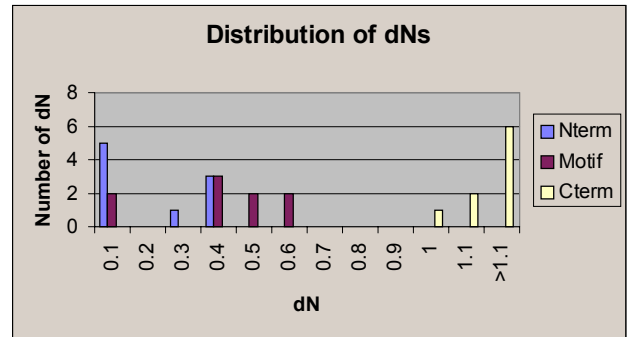
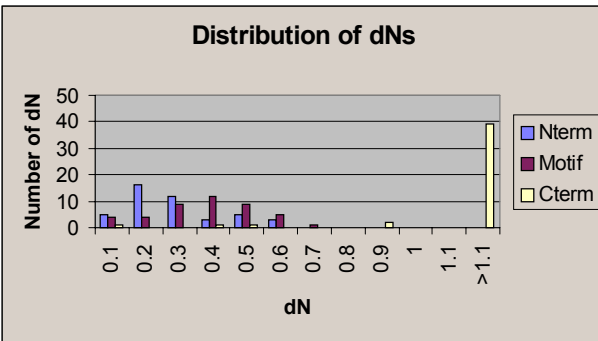


