.55	86.8822	TRUE
tlen_H0-tlen_H6	554.15	86.8822	TRUE
tlen_H1-tlen_H2	125.89	86.8822	TRUE
tlen_H1-tlen_H3	134.05	86.8822	TRUE
tlen_H1-tlen_H4	281.39	86.8822	TRUE
tlen_H1-tlen_H5	310.28	86.8822	TRUE
tlen_H1-tlen_H6	475.88	86.8822	TRUE
tlen_H2-tlen_H3	8.16	86.8822	FALSE
tlen_H2-tlen_H4	155.50	86.8822	TRUE
tlen_H2-tlen_H5	184.39	86.8822	TRUE
tlen_H2-tlen_H6	349.99	86.8822	TRUE
tlen_H3-tlen_H4	147.34	86.8822	TRUE
tlen_H3-tlen_H5	176.23	86.8822	TRUE
tlen_H3-tlen_H6	341.83	86.8822	TRUE
tlen_H4-tlen_H5	28.89	86.8822	FALSE
tlen_H4-tlen_H6	194.49	86.8822	TRUE
tlen_H5-tlen_H6	165.60	86.8822	TRUE

Kruskal-Wallis rank sum test on the Log likelihood
chi-squared = 45.187, df = 6, p-value = 4.296e-08

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

	obs.dif	critical.dif	difference
lnl_H0-lnl_H1	13.35	86.8822	FALSE
lnl_H0-lnl_H2	5.61	86.8822	FALSE
lnl_H0-lnl_H3	24.33	86.8822	FALSE
lnl_H0-lnl_H4	79.77	86.8822	FALSE
lnl_H0-lnl_H5	14.61	86.8822	FALSE
lnl_H0-lnl_H6	151.92	86.8822	TRUE
lnl_H1-lnl_H2	7.74	86.8822	FALSE
lnl_H1-lnl_H3	10.98	86.8822	FALSE
lnl_H1-lnl_H4	66.42	86.8822	FALSE
lnl_H1-lnl_H5	1.26	86.8822	FALSE
lnl_H1-lnl_H6	138.57	86.8822	TRUE
lnl_H2-lnl_H3	18.72	86.8822	FALSE
lnl_H2-lnl_H4	74.16	86.8822	FALSE
lnl_H2-lnl_H5	9.00	86.8822	FALSE
lnl_H2-lnl_H6	146.31	86.8822	TRUE
lnl_H3-lnl_H4	55.44	86.8822	FALSE
lnl_H3-lnl_H5	9.72	86.8822	FALSE
lnl_H3-lnl_H6	127.59	86.8822	TRUE
lnl_H4-lnl_H5	65.16	86.8822	FALSE
lnl_H4-lnl_H6	72.15	86.8822	FALSE
lnl_H5-lnl_H6	137.31	86.8822	TRUE



Kruskal-Wallis rank sum test on the ΔBF
chi-squared = 429.29, 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	44.57	71.9573	FALSE
bf_H1-bf_H3	63.40	71.9573	FALSE
bf_H1-bf_H4	250.97	71.9573	TRUE
bf_H1-bf_H5	3.25	71.9573	FALSE
bf_H1-bf_H6	354.43	71.9573	TRUE
bf_H2-bf_H3	107.97	71.9573	TRUE
bf_H2-bf_H4	295.54	71.9573	TRUE
bf_H2-bf_H5	47.82	71.9573	FALSE
bf_H2-bf_H6	399.00	71.9573	TRUE
bf_H3-bf_H4	187.57	71.9573	TRUE
bf_H3-bf_H5	60.15	71.9573	FALSE
bf_H3-bf_H6	291.03	71.9573	TRUE
bf_H4-bf_H5	247.72	71.9573	TRUE
bf_H4-bf_H6	103.46	71.9573	TRUE
bf_H5-bf_H6	351.18	71.9573	TRUE

