Supplementary table 1: Characterisation of microsatellite loci in *Sturnus vulgaris* (*N*=94) including locus name, GenBank accession number, primer sequences, repeat motif, number of alleles and allele size range.

| **Locus****GenBank** | **Primer Sequence (5’ to 3’)\*** | **Repeat Motif** | **Number** **of Alleles** | **Size Range\*** | **Dye** | **Multi-plex** |
| --- | --- | --- | --- | --- | --- | --- |
| *Svu002^*KF535925 | F: TACCAACCAGCCACAGATTGR: TACCAGCTGCATTTCCTCCT | GT | 12 | 100-129 | NED | 1 |
| *Svu004* KF535926 | F: ATTCCACTACCAGCCACCAGR: AGTGCAGGTGTTGGAAAGGT | CATC | 11 | 220-255 | VIC | 1 |
| *Svu005* KF535927 | F: TTTCGCAAGCACAATTTCTTTR: ACTGGCTCTCCTGAGTCCAA | CCAT | 15 | 150-224 | 6-FAM | 1 |
| *Svu006* KF535928 | F: CCTTTCCAATTCTCTTCCCCR: AGTCAGCCACCAGGTACCAC | GTGA | 14 | 77-144 | VIC | 1 |
| *Svu007* KF535929 | F: CCAAGGGATAGCAATAGGCAR: CTGGCCCAGTTAGCATAGAGA | TAGG | 12 | 153-184 | PET | 1 |
| *Svu010^* KF535930 | F: CAGTTCCTGGGTTGGTTTTGR: ATTTCATGCTTTGTTGTGCG | AC | 9 | 98-130 | NED | 2 |
| *Svu012* KF535931 | F: CCTCATCCTCCTAGCACAGCR: AGGGAGAAGCTGGTGTCAGA | CA | 9 | 128-171 | PET | 2 |
| *Svu013* KF535932 | F: TGTACTGGCTAACGGAGCACR: GCTGTGATTGTGAGTCGTGG | GT | 13 | 86-115 | 6-FAM | 2 |
| *Svu015*KF535933 | F: CAGCACAACAGAGCAGGAGAR: AATTTGCTCCCCACAGAAGA | AAAC | 5 | 123-139 | 6-FAM | 3 |
| *Svu016* KF535934 | F: GCTTCTATTATCTTCTGCCATCCTR: GATGAGGCATGGATGGAGTG | TCCA | 9 | 139-169 | PET | 3 |
| *Svu017* KF535935 | F: TTGAACAAGCTGGTCTTGGAR: ATATCCACGGAACAGAGCCA | GATA | 12 | 244-295 | 6-FAM | 3 |
| *Svu018* KF535936 | F: TGAAAGGCTTTTGTAGCAGTCAR: ACTGGATAAGCTTCCTGGGG | TAGA | 11 | 168-215 | 6-FAM | 2 |
| *Svu021*KF535937 | F: AAGGCTGACGTGGCAATTATR: CACGTGAGGTGTGCTTGTCT | AC | 5 | 89-100 | NED | 3 |
| *Svu022* KF535938 | F: GCGCCTGTGTTTTGCATTATR: TCAGGTACTGCTTGGTGCAT | CA | 12 | 92-121 | VIC | 3 |
| *Svu025* KF535939 | F: AGCTCACTGGAGCAGCCTACR: TCACAGCATTCAGGGAATCA | GT | 8 | 104-123 | PET | 3 |
| *Svu030*KF535940 | F: ACACACAAGAGGGAACCTGGR: TTTGGTGGATGGATAGAGGG | TA | 6 | 186-214 | VIC | 2 |
| *Svu033* KF535941 | F: TGACATGATCACAGTGGAAGGR: TGAGTCACTGCATAGGCATACA | ATCA | 8 | 74-109 | 6-FAM | 1 |
| *Svu034* KF535942 | F: ACTCTGGCATAGGAGGGGACR: GCTCAGCATGGCTGTATTGA | CA | 13 | 163-200 | VIC | 3 |
| *Svu038* KF535943 | F: CCTGTAGGACCATGGAGCATR: TAGACCGGAACCTTGTCTGG | ATGG | 7 | 242-266 | NED | 1 |
| *Svu039* KF535944 | F: CCACTGCTTCTCTGGGGTAAR: GCATAGCTACACCGTGGGAT | ATCA | 4 | 93-112 | PET | 1 |

\* Universal primer sequence removed. ^These loci were not in Hardy-Weinberg equilibrium and were removed from downstream analyse

# Simulated Disperser Analysis: determining the number of loci required to genetically identify dispersers

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