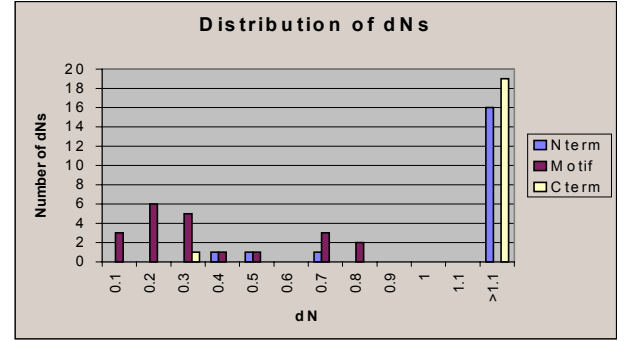
Ex1



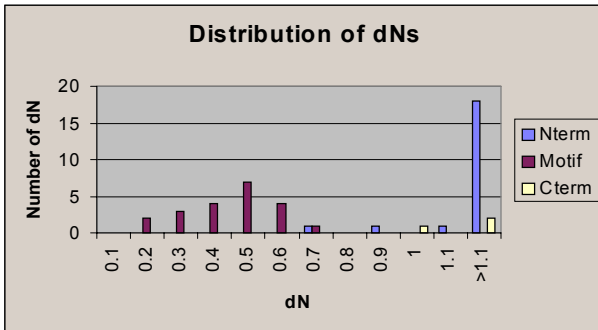
Ex2



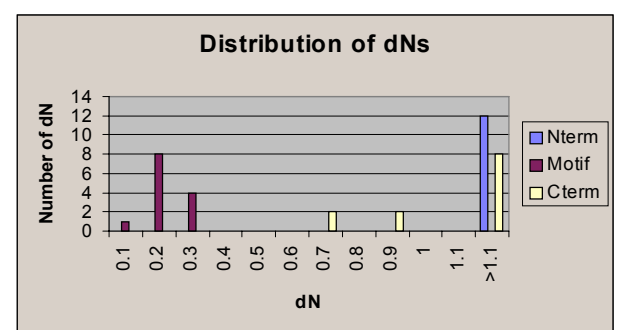
Ex3



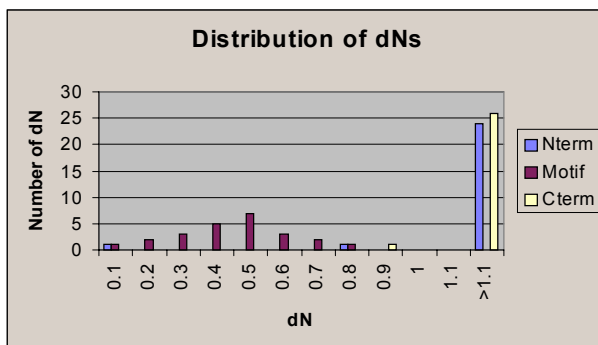
M1



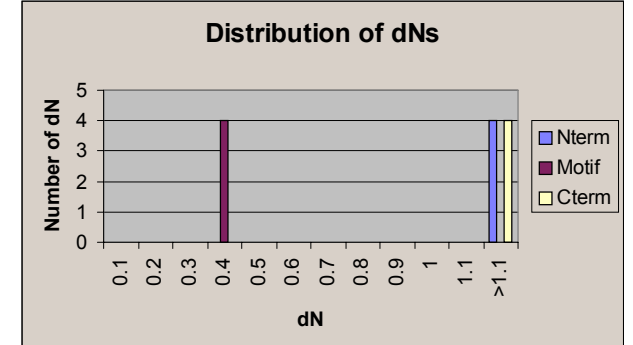
M2



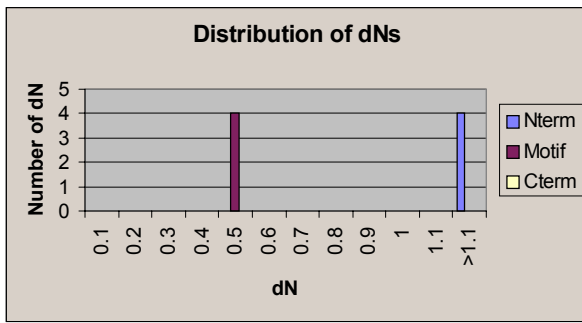
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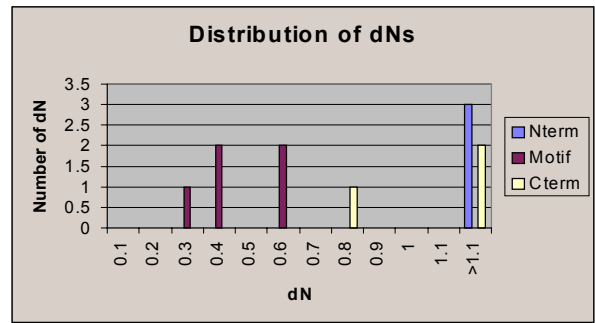
M4



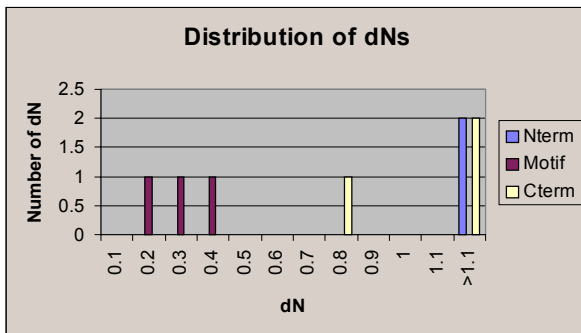
M5



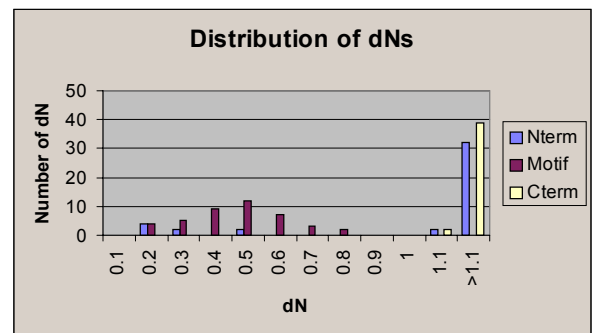
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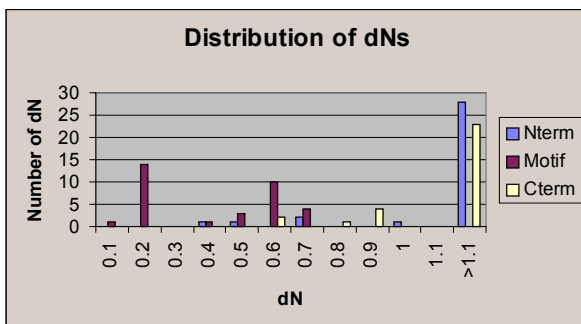
M7



