

## SUPPLEMENTARY MATERIAL

### **Delineation of conservation units in an endangered marsupial, the southern brown bandicoot (*Isoodon obesulus obesulus*) in South Australia/Western Victoria, Australia**

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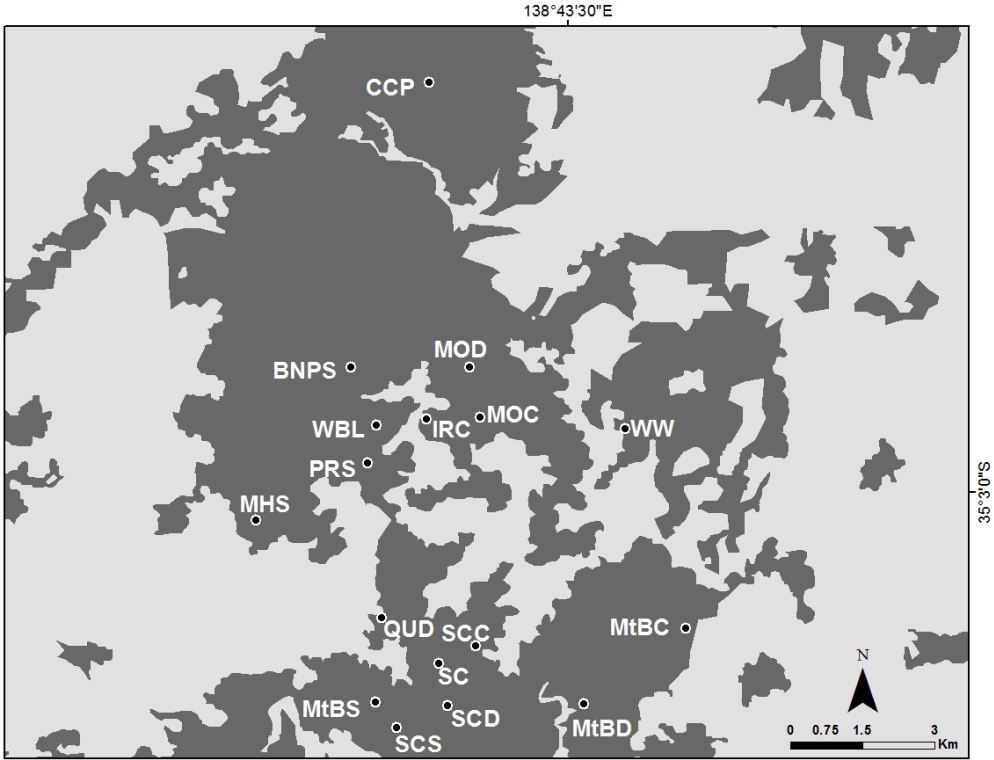
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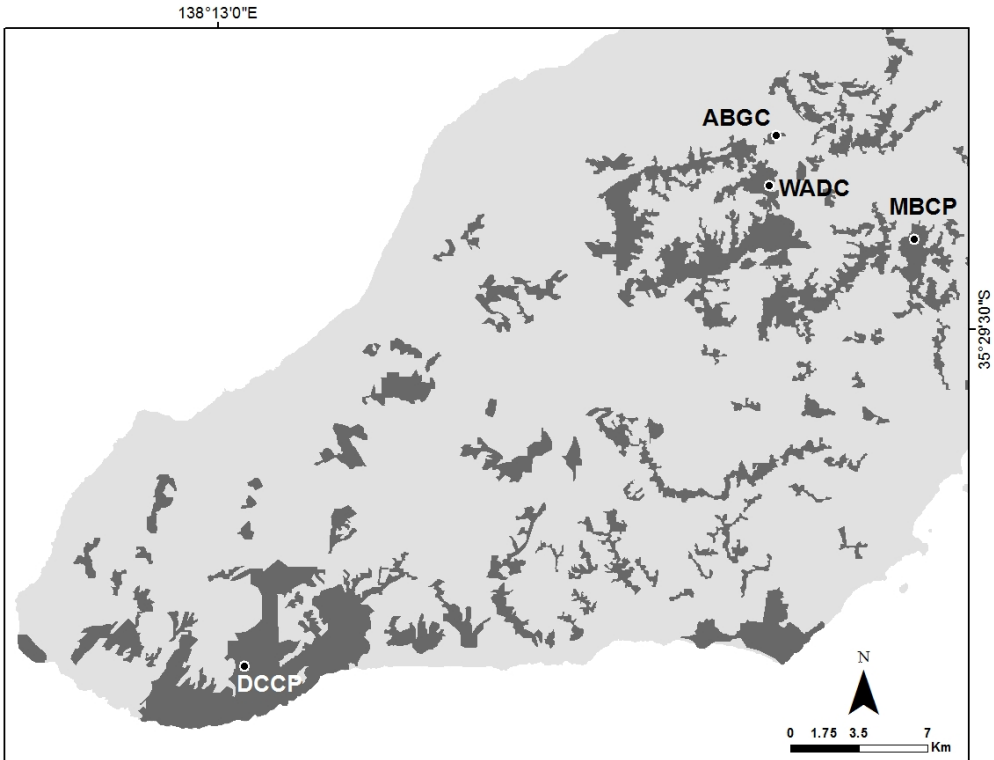
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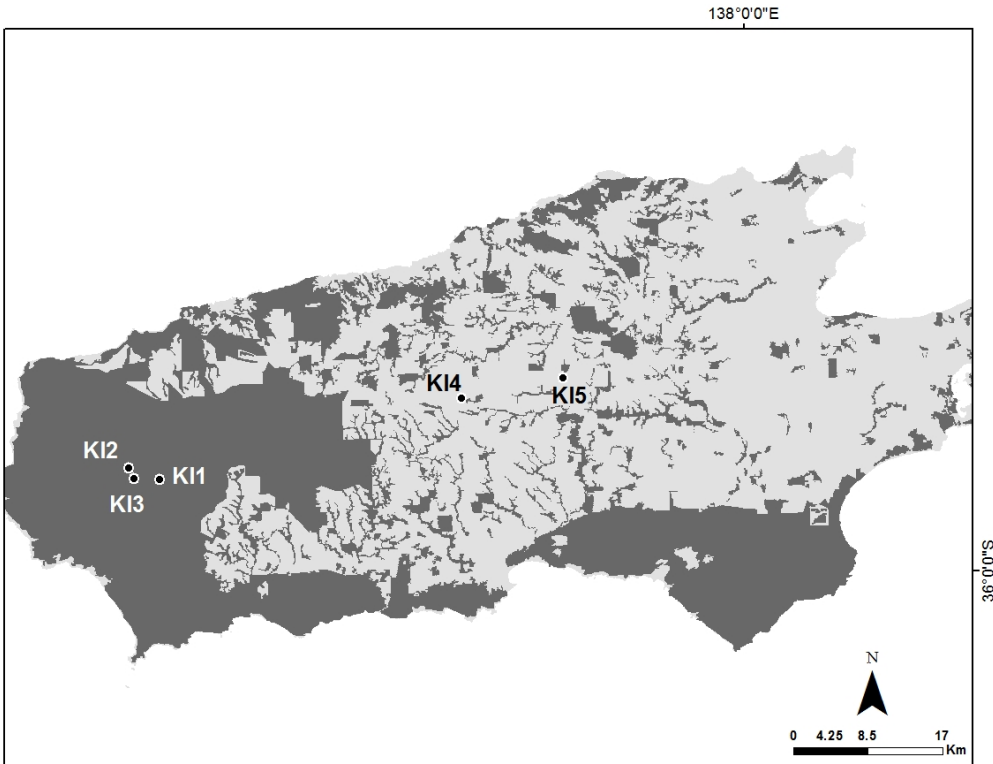
(a) The Mt Lofty Ranges



