<table>
<thead>
<tr>
<th>Source</th>
<th>Panel 1 (1-12)</th>
<th>Panel 2 (13-25)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
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</tr>
<tr>
<td>Marker</td>
<td>FTDNA</td>
<td>Wikipedia</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>DYS393</td>
<td>0.250%</td>
<td>0.204%</td>
</tr>
<tr>
<td>DYS390</td>
<td>0.076% as Wikipedia</td>
<td>0.150%</td>
</tr>
<tr>
<td>DYS19</td>
<td>0.311%</td>
<td>do</td>
</tr>
<tr>
<td></td>
<td>0.151%</td>
<td>do</td>
</tr>
<tr>
<td>DYS391</td>
<td>0.265%</td>
<td>do</td>
</tr>
<tr>
<td>DYS385a</td>
<td>0.226%</td>
<td>do</td>
</tr>
<tr>
<td>DYS385b</td>
<td>0.226%</td>
<td>do</td>
</tr>
<tr>
<td>DYS426</td>
<td>0.009%</td>
<td>do</td>
</tr>
<tr>
<td>DYS388</td>
<td>0.222%</td>
<td>do</td>
</tr>
<tr>
<td>DYS439</td>
<td>0.477%</td>
<td>do</td>
</tr>
<tr>
<td>DYS389i</td>
<td>0.186%</td>
<td>do</td>
</tr>
<tr>
<td>DYS392</td>
<td>0.052%</td>
<td>do</td>
</tr>
<tr>
<td>DYS389ii</td>
<td>0.242%</td>
<td>do</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS458</td>
<td>0.814%</td>
<td>do</td>
</tr>
<tr>
<td>DYS459a</td>
<td>0.132%</td>
<td>do</td>
</tr>
<tr>
<td>DYS459b</td>
<td>0.132%</td>
<td>do</td>
</tr>
<tr>
<td>DYS455</td>
<td>0.016%</td>
<td>do</td>
</tr>
<tr>
<td>DYS454</td>
<td>0.016%</td>
<td>do</td>
</tr>
</tbody>
</table>

23 of 30 test results to date are haplogroup R1b (mostly R1b1a2). 7 x DNAH, 2 x FTDNA = 9 2 x DNAH, 2 x FTDNA = 4 8 x DNAH, 2 x FTDNA = 10

* = most common allele unless noted
### R1b Mutation Rates and Allele Distributions

