Supplementary Table S4. Benchmark results for the recall and precision of CS prediction in Tat/SPI in four tolerance windows. The PEFT-SP (LoRA) represents PEFT-SP using LoRA with ESM2-3B backbone. The bold value represents the highest recall or precision among the predictors in a particular tolerance window. The n.d. represents the model was not trained on the data. The * denotes the performance reported in SignalP 6.0.

	Archaea				**Gram-negative bacteria**				**Gram-positive bacteria**			
Method	**± 0**	**± 1**	**± 2**	**± 3**	**± 0**	**± 1**	**± 2**	**± 3**	**± 0**	**± 1**	**± 2**	**± 3**
CS recall												
PEFT-SP (LoRA)	0.268	0.292	0.339	0.405	0.711	0.764	0.878	0.904	**0.550**	**0.550**	**0.765**	**0.765**
SignalP 6.0 retrained	0.292	0.363	0.363	0.429	**0.782**	**0.839**	**0.892**	**0.914**	0.396	0.457	0.669	0.669
SignalP 6.0 *	**0.333**	**0.444**	0.444	0.444	0.706	0.765	0.784	0.804	0.556	0.556	0.667	0.667
SignalP 5.0 *	0.222	**0.444**	0.444	0.444	0.412	0.451	0.490	0.490	0.167	0.222	0.222	0.278
PRED - TAT *	**0.333**	**0.444**	**0.667**	**0.667**	0.725	0.765	0.784	0.824	0.611	0.611	0.667	0.722
TatP *	0.222	0.333	0.444	0.444	0.588	0.608	0.608	0.627	0.333	0.333	0.389	0.389
TATFIND *	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
CS precision												
PEFT-SP (LoRA)	0.417	0.444	0.514	0.618	0.712	0.763	**0.873**	**0.899**	0.611	0.611	0.889	0.889
SignalP 6.0 retrained	**0.469**	**0.562**	**0.562**	**0.656**	**0.764**	**0.820**	0.872	0.895	0.518	0.595	**0.921**	**0.921**
SignalP 6.0 *	0.375	0.500	0.500	0.500	0.679	0.736	0.755	0.774	**0.714**	**0.714**	0.857	0.857
SignalP 5.0 *	0.182	0.364	0.364	0.364	0.488	0.535	0.581	0.581	0.273	0.364	0.364	0.455
PRED - TAT *	0.231	0.308	0.462	0.462	0.638	0.672	0.690	0.724	0.458	0.458	0.500	0.542
TatP *	0.133	0.200	0.267	0.267	0.326	0.337	0.337	0.348	0.167	0.167	0.194	0.194
TATFIND *	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.