Supplementary information

Roved J., Hansson B., Stervander, M., Hasselquist D., & Westerdahl H. (2022). MHCtools – an R package for MHC high-throughput sequencing data: genotyping, haplotype and supertype inference, and downstream genetic analyses in non-model organisms.

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Supplementary methods

PCR amplification and library preparation for Illumina MiSeq
We prepared both amplicon libraries for Illumina sequencing in a two-step amplification. First, individual samples were amplified using the HNalla and HN46, modified with 5′-overhangs designed to match the Illumina sequencing adapters and molecular identifiers (MIDs) of the Nextera® XT v2 Index Kit (Illumina Inc., San Diego, CA, USA). The reactions comprised 25 μl and used 25 ng template DNA, 0.5 μM of each primer, and 12.5 μl 2X Phusion High-Fidelity PCR Master Mix (ThermoFisher Scientific, Waltham, USA). The PCR was initiated with a 30 s denaturation step at 98°C followed by 25 cycles of 10 s denaturation at 98°C, 10 s annealing at 66.8°C, and 15 s elongation at 72°C. A 10 min final extension 72°C completed the program.

The PCR product was cleaned with Agencourt AMPure XP-PCR Purification Kit (Beckman Coulter, Indianapolis, USA), following the manufacturer’s instruction with some modifications: The ratio of PCR product to beads was 1:0.8, 80% ethanol was used in the bead cleaning steps, and the elution was made with 43 μl double-distilled water, which incubated at room temperature for two minutes. An aliquot of the clean PCR product was run on a 2% agarose gel, to verify fragment length and to roughly estimate concentration of the PCR product based on band intensity. The individual PCR products were then differentially evaporated at room temperature, to achieve even concentrations.

To be able to assign sequences to individual samples after multiplexing, we added unique combinations of forward and reverse Illumina indices to each sample using the Nextera XT v2 Index Kit (Illumina Inc., San Diego, CA, USA). A second PCR was run in 50 μl reactions that contained 25 μl 2X Phusion High-Fidelity PCR Master Mix (ThermoFisher Scientific, Waltham, USA), 5 μl of each index primer, and a varying amount of cleaned PCR product depending on estimated concentration (5, 10, or 15 μl for the first library; 5, 7.5, or 10 μl for the second library). The PCRs were initiated with a 30 s heating phase at 98°C, followed by eight cycles of 10 s denaturation at 98°C, 15 s annealing at 62°C, and 15 s elongation at 72°C, and ended with 10 min final extension at 72°C.

The indexed amplicons were cleaned with Agencourt AMPure XP-PCR Purification Kit (Beckman Coulter, Indianapolis, USA), following the manufacturer’s instruction with some modifications: The ratio of PCR product to beads was 1:1.12, 80% ethanol was used in the bead cleaning steps, and the elution was made with 43 μl double-distilled water and incubated at room temperature for two minutes. The cleaned PCR products were checked on a 2% agarose gel, and quantified using a Quant-iT PicoGreen dsDNA Assay Kit (ThermoFisher Scientific/Invitrogen, Waltham, USA) modified for a 96-well plate, measured on a plate reader.

For each library, we pooled an equimolar quantity of each of 384 samples (including samples unrelated to this study) into pools (nine for the first library and four for the second library), depending on amplicon length, concentration, and primer combination. These pools were then quantified with Qubit Broad Range and High Sensitivity kits (ThermoFisher Scientific, Waltham, USA), after which we ran them on a Bioanalyzer DNA 2100 chip for validation of quality and size. In a final step, equimolar quantities of all pools were combined in a 20 nM library.

Technical replicates & filtering
The data set that was sequenced using the Roche 454 platform included 50 sets of technical replicates, see Roved et al. 2018 for details.

The first Illumina MiSeq data set did not incorporate formal technical replicates, but as the data set included samples from 69 complete great reed warbler families, we were able to identify 52 samples that had identical genotypes to one or more other samples (predominantly full...
siblings). We grouped these samples into 25 replicate sets. The inference of these genotype replicates was done after preliminary filtering of the data set using DADA2 and it allowed us to optimize the final settings for filtering this data set (see main text). The filtering settings were applied uniformly on the entire data set and were thus independent of variation in e.g. coverage or error rates between individual samples. We were therefore able to perform all optimizations and repeatability evaluations using sets of genotype replicates, and we proceeded to treat these equivalently to formal technical replicates.

The second Illumina MiSeq data set included 30 samples in total, of which 3 were technical replicates. Two of the replicated samples failed due to low read numbers, leaving one replicated sample. Given that these were samples of the same species, population, and time period (i.e., age of the DNA material), and were genotyped with identical primers and protocols, we proceeded to filter this data set with the settings that we identified when optimizing for the first Illumina MiSeq data set. Filtering the second Illumina MiSeq with these settings resulted in a complete match between the two copies of the replicated sample. Because the two failed samples were both replicated, all 30 individuals included in this sequencing run were successfully genotyped.

Purifying putative MHC-I haplotypes

1. We used the HpltFind function in MHCtools to construct putative haplotypes for each individual in 67 concurrent families of the 1998 and 1999 cohorts in our study population, one family from 1991, and one family from 1996.
2. We constructed putative haplotypes for each individual in ancestral families of 26 parents, that we were able to trace in the pedigree of our study population (Table S1). This step was also carried out using HpltFind.
3. We then traced the inheritance of putative haplotypes through generations as far as data was available within each family line. When a haplotype mismatched between generations by alleles that had been marked as unresolved by HpltFind, we manually reconstructed the allele segregation within each family to resolve the allele assignments and corrected the putative haplotypes accordingly.
4. We then applied each corrected haplotype in all families where it occurred and resolved lateral mismatches of unresolved alleles between concurrent families by manually reconstructing the allele segregation within each family.
5. If incongruences were found between individuals that shared a putative haplotype, and these incongruences could not be resolved by manual inspection of the segregation patterns within families (steps 3–4), we investigated whether the incongruences were caused by genotyping errors. We considered the following types of genotyping errors:
   a. Null alleles (i.e., alleles that failed to amplify during PCR or had low PCR amplification success, and therefore had been deleted from samples in the filtering process).
   b. Sequencing errors that survived the filtering process. We only assigned an incongruent allele to this category, if it had low read numbers (relative, within each sample) and could be derived from more abundant alleles in the same sample by single nucleotide substitutions.

Each such incongruence was investigated by manually inspecting the raw sequencing output files for presence or absence (and read numbers, if present) of the mismatching allele prior to filtering. In cases of multiple solutions to an incongruence, the solution involving the fewest assumptions was applied. By comparing haplotypes both vertically through family
lines and laterally between concurrent families (steps 3–5), we were able to resolve a large proportion of the unresolved allele assignments (Table S2).

6. Finally, we identified sets of haplotypes that overlapped by a proportion of at least 0.66 of the assigned alleles. Whenever a set of haplotypes only mismatched by alleles that had been assigned as unresolved, we manually inspected the segregation patterns of the unresolved alleles to determine whether we could assume identity between the potentially matching haplotypes. This enabled us to resolve some additional unresolved allele assignments (Table S2).

We repeated steps 3–6, further improving the accuracy of our haplotype inference by reapplying corrected haplotypes both within and between families and family lines. This process was repeated until all incongruences had been addressed and no more unresolved allele assignments could be settled with the available data.

Our stepwise protocol for haplotype inference and purification is outlined in the flow chart in Fig. 1. The number of corrections applied in the purification of putative haplotypes in our data set is summarized in Table S2.

**Phylogenetic analyses**

For phylogenetic inference and selection analyses, we first aligned the MHC-I exon 3 alleles in open reading frame according to conserved residues and sequence motifs (Bjorkman et al., 1987; Hughes & Nei, 1989) and trimmed them to a length of 261 nucleotides. We then tested 12 different substitution models in PhyML version 3.1 (Guindon et al., 2010; Guindon & Gascuel, 2003) using maximum likelihood estimation of the nucleotide frequencies and tree topology optimization (Table S3). The generalized time-reversible (GTR) model with no additional parameters had the lowest Akaike Information Criterion (AIC) value and a tree with Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) support values was created using this model. The phylogenetic tree was visualized using the R package ggtree version 3.0.2 (Yu, Smith, Zhu, Guan, & Lam, 2017). We indicated MHC-I supertype associations (see below) in the phylogenetic tree with coloured circles at the tip of each branch. Note that when plotting the tree, we flipped a central node in group N.C. to make it easier to distinguish the different groups. This did not alter the topology of the tree.

In the phylogenetic tree, we identified five tentative groups based on the tree topology and SH-aLRT support values, which may typically be interpreted to confer clade support from a level of ~0.8 (Anisimova, Gil, Dufayard, Dessimoz, & Gascuel, 2011; Guindon et al., 2010; Minh, Nguyen, & Von Haeseler, 2013). The five groups were distinguished by the following properties of the phylogeny of our MHC-I alleles: (i) Group A forms a monophyletic clade which separates from the rest of the tree with a support value of 1. (ii) A large monophyletic clade with a support value of 0.96 is formed by the groups B, C, D, and E. Within this large clade, group E and groups B–D form two monophyletic clades, both with support value 0.79. (iii) Groups C and D are monophyletic sister clades with individual supports of 0.72 and 0.82, respectively, and are grouped together with a support of 0.82. (iv) Note that the group of alleles denoted B are paraphyletic and given the tree topology and support values, they may or may not form a clade. While most alleles of group B are included in a monophyletic clade representing MHC-I supertypes 3 and 14, its SH-aLRT support value (0.59) is poor and we therefore chose to maintain all of group B as a working definition for reference throughout this paper. (v) Finally, seven alleles remain that form a diverse paraphyletic group between the well-supported monophyletic clades A and B–E (Fig. 2).
Estimating positive selection
We used codeml from the PAML software package (Yang, 1997, 2007) to test for positive selection on an alignment of all alleles in our data set, using our GTR tree as input for codeml. We set codeml to calculate codon frequencies from the average nucleotide frequencies at the three codon positions and to assume a single $\Omega$ (i.e., $dN/dS$) ratio for all branches in the phylogeny. We specified the nested site models (as defined in Yang et al. (2000)) M1 (nearly neutral selection) vs. M2 (some sites evolved under positive selection ($\Omega > 1$)), and M7 ($\Omega$ following a beta distribution) vs. M8 ($\Omega$ following a beta distribution while allowing some sites to evolve under positive selection ($\Omega > 1$)). We tested the nested models using likelihood ratio tests with the formula: $2 \times \Delta\ln(L) \sim \chi^2$, where the degrees of freedom of the $\chi^2$ distribution equals the difference in the number of parameters between the models (Anisimova, Bielawski, & Yang, 2001; Yang et al., 2000). Codons under positive selection from model M8 were inferred by Bayes Empirical Bayes analysis (Yang, Wong, & Nielsen, 2005).

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**Fig. S1**  

**a** Repeatability obtained by filtering in DADA2 with truncQ settings between 18 and 30;  

**b** Repeatability obtained by filtering in DADA2 with MaxEE fw and rv settings between 0.05 and 2.0 (truncQ = 20);  

**c** Repeatability obtained by filtering the DADA2 output (truncQ = 20, MaxEE fw/rv = 0.1) by per amplicon frequency thresholds between 0.005 and 0.03. Note: Repeatability was calculated as 1 minus the mean across all replicate sets of the mean proportion of mismatching sequence variants within each replicate set.

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**a**

![truncQ & repeatability graph](image)

**b**

![MaxEE & repeatability graph](image)
**Fig. S2** Stepwise protocol for haplotype inference and resolution of problematic allele segregation patterns.

**Step 1** Construct putative MHC haplotypes by analyzing segregation of MHC alleles in concurrent families using HpltFind (MHCtools).

**Step 2** Construct putative MHC haplotypes by analyzing segregation of MHC alleles in ancestral families using HpltFind (MHCtools).

**Step 3** Trace putative MHC haplotypes vertically through lines of ancestry and manually inspect the segregation of unresolved alleles in each family. Correct unresolved allele assignments to putative haplotypes when possible.

**Step 4** Apply corrected MHC haplotypes laterally among concurrent families and manually inspect the segregation of unresolved alleles in each family. Correct unresolved allele assignments when possible.

**Step 5** Resolve incongruences among samples that share MHC haplotypes by inspecting raw sequencing output files to identify potential genotyping errors.

**Step 6** Identify sets of potentially identical MHC haplotypes, e.g. by applying a threshold for the proportion of overlapping allele assignments. For each set, manually inspect the segregation of unresolved alleles in families and correct unresolved allele assignments, when identity between haplotypes can be inferred. *Repeat steps 3-6, until all incongruences have been addressed and no more unresolved allele assignments can be settled.*

Final haplotypes
Fig. S3 Family table from nest number 12 of the 1998 cohort showing MHC-I allele segregation patterns with inferred segregating MHC-I haplotypes including a recombination event (indicated by the arrow). Dark gray color indicates that a segregation pattern could not be determined for an allele (uncertain allele).

| Nest 12 of the 1998 cohort | Alleles       | Mother | Father | Offspring 1 | Offspring 2 | Offspring 3 | Offspring 4 | Offspring 5 |
|---------------------------|---------------|--------|--------|-------------|-------------|-------------|-------------|-------------|
| Acar-UA*144               | X             | X      |        | X           | -           | -           | -           | -           |
| Acar-UA*9                 | X             | X      |        | X           | X           | -           | -           | -           |
| Acar-UA*14                | X             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*54                | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*30                | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*39                | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*61                | X             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*12                | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*136               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*241               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*364               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*300               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*133               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*153               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*157               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*201               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*223               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*239               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*296               | -             | X      |        | -           | -           | -           | -           | -           |
| Acar-UA*107               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*110               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*143               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*304               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*368               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*392               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*51                | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*52                | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*55                | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*186               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*231               | X             | -      |        | -           | -           | -           | -           | -           |
| Acar-UA*255               | X             | -      |        | -           | -           | -           | -           | -           |

| Final haplotypes          | Mother A      | Mother B | Recombinant |
|---------------------------|---------------|-----------|-------------|
| Acar-UA*144              | Acar-UA*144   | Acar-UA*144 |             |
| Acar-UA*4                | Acar-UA*9     | Acar-UA*4  |             |
| Acar-UA*9                | Acar-UA*107   | Acar-UA*9  |             |
| Acar-UA*12               | Acar-UA*110   | Acar-UA*136|             |
| Acar-UA*136              | Acar-UA*143   | Acar-UA*107|             |
| Acar-UA*191              | Acar-UA*304   | Acar-UA*143|             |
| Acar-UA*241              | Acar-UA*368   | Acar-UA*304|             |
| Acar-UA*364              | Acar-UA*392   | Acar-UA*368|             |
| Acar-UA*51               | Acar-UA*51    | Acar-UA*51 |             |
| Acar-UA*52               | Acar-UA*52    | Acar-UA*52 |             |
| Acar-UA*55               | Acar-UA*55    | Acar-UA*55 |             |
| Acar-UA*186              | Acar-UA*186   | Acar-UA*186|             |
| Acar-UA*231              | Acar-UA*231   | Acar-UA*231|             |
| Acar-UA*255              | Acar-UA*255   | Acar-UA*255|             |
Fig. S4  Family table from nest number 8 of the 1999 cohort showing MHC-I allele segregation patterns with inferred segregating MHC-I haplotypes including a recombination event (indicated by the arrow). Dark gray color indicates that a segregation pattern could not be determined for an allele (uncertain allele).

| Alleles         | Mother | Father | Offspring 1 | Offspring 2 | Offspring 3 | Offspring 4 | Offspring 5 | Offspring 6 |
|-----------------|--------|--------|-------------|-------------|-------------|-------------|-------------|-------------|
| Acar-UA*4       | X      | X      | X           | X           | X           | X           | X           | X           |
| Acar-UA*55      | X      | X      | X           | X           | X           | X           | X           | X           |
| Acar-UA*9       | X      | X      | X           | X           | X           | X           | X           | X           |
| Acar-UA*129     | -      | -      | -           | -           | -           | -           | -           | -           |
| Acar-UA*42      | -      | -      | X           | X           | X           | -           | -           | -           |
| Acar-UA*144     | X      | X      | -           | -           | X           | -           | X           | X           |
| Acar-UA*143     | -      | -      | X           | X           | -           | X           | -           | -           |
| Acar-UA*155     | -      | X      | -           | X           | -           | X           | -           | -           |
| Acar-UA*255     | -      | X      | -           | X           | -           | X           | -           | -           |
| Acar-UA*59      | -      | X      | -           | X           | -           | X           | -           | -           |
| Acar-UA*65      | -      | X      | -           | X           | -           | X           | -           | -           |
| Acar-UA*12      | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*122     | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*145     | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*163     | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*33      | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*391     | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*74      | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*8       | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*95      | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*192     | X      | -      | -           | X           | -           | X           | -           | -           |
| Acar-UA*31      | X      | X      | -           | X           | -           | X           | -           | -           |
| Acar-UA*332     | X      | X      | -           | X           | -           | X           | -           | -           |
| Acar-UA*285     | X      | -      | -           | X           | -           | -           | -           | X           |
| Acaru_UA_23     | X      | -      | -           | X           | -           | -           | -           | X           |
| Acar-UA*349     | -      | X      | X           | -           | X           | -           | -           | X           |
| Acar-UA*94      | -      | X      | X           | -           | X           | -           | -           | X           |

Final haplotypes

| Mother A | Mother B |
|----------|----------|
| Acar-UA*285 | Acar-UA*12 |
| Acar-UA*4   | Acar-UA*122 |
| Acar-UA*55  | Acar-UA*144 |
| Acar-UA*129 | Acar-UA*145 |
| Acar-UA*23  | Acar-UA*163 |