<table>
<thead>
<tr>
<th>Marker</th>
<th>FTDNA</th>
<th>RogersDNA</th>
<th>Hawgood DNA</th>
<th>R1b Allele Frequency</th>
<th>Cheshire Clan Experience</th>
<th>Lancashire Clan</th>
<th>Other R1b Experience</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS447</td>
<td>0.264%</td>
<td>do</td>
<td>0.300%</td>
<td>25 = 69%, 24 = 17%</td>
<td>all 24</td>
<td>2 x 24</td>
<td>2 x 24</td>
</tr>
<tr>
<td>DYS437</td>
<td>0.099%</td>
<td>do</td>
<td>0.170%</td>
<td>15 = 85%, 14 = 12%</td>
<td>All = 14</td>
<td>2 x 14</td>
<td></td>
</tr>
<tr>
<td>DYS448</td>
<td>0.135%</td>
<td>do</td>
<td>0.170%</td>
<td>19 = 78%, 20 = 5%</td>
<td></td>
<td>1 x 20</td>
<td></td>
</tr>
<tr>
<td>DYS449</td>
<td>0.838%</td>
<td>do</td>
<td>0.880%</td>
<td>15 = 60%, 14 = 16%, 16 = 2%</td>
<td>All = 30</td>
<td>7 x 29, 1 x 30, 2 x 28</td>
<td></td>
</tr>
<tr>
<td>DYS464a</td>
<td>0.566%</td>
<td>do</td>
<td>0.500%</td>
<td>15 = 71%, 16 = 24%</td>
<td></td>
<td>4 x 16</td>
<td></td>
</tr>
<tr>
<td>DYS464b</td>
<td>0.566%</td>
<td>do</td>
<td>0.500%</td>
<td>17 = 48%, 16 = 39%, 15 = 11%</td>
<td>3 x 17, 1 x 16</td>
<td>3 x 15, 3 x 16, 3 x 17</td>
<td></td>
</tr>
<tr>
<td>DYS464c</td>
<td>0.566%</td>
<td>do</td>
<td>0.500%</td>
<td>17 = 69%, 18 = 20%, 16 = 8%, 15 = 1%, 19 = 2%</td>
<td>All = 16</td>
<td>4 x 15, 2 x 16, 4 x 17, 2 x 18, 1 x 19</td>
<td></td>
</tr>
<tr>
<td>DYS464d</td>
<td>0.566%</td>
<td>do</td>
<td>0.550%</td>
<td>17 = 69%, 18 = 20%, 16 = 8%, 15 = 1%, 19 = 2%</td>
<td>All = 16</td>
<td>4 x 15, 2 x 16, 4 x 17, 2 x 18, 1 x 19</td>
<td></td>
</tr>
<tr>
<td>DYS460</td>
<td>0.402%</td>
<td>do</td>
<td>0.340%</td>
<td>11 = 64%, 10 = 19%</td>
<td></td>
<td>2 x 10</td>
<td></td>
</tr>
<tr>
<td>Y-GATA-H4</td>
<td>0.208%</td>
<td>do</td>
<td>0.320%</td>
<td>11 = 71%, 12 = 9%</td>
<td></td>
<td>1 x 12</td>
<td></td>
</tr>
<tr>
<td>YCAIIa</td>
<td>0.123%</td>
<td>do</td>
<td>0.160%</td>
<td>19 = 95%, 20 = 1%</td>
<td></td>
<td>2 x 20</td>
<td></td>
</tr>
<tr>
<td>YCAIIb</td>
<td>0.123%</td>
<td>do</td>
<td>0.160%</td>
<td>23 = 81%, 22 = 9%, 24 = 6%</td>
<td></td>
<td>1 x 22, 1 x 24</td>
<td></td>
</tr>
<tr>
<td>DYS456</td>
<td>0.735%</td>
<td>do</td>
<td>0.540%</td>
<td>16 = 40%, 15 = 36%</td>
<td>6 x 16, 3 x 15</td>
<td>4 x 15</td>
<td></td>
</tr>
<tr>
<td>DYS607*</td>
<td>0.411%</td>
<td>do</td>
<td>0.390%</td>
<td>15 = 70%, 16 = 14%</td>
<td>2 x 15</td>
<td>1 x 15, 1 x 16</td>
<td></td>
</tr>
<tr>
<td>DYS576*</td>
<td>1.022%</td>
<td>do</td>
<td>0.860%</td>
<td>18 = 42%, 17 = 28%, 19 = 17%, 20 = 5%</td>
<td>1 x 17, 1 x 18</td>
<td>1 x 17, 1 x 20</td>
<td></td>
</tr>
<tr>
<td>DYS570*</td>
<td>0.790%</td>
<td>do</td>
<td>0.750%</td>
<td>17 = 57%, 18 = 20%</td>
<td></td>
<td>1 x 17, 1 x 18</td>
<td></td>
</tr>
</tbody>
</table>

### Panel 3 (26-37)

- DNAH present: 0.710% DNAH 0.936% other specific 0.930%
- FTDNA Specific: 1.857% DNAH 1.812% other specific 0.710%
### R1b Mutation Rates and Allele Distributions

<table>
<thead>
<tr>
<th>Marker</th>
<th>FTDNA</th>
<th>Wikipedia</th>
<th>RogersDNA</th>
<th>Hawgood DNA</th>
<th>R1b Allele Frequency</th>
<th>Cheshire Clan Experience</th>
<th>Lancashire Clan</th>
<th>Other R1b Experience</th>
</tr>
</thead>
<tbody>
<tr>
<td>CDYa*</td>
<td>3.531%</td>
<td>do</td>
<td></td>
<td>36 = 30%, 35 = 14%, 34 = 4%, 37 = 29%, 38 = 16%</td>
<td>1 x 34, 1 x 35</td>
<td>1 x 37, 1 x 38</td>
<td>1 x 34, 1 x 38</td>
<td></td>
</tr>
<tr>
<td>CDYb*</td>
<td>3.531%</td>
<td>do</td>
<td></td>
<td>38 = 31%, 39 = 32%, 36 = 7%</td>
<td>2 x 38</td>
<td>2 x 39</td>
<td>1 x 36, 1 x 38</td>
<td></td>
</tr>
<tr>
<td>DYS442</td>
<td>0.324%</td>
<td>do</td>
<td>0.500%</td>
<td>12 = 74%, 13 = 12%</td>
<td>One mutation at 11</td>
<td>all 13</td>
<td>3 x 11, 2 x 13</td>
<td></td>
</tr>
<tr>
<td>DYS438</td>
<td>0.035%</td>
<td>do</td>
<td>0.080%</td>
<td>12 = 94%, 10 = &lt;1%</td>
<td>1 x 10</td>
<td></td>
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<td></td>
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</tbody>
</table>