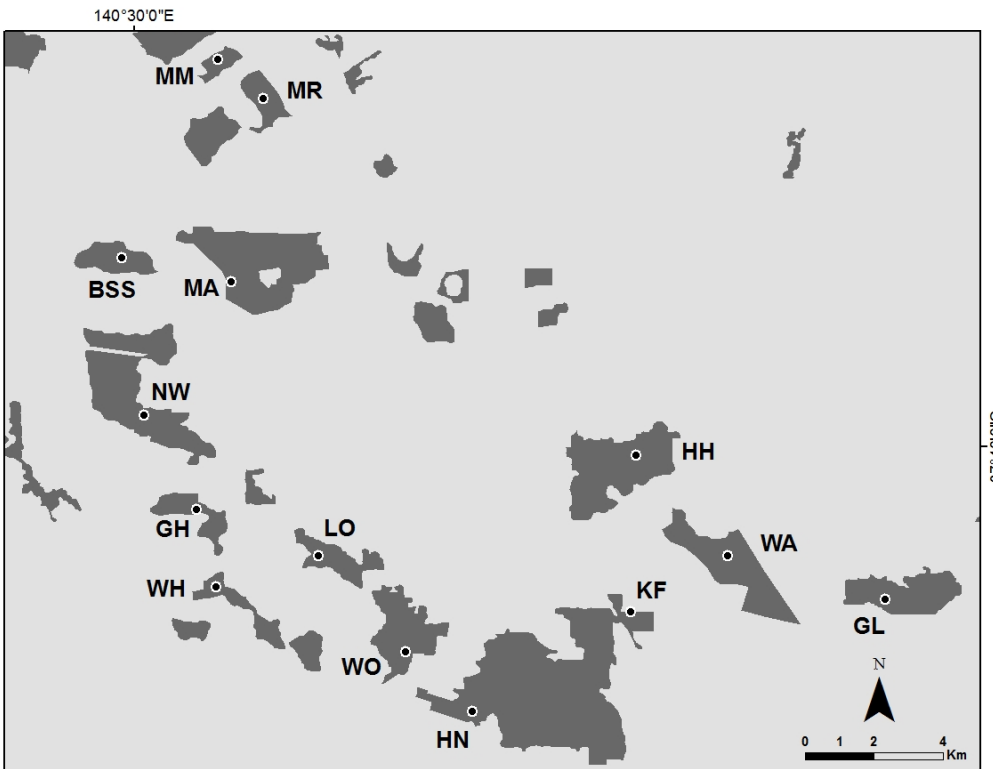
(b) Fleurieu Peninsula



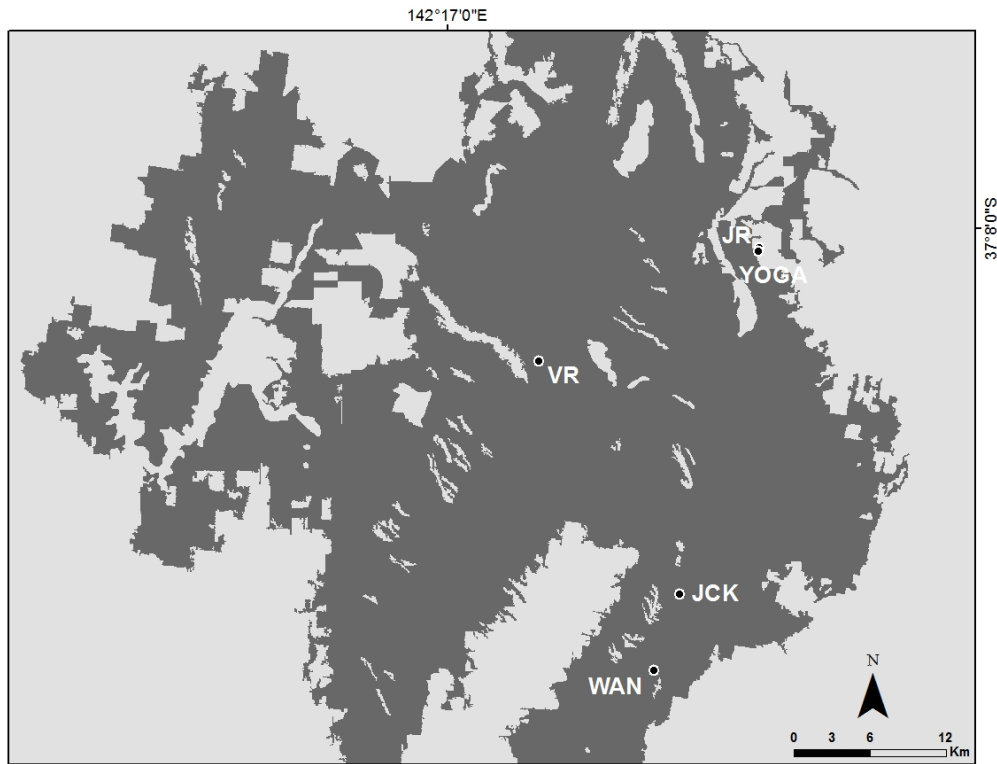
(c) Kangaroo Island



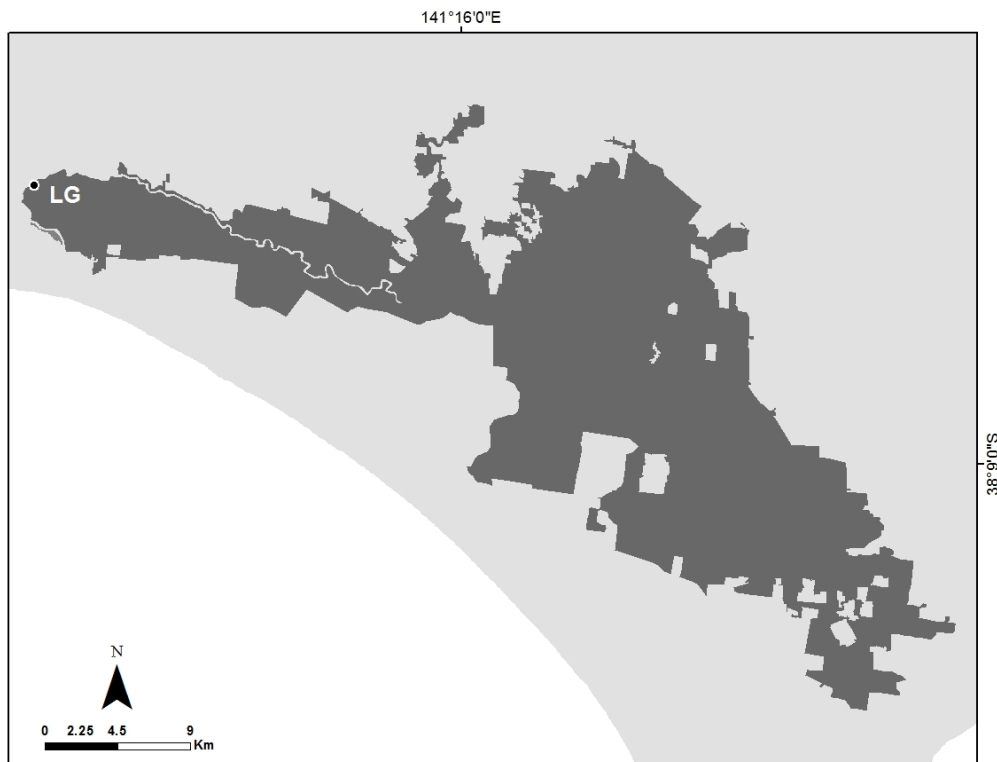
(d) The Mt Burr Range



(e) The Grampians



(f) Lower Glenelg



**Fig. S1** Detailed maps showing sampled locations (marked with black dots) in each region: (a) the Mt Lofty Ranges; (b) Fleurieu Peninsula; (c) Kangaroo Island; (d) the Mt Burr Range; (e) the Grampians; (f) Lower Glenelg.