Father A | Father B | Recombinant
----------|----------|----------------|
Acar-UA*129 | Acar-UA*143 | Acar-UA*129 |
Acar-UA*31  | Acar-UA*144 | Acar-UA*42 |
Acar-UA*332 | Acar-UA*155 | Acar-UA*349 |
Acar-UA*95  | Acar-UA*255 | Acar-UA*94 |
Acar-UA*4   | Acar-UA*4   | Acar-UA*94 |
Acar-UA*55  | Acar-UA*55  | Acar-UA*95 |
Acar-UA*9   | Acar-UA*65  | Acar-UA*94 |
Acar-UA*94  | Acar-UA*59  | Acar-UA*65 |
Acar-UA*8   | Acar-UA*9   | Acar-UA*94 |
**Fig. S5** Elbow plot showing BIC in relation to the number of clusters (k) in model 575 of our bootstrapped k-means clustering approach. The stippled red line indicates the smallest value of k for which \( \Delta \text{BIC} \) was < 1% of the largest \( \Delta \text{BIC} \) observed in the model. Model 575 was one of the six final selected models.
Fig. S6 Scatterplot of cluster assignments for each MHC-I allele in two different k-means clustering models. This plot compares two models with $k_{est} = 14$. Individual clusters within each model are designated by index numbers on the x- and y-axis, and each data point represents one MHC-I allele ($N = 390$). Jitter was used to separate individual data points. In this comparison, three allele assignments fell outside of the 14 most abundant clusters. Model 575 was one of the six final selected models.
Fig. S7 Distribution of the number of different MHC-I alleles per individual in our data set. The line shows a normal distribution with the observed mean (14.3) and standard deviation (3.42).
**Fig. S8** Distribution of the number of different MHC-I alleles on haplotypes. The line shows a normal distribution with the observed mean (9.2) and standard deviation (2.80).
Fig. S9 Amino acid codons estimated to be under positive selection in the MHC-I exon 3 sequences in our data set. The upper line indicates which codons were estimated to be under positive selection, when the selection analysis was carried out using all sequences in our data set, and the remaining lines indicate which codons were estimated to be under positive selection, when selection analyses were carried out using the sequences belonging to each MHC-I exon 3 supertype. The supertypes Acar-ST*3, Acar-ST*5, and Acar-ST*14 did not show evidence of positive selection. * indicates $p < 0.05$ for each site; † indicates $0.05 < p < 0.10$. Estimated $dN/dS$ and p-values for each site are specified in Table S6a–l.

| Codon position | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|----------------|----|----|----|----|----|----|----|----|
| All sequences  | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*1      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*2      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*3      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*4      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*5      |   |   |   |   |   |   |   |   |
| Acar-ST*6      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*7      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*8      | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*9      |   |   | *  | *  | *  | *  | *  | *  |
| Acar-ST*10     |   | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*11     |   | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*12     | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*13     | *  | *  | *  | *  | *  | *  | *  | *  |
| Acar-ST*14     |   |   |   |   |   |   |   |   |
Fig. S10  Barplot showing the number of different MHC-I alleles associated with each MHC-I supertype.
Fig. S11 The relationship between the number of different MHC-I alleles per haplotype and the number of MHC-I supertypes per haplotype. Correlation coefficient = 0.86 (Pearson’s product-moment correlation).

Next page:
Fig. S12 a Histogram showing the distribution of mean Sandberg distance between centroids of positively selected (pos. sel.) MHC-I supertypes within MHC-I haplotypes. b Histogram showing the distribution of mean Sandberg distance overlap between pos. sel. MHC-I supertypes within MHC-I haplotypes. Notes: Haplotypes that harboured fewer than two pos. sel. MHC-I supertypes were excluded from the analysis. Values were calculated based on 14 amino acid codons that showed evidence of positive selection.
This page contains a table and a chart. The table appears to be a pedigree chart with symbols indicating relationships and breeding years. The chart is not clearly visible due to the resolution and angle of the image.

The table includes columns for different generations and relationships, such as 'Pat pat great grandmother', 'Mat mat great grandmother', 'Pat mat great grandfather', and so on. Each row seems to represent a specific individual or relationship, with entries such as '554_ad' and dates like '1991'.

The chart has a patterned background that might represent different generations or statuses, such as '371_ad' and '547_ad', which could indicate family lines or other categorizations.

The chart and table are likely used to document family relationships and breeding information over time, possibly for a study or genetic analysis.
Table S2 *Summary of the corrections applied to putative MHC-I haplotypes.*

| Steps 1–2 |          |
|-----------|----------|
| Initial number of putative haplotypes | 225      |
| Initial mean proportion of unresolved alleles in putative haplotypes | 0.446    |

| Steps 3–5 |          |
|-----------|----------|
| Number of putative haplotypes shared within lines of ancestry | 165      |
| Number of unresolved alleles settled in putative haplotypes | 358      |
| Number of alleles added to putative haplotypes | 162      |
| Number of alleles removed from putative haplotypes | 154      |
| Number of null alleles added to individual samples | 430      |
| – *proportion of the total number of allele assignments to genotypes* | 0.051    |
| Number of sequencing errors called as alleles, removed from individual samples | 15       |
| – *proportion of the total number of allele assignments to genotypes* | 0.0019   |

| Step 6 |          |
|--------|----------|
| Number of haplotypes inferred to be identical to other haplotypes | 41       |
| Number of unresolved alleles verified in putative haplotypes | 128      |

**Final number of putative haplotypes** | 107

**Final mean proportion of unresolved alleles in putative haplotypes** | 0.255
Table S3 Log likelihood, number of parameters, and AIC values for 12 different substitution models evaluated in PhyML: JC69, HKY85, and generalized time-reversible model (GTR), each with no additional parameters, and with the additional estimation of the gamma shape parameter (gamma distribution with 4 classes; G), the proportion of invariable sites (I), or both (G + I). The number of parameters in each model was estimated using the formula: no. parameters in model = (2 × no. sequences – 3) + no. parameters in substitution model + extra parameters, where no. sequences = 390 and no. substitution model parameters are: JC = 0 parameters, HKY = 4 parameters, GTR = 8 parameters. Extra parameters are: Invariable sites = +1 parameter, and gamma rates = +1 parameter. AIC values were calculated for each model by the formula: $AIC = 2k - 2 \times \log(L)$, where $\log(L)$ is the log-likelihood ratio value obtained for each model.

| Model     | Log likelihood | No. parameters | AIC     |
|-----------|----------------|----------------|---------|
| GTR       | -7059.73       | 787            | 15693.47|
| GTR + I   | -7060.23       | 788            | 15696.46|
| GTR + G + I | -7093.55     | 789            | 15765.10|
| HKY + I   | -7105.83       | 784            | 15779.65|
| HKY       | -7125.53       | 783            | 15817.07|
| GTR + G   | -7121.32       | 788            | 15818.65|
| HKY + G   | -7147.98       | 784            | 15863.95|
| HKY + G + I | -7162.26     | 785            | 15894.52|
| JC + I    | -7293.09       | 780            | 16146.18|
| JC + G + I | -7307.02     | 781            | 16176.03|
| JC        | -7315.96       | 779            | 16189.92|
| JC + G    | -7329.97       | 780            | 16219.94|
Table S4 a–f Specification of allele associations with phylogenetic groups.

| a. Group A          | b. Group B          |
|---------------------|---------------------|
| Acar-UA*54          | Acar-UA*4           |
| Acar-UA*55          | Acar-UA*217         |
| Acar-UA*105         | Acar-UA*6           |
| Acar-UA*108         | Acar-UA*218         |
| Acar-UA*109         | Acar-UA*9           |
| Acar-UA*114         | Acar-UA*219         |
| Acar-UA*115         | Acar-UA*31          |
| Acar-UA*116         | Acar-UA*222         |
| Acar-UA*117         | Acar-UA*41          |
| Acar-UA*118         | Acar-UA*224         |
| Acar-UA*129         | Acar-UA*60          |
| Acar-UA*130         | Acar-UA*61          |
| Acar-UA*131         | Acar-UA*225         |
| Acar-UA*132         | Acar-UA*69          |
| Acar-UA*133         | Acar-UA*71          |
| Acar-UA*134         | Acar-UA*142         |
| Acar-UA*135         | Acar-UA*148         |
| Acar-UA*136         | Acar-UA*152         |
| Acar-UA*137         | Acar-UA*199         |
| Acar-UA*138         | Acar-UA*201         |
| Acar-UA*139         | Acar-UA*204         |
| Acar-UA*144         | Acar-UA*205         |
| Acar-UA*159         | Acar-UA*206         |
| Acar-UA*393         | Acar-UA*207         |
| Acar-UA*394         | Acar-UA*208         |
| Acar-UA*395         | Acar-UA*209         |
| Acar-UA*396         | Acar-UA*210         |
| Acar-UA*397         | Acar-UA*211         |
| Acar-UA*399         | Acar-UA*212         |
| Acar-UA*400         | Acar-UA*213         |
| Acar-UA*401         | Acar-UA*214         |
| Acar-UA*402         | Acar-UA*215         |
| Acar-UA*423         | Acar-UA*216         |
| Acar-UA*446         |                     |
| c. Group C         |        |
|--------------------|--------|
| Acar-UA*42         | Acar-UA*270 |
| Acar-UA*44         | Acar-UA*271 |
| Acar-UA*45         | Acar-UA*272 |
| Acar-UA*47         | Acar-UA*273 |
| Acar-UA*88         | Acar-UA*274 |
| Acar-UA*125        | Acar-UA*275 |
| Acar-UA*128        | Acar-UA*276 |
| Acar-UA*155        | Acar-UA*277 |
| Acar-UA*157        | Acar-UA*278 |
| Acar-UA*164        | Acar-UA*279 |
| Acar-UA*185        | Acar-UA*280 |
| Acar-UA*186        | Acar-UA*281 |
| Acar-UA*223        | Acar-UA*282 |
| Acar-UA*228        | Acar-UA*283 |
| Acar-UA*234        | Acar-UA*284 |
| Acar-UA*235        | Acar-UA*285 |
| Acar-UA*238        | Acar-UA*317 |
| Acar-UA*239        | Acar-UA*318 |
| Acar-UA*240        | Acar-UA*331 |
| Acar-UA*241        | Acar-UA*364 |
| Acar-UA*242        | Acar-UA*365 |
| Acar-UA*245        | Acar-UA*367 |
| Acar-UA*248        | Acar-UA*368 |
| Acar-UA*250        | Acar-UA*409 |
| Acar-UA*251        | Acar-UA*416 |
| Acar-UA*254        | Acar-UA*419 |
| Acar-UA*262        | Acar-UA*420 |
| Acar-UA*263        | Acar-UA*428 |
| Acar-UA*265        | Acar-UA*432 |
| Acar-UA*266        | Acar-UA*456 |
| Acar-UA*267        | Acar-UA*457 |
| Acar-UA*268        | Acar-UA*458 |
| Acar-UA*269        | Acar-UA*462 |

| d. Group NC       |        |
|--------------------|--------|
| Acar-UA*13         |        |
| Acar-UA*110        |        |
| Acar-UA*112        |        |
| Acar-UA*127        |        |
| Acar-UA*140        |        |
| Acar-UA*141        |        |
| Acar-UA*158        |        |
| e. Group D |
|------------|
| Acar-UA*11 | Acar-UA*260 | Acar-UA*351 |
| Acar-UA*12 | Acar-UA*306 | Acar-UA*352 |
| Acar-UA*30 | Acar-UA*308 | Acar-UA*354 |
| Acar-UA*48 | Acar-UA*309 | Acar-UA*355 |
| Acar-UA*49 | Acar-UA*310 | Acar-UA*360 |
| Acar-UA*51 | Acar-UA*311 | Acar-UA*375 |
| Acar-UA*52 | Acar-UA*312 | Acar-UA*376 |
| Acar-UA*53 | Acar-UA*313 | Acar-UA*379 |
| Acar-UA*59 | Acar-UA*314 | Acar-UA*384 |
| Acar-UA*62 | Acar-UA*315 | Acar-UA*386 |
| Acar-UA*63 | Acar-UA*316 | Acar-UA*387 |
| Acar-UA*64 | Acar-UA*320 | Acar-UA*388 |
| Acar-UA*65 | Acar-UA*321 | Acar-UA*391 |
| Acar-UA*66 | Acar-UA*322 | Acar-UA*404 |
| Acar-UA*67 | Acar-UA*324 | Acar-UA*406 |
| Acar-UA*68 | Acar-UA*325 | Acar-UA*407 |
| Acar-UA*72 | Acar-UA*326 | Acar-UA*410 |
| Acar-UA*73 | Acar-UA*327 | Acar-UA*411 |
| Acar-UA*74 | Acar-UA*328 | Acar-UA*412 |
| Acar-UA*77 | Acar-UA*329 | Acar-UA*414 |
| Acar-UA*78 | Acar-UA*330 | Acar-UA*417 |
| Acar-UA*79 | Acar-UA*332 | Acar-UA*418 |
| Acar-UA*83 | Acar-UA*333 | Acar-UA*422 |
| Acar-UA*84 | Acar-UA*334 | Acar-UA*424 |
| Acar-UA*91 | Acar-UA*335 | Acar-UA*426 |
| Acar-UA*93 | Acar-UA*336 | Acar-UA*430 |
| Acar-UA*94 | Acar-UA*337 | Acar-UA*431 |
| Acar-UA*95 | Acar-UA*338 | Acar-UA*437 |
| Acar-UA*96 | Acar-UA*339 | Acar-UA*442 |
| Acar-UA*123| Acar-UA*340 | Acar-UA*445 |
| Acar-UA*124| Acar-UA*341 | Acar-UA*447 |
| Acar-UA*154| Acar-UA*342 | Acar-UA*448 |
| Acar-UA*156| Acar-UA*344 | Acar-UA*449 |
| Acar-UA*168| Acar-UA*345 | Acar-UA*455 |
| Acar-UA*169| Acar-UA*346 | Acar-UA*459 |
| Acar-UA*171| Acar-UA*347 | Acar-UA*460 |
| Acar-UA*187| Acar-UA*348 | Acar-UA*463 |
| Acar-UA*188| Acar-UA*349 | Acar-UA*464 |
| Acar-UA*189| Acar-UA*350 | Acar-UA*464 |
| f. Group E |  |  |
|------------|-----------------|-----------------|
| Acar-UA*8  | Acar-UA*145     | Acar-UA*300     |
| Acaru-UA*23| Acar-UA*146     | Acar-UA*302     |
| Acar-UA*32 | Acar-UA*147     | Acar-UA*303     |
| Acar-UA*33 | Acar-UA*149     | Acar-UA*304     |
| Acar-UA*34 | Acar-UA*150     | Acar-UA*307     |
| Acar-UA*35 | Acar-UA*151     | Acar-UA*319     |
| Acar-UA*36 | Acar-UA*153     | Acar-UA*323     |
| Acar-UA*37 | Acar-UA*160     | Acar-UA*366     |
| Acar-UA*38 | Acar-UA*161     | Acar-UA*357     |
| Acar-UA*39 | Acar-UA*162     | Acar-UA*358     |
| Acar-UA*40 | Acar-UA*163     | Acar-UA*359     |
| Acar-UA*43 | Acar-UA*165     | Acar-UA*362     |
| Acar-UA*46 | Acar-UA*166     | Acar-UA*363     |
| Acar-UA*50 | Acar-UA*173     | Acar-UA*366     |
| Acar-UA*57 | Acar-UA*174     | Acar-UA*371     |
| Acar-UA*58 | Acar-UA*175     | Acar-UA*372     |
| Acar-UA*75 | Acar-UA*177     | Acar-UA*373     |
| Acar-UA*80 | Acar-UA*178     | Acar-UA*377     |
| Acar-UA*81 | Acar-UA*181     | Acar-UA*378     |
| Acar-UA*82 | Acar-UA*182     | Acar-UA*380     |
| Acar-UA*85 | Acar-UA*183     | Acar-UA*408     |
| Acar-UA*86 | Acar-UA*184     | Acar-UA*413     |
| Acar-UA*87 | Acar-UA*190     | Acar-UA*421     |
| Acar-UA*89 | Acar-UA*191     | Acar-UA*425     |
| Acar-UA*90 | Acar-UA*192     | Acar-UA*427     |
| Acar-UA*97 | Acar-UA*195     | Acar-UA*429     |
| Acar-UA*99 | Acar-UA*196     | Acar-UA*433     |
| Acar-UA*100| Acar-UA*200     | Acar-UA*434     |
| Acar-UA*101| Acar-UA*233     | Acar-UA*435     |
| Acar-UA*102| Acar-UA*236     | Acar-UA*438     |
| Acar-UA*103| Acar-UA*243     | Acar-UA*439     |
| Acar-UA*107| Acar-UA*247     | Acar-UA*440     |
| Acar-UA*111| Acar-UA*255     | Acar-UA*441     |
| Acar-UA*119| Acar-UA*257     | Acar-UA*444     |
| Acar-UA*120| Acar-UA*258     | Acar-UA*451     |
| Acar-UA*122| Acar-UA*264     | Acar-UA*452     |
| Acar-UA*126| Acar-UA*298     | Acar-UA*453     |
| Acar-UA*143| Acar-UA*299     | Acar-UA*454     |
Table S5 Results from tests of positive selection on our great reed warbler MHC-I exon 3 sequences using codeml from the software package PAML (Yang, 1997, 2007) a across all sequence variants in our data set, and b–o among the sequences belonging to each MHC-I exon 3 supertype. P-values were obtained by the formula \(2 \times \Delta \ln L \sim \chi^2\) (d.f. = difference in no. parameters between the models) and indicate the probability that two models have similar log likelihood (i.e., that \(2 \times \Delta \ln L = 0\)).

