Table S1. General Aspects. Participants Characterization.

<table>
<thead>
<tr>
<th>Kind of cases that your laboratory examine</th>
<th>GHEP-MIX1 (N = 32)</th>
<th>GHEP-MIX2 (N = 24)</th>
<th>GHEP-MIX3 (N = 17)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n (labs)</td>
<td>%</td>
<td>n (labs)</td>
</tr>
<tr>
<td>Forensic</td>
<td>3</td>
<td>9.4</td>
<td>3</td>
</tr>
<tr>
<td>Paternity</td>
<td>5</td>
<td>15.6</td>
<td>3</td>
</tr>
<tr>
<td>Both</td>
<td>24</td>
<td>75.0</td>
<td>18</td>
</tr>
</tbody>
</table>

2. Send DNA profile to Criminal DataBase:

| National                                 | 7       | 21.9 | 8       | 33.3 | 5        | 29.4 |
| Own                                      | 2       | 6.3  | 2       | 8.3  | 2        | 11.8 |
| Both                                     | 4       | 12.5 | 4       | 16.7 | 6        | 35.3 |
| No                                       | 19      | 59.4 | 11      | 45.8 | 4        | 23.5 |

3. Report results about mixture profiles of autosomal markers:

| Yes                                      | 14      | 43.8 | 16      | 66.7 | 12       | 70.6 |
| No                                       | 5       | 28.1 | 4       | 16.7 | 2        | 11.8 |
| Only if there is reference sample        | 5       | 26.3 | 5       | 20.8 | 3        | 17.6 |

4. In case of obtaining a mixture profiles:

| They are sent to Criminal DataBases      | 3       | 9.4  | 5       | 20.8 | 2        | 11.8 |
| They are not sent to Criminal DataBases  | 14      | 43.8 | 8       | 33.3 | 1        | 5.9  |
| They are only registered on the reports  | 15      | 46.9 | 10      | 41.7 | 8        | 47.1 |
| They are registered on both reports and Criminal DataBases | N/D | N/D | N/D | N/D | 6 | 35.3 |

5. When mixture profiles are interpreted, allelic assignment has been carried out by procedure:

| Automatic                                 | 3       | 9.4  | 5       | 20.8 | 6        | 35.3 |
| Manual                                   | 18      | 56.3 | 12      | 50.0 | 2        | 11.8 |
| Both                                     | 10      | 31.3 | 6       | 25.0 | 9        | 52.9 |

6. Your laboratory’s mixture interpretation criterias have been validated:

| Yes                                      | 5       | 15.6 | 3       | 12.5 | 4        | 23.5 |
| No                                       | 26      | 81.3 | 21      | 87.5 | 5        | 29.4 |
| Validation in progress                    | N/D     | N/D  | N/D     | N/D  | 8        | 47.1 |

N/D = No Data
### Table S2. Technical Aspects. Edition Tools.

<table>
<thead>
<tr>
<th></th>
<th>GHEP-MIX1 (N = 32)</th>
<th>GHEP-MIX2 (N = 24)</th>
<th>GHEP-MIX3 (N = 17)</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (labs)</td>
<td>%</td>
<td>n (labs)</td>
<td>%</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Edition Tool</th>
<th>n (labs)</th>
<th>%</th>
<th>n (labs)</th>
<th>%</th>
<th>n (labs)</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>GeneMapper</td>
<td>29</td>
<td>90.6</td>
<td>23</td>
<td>95.8</td>
<td>17</td>
<td>100.0</td>
</tr>
<tr>
<td>GeneScan</td>
<td>2</td>
<td>6.3</td>
<td>0</td>
<td>0.0</td>
<td>0</td>
<td>0.0</td>
</tr>
<tr>
<td>Genotyper</td>
<td>1</td>
<td>3.1</td>
<td>0</td>
<td>0.0</td>
<td>0</td>
<td>0.0</td>
</tr>
<tr>
<td>PeakScanner</td>
<td>0</td>
<td>0.0</td>
<td>1</td>
<td>4.2</td>
<td>0</td>
<td>0.0</td>
</tr>
</tbody>
</table>

7. Which edition software have you used:

<table>
<thead>
<tr>
<th>Criteria</th>
<th>GHEP-MIX1</th>
<th>GHEP-MIX2</th>
<th>GHEP-MIX3</th>
</tr>
</thead>
<tbody>
<tr>
<td>&gt; 4 STRs with &gt;3 alleles</td>
<td>2</td>
<td>6.3</td>
<td>0</td>
</tr>
<tr>
<td>&gt; 3 STRs with &gt;3 alleles</td>
<td>2</td>
<td>6.3</td>
<td>0</td>
</tr>
<tr>
<td>&gt; 2 STRs with &gt;3 alleles</td>
<td>6</td>
<td>18.8</td>
<td>3</td>
</tr>
<tr>
<td>Alleles imbalance</td>
<td>0</td>
<td>0.0</td>
<td>0</td>
</tr>
<tr>
<td>Amelogenin imbalance (exclusively)</td>
<td>0</td>
<td>0.0</td>
<td>0</td>
</tr>
<tr>
<td>&gt; 4 STRs with &gt;3 alleles and Alleles imbalance</td>
<td>2</td>
<td>6.3</td>
<td>0</td>
</tr>
<tr>
<td>&gt; 3 STRs with &gt;3 alleles and Alleles imbalance</td>
<td>4</td>
<td>12.5</td>
<td>2</td>
</tr>
<tr>
<td>&gt; 2 STRs with &gt;3 alleles and Alleles imbalance</td>
<td>10</td>
<td>31.3</td>
<td>11</td>
</tr>
<tr>
<td>&gt; 3 STRs with &gt;3 alleles and Amelogenin imbalance</td>
<td>1</td>
<td>3.1</td>
<td>0</td>
</tr>
<tr>
<td>&gt; 2 STRs with &gt;3 alleles and Amelogenin imbalance</td>
<td>1</td>
<td>3.1</td>
<td>0</td>
</tr>
<tr>
<td>Others</td>
<td>4</td>
<td>12.5</td>
<td>1</td>
</tr>
</tbody>
</table>

8. Which criterias do you use to define a profile as a mixture:

9. In the present exercise, the alleles have been assigned when the peak is higher than:

<table>
<thead>
<tr>
<th>RFUs</th>
<th>GHEP-MIX1</th>
<th>GHEP-MIX2</th>
<th>GHEP-MIX3</th>
</tr>
</thead>
<tbody>
<tr>
<td>150 RFUs</td>
<td>1</td>
<td>3.1</td>
<td>0</td>
</tr>
<tr>
<td>100 RFUs</td>
<td>10</td>
<td>31.3</td>
<td>1</td>
</tr>
<tr>
<td>50 RFUs</td>
<td>21</td>
<td>65.6</td>
<td>15</td>
</tr>
<tr>
<td>Others</td>
<td>0</td>
<td>0.0</td>
<td>1</td>
</tr>
</tbody>
</table>
### Table S2. Technical Aspects. Edition Tools.

<table>
<thead>
<tr>
<th></th>
<th>GHEP-MIX1 (N = 32)</th>
<th>GHEP-MIX2 (N = 24)</th>
<th>GHEP-MIX3 (N = 17)</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (labs) %</td>
<td>0 0.0</td>
<td>0 0.0</td>
<td>1 5.9</td>
</tr>
<tr>
<td>Every</td>
<td>0 0.0</td>
<td>0 0.0</td>
<td>1 5.9</td>
</tr>
<tr>
<td>&gt; 15% from principal allele</td>
<td>8 25.0</td>
<td>7 29.2</td>
<td>2 11.8</td>
</tr>
<tr>
<td>&gt; 150 RFUs</td>
<td>0 0.0</td>
<td>0 0.0</td>
<td>0 0.0</td>
</tr>
<tr>
<td>&gt; 100 RFUs</td>
<td>0 0.0</td>
<td>1 4.2</td>
<td>0 0.0</td>
</tr>
<tr>
<td>&gt; 50 RFUs</td>
<td>0 0.0</td>
<td>1 4.2</td>
<td>0 0.0</td>
</tr>
<tr>
<td>The assignment has been variable depending on which STR marker is taken into account</td>
<td>13 40.6</td>
<td>9 37.5</td>
<td>8 47.1</td>
</tr>
<tr>
<td>&gt; 15% from principal allele and &gt; 150 RFUs</td>
<td>2 6.3</td>
<td>0 0.0</td>
<td>0 0.0</td>
</tr>
<tr>
<td>&gt; 15% from principal allele and &gt; 100 RFUs</td>
<td>2 6.3</td>
<td>0 0.0</td>
<td>0 0.0</td>
</tr>
<tr>
<td>&gt; 15% from principal allele and &gt; 50 RFUs</td>
<td>1 3.1</td>
<td>4 16.7</td>
<td>2 11.8</td>
</tr>
<tr>
<td>The assignment has been variable depending on which STR marker is taken into account, and &gt; 150 RFUs</td>
<td>0 0.0</td>
<td>0 0.0</td>
<td>0 0.0</td>
</tr>
<tr>
<td>The assignment has been variable depending on which STR marker is taken into account, and &gt; 100 RFUs</td>
<td>0 0.0</td>
<td>0 0.0</td>
<td>1 5.9</td>
</tr>
<tr>
<td>The assignment has been variable depending on which STR marker is taken into account, and &gt; 50 RFUs</td>
<td>3 9.4</td>
<td>1 4.2</td>
<td>3 17.6</td>
</tr>
<tr>
<td>The assignment has been variable depending on which STR marker is taken into account, and &gt; 15% from principal allele</td>
<td>3 9.4</td>
<td>1 4.2</td>
<td>0 0.0</td>
</tr>
</tbody>
</table>

10. The "stutter" positions (n-4/n+4) have been assigned as possible alleles:

11. Which is / are the principal obstacle/s that your laboratory have to face up to interpret a mixture profiles?

<table>
<thead>
<tr>
<th></th>
<th>GHEP-MIX1</th>
<th>GHEP-MIX2</th>
<th>GHEP-MIX3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lack of an unique criterion on the laboratory</td>
<td>13 40.6</td>
<td>2 8.3</td>
<td>3 17.6</td>
</tr>
<tr>
<td>Lack of training</td>
<td>16 50.0</td>
<td>6 25.0</td>
<td>3 17.6</td>
</tr>
<tr>
<td>Lack of an unique criterion on the laboratory and Lack of training</td>
<td>1 3.1</td>
<td>6 25.0</td>
<td>5 29.4</td>
</tr>
<tr>
<td>There are not any obstacle</td>
<td>2 6.3</td>
<td>3 12.5</td>
<td>0 0.0</td>
</tr>
<tr>
<td>Others</td>
<td>N/D</td>
<td>N/D</td>
<td>7 29.2</td>
</tr>
</tbody>
</table>

N/D = No Data
Table S3. Statistical Aspects.

<table>
<thead>
<tr>
<th></th>
<th>GHEP-MIX1 (N = 32)</th>
<th>GHEP-MIX2 (N = 24)</th>
<th>GHEP-MIX3 (N = 17)</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (labs)</td>
<td>%</td>
<td>n (labs)</td>
<td>%</td>
</tr>
<tr>
<td>Automatic (software)</td>
<td>N/D</td>
<td>11</td>
<td>45.8</td>
</tr>
<tr>
<td>Manual</td>
<td>N/D</td>
<td>7</td>
<td>29.2</td>
</tr>
<tr>
<td>Both</td>
<td>N/D</td>
<td>6</td>
<td>25.0</td>
</tr>
</tbody>
</table>

N/D = No Data

13. LR calculation is carried out by using: Table S3. Statistical Aspects.
### Table S4. Samples Discrepancies.

<table>
<thead>
<tr>
<th></th>
<th>GHEP-MIX1 (N = 32)</th>
<th>GHEP-MIX2 (N = 24)</th>
<th>GHEP-MIX3 (N = 17)</th>
<th>Total (N = 79)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>M1 (1:5)</td>
<td>M2 (1:10)</td>
<td>M3 (1:1)</td>
<td>M4 (1:5)</td>
</tr>
<tr>
<td>Group A</td>
<td>-A</td>
<td>31 37.3</td>
<td>21 13.0</td>
<td>0 0.0</td>
</tr>
<tr>
<td></td>
<td>+A</td>
<td>10 12.0</td>
<td>69 42.6</td>
<td>5 71.4</td>
</tr>
<tr>
<td>Group B</td>
<td>-B</td>
<td>1 1.2</td>
<td>70 43.2</td>
<td>0 0.0</td>
</tr>
<tr>
<td></td>
<td>+B</td>
<td>40 48.2</td>
<td>2 1.2</td>
<td>1 14.3</td>
</tr>
<tr>
<td>Group C</td>
<td>-C</td>
<td>1 1.2</td>
<td>0 0.0</td>
<td>1 14.3</td>
</tr>
<tr>
<td></td>
<td>+C</td>
<td>1 0.8</td>
<td>0 0.0</td>
<td>0 0.0</td>
</tr>
<tr>
<td></td>
<td>Total</td>
<td>83 31.7</td>
<td>182 61.8</td>
<td>7 2.7</td>
</tr>
</tbody>
</table>

**Group A**: those which take place at a stutter position (n-4, n+4 or n-3, n+3).
- **-A**: No report of a real allele which is located at a stutter position, which represents a false allelic loss in the profile.
- **+A**: Report of a non-existent allele (actual stutter peak), which represents a false allelic gain in the genetic profile.

**Group B**: those which occur in a position non-stutter.
- **-B**: No report of a real allele in a non-stutter position, which represents a false allelic loss in the profile.
- **+B**: Report of a non-existent allele in a non-stutter position, which represents a false allelic gain in the genetic profile.

**Group C**: discrepancies attributable to an incorrect transcription.
### Table S5. Statistical Treatment. Locked Hypothesis. (GHEP-MIX2)

#### Case 1

<table>
<thead>
<tr>
<th>Suspect</th>
<th>Mixture</th>
<th>$H_p/H_d$</th>
<th>$LR = (H_p:S+U)/(H_d:2U)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>D21S11</td>
<td>29-31.2</td>
<td>29-30-31.2-32.2</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D7S820</td>
<td>8-12</td>
<td>8-11-12</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D16S539</td>
<td>11-14</td>
<td>11-12-14</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D2S1338</td>
<td>17-19</td>
<td>17-19-25</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>TPOX</td>
<td>8-9</td>
<td>8-9</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D5S818</td>
<td>11</td>
<td>11-12</td>
<td>LR\textsubscript{total}</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Suspect</th>
<th>Mixture</th>
<th>$H_p/H_d$</th>
<th>$LR = (H_p:S+V)/(H_d:V+U)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>D21S11</td>
<td>29-31.2</td>
<td>29-30-31.2-32.2</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D7S820</td>
<td>8-12</td>
<td>8-11-12</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D16S539</td>
<td>11-14</td>
<td>11-12-14</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D2S1338</td>
<td>17-19</td>
<td>17-19-25</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>TPOX</td>
<td>8-9</td>
<td>8-9</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D5S818</td>
<td>11</td>
<td>11-12</td>
<td>LR\textsubscript{total}</td>
</tr>
</tbody>
</table>

#### Case 2

<table>
<thead>
<tr>
<th>Suspect</th>
<th>Mixture</th>
<th>$H_p/H_d$</th>
<th>$LR = (H_p:S+V)/(H_d:V+U)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>D21S11</td>
<td>29-31.2</td>
<td>29-30-31.2-32.2</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D7S820</td>
<td>8-12</td>
<td>8-11-12</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D16S539</td>
<td>11-14</td>
<td>11-12-14</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D2S1338</td>
<td>17-19</td>
<td>17-19-25</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>TPOX</td>
<td>8-9</td>
<td>8-9</td>
<td>LR\textsubscript{partial}</td>
</tr>
<tr>
<td>D5S818</td>
<td>11</td>
<td>11-12</td>
<td>LR\textsubscript{total}</td>
</tr>
</tbody>
</table>

#### Notes

- **LR** = Likelihood Ratio
- **N** = Number of samples
- **%** = Percentage

**Mixture**

- **D21S11**: 1/12 $l_{29}f_{31.2}$
- **D7S820**: 1/12 $l_{12}f_{8}$
- **D16S539**: 1/12 $l_{14}f_{12}$
- **D2S1338**: 1/12 $l_{18}f_{18}$
- **TPOX**: 1/12 $l_{17}f_{17}$
- **D5S818**: 1/12 $l_{18}f_{18}$

**Suspect**

- **D21S11**: 29-31.2
- **D7S820**: 8-12
- **D16S539**: 11-14
- **D2S1338**: 17-19
- **TPOX**: 8-9
- **D5S818**: 11

**Victim**

- **D21S11**: 30-32.2
- **D7S820**: 8-11
- **D16S539**: 12
- **D2S1338**: 19-25
- **TPOX**: 8
- **D5S818**: 11-12
## Table S6. Statistical Treatment. Open Hypothesis. (GHEP-MIX3)

