

| Region | Sampling location | N | Number of haplotypes | Haplotype diversity (Hd) ± SD | Nucleotide diversity (π) ± SD |
|-----------------------------|-------------------|----|----------------------|-------------------------------|-------------------------------|
| A | | | | | |
| Overall within BS lineage | | 96 | 20 | 0.598 ± 0.058 | 0.004 ± 0.0025 |
| | Himmerfjarden | 22 | 12 | 0.905 ± 0.044 | 0.003 ± 0.0004 |
| | Baltic Sea | 9 | 5 | 0.833 ± 0.098 | 0.006 ± 0.0020 |
| | Riga | 12 | 5 | 0.803 ± 0.09 | 0.003 ± 0.0007 |
| | Luga | 19 | 8 | 0.614 ± 0.130 | 0.015 ± 0.0120 |
| | Vistula | 4 | 4 | 1 ± 0.177 | 0.003 ± 0.0007 |
| | Vyborg | 30 | 8 | 0.467 ± 0.112 | 0.001 ± 0.0003 |
| Overall within NSEC lineage | | 79 | 15 | 0.441 ± 0.071 | 0.002 ± 0.0006 |
| | N. Dvina | 3 | 2 | 0.667 ± 0.314 | 0.001 ± 0.0006 |
| | Elbe | 29 | 8 | 0.431 ± 0.116 | 0.001 ± 0.0004 |
| | Scheldt | 22 | 5 | 0.338 ± 0.128 | 0.001 ± 0.0003 |
| | Seine | 20 | 4 | 0.284 ± 0.128 | 0.003 ± 0.0020 |
| | Tamar | 5 | 2 | 0.400 ± 0.237 | 0.002 ± 0.0010 |
| Overall within EAt lineage | | 40 | 16 | 0.814 ± 0.053 | 0.003 ± 0.0004 |
| | Gironde | 20 | 6 | 0.711 ± 0.089 | 0.002 ± 0.0004 |
| | Loire | 20 | 10 | 0.842 ± 0.061 | 0.003 ± 0.0006 |
| B | | | | | |
| Overall within EU lineage | | 27 | 7 | 0.758 ± 0.065 | 0.003 ± 0.0004 |
| | Scheldt | 20 | 4 | 0.605 ± 0.101 | 0.002 ± 0.0004 |
| | Oder | 2 | 2 | 1 ± 0.500 | 0.004 ± 0.0019 |
| | Feofania | 3 | 2 | 0.667 ± 0.314 | 0.001 ± 0.0006 |
| | Cheboksary | 2 | 1 | | |
| Overall within TU lineage | | 3 | 2 | 0.667 ± 0.314 | 0.003 ± 0.0012 |