<table>
<thead>
<tr>
<th>Parameter</th>
<th>Definition</th>
<th>Estimate (95% credible interval)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mu$</td>
<td>Primary boosting</td>
<td>3.01 (2.64–3.42)</td>
</tr>
<tr>
<td>$\epsilon$</td>
<td>Measurement error</td>
<td>0.00 (0.00–0.02)</td>
</tr>
<tr>
<td>$\sigma$</td>
<td>Specific cross-reactivity</td>
<td>0.29 (0.25–0.33)</td>
</tr>
<tr>
<td>$\alpha$</td>
<td>Broad cross-reactivity</td>
<td>0.00 (0.00–0.01)</td>
</tr>
<tr>
<td>$\tau_1$</td>
<td>Antigenic seniority (boost prior response)</td>
<td>0.00 (0.00–0.01)</td>
</tr>
<tr>
<td>$\tau_2$</td>
<td>Antigenic seniority (suppress new response)</td>
<td>0.06 (0.02–0.09)</td>
</tr>
</tbody>
</table>

Table S1: Parameter estimates for extended model that includes specific and broad cross-reactivity (details in Supplementary Text S1).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>$w = 0$</th>
<th>$w = 0.01$</th>
<th>$w = 0.1$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mu$</td>
<td>3.01 (2.64–3.42)</td>
<td>4.29 (3.12–4.99)</td>
<td>5.01 (4.03–6.33)</td>
</tr>
<tr>
<td>$\epsilon$</td>
<td>0.00 (0.00–0.02)</td>
<td>0.01 (0.00–0.03)</td>
<td>0.01 (0.01–0.02)</td>
</tr>
<tr>
<td>$\sigma$</td>
<td>0.29 (0.25–0.33)</td>
<td>0.29 (0.23–0.33)</td>
<td>0.29 (0.25–0.33)</td>
</tr>
<tr>
<td>$\tau_1$</td>
<td>0.00 (0.00–0.01)</td>
<td>0.00 (0.00–0.03)</td>
<td>0.05 (0.03–0.08)</td>
</tr>
<tr>
<td>$\tau_2$</td>
<td>0.06 (0.02–0.09)</td>
<td>0.11 (0.08–0.15)</td>
<td>0.13 (0.09–0.17)</td>
</tr>
</tbody>
</table>

Table S2: Parameter estimates for different values of waning, $w$. We assume waning reduces titres to strains in the infection history by a factor $e^{-w}$ per year post-infection (details in Supplementary Text S1).