

Supplementary Figure 2: Protein sequence alignment between *P. chabaudi* rpn2, *P. falciparum* rpn2 and chimeric rpn2.

Consensus	MRFENQFSKHDIVTSASGVIALNNEEETSCLKLFGLEKLNLAIVDVYWPPELADSIKIEELCEDEDFVGRELANLLASKIYFHLEKYSEALKYALCAGKLFNIKEKSQYVETMLAKCIEKYVEIREMOYD-----IDYN-----NQHNI-----NDGITNNN-----DIFNAY-----NN	153
pcRPN2	MDVEKTIHENDIVTSASGVIALNNEEETSCLKLFGLEKLNLAIVDVYWPPELADSIKIEELCEDEDFVGRELANLLASKIYFHLEKYSEALKYALCAGKLFNIKEKSQYVETMLAKCIEKYVEIREMOYD-----IDYN-----NQHNI-----NDGITNNN-----DIFNAY-----NN	207
pfRPN2	MRFENQFSKHDIVTSASGVIALNNEEETSCLKLFGLEKLNLAIVDVYWPPELADSIKIEELCEDEDFVGRELANLLASKIYFHLEKYSEALKYALCAGKLFNIKEKSQYVETMLAKCIEKYVEIREMOYD-----IDYN-----NQHNI-----NDGITNNN-----DIFNAY-----NN	153
chimeric_RPN2	MRFENQFSKHDIVTSASGVIALNNEEETSCLKLFGLEKLNLAIVDVYWPPELADSIKIEELCEDEDFVGRELANLLASKIYFHLEKYSEALKYALCAGKLFNIKEKSQYVETMLAKCIEKYVEIREMOYD-----IDYN-----NQHNI-----NDGITNNN-----DIFNAY-----NN	153
Consensus	NDLVELNSHNELLNKETDIFRFDINNEINQRMELLVDEMDVCIKSNDIKEALGVLDARRLDKVEYIIANAENKIEILAHNSINNEKHNMNKSFRNEYFKLLVNLVLSLSEELKTEYINLCECLYIIDDYKVAEILKLLHNYHLMAYQISFDLVDVFENKIFLRNLIQIENLQNKAYYFGEYFVTTPOEENNDADNKENE	360
pcRPN2	NHLFSRDNENDKVKENNIKDKDNNINNKMETFVDMLEICIKNNSIKEALGVLDARRLDKVEYIIANAENKIEILAHNSINNEKHNMNKSFRNEYFKLLVNLVLSLSEELKTEYINLCECLYIIDDYKVAEILKLLHNYHLMAYQISFDLVDVFENKIFLRNLIQIENLQNKAYYFGEYFVTTPOEENNDADNKENE	409
pfRPN2	NDLVELNSHNELLNKETDIFRFDINNEINQRMELLVDEMDVCIKSNDIKEALGVLDARRLDKVEYIIANAENKIEILAHNSINNEKHNMNKSFRNEYFKLLVNLVLSLSEELKTEYINLCECLYIIDDYKVAEILKLLHNYHLMAYQISFDLVDVFENKIFLRNLIQIENLQNKAYYFGEYFVTTPOEENNDADNKENE	360
chimeric_RPN2	NDLVELNSHNELLNKETDIFRFDINNEINQRMELLVDEMDVCIKSNDIKEALGVLDARRLDKVEYIIANAENKIEILAHNSINNEKHNMNKSFRNEYFKLLVNLVLSLSEELKTEYINLCECLYIIDDYKVAEILKLLHNYHLMAYQISFDLVDVFENKIFLRNLIQIENLQNKAYYFGEYFVTTPOEENNDADNKENE	360
Consensus	SNAIITNEQQDENNNEKEDKDNNDGKNPEHNDNNKPNDLTNDEPTYNNDDKAINDGNDNNDNNNNNNNNNNIIVEDVLKYISKKHIFYNKMKLLYILTGVKVTGNLYIEFLHRNHADLILLDTYKNIIVDSRSSITHHGIVIAHALMQTGTTCDFVFLRSNIEWLSKAINWEKFSATASLGVVYKGHVNESFMVLSTHLPYNDVS	567
pcRPN2	SNSAISGEGTNGV-KSBNTEQDAQKENSQSSNTEQAQDSEGDSAMPSTAVN---TDDKMAKDNEEKDRIPEDVLMVYVNEQHLEKMKLLIHLTGKIPSTLYIEFLHRNHADLILLDTYKNIIVDSRSSITHHGIVIAHALMQTGTTCDFVFLRSNIEWLSKAINWEKFSATASLGVVYKGHVNESFMVLSTHLPYNDVS	611
pfRPN2	SNAIITNEQQDENNNEKEDKDNNDGKNPEHNDNNKPNDLTNDEPTYNNDDKAINDGNDNNDNNNNNNNNNNIIVEDVLKYISKKHIFYNKMKLLYILTGVKVTGNLYIEFLHRNHADLILLDTYKNIIVDSRSSITHHGIVIAHALMQTGTTCDFVFLRSNIEWLSKAINWEKFSATASLGVVYKGHVNESFMVLSTHLPYNDVS	567
chimeric_RPN2	SNAIITNEQQDENNNEKEDKDNNDGKNPEHNDNNKPNDLTNDEPTYNNDDKAINDGNDNNDNNNNNNNNNNIIVEDVLKYISKKHIFYNKMKLLYILTGVKVTGNLYIEFLHRNHADLILLDTYKNIIVDSRSSITHHGIVIAHALMQTGTTCDFVFLRSNIEWLSKAINWEKFSATASLGVVYKGHVNESFMVLSTHLPYNDVS	567
