# all differences – 100%

“diff” is the difference in landmark length between the ones from the partition and all the other. “overlap” is the probability of overlap between the distribution of the landmark lengths in the partitions and all the other. The p values are adjusted using a Bonferroni-Holm correction. Because of the number of bootstrap pseudo-replicates involved in the test (1000), we lowered our threshold for rejecting H0 to p <= 0.01. Signif. codes: 0 `\*\*` 0.001 `\*` 0.01 `.` 0.05 ` ` 1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | test | Cranium 1 - Zygomatic | Cranium 2 - Rest | Cranium 3 – Tip of snout | Mandible 1 - Back | Mandible 2 Snout | Mandible 3 - Rest |
| All species | diff | 0.425 | -0.519 | 0.098 | -0.022 | 0.049 | -0.03 |
|  | p | 0.003\* | 0.003\* | 0.003\* | 0.509 | 1 | 1 |
|  | overlap | 0.95 | 0.95 | 0.78 | 0.83 | 0.99 | 0.98 |
|  | p | 0.003\* | 0.003\* | 0.003\* | 0.024. | 0.045. | 1 |
| *l*  *krefftii* | diff | 0.092 | -0.133 | 0.043 | 0.029 | -0.112 | 0.081 |
|  | p | 0.006\* | 0.003\* | 0.003\* | 0.057 | 0.045. | 0.045. |
|  | overlap | 0.97 | 0.98 | 0.58 | 0.79 | 0.98 | 0.99 |
|  | p | 0.132 | 0.95 | 0.003\* | 0.003\* | 1 | 0.438 |
| *Lasiorhinus latifrons* | diff | 0.004 | -0.145 | 0.14 | 0.104 | -0.22 | 0.114 |
|  | p | 1 | 0.003\* | 0.003\* | 0.003\* | 0.003\* | 0.003\* |
|  | overlap | 0.97 | 0.98 | 0.35 | 0.58 | 0.93 | 0.95 |
|  | p | 0.165 | 1 | 0.003\* | 0.003\* | 0.003\* | 0.015. |
| *Vombatus ursinus* | diff | 0.395 | -0.333 | -0.06 | -0.012 | -0.148 | 0.165 |
|  | P | 0.003\* | 0.003\* | 0.003\* | 0.959 | 0.003\* | 0.003\* |
|  | overlap | 0.9 | 0.92 | 0.72 | 0.88 | 0.98 | 0.97 |
|  | p | 0.003\* | 0.003\* | 0.003\* | 0.174 | 1 | 0.18 |
| *Lasiorhinus* | diff | 0.027 | -0.068 | 0.04 | 0.112 | -0.26 | 0.156 |
|  | p | 1 | 0.309 | 0.003\* | 0.003\* | 0.003\* | 0.003\* |
|  | overlap | 0.97 | 0.98 | 0.87 | 0.59 | 0.94 | 0.97 |
|  | p | 0.003\* | 0.051 | 0.126 | 0.003\* | 0.003\* | 1 |

