

Table S1 - Average MCC distributions of secondary structure predictions done with the *P-DCfold* algorithm and using different homologous sequence selection models on SRP RNA (top), U1 RNA (center) and 5S RNA (bottom).

	All	M_{HC}	$\mathcal{M}_{GU}$	$\mathcal{M}_{GC}$	$\mathcal{M}_{GC+GU}$
Avg MCC	51.83	68.98	73.74	67.23	75.39
Max MCC	91	90	89	90	85
Min MCC	3	37	40	37	45
% of predictions with MCC > 75	6.4%	33%	61%	24%	67%

	All	M_{HC}	$\mathcal{M}_{GU}$	$\mathcal{M}_{GC}$	$\mathcal{M}_{GC+GU}$
Avg MCC	62.56	74.02	84.05	80.95	84.63
Max MCC	96	93	93	93	93
Min MCC	4	28	49	55	57
% of predictions with MCC > 75	25.7%	61%	95%	70%	96%

	All	M_{HC}	$\mathcal{M}_{GU}$	$\mathcal{M}_{GC}$	$\mathcal{M}_{GC+GU}$
Avg MCC	79.48	70.58	84.78	90.1	90.12
Max MCC	97	92	95	94	92
Min MCC	14	19	74	74	81
% of predictions with MCC > 75	67.7%	45%	90%	98%	100%