* = FTDNA specific

### DNAH Specific

<table>
<thead>
<tr>
<th>Marker</th>
<th>FTDNA</th>
<th>RogersDNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS441</td>
<td>0.132%</td>
<td></td>
</tr>
<tr>
<td>DYS444</td>
<td>0.321%</td>
<td>0.290%</td>
</tr>
<tr>
<td>DYS445</td>
<td>0.296%</td>
<td>0.260%</td>
</tr>
<tr>
<td>DYS446</td>
<td>0.095%</td>
<td>0.310%</td>
</tr>
<tr>
<td>DYS452</td>
<td>0.314%</td>
<td></td>
</tr>
<tr>
<td>DYS461</td>
<td>0.233%</td>
<td></td>
</tr>
<tr>
<td>DYS462</td>
<td>0.053%</td>
<td></td>
</tr>
<tr>
<td>DYS463</td>
<td>0.162%</td>
<td></td>
</tr>
<tr>
<td>DYS465</td>
<td>0.492%</td>
<td>0.340%</td>
</tr>
<tr>
<td>GATA A10</td>
<td>0.379%</td>
<td>0.340%</td>
</tr>
<tr>
<td>GATA 1B</td>
<td>0.130%</td>
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</table>

### Overall

<table>
<thead>
<tr>
<th></th>
<th>FTDNA +</th>
<th>RogersDNA</th>
<th>Hawgood DNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>FTDNA - 37 Markers</td>
<td>0.420%</td>
<td>0.497%</td>
<td>0.513%</td>
</tr>
<tr>
<td>DNH - 43 Markers</td>
<td>0.228%</td>
<td>0.232%</td>
<td>0.244%</td>
</tr>
<tr>
<td>Common - 32 Markers</td>
<td>0.277%</td>
<td>0.284%</td>
<td>0.309%</td>
</tr>
</tbody>
</table>

FTDNA + is FTDNA panels 1 and 2 plus RogersDNA values
Hawgood DNA uses values from RogersDNA where missing from Hawgood DNA

### Sources

1. [http://www.kerchner.com/cgi-bin/ystrmutationrate.cgi](http://www.kerchner.com/cgi-bin/ystrmutationrate.cgi)
4. [http://orders.hawgoodfamily.co.uk/str%20data.html](http://orders.hawgoodfamily.co.uk/str%20data.html)
# R1b Mutation Rates and Allele Distributions

<table>
<thead>
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<th>Cheshire Clan Experience</th>
<th>Lancashire Clan</th>
<th>Other R1b Experience</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>10.0%</td>
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<tr>
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<td></td>
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<td>25.00%</td>
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<tr>
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<td>75.00%</td>
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<td></td>
<td>90.0%</td>
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## Probabilities

<table>
<thead>
<tr>
<th>No of Mismatches</th>
<th>DNAH (43 markers) mutation rate 0.23%</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1 2 4 7 12</td>
</tr>
<tr>
<td>1</td>
<td>3 5 9 14 20</td>
</tr>
<tr>
<td>2</td>
<td>6 9 14 20 28</td>
</tr>
<tr>
<td>3</td>
<td>10 13 19 27 35</td>
</tr>
<tr>
<td>4</td>
<td>13 18 25 34 43</td>
</tr>
<tr>
<td>5</td>
<td>17 23 31 40 50</td>
</tr>
</tbody>
</table>

## FTDNA (37 markers) mutation rate 0.42%

<table>
<thead>
<tr>
<th>No of Mismatches</th>
<th>FTDNA (37 markers) mutation rate 0.42%</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1 1 2 5 8</td>
</tr>
<tr>
<td>1</td>
<td>2 3 6 9 13</td>
</tr>
<tr>
<td>2</td>
<td>4 6 9 13 18</td>
</tr>
<tr>
<td>3</td>
<td>6 9 13 17 23</td>
</tr>
<tr>
<td>4</td>
<td>9 12 16 22 27</td>
</tr>
<tr>
<td>5</td>
<td>11 15 20 26 32</td>
</tr>
</tbody>
</table>

## Common (32 markers) mutation rate 0.28%

<table>
<thead>
<tr>
<th>No of Mismatches</th>
<th>Common (32 markers) mutation rate 0.28%</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1 2 4 8 13</td>
</tr>
<tr>
<td>1</td>
<td>3 6 10 15 22</td>
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<tr>
<td>2</td>
<td>7 10 16 23 31</td>
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<tr>
<td>3</td>
<td>11 15 22 30 39</td>
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<tr>
<td>4</td>
<td>15 20 28 38 48</td>
</tr>
<tr>
<td>5</td>
<td>20 26 35 45 57</td>
</tr>
</tbody>
</table>

The above table is based on the MRCA calculator at http://www.moseswalker.com/mrca/calculator.asp?q=1