

664 **Supplementary files**

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666 **Table S1** Microsatellite primers developed for *Bombus terrestris* by Stolle et al. (2011; see
667 Table S1 of Stolle et al. 2011) and employed in this study to genotype the *lucorum* complex
668 of three putative species: *B. cryptarum*, *B. lucorum s. str.* and *B. magnus*

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670 **Table S2.** Details of the eight individuals of the *lucorum* complex whose RFLP-based mt
671 haplotype did not concur with nuclear (microsatellite) genotypes, as defined by
672 STRUCTURE Q value (Supplementary Table S5) or visually by PCoA (Figure 4). Code: the
673 unique identifier to the specimen; Location: site of collection; RFLP ID: haplotype
674 designation by RFLP (from Murray et al. 2008); PCoA ID: microsatellite genetic cluster
675 membership (see Figure 4); STRUCTURE Q ID: microsatellite genetic cluster membership
676 by STRUCTURE Q value (see Supplementary Table S5); COI-BLAST: COI barcode DNA
677 sequence identity by BLASTn search;

678

679 **Table S3** Linkage disequilibrium for seven microsatellite loci in the three putative species of
680 the *lucorum* complex of bumble bees collected at 11 sites in Ireland; columns represent
681 respectively the pairwise combination of loci, probability of linkage disequilibrium (P) and
682 standard error of that P value (SE), calculated in GENPOP

683

684 **Table S4** Deviation from Hardy-Weinberg equilibrium (HWE) for seven microsatellite loci
685 in the three putative species of the *lucorum* complex of bumble bees collected from 11 sites
686 in Ireland, including the inbreeding coefficient, F_{IS} , and probability of deviation from HWE,
687 as calculated in GENPOP

688

689 **Table S5** Mitochondrial lineage and multilocus probability of group membership
690 (STRUCTURE Q value; admixture model) at seven microsatellite loci in the three putative
691 species of the *lucorum* complex of bumble bees collected at 11 sites in Ireland (see Table 1
692 for site names and location); the one individual with aberrant correspondence between
693 mtDNA lineage (mt sp.) and nuclear genotype (nuc mag, nuc cryp, nuc luc for *B. magnus*, *B.*
694 *cryptarum* and *B. lucorum s. str.* respectively) is highlighted in blue; the 23 individuals with
695 non-aberrant but low probability (STRUCTURE Q value, 0.5-0.9) of membership to their
696 mtDNA lineage are highlighted in yellow

697

698 **Fig. S1** Barplot of STRUCTURE (using the non-admixture model) output showing percentage
699 assignment of individuals of the three *lucorum* complex species of bumble bees genotyped at
700 seven microsatellite loci to a given putative species for $K = 2$ and $K = 3$ (species designation
701 based on mtDNA COI haplotypes)

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