### a. Selection models – all sequences

| Model | Parameter estimates | Log likelihood (ln L) | \(2\Delta\ln L\) | P-value | Sign. level |
|-------|---------------------|-----------------------|-----------------|---------|-------------|
| M1    | \(p = 0.701, dN/dS = 0.084\) \(p = 0.299, dN/dS = 1\) | -7915.96 | 353.5 | < 0.0001 | *** |
| M2    | \(p = 0.655, dN/dS = 0.116\) \(p = 0.182, dN/dS = 1\) \(p = 0.163, dN/dS = 3.73\) | -7739.21 | - | - | - |
| M7    | \(p = 0.247, q = 0.389\) | -7901.34 | 342.7 | < 0.0001 | *** |
| M8    | \(p0 = 0.835, p = 0.356, q = 0.826\) \(p1 = 0.165, dN/dS = 3.44\) | -7729.94 | - | - | - |

### b. Selection models – Acar-ST*1

| Model | Parameter estimates | Log likelihood (ln L) | \(2\Delta\ln L\) | P-value | Sign. level |
|-------|---------------------|-----------------------|-----------------|---------|-------------|
| M1    | \(p = 0.725, dN/dS = 0.037\) \(p = 0.275, dN/dS = 1\) | -907.99 | 10.04 | 0.0066 | ** |
| M2    | \(p = 0.798, dN/dS = 0.089\) \(p = 0.070, dN/dS = 1\) \(p = 0.132, dN/dS = 2.84\) | -902.97 | - | - | - |
| M7    | \(p = 0.012, q = 0.024\) | -908.32 | 10.67 | 0.0048 | ** |
| M8    | \(p0 = 0.853, p = 0.523, q = 3.27\) \(p1 = 0.147, dN/dS = 2.73\) | -902.98 | - | - | - |
### c. Selection models - Acar-ST*2

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|--------|---------|-------------|
| M1    | p = 0.662, dN/dS = 0.033  
       | p = 0.338, dN/dS = 1   | -1041.84 | 27.33  | < 0.0001 | ***         |
| M2    | p = 0.632, dN/dS = 0.045  
       | p = 0.240, dN/dS = 1  
       | p = 0.128, dN/dS = 4.94 | -1028.17 | 28.79  | < 0.0001 | ***         |
| M7    | p = 0.018, q = 0.035  | -1042.47  | 28.79  | < 0.0001 | ***         |
| M8    | p0 = 0.864, p = 0.115, q = 0.292  
       | p1 = 0.136, dN/dS = 4.70 | -1028.08 | 28.79  | < 0.0001 | ***         |

### d. Selection models - Acar-ST*3

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|--------|---------|-------------|
| M1    | p = 0.54, dN/dS = 0.033 
       | p = 0.46, dN/dS = 1   | -1010.79 | 0.37  | 0.83      | n.s.        |
| M2    | p = 0.57, dN/dS = 0.054  
       | p = 0.27, dN/dS = 1  
       | p = 0.15, dN/dS = 1.46 | -1010.61 | 0.87  | 0.65      | n.s.        |
| M7    | p = 0.073, q = 0.084  | -1010.86  | 0.87  | 0.65    | n.s.        |
| M8    | p0 = 0.75, p = 0.226, q = 0.771  
       | p1 = 0.25, dN/dS = 1.44 | -1010.42 | 0.87  | 0.65      | n.s.        |
**e. Selection models - Acar-ST*4**

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|---------|---------|-------------|
| M1    | $p = 0.75, dN/dS = 0.04$ | -1185.63              | 48.09   | < 0.0001 | ***         |
|       | $p = 0.25, dN/dS = 1$  |                      |         |         |             |
| M2    | $p = 0.71, dN/dS = 0.047$ | -1161.59              |         |         |             |
|       | $p = 0.24, dN/dS = 1$  |                      |         |         |             |
|       | $p = 0.05, dN/dS = 7.61$ |                      |         |         |             |
| M7    | $p = 0.017, q = 0.034$ | -1188.08              |         |         |             |
| M8    | $p0 = 0.88, p = 0.135, q = 0.445$ | -1162.74              |         |         |             |
|       | $p1 = 0.12, dN/dS = 4.99$ |                      |         |         |             |

**f. Selection models - Acar-ST*5**

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|---------|---------|-------------|
| M1    | $p = 0.54, dN/dS = 0.14$ | -831.27               | 0       | 1       | n.s.        |
|       | $p = 0.46, dN/dS = 1$  |                      |         |         |             |
| M2    | $p = 0.54, dN/dS = 0.14$ | -831.27               | 0       | 1       | n.s.        |
|       | $p = 0.32, dN/dS = 1$  |                      |         |         |             |
|       | $p = 0.14, dN/dS = 1$  |                      |         |         |             |
| M7    | $p = 0.324, q = 0.310$ | -831.24               | 0       | 1       | n.s.        |
| M8    | $p0 = 1, p = 0.324, q = 0.310$ | -831.24               | 0       | 1       | n.s.        |
|       | $p1 = 0, dN/dS = 1$    |                      |         |         |             |
### g. Selection models - Acar-ST*6

| Model | Parameter estimates | Log likelihood (ln L) | $2\Delta\ln L$ | P-value | Sign. level |
|-------|---------------------|-----------------------|----------------|---------|-------------|
| M1    | $p = 0.72$, $dN/dS = 0.062$  
$p = 0.28$, $dN/dS = 1$ | -985.81 | 7.32 | 0.026 | * |
| M2    | $p = 0.82$, $dN/dS = 0.127$  
$p = 0$, $dN/dS = 1$  
$p = 0.18$, $dN/dS = 2.23$ | -982.15 | 7.32 | 0.026 | * |
| M7    | $p = 0.093$, $q = 0.175$ | -987.07 | 7.32 | 0.026 | ** |
| M8    | $p = 0.83$, $p = 0.996$, $q = 5.63$  
$p = 0.17$, $dN/dS = 2.36$ | -982.03 | 7.32 | 0.026 | ** |

### h. Selection models - Acar-ST*7

| Model | Parameter estimates | Log likelihood (ln L) | $2\Delta\ln L$ | P-value | Sign. level |
|-------|---------------------|-----------------------|----------------|---------|-------------|
| M1    | $p = 0.70$, $dN/dS = 0.043$  
$p = 0.30$, $dN/dS = 1$ | -928.69 | 34.63 | < 0.0001 | *** |
| M2    | $p = 0.62$, $dN/dS = 0.035$  
$p = 0.32$, $dN/dS = 1$  
$p = 0.06$, $dN/dS = 9.72$ | -911.37 | 34.63 | < 0.0001 | *** |
| M7    | $p = 0.018$, $q = 0.035$ | -929.27 | 34.63 | < 0.0001 | *** |
| M8    | $p = 0.94$, $p = 0.052$, $q = 0.091$  
$p = 0.06$, $dN/dS = 9.72$ | -911.47 | 34.63 | < 0.0001 | *** |
### i. Selection models - Acar-ST*8

| Model | Parameter estimates | Log likelihood (ln L) | $2^\Delta ln L$ | P-value | Sign. level |
|-------|---------------------|-----------------------|-----------------|---------|-------------|
| M1    | $p = 0.74$, dN/dS = 0.046  
$p = 0.26$, dN/dS = 1 | -936.87 | 25.16 | < 0.0001 | *** |
| M2    | $p = 0.69$, dN/dS = 0.046  
$p = 0.25$, dN/dS = 1  
$p = 0.06$, dN/dS = 6.41 | -924.29 | 25.16 | < 0.0001 | *** |
| M7    | $p = 0.017$, q = 0.033 | -937.04 | 26.59 | < 0.0001 | *** |
| M8    | $p_0 = 0.93$, $p = 0.177$, q = 0.526  
$p_1 = 0.07$, dN/dS = 5.60 | -923.75 | 26.59 | < 0.0001 | *** |

### j. Selection models - Acar-ST*9

| Model | Parameter estimates | Log likelihood (ln L) | $2^\Delta ln L$ | P-value | Sign. level |
|-------|---------------------|-----------------------|-----------------|---------|-------------|
| M1    | $p = 0.79$, dN/dS = 0.017  
$p = 0.21$, dN/dS = 1 | -919.68 | 28.53 | < 0.0001 | *** |
| M2    | $p = 0.77$, dN/dS = 0.020  
$p = 0.16$, dN/dS = 1  
$p = 0.07$, dN/dS = 4.91 | -905.42 | 28.53 | < 0.0001 | *** |
| M7    | $p = 0.009$, q = 0.030 | -920.17 | 27.87 | < 0.0001 | *** |
| M8    | $p_0 = 0.83$, $p = 5.23$, q = 99.00  
$p_1 = 0.17$, dN/dS = 3.47 | -906.24 | 27.87 | < 0.0001 | *** |
### k. Selection models - Acar-ST*10

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|--------|---------|-------------|
| **M1** | p = 0.56, dN/dS = 0<br>p = 0.44, dN/dS = 1 | -661.14 | 8.93 | 0.011 | * |
| **M2** | p = 0.88, dN/dS = 0.257<br>p = 0, dN/dS = 1<br>p = 0.12, dN/dS = 4.80 | -656.67 |  |  |
| **M7** | p = 0.005, q = 0.006 | -661.20 | 9.05 | 0.011 | * |
| **M8** | p0 = 0.88, p = 34.55, q = 99.00<br>p1 = 0.12, dN/dS = 4.81 | -656.68 |  |  |

### l. Selection models - Acar-ST*11

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|--------|---------|-------------|
| **M1** | p = 0.66, dN/dS = 0.040<br>p = 0.34, dN/dS = 1 | -1124.07 | 67.67 | < 0.0001 | *** |
| **M2** | p = 0.53, dN/dS = 0.013<br>p = 0.38, dN/dS = 1<br>p = 0.09, dN/dS = 9.53 | -1090.23 |  |  |
| **M7** | p = 0.017, q = 0.022 | -1124.98 | 69.38 | < 0.0001 | *** |
| **M8** | p0 = 0.91, p = 0.013, q = 0.017<br>p1 = 0.09, dN/dS = 9.39 | -1090.29 |  |  |
## Selection models - Acar-ST*12

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|--------|---------|-------------|
| M1    | p = 0.78, dN/dS = 0.046 |
|       | p = 0.22, dN/dS = 1   |
|       | -772.89              |
|       | 31.67                |
|       | < 0.0001            | ***                   |
| M2    | p = 0.87, dN/dS = 0.146 |
|       | p = 0.13, dN/dS = 5.94 |
|       | -757.06              |
| M7    | p = 0.014, q = 0.027 |
|       | -774.00              |
| M8    | p0 = 0.87, p = 17.31, q = 99.00 |
|       | p1 = 0.13, dN/dS = 5.94 |
|       | -757.06              |

## Selection models - Acar-ST*13

| Model | Parameter estimates | Log likelihood (ln L) | 2*ΔlnL | P-value | Sign. level |
|-------|---------------------|-----------------------|--------|---------|-------------|
| M1    | p = 0.66, dN/dS = 0.075 |
|       | p = 0.34, dN/dS = 1   |
|       | -883.98              |
| M2    | p = 0.71, dN/dS = 0.147 |
|       | p = 0.22, dN/dS = 1   |
|       | p = 0.08, dN/dS = 4.36 |
|       | -878.12              |
| M7    | p = 0.021, q = 0.026 |
|       | -884.43              |
| M8    | p0 = 0.92, p = 0.466, q = 0.992 |
|       | p1 = 0.08, dN/dS = 4.14 |
|       | -877.92              |

|       | 13.01                |
|       | 0.0015              | **                  |
| Model | Parameter estimates | Log likelihood (ln L) | $2\Delta \ln L$ | P-value | Sign. level |
|-------|---------------------|-----------------------|-----------------|---------|-------------|
| M1    | $p = 1$, dN/dS = 0.208 | -441.23               | 0               | 1       | n.s.        |
|       | $p = 0$, dN/dS = 1   |                      |                 |         |             |
| M2    | $p = 1$, dN/dS = 0.208 | -441.23               | 0               | 1       | n.s.        |
|       | $p = 0$, dN/dS = 1   |                      |                 |         |             |
|       | $p = 0$, dN/dS = 1   |                      |                 |         |             |
| M7    | $p = 26.35$, q = 99.00 | -441.23               | 0               | 1       | n.s.        |
| M8    | $p^0 = 1$, $p = 26.05$, q = 99.00 | -441.23 | 0 | 1 | n.s. |
Table S6 Results of Bayes Empirical Bayes analyses (Yang et al., 2005) of positively selected sites (i.e. sites for which dN/dS is estimated to be greater than 1) in our great reed warbler MHC-I exon 3 sequences. a Results of a Bayes Empirical Bayes analysis across all sequence variants in our data set, b–l Results of Bayes Empirical Bayes analyses among the sequences belonging to each of the MHC-I exon 3 supertypes, that showed evidence of positive selection. P-values indicate the probability that dN/dS ≤ 1.

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 3.500 ± 0.000            | < 0.001 | ***         |
| 3          | 3.500 ± 0.000            | < 0.001 | ***         |
| 5          | 3.500 ± 0.000            | < 0.001 | ***         |
| 18         | 3.494 ± 0.120            | 0.002   | **          |
| 21         | 3.500 ± 0.000            | < 0.001 | ***         |
| 34         | 3.481 ± 0.220            | 0.007   | **          |
| 40         | 3.499 ± 0.039            | < 0.001 | ***         |
| 44         | 3.500 ± 0.007            | < 0.001 | ***         |
| 58         | 3.500 ± 0.002            | < 0.001 | ***         |
| 61         | 3.500 ± 0.000            | < 0.001 | ***         |
| 62         | 3.500 ± 0.000            | < 0.001 | ***         |
| 69         | 3.500 ± 0.000            | < 0.001 | ***         |
| 76         | 3.498 ± 0.071            | < 0.001 | ***         |
| 79         | 3.500 ± 0.014            | < 0.001 | ***         |
b. Positively selected sites – Acar-ST*1

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 16         | 2.495 ± 1.062            | 0.18    | n.s.        |
| 18         | 2.854 ± 0.793            | 0.037   | *           |
| 19         | 2.267 ± 1.075            | 0.26    | n.s.        |
| 20         | 2.766 ± 0.850            | 0.069   |             |
| 21         | 2.705 ± 0.913            | 0.095   |             |
| 26         | 2.412 ± 1.038            | 0.20    | n.s.        |
| 32         | 2.918 ± 0.724            | 0.010   | **          |
| 34         | 2.778 ± 0.867            | 0.068   |             |
| 37         | 2.423 ± 1.090            | 0.20    | n.s.        |
| 40         | 2.936 ± 0.712            | 0.003   | **          |

c. Positively selected sites – Acar-ST*2

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 4.347 ± 0.962            | 0.011   | *           |
| 3          | 4.385 ± 0.908            | 0.002   | **          |
| 5          | 4.392 ± 0.894            | < 0.001 | ***         |
| 18         | 3.623 ± 1.588            | 0.19    | n.s.        |
| 19         | 4.369 ± 0.928            | 0.006   | **          |
| 21         | 4.329 ± 0.987            | 0.016   | *           |
| 26         | 2.692 ± 1.790            | 0.42    | n.s.        |
| 34         | 2.732 ± 1.864            | 0.41    | n.s.        |
| 36         | 2.913 ± 1.739            | 0.36    | n.s.        |
| 40         | 4.294 ± 1.029            | 0.024   | *           |
| 44         | 4.248 ± 1.119            | 0.038   | *           |
| 61         | 4.338 ± 0.987            | 0.015   | *           |
| 76         | 3.185 ± 1.807            | 0.30    | n.s.        |
| 79         | 4.246 ± 1.119            | 0.039   | *           |
### d. Positively selected sites – Acar-ST*4

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
|  1         | 4.789 ± 0.977            | < 0.001 | ***         |
|  3         | 4.770 ± 1.008            | 0.004   | **          |
|  5         | 4.789 ± 0.977            | < 0.001 | ***         |
|  18        | 4.577 ± 1.142            | 0.039   | *           |
|  19        | 3.638 ± 1.710            | 0.244   | n.s.        |
|  21        | 4.789 ± 0.977            | < 0.001 | ***         |
|  34        | 4.245 ± 1.431            | 0.111   | n.s.        |
|  40        | 4.656 ± 1.043            | 0.022   | *           |
|  44        | 4.210 ± 1.517            | 0.124   | n.s.        |
|  55        | 3.716 ± 1.709            | 0.228   | n.s.        |
|  61        | 2.980 ± 1.922            | 0.404   | n.s.        |
|  69        | 4.344 ± 1.299            | 0.084   | .           |

### e. Positively selected sites – Acar-ST*6

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
|  1         | 1.965 ± 1.000            | 0.293   | n.s.        |
|  3         | 1.962 ± 1.099            | 0.296   | n.s.        |
|  5         | 2.430 ± 0.834            | 0.092   | .           |
|  19        | 2.420 ± 0.817            | 0.092   | .           |
|  21        | 2.478 ± 0.772            | 0.065   | .           |
|  51        | 1.717 ± 0.978            | 0.404   | n.s.        |
|  55        | 2.572 ± 0.722            | 0.024   | *           |
|  57        | 1.997 ± 0.964            | 0.278   | n.s.        |
|  58        | 2.578 ± 0.712            | 0.020   | *           |
|  61        | 2.073 ± 0.974            | 0.25    | n.s.        |
|  62        | 2.549 ± 0.735            | 0.034   | *           |
f. Positively selected sites – Acar-ST*7

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 8.229 ± 1.725            | < 0.001 | ***         |
| 3          | 8.222 ± 1.739            | 0.001   | ***         |
| 5          | 8.205 ± 1.771            | 0.003   | **          |
| 21         | 8.210 ± 1.759            | 0.003   | **          |
| 61         | 8.231 ± 1.719            | < 0.001 | ***         |

g. Positively selected sites – Acar-ST*8

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 3.039 ± 2.406            | 0.498   | n.s.        |
| 3          | 5.907 ± 1.535            | 0.005   | **          |
| 5          | 5.872 ± 1.569            | 0.010   | **          |
| 18         | 5.559 ± 1.843            | 0.060   | .           |
| 19         | 5.499 ± 1.854            | 0.067   | .           |
| 21         | 5.929 ± 1.497            | < 0.001 | ***         |
### h. Positively selected sites – Acar-ST*9

