Supplementary Note:

Marginal probability landscape visualizations

(a) COX24 (Average PAM = 213, compr=14)

(b) PET100 (Average PAM = 183, compr=5.1)

(c) COA3 (Average n = 314, compr=0.9)

(d) PET117 (Average n = 91, compr=35)

(e) COA1 (Average n = 408, compr=-3.1)

(f) MSS51 (Average n = 300, compr=1.8)

(g) PET191 (Average n = 216, compr=29.4)

(h) COX23 (Average n = 245, compr=16.6)
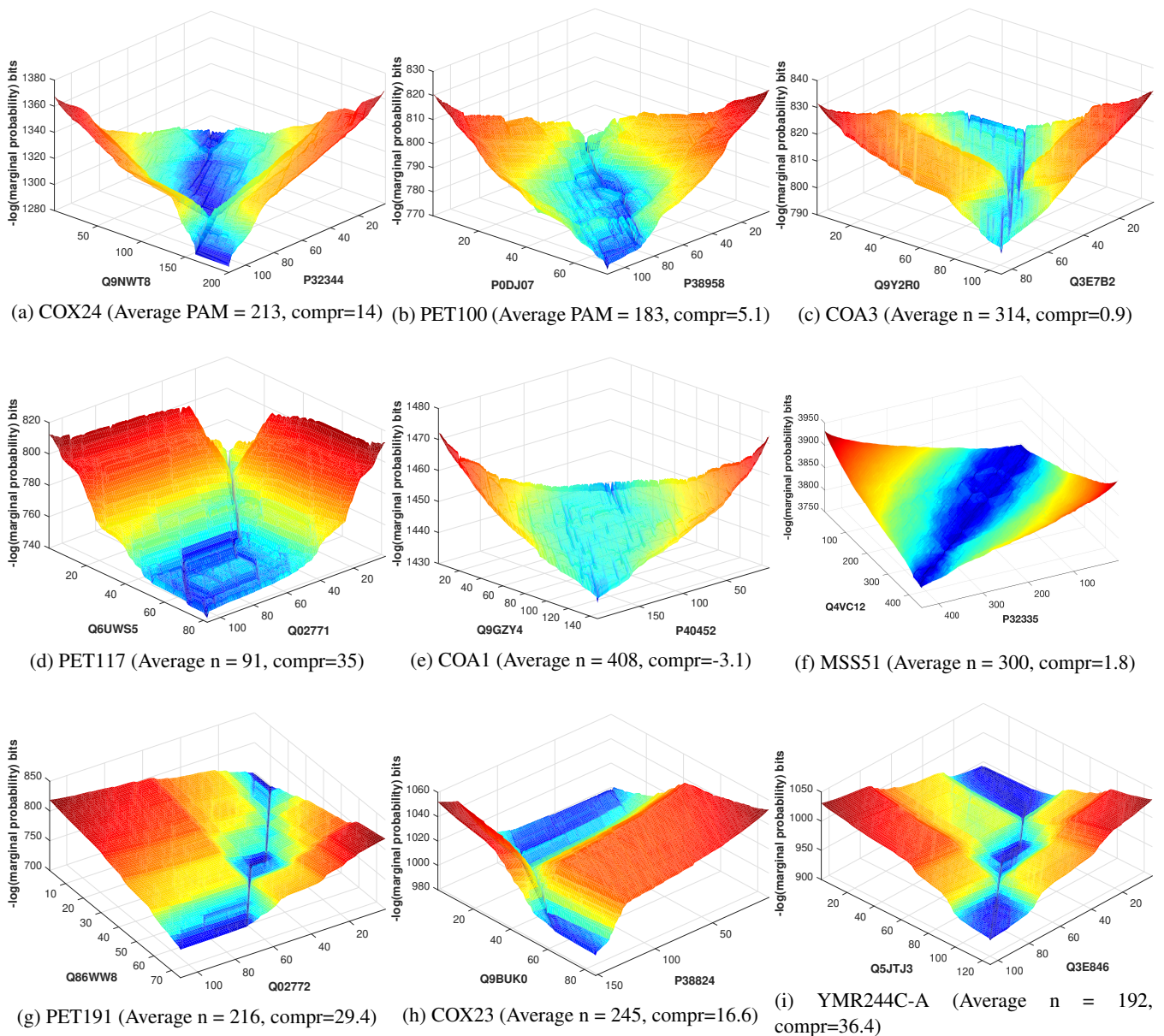
(i) YMR244C-A (Average n = 192, compr=36.4)

Fig. 1: A gallery of marginal probability landscapes inferred for 9 human vs yeast ortholog pairs: COX24, PET100, COA3, PET117, COA1, MSS51, PET191, COX23 and YMR244C-A, from the fungal mitochondrial remote ortholog dataset by Szklarczyk et al. (*Genome Biology, 2012*)(Note: compr refers to the compression gain of the marginal probability based *alignment-model* in bits, with respect to the *null-model*)