

# Prediction of malarial signal peptides using signalHsmm

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## 1 Introduction

Medically significant *Plasmodiidae* have unique composition of signal peptides

Heavy adenine-thymine bias of malarial genomes alters amino acid composition of malarial signal peptides making them hard to predict using software trained on other eukaryotes.

## 2 Reduced alphabet

## 3 Benchmark

## References

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- Hiller, K., Grote, A., Scheer, M., Münch, R., and Jahn, D. (2004). PrediSi: prediction of signal peptides and their cleavage positions. *Nucleic Acids Research*, 32(suppl 2):W375–W379.
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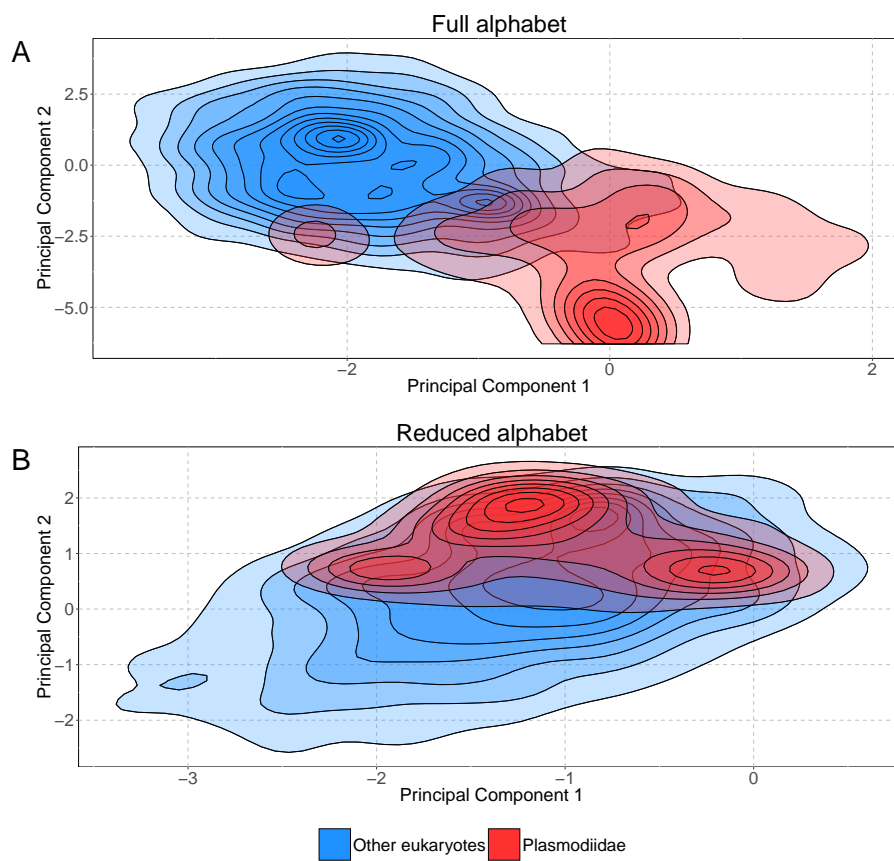


Figure 1: Principal component analysis of amino acid frequency in signal peptides belonging to *Plasmodiidae* and other eukaryotes. A) Frequency of amino acids. B) Frequency of amino acids encoded using the reduced alphabet.

	Sensitivity	Specificity	MCC	AUC
signalP 4.1 (no tm) (Petersen et al., 2011)	0.8235	0.9100	0.6872	0.8667
signalP 4.1 (tm) (Petersen et al., 2011)	0.6471	0.9431	0.6196	0.7951
signalP 3.0 (NN) (Bendtsen et al., 2004)	0.8824	0.9052	0.7220	0.8938
signalP 3.0 (HMM) (Bendtsen et al., 2004)	0.6275	0.9194	0.5553	0.7734
PrediSi (Hiller et al., 2004)	0.3333	<b>0.9573</b>	0.3849	0.6453
Philius (Reynolds et al., 2008)	0.6078	0.9336	0.5684	0.7707
Phobius (Käll et al., 2004)	0.6471	0.9289	0.5895	0.7880
signalHsmm-2010	0.9804	0.8720	0.7409	0.9262
signalHsmm-2010 (hom. 50%)	<b>1.0000</b>	0.8768	<b>0.7621</b>	<b>0.9384</b>
signalHsmm-2010 (raw aa)	0.8431	0.9005	0.6853	0.8718