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 3.420 ± 1.306            | 0.153   | n.s.        |
| 5          | 4.035 ± 0.844            | < 0.001 | ***         |
| 18         | 3.335 ± 1.419            | 0.178   | n.s.        |
| 19         | 3.990 ± 0.871            | 0.010   | **          |
| 21         | 4.036 ± 0.844            | < 0.001 | ***         |
| 34         | 2.669 ± 1.648            | 0.357   | n.s.        |
| 39         | 2.937 ± 1.511            | 0.283   | n.s.        |
| 40         | 2.777 ± 1.550            | 0.328   | n.s.        |
| 44         | 3.511 ± 1.327            | 0.134   | n.s.        |
| 57         | 3.974 ± 0.875            | 0.013   | *           |
| 58         | 3.586 ± 1.159            | 0.106   | n.s.        |
| 62         | 4.036 ± 0.844            | < 0.001 | ***         |
| 69         | 3.475 ± 1.229            | 0.135   | n.s.        |

### i. Positively selected sites – Acar-ST*10

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 5          | 5.173 ± 2.232            | 0.059   |             |
| 19         | 4.458 ± 2.436            | 0.176   | n.s.        |
| 21         | 5.412 ± 2.061            | 0.013   | *           |
| 44         | 4.432 ± 2.560            | 0.197   | n.s.        |
| 57         | 2.955 ± 2.428            | 0.449   | n.s.        |
| 69         | 5.091 ± 2.242            | 0.069   |             |
| 79         | 4.525 ± 2.544            | 0.181   | n.s.        |
### j. Positively selected sites – Acar-ST*11

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 3          | 8.623 ± 1.323            | < 0.001 | ***         |
| 21         | 8.624 ± 1.319            | < 0.001 | ***         |
| 44         | 8.514 ± 1.590            | 0.014   | *           |
| 58         | 8.624 ± 1.318            | < 0.001 | ***         |
| 61         | 4.643 ± 3.806            | 0.484   | n.s.        |
| 69         | 8.624 ± 1.318            | < 0.001 | ***         |
| 76         | 5.909 ± 3.704            | 0.328   | n.s.        |
| 79         | 8.267 ± 2.031            | 0.043   | *           |
| 82         | 8.593 ± 1.396            | 0.004   | **          |

### k. Positively selected sites – Acar-ST*12

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 6.629 ± 1.438            | < 0.001 | ***         |
| 3          | 5.850 ± 2.349            | 0.122   | n.s.        |
| 5          | 6.614 ± 1.462            | 0.002   | **          |
| 19         | 6.594 ± 1.496            | 0.006   | **          |
| 21         | 4.498 ± 2.922            | 0.328   | n.s.        |
| 26         | 6.164 ± 1.981            | 0.067   |             |
| 34         | 4.413 ± 2.919            | 0.339   | n.s.        |
| 40         | 4.869 ± 2.743            | 0.264   | n.s.        |
| 58         | 6.626 ± 1.443            | < 0.001 | ***         |
| 61         | 6.595 ± 1.495            | 0.005   | **          |
## I. Positively selected sites – Acar-ST*13

| a.a. codon | post mean ± SE for dN/dS | P-value | sign. level |
|------------|--------------------------|---------|-------------|
| 1          | 4.352 ± 1.567            | 0.038   | *           |
| 5          | 4.396 ± 1.540            | 0.029   | *           |
| 21         | 4.497 ± 1.451            | 0.004   | **          |
| 44         | 2.505 ± 2.011            | 0.478   | n.s.        |
| 58         | 4.311 ± 1.587            | 0.047   | *           |
| 61         | 3.055 ± 1.960            | 0.334   | n.s.        |
Table S7 Summary of model statistics from bootstrapped k-means clustering models for each estimated value of k. No. models specifies the number of models that estimated each value of k. Mean no. ass. low-ranking clusters and Mean prop. ass. low-ranking clusters are the number and proportion of allele assignments to low-ranking clusters.

| k   | No. models | Mean residual total within SS | Mean residual AIC | Mean residual BIC |
|-----|------------|-------------------------------|-------------------|------------------|
| 13  | 14         | 21605.52                      | 23425.52          | 27034.71         |
| 14  | 54         | 20598.90                      | 22558.90          | 26445.72         |
| 15  | 86         | 19749.09                      | 21849.09          | 26013.55         |
| 16  | 123        | 18960.16                      | 21200.16          | 25642.24         |
| 17  | 191        | 18231.97                      | 20611.97          | 25331.69         |
| 18  | 184        | 17573.44                      | 20093.44          | 25090.78         |
| 19  | 188        | 16954.26                      | 19614.26          | 24889.24         |
| 20  | 110        | 16399.76                      | 19199.76          | 24752.36         |
| 21  | 37         | 15868.94                      | 18808.94          | 24639.17         |
| 22  | 12         | 15359.48                      | 18439.48          | 24547.35         |
| 23  | 1          | 14922.99                      | 18142.99          | 24528.49         |

Table S7 cont.

| k   | Mean prop. ΔBIC | Mean ΔBIC/k | Mean no. ass. low-ranking clusters | Mean prop. ass. low-ranking clusters |
|-----|----------------|-------------|-----------------------------------|-------------------------------------|
| 13  | 0.926          | 2475.86     | 27.85                             | 0.036                               |
| 14  | 0.944          | 2341.08     | 24.97                             | 0.032                               |
| 15  | 0.956          | 2213.82     | 44.99                             | 0.058                               |
| 16  | 0.966          | 2098.66     | 51.25                             | 0.066                               |
| 17  | 0.976          | 1993.48     | 58.78                             | 0.075                               |
| 18  | 0.983          | 1896.12     | 64.45                             | 0.083                               |
| 19  | 0.988          | 1806.93     | 64.50                             | 0.083                               |
| 20  | 0.992          | 1723.43     | 63.29                             | 0.081                               |
| 21  | 0.995          | 1646.75     | 61.21                             | 0.078                               |
| 22  | 0.996          | 1576.07     | 50.30                             | 0.064                               |
| 23  | 1.000          | 1508.36     | NA                                | NA                                  |
Table S8 a–n Allele associations with MHC-I supertypes.

| a. Acar-ST*1          |          |
|-----------------------|----------|
| Acar-UA*11            | Acar-UA*348 |
| Acar-UA*12            | Acar-UA*349 |
| Acar-UA*123           | Acar-UA*350 |
| Acar-UA*154           | Acar-UA*351 |
| Acar-UA*308           | Acar-UA*352 |
| Acar-UA*309           | Acar-UA*354 |
| Acar-UA*310           | Acar-UA*355 |
| Acar-UA*311           | Acar-UA*356 |
| Acar-UA*312           | Acar-UA*357 |
| Acar-UA*313           | Acar-UA*358 |
| Acar-UA*314           | Acar-UA*359 |
| Acar-UA*315           | Acar-UA*360 |
| Acar-UA*316           | Acar-UA*361 |
| Acar-UA*320           | Acar-UA*362 |
| Acar-UA*321           | Acar-UA*363 |
| Acar-UA*322           | Acar-UA*364 |
| Acar-UA*324           | Acar-UA*365 |
| Acar-UA*325           | Acar-UA*366 |
| Acar-UA*326           | Acar-UA*367 |
| Acar-UA*327           | Acar-UA*368 |
| Acar-UA*328           | Acar-UA*369 |
| Acar-UA*329           | Acar-UA*370 |
| Acar-UA*330           | Acar-UA*371 |
| Acar-UA*332           | Acar-UA*372 |
| Acar-UA*333           | Acar-UA*373 |
| Acar-UA*334           | Acar-UA*374 |
| Acar-UA*335           | Acar-UA*375 |
| Acar-UA*336           | Acar-UA*376 |
| Acar-UA*337           | Acar-UA*377 |
| Acar-UA*338           | Acar-UA*378 |
| Acar-UA*339           | Acar-UA*379 |
| Acar-UA*340           | Acar-UA*380 |
| Acar-UA*341           | Acar-UA*381 |
| Acar-UA*342           | Acar-UA*382 |
| Acar-UA*344           | Acar-UA*383 |
| Acar-UA*345           | Acar-UA*384 |
| Acar-UA*346           | Acar-UA*385 |
| Acar-UA*347           | Acar-UA*386 |

| b. Acar-ST*2          |          |
|-----------------------|----------|
| Acar-UA*111           |          |
| Acar-UA*122           |          |
| Acar-UA*123           |          |
| Acar-UA*146           |          |
| Acar-UA*153           |          |
| Acar-UA*164           |          |
| Acar-UA*185           |          |
| Acar-UA*186           |          |
| Acar-UA*195           |          |
| Acar-UA*196           |          |
| Acar-UA*223           |          |
| Acar-UA*299           |          |
| Acar-UA*300           |          |
| Acar-UA*302           |          |
| Acar-UA*303           |          |
| Acar-UA*304           |          |
| Acar-UA*356           |          |
| Acar-UA*357           |          |
| Acar-UA*358           |          |
| Acar-UA*359           |          |
| Acar-UA*360           |          |
| Acar-UA*361           |          |
| Acar-UA*362           |          |
| Acar-UA*363           |          |
| Acar-UA*364           |          |
| Acar-UA*365           |          |
| Acar-UA*366           |          |
| Acar-UA*367           |          |
| Acar-UA*368           |          |
| Acar-UA*369           |          |
| Acar-UA*370           |          |
| Acar-UA*371           |          |
| Acar-UA*372           |          |
| Acar-UA*373           |          |
| Acar-UA*374           |          |
| Acar-UA*375           |          |
| Acar-UA*376           |          |
| Acar-UA*377           |          |
| Acar-UA*378           |          |
| Acar-UA*379           |          |
| Acar-UA*380           |          |
| Acar-UA*381           |          |
| Acar-UA*382           |          |
| Acar-UA*383           |          |
| Acar-UA*384           |          |
| Acar-UA*385           |          |
| Acar-UA*386           |          |
| Acar-UA*426           |          |
| Acar-UA*429           |          |
| Acar-UA*440           |          |
| Acar-UA*452           |          |
| c. Acar-ST*3 | d. Acar-ST*4 | e. Acar-ST*5 |
|-------------|-------------|-------------|
| Acar-UA*127 | Acar-UA*101 | Acar-UA*105 |
| Acar-UA*13  | Acar-UA*102 | Acar-UA*108 |
| Acar-UA*140 | Acar-UA*112 | Acar-UA*109 |
| Acar-UA*142 | Acar-UA*141 | Acar-UA*114 |
| Acar-UA*148 | Acar-UA*151 | Acar-UA*115 |
| Acar-UA*158 | Acar-UA*155 | Acar-UA*116 |
| Acar-UA*199 | Acar-UA*156 | Acar-UA*117 |
| Acar-UA*201 | Acar-UA*230 | Acar-UA*118 |
| Acar-UA*204 | Acar-UA*231 | Acar-UA*129 |
| Acar-UA*205 | Acar-UA*276 | Acar-UA*130 |
| Acar-UA*206 | Acar-UA*360 | Acar-UA*131 |
| Acar-UA*207 | Acar-UA*367 | Acar-UA*132 |
| Acar-UA*208 | Acar-UA*368 | Acar-UA*133 |
| Acar-UA*209 | Acar-UA*384 | Acar-UA*134 |
| Acar-UA*210 | Acar-UA*387 | Acar-UA*135 |
| Acar-UA*211 | Acar-UA*388 | Acar-UA*136 |
| Acar-UA*212 | Acar-UA*390 | Acar-UA*137 |
| Acar-UA*213 | Acar-UA*391 | Acar-UA*138 |
| Acar-UA*214 | Acar-UA*53  | Acar-UA*139 |
| Acar-UA*215 | Acar-UA*80  | Acar-UA*144 |
| Acar-UA*216 | Acar-UA*81  | Acar-UA*159 |
| Acar-UA*217 | Acar-UA*82  | Acar-UA*248 |
| Acar-UA*218 | Acar-UA*86  | Acar-UA*254 |
| Acar-UA*219 | Acar-UA*87  | Acar-UA*393 |
| Acar-UA*222 | Acar-UA*89  | Acar-UA*394 |
| Acar-UA*224 | Acar-UA*439 | Acar-UA*395 |
| Acar-UA*241 | Acar-UA*444 | Acar-UA*396 |
| Acar-UA*392 | Acar-UA*445 | Acar-UA*397 |
| Acar-UA*4   |               | Acar-UA*399 |
| Acar-UA*41  |               | Acar-UA*400 |
| Acar-UA*6   |               | Acar-UA*401 |
| Acar-UA*407 |               | Acar-UA*402 |
| Acar-UA*443 |               | Acar-UA*54  |
| Acar-UA*450 |               | Acar-UA*55  |
| Acar-UA*461 |               | Acar-UA*423 |
|               |               | Acar-UA*446 |
| f. Acar-ST*6  | g. Acar-ST*7  | h. Acar-ST*8  |
|---------------|---------------|---------------|
| Acar-UA*110   | Acar-UA*147   | Acar-UA*143   |
| Acar-UA*128   | Acar-UA*200   | Acar-UA*168   |
| Acar-UA*157   | Acar-UA*228   | Acar-UA*169   |
| Acar-UA*229   | Acar-UA*233   | Acar-UA*171   |
| Acar-UA*245   | Acar-UA*255   | Acar-UA*242   |
| Acar-UA*261   | Acar-UA*257   | Acar-UA*30    |
| Acar-UA*263   | Acar-UA*258   | Acar-UA*306   |
| Acar-UA*265   | Acar-UA*268   | Acar-UA*31    |
| Acar-UA*266   | Acar-UA*298   | Acar-UA*59    |
| Acar-UA*273   | Acar-UA*362   | Acar-UA*60    |
| Acar-UA*274   | Acar-UA*366   | Acar-UA*61    |
| Acar-UA*275   | Acar-UA*372   | Acar-UA*62    |
| Acar-UA*277   | Acar-UA*373   | Acar-UA*63    |
| Acar-UA*278   | Acar-UA*39    | Acar-UA*64    |
| Acar-UA*279   | Acar-UA*40    | Acar-UA*65    |
| Acar-UA*280   | Acar-UA*43    | Acar-UA*66    |
| Acar-UA*281   | Acar-UA*425   | Acar-UA*67    |
| Acar-UA*282   | Acar-UA*438   | Acar-UA*68    |
| Acar-UA*283   |                | Acar-UA*69    |
| Acar-UA*284   |                | Acar-UA*71    |
| Acar-UA*45    |                | Acar-UA*72    |
| Acar-UA*409   |                | Acar-UA*77    |
| Acar-UA*412   |                | Acar-UA*78    |
| Acar-UA*416   |                | Acar-UA*79    |
| Acar-UA*428   |                | Acar-UA*83    |
| Acar-UA*432   |                | Acar-UA*84    |
| Acar-UA*456   |                | Acar-UA*404   |
| Acar-UA*458   |                | Acar-UA*411   |
| Acar-UA*462   |                |                |
### Table i. Acar-ST*9

| Acar-UA*124 | Acar-UA*234 |
|-------------|-------------|
| Acar-UA*238 | Acar-UA*239 |
| Acar-UA*240 | Acar-UA*250 |
| Acar-UA*251 | Acar-UA*260 |
| Acar-UA*262 | Acar-UA*267 |
| Acar-UA*270 | Acar-UA*285 |
| Acar-UA*375 | Acar-UA*376 |
| Acar-UA*379 | Acar-UA*386 |
| Acar-UA*42  | Acar-UA*44  |
| Acar-UA*418 | Acar-UA*419 |
| Acar-UA*420 | Acar-UA*459 |

### Table j. Acar-ST*10

| Acar-UA*73  | Acar-UA*74  |
|-------------|-------------|
| Acar-UA*88  | Acar-UA*91  |
| Acar-UA*93  | Acar-UA*94  |
| Acar-UA*95  | Acar-UA*96  |
| Acar-UA*10  | Acar-UA*11  |
| Acar-UA*14  | Acar-UA*22  |
| Acar-UA*25  | Acar-UA*26  |
| Acar-UA*30  | Acar-UA*31  |
| Acar-UA*35  | Acar-UA*36  |
| Acar-UA*42  | Acar-UA*43  |
| Acar-UA*45  | Acar-UA*46  |
| Acar-UA*49  | Acar-UA*50  |
| Acar-UA*55  | Acar-UA*56  |
| Acar-UA*60  | Acar-UA*61  |
| Acar-UA*63  | Acar-UA*64  |

### Table k. Acar-ST*11

| Acar-UA*107 | Acar-UA*162 |
|-------------|-------------|
| Acar-UA*163 | Acar-UA*165 |
| Acar-UA*166 | Acar-UA*173 |
| Acar-UA*174 | Acar-UA*175 |
| Acar-UA*177 | Acar-UA*178 |
| Acar-UA*181 | Acar-UA*187 |
| Acar-UA*188 | Acar-UA*189 |
| Acar-UA*225 | Acar-UA*226 |
| Acar-UA*32  | Acar-UA*33  |
| Acar-UA*34  | Acar-UA*57  |
| Acar-UA*58  | Acar-UA*75  |
| Acar-UA*99  | Acar-UA*433 |
| Acar-UA*435 | Acar-UA*441 |
| Acar-UA*451 |              |
| l. Acar-ST*12 | m. Acar-ST*13 | n. Acar-ST*14 |
|--------------|---------------|---------------|
| Acar-UA*120  | Acar-UA*100   | Acar-UA*152   |
| Acar-UA*125  | Acar-UA*103   | Acar-UA*288   |
| Acar-UA*235  | Acar-UA*119   | Acar-UA*289   |
| Acar-UA*236  | Acar-UA*145   | Acar-UA*290   |
| Acar-UA*243  | Acar-UA*149   | Acar-UA*292   |
| Acar-UA*269  | Acar-UA*150   | Acar-UA*293   |
| Acar-UA*271  | Acar-UA*160   | Acar-UA*294   |
| Acar-UA*272  | Acar-UA*161   | Acar-UA*296   |
| Acar-UA*307  | Acar-UA*182   | Acar-UA*9     |
| Acar-UA*317  | Acar-UA*183   | Acar-UA*405   |
| Acar-UA*318  | Acar-UA*184   | Acar-UA*415   |
| Acar-UA*319  | Acar-UA*190   | Acar-UA*436   |
| Acar-UA*323  | Acar-UA*191   |               |
| Acar-UA*331  | Acar-UA*192   |               |
| Acar-UA*364  | Acar-UA*247   |               |
| Acar-UA*365  | Acar-UA*264   |               |
| Acar-UA*380  | Acar-UA*35    |               |
| Acar-UA*47   | Acar-UA*36    |               |
| Acar-UA*50   | Acar-UA*85    |               |
| Acar-UA*453  | Acar-UA*90    |               |
| Acar-UA*454  | Acar-UA*97    |               |
| Acar-UA*457  | Acaru-UA*23   |               |
|              | Acar-UA*408   |               |
|              | Acar-UA*413   |               |
|              | Acar-UA*421   |               |
|              | Acar-UA*427   |               |
|              | Acar-UA*434   |               |
Table S9  Number of different alleles, mean Grantham distance, mean amino acid p-distance, and mean Sandberg distance measured between alleles within each MHC-I supertype.

