

**Supplementary Table S3.** Results of the ROHan analysis specifying a ROH if 1Mb of data contains an average proportion of heterozygous sites less than  $5 \times 10^{-5}$  for the definition of a ROH.

<b>Sample</b>	<b>% of segments in ROH</b>	<b>Lower bound estimate</b>	<b>Upper bound estimate</b>	<b>Avg. length of ROH</b>
<b>17-05</b>	0.1490	0.1490	0.1490	2,000,000
<b>17-07</b>	0.0746	0.0000	0.1493	1,000,000
<b>17-08</b>	0.5975	0.3734	0.9767	2,000,000
<b>17-10</b>	1.7280	0.9738	2.3538	1,916,670
<b>17-12</b>	0.1494	0.1493	0.2240	2,000,000
<b>17-17</b>	1.4211	1.0471	2.1164	1,900,000
<b>17-18</b>	0.0000	0.0000	0.0000	0
<b>17-19</b>	0.0000	0.0000	0.0000	0
<b>17-20</b>	0.5970	0.1491	0.8258	2,000,000
<b>17-21</b>	0.1490	0.1490	0.1490	2,000,000
<b>18-05</b>	0.6726	0.5966	1.1244	1,800,000
<b>18-06</b>	0.5220	0.2983	0.5232	1,750,000