README file for data file, “Raw\_male\_typing\_matrix”, containing data for Figure 2 and Table S6 in Brock *et al.* “No severe genetic bottleneck in a rapidly range expanding bumblebee pollinator”.

Column headings are as follows:

**Type:** The colony type from which males were sampled. FC = mature *Bombus hypnorum* colony collected from the field; EM = *B. hypnorum* colony reared from a field-collected queen that exhibited first-brood male production (where only males eclosed, or where males eclosed within one week of first worker eclosion), LM = *B. hypnorum* colony reared from a field-collected queen that exhibited late male production (where males eclosed a week or more after first worker eclosion).

**Round:** The round of genotyping for sampled males. 1 = first round of DNA extraction and genotyping; 2 = second round of DNA extraction and genotyping; 3 = third round of DNA extraction and genotyping.

**Colony:** Unique numeric ID of each individual colony males were sampled from.

**ID:** Unique numeric ID for each genotyped male. In colonies reared from field-collected queens (Types EM & LM), the male ID is in chronological order of eclosion, i.e. M1 is the first male to eclose within the colony, M2 is the second male to eclose and so on.

**B131\_1:** The allele length in base pairs at the first position at the B131 marker. 0s indicate a missing genotype.

**B131\_2:** The allele length in base pairs at the second position at the B131 marker. 0s indicate a missing genotype.

**BL03\_1:** The allele length in base pairs at the first position at the BL03 marker. 0s indicate a missing genotype.

**BL03\_2:** The allele length in base pairs at the second position at the BL03 marker. 0s indicate a missing genotype.

**BT26\_1:** The allele length in base pairs at the first position at the BT26 marker. 0s indicate a missing genotype.

**BT26\_2:** The allele length in base pairs at the second position at the BT26 marker. 0s indicate a missing genotype.

**BTMS0132\_1:** The allele length in base pairs at the first position at the BTMS0132 marker. 0s indicate a missing genotype.

**BTMS0132\_2:** The allele length in base pairs at the second position at the BTMS0132 marker. 0s indicate a missing genotype.

**BTMS0125\_1:** The allele length in base pairs at the first position at the BTMS0125 marker. 0s indicate a missing genotype.

**BTMS0125\_2:** The allele length in base pairs at the second position at the BTMS0125 marker. 0s indicate a missing genotype.

**B11\_1:** The allele length in base pairs at the first position at the B11 marker. 0s indicate a missing genotype.

**B11\_2:** The allele length in base pairs at the second position at the B11 marker. 0s indicate a missing genotype.

**B10\_1:** The allele length in base pairs at the first position at the B10 marker. 0s indicate a missing genotype.

**B10\_2:** The allele length in base pairs at the second position at the B10 marker. 0s indicate a missing genotype.

**BTMS0057\_1:** The allele length in base pairs at the first position at the BTMS0057 marker. 0s indicate a missing genotype.

**BTMS0057\_2:** The allele length in base pairs at the second position at the BTMS0057 marker. 0s indicate a missing genotype.

**BT05\_1:** The allele length in base pairs at the first position at the BT05 marker. 0s indicate a missing genotype.

**BT05\_2:** The allele length in base pairs at the second position at the BT05 marker. 0s indicate a missing genotype.

**BTMS0056\_1:** The allele length in base pairs at the first position at the BTMS0056 marker. 0s indicate a missing genotype.

**BTMS0056\_2:** The allele length in base pairs at the second position at the BTMS0056 marker. 0s indicate a missing genotype.

**B121\_1:** The allele length in base pairs at the first position at the B121 marker. 0s indicate a missing genotype.

**B121\_2:** The allele length in base pairs at the second position at the B121 marker. 0s indicate a missing genotype.

**BTERN02\_1:** The allele length in base pairs at the first position at the BTERN02 marker. 0s indicate a missing genotype.

**BTERN02\_2:** The allele length in base pairs at the second position at the BTERN02 marker. 0s indicate a missing genotype.

**BTMS0083\_1:** The allele length in base pairs at the first position at the BTMS0083 marker. 0s indicate a missing genotype.

**BTMS0083\_2:** The allele length in base pairs at the second position at the BTMS0083 marker. 0s indicate a missing genotype.

**BL08\_1:** The allele length in base pairs at the first position at the BL08 marker. 0s indicate a missing genotype.

**BL08\_1:** The allele length in base pairs at the second position at the BL08 marker. 0s indicate a missing genotype.

**Het\_loci:** The total number of heterozygous loci (where the allele length at position 1 does not match the allele length at position 2 for a given marker) for each genotyped male.