| No. alleles | Mean Grantham distance | Mean a.a. p-distance | Mean Sandberg distance |
|-------------|-------------------------|----------------------|------------------------|
| Acar-ST*1   | 55                      | 9.90                 | 0.128                  | 0.599                  |
| Acar-ST*2   | 32                      | 27.26                | 0.378                  | 1.985                  |
| Acar-ST*3   | 35                      | 12.39                | 0.186                  | 0.806                  |
| Acar-ST*4   | 28                      | 32.44                | 0.405                  | 2.136                  |
| Acar-ST*5   | 36                      | 3.80                 | 0.081                  | 0.263                  |
| Acar-ST*6   | 29                      | 14.67                | 0.190                  | 1.031                  |
| Acar-ST*7   | 18                      | 29.33                | 0.357                  | 1.944                  |
| Acar-ST*8   | 28                      | 27.79                | 0.333                  | 1.831                  |
| Acar-ST*9   | 22                      | 26.95                | 0.290                  | 1.722                  |
| Acar-ST*10  | 19                      | 16.40                | 0.203                  | 1.085                  |
| Acar-ST*11  | 27                      | 29.35                | 0.408                  | 1.959                  |
| Acar-ST*12  | 22                      | 23.07                | 0.266                  | 1.573                  |
| Acar-ST*13  | 27                      | 25.59                | 0.293                  | 1.692                  |
| Acar-ST*14  | 12                      | 0.31                 | 0.012                  | 0.028                  |
Table S10 Pairwise Sandberg distances between MHC-I supertype centroids (upper right matrix) and pairwise overlap between MHC-I supertypes (lower left matrix). The pairwise overlap between supertypes was calculated as the sum of the mean Sandberg distances between the alleles in each supertype (Table S9) minus the Sandberg distance between the supertype centroids.

|       | Acar-ST*1 | Acar-ST*2 | Acar-ST*3 | Acar-ST*4 | Acar-ST*5 | Acar-ST*6 | Acar-ST*7 | Acar-ST*8 | Acar-ST*9 | Acar-ST*10 | Acar-ST*11 | Acar-ST*12 | Acar-ST*13 | Acar-ST*14 |
|-------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Acar-ST*1 | 3.211     | 3.106     | 2.948     | 4.754     | 2.727     | 3.088     | 2.049     | 3.189     | 3.076     | 3.041     | 3.786     | 3.736     | 2.570     |
| Acar-ST*2 | -0.626    | 2.734     | 2.849     | 2.430     | 3.321     | 2.231     | 2.684     | 2.133     | 2.850     | 2.388     | 2.494     | 3.009     | 3.036     |
| Acar-ST*3 | -1.700    | 0.057     | 2.445     | 2.576     | 2.041     | 3.189     | 2.393     | 2.302     | 3.111     | 3.278     | 3.280     | 3.815     | 2.317     |
| Acar-ST*4 | -0.212    | 1.272     | 0.497     | 3.482     | 2.296     | 2.876     | 2.620     | 2.489     | 3.056     | 2.310     | 2.556     | 1.934     | 3.007     |
| Acar-ST*5 | -3.892    | -0.182    | -1.507    | -1.083    | 3.229     | 2.286     | 4.275     | 2.247     | 3.627     | 3.201     | 2.197     | 3.041     | 4.094     |
| Acar-ST*6 | -1.097    | -0.305    | -0.204    | 0.870     | -1.936    | 3.190     | 2.473     | 1.734     | 2.563     | 2.757     | 3.543     | 3.540     | 2.557     |
| Acar-ST*7 | -0.544    | 1.698     | -0.439    | 1.204     | -0.079    | -0.215    | 2.987     | 2.275     | 2.860     | 2.227     | 3.076     | 2.489     | 4.076     |
| Acar-ST*8 | 0.381     | 1.133     | 0.245     | 1.347     | -2.181    | 0.389     | 0.789     | 2.902     | 2.555     | 2.421     | 4.125     | 3.278     | 3.206     |
| Acar-ST*9 | -0.868    | 1.574     | 0.227     | 1.369     | -0.262    | 1.019     | 1.391     | 0.651     | 1.912     | 2.948     | 2.327     | 2.534     | 2.950     |
| Acar-ST*10| -1.391    | 0.220     | -1.220    | 0.165     | -2.280    | -0.448    | 0.169     | 0.362     | 0.894     | 2.482     | 3.622     | 2.351     | 2.908     |
| Acar-ST*11| -0.483    | 1.557     | -0.513    | 1.786     | -0.979    | 0.233     | 1.676     | 1.370     | 0.733     | 0.562     | 3.824     | 2.367     | 3.465     |
| Acar-ST*12| -1.613    | 1.064     | -0.900    | 1.153     | -0.362    | -0.939    | 0.441     | -0.721    | 0.968     | -0.965    | -0.292    | 2.195     | 3.671     |
| Acar-ST*13| -1.444    | 0.668     | -1.317    | 1.894     | -1.086    | -0.817    | 1.147     | 0.245     | 0.880     | 0.426     | 1.285     | 1.069     | 4.036     |
| Acar-ST*14| -1.942    | -1.023    | -1.482    | -0.842    | -3.803    | -1.499    | -2.104    | -1.346    | -1.200    | -1.795    | -1.478    | -2.070    | -2.316    |
Table S11  

| Haplotype | No. ST | Haplotype | No. ST | Haplotype | No. ST | Haplotype | No. ST | Haplotype | No. ST | Haplotype | No. ST |
|-----------|--------|-----------|--------|-----------|--------|-----------|--------|-----------|--------|-----------|--------|
| Acar-HPLT*01 | 9      | Acar-HPLT*28 | 6      | Acar-HPLT*55 | 6      | Acar-HPLT*82 | 3      |
| Acar-HPLT*02 | 8      | Acar-HPLT*29 | 9      | Acar-HPLT*56 | 8      | Acar-HPLT*83 | 6      |
| Acar-HPLT*03 | 6      | Acar-HPLT*30 | 7      | Acar-HPLT*57 | 4      | Acar-HPLT*84 | 13     |
| Acar-HPLT*04 | 7      | Acar-HPLT*31 | 6      | Acar-HPLT*58 | 10     | Acar-HPLT*85 | 6      |
| Acar-HPLT*05 | 4      | Acar-HPLT*32 | 9      | Acar-HPLT*59 | 6      | Acar-HPLT*86 | 8      |
| Acar-HPLT*06 | 10     | Acar-HPLT*33 | 8      | Acar-HPLT*60 | 6      | Acar-HPLT*87 | 5      |
| Acar-HPLT*07 | 7      | Acar-HPLT*34 | 9      | Acar-HPLT*61 | 4      | Acar-HPLT*88 | 9      |
| Acar-HPLT*08 | 5      | Acar-HPLT*35 | 9      | Acar-HPLT*62 | 7      | Acar-HPLT*89 | 7      |
| Acar-HPLT*09 | 6      | Acar-HPLT*36 | 6      | Acar-HPLT*63 | 9      | Acar-HPLT*90 | 8      |
| Acar-HPLT*10 | 5      | Acar-HPLT*37 | 5      | Acar-HPLT*64 | 10     | Acar-HPLT*91 | 8      |
| Acar-HPLT*11 | 6      | Acar-HPLT*38 | 7      | Acar-HPLT*65 | 10     | Acar-HPLT*92 | 9      |
| Acar-HPLT*12 | 9      | Acar-HPLT*39 | 7      | Acar-HPLT*66 | 4      | Acar-HPLT*93 | 7      |
| Acar-HPLT*13 | 5      | Acar-HPLT*40 | 8      | Acar-HPLT*67 | 4      | Acar-HPLT*94 | 7      |
| Acar-HPLT*14 | 6      | Acar-HPLT*41 | 7      | Acar-HPLT*68 | 4      | Acar-HPLT*95 | 10     |
| Acar-HPLT*15 | 10     | Acar-HPLT*42 | 3      | Acar-HPLT*69 | 8      | Acar-HPLT*96 | 7      |
| Acar-HPLT*16 | 8      | Acar-HPLT*43 | 7      | Acar-HPLT*70 | 6      | Acar-HPLT*97 | 7      |
| Acar-HPLT*17 | 6      | Acar-HPLT*44 | 8      | Acar-HPLT*71 | 8      | Acar-HPLT*98 | 5      |
| Acar-HPLT*18 | 6      | Acar-HPLT*45 | 6      | Acar-HPLT*72 | 8      | Acar-HPLT*99 | 8      |
| Acar-HPLT*19 | 8      | Acar-HPLT*46 | 5      | Acar-HPLT*73 | 7      | Acar-HPLT*100 | 7     |
| Acar-HPLT*20 | 5      | Acar-HPLT*47 | 6      | Acar-HPLT*74 | 3      | Acar-HPLT*101 | 7     |
| Acar-HPLT*21 | 6      | Acar-HPLT*48 | 7      | Acar-HPLT*75 | 8      | Acar-HPLT*102 | 8     |
| Acar-HPLT*22 | 7      | Acar-HPLT*49 | 4      | Acar-HPLT*76 | 4      | Acar-HPLT*103 | 7     |
| Acar-HPLT*23 | 6      | Acar-HPLT*50 | 10     | Acar-HPLT*77 | 7      | Acar-HPLT*104 | 5     |
| Acar-HPLT*24 | 6      | Acar-HPLT*51 | 8      | Acar-HPLT*78 | 6      | Acar-HPLT*105 | 7     |
| Acar-HPLT*25 | 8      | Acar-HPLT*52 | 10     | Acar-HPLT*79 | 7      | Acar-HPLT*106 | 10    |
| Acar-HPLT*26 | 6      | Acar-HPLT*53 | 7      | Acar-HPLT*80 | 10     | Acar-HPLT*107 | 8     |
| Acar-HPLT*27 | 7      | Acar-HPLT*54 | 7      | Acar-HPLT*81 | 7      |
| No. haplotypes | Acar-ST*1 | Acar-ST*2 | Acar-ST*3 | Acar-ST*4 | Acar-ST*5 | Acar-ST*6 | Acar-ST*7 | Acar-ST*8 | Acar-ST*9 | Acar-ST*10 | Acar-ST*11 | Acar-ST*12 | Acar-ST*13 | Acar-ST*14 |
|----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
Table S12  Number of alleles from positively selected (pos. sel.) MHC-I supertypes, number of pos. sel. MHC-I supertypes, mean Sandberg distance between centroids of pos. sel. MHC-I supertypes, and mean Sandberg distance overlap between pos. sel. MHC-I supertypes observed in each haplotype.  
Notes:  Haplotypes that harboured fewer than two pos. sel. MHC-I supertypes were assigned NA.  Distance values were calculated based on 14 amino acid codons that showed evidence of positive selection.

|                  | No. alleles pos. sel. STs | No. pos. sel. STs | Mean centroid dist. pos. sel. STs | Mean overlap pos. sel. STs |
|------------------|---------------------------|------------------|----------------------------------|---------------------------|
| Acar-HPLT*01     | 10                        | 6                | 2.77                             | 0.378                     |
| Acar-HPLT*02     | 6                         | 5                | 2.96                             | 0.020                     |
| Acar-HPLT*03     | 4                         | 3                | 2.40                             | 0.763                     |
| Acar-HPLT*04     | 4                         | 4                | 2.97                             | -0.391                    |
| Acar-HPLT*05     | 1                         | 1                | NA                               | NA                        |
| Acar-HPLT*06     | 12                        | 7                | 2.64                             | 0.576                     |
| Acar-HPLT*07     | 4                         | 4                | 2.96                             | 0.159                     |
| Acar-HPLT*08     | 2                         | 2                | 2.53                             | 0.880                     |
| Acar-HPLT*09     | 4                         | 3                | 3.10                             | -0.061                    |
| Acar-HPLT*10     | 2                         | 2                | 4.12                             | -0.721                    |
| Acar-HPLT*11     | 4                         | 3                | 2.83                             | 0.406                     |
| Acar-HPLT*12     | 9                         | 6                | 2.67                             | 0.362                     |
| Acar-HPLT*13     | 2                         | 2                | 3.28                             | 0.245                     |
| Acar-HPLT*14     | 5                         | 3                | 2.83                             | 1.113                     |
| Acar-HPLT*15     | 10                        | 7                | 2.70                             | 0.582                     |
| Acar-HPLT*16     | 6                         | 5                | 2.66                             | 0.233                     |
| Acar-HPLT*17     | 4                         | 3                | 3.32                             | -0.468                    |
| Acar-HPLT*18     | 6                         | 4                | 2.73                             | 0.549                     |
| Acar-HPLT*19     | 7                         | 5                | 2.93                             | 0.318                     |
| Acar-HPLT*20     | 3                         | 2                | 2.99                             | 0.789                     |
| Acar-HPLT*21     | 3                         | 3                | 3.24                             | -0.663                    |
| Acar-HPLT*22     | 4                         | 4                | 2.69                             | 0.374                     |
| Acar-HPLT*23     | 4                         | 3                | 2.50                             | 0.423                     |
| Acar-HPLT*24     | 4                         | 3                | 3.10                             | -0.280                    |
| Acar-HPLT*25     | 7                         | 5                | 3.01                             | 0.118                     |
| Acar-HPLT*26     | 4                         | 3                | 3.35                             | -1.217                    |
| Acar-HPLT*27     | 5                         | 4                | 2.61                             | 0.005                     |
| No. alleles pos. sel. STs | No. pos. sel. STs | Mean centroid dist. pos. sel. STs | Mean overlap pos. sel. STs |
|--------------------------|-------------------|---------------------------------|--------------------------|
| Acar-HPLT*28             | 4                 | 3                               | 2.82                     | 0.495                    |
| Acar-HPLT*29             | 6                 | 6                               | 3.06                     | -0.116                   |
| Acar-HPLT*30             | 4                 | 4                               | 3.17                     | -0.136                   |
| Acar-HPLT*31             | 4                 | 3                               | 3.32                     | -0.468                   |
| Acar-HPLT*32             | 7                 | 6                               | 2.81                     | 0.296                    |
| Acar-HPLT*33             | 5                 | 5                               | 3.08                     | -0.020                   |
| Acar-HPLT*34             | 6                 | 6                               | 2.83                     | 0.478                    |
| Acar-HPLT*35             | 6                 | 6                               | 2.93                     | 0.060                    |
| Acar-HPLT*36             | 7                 | 4                               | 2.99                     | 0.059                    |
| Acar-HPLT*37             | 2                 | 2                               | 3.74                     | -1.444                   |
| Acar-HPLT*38             | 4                 | 4                               | 2.72                     | -0.051                   |
| Acar-HPLT*39             | 5                 | 4                               | 2.66                     | 0.927                    |
| Acar-HPLT*40             | 5                 | 5                               | 3.00                     | -0.147                   |
| Acar-HPLT*41             | 5                 | 4                               | 3.07                     | -0.147                   |
| Acar-HPLT*42             | 1                 | 1                               | NA                       | NA                       |
| Acar-HPLT*43             | 7                 | 4                               | 3.26                     | -0.604                   |
| Acar-HPLT*44             | 5                 | 5                               | 3.04                     | -0.482                   |
| Acar-HPLT*45             | 3                 | 3                               | 2.55                     | -0.315                   |
| Acar-HPLT*46             | 2                 | 2                               | 2.55                     | 0.362                    |
| Acar-HPLT*47             | 5                 | 3                               | 3.35                     | -1.217                   |
| Acar-HPLT*48             | 5                 | 4                               | 2.54                     | 0.743                    |
| Acar-HPLT*49             | 2                 | 1                               | NA                       | NA                       |
| Acar-HPLT*50             | 8                 | 7                               | 2.70                     | 0.582                    |
| Acar-HPLT*51             | 6                 | 5                               | 2.85                     | -0.082                   |
| Acar-HPLT*52             | 8                 | 7                               | 2.79                     | 0.455                    |
| Acar-HPLT*53             | 8                 | 4                               | 3.17                     | -0.477                   |
| Acar-HPLT*54             | 4                 | 4                               | 2.82                     | 0.226                    |
| No. alleles pos. sel. STs | No. pos. sel. STs | Mean centroid dist. pos. sel. STs | Mean overlap pos. sel. STs |
|--------------------------|------------------|----------------------------------|--------------------------|
| Acar-HPLT*55             | 6                | 2.65                             | 0.296                    |
| Acar-HPLT*56             | 7                | 2.85                             | -0.082                   |
| Acar-HPLT*57             | 1                | NA                               | NA                       |
| Acar-HPLT*58             | 9                | 2.80                             | 0.106                    |
| Acar-HPLT*59             | 3                | 3.09                             | -0.676                   |
| Acar-HPLT*60             | 3                | 2.72                             | 0.177                    |
| Acar-HPLT*61             | 1                | NA                               | NA                       |
| Acar-HPLT*62             | 4                | 2.86                             | 0.141                    |
| Acar-HPLT*63             | 10               | 2.83                             | 0.119                    |
| Acar-HPLT*64             | 8                | 2.87                             | 0.125                    |
| Acar-HPLT*65             | 10               | 2.80                             | 0.424                    |
| Acar-HPLT*66             | 1                | NA                               | NA                       |
| Acar-HPLT*67             | 1                | NA                               | NA                       |
| Acar-HPLT*68             | 1                | NA                               | NA                       |
| Acar-HPLT*69             | 6                | 2.96                             | 0.020                    |
| Acar-HPLT*70             | 3                | 2.57                             | 1.119                    |
| Acar-HPLT*71             | 8                | 2.84                             | 0.506                    |
| Acar-HPLT*72             | 5                | 2.65                             | 0.752                    |
| Acar-HPLT*73             | 6                | 2.69                             | 1.125                    |
| Acar-HPLT*74             | 0                | NA                               | NA                       |
| Acar-HPLT*75             | 5                | 3.01                             | 0.118                    |
| Acar-HPLT*76             | 2                | NA                               | NA                       |
| Acar-HPLT*77             | 5                | 2.91                             | -0.120                   |
| Acar-HPLT*78             | 4                | 3.17                             | -0.136                   |
| Acar-HPLT*79             | 5                | 2.51                             | 0.079                    |
| Acar-HPLT*80             | 8                | 2.70                             | 0.582                    |
| Acar-HPLT*81             | 5                | 3.25                             | -0.807                   |
| Allele              | No. alleles | No. pos. sel. | Mean centroid dist. | Mean overlap pos. sel. |
|---------------------|-------------|---------------|---------------------|-----------------------|
| Acar-HPLT*82        | 0           | 0             | NA                  | NA                    |
| Acar-HPLT*83        | 3           | 3             | 3.15                | -0.477                |
| Acar-HPLT*84        | 18          | 10            | 2.85                | 0.321                 |
| Acar-HPLT*85        | 4           | 3             | 3.00                | -0.619                |
| Acar-HPLT*86        | 6           | 6             | 2.96                | 0.097                 |
| Acar-HPLT*87        | 2           | 2             | 2.53                | 0.880                 |
| Acar-HPLT*88        | 8           | 6             | 2.89                | -0.111                |
| Acar-HPLT*89        | 8           | 4             | 2.79                | 0.509                 |
| Acar-HPLT*90        | 6           | 5             | 2.75                | 0.610                 |
| Acar-HPLT*91        | 6           | 5             | 2.93                | -0.092                |
| Acar-HPLT*92        | 8           | 6             | 3.07                | -0.413                |
| Acar-HPLT*93        | 6           | 5             | 2.93                | 0.318                 |
| Acar-HPLT*94        | 6           | 5             | 2.93                | -0.114                |
| Acar-HPLT*95        | 9           | 7             | 2.93                | -0.055                |
| Acar-HPLT*96        | 5           | 4             | 2.76                | 0.369                 |
| Acar-HPLT*97        | 5           | 5             | 3.04                | -0.482                |
| Acar-HPLT*98        | 2           | 2             | 1.73                | 1.019                 |
| Acar-HPLT*99        | 7           | 5             | 3.16                | -0.404                |
| Acar-HPLT*100       | 6           | 4             | 2.93                | -0.273                |
| Acar-HPLT*101       | 5           | 4             | 2.63                | 0.555                 |
| Acar-HPLT*102       | 6           | 5             | 2.95                | -0.003                |
| Acar-HPLT*103       | 4           | 4             | 3.00                | -0.095                |
| Acar-HPLT*104       | 3           | 2             | 2.05                | 0.381                 |
| Acar-HPLT*105       | 4           | 4             | 3.04                | -0.358                |
| Acar-HPLT*106       | 7           | 7             | 2.93                | -0.055                |
| Acar-HPLT*107       | 6           | 5             | 2.78                | 0.300                 |
Haplotype tables

