

			Name	Max. Score
A)	50-150bp 5' —CGGTTATAACAAACGGTTCAAG-CTTAACGGGGCGTTATAACCG— 3' 3' —GCCAATATTGTTTGGCAAGTTC-GAATTGGCCCCCAATATTGGC— 5'	Find candidate regions on bottom strand based on recombination sites		
B)	5' —TTATAACGCCCGGTT-AAG— 3' —AATATTGTTC— R' L' R'' L''	Score 1 pt per match in folded bottom strand between remaining sites of R' and R'' Intl binding domains	R	4
C)	5' —TTATAACGCCCGGTT-AAG— 3' —AATATTGTTC— L' L''	Score 1 pt per match within two 3 bp segments in L' and L'' Intl binding domains, then multiply scores	$L_A \times L_B$	(3x3)
D)	5' —TTATAACGCCCGGTT-AAG— 3' —AATATTGTTC—	Score 1 pt for presence of extra-helical base	E	1
E)	5' —TTATAACGCCCGGTT-AAG— 3' —AATATTGTTC—	Score 1 pt per mismatch for the 2 bp adjacent to the R' Intl binding domain	S	2