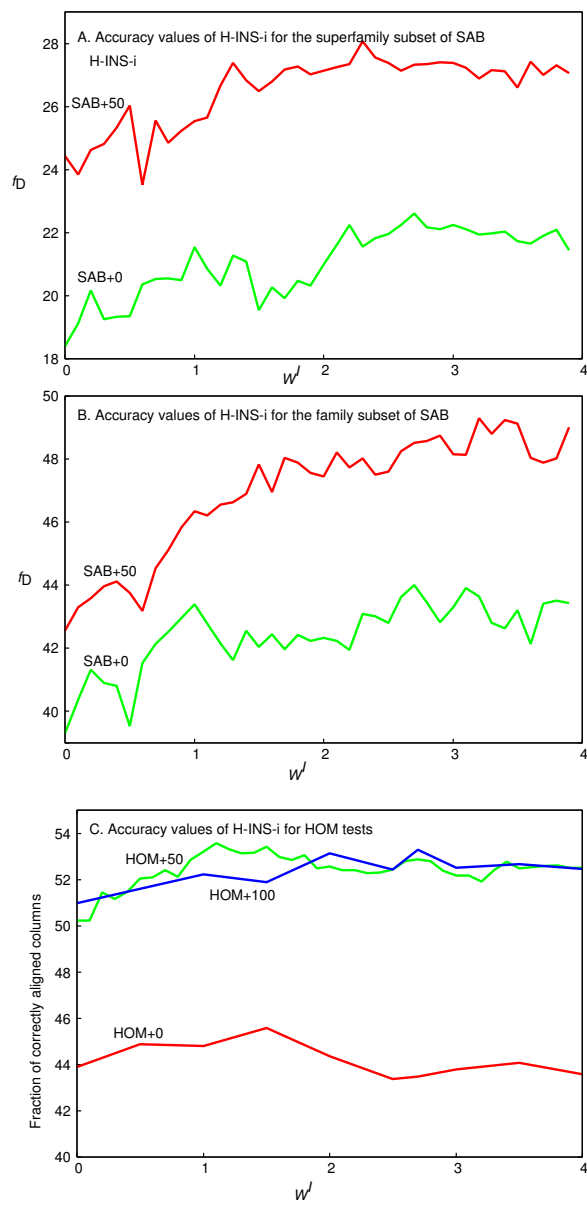# SUPPLEMENTARY DATA

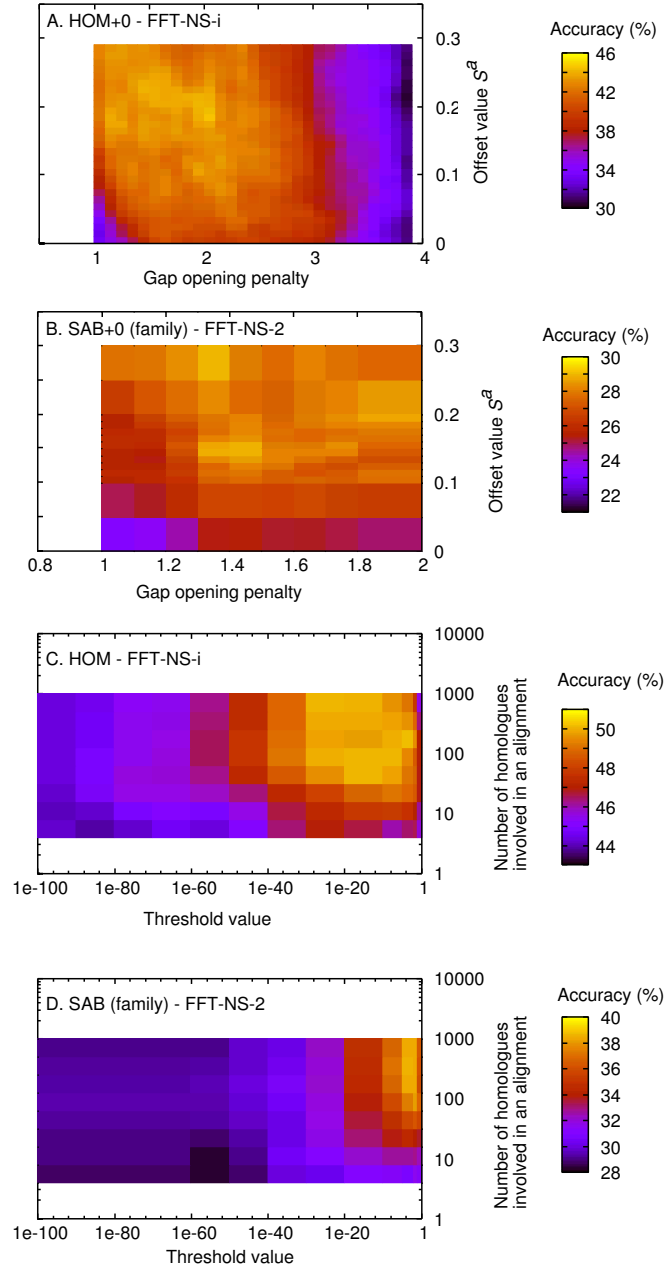Figure 1: W^I value versus the accuracy value for the SAB tests (A,B) and the HOM test (C).