Unique haplotypes in our data set with the proportion of unresolved allele assignments on each haplotype. The tables show the alleles found on each haplotype, with specification of allele assignment status (1 = unresolved allele assignment, 0 = definite allele assignment).

### Acar-HPLT*01

| Allele     | Unresolved |
|------------|------------|
| Acar-UA*4  | 0          |
| Acar-UA*8  | 0          |
| Acar-UA*9  | 1          |
| Acar-UA*12 | 0          |
| Acar-UA*33 | 0          |
| Acar-UA*55 | 0          |
| Acar-UA*74 | 0          |
| Acar-UA*95 | 0          |
| Acar-UA*122| 0          |
| Acar-UA*144| 0          |
| Acar-UA*145| 0          |
| Acar-UA*163| 0          |
| Acar-UA*192| 0          |
| Acar-UA*391| 0          |

| Prop. unresolved alleles | 0.071429 |

### Acar-HPLT*02

| Allele     | Unresolved |
|------------|------------|
| Acar-UA*9  | 1          |
| Acar-UA*48 | 0          |
| Acar-UA*55 | 0          |
| Acar-UA*82 | 0          |
| Acar-UA*126| 0          |
| Acar-UA*145| 0          |
| Acar-UA*157| 0          |
| Acar-UA*241| 0          |
| Acar-UA*330| 0          |

| Prop. unresolved alleles | 0.111111 |

### Acar-HPLT*03

| Allele     | Unresolved |
|------------|------------|
| Acar-UA*9  | 1          |
| Acar-UA*54 | 0          |
| Acar-UA*130| 0          |
| Acar-UA*133| 0          |
| Acar-UA*153| 0          |
| Acar-UA*157| 0          |
| Acar-UA*201| 0          |
| Acar-UA*223| 0          |
| Acar-UA*239| 0          |
| Acar-UA*296| 0          |

| Prop. unresolved alleles | 0.1      |
| Allele       | Acar-HPLT*04 Prop. unresolved alleles | Acar-HPLT*05 Prop. unresolved alleles | Acar-HPLT*06 Prop. unresolved alleles | Acar-HPLT*07 Prop. unresolved alleles |
|--------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|
|              | 0.142857                              | 0                                     | 0.2                                   | 0.125                                 |
| Acar-UA*4    | 0                                     | 0                                     | 1                                     | 0                                     |
| Acar-UA*9    | 0                                     | 0                                     | 1                                     | 1                                     |
| Acar-UA*11   | 0                                     | 0                                     | 0                                     | 0                                     |
| Acar-UA*55   | 1                                     | 0                                     | 1                                     | 0                                     |
| Acar-UA*69   | 0                                     | 0                                     | 0                                     | 0                                     |
| Acar-UA*157  | 0                                     | 0                                     | 0                                     | 0                                     |
| Acar-UA*247  | 0                                     | 0                                     | 0                                     | 0                                     |

The table above shows the allele frequencies for different HLA alleles under the test conditions specified.
| Allele   | Prop. unresolved alleles | Unresolved |
|----------|--------------------------|------------|
| Acar-HPLT*08 | 0.2                      | Unresolved |
| Acar-UA*4  | 0                        |            |
| Acar-UA*9  | 1                        |            |
| Acaru-UA*23 | 0                        |            |
| Acar-UA*55 | 0                        |            |
| Acar-UA*285 | 0                       |            |

| Allele   | Prop. unresolved alleles | Unresolved |
|----------|--------------------------|------------|
| Acar-HPLT*09 | 0.285714                 | Unresolved |
| Acar-UA*4  | 0                        |            |
| Acar-UA*9  | 1                        |            |
| Acar-UA*35 | 0                        |            |
| Acar-UA*55 | 1                        |            |
| Acar-UA*66 | 0                        |            |
| Acar-UA*192 | 0                       |            |
| Acar-UA*265 | 0                       |            |

| Allele   | Prop. unresolved alleles | Unresolved |
|----------|--------------------------|------------|
| Acar-HPLT*10 | 0.4                    | Unresolved |
| Acar-UA*4  | 0                        |            |
| Acar-UA*9  | 1                        |            |
| Acar-UA*31 | 0                        |            |
| Acar-UA*47 | 0                        |            |
| Acar-UA*55 | 1                        |            |

| Allele   | Prop. unresolved alleles | Unresolved |
|----------|--------------------------|------------|
| Acar-HPLT*11 | 0.25                   | Unresolved |
| Acar-UA*9  | 1                        |            |
| Acar-UA*31 | 0                        |            |
| Acar-UA*55 | 1                        |            |
| Acar-UA*78 | 0                        |            |
| Acar-UA*208 | 0                       |            |
| Acar-UA*265 | 0                       |            |
| Acar-UA*357 | 0                       |            |
| Acar-UA*397 | 0                       |            |
| Allele       | Unresolved | Prop. unresolved alleles |
|--------------|------------|--------------------------|
| Acar-HPLT*12 |            | 0.076923                 |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*11   | 0          |                          |
| Acar-UA*12   | 0          |                          |
| Acar-UA*55   | 0          |                          |
| Acar-UA*62   | 0          |                          |
| Acar-UA*173  | 0          |                          |
| Acar-UA*214  | 0          |                          |
| Acar-UA*233  | 0          |                          |
| Acar-UA*279  | 0          |                          |
| Acar-UA*328  | 0          |                          |
| Acar-UA*336  | 0          |                          |
| Acar-UA*419  | 0          |                          |

| Allele       | Unresolved | Prop. unresolved alleles |
|--------------|------------|--------------------------|
| Acar-HPLT*13 |            | 0.333333                 |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*31   | 0          |                          |
| Acar-UA*36   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*144  | 0          |                          |

| Allele       | Unresolved | Prop. unresolved alleles |
|--------------|------------|--------------------------|
| Acar-HPLT*14 |            | 0.111111                 |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*59   | 0          |                          |
| Acar-UA*65   | 0          |                          |
| Acar-UA*143  | 0          |                          |
| Acar-UA*144  | 0          |                          |
| Acar-UA*155  | 0          |                          |
| Acar-UA*255  | 0          |                          |
| Allele       | Unresolved |
|--------------|------------|
| Acar-UA*9    | 1          |
| Acar-UA*51   | 0          |
| Acar-UA*52   | 0          |
| Acar-UA*55   | 0          |
| Acar-UA*107  | 0          |
| Acar-UA*110  | 0          |
| Acar-UA*143  | 0          |
| Acar-UA*144  | 0          |
| Acar-UA*186  | 0          |
| Acar-UA*231  | 0          |
| Acar-UA*255  | 0          |
| Acar-UA*304  | 0          |
| Acar-UA*368  | 0          |
| Acar-UA*392  | 0          |

| Allele       | Unresolved |
|--------------|------------|
| Acar-UA*9    | 0          |
| Acar-UA*37   | 0          |
| Acar-UA*55   | 0          |
| Acar-UA*60   | 0          |
| Acar-UA*94   | 0          |
| Acar-UA*144  | 0          |
| Acar-UA*224  | 0          |
| Acar-UA*250  | 0          |
| Acar-UA*349  | 0          |
| Acar-UA*350  | 0          |

| Allele       | Unresolved |
|--------------|------------|
| Acar-UA*4    | 0          |
| Acar-UA*9    | 1          |
| Acar-UA*12   | 0          |
| Acar-UA*55   | 1          |
| Acar-UA*191  | 0          |
| Acar-UA*304  | 0          |
| Acar-UA*363  | 0          |
| Allele          | Unresolved | Prop. unresolved alleles |
|-----------------|------------|--------------------------|
| **Acar-HPLT*18** |            | 0.444444                 |
| Acar-UA*9       | 1          |                          |
| Acar-UA*12      | 0          |                          |
| Acar-UA*31      | 1          |                          |
| Acar-UA*48      | 0          |                          |
| Acar-UA*55      | 1          |                          |
| Acar-UA*86      | 0          |                          |
| Acar-UA*122     | 0          |                          |
| Acar-UA*144     | 1          |                          |
| Acar-UA*330     | 0          |                          |
| **Acar-HPLT*19** |            | 0.166667                 |
| Acar-UA*9       | 1          |                          |
| Acar-UA*12      | 0          |                          |
| Acar-UA*55      | 1          |                          |
| Acar-UA*79      | 0          |                          |
| Acar-UA*122     | 0          |                          |
| Acar-UA*125     | 0          |                          |
| Acar-UA*133     | 0          |                          |
| Acar-UA*201     | 0          |                          |
| Acar-UA*276     | 0          |                          |
| Acar-UA*296     | 0          |                          |
| Acar-UA*340     | 0          |                          |
| Acar-UA*348     | 0          |                          |
| **Acar-HPLT*20** |            | 0.285714                 |
| Acar-UA*4       | 1          |                          |
| Acar-UA*9       | 1          |                          |
| Acar-UA*30      | 0          |                          |
| Acar-UA*39      | 0          |                          |
| Acar-UA*54      | 0          |                          |
| Acar-UA*61      | 0          |                          |
| Acar-UA*144     | 0          |                          |
| **Acar-HPLT*21** |            | 0.125                    |
| Acar-UA*4       | 0          |                          |
| Acar-UA*9       | 1          |                          |
| Acar-UA*12      | 0          |                          |
| Acar-UA*136     | 0          |                          |
| Acar-UA*144     | 0          |                          |
| Acar-UA*191     | 0          |                          |
| Acar-UA*241     | 0          |                          |
| Acar-UA*364     | 0          |                          |
| Allele          | Unresolved | Acar-HPLT*22 | Prop. unresolved alleles |
|----------------|------------|--------------|--------------------------|
| Acar-UA*4      | 0          |              |                          |
| Acar-UA*9      | 1          |              |                          |
| Acar-UA*12     | 0          |              |                          |
| Acar-UA*55     | 1          |              |                          |
| Acar-UA*77     | 0          |              |                          |
| Acar-UA*144    | 0          |              |                          |
| Acar-UA*223    | 0          |              |                          |
| Acar-UA*238    | 0          |              |                          |

| Allele          | Unresolved | Acar-HPLT*23 | Prop. unresolved alleles |
|----------------|------------|--------------|--------------------------|
| Acar-UA*4      | 0          |              |                          |
| Acar-UA*9      | 1          |              |                          |
| Acar-UA*48     | 0          |              |                          |
| Acar-UA*55     | 1          |              |                          |
| Acar-UA*62     | 0          |              |                          |
| Acar-UA*144    | 1          |              |                          |
| Acar-UA*152    | 0          |              |                          |
| Acar-UA*177    | 0          |              |                          |
| Acar-UA*188    | 0          |              |                          |

| Allele          | Unresolved | Acar-HPLT*24 | Prop. unresolved alleles |
|----------------|------------|--------------|--------------------------|
| Acar-UA*9      | 1          |              |                          |
| Acar-UA*41     | 0          |              |                          |
| Acar-UA*55     | 1          |              |                          |
| Acar-UA*103    | 0          |              |                          |
| Acar-UA*144    | 0          |              |                          |
| Acar-UA*192    | 0          |              |                          |
| Acar-UA*200    | 0          |              |                          |
| Acar-UA*342    | 0          |              |                          |

| Allele          | Unresolved | Acar-HPLT*25 | Prop. unresolved alleles |
|----------------|------------|--------------|--------------------------|
| Acar-UA*4      | 0          |              |                          |
| Acar-UA*8      | 0          |              |                          |
| Acar-UA*9      | 0          |              |                          |
| Acar-UA*12     | 0          |              |                          |
| Acar-UA*48     | 0          |              |                          |
| Acar-UA*55     | 1          |              |                          |
| Acar-UA*58     | 0          |              |                          |
| Acar-UA*144    | 0          |              |                          |
| Acar-UA*145    | 0          |              |                          |
| Acar-UA*236    | 0          |              |                          |
| Acar-UA*304    | 0          |              |                          |
| Allele   | Unresolved | Prop. unresolved alleles |
|----------|------------|--------------------------|
| Acar-HPLT*26 |            | 0.125                    |
| Acar-UA*9     | 1          |                          |
| Acar-UA*12    | 0          |                          |
| Acar-UA*47    | 0          |                          |
| Acar-UA*137   | 0          |                          |
| Acar-UA*144   | 0          |                          |
| Acar-UA*208   | 0          |                          |
| Acar-UA*279   | 0          |                          |
| Acar-UA*280   | 0          |                          |
| Acar-HPLT*27  |            | 0.111111                 |
| Acar-UA*4     | 0          |                          |
| Acar-UA*9     | 1          |                          |
| Acar-UA*31    | 0          |                          |
| Acar-UA*42    | 0          |                          |
| Acar-UA*55    | 0          |                          |
| Acar-UA*94    | 0          |                          |
| Acar-UA*129   | 0          |                          |
| Acar-UA*332   | 0          |                          |
| Acar-UA*349   | 0          |                          |
| Acar-HPLT*28  |            | 0.125                    |
| Acar-UA*32    | 0          |                          |
| Acar-UA*55    | 1          |                          |
| Acar-UA*144   | 0          |                          |
| Acar-UA*166   | 0          |                          |
| Acar-UA*224   | 0          |                          |
| Acar-UA*229   | 0          |                          |
| Acar-UA*290   | 0          |                          |
| Acar-UA*378   | 0          |                          |
| Acar-HPLT*29  |            | 0                        |
| Acar-UA*9     | 0          |                          |
| Acar-UA*48    | 0          |                          |
| Acar-UA*55    | 0          |                          |
| Acar-UA*97    | 0          |                          |
| Acar-UA*144   | 0          |                          |
| Acar-UA*188   | 0          |                          |
| Acar-UA*208   | 0          |                          |
| Acar-UA*229   | 0          |                          |
| Acar-UA*236   | 0          |                          |
| Acar-UA*304   | 0          |                          |
| Allele   | Unresolved | Prop. unresolved alleles |
|----------|------------|--------------------------|
| Acar-HPLT*30 | 0          | 0                        |
| Acar-UA*9   | 0          |                          |
| Acar-UA*12  | 0          |                          |
| Acar-UA*50  | 0          |                          |
| Acar-UA*55  | 0          |                          |
| Acar-UA*181 | 0          |                          |
| Acar-UA*208 | 0          |                          |
| Acar-UA*373 | 0          |                          |

| Allele   | Unresolved | Prop. unresolved alleles |
|----------|------------|--------------------------|
| Acar-HPLT*31 | 0.333333  |                          |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*123 | 0          |                          |
| Acar-UA*144 | 1          |                          |
| Acar-UA*149 | 0          |                          |
| Acar-UA*183 | 0          |                          |
| Acar-UA*196 | 0          |                          |
| Acar-UA*401 | 0          |                          |