**Table S1**

| Locus | Repeat motif        | Size range | Primer sequences (5'-3')                                     | Genbank accession number | Source                     |
|-------|---------------------|------------|--|--------------------------|----------------------------|
| Ioo2  | (GAT)16             | 260-280    | F:TTGCTATCAAATAACTATCAGGGG<br>R:ACTGTGTGACATGCTGAAATCC       | JX188445                 | Li <i>et al.</i> (2013)    |
| Ioo3  | (CATATA)16          | 160-300    | F:CAGTTGCAAGTAAATTCATTCATGG<br>R:ATACATTCACACAGCATCCAC       | JX188446                 | Li <i>et al.</i> (2013)    |
| Ioo4  | (GATA)17            | 220-280    | F:GTTTTAGTCCATGGGGTCCTG<br>R:AGCTGGTCTATATCAACTTTGAGG        | JX188447                 | Li <i>et al.</i> (2013)    |
| Ioo5  | (GTATAT)14(GTGTAT)4 | 130-250    | F:TCCTTGACTTAGACAGTGTTCCTC<br>R:TGGGCTAGGATGTTTAAGGG         | JX188448                 | Li <i>et al.</i> (2013)    |
| Ioo6  | (GAT)13GAG(GAT)7    | 210-240    | F:AGAAAAGGATGGTTTGCGGG<br>R:CTTTGCCCTGGGATTCACG              | JX188449                 | Li <i>et al.</i> (2013)    |
| Ioo7  | (AT)8GT(AT)9        | 170-200    | F:TGTGCCTCCTCCTAAAGGC<br>R:TGAGGAGACTGAGGTTCAAAG             | JX188450                 | Li <i>et al.</i> (2013)    |
| Ioo8  | (GGAA)17            | 270-290    | F:AGGAATTTCTCTTGATTCCACTTG<br>R:AAGTAGTAAATTTTGGAGGCAGG      | JX188451                 | Li <i>et al.</i> (2013)    |
| Ioo10 | (GTATA)20           | 240-290    | F:TGTGTGATGCTGCACAAGTC<br>R:CTCAGCCTCAATCTCTAACTGC           | JX188452                 | Li <i>et al.</i> (2013)    |
| Ioo16 | (AAC)26             | 220-270    | F:TGGCCAATGGGTGGATGTG<br>R:ACTTCTACTGCTTTCTGTTCG             | JX188453                 | Li <i>et al.</i> (2013)    |
| B3-2  | (GT)21              | 132 – 148  | F: GGGAGTAATGTGTTTGTGCTTG<br>R: TCCAGTCATTATCCCCTAGAATG      | AF322578                 | Zenger and Johnston (2001) |
| B15-1 | (GT)21              | 110 – 136  | F: GAGGCAAGTGACAGTATGATGC<br>R: TTCTGTCTCTCTATCTCTGTTTCTGTC  | AF322580                 | Zenger and Johnston (2001) |
| B20-5 | (GT)14              | 160 – 166  | F: TTCTGACCATTTCTCACCTTTG<br>R: ACAAATCTCCTAGGCTCTGGTG       | AF322581                 | Zenger and Johnston (2001) |
| B34-2 | (CA)20              | 138 – 150  | F: CAGGAATAATCTTGTATTTTCTCCAG<br>R: TGAACTTTTCAACATCCAATCATC | AF322583                 | Zenger and Johnston (2001) |
| B38-1 | (CA)3GA(CA)13       | 130 – 148  | F: GTGATCTTTTGCACGTTGTCTC<br>R: GGGTCTTCCAGTAAAGATTTGG       | AF322585                 | Zenger and Johnston (2001) |

**Table S2** Pairwise  $F_{ST}$  (below diagonal) and  $D_{EST}$  (above diagonal) values among the six regions (following Sequential Bonferroni correction). Significant values at the 0.001 level are denoted by \*\*\*

|    | MB       | GP       | LG       | ML       | FP       | KI       |
|----|----------|----------|----------|----------|----------|----------|
| MB | -        | 0.396*** | 0.309*** | 0.877*** | 0.896*** | 0.901*** |
| GP | 0.211*** | -        | 0.352*** | 0.895*** | 0.873*** | 0.894*** |
| LG | 0.102*** | 0.173*** | -        | 0.957*** | 0.967*** | 0.971*** |
| ML | 0.375*** | 0.383*** | 0.373*** | -        | 0.341*** | 0.518*** |
| FP | 0.418*** | 0.441*** | 0.437*** | 0.122*** | -        | 0.553*** |
| KI | 0.477*** | 0.557*** | 0.616*** | 0.266*** | 0.304*** | -        |

Abbreviation: MB, Mount Burr Range; LG, Lower Glenelg; GP, Grampians; ML, Mount Lofty Ranges; KI, Kangaroo Island; FP, Fleurieu Peninsula.

