

calculated with PAML version 3.14 (Yang 1997, Comput. Appl. Biosci 13:555-556; Yang and Nielsen, 2000, Mol. Biol. Evol. 17:32-43)

Legend

krab_A, _B	input sequences: KRAB-A or KRAB-B, respectively
link	input is non-conserved sequence between KRAB-B and zinc finger array
ZnF	input is whole sequence encoding the C2H2 zinc fingers based on nucleotide sequence specifying amino acids that are considered important for DNA binding specificity of a C2H2 zinc finger (amino acids -2 to 6 with respect to start of the alpha helix; see also Supplement 8); however, the codon encoding the conserved hydrophobic amino acid, in the vast majority leucine, on position 4 was removed; this sequences are arteficially linked together for all C2H2 zinc fingers of a particular gene
7AA DBD	
S	Number of synonymous sites in a sequence
N	Number of non-synonymous sites in a sequence
t	Time (distance), measured by the expected number of nucleotide substitutions per codon ($= dS \times 3S/(S+N) + dN \times 3N/(S+N)$)
Kappa	ratio of transition/transversion (mutation) rates
Omega	ratio of non-synonymous/synonymous rates ($= dN/dS$)
dN	Number of non-synonymous substitutions per non-synonymous site
dN_SE	Standard error of the mean of the dN calculation
dS	Number of synonymous substitutions per synonymous site
dS_SE	Standard error of the mean of the dS calculation
Z score	$Z = (dN-dS) / \sqrt{dN_SE^2 + dS_SE^2}$
p-value	$p = 1 - \text{normsdist}(\text{abs}(Z \text{ score}))$

Note: "99" or "#DIV/0" values reflect non-productive calculations, e.g. if two sequences do not show differences