Figure 2: Alignment accuracies on various conditions.
A, Accuracy values of the FFT-NS-i option for the HOM+0 test on various gap opening penalty S^{op} and offset value S^{a}; B, Accuracy values of the FFT-NS-2 option for the family subset of the SAB+0 test on various gap opening penalty S^{op} and offset value S^{a}; C, Accuracy values of the FFT-NS-i option for the HOM test on various conditions. D, Accuracy values of the FFT-NS-2 option for the family subset of the SAB test on various conditions.

Table 1: Comparison of accuracy values (%) of multiple sequence alignment programs

Method	Dataset						
	HOM+0	HOM+50	TWIs+0	TWIs+50	TWIf+0	TWIf+50	PREFAB (%id=0-20)
G-INS-i	42.58	53.85	20.73	**29.58**	41.68	**51.11**	46.75
H-INS-i	43.20	**53.37**	**23.36**	27.87	42.78	50.29	**48.22**
F-INS-i	43.14	53.72	22.03	27.25	43.21	47.59	48.00
NW-NS-i	43.57	50.68	18.16	22.79	37.46	44.90	46.00
FFT-NS-i	43.57	50.68	18.16	22.76	37.46	44.85	45.72
FFT-NS-i2	43.40	50.22	17.03	22.19	36.09	44.56	45.36
NW-NS-2	35.94	44.42	12.89	17.49	30.27	36.95	43.15
FFT-NS-2	35.94	44.42	12.89	17.49	30.27	37.08	43.19
FFT-NS-1	33.30	42.59	11.01	16.72	25.35	32.16	40.90
PROBCONS	**47.95**	51.59	22.06	22.53	**44.48**	44.86	45.63
TCoffee 2.02	43.49	49.71	21.80	21.85	44.20	45.18	45.30
TCoffee 1.37	41.97	42.63	17.12	15.20	34.14	22.62	40.92
FFT-NS-i 3.88	38.12	45.18	12.88	17.56	30.67	34.67	42.11
MUSCLE-i	43.44	46.90	15.67	19.61	36.38	38.17	42.77
MUSCLE-p	39.46	43.39	11.90	17.45	30.95	36.13	40.85
MUSCLE-2	35.59	42.44	10.64	15.09	26.02	32.77	39.37
MUSCLE-fast	33.95	37.97	11.00	12.37	28.28	30.06	38.44
CLUSTAL W 1.38	36.77	37.33	12.76	12.91	34.28	34.95	33.96
CLUSTAL W 1.38 -quicktree	34.25	38.07	11.48	12.46	32.78	33.89	33.89
Align-m	31.26	31.41	17.08	15.63	33.74	29.40	
POA progressive, local	21.15	33.30	8.990	6.142	22.75	20.58	29.85
POA progressive, global	26.35	33.66	9.431	8.108	27.29	23.76	28.57