

A *C. albicans*

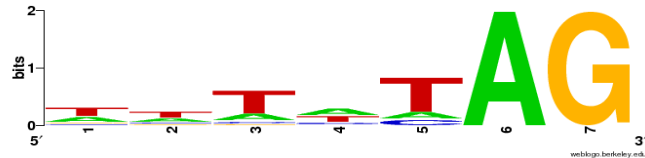
5 prime

A	0.00	0.00	0.98	0.06	0.01	0.02
C	0.00	0.00	0.00	0.08	0.00	0.01
G	1.00	0.00	0.01	0.01	0.99	0.00
T	0.00	1.00	0.01	0.85	0.00	0.97



3 prime

A	0.32	0.30	0.20	0.42	0.15	1.00	0.00
C	0.09	0.12	0.07	0.16	0.13	0.00	0.00
G	0.10	0.10	0.06	0.04	0.00	0.00	1.00
T	0.49	0.48	0.67	0.38	0.72	0.00	0.00



C. parapsilosis

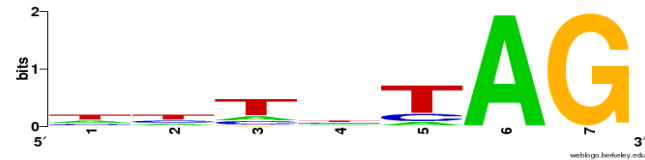
5 prime

A	0.00	0.00	0.97	0.06	0.01	0.02
C	0.00	0.00	0.00	0.11	0.01	0.02
G	1.00	0.00	0.01	0.01	0.97	0.00
T	0.00	1.00	0.02	0.82	0.01	0.96

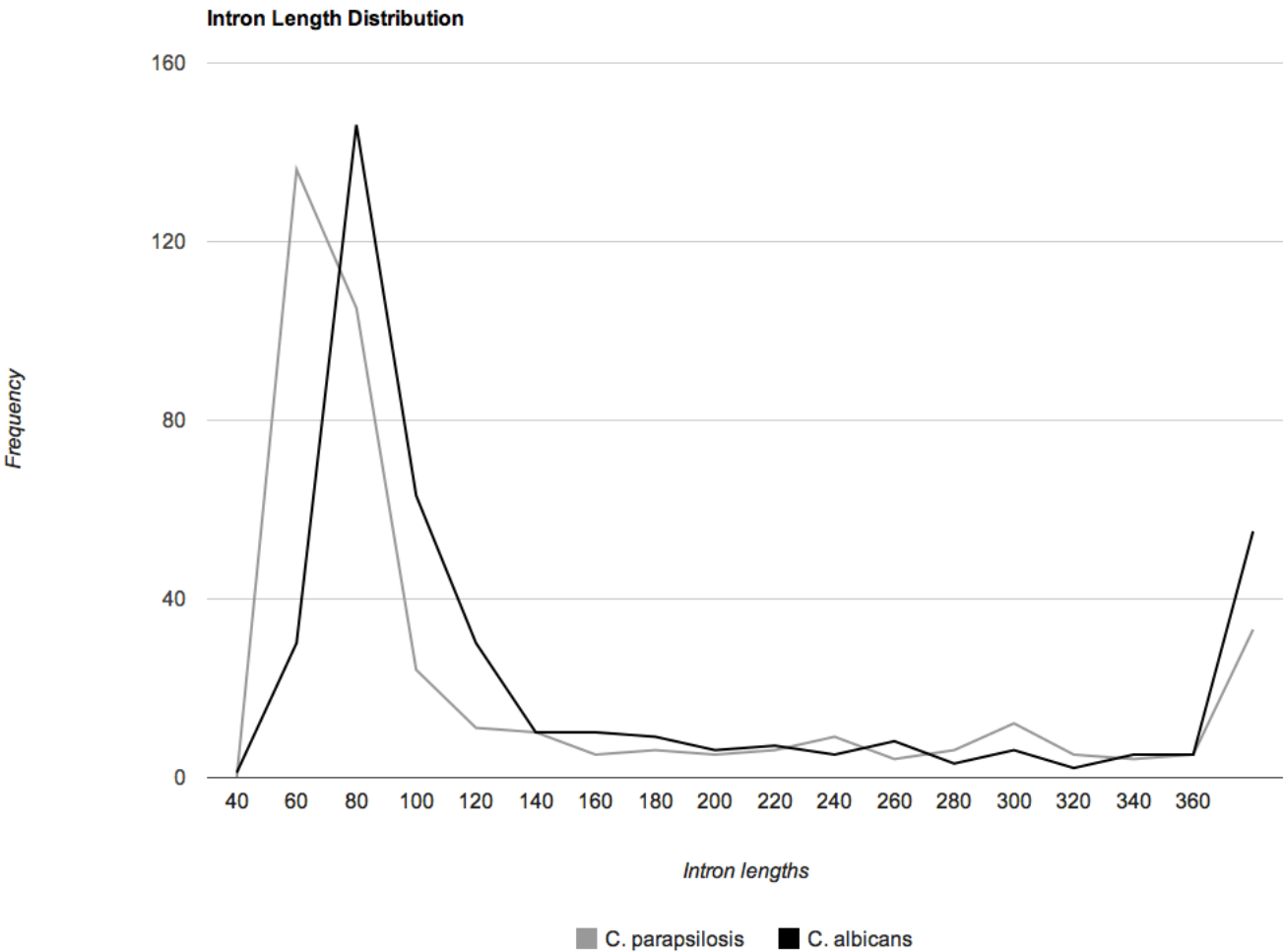


3 prime

A	0.26	0.22	0.18	0.27	0.11	0.99	0.00
C	0.20	0.24	0.17	0.29	0.21	0.00	0.00
G	0.08	0.08	0.04	0.09	0.00	0.01	1.00
T	0.46	0.46	0.61	0.35	0.68	0.00	0.00



B



(A) Intron length comparison between *C. parapsilosis* and *C. albicans*. (B) Intron consensus sequence comparison between *Candida parapsilosis* and *Candida albicans*. The frequency matrixes were calculated from the intron sequences according to the *C. albicans* and *C. parapsilosis* latest annotation. The motif logo were generated by using the webtool <http://www.benoslab.pitt.edu/stamp/index.php>