# 

# all differences rarefied – 100%

“diff” is the difference in landmark length between the ones from the partition and all the other. “overlap” is the probability of overlap between the distribution of the landmark lengths in the partitions and all the other. The p values are adjusted using a Bonferroni-Holm correction. Because of the number of bootstrap pseudo-replicates involved in the test (1000), we lowered our threshold for rejecting H0 to p <= 0.01. Signif. codes: 0 `\*\*` 0.001 `\*` 0.01 `.` 0.05 ` ` 1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | test | Cranium 1 | Cranium 2 | Cranium 3 | Mandible 1 - Back | Mandible 2 Snout | Mandible 3 - Rest |
| All species | diff | 0.071 | -0.052 | 0.105 | -0.023 | 0.008 | -0.005 |
|  | p | 0.003\* | 0.012. | 0.003\* | 0.426 | 1 | 1 |
|  | overlap | 0.85 | 0.86 | 0.69 | 0.87 | 0.91 | 0.92 |
|  | p | 0.153 | 0.297 | 0.003\* | 0.141 | 1 | 1 |
| *Lasiorhinus* *krefftii* | diff | 0.015 | -0.013 | 0.046 | 0.031 | -0.018 | 0.017 |
|  | p | 0.225 | 0.378 | 0.003\* | 0.015. | 0.42 | 0.438 |
|  | overlap | 0.89 | 0.9 | 0.52 | 0.75 | 0.91 | 0.91 |
|  | p | 1 | 1 | 0.003\* | 0.003\* | 1 | 1 |
| *Lasiorhinus* *latifrons* | diff | 0.001 | -0.014 | 0.147 | 0.113 | -0.035 | 0.023 |
|  | p | 1 | 0.333 | 0.003\* | 0.003\* | 0.006\* | 0.069 |
|  | overlap | 0.9 | 0.91 | 0.19 | 0.46 | 0.85 | 0.87 |
|  | p | 1 | 1 | 0.003\* | 0.003\* | 0.018. | 0.333 |
| *Vombatus ursinus* | diff | 0.067 | -0.033 | -0.062 | -0.013 | -0.025 | 0.033 |
|  | p | 0.003\* | 0.006\* | 0.003\* | 0.797 | 0.132 | 0.012. |
|  | overlap | 0.8 | 0.85 | 0.69 | 0.88 | 0.9 | 0.91 |
|  | p | 0.003\* | 0.048. | 0.003\* | 0.117 | 0.839 | 1 |
| *Lasiorhinus* | diff | 0.005 | -0.006 | 0.042 | 0.119 | -0.042 | 0.03 |
|  | p | 1 | 1 | 0.003\* | 0.003\* | 0.006\* | 0.06 |
|  | overlap | 0.9 | 0.9 | 0.87 | 0.52 | 0.88 | 0.88 |
|  | p | 0.812 | 1 | 0.078 | 0.003\* | 0.414 | 0.384 |

# all differences – 95%

“diff” is the difference in landmark length between the ones from the partition and all the other. “overlap” is the probability of overlap between the distribution of the landmark lengths in the partitions and all the other. The p values are adjusted using a Bonferroni-Holm correction. Because of the number of bootstrap pseudo-replicates involved in the test (1000), we lowered our threshold for rejecting H0 to p <= 0.01. Signif. codes: 0 `\*\*` 0.001 `\*` 0.01 `.` 0.05 ` ` 1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | test | Cranium 1 | Cranium 2 | Cranium 3 | Mandible 1 - Back | Mandible 2 Snout | Mandible 3 - Rest |
| All species | diff | 0.113 | -0.192 | 0.08 | 0.041 | -0.047 | 0.003 |
|  | p | 0.009\* | 0.003\* | 0.003\* | 0.006\* | 0.779 | 1 |
|  | overlap | 0.96 | 0.98 | 0.8 | 0.84 | 0.99 | 0.98 |
|  | p | 0.012. | 1 | 0.003\* | 0.009\* | 1 | 1 |
| *L* *krefftii* | diff | -0.096 | 0.002 | 0.096 | -0.01 | -0.079 | 0.093 |
|  | p | 0.003\* | 1 | 0.003\* | 1 | 0.117 | 0.009\* |
|  | overlap | 0.95 | 0.99 | 0.49 | 0.78 | 0.99 | 0.99 |
|  | p | 0.003\* | 0.387 | 0.003\* | 0.003\* | 0.135 | 0.177 |
| *Lasiorhinus* *latifrons* | diff | 0.173 | -0.255 | 0.086 | -0.061 | -0.138 | 0.199 |
|  | p | 0.003\* | 0.003\* | 0.003\* | 0.003\* | 0.003\* | 0.003\* |
|  | overlap | 0.97 | 0.96 | 0.65 | 0.67 | 0.97 | 0.94 |
|  | p | 0.018. | 0.003\* | 0.003\* | 0.003\* | 1 | 0.003\* |
| *Vombatus ursinus* | diff | 0.208 | -0.187 | -0.022 | 0.046 | -0.138 | 0.098 |
|  | p | 0.003\* | 0.003\* | 0.012. | 0.003\* | 0.003\* | 0.006\* |
|  | overlap | 0.91 | 0.98 | 0.74 | 0.69 | 0.97 | 0.97 |
|  | p | 0.003\* | 0.53 | 0.003\* | 0.003\* | 1 | 1 |
| *Lasiorhinus* | diff | 0.204 | -0.228 | 0.021 | 0.07 | -0.09 | 0.021 |
|  | p | 0.003\* | 0.003\* | 0.264 | 0.003\* | 0.03. | 1 |
|  | overlap | 0.97 | 0.96 | 0.81 | 0.61 | 0.98 | 0.98 |
|  | p | 0.018. | 0.003\* | 0.003\* | 0.003\* | 0.8 | 0.423 |

