

Graf, Ludin et al. 2015

**Comparative genomics of drug resistance of the sleeping sickness parasite
*Trypanosoma brucei rhodesiense***

	STIB900	STIB900-M	STIB900-P
High-quality (HQ) reads	1,418,416	1,513,957	1,482,415
Average read length	330 b	362 b	371 b
Calculated coverage	18-fold	21-fold	21-fold
Mapped reads (all mapping quality)	1,212,557	1,205,716	1,201,165
Mapped reads (mapq \geq 20)	897,213	959,151	959,663
Coverage with HQ bases (DP4 \geq 5)	82%	82%	82%
Gene coverage (gene length \geq 95%)	84%	81%	83%

Table S1. Whole genome sequencing (on the Roche-454 platform) and mapping statistics of parental, drug-sensitive *T. b. rhodesiense* STIB900 and its two drug-resistant derivatives STIB900-M and STIB900-P compared to the *T. b. brucei* TREU927 reference genome.