| Allele   | Unresolved | Prop. unresolved alleles |
|----------|------------|--------------------------|
| Acar-HPLT*32 | 0.363636  |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*31  | 1          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*77  | 0          |                          |
| Acar-UA*82  | 0          |                          |
| Acar-UA*91  | 0          |                          |
| Acar-UA*144 | 1          |                          |
| Acar-UA*183 | 0          |                          |
| Acar-UA*196 | 0          |                          |
| Acar-UA*204 | 0          |                          |
| Acar-UA*349 | 0          |                          |

| Allele   | Unresolved | Prop. unresolved alleles |
|----------|------------|--------------------------|
| Acar-HPLT*33 | 0.125     |                          |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*12  | 0          |                          |
| Acar-UA*30  | 0          |                          |
| Acar-UA*33  | 0          |                          |
| Acar-UA*55  | 0          |                          |
| Acar-UA*145 | 0          |                          |
| Acar-UA*235 | 0          |                          |
| Allele          | Unresolved | Prop. unresolved alleles |
|-----------------|------------|--------------------------|
| Acar-HPLT*34    |            |                          |
| Acar-UA*4       | 0          |                          |
| Acar-UA*9       | 1          |                          |
| Acar-UA*43      | 0          |                          |
| Acar-UA*48      | 0          |                          |
| Acar-UA*55      | 0          |                          |
| Acar-UA*190     | 0          |                          |
| Acar-UA*236     | 0          |                          |
| Acar-UA*304     | 0          |                          |
| Acar-UA*367     | 0          |                          |
| Acar-HPLT*35    |            |                          |
| Acar-UA*4       | 1          |                          |
| Acar-UA*9       | 1          |                          |
| Acar-UA*40      | 0          |                          |
| Acar-UA*55      | 1          |                          |
| Acar-UA*144     | 0          |                          |
| Acar-UA*191     | 0          |                          |
| Acar-UA*281     | 0          |                          |
| Acar-UA*290     | 0          |                          |
| Acar-UA*310     | 0          |                          |
| Acar-UA*380     | 0          |                          |
| Acar-UA*384     | 0          |                          |
| Acar-HPLT*36    |            |                          |
| Acar-UA*9       | 1          |                          |
| Acar-UA*31      | 0          |                          |
| Acar-UA*48      | 0          |                          |
| Acar-UA*122     | 0          |                          |
| Acar-UA*123     | 0          |                          |
| Acar-UA*145     | 0          |                          |
| Acar-UA*217     | 0          |                          |
| Acar-UA*241     | 0          |                          |
| Acar-UA*306     | 0          |                          |
| Acar-UA*325     | 0          |                          |
| Acar-HPLT*37    |            |                          |
| Acar-UA*9       | 1          |                          |
| Acar-UA*11      | 0          |                          |
| Acar-UA*55      | 1          |                          |
| Acar-UA*144     | 0          |                          |
| Acar-UA*183     | 0          |                          |
| Allele       | Unresolved | Prop. unresolved alleles |
|--------------|------------|--------------------------|
| Acar-HPLT*38 |            | 0.5                      |
| Acar-UA*4    | 1          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*12   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*144  | 1          |                          |
| Acar-UA*223  | 0          |                          |
| Acar-UA*270  | 0          |                          |
| Acar-UA*279  | 0          |                          |
| Acar-UA*38   |            |                          |
| Acar-UA*4    | 1          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*12   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*144  | 1          |                          |
| Acar-UA*146  | 0          |                          |
| Acar-UA*223  | 0          |                          |
| Acar-HPLT*39 |            | 0.444444                 |
| Acar-UA*4    | 1          |                          |
| Acar-UA*8    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*73   | 0          |                          |
| Acar-UA*144  | 1          |                          |
| Acar-UA*156  | 0          |                          |
| Acar-UA*175  | 0          |                          |
| Acar-UA*225  | 0          |                          |
| Acar-HPLT*40 |            | 0.333333                 |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acaru-UA*23  | 0          |                          |
| Acar-UA*31   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*144  | 1          |                          |
| Acar-UA*146  | 0          |                          |
| Acar-UA*277  | 0          |                          |
| Acar-UA*322  | 0          |                          |
| Acar-HPLT*41 |            | 0.25                     |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*12   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*122  | 0          |                          |
| Acar-UA*190  | 0          |                          |
| Acar-UA*192  | 0          |                          |
| Acar-UA*235  | 0          |                          |
| Allele       | Unresolved | Prop. unresolved alleles |
|--------------|------------|--------------------------|
| Acar-HPLT*42 | 0          | 0                        |
| Acar-UA*137  | 0          |                          |
| Acar-UA*144  | 0          |                          |
| Acar-UA*187  | 0          |                          |
| Acar-UA*208  | 0          |                          |
| Acar-HPLT*43 | 0.090909   |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*48   | 0          |                          |
| Acar-UA*55   | 0          |                          |
| Acar-UA*122  | 0          |                          |
| Acar-UA*144  | 0          |                          |
| Acar-UA*164  | 0          |                          |
| Acar-UA*208  | 0          |                          |
| Acar-UA*229  | 0          |                          |
| Acar-UA*304  | 0          |                          |
| Acar-UA*330  | 0          |                          |
| Acar-UA*408  | 0          |                          |
| Acar-HPLT*44 | 0.111111   |                          |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*55   | 0          |                          |
| Acar-UA*128  | 0          |                          |
| Acar-UA*144  | 0          |                          |
| Acar-UA*191  | 0          |                          |
| Acar-UA*337  | 0          |                          |
| Acar-UA*371  | 0          |                          |
| Acar-UA*410  | 0          |                          |
| Acar-HPLT*45 | 0.166667   |                          |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*44   | 0          |                          |
| Acar-UA*45   | 0          |                          |
| Acar-UA*55   | 0          |                          |
| Acar-UA*347  | 0          |                          |
| Allele     | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| Acar-HPLT*46 |            | 0.333333                 |
| Acar-UA*4   | 1          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*31  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*73  | 0          |                          |
| Acar-UA*114 | 0          |                          |
| Acar-UA*115 | 0          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*159 | 0          |                          |
| Acar-HPLT*47 |            | 0.1                      |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 0          |                          |
| Acar-UA*12  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*208 | 0          |                          |
| Acar-UA*279 | 0          |                          |
| Acar-UA*280 | 0          |                          |
| Acar-UA*318 | 0          |                          |
| Acar-UA*326 | 0          |                          |
| Acar-HPLT*48 |            | 0                        |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 0          |                          |
| Acar-UA*31  | 0          |                          |
| Acar-UA*55  | 0          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*153 | 0          |                          |
| Acar-UA*157 | 0          |                          |
| Acar-UA*223 | 0          |                          |
| Acar-UA*239 | 0          |                          |
| Acar-HPLT*49 |            | 0.333333                 |
| Acar-UA*6   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*33  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*187 | 0          |                          |
### Acar-HPLT*50

| Allele         | Unresolved |
|----------------|------------|
| Acar-UA*9      | 1          |
| Acar-UA*12     | 0          |
| Acar-UA*41     | 0          |
| Acar-UA*55     | 0          |
| Acar-UA*107    | 0          |
| Acar-UA*143    | 0          |
| Acar-UA*144    | 0          |
| Acar-UA*186    | 0          |
| Acar-UA*231    | 0          |
| Acar-UA*255    | 0          |
| Acar-UA*277    | 0          |
| Acar-UA*368    | 0          |

Prop. unresolved alleles: 0.083333

### Acar-HPLT*51

| Allele         | Unresolved |
|----------------|------------|
| Acar-UA*4      | 1          |
| Acar-UA*12     | 0          |
| Acar-UA*50     | 0          |
| Acar-UA*54     | 0          |
| Acar-UA*55     | 1          |
| Acar-UA*128    | 0          |
| Acar-UA*144    | 0          |
| Acar-UA*250    | 0          |
| Acar-UA*288    | 0          |
| Acar-UA*304    | 0          |
| Acar-UA*351    | 0          |

Prop. unresolved alleles: 0.181818

### Acar-HPLT*52

| Allele         | Unresolved |
|----------------|------------|
| Acar-UA*4      | 1          |
| Acar-UA*9      | 1          |
| Acar-UA*49     | 0          |
| Acar-UA*55     | 1          |
| Acar-UA*81     | 0          |
| Acar-UA*122    | 0          |
| Acar-UA*128    | 0          |
| Acar-UA*144    | 1          |
| Acar-UA*147    | 0          |
| Acar-UA*160    | 0          |
| Acar-UA*187    | 0          |
| Acar-UA*229    | 0          |

Prop. unresolved alleles: 0.333333
| Allele     | Acar-HPLT*53 | Unresolved | Pro. unresolved alleles |
|------------|--------------|------------|-------------------------|
| Acar-UA*4  |              | 0          |                         |
| Acar-UA*9  |              | 1          |                         |
| Acar-UA*11 |              | 0          |                         |
| Acar-UA*12 |              | 0          |                         |
| Acar-UA*48 |              | 0          |                         |
| Acar-UA*50 |              | 0          |                         |
| Acar-UA*53 |              | 0          |                         |
| Acar-UA*55 |              | 1          |                         |
| Acar-UA*91 |              | 0          |                         |
| Acar-UA*241|              | 0          |                         |
| Acar-UA*330|              | 0          |                         |
| Acar-UA*336|              | 0          |                         |
|            | Acar-HPLT*54 |            |                         |
| Acar-UA*4  |              | 1          | 0.375                   |
| Acar-UA*9  |              | 1          |                         |
| Acar-UA*30 |              | 0          |                         |
| Acar-UA*48 |              | 0          |                         |
| Acar-UA*55 |              | 1          |                         |
| Acar-UA*57 |              | 0          |                         |
| Acar-UA*144|              | 0          |                         |
| Acar-UA*145|              | 0          |                         |
|            | Acar-HPLT*55 |            |                         |
| Acar-UA*4  |              | 0          | 0.2                     |
| Acar-UA*9  |              | 1          |                         |
| Acar-UA*31 |              | 1          |                         |
| Acar-UA*48 |              | 0          |                         |
| Acar-UA*55 |              | 0          |                         |
| Acar-UA*122|              | 0          |                         |
| Acar-UA*144|              | 0          |                         |
| Acar-UA*164|              | 0          |                         |
| Acar-UA*304|              | 0          |                         |
| Acar-UA*330|              | 0          |                         |
| Allele     | Prop. unresolved alleles | Unresolved |
|------------|--------------------------|------------|
| Acar-HPLT*56 | 0.090909                |            |
| Acar-UA*4   | 0                        |            |
| Acar-UA*12  | 0                        |            |
| Acar-UA*48  | 0                        |            |
| Acar-UA*50  | 0                        |            |
| Acar-UA*54  | 0                        |            |
| Acar-UA*128 | 0                        |            |
| Acar-UA*144 | 1                        |            |
| Acar-UA*250 | 0                        |            |
| Acar-UA*288 | 0                        |            |
| Acar-UA*304 | 0                        |            |
| Acar-UA*351 | 0                        |            |
| Acar-HPLT*57 | 0                        |            |
| Acar-UA*4   | 0                        |            |
| Acar-UA*9   | 0                        |            |
| Acar-UA*55  | 0                        |            |
| Acar-UA*144 | 0                        |            |
| Acar-UA*158 | 0                        |            |
| Acar-UA*368 | 0                        |            |
| Acar-HPLT*58 | 0.230769                |            |
| Acar-UA*4   | 1                        |            |
| Acar-UA*9   | 1                        |            |
| Acar-UA*12  | 0                        |            |
| Acar-UA*30  | 0                        |            |
| Acar-UA*55  | 1                        |            |
| Acar-UA*57  | 0                        |            |
| Acar-UA*91  | 0                        |            |
| Acar-UA*144 | 0                        |            |
| Acar-UA*274 | 0                        |            |
| Acar-UA*282 | 0                        |            |
| Acar-UA*303 | 0                        |            |
| Acar-UA*421 | 0                        |            |
| Acar-UA*424 | 0                        |            |
| Acar-HPLT*59 | 0.428571                |            |
| Acar-UA*4   | 1                        |            |
| Acar-UA*9   | 1                        |            |
| Acar-UA*12  | 0                        |            |
| Acaru-UA*23 | 0                        |            |
| Acar-UA*55  | 1                        |            |
| Acar-UA*122 | 0                        |            |
| Acar-UA*277 | 0                        |            |
| Allele     | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| Acar-HPLT*60 |            | 0.166667                 |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*55  | 0          |                          |
| Acar-UA*94  | 0          |                          |
| Acar-UA*119 | 0          |                          |
| Acar-UA*271 | 0          |                          |
| Acar-HPLT*61 |            | 0.2                      |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*55  | 0          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*200 | 0          |                          |
| Acar-HPLT*62 |            | 0.375                    |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*50  | 0          |                          |
| Acar-UA*53  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*144 | 1          |                          |
| Acar-UA*184 | 0          |                          |
| Acar-UA*308 | 0          |                          |
| Acar-HPLT*63 |            | 0.2                      |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*12  | 0          |                          |
| Acar-UA*30  | 0          |                          |
| Acar-UA*31  | 0          |                          |
| Acar-UA*31  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*122 | 0          |                          |
| Acar-UA*144 | 1          |                          |
| Acar-UA*145 | 0          |                          |
| Acar-UA*157 | 0          |                          |
| Acar-UA*208 | 0          |                          |
| Acar-UA*240 | 0          |                          |
| Acar-UA*278 | 0          |                          |
| Acar-UA*315 | 0          |                          |
| Acar-UA*327 | 0          |                          |
| Allele       | Unresolved | Prop. unresolved alleles |
|--------------|------------|--------------------------|
| Acar-HPLT*64 |             |                          |
| Acar-UA*4    | 1          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*40   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*128  | 0          |                          |
| Acar-UA*144  | 1          |                          |
| Acar-UA*160  | 0          |                          |
| Acar-UA*304  | 0          |                          |
| Acar-UA*342  | 0          |                          |
| Acar-UA*384  | 0          |                          |
| Acar-UA*406  | 0          |                          |
| Acar-UA*422  | 0          |                          |
| Acar-HPLT*65 |             | 0.266667                 |
| Acar-UA*4    | 1          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*12   | 0          |                          |
| Acar-UA*48   | 0          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*72   | 0          |                          |
| Acar-UA*91   | 0          |                          |
| Acar-UA*122  | 0          |                          |
| Acar-UA*144  | 1          |                          |
| Acar-UA*145  | 0          |                          |
| Acar-UA*148  | 0          |                          |
| Acar-UA*268  | 0          |                          |
| Acar-UA*304  | 0          |                          |
| Acar-UA*336  | 0          |                          |
| Acar-UA*384  | 0          |                          |
| Acar-HPLT*66 |             | 0.333333                 |
| Acar-UA*9    | 1          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*124  | 0          |                          |
| Acar-UA*138  | 0          |                          |
| Acar-UA*144  | 0          |                          |
| Acar-UA*208  | 0          |                          |
| Acar-HPLT*67 |             | 0.4                      |
| Acar-UA*4    | 0          |                          |
| Acar-UA*9    | 1          |                          |
| Acar-UA*55   | 1          |                          |
| Acar-UA*144  | 0          |                          |
| Acar-UA*187  | 0          |                          |
| Allele        | Unresolved | Acar-HPLT*68 | Prop. unresolved alleles |
|--------------|------------|--------------|--------------------------|
| Acar-UA*4    | 1          |              |                          |
| Acar-UA*9    | 1          |              |                          |
| Acar-UA*55   | 1          |              |                          |
| Acar-UA*365  | 0          |              |                          |
| Acar-HPLT*68 |            | Prop. unresolved alleles | 0.75                    |
| Acar-UA*4    | 0          |              |                          |
| Acar-UA*9    | 1          |              |                          |
| Acar-UA*48   | 0          |              |                          |
| Acar-UA*55   | 1          |              |                          |
| Acar-UA*82   | 0          |              |                          |
| Acar-UA*126  | 0          |              |                          |
| Acar-UA*145  | 0          |              |                          |
| Acar-UA*157  | 0          |              |                          |
| Acar-UA*241  | 0          |              |                          |
| Acar-UA*330  | 0          |              |                          |

| Allele        | Unresolved | Acar-HPLT*69 | Prop. unresolved alleles |
|--------------|------------|--------------|--------------------------|
| Acar-UA*4    | 0          |              |                          |
| Acar-UA*9    | 1          |              |                          |
| Acar-UA*48   | 0          |              |                          |
| Acar-UA*55   | 1          |              |                          |
| Acar-UA*126  | 0          |              |                          |
| Acar-UA*145  | 0          |              |                          |
| Acar-UA*157  | 0          |              |                          |
| Acar-UA*241  | 0          |              |                          |
| Acar-UA*330  | 0          |              |                          |

| Allele        | Unresolved | Acar-HPLT*70 | Prop. unresolved alleles |
|--------------|------------|--------------|--------------------------|
| Acar-UA*4    | 0          |              |                          |
| Acar-UA*9    | 1          |              |                          |
| Acar-UA*31   | 0          |              |                          |
| Acar-UA*55   | 1          |              |                          |
| Acar-UA*144  | 1          |              |                          |
| Acar-UA*260  | 0          |              |                          |
| Acar-UA*304  | 1          |              |                          |

