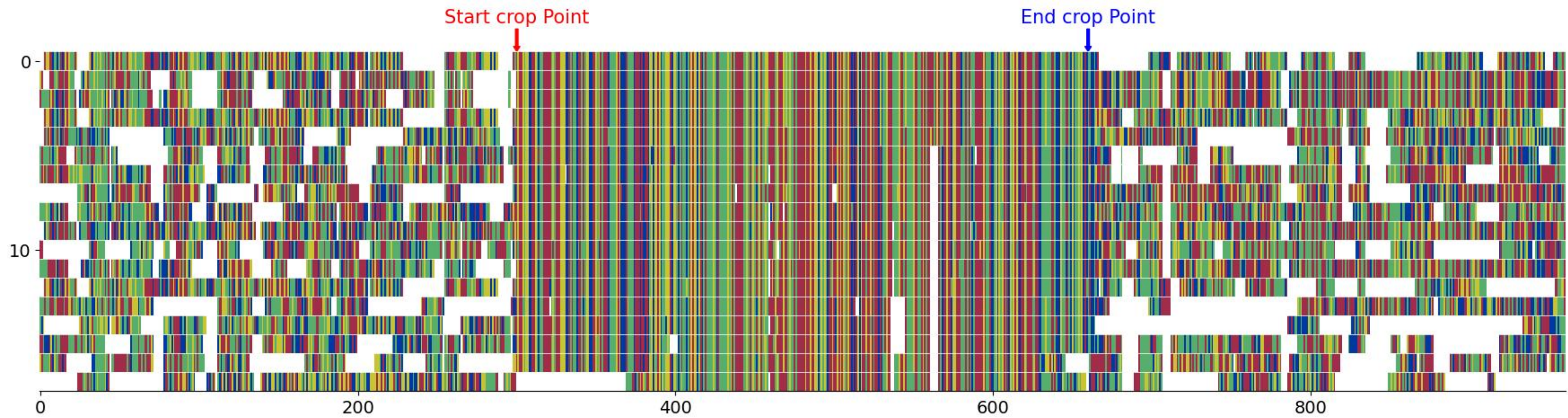


MSA length = 361

Start crop Point

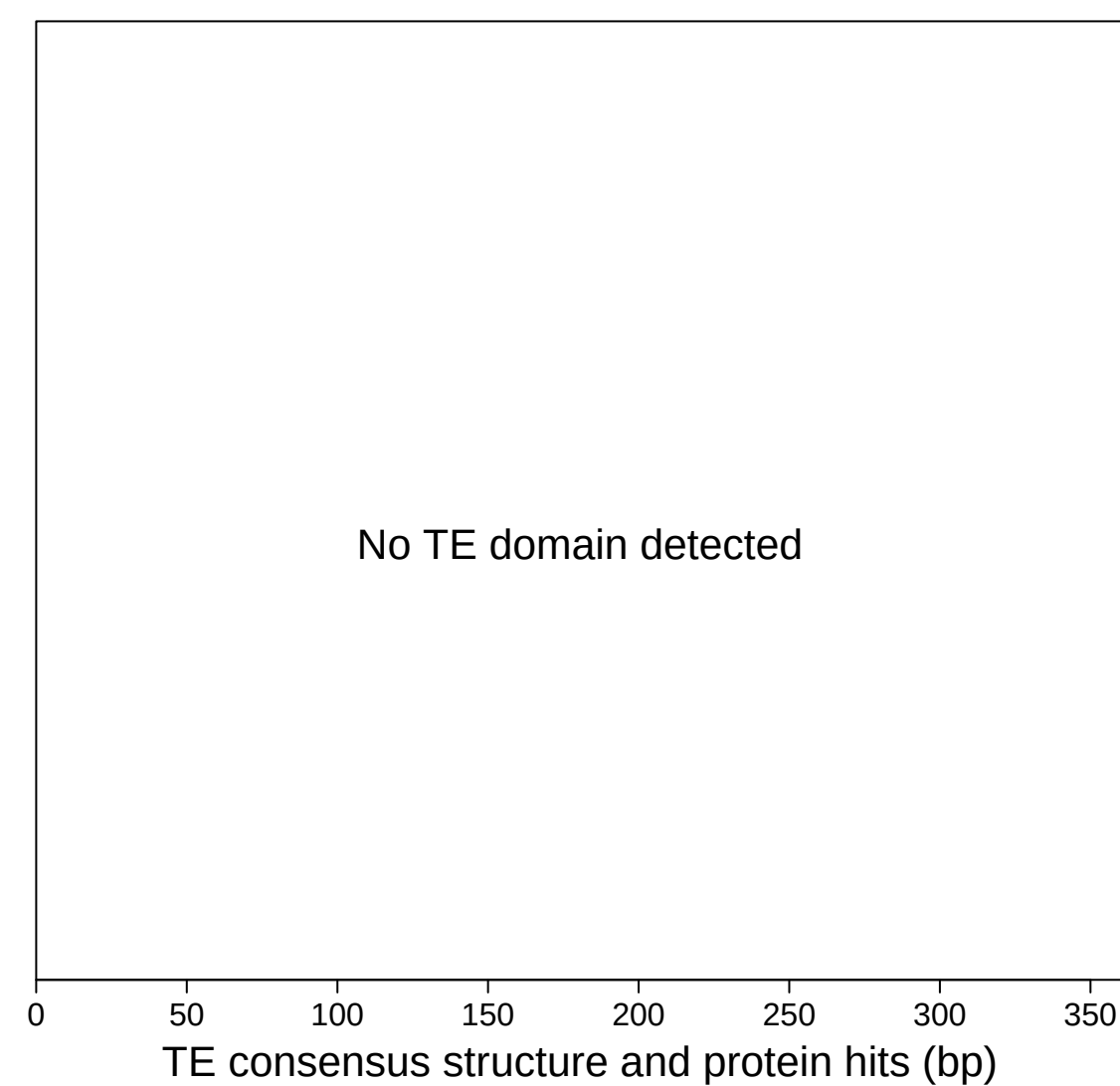
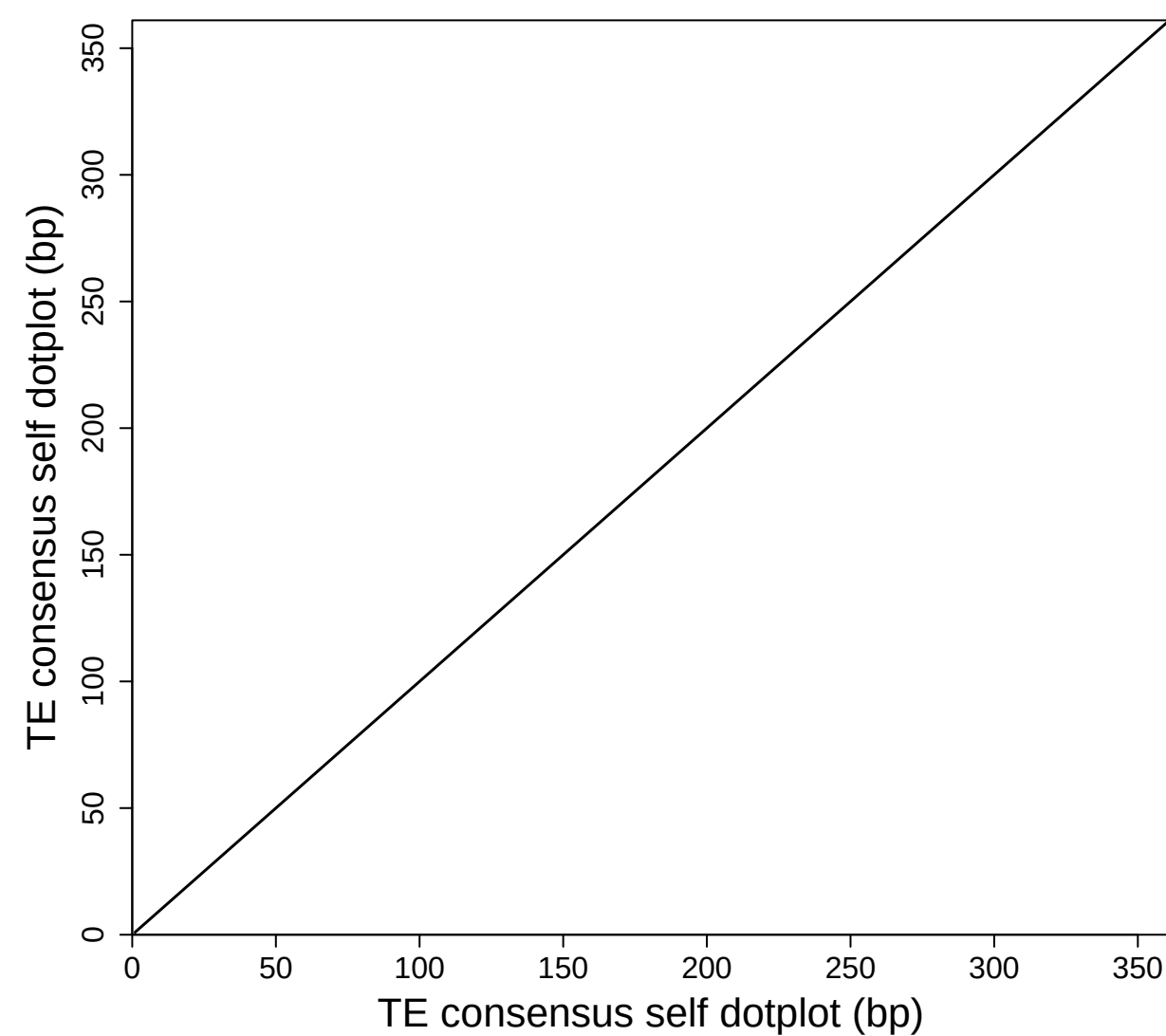
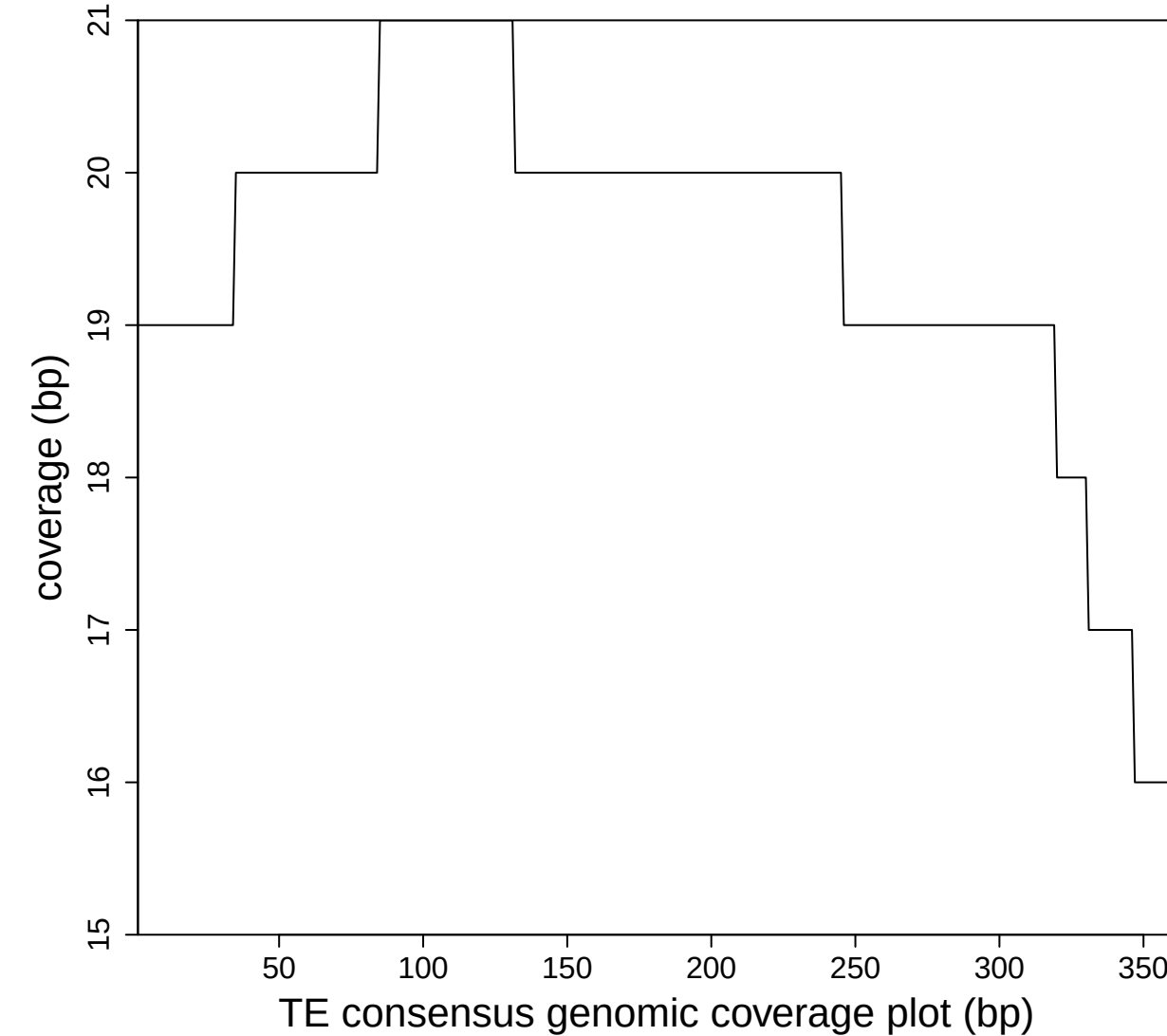
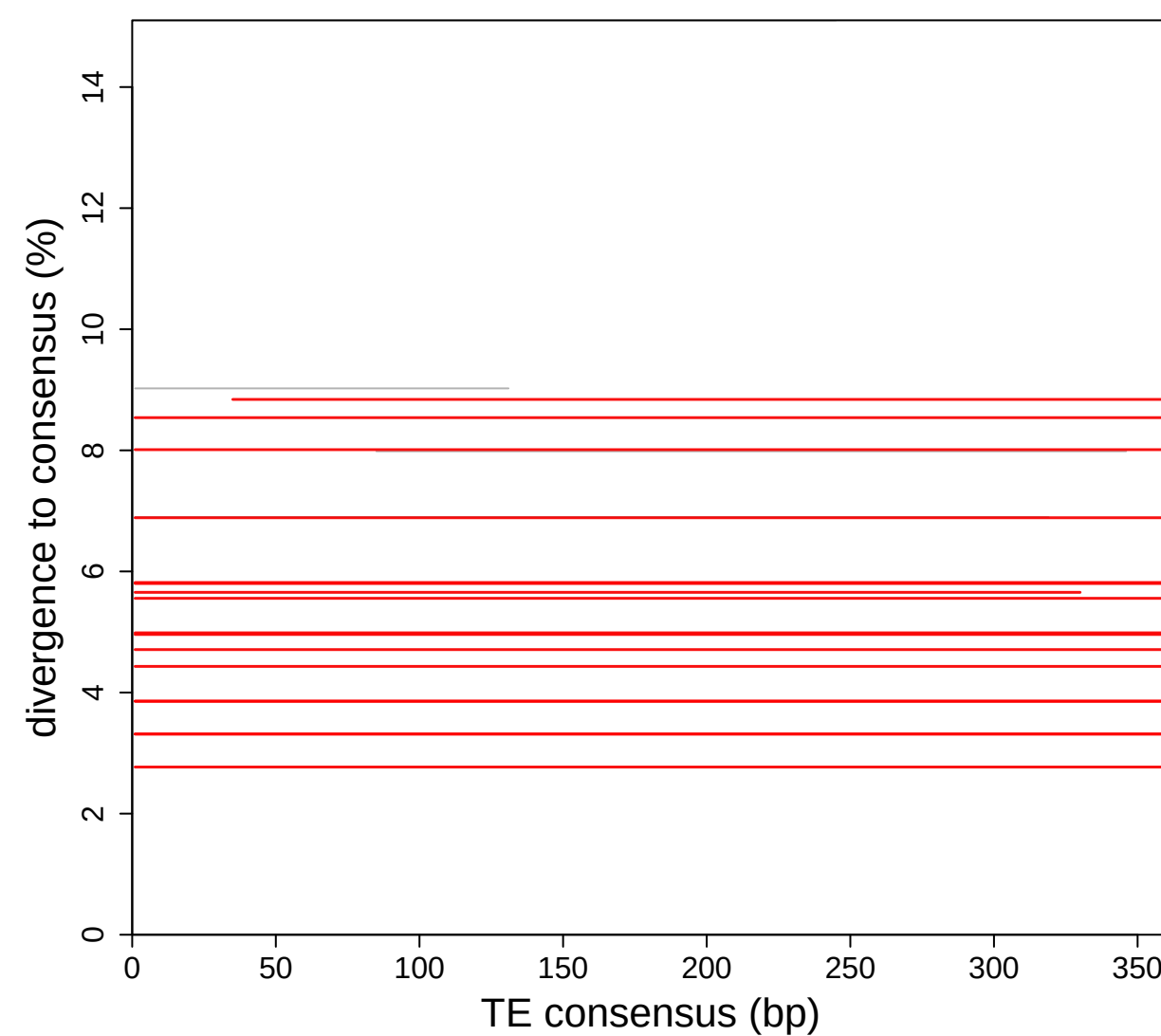
End crop Point

Sequence alignment visualization showing 16 sequences. The alignment is color-coded by amino acid type: red for acidic (D, E), blue for basic (K, R, H), green for polar (S, T, N, Q, Y, C), grey for non-polar (A, V, L, I, M, F, P, G), and black for glycine (G). A red arrow labeled 'Start crop Point' points to position 100, and a blue arrow labeled 'End crop Point' points to position 250. The sequences are aligned in a grid format with gaps represented by dashes.



