

Table S2. Deduced amino acid sequence information for PfMAAP for the *Laverania* species compared to the 3D7 reference isolate.

ID	Size of protein	Size of repeat	Repeat coordinates	Isolate	References
PF3D7_1035900	566	362	144-506	Laboratory isolate	1
PRG01_1034400	571	367	144-511	<i>P. reichenowi</i> G01 isolate	2
PRCDC_1035200	545	341	144-485	<i>P. reichenowi</i> CDC isolate	3
PBILCG01_1034800	394	192	142-334	<i>P. billcollinsi</i> G01 isolate	2
PGSY75_0012400*	207	n/a	n/a	<i>P.gaboni</i> SY75 isolate	3
PPRFG01_1036900	602	402	144-546	<i>P. praefalciparum</i> G01 isolate	4
PADL01_1034600	354	190	142-332	<i>P. adleri</i> G01 isolate	5

Note: All isolates had a repeat periodicity of 3.92 with the exception of *P.adleri* and *P.gaboni*. The asterisk indicates that the database sequence for *P.gaboni* was deposited as a truncated sequence.

References:

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2. Otto TD, Gilabert A, Crellen T, Böhme U, Arnathau C, Sanders M, Oyola SO, Okouga AP, Boundenga L, Willaume E, Ngoubangoye B, Moukoudoum ND, Paupy C, Durand P, Rougeron V, Ollomo B, Renaud F, Newbold C, Berriman M, Prugnolle F. Genomes of all known members of a *Plasmodium* subgenus reveal paths to virulent human malaria. Nat Microbiol. 2018 Jun;3(6):687-697. doi: 10.1038/s41564-018-0162-2.
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