[1] 1 2 3 4 5 6 7 8 9 10 11 12

[1] 1 2 3 4 5 6 7 8 9 10 11 12

[1] 1 2 3 4 5 6 7 8 9 10 11 12

11 214605 1933

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid -30.97482 -49.34524 -12.6044 0.0011372

[1] "bio2"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 3 3.454 0.121 0.729

Residuals 111 3169 28.547

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid -0.3918175 -2.624063 1.840429 0.7286365

[1] "bio3"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 81.7 81.65 24.91 2.24e-06 \*\*\*

Residuals 111 363.8 3.28

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 1.905193 1.148814 2.661571 2.2e-06

[1] "bio5"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 403 403.3 10.47 0.0016 \*\*

Residuals 111 4275 38.5

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 4.234068 1.64133 6.826805 0.0015979

[1] "bio6"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 8882 8882 27.34 8.11e-07 \*\*\*

Residuals 111 36065 325

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 19.87097 12.34011 27.40183 8e-07

[1] "bio8"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 273 273.2 0.964 0.328

Residuals 111 31469 283.5

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 3.485051 -3.549554 10.51966 0.3283833

[1] "bio9"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 8454 8454 24.2 3.03e-06 \*\*\*

Residuals 111 38770 349

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 19.38552 11.57736 27.19369 3e-06

[1] "bio12"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 75125 75125 18.62 3.48e-05 \*\*\*

Residuals 111 447907 4035

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 57.78875 31.24925 84.32824 3.48e-05

[1] "bio13"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 2746 2746.4 7.134 0.0087 \*\*

Residuals 111 42729 384.9

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 11.04917 2.85204 19.24631 0.0086994

[1] "bio14"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 489.4 489.4 19.74 2.11e-05 \*\*\*

Residuals 111 2751.2 24.8

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid -4.664044 -6.744032 -2.584056 2.11e-05

[1] "bio19"

Df Sum Sq Mean Sq F value Pr(>F)

species 1 732 732.1 2.134 0.147

Residuals 111 38086 343.1

Tukey multiple comparisons of means

95% family-wise confidence level

Fit: aov(formula = bothPts[, i] ~ species, data = bothPts)

$species

diff lwr upr p adj

tetraploid-diploid 5.704563 -2.034346 13.44347 0.1469315