**Supplemental material**

**S1**

<table>
<thead>
<tr>
<th>sample</th>
<th>cohort</th>
<th>day 2</th>
<th>day 3</th>
<th>day 4</th>
<th>day 5</th>
<th>day 7</th>
<th>day 31</th>
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<tbody>
<tr>
<td>tears</td>
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<td>1.1x10E+4</td>
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<td>4.9x10E+3</td>
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<td>6.5x10E+5</td>
<td>8.8x10E+6</td>
<td>3.7x10E+5</td>
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<td>1.3x10E+4</td>
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<td>3.7x10E+4</td>
<td>8.1x10E+3</td>
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<td>5.6x10E+3</td>
<td>1.4x10E+3</td>
<td>&lt;LLOQ</td>
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<tr>
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<td>3.6x10E+3</td>
<td>&lt;LLOQ</td>
</tr>
<tr>
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<td>9.1x10E+3</td>
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</table>

**Supplement 1:** Cohort mean copy numbers per ml of biofluid sample.

**S2**

<table>
<thead>
<tr>
<th>Tissue</th>
<th>Spleen</th>
<th>Liver</th>
<th>Lungs</th>
<th>Heart</th>
<th>Gonads</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>342.1 ± 62.2</td>
<td>602.9 ± 185.3</td>
<td>858.0 ± 191.7</td>
<td>1689.9 ± 380.4</td>
<td>432.0 ± 112.6</td>
</tr>
</tbody>
</table>

Blood | DC | RP | MA | ME |
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>40.1 ± 17.8</td>
<td>403.1 ± 148.4</td>
<td>372.3 ± 114.5</td>
<td>481.1 ± 213.8</td>
<td>434.2 ± 78.5</td>
</tr>
</tbody>
</table>

**Supplement 2:** Corresponding amount of tissue (µg) and blood (µl) per µgDNA, across all samples: mean ± standard deviation. Individual samples from the visual system were processed directly to minimize loss of tissue. Therefore, sample weights could not be determined. Lymph node abbreviations, DC: deep cervical, RP: retropharyngeal, MA: mandibular, ME: mesenteric.
### Supplement 3

Results given as copies per diploid genome (1dg = 6pg DNA): mean ± standard deviation. LLOQ: 50 copies/reaction. For blood, the day with maximal mean vector presence was chosen. Lymph node abbreviations, DC: deep cervical, RP: retropharyngeal, MA: mandibular, ME: mesenteric.