**Table S3** Pairwise  $F_{ST}$  (below diagonal) and  $D_{EST}$  (above diagonal) values among the seven sub-clusters detected in STRUCTURE (following Sequential Bonferroni correction). Significant values at the 0.001 level are denoted by \*\*\*

|      | MB1      | MB2      | GPLG     | ML1      | ML2      | ML3      | KIFP     |
|------|----------|----------|----------|----------|----------|----------|----------|
| MB1  | -        | 0.233*** | 0.362*** | 0.903*** | 0.866*** | 0.909*** | 0.886*** |
| MB2  | 0.189*** | -        | 0.391*** | 0.882*** | 0.872*** | 0.897*** | 0.901*** |
| GPLG | 0.179*** | 0.249*** | -        | 0.915*** | 0.909*** | 0.910*** | 0.877*** |
| ML1  | 0.421*** | 0.354*** | 0.390*** | -        | 0.387*** | 0.199*** | 0.310*** |
| ML2  | 0.533*** | 0.534*** | 0.575*** | 0.268*** | -        | 0.346*** | 0.443*** |
| ML3  | 0.439*** | 0.384*** | 0.410*** | 0.095*** | 0.273*** | -        | 0.408*** |
| KIFP | 0.437*** | 0.375*** | 0.412*** | 0.123*** | 0.312*** | 0.175*** | -        |

Abbreviation: MB1, Mount Burr Range-sub-cluster1; MB2, Mount Burr Range-sub-cluster2; GPLG, Grampians / Lower Glenelg; ML1, Mount Lofty Ranges-sub-cluster1; ML2, Mount Lofty Ranges-sub-cluster2; ML3, Mount Lofty Ranges-sub-cluster3; KIFP, Kangaroo Island/ Fleurieu Peninsula.

**Table S4** Hierarchical AMOVA performed by grouping populations according to the regions and sub-clusters detected in STRUCTURE/sPCA

| Comparison        | Source of variation | Variance components | Percentage of variation | <i>P</i> value |
|-------------------|---------------------|---------------------|-------------------------|----------------|
| MB1-MB2-GP-LG     | Among population    | 0.622               | 20.00%                  | < 0.01         |
|                   | Within population   | 2.487               | 80.00%                  | < 0.01         |
| MB1-MB2-GPLG      | Among population    | 0.536               | 17.39%                  | < 0.01         |
|                   | Within population   | 2.543               | 82.61%                  | < 0.01         |
| MB-GP-LG          | Among population    | 0.550               | 17.30%                  | < 0.01         |
|                   | Within population   | 2.629               | 82.70%                  | < 0.01         |
| MBLG-GP           | Among population    | 0.502               | 15.68%                  | < 0.01         |
|                   | Within population   | 2.697               | 84.32%                  | < 0.01         |
| MB-GPLG           | Among population    | 0.412               | 13.31%                  | < 0.01         |
|                   | Within population   | 2.685               | 86.69%                  | < 0.01         |
| ML1-ML2-ML3-KI-FP | Among population    | 0.658               | 19.62%                  | < 0.01         |
|                   | Within population   | 2.694               | 80.38%                  | < 0.01         |
| ML-KI-FP          | Among population    | 0.624               | 17.31%                  | < 0.01         |
|                   | Within population   | 2.983               | 82.69%                  | < 0.01         |
| ML1-ML2-ML3-KIFP  | Among population    | 0.571               | 17.14%                  | < 0.01         |
|                   | Within population   | 2.762               | 82.86%                  | < 0.01         |
| ML-KIFP           | Among population    | 0.406               | 11.76%                  | < 0.01         |
|                   | Within population   | 3.050               | 88.24%                  | < 0.01         |

