

Additional file 5

A

B

Name	Location	Position in query	Coordinates	Annotations
1 P{lacW}		1 .. 31	31 .. 1 (-)	lacZY 1 5'TIR
2 Dmel_r5.57_genes_3R		32 .. 419	1439101 .. 1438713 (-)	Spec2 2 Atu CR43628 and 1 other gene..

Tag Sequence	From 1 to 31 on the FWD strand
Alignment	CGACGGGACCACCTTATGTTATