

**Pilot 1 Sample Summary (low coverage) 1000 Genomes Project 05-Mar-10**

|                                |         | Number of Samples |           |           |           |            |
|--------------------------------|---------|-------------------|-----------|-----------|-----------|------------|
|                                |         | CEU               | YRI       | CHB       | JPT       | Total      |
| Broad                          | Solexa  | 10                | 20        | 0         | 5         | 35         |
| BGI                            | Solexa  | 0                 | 0         | 30        | 0         | 30         |
| Illumina                       | Solexa  | 10                | 0         | 0         | 0         | 10         |
| MPIMG                          | Solexa  | 0                 | 7         | 0         | 0         | 7          |
| Sanger                         | Solexa  | 22                | 20        | 0         | 15        | 57         |
| WashU                          | Solexa  | 9                 | 17        | 0         | 8         | 34         |
| AB                             | SOLiD   | 8                 | 0         | 0         | 0         | 8          |
| Baylor                         | SOLiD   | 32                | 0         | 0         | 0         | 32         |
| MPIMG                          | SOLiD   | 0                 | 5         | 0         | 0         | 5          |
| Baylor                         | 454 FLX | 6                 | 0         | 0         | 0         | 6          |
| Roche                          | 454FLX  | 10                | 0         | 0         | 0         | 10         |
| WashU                          | 454 FLX | 2                 | 3         | 0         | 2         | 7          |
| <b>Total redundant samples</b> |         | <b>49</b>         | <b>12</b> | <b>0</b>  | <b>0</b>  | <b>61</b>  |
| <b>Total unique samples</b>    |         | <b>60</b>         | <b>60</b> | <b>30</b> | <b>30</b> | <b>180</b> |

Redundant samples were sequenced by more than one center

**Pilot 2 Sample  
Summary (trios)**

**1000 Genomes Project**

05-Mar-10

|          |         | CEU     |         |          | YRI     |         |          |
|----------|---------|---------|---------|----------|---------|---------|----------|
|          |         | Mother  | Father  | Daughter | Mother  | Father  | Daughter |
|          |         | NA12892 | NA12891 | NA12878  | NA19238 | NA19239 | NA19240  |
| BGI      | Solexa  | 0       | 0       | 0        | 1       | 1       | 1        |
| Broad    | Solexa  | 1       | 1       | 1        | 0       | 0       | 0        |
| Illumina | Solexa  | 0       | 0       | 0        | 0       | 0       | 1        |
| MPIMG    | Solexa  | 0       | 0       | 1        | 0       | 0       | 0        |
| Sanger   | Solexa  | 1       | 1       | 1        | 0       | 0       | 0        |
| WashU    | Solexa  | 0       | 0       | 0        | 1       | 1       | 1        |
| AB       | SOLiD   | 0       | 0       | 1        | 0       | 0       | 0        |
| Baylor   | SOLiD   | 0       | 0       | 1        | 0       | 0       | 1        |
| Broad    | SOLiD   | 0       | 0       | 0        | 0       | 0       | 0        |
| Baylor   | 454 FLX | 0       | 0       | 1        | 0       | 0       | 0        |
| Roche    | 454 FLX | 0       | 0       | 0        | 0       | 0       | 1        |

This table shows which trio samples were sequenced by which centers and platforms

**Pilot 3 Sample Summary (gene regions)**

**1000 Genomes Project**

05-Mar-10

|   |         | Number of Samples |            |           |            |            |            |            |            |            |
|---|---------|-------------------|------------|-----------|------------|------------|------------|------------|------------|------------|
|   |         | Trio samples      | CEU        | TSI       | YRI        | LWK        | CHB        | JPT        | CHD        | Total      |
| Broad                                       | Solexa  | 6                 | 30         | 4         | 31         | 0          | 14         | 54         | 28         | 161        |
| Sanger                                      | Solexa  | 1                 | 18         | 62        | 14         | 0          | 14         | 9          | 0          | 117        |
| Baylor                                      | 454 FLX | 6                 | 40         | 0         | 45         | 108        | 63         | 16         | 79         | 351        |
| Broad                                       | 454FLX  | 3                 | 3          | 0         | 0          | 0          | 0          | 0          | 0          | 3          |
| WashU                                       | 454 FLX | 6                 | 20         | 0         | 29         | 0          | 18         | 26         | 0          | 93         |
| <b>Total redundant samples</b>              |         | <b>16</b>         | <b>21</b>  | <b>0</b>  | <b>7</b>   | <b>0</b>   | <b>0</b>   | <b>0</b>   | <b>0</b>   | <b>28</b>  |
| <b>Total unique samples</b>                 |         | <b>6</b>          | <b>90</b>  | <b>66</b> | <b>112</b> | <b>108</b> | <b>109</b> | <b>105</b> | <b>107</b> | <b>697</b> |
| <b>Total unique samples in related pops</b> |         | <b>6</b>          | <b>156</b> |           | <b>220</b> |            | <b>321</b> |            |            |            |

Redundant samples were sequenced by more than one center