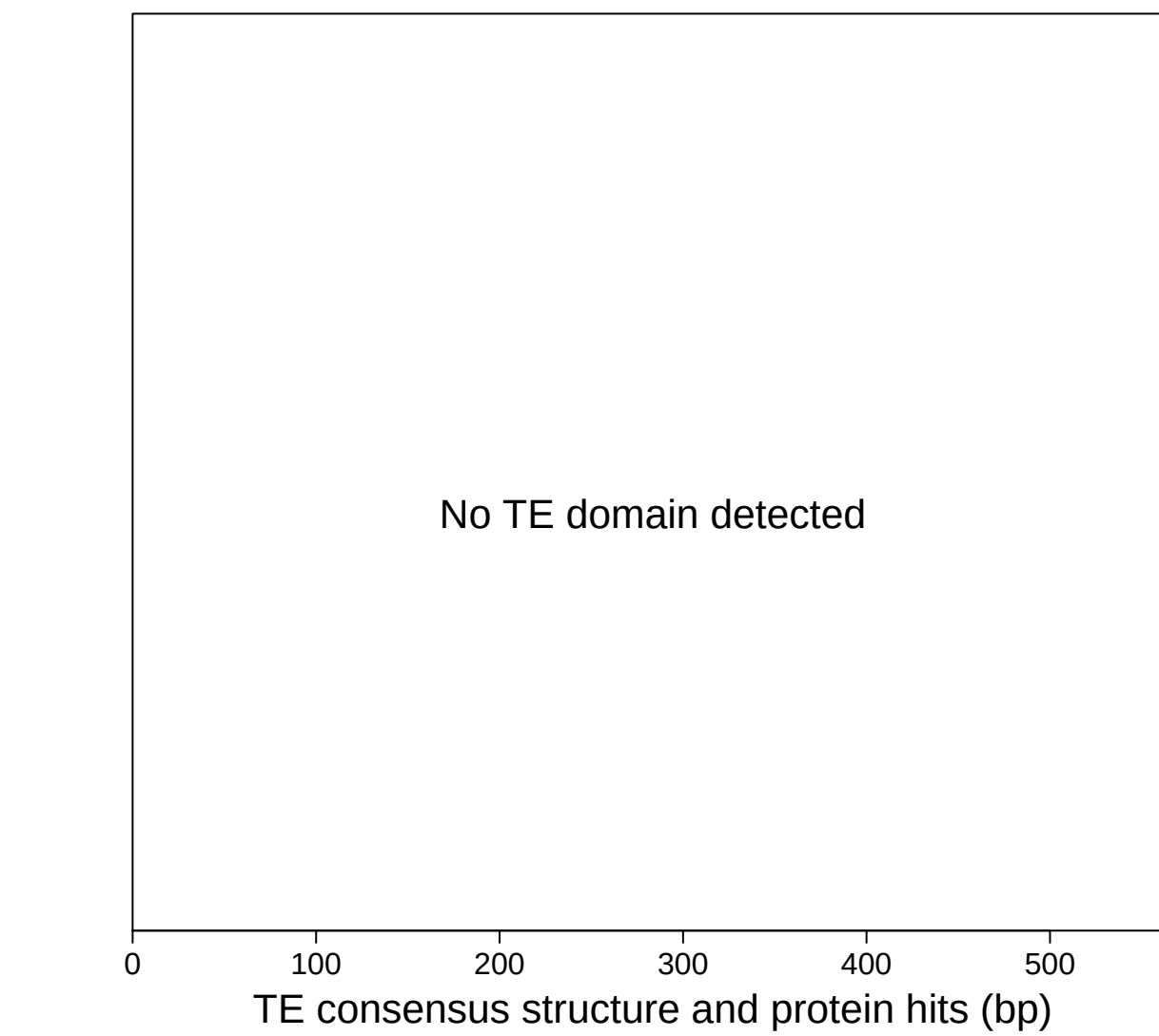
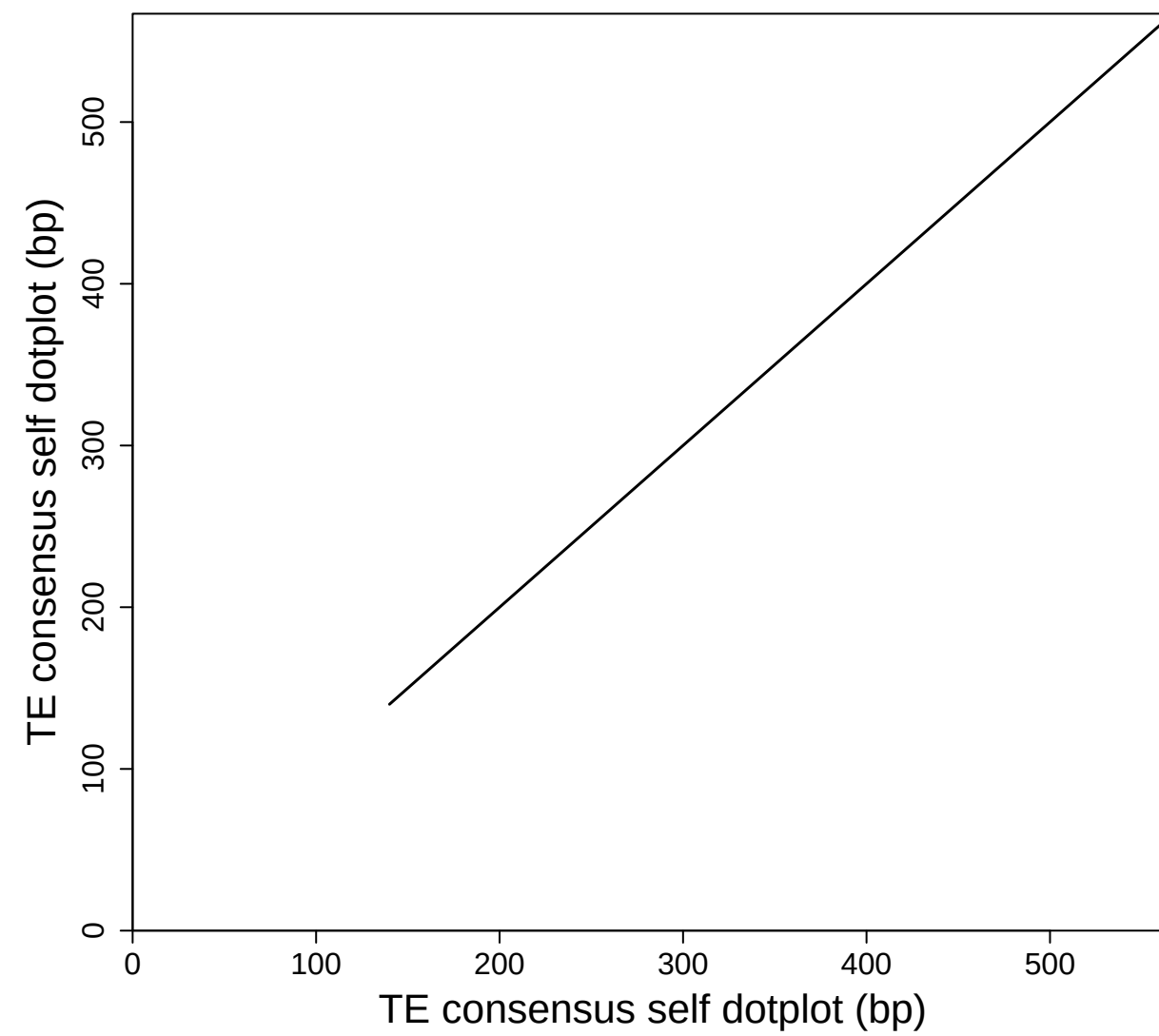
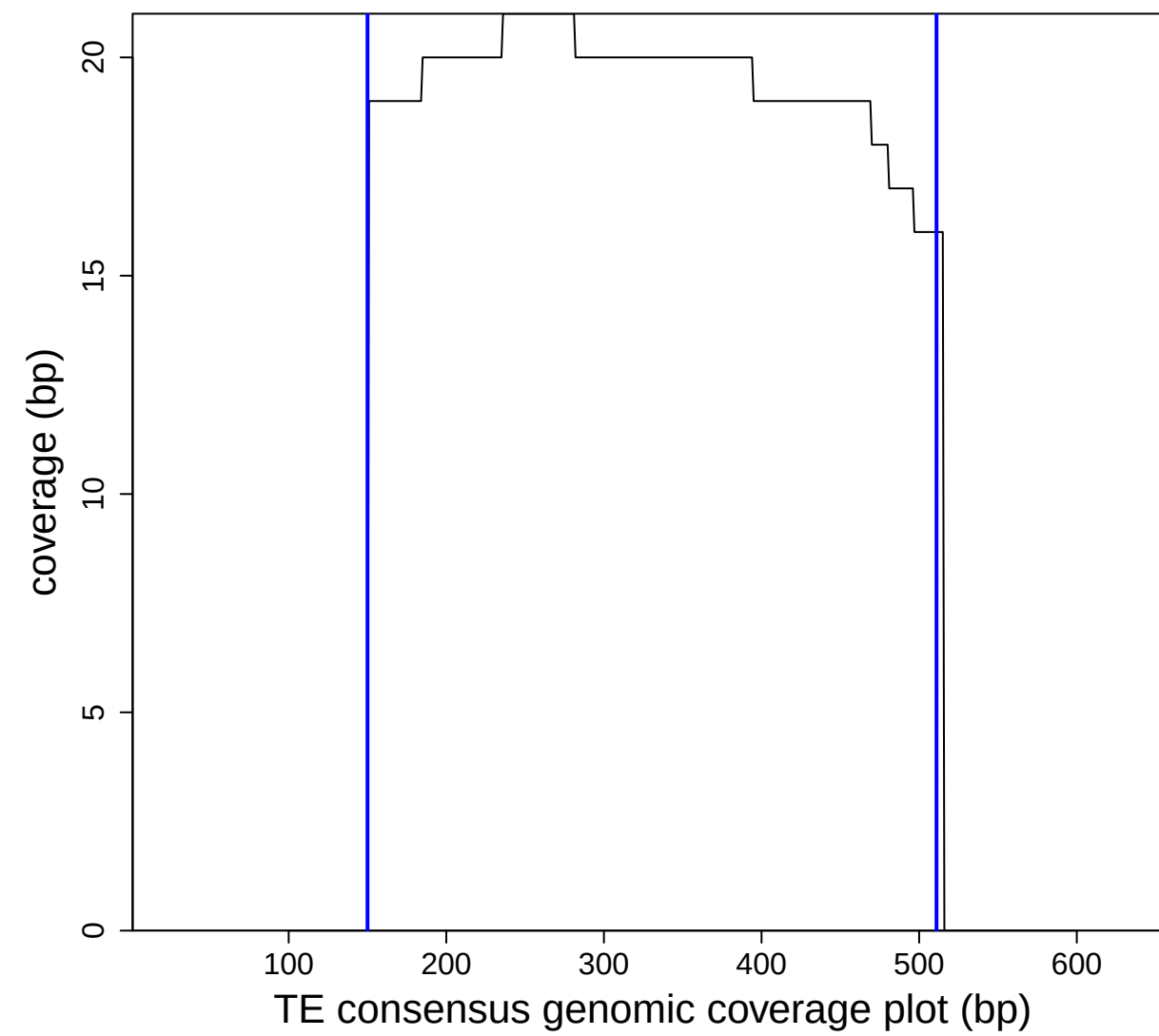
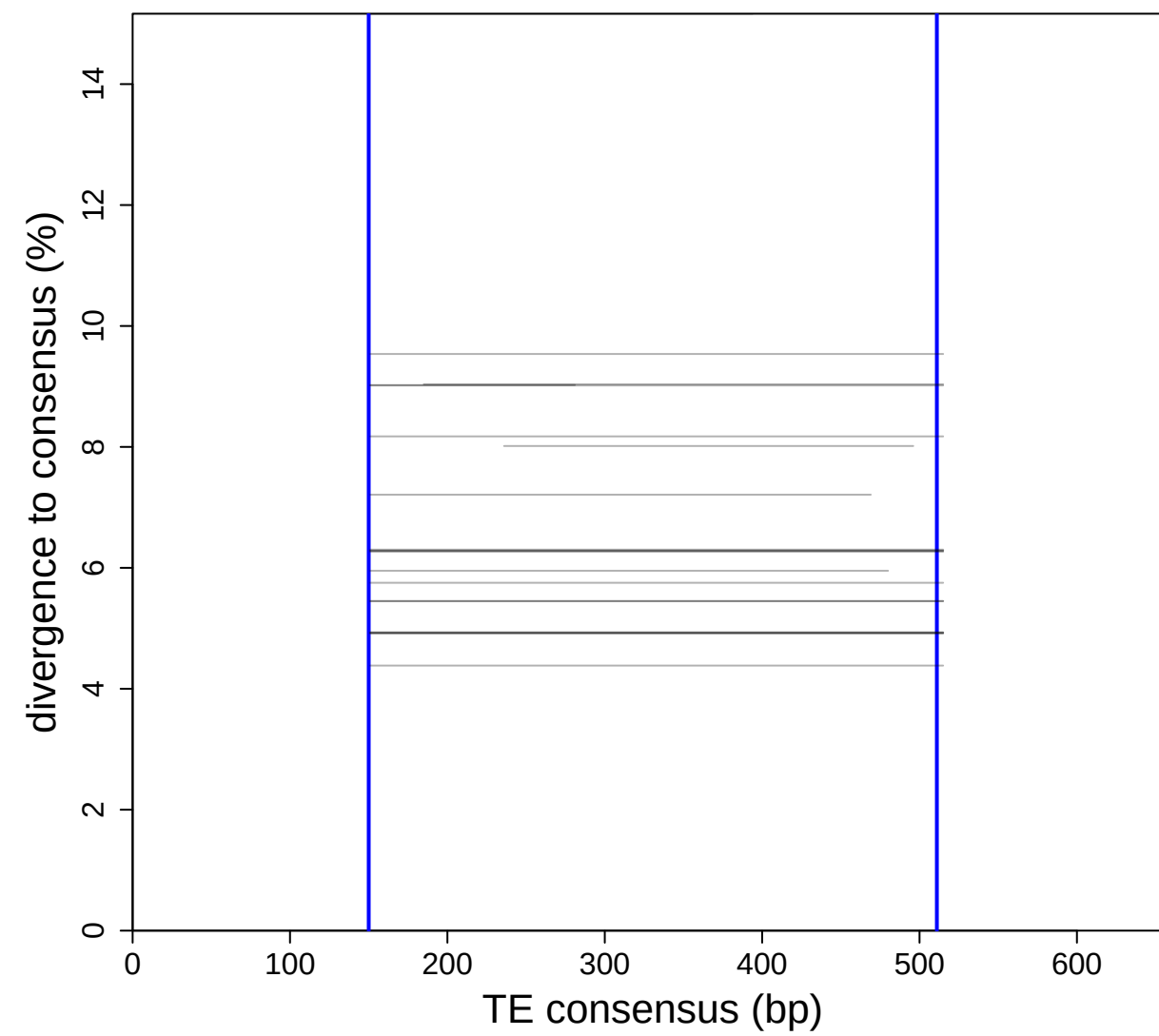