<table>
<thead>
<tr>
<th>Case 1 (N = 17)</th>
<th>n (labs)</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hypothesis Couples (LR = Hₚ/Hₐ)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2S/2U</td>
<td></td>
<td>29.4</td>
</tr>
<tr>
<td>(2S/2U) + [(S1+U)/2U] + [(S2+U)/2U]</td>
<td>11</td>
<td>64.7</td>
</tr>
<tr>
<td>[(S1+U)/2U] + [(S2+U)/2U]</td>
<td>1</td>
<td>5.9</td>
</tr>
<tr>
<td>(S+V)/(V+U)</td>
<td></td>
<td>11.8</td>
</tr>
<tr>
<td>(S+V)/2U</td>
<td></td>
<td>17.6</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Case 2 (N = 17)</th>
<th>n (labs)</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hypothesis Couples (LR = Hₚ/Hₐ)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>(S+V)/(V+U)</td>
<td></td>
<td>47.1</td>
</tr>
<tr>
<td>[(S+V)/(V+U)] + [(S+V)/2U]</td>
<td>2</td>
<td>11.8</td>
</tr>
<tr>
<td>[(S+V)/(V+U)] + [(S+V)/2U] + [(S+V)/(S+U)]</td>
<td>1</td>
<td>5.9</td>
</tr>
<tr>
<td>(S+V)/2U</td>
<td></td>
<td>17.6</td>
</tr>
<tr>
<td>[(S+V)/(V+U)] + [(S+V)/2U] + [(V+U)/2U]</td>
<td>1</td>
<td>5.9</td>
</tr>
</tbody>
</table>

Hₚ = Prosecution hypothesis
Hₐ = Defence hypothesis
S = Suspect
V = Victim
U = Unknown
Table S7. Statistical Treatment. Open Hypothesis. LRs combined of Case 1. (GHEP-MIX3)

<table>
<thead>
<tr>
<th>( H_p/H_d = S1+S2 ) / 2U</th>
<th>LR(_{combined})</th>
<th>n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.17E+10</td>
<td>1</td>
<td>6.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>1.12E+11</td>
<td>9</td>
<td>56.3</td>
<td>52.9</td>
<td></td>
</tr>
<tr>
<td>3.25E+11</td>
<td>4</td>
<td>25.0</td>
<td>23.5</td>
<td></td>
</tr>
<tr>
<td>2.01E+12</td>
<td>1</td>
<td>6.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>2.64E+17</td>
<td>1</td>
<td>6.3</td>
<td>5.9</td>
<td></td>
</tr>
</tbody>
</table>

| min.  | 6.17E+10 |
| Max.  | 2.64E+17 |

<table>
<thead>
<tr>
<th>( H_p/H_d = S1+U ) / 2U</th>
<th>LR(_{combined})</th>
<th>n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.48E+05</td>
<td>10</td>
<td>83.3</td>
<td>58.8</td>
<td></td>
</tr>
<tr>
<td>1.55E+06</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>6.96E+08</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
</tbody>
</table>

| min.  | 1.48E+05 |
| Max.  | 6.96E+08 |

\( N_{partial} \) = 12
\( N_{total} \) = 17

<table>
<thead>
<tr>
<th>( H_p/H_d = S2+U ) / 2U</th>
<th>LR(_{combined})</th>
<th>n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.74E+02</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>1.98E+03</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>3.14E+03</td>
<td>6</td>
<td>50.0</td>
<td>35.3</td>
<td></td>
</tr>
<tr>
<td>3.86E+03</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>8.73E+03</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>9.16E+03</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
<tr>
<td>3.80E+08</td>
<td>1</td>
<td>8.3</td>
<td>5.9</td>
<td></td>
</tr>
</tbody>
</table>

| min.  | 7.74E+02 |
| Max.  | 3.80E+08 |

\( H_p = \) Prosecution hypothesis
\( H_d = \) Defence hypothesis
### Table S8. Statistical Treatment. Open Hypothesis. LRs combined of Case 2. (GHEP-MIX3)

