**Supplementary File 2. Amino acid sequences of the TRAP variants expressed by the parasite lines *TRAP-I*, *MIC2-I*, *αX-I,* *αL-I, and RevCharge*.**

Shown are the sequences of each TRAP replacement. Residues that are part of the extendable ß-ribbon are written in green, residues that form the remainder of the I domain are written in red, residues of the thrombospondin domain are written in orange, and the remaining native residues of *Pb*TRAP are written in black. Residues written in blue were introduced into wild type *Pb*TRAP to generate a more negative charge on the portion of the I domain surface surrounding the MIDAS in the *RevCharge* mutant. Residues written in white on a black background were mutated to create a better fitting of the exchanged portion of the I domain with the N- and C-terminal segments of the *Pb*TRAP I domain/extendable ß-ribbon. The calculated pI of the I domain region is shown in parentheses.

***Pb*TRAP-αL**

MKLLGNSKYFFVVLLLCISVFLNGQEILDEIKYSEEVCNEQSDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAVQFSTSYKTEFDFSDYVKRKDPDALLKHVKHMLLLTNTFGAINYVATEVFREELGARPDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTELQKKICQEVEKVALCGKWEEWSECSTTCDNGTKIRKRKVLHPNCAGEMTAPCKVRDCPPKPVAPPVIPIKVPDVPVKPVEPIEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAKPAEPAEPAEPAEPAEPVNPDNPILPIKPEEPSGGAEPLNPEVENPFIIPDEPIEPIIAPGAVPDKPIIPEESNELPNNLPESPSDSQVEYPRPNDNGDNSNNTINSNKNIPNKHVPPTDDNPYKGQEERIPKPHRSNDEYIYYNNANNNDKLEPEIPSKDYEENKSKKQSKSNNGYKIAGGIIGGLAIIGCIGVGYNFIAGSSAAAMAGEAAPFEDVMADDEKGIVENEQFKLPEDNDWN (pI 5.8)

***Pb*TRAP-αX**

MKLLGNSKYFFVVLLLCISVFLNGQEILDEIKYSEEVCNEQQDIVFLIDGSGSISSRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRSSNPLSLLASVHQLQGFTYTATAIQNVVHRLFHASYGARRDAAKILIVITDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFQNRNSWKELNDIASKPSQEHIFKVEDFDALKDIQNQLKEKICQEVEKVALCGKWEEWSECSTTCDNGTKIRKRKVLHPNCAGEMTAPCKVRDCPPKPVAPPVIPIKVPDVPVKPVEPIEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAKPAEPAEPAEPAEPAEPVNPDNPILPIKPEEPSGGAEPLNPEVENPFIIPDEPIEPIIAPGAVPDKPIIPEESNELPNNLPESPSDSQVEYPRPNDNGDNSNNTINSNKNIPNKHVPPTDDNPYKGQEERIPKPHRSNDEYIYYNNANNNDKLEPEIPSKDYEENKSKKQSKSNNGYKIAGGIIGGLAIIGCIGVGYNFIAGSSAAAMAGEAAPFEDVMADDEKGIVENEQFKLPEDNDWN (pI 8.9)

***Pb*TRAP-MIC2**

MKLLGNSKYFFVVLLLCISVFLNGQEILDEIKYSEEVCNEQVDICFLIDSSGSIGIQNFRLVKQFLHTFLMVLPIGPEEVNNAVVTYSTDVHLQWDLQSPNAVDKQLAAHAVLEMPYKKGSTNTSDGLKACKQILFTGSRPGREHVPKLVIGMTDGESDSDFRTVRAAKEIRELGGIVTVLAVGHYVKHSECRSMCGCSGTSDDDSPCPLYLRADWGQLATAIKPMLKEVCQEVEKVALCGKWEEWSECSTTCDNGTKIRKRKVLHPNCAGEMTAPCKVRDCPPKPVAPPVIPIKVPDVPVKPVEPIEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAKPAEPAEPAEPAEPAEPVNPDNPILPIKPEEPSGGAEPLNPEVENPFIIPDEPIEPIIAPGAVPDKPIIPEESNELPNNLPESPSDSQVEYPRPNDNGDNSNNTINSNKNIPNKHVPPTDDNPYKGQEERIPKPHRSNDEYIYYNNANNNDKLEPEIPSKDYEENKSKKQSKSNNGYKIAGGIIGGLAIIGCIGVGYNFIAGSSAAAMAGEAAPFEDVMADDEKGIVENEQFKLPEDNDWN (pI 6.1)

***Pb*TRAP**

MKLLGNSKYFFVVLLLCISVFLNGQEILDEIKYSEEVCNEQIDLHILLDGSGSIGHSNWISHVIPMLTTLVDNLNISRDEINISMTLFSTYARELVRLKRYGSTSKASLRFIIAQLQNNYSPHGTTNLTSALLNVDNLIQKKMNRPNAIQLVIILTDGIPNNLKKSTTVVNQLKKKDVNVAIIGVGAGVNNMFNRILVGCGKLGPCPYYSYGSWDQAQTMIKPFLSKVCQEVEKVALCGKWEEWSECSTTCDNGTKIRKRKVLHPNCAGEMTAPCKVRDCPPKPVAPPVIPIKVPDVPVKPVEPIEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAKPAEPAEPAEPAEPAEPVNPDNPILPIKPEEPSGGAEPLNPEVENPFIIPDEPIEPIIAPGAVPDKPIIPEESNELPNNLPESPSDSQVEYPRPNDNGDNSNNTINSNKNIPNKHVPPTDDNPYKGQEERIPKPHRSNDEYIYYNNANNNDKLEPEIPSKDYEENKSKKQSKSNNGYKIAGGIIGGLAIIGCIGVGYNFIAGSSAAAMAGEAAPFEDVMADDEKGIVENEQFKLPEDNDWN (pI 9.7)

***Pb*RevCharge**

MKLLGNSKYFFVVLLLCISVFLNGQEILDEIKYSEEVCNEQIDLHILLDGSGSIGESNWISEVIPMLTTLVDNLNISRDEINISMTLFSTYARELVRLKRYGSTSKASLRFIIAQLQNNYSPEGTTNLTSALLNVDNLIQKKMNRPNAIQLVIILTDGIPNNLQDSTTVVNQLKKKDVNVAIIGVGAGVNNMFNEILVGCGALGPCPYYSYGSWDQAQTMIKPFLSKVCQEVEKVALCGKWEEWSECSTTCDNGTKIRKRKVLHPNCAGEMTAPCKVRDCPPKPVAPPVIPIKVPDVPVKPVEPIEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAEPAKPAEPAEPAEPAEPAEPVNPDNPILPIKPEEPSGGAEPLNPEVENPFIIPDEPIEPIIAPGAVPDKPIIPEESNELPNNLPESPSDSQVEYPRPNDNGDNSNNTINSNKNIPNKHVPPTDDNPYKGQEERIPKPHRSNDEYIYYNNANNNDKLEPEIPSKDYEENKSKKQSKSNNGYKIAGGIIGGLAIIGCIGVGYNFIAGSSAAAMAGEAAPFEDVMADDEKGIVENEQFKLPEDNDWN (pI 6.8)