_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bcIn.fa_al
size: 361bp; fragments: 21; full length: 17 (>=324.9bp)

After TEtrimmer 361 bp

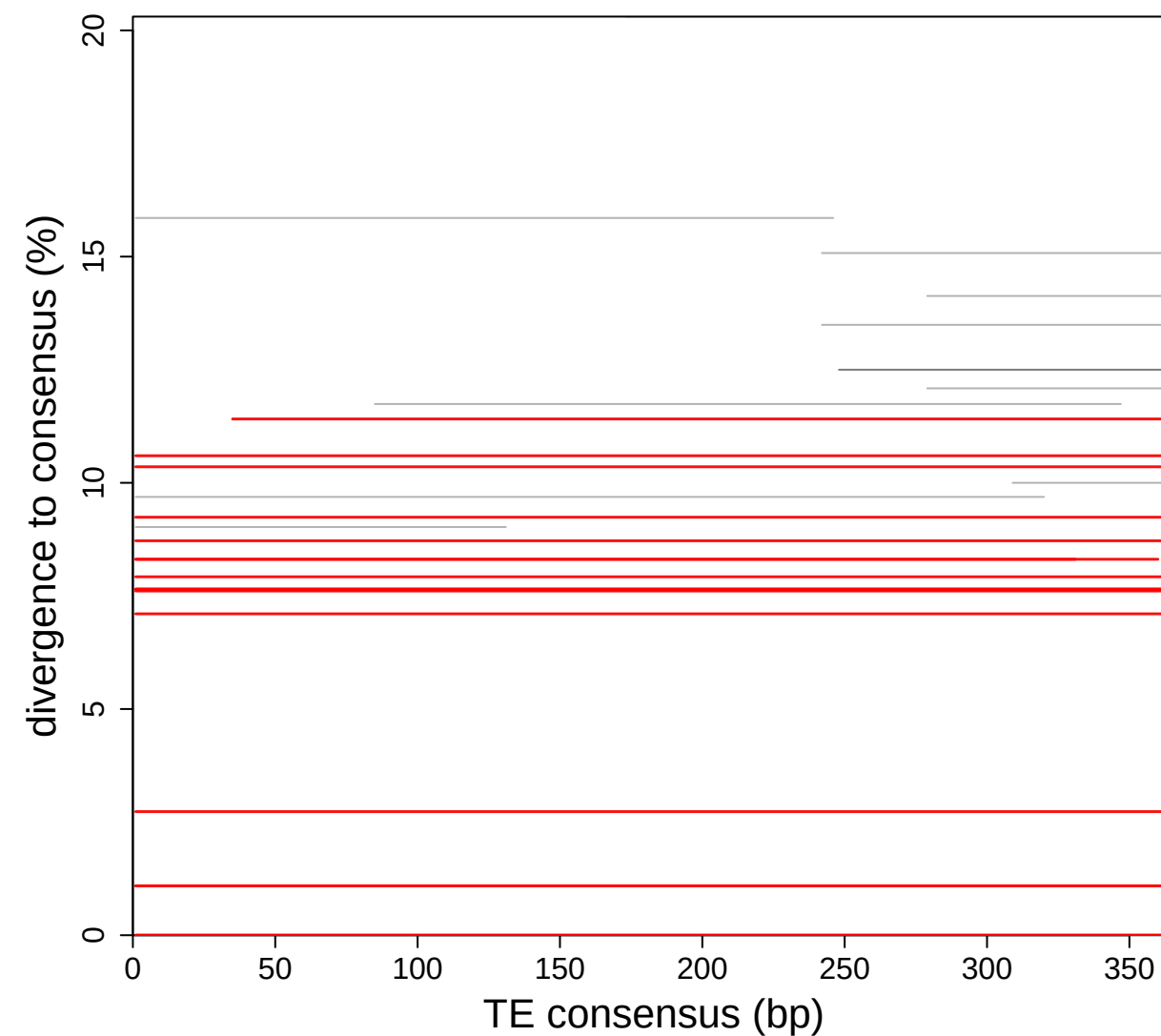


bed_g_1.bed_fm_1.bed_0_0_n.bed_g_1.bed_fm_2.bed_0_0_bclr
size: 661bp; fragments: 21; full length: 0 (>=594.9bp)

