

**Supplementary Table 8. The quality score Q distribution for our custom resequencing array.** At a 0.67 threshold, 5.7% (5,973/104,753) of all positions on the resequencing array have at least one probe quartet presenting low performance and therefore will not provide reliable variant calls. SRMA called variant samples in 3% (185/5,973) of these positions, which were replaced with “N”

	Q≤0.67	Q>0.67	Total
Called SNP positions	185	374	559
Called reference positions	5,788	98,221	104,009
Total	5,973	98,595	104,568