| Allele        | Unresolved | Acar-HPLT*71 | Prop. unresolved alleles |
|--------------|------------|--------------|--------------------------|
| Acar-UA*4    | 0          |              |                          |
| Acar-UA*9    | 1          |              |                          |
| Acar-UA*12   | 0          |              |                          |
| Acar-UA*55   | 1          |              |                          |
| Acar-UA*82   | 0          |              |                          |
| Acar-UA*122  | 0          |              |                          |
| Acar-UA*144  | 1          |              |                          |
| Acar-UA*147  | 0          |              |                          |
| Acar-UA*160  | 0          |              |                          |
| Acar-UA*208  | 0          |              |                          |
| Acar-UA*233  | 0          |              |                          |
| Acar-UA*304  | 1          |              |                          |
| Acar-UA*384  | 0          |              |                          |
| Allele     | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| **Acar-HPLT*72** |            | 0.333333                 |
| Acar-UA*4  | 1          |                          |
| Acar-UA*9  | 1          |                          |
| Acar-UA*51 | 0          |                          |
| Acar-UA*107| 0          |                          |
| Acar-UA*136| 0          |                          |
| Acar-UA*143| 0          |                          |
| Acar-UA*144| 1          |                          |
| Acar-UA*304| 0          |                          |
| Acar-UA*368| 0          |                          |

| Allele     | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| **Acar-HPLT*73** |            | 0.272727                 |
| Acar-UA*4  | 1          |                          |
| Acar-UA*9  | 1          |                          |
| Acar-UA*42 | 0          |                          |
| Acar-UA*55 | 1          |                          |
| Acar-UA*59 | 0          |                          |
| Acar-UA*65 | 0          |                          |
| Acar-UA*129| 0          |                          |
| Acar-UA*143| 0          |                          |
| Acar-UA*144| 0          |                          |
| Acar-UA*155| 0          |                          |
| Acar-UA*255| 0          |                          |

| Allele     | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| **Acar-HPLT*74** |            | 0.142857                 |
| Acar-UA*4  | 0          |                          |
| Acar-UA*9  | 0          |                          |
| Acar-UA*55 | 0          |                          |
| Acar-UA*144| 1          |                          |
| Acar-UA*199| 0          |                          |
| Acar-UA*254| 0          |                          |
| Acar-UA*394| 0          |                          |

| Allele     | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| **Acar-HPLT*75** |            | 0.111111                 |
| Acar-UA*6  | 0          |                          |
| Acar-UA*9  | 0          |                          |
| Acar-UA*48 | 0          |                          |
| Acar-UA*55 | 0          |                          |
| Acar-UA*97 | 0          |                          |
| Acar-UA*144| 1          |                          |
| Acar-UA*188| 0          |                          |
| Acar-UA*243| 0          |                          |
| Acar-UA*304| 0          |                          |
| Allele        | Unresolved |
|--------------|------------|
| Acar-UA*4    | 0          |
| Acar-UA*9    | 1          |
| Acar-UA*30   | 0          |
| Acar-UA*55   | 0          |
| Acar-UA*144  | 0          |
| Acar-UA*242  | 0          |

| Allele        | Unresolved |
|--------------|------------|
| Acar-UA*4    | 1          |
| Acar-UA*9    | 1          |
| Acar-UA*48   | 0          |
| Acar-UA*55   | 1          |
| Acar-UA*122  | 0          |
| Acar-UA*144  | 1          |
| Acar-UA*162  | 0          |
| Acar-UA*174  | 0          |
| Acar-UA*277  | 0          |

| Allele        | Unresolved |
|--------------|------------|
| Acar-UA*12   | 0          |
| Acar-UA*50   | 0          |
| Acar-UA*55   | 0          |
| Acar-UA*181  | 0          |
| Acar-UA*208  | 0          |
| Acar-UA*248  | 0          |
| Acar-UA*373  | 0          |

| Allele        | Unresolved |
|--------------|------------|
| Acar-UA*4    | 1          |
| Acar-UA*9    | 1          |
| Acar-UA*55   | 1          |
| Acar-UA*71   | 0          |
| Acar-UA*137  | 0          |
| Acar-UA*144  | 1          |
| Acar-UA*250  | 0          |
| Acar-UA*279  | 0          |
| Acar-UA*322  | 0          |
| Acar-UA*328  | 0          |
| Allele       | Unresolved | Prop. unresolved alleles |
|-------------|------------|--------------------------|
| Acar-HPLT*80|            | 0.230769                 |
| Acar-UA*4   | 1          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*51  | 0          |                          |
| Acar-UA*52  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*107 | 0          |                          |
| Acar-UA*110 | 0          |                          |
| Acar-UA*143 | 0          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*255 | 0          |                          |
| Acar-UA*304 | 0          |                          |
| Acar-UA*368 | 0          |                          |
| Acar-UA*392 | 0          |                          |
| Acar-HPLT*81|            | 0.333333                 |
| Acar-UA*4   | 1          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*11  | 0          |                          |
| Acar-UA*47  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*128 | 0          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*150 | 0          |                          |
| Acar-UA*332 | 0          |                          |
| Acar-HPLT*82|            | 0.75                     |
| Acar-UA*4   | 1          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*254 | 0          |                          |
| Acar-HPLT*83|            | 0.333333                 |
| Acar-UA*4   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*23  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*285 | 0          |                          |
| Acar-UA*342 | 0          |                          |
| Allele     | Acar-HPLT*84 Unresolved | Prop. unresolved alleles |
|------------|-------------------------|--------------------------|
| Acar-UA*4  | 0                       | 0.095238                 |
| Acar-UA*9  | 1                       |                          |
| Acar-UA*46 | 0                       |                          |
| Acar-UA*48 | 0                       |                          |
| Acar-UA*49 | 0                       |                          |
| Acar-UA*53 | 0                       |                          |
| Acar-UA*55 | 1                       |                          |
| Acar-UA*77 | 0                       |                          |
| Acar-UA*94 | 0                       |                          |
| Acar-UA*103| 0                       |                          |
| Acar-UA*107| 0                       |                          |
| Acar-UA*143| 0                       |                          |
| Acar-UA*150| 0                       |                          |
| Acar-UA*154| 0                       |                          |
| Acar-UA*255| 0                       |                          |
| Acar-UA*273| 0                       |                          |
| Acar-UA*307| 0                       |                          |
| Acar-UA*332| 0                       |                          |
| Acar-UA*349| 0                       |                          |
| Acar-UA*356| 0                       |                          |
| Acar-UA*417| 0                       |                          |

| Allele     | Acar-HPLT*85 Unresolved | Prop. unresolved alleles |
|------------|-------------------------|--------------------------|
| Acar-UA*4  | 1                       | 0.5                      |
| Acar-UA*9  | 1                       |                          |
| Acar-UA*12 | 0                       |                          |
| Acar-UA*55 | 1                       |                          |
| Acar-UA*128| 0                       |                          |
| Acar-UA*144| 1                       |                          |
| Acar-UA*200| 0                       |                          |
| Acar-UA*328| 0                       |                          |

| Allele     | Acar-HPLT*86 Unresolved | Prop. unresolved alleles |
|------------|-------------------------|--------------------------|
| Acar-UA*9  | 1                       | 0.222222                 |
| Acar-UA*33 | 0                       |                          |
| Acar-UA*55 | 1                       |                          |
| Acar-UA*94 | 0                       |                          |
| Acar-UA*144| 0                       |                          |
| Acar-UA*151| 0                       |                          |
| Acar-UA*341| 0                       |                          |
| Acar-UA*364| 0                       |                          |
| Acar-UA*404| 0                       |                          |
| Allele          | Unresolved | Acar-HPLT*87 Prop. unresolved alleles | 0.333333 |
|-----------------|------------|--------------------------------------|----------|
| Acar-UA*4       | 0          |                                      |          |
| Acar-UA*9       | 1          |                                      |          |
| Acaru-UA*23     | 0          |                                      |          |
| Acar-UA*55      | 1          |                                      |          |
| Acar-UA*144     | 0          |                                      |          |
| Acar-UA*285     | 0          |                                      |          |

| Allele          | Unresolved | Acar-HPLT*88 Prop. unresolved alleles | 0.25     |
|-----------------|------------|--------------------------------------|----------|
| Acar-UA*4       | 1          |                                      |          |
| Acar-UA*9       | 1          |                                      |          |
| Acar-UA*12      | 0          |                                      |          |
| Acar-UA*48      | 0          |                                      |          |
| Acar-UA*55      | 1          |                                      |          |
| Acar-UA*96      | 0          |                                      |          |
| Acar-UA*145     | 0          |                                      |          |
| Acar-UA*173     | 0          |                                      |          |
| Acar-UA*214     | 0          |                                      |          |
| Acar-UA*279     | 0          |                                      |          |
| Acar-UA*304     | 0          |                                      |          |
| Acar-UA*330     | 0          |                                      |          |

| Allele          | Unresolved | Acar-HPLT*89 Prop. unresolved alleles | 0.384615 |
|-----------------|------------|--------------------------------------|----------|
| Acar-UA*4       | 1          |                                      |          |
| Acar-UA*9       | 1          |                                      |          |
| Acar-UA*31      | 0          |                                      |          |
| Acar-UA*55      | 1          |                                      |          |
| Acar-UA*91      | 0          |                                      |          |
| Acar-UA*96      | 0          |                                      |          |
| Acar-UA*103     | 0          |                                      |          |
| Acar-UA*122     | 1          |                                      |          |
| Acar-UA*144     | 1          |                                      |          |
| Acar-UA*150     | 0          |                                      |          |
| Acar-UA*183     | 0          |                                      |          |
| Acar-UA*196     | 0          |                                      |          |
| Acar-UA*204     | 0          |                                      |          |
| Allele      | Unresolved | Prop. unresolved alleles |
|------------|------------|--------------------------|
| Acar-HPLT*90 |            | 0.272727                 |
| Acar-UA*4   | 0          |                          |
| Acar-UA*8   | 0          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*12  | 1          |                          |
| Acar-UA*33  | 0          |                          |
| Acar-UA*42  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*156 | 0          |                          |
| Acar-UA*163 | 0          |                          |
| Acar-UA*248 | 0          |                          |
| Acar-HPLT*91 |            | 0.363636                 |
| Acar-UA*4   | 1          |                          |
| Acar-UA*9   | 1          |                          |
| Acar-UA*48  | 1          |                          |
| Acar-UA*50  | 0          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*86  | 0          |                          |
| Acar-UA*91  | 0          |                          |
| Acar-UA*144 | 0          |                          |
| Acar-UA*150 | 0          |                          |
| Acar-UA*332 | 0          |                          |
| Acar-UA*415 | 0          |                          |
| Acar-HPLT*92 |            | 0.230769                 |
| Acar-UA*9   | 1          |                          |
| Acar-UA*55  | 1          |                          |
| Acar-UA*126 | 0          |                          |
| Acar-UA*144 | 1          |                          |
| Acar-UA*150 | 0          |                          |
| Acar-UA*208 | 0          |                          |
| Acar-UA*229 | 0          |                          |
| Acar-UA*328 | 0          |                          |
| Acar-UA*349 | 0          |                          |
| Acar-UA*380 | 0          |                          |
| Acar-UA*407 | 0          |                          |
| Acar-UA*412 | 0          |                          |
| Acar-UA*414 | 0          |                          |
| Allele   | Unresolved | Prop. unresolved alleles |
|---------|------------|--------------------------|
| Acar-HPLT*93 | 0.555556  |
| Acar-UA*4     | 1          |                          |
| Acar-UA*12    | 1          |                          |
| Acar-UA*31    | 0          |                          |
| Acar-UA*48    | 0          |                          |
| Acar-UA*50    | 0          |                          |
| Acar-UA*55    | 1          |                          |
| Acar-UA*82    | 0          |                          |
| Acar-UA*144   | 1          |                          |
| Acar-UA*304   | 1          |                          |

| Allele   | Unresolved | Prop. unresolved alleles |
|---------|------------|--------------------------|
| Acar-HPLT*94 | 0.222222  |
| Acar-UA*9     | 1          |                          |
| Acar-UA*11    | 0          |                          |
| Acar-UA*47    | 0          |                          |
| Acar-UA*55    | 1          |                          |
| Acar-UA*128   | 0          |                          |
| Acar-UA*141   | 0          |                          |
| Acar-UA*144   | 0          |                          |
| Acar-UA*150   | 0          |                          |
| Acar-UA*332   | 0          |                          |

| Allele   | Unresolved | Prop. unresolved alleles |
|---------|------------|--------------------------|
| Acar-HPLT*95 | 0.166667  |
| Acar-UA*4     | 0          |                          |
| Acar-UA*9     | 1          |                          |
| Acar-UA*40    | 0          |                          |
| Acar-UA*55    | 1          |                          |
| Acar-UA*91    | 0          |                          |
| Acar-UA*191   | 0          |                          |
| Acar-UA*230   | 0          |                          |
| Acar-UA*281   | 0          |                          |
| Acar-UA*313   | 0          |                          |
| Acar-UA*360   | 0          |                          |
| Acar-UA*380   | 0          |                          |
| Acar-UA*384   | 0          |                          |
| Allele    | Unresolved | Prop. unresolved alleles |
|-----------|------------|--------------------------|
| Acar-UA*4 | 1          |                          |
| Acar-UA*9 | 1          |                          |
| Acar-UA*11| 0          |                          |
| Acar-UA*12| 1          |                          |
| Acar-UA*31| 0          |                          |
| Acar-UA*55| 1          |                          |
| Acar-UA*144| 1          |                          |
| Acar-UA*183| 0          |                          |
| Acar-UA*387| 0         |                          |
| Acar-UA*9 | 1          | 0.555556                 |
| Acar-UA*55| 1          |                          |
| Acar-UA*128| 0          |                          |
| Acar-UA*144| 0          |                          |
| Acar-UA*191| 0          |                          |
| Acar-UA*337| 0          |                          |
| Acar-UA*371| 0          |                          |
| Acar-UA*410| 0         |                          |
| Acar-UA*9 | 1          | 0.25                     |
| Acar-UA*55| 1          |                          |
| Acar-UA*128| 0          |                          |
| Acar-UA*144| 0          |                          |
| Acar-UA*191| 0          |                          |
| Acar-UA*337| 0          |                          |
| Acar-UA*371| 0          |                          |
| Acar-UA*410| 0         |                          |
| Acar-UA*9 | 1          | 0.5                      |
| Acar-UA*55| 1          |                          |
| Acar-UA*144| 1          |                          |
| Acar-UA*210| 0          |                          |
| Acar-UA*229| 0          |                          |
| Acar-UA*375| 0          |                          |
| Acar-UA*9 | 1          | 0.333333                 |
| Acar-UA*48| 0          |                          |
| Acar-UA*50 | 0          |                          |
| Acar-UA*55| 1          |                          |
| Acar-UA*90 | 0          |                          |
| Acar-UA*144| 0          |                          |
| Acar-UA*146| 1          |                          |
| Acar-UA*216| 0          |                          |
| Acar-UA*265| 0          |                          |
| Acar-UA*266| 0          |                          |
| Acar-UA*378| 0          |                          |
| Allele          | Unresolved |
|-----------------|------------|
| Acar-UA*4       | 1          |
| Acar-UA*9       | 1          |
| Acar-UA*55      | 1          |
| Acar-UA*66      | 0          |
| Acar-UA*111     | 0          |
| Acar-UA*144     | 1          |
| Acar-UA*181     | 0          |
| Acar-UA*406     | 0          |
| Acar-UA*411     | 0          |

| Allele          | Unresolved |
|-----------------|------------|
| Acar-UA*4       | 1          |
| Acar-UA*9       | 1          |
| Acar-UA*55      | 1          |
| Acar-UA*94      | 0          |
| Acar-UA*122     | 0          |
| Acar-UA*125     | 0          |
| Acar-UA*144     | 1          |
| Acar-UA*304     | 0          |
| Acar-UA*405     | 0          |
| Acar-UA*409     | 0          |
| Acar-UA*413     | 0          |
| Allele       | Acar-HPLT*103 | Prop. unresolved alleles |
|--------------|---------------|--------------------------|
|              | Acar-UA*4     | 1                        |
|              | Acar-UA*6     | 0                        |
|              | Acar-UA*8     | 0                        |
|              | Acar-UA*9     | 1                        |
|              | Acar-UA*11    | 0                        |
|              | Acar-UA*55    | 0                        |
|              | Acar-UA*73    | 0                        |
|              | Acar-UA*144   | 1                        |
|              | Acar-UA*156   | 0                        |
|              | Acar-HPLT*104 | 0.222222                 |
|              | Acar-UA*4     | 1                        |
|              | Acar-UA*9     | 0                        |
|              | Acar-UA*31    | 0                        |
|              | Acar-UA*48    | 0                        |
|              | Acar-UA*109   | 0                        |
|              | Acar-UA*144   | 1                        |
|              | Acar-UA*241   | 0                        |
|              | Acar-UA*330   | 0                        |
|              | Acar-UA*400   | 0                        |
|              | Acar-HPLT*105 | 0.5                      |
|              | Acar-UA*4     | 1                        |
|              | Acar-UA*9     | 1                        |
|              | Acar-UA*40    | 0                        |
|              | Acar-UA*55    | 1                        |
|              | Acar-UA*144   | 1                        |
|              | Acar-UA*191   | 0                        |
|              | Acar-UA*337   | 0                        |
|              | Acar-UA*371   | 0                        |
|              | Acar-UA*410   | 0                        |
|              | Acar-HPLT*106 | 0.25                     |
|              | Acar-UA*4     | 1                        |
|              | Acar-UA*9     | 1                        |
|              | Acar-UA*40    | 0                        |
|              | Acar-UA*55    | 1                        |
|              | Acar-UA*91    | 0                        |
|              | Acar-UA*144   | 0                        |
|              | Acar-UA*191   | 0                        |
|              | Acar-UA*281   | 0                        |
|              | Acar-UA*290   | 0                        |
|              | Acar-UA*310   | 0                        |
|              | Acar-UA*380   | 0                        |
|              | Acar-UA*384   | 0                        |
| Allele     | Unresolved |
|-----------|------------|
| Acar-UA*4 | 1          |
| Acar-UA*9 | 1          |
| Acar-UA*33| 0          |
| Acar-UA*48| 1          |
| Acar-UA*55| 1          |
| Acar-UA*122| 0         |
| Acar-UA*144| 0         |
| Acar-UA*163| 0         |
| Acar-UA*277| 0         |
| Acar-UA*384| 0         |

|         | Prop. unresolved alleles |
|---------|--------------------------|
| Acar-HPLT*107 | 0.4                     |