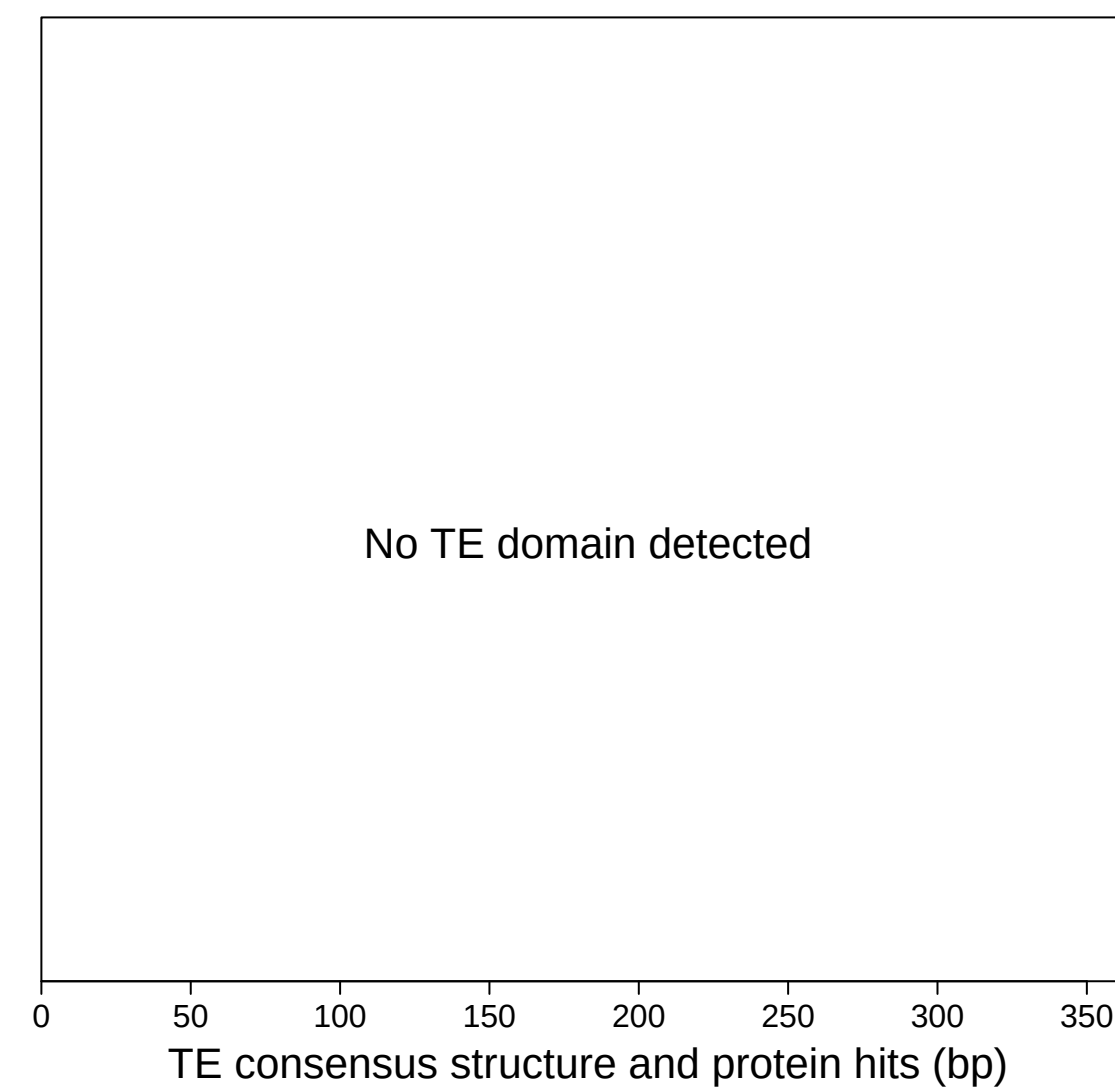
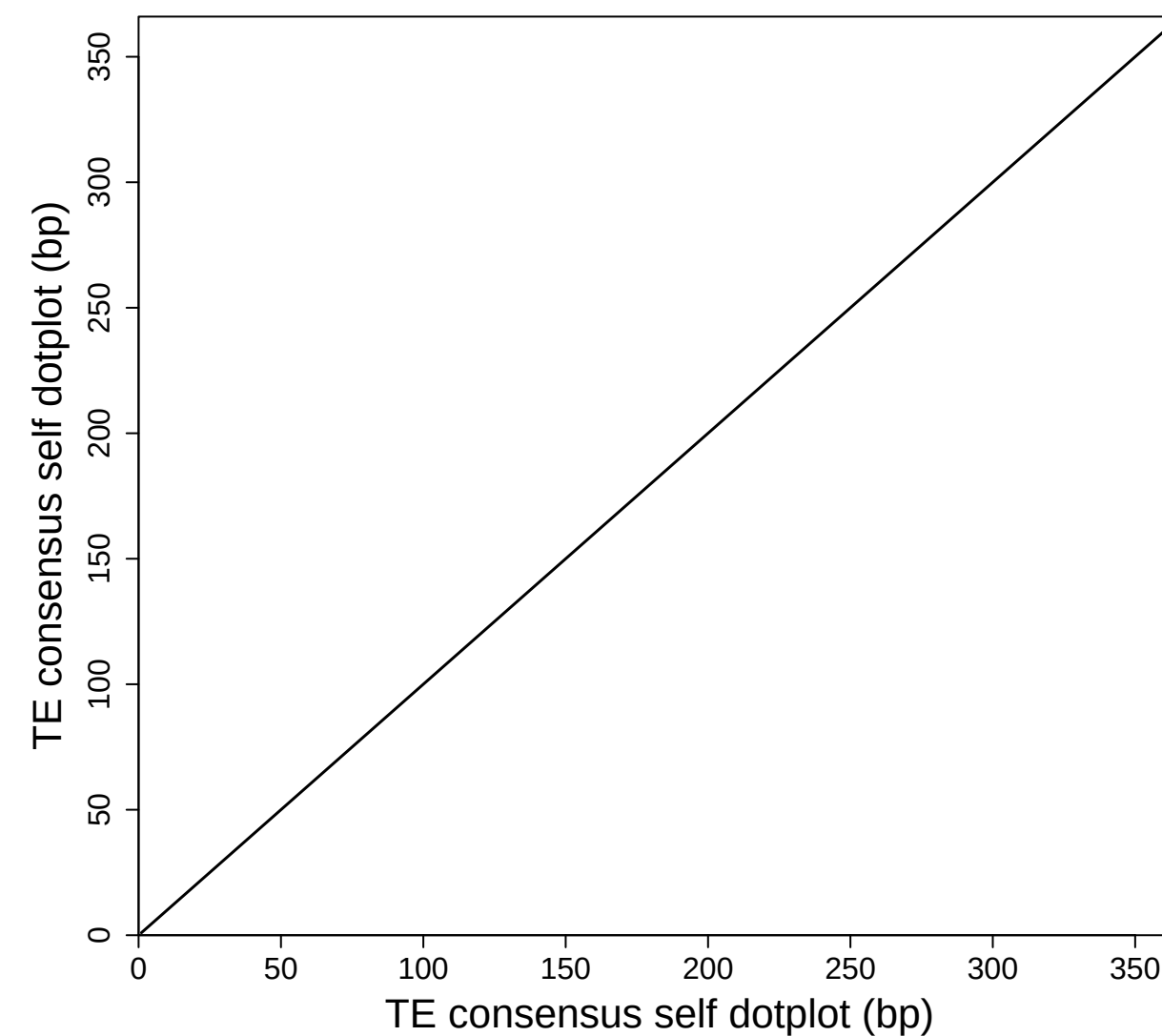
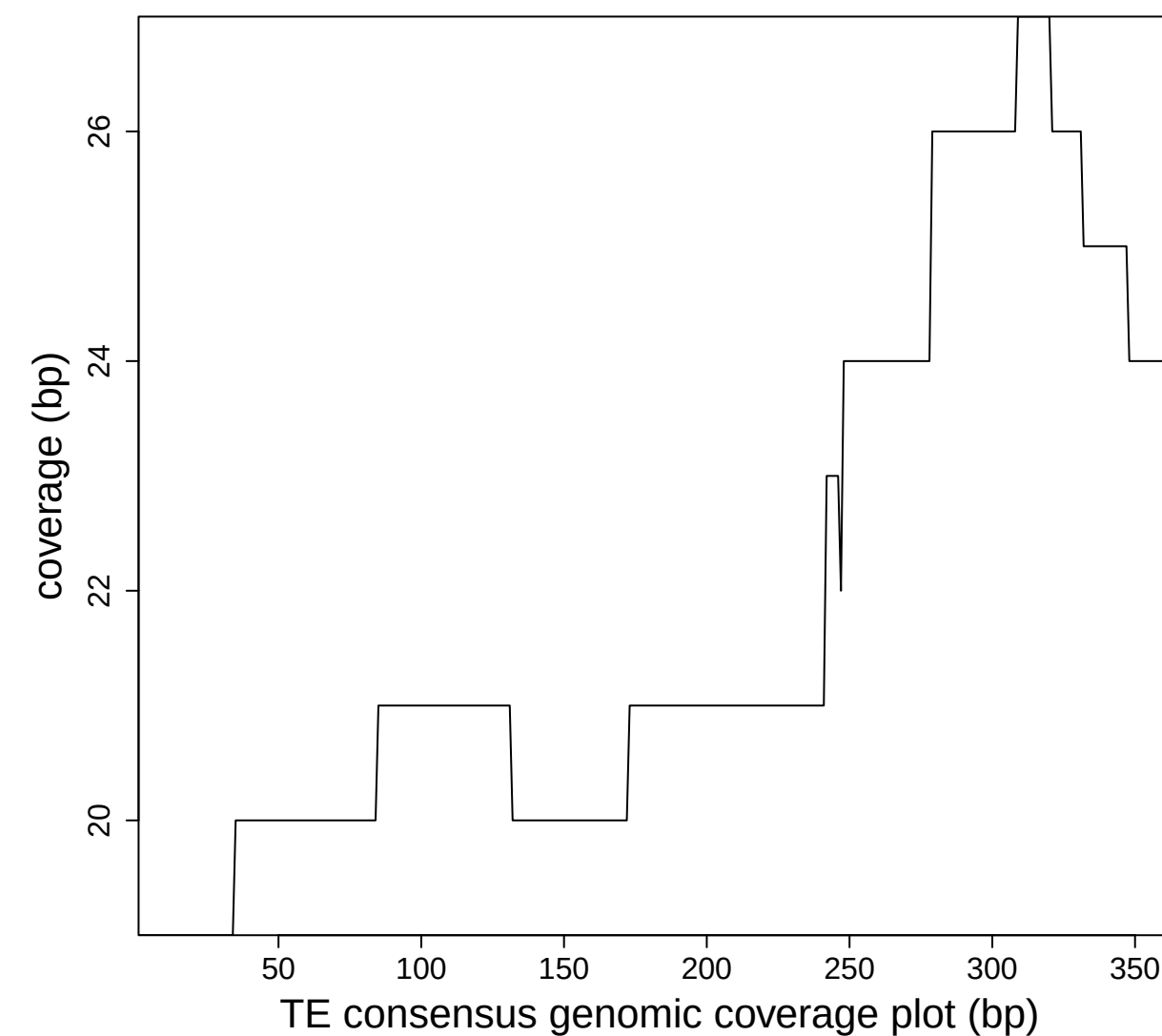
After TEtrimmer Extended plot Blue lines are boundaries



TE: ltr_1_family_318
size: 366bp; fragments: 29; full length: 17 (≥ 329.4 bp)



Before TEtrimmer 366 bp



Dotplot

(windowsize = 25, threshold = 50.00 09/10/25)