Abbreviation: MB, Mount Burr Range; MB1, Mount Burr Range-sub-cluster1; MB2, Mount Burr Range-sub-cluster2; LG, Lower Glenelg; GP, Grampians; GPLG, Grampians / Lower Glenelg; MBLG, Mount Burr Range / Lower Glenelg; ML, Mount Lofty Ranges; ML1, Mount Lofty Ranges-sub-cluster1; ML2, Mount Lofty Ranges-sub-cluster2; ML3, Mount Lofty Ranges-sub-cluster3; KI, Kangaroo Island; FP, Fleurieu Peninsula; KIFP, Kangaroo Island/ Fleurieu Peninsula.

**Table S5** Pairwise distance among haplotypes for concatenated mtDNA. The distance values were showed in lower left and the standard errors were showed in upper right

| mtDNA | H1    | H2    | H3    | H4    | H5    | H6    | H7    | H8    | H9    | H10   | H11   | H12   | H13   | H14   |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| H1    |       | 0.004 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.002 | 0.002 | 0.000 |
| H2    | 0.019 |       | 0.005 | 0.005 | 0.004 | 0.005 | 0.004 | 0.005 | 0.005 | 0.005 | 0.005 | 0.004 | 0.004 | 0.004 |
| H3    | 0.032 | 0.028 |       | 0.004 | 0.001 | 0.003 | 0.003 | 0.003 | 0.004 | 0.004 | 0.004 | 0.005 | 0.005 | 0.005 |
| H4    | 0.037 | 0.035 | 0.017 |       | 0.003 | 0.001 | 0.002 | 0.001 | 0.001 | 0.004 | 0.004 | 0.005 | 0.005 | 0.005 |
| H5    | 0.031 | 0.027 | 0.002 | 0.016 |       | 0.003 | 0.003 | 0.003 | 0.003 | 0.003 | 0.003 | 0.005 | 0.005 | 0.005 |
| H6    | 0.036 | 0.032 | 0.015 | 0.002 | 0.014 |       | 0.002 | 0.001 | 0.001 | 0.003 | 0.003 | 0.005 | 0.005 | 0.005 |
| H7    | 0.033 | 0.030 | 0.014 | 0.006 | 0.013 | 0.004 |       | 0.002 | 0.002 | 0.003 | 0.003 | 0.005 | 0.005 | 0.005 |
| H8    | 0.036 | 0.033 | 0.015 | 0.002 | 0.015 | 0.001 | 0.005 |       | 0.001 | 0.003 | 0.003 | 0.005 | 0.005 | 0.005 |
| H9    | 0.036 | 0.032 | 0.015 | 0.002 | 0.014 | 0.002 | 0.006 | 0.001 |       | 0.003 | 0.003 | 0.005 | 0.005 | 0.005 |
| H10   | 0.035 | 0.033 | 0.015 | 0.019 | 0.015 | 0.017 | 0.015 | 0.018 | 0.017 |       | 0.000 | 0.005 | 0.005 | 0.005 |
| H11   | 0.035 | 0.033 | 0.015 | 0.019 | 0.015 | 0.017 | 0.015 | 0.018 | 0.017 | 0.000 |       | 0.005 | 0.005 | 0.005 |
| H12   | 0.005 | 0.023 | 0.032 | 0.040 | 0.032 | 0.038 | 0.036 | 0.039 | 0.038 | 0.036 | 0.036 |       | 0.000 | 0.002 |
| H13   | 0.005 | 0.023 | 0.032 | 0.040 | 0.032 | 0.038 | 0.036 | 0.039 | 0.038 | 0.036 | 0.036 | 0.000 |       | 0.002 |
| H14   | 0.000 | 0.019 | 0.032 | 0.037 | 0.031 | 0.036 | 0.033 | 0.036 | 0.036 | 0.035 | 0.035 | 0.005 | 0.005 |       |