

Table S2. Summary of the exome sequencing raw data.

<b>Total reads</b>	<b>77,230,042</b>
<b>Total yield</b>	<b>(bp)</b> <b>7,800,234,242</b>
<b>Average read length (bp)</b>	<b>101</b>
<b>Mappable reads (=reads mapped to human genome)</b>	<b>69,175,606</b>
<b>Mappable yield (bp)</b>	<b>6,645,096,198</b>
<b>% Mappable reads (out of total reads)</b>	<b>89.60%</b>
<b>On-target reads (=reads mapped to target regions)</b>	<b>49,270,671</b>
<b>On-target yield (bp)</b>	<b>3,868,803,760</b>
<b>% On-target reads (out of mappable reads)</b>	<b>71.20%</b>
<b>% On-target reads (out of total reads)</b>	<b>63.80%</b>
<b>Target regions (bp)</b>	<b>62,085,286</b>
<b>% Coverage of target regions (more than 1X)</b>	<b>92.20%</b>
<b>Number of on-target genotypes (more than 1X)</b>	<b>57,262,647</b>
<b>% Coverage of target regions (more than 10X)</b>	<b>78.80%</b>
<b>Number of on-target genotypes (more than 10X)</b>	<b>48,896,848</b>
<b>Median read depth of target regions</b>	<b>47.0X</b>
<b>Mean read depth of target regions</b>	<b>62.3X</b>
<b>Number of SNPs</b>	<b>65,124</b>
<b>Number of coding SNPs</b>	<b>18,747</b>
<b>Number of Indels</b>	<b>13,871</b>
<b>Number of coding Indels</b>	<b>667</b>