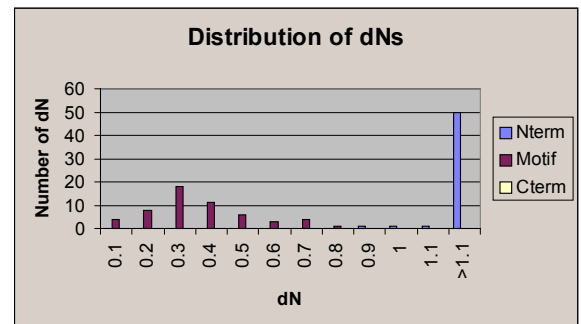
M8



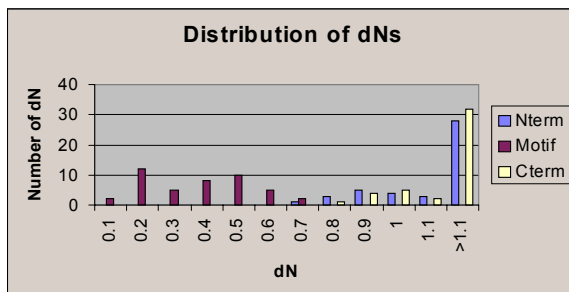
M9



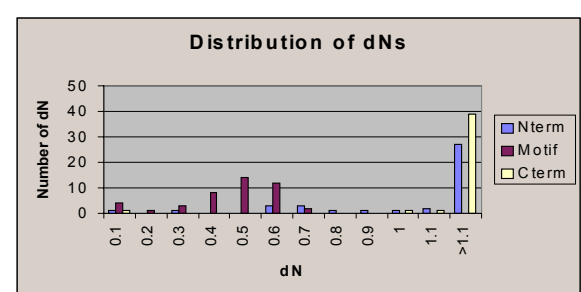
M10



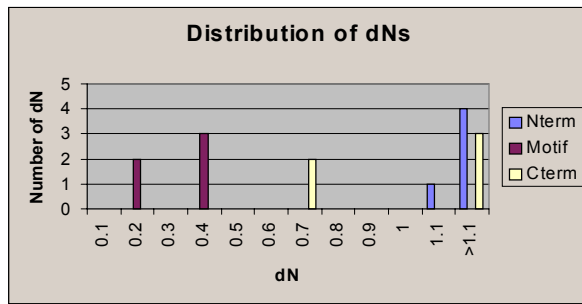
M11



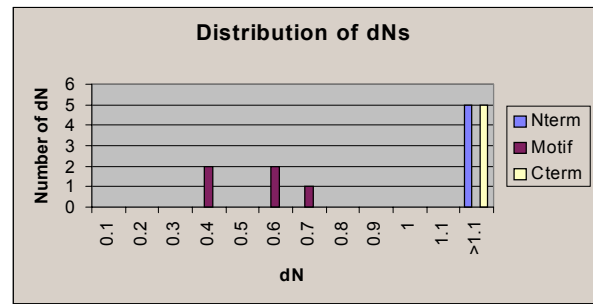
M12



M13



M14



M15

Figure Distribution of pairwise dN values of motif, and flanking regions (Nterm and Cterm). Most dNs of motifs are ≤ 0.6 . In contrast, those of flanking regions are ≥ 1 . This result indicates that sites in motif region are highly conserved and less frequently subject to substitution than in flanking regions. Notes: N-term flanking regions of the four extension motifs are partial R3 Myb repeat so that they have low dN values. Some sequences in Motif 6 and 11 are not long enough to have C-terminal following the motif for dN analysis. Thus, the Cterm dN values are not available. Some dN values in the flanking regions are 99.0 which is the preset boundary for YN00 indicating too divergence in the regions. These outliers were removed in our analysis. In contrast, no such outliers in motif regions. Therefore, the total number of dNs in the above three categories may not be the same.