

Convolution	Encoder	Decoder	Evaluate	Failed alignment	Short alignment	No prediction	Match	Mismatch	Insertion	Deletion	Adenine	Cytosine	Guanine	Thymine	AUC	PhredQ score
URN	LS5	CRF	99.4	0.20	0.32	0.06	93.3	2.08	1.86	2.76	9.94	13.1	16.4	11.9	94.4	20.6
URN	BFW	CRF	99.4	0.21	0.33	0.06	93.3	2.04	1.72	2.89	9.62	13.5	16.3	11.9	94.4	19.0
CAT	BFW	CRF	99.4	0.23	0.33	0.05	93.4	1.98	1.56	3.00	9.90	14.2	16.6	12.2	94.5	18.1
CAT	LS5	CRF	99.4	0.25	0.32	0.05	93.6	1.94	1.47	3.02	10.0	14.0	16.5	12.5	94.5	21.0
BON	LS5	CRF	99.4	0.25	0.32	0.01	93.3	2.03	1.74	2.92	9.65	14.2	17.1	12.5	94.3	22.3
CAU	LS5	CRF	99.4	0.23	0.33	0.04	93.2	2.11	1.88	2.79	9.15	14.0	17.0	11.5	94.3	21.2
BON	BRE	CRF	99.4	0.25	0.32	0.02	93.0	2.16	1.79	3.07	9.73	16.0	17.7	13.8	93.9	24.5
SAC	LS5	CRF	99.4	0.19	0.33	0.09	93.2	2.07	1.61	3.10	10.6	15.0	19.1	14.0	94.2	19.0
BON	BFW	CRF	99.4	0.22	0.33	0.02	92.8	2.23	1.97	2.98	10.0	15.1	19.2	13.6	93.8	17.9
URN	LS3	CRF	99.4	0.21	0.32	0.08	92.8	2.22	1.92	3.02	9.99	15.3	18.8	13.7	93.7	21.9