Consensus	TEIANNINVLAPSGVYSEGGSYALGLIHANYNTNDKKVKNYLSQLKSNMDEVLQHGCLGLGLVCLGDSNDENTYDELKAILYSDS AVAGE SAAYAIGLLKLGSGDDKCIDELLAYAHTQHEKITRACISILGFVMPQKEREADNLIIEELINDKDAIIRYGGMFTIALAYCGLSNYNKHVIKKLLHPSVSDVSDVRRAAVI	774
pcRPN2	ROIANNINANISQSDVYSEGGSYALGLIHANYNTNDKKVKNYLSQLKSNMDEVLQHGCLGLGLVCLGDSNDENTYDELKAILYSDS AVAGE SAAYAIGLLKLGSGDDKCIDELLAYAHTQHEKITRACISILGFVMPQKEREADNLIIEELINDKDAIIRYGGMFTIALAYCGLSNYNKHVIKKLLHPSVSDVSDVRRAAVI	818
pfRPN2	TEIANNINVLAPSGVYSEGGSYALGLIHANYNTNDKKVKNYLSQLKSNMDEVLQHGCLGLGLVCLGDSNDENTYDELKAILYSDS AVAGE SAAYAIGLLKLGSGDDKCIDELLAYAHTQHEKITRACISILGFVMPQKEREADNLIIEELINDKDAIIRYGGMFTIALAYCGLSNYNKHVIKKLLHPSVSDVSDVRRAAVI	774
chimeric_RPN2	TEIANNINVLAPSGVYSEGGSYALGLIHANYNTNDKKVKNYLSQLKSNMDEVLQHGCLGLGLVCLGDSNDENTYDELKAILYSDS AVAGE SAAYAIGLLKLGSGDDKCIDELLAYAHTQHEKITRACISILGFVMPQKEREADNLIIEELINDKDAIIRYGGMFTIALAYCGLSNYNKHVIKKLLHPSVSDVSDVRRAAVI	774
Consensus	ALGFVLCNTPAQVPMFNLNLLIESYNPHVRYGAALALGIACAATGNEEAVNMLPLLLTDTDFVFRQSAFISLGLIFQQSNENVNPFFKFKDEIMKILSDKHEDIIAKFGATVGLGLLDICGRNAISTFFTRRANIIRPQSAVGFCLFCQLWYWPFLIHMISLTFPLPTCLIGLTEDLKVKNFTIIST-KNOAFDYPFSLSKVKQEK	980
pcRPN2	ALGFVLCNTPAQVPMFNLNLLIESYNPHVRYGAALALGIACAATGNEEAVNMLPLLLTDTDFVFRQSAFISLGLIFQQSNENVNPFFKFKDEIMKILSDKHEDIIAKFGATVGLGLLDICGRNAISTFFTRRANIIRPQSAVGFCLFCQLWYWPFLIHMISLTFPLPTCLIGLTEDLKVKNFTIIST-KNOAFDYPFSLSKVKQEK	1024
pfRPN2	ALGFVLCNSFNQVPMFNLNLLIESYNPHVRYGAALALGIACAATGNEEAVNMLPLLLTDTDFVFRQSAFISLGLIFQQSNENVNPFFKFKDEIMKILSDKHEDIIAKFGATVGLGLLDICGRNAISTFFTRRANIIRPQSAVGFCLFCQLWYWPFLIHMISLTFPLPTCLIGLTEDLKVKNFTIIST-KNOAFDYPFSLSKVKQEK	981
chimeric_RPN2	ALGFVLCNTPAQVPMFNLNLLIESYNPHVRYGAALALGIACAATGNEEAVNMLPLLLTDTDFVFRQSAFISLGLIFQQSNENVNPFFKFKDEIMKILSDKHEDIIAKFGATVGLGLLDICGRNAISTFFTRRANIIRPQSAVGFCLFCQLWYWPFLIHMISLTFPLPTCLIGLTEDLKVKNFTIIST-KNOAFDYPFSLSKVKQEK	980
Consensus	KETVTAIILSTTDKRRSLKLRKQKNENKLTKEKNPQDDSSSVLSDGKSMKNLEILSTAATIGQSSHVSHAESVEGSANDENSNDHQNDANQFSQLQRIKSD-KSKSASL--SHATTVDMKNPCRVIKTQEKYIEYPPNSRFKPIISIRKSGFIMLSDTTPTEPFDIEPKLESGNKKEVPPPEPPTWKDEN	1168
pcRPN2	KETVTAIILSTTDKRRSLKLRKQKNENKLTKEKNPQDDSSSVLSDGKSMKNLEILSTAATIGQSSHVSHAESVEGSANDENSNDHQNDANQFSQLQRIKSD-KSKSASL--SHATTVDMKNPCRVIKTQEKYIEYPPNSRFKPIISIRKSGFIMLSDTTPTEPFDIEPKLESGNKKEVPPPEPPTWKDEN	1212
pfRPN2	KETVTAIILSTTDKRRSLKLRKQKNENKLTKEKNPQDDSSSVLSDGKSMKNLEILSTAATIGQSSHVSHAESVEGSANDENSNDHQNDANQFSQLQRIKSD-KSKSASL--SHATTVDMKNPCRVIKTQEKYIEYPPNSRFKPIISIRKSGFIMLSDTTPTEPFDIEPKLESGNKKEVPPPEPPTWKDEN	1172
chimeric_RPN2	KETVTAIILSTTDKRRSLKLRKQKNENKLTKEKNPQDDSSSVLSDGKSMKNLEILSTAATIGQSSHVSHAESVEGSANDENSNDHQNDANQFSQLQRIKSD-KSKSASL--SHATTVDMKNPCRVIKTQEKYIEYPPNSRFKPIISIRKSGFIMLSDTTPTEPFDIEPKLESGNKKEVPPPEPPTWKDEN	1168