# all differences rarefied – 95%

“diff” is the difference in landmark length between the ones from the partition and all the other. “overlap” is the probability of overlap between the distribution of the landmark lengths in the partitions and all the other. The p values are adjusted using a Bonferroni-Holm correction. Because of the number of bootstrap pseudo-replicates involved in the test (1000), we lowered our threshold for rejecting H0 to p <= 0.01. Signif. codes: 0 `\*\*` 0.001 `\*` 0.01 `.` 0.05 ` ` 1

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | test | Cranium 1 | Cranium 2 | Cranium 3 | Mandible 1 - Back | Mandible 2 Snout | Mandible 3 - Rest |
| All species | diff | 0.019 | -0.02 | 0.085 | 0.046 | -0.008 | 0.001 |
|  | p | 0.414 | 0.312 | 0.003\* | 0.003\* | 1 | 1 |
|  | overlap | 0.89 | 0.88 | 0.78 | 0.82 | 0.91 | 0.91 |
|  | p | 1 | 1 | 0.003\* | 0.006\* | 1 | 1 |
| *Lasiorhinus* *krefftii* | diff | -0.016 | 0 | 0.101 | -0.01 | -0.013 | 0.018 |
|  | p | 0.099 | 1 | 0.003\* | 0.992 | 0.692 | 0.327 |
|  | overlap | 0.9 | 0.91 | 0.38 | 0.79 | 0.89 | 0.9 |
|  | p | 1 | 1 | 0.003\* | 0.003\* | 1 | 1 |
| *Lasiorhinus* *latifrons* | diff | 0.029 | -0.026 | 0.091 | -0.065 | -0.023 | 0.041 |
|  | p | 0.009\* | 0.045. | 0.003\* | 0.003\* | 0.117 | 0.003\* |
|  | overlap | 0.88 | 0.87 | 0.6 | 0.63 | 0.88 | 0.84 |
|  | p | 1 | 0.593 | 0.003\* | 0.003\* | 0.833 | 0.06 |
| *Vombatus* *ursinus* | diff | 0.035 | -0.019 | -0.022 | 0.05 | -0.023 | 0.019 |
|  | p | 0.003\* | 0.03. | 0.006\* | 0.003\* | 0.021. | 0.165 |
|  | overlap | 0.82 | 0.9 | 0.67 | 0.65 | 0.89 | 0.89 |
|  | p | 0.006\* | 1 | 0.003\* | 0.003\* | 1 | 1 |
| *Lasiorhinus* | diff | 0.035 | -0.023 | 0.024 | 0.074 | -0.015 | 0.005 |
|  | p | 0.015. | 0.204 | 0.177 | 0.003\* | 0.39 | 1 |
|  | overlap | 0.89 | 0.9 | 0.78 | 0.55 | 0.89 | 0.91 |
|  | p | 0.74 | 1 | 0.003\* | 0.003\* | 1 | 1 |