

**The N-terminal zinc finger domain of *Tgf2* transposase contributes to DNA
binding and to transposition activity**

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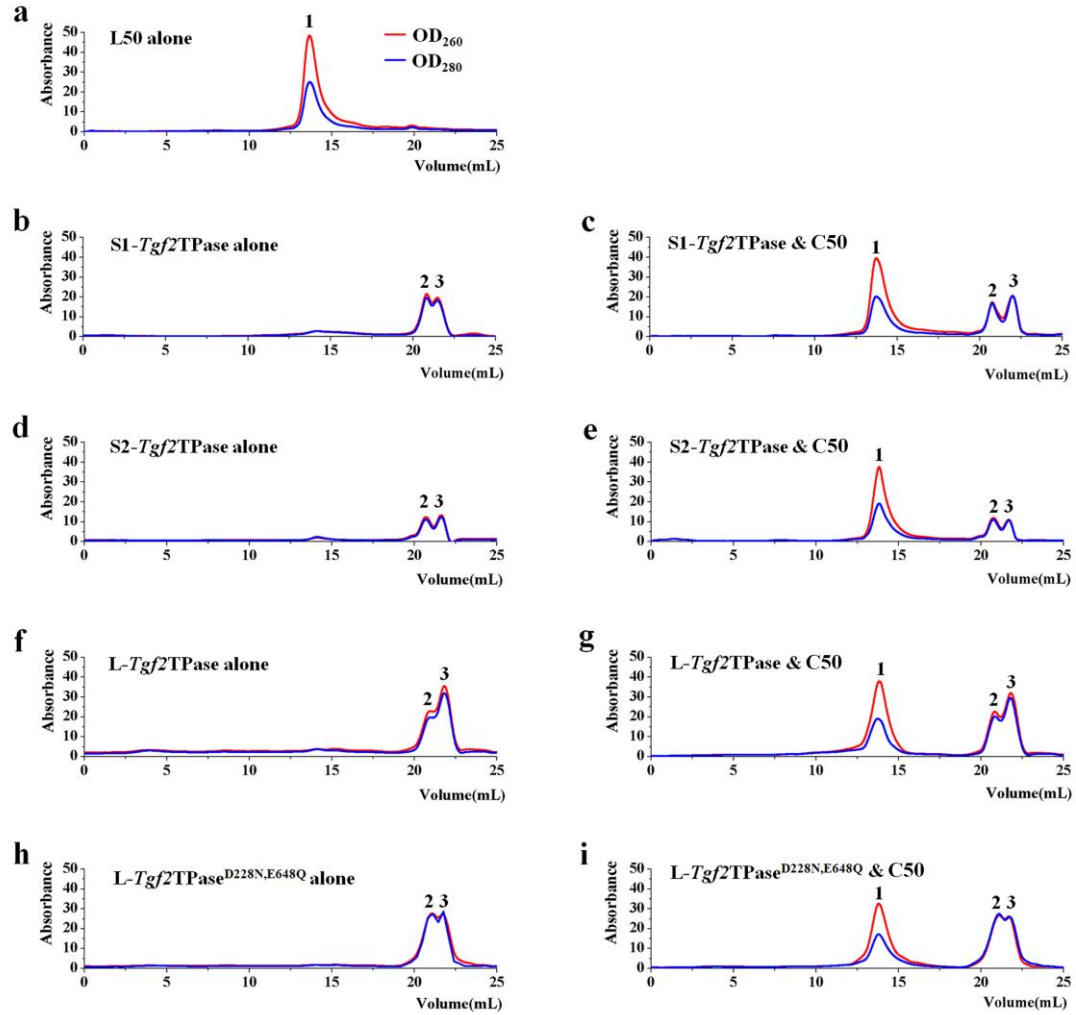
SUPPLEMENTARY FIGURES

Supplemental Figure 1: Size exclusion chromatography analysis of S1-, S2- or L-*Tgf2*TPases binding with random 50-mer double stranded DNA control C50.

(a) Elution profiles of C50 double stranded DNA probe alone; (b-c) Elution profiles of S1-*Tgf2*TPase alone (b) or a mixture of S1-*Tgf2*TPase and C50 (c); (d-e) Elution profiles of S2-*Tgf2*TPase alone (d) or a mixture of S2-*Tgf2*TPase and C50 (e). (f-g) Elution profiles of L-*Tgf2*TPase alone (f) or a mixture of L-*Tgf2*TPase and C50 (g). (h-i) Elution profiles of L-*Tgf2*TPase^{D228N, E648Q} alone (h) or a mixture of L-*Tgf2*TPase^{D228N, E648Q} and C50 (i). Based on elution times, peak 1 corresponds to C50 probes and peaks 2 and 3 represent *Tgf2*TPase dimers and monomers, respectively.

Supplemental Figure 2: Terminal inverted repeats (TIRs) and subterminal repeats (STRs) within the left (220bp) and right (185bp) ends of the *Tgf2* element. The 11 bp TIRs are underscored. Arrows suggest the occurrence of A/GAGTA STR motifs. Gray sequences show double-stranded DNA L50 probe for size exclusion chromatography.

Supplemental Figure 1:



Supplemental Figure 2:

Tgf2 left-end

..... 10 20 30 40 50 60 70
CAGAGGTGTAAAAGTACTTGAGTAAATTTACTTGATTACTGTACTTAAGTATTATTTTTGGGGATTTTTA
GTCTCCACATTTTCATGAACTCATTAAAATGAACTAATGACATGAATT CATAATAAAAAACCCCTAAAAAT

..... 80 90 100 110 120 130 140
CTTTACTTGAGTACAATTAATAAATCAATACTTTTACTTTTACTTAATTACATTTTTTTAGAAAAAAGT
GAAATGAACTCATGTTAATTTTTAGTTATGAAAATGAAAATGAATTAATGTAATAAAAAATCTTTTTTCA

..... 150 160 170 180 190 200 210
ACTTTTTACTCCTTACAATTTTATTTACAGTCAAAAAGTACTTATTTTTGGAGATCACTTCATTCTATT
TGAATAATGAGGAATGTTAAAATAAATGTCAGTTTTTCATGAATAAAAAACCTCTAGTGAAGTAAGATAA

..... 220 4540 4550 4560 4570 4580
TTCCCTTGCT TCTAGTTTTCATTCTTGCTTTTACTTTTACTTCTTTAATACTCAA
AAGGGAACGA AGATCAAAAAGTAAGAACGAAAATGAAAATGAAAGAAATTATGAGTT

..... 4590 4600 4610 4620 4630 4640 4650
GTACAATTTTAAATGGAGTACTTTTTTACTTTTACTCAAGTAAGATTCTAGCCAGATACTTTTACTTTTAA
CATGTTAAAATTACCTCATGAAAAAATGAAAATGAGTTCATTCTAAGATCGGTCTATGAAAATGAAAATT

..... 4660 4670 4680 4690 4700 4710 4720
TTGAGTAAAATTTCCCTAAGTACTTGTACTTTCACTTGAGTAAAATTTTGGAGTACTTTTACACCTCTG
AACTCATTTTTAAAAGGGATT CATGAACATGAAAGTGAACCTATTTTAAAAACTCATGAAAATGTGGAGAC

Tgf2 right-end