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>LR&lt;sub&gt;combined&lt;/sub&gt; n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hp/Hd = S+V / V+U</strong></td>
<td>3.30E+07</td>
<td>1</td>
<td>7.7</td>
</tr>
<tr>
<td></td>
<td>3.52E+07</td>
<td>11</td>
<td>84.6</td>
</tr>
<tr>
<td></td>
<td>6.96E+08</td>
<td>1</td>
<td>7.7</td>
</tr>
<tr>
<td><strong>min.</strong></td>
<td>3.30E+07</td>
<td>1</td>
<td>7.7</td>
</tr>
<tr>
<td><strong>Max.</strong></td>
<td>6.96E+08</td>
<td>1</td>
<td>7.7</td>
</tr>
<tr>
<td>N&lt;sub&gt;partial&lt;/sub&gt;</td>
<td>13</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;total&lt;/sub&gt;</td>
<td>17</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>LR&lt;sub&gt;combined&lt;/sub&gt; n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hp/Hd = S+V / 2U</strong></td>
<td>1.12E+11</td>
<td>7</td>
<td>87.5</td>
</tr>
<tr>
<td></td>
<td>2.01E+12</td>
<td>1</td>
<td>12.5</td>
</tr>
<tr>
<td><strong>min.</strong></td>
<td>1.12E+11</td>
<td>7</td>
<td>87.5</td>
</tr>
<tr>
<td><strong>Max.</strong></td>
<td>2.01E+12</td>
<td>1</td>
<td>12.5</td>
</tr>
<tr>
<td>N&lt;sub&gt;partial&lt;/sub&gt;</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;total&lt;/sub&gt;</td>
<td>17</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>LR&lt;sub&gt;combined&lt;/sub&gt; n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hp/Hd = S+V / S+U</strong></td>
<td>7.52E+05</td>
<td>1</td>
<td>100.0</td>
</tr>
<tr>
<td><strong>min.</strong></td>
<td>7.52E+05</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Max.</strong></td>
<td>7.52E+05</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;partial&lt;/sub&gt;</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;total&lt;/sub&gt;</td>
<td>17</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>LR&lt;sub&gt;combined&lt;/sub&gt; n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hp/Hd = S+U / 2U</strong></td>
<td>1.48E+05</td>
<td>2</td>
<td>100.0</td>
</tr>
<tr>
<td><strong>min.</strong></td>
<td>1.48E+05</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Max.</strong></td>
<td>1.48E+05</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;partial&lt;/sub&gt;</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;total&lt;/sub&gt;</td>
<td>17</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hypothesis</th>
<th>LR&lt;sub&gt;combined&lt;/sub&gt; n (labs)</th>
<th>%partial</th>
<th>%total</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hp/Hd = V+U / 2U</strong></td>
<td>3.14E+03</td>
<td>2</td>
<td>100.0</td>
</tr>
<tr>
<td><strong>min.</strong></td>
<td>3.14E+03</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Max.</strong></td>
<td>3.14E+03</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;partial&lt;/sub&gt;</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>N&lt;sub&gt;total&lt;/sub&gt;</td>
<td>17</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Hp = Prosecution hypothesis
Hd = Defence hypothesis
Classification of discrepancies

**Group A:** those which take place at a stutter position (n-4, n+4 or n-3, n+3)

- **Type -A**
  - Contributor 1: 9-12
  - Contributor 2: 11-13
  - Reported by lab: 9-12-13
  - Expected DNA profile: 9-11-12-13

- **Type +A**
  - Contributor 1: 9-12
  - Contributor 2: 9-12
  - Reported by lab: 9-11-12
  - Expected DNA profile: 9-12

**Group B:** those which occur in a non-stutter position.

- **Type -B**
  - Contributor 1: 16
  - Contributor 2: 11-18
  - Reported by lab: 16-18
  - Expected DNA profile: 11-16-18

- **Type +B**
  - Contributor 1: 20
  - Contributor 2: 23-25
  - Reported by lab: 20-21-23-25
  - Expected DNA profile: 20-23-25
GHEP-MIX01
-M2 (1:10)-

Penta E

18?

Powerplex®

<table>
<thead>
<tr>
<th>Penta E</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Contributor A</td>
<td>Contributor B</td>
</tr>
<tr>
<td>(minor)</td>
<td>(major)</td>
</tr>
<tr>
<td>9-18</td>
<td>8-9</td>
</tr>
</tbody>
</table>

Slide 2
### D8S1179

<table>
<thead>
<tr>
<th></th>
<th>11-13</th>
<th>11-13-15</th>
<th>(11)-13-(15)</th>
<th>11-12-13</th>
<th>11-12-13-15</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>26</td>
<td></td>
<td></td>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>

### D8S1179

<table>
<thead>
<tr>
<th>Contributor A (minor component)</th>
<th>Contributor B (major component)</th>
</tr>
</thead>
<tbody>
<tr>
<td>11-15</td>
<td>13</td>
</tr>
</tbody>
</table>

**Contributor A** (minor component)

**Contributor B** (major component)
GHEP-MIX01
-M1 (1:5)-

Penta E

<table>
<thead>
<tr>
<th>Contributor A</th>
<th>Contributor B</th>
</tr>
</thead>
<tbody>
<tr>
<td>(minor component)</td>
<td>(major component)</td>
</tr>
<tr>
<td>12-13</td>
<td>14-17</td>
</tr>
</tbody>
</table>
GHEP-MIX03
-M2 (1:10)-

Slide 7
GHEP-MIX03
-M2 (1:10)-