

Table 1: Breakdown of runtime analysis comparison, all times are given per sample.

	<b>popSTR</b>	<b>popSTR2</b>
samples	15,220	40,121
markers	880,355	5,401,401
polymorphic markers	380,261	1,636,021
Read selection	9.2 h	9.45 h
Sample slippage	0.25 h	0.065 h
Genotyping	0.35 h	2.19 h
CPU hours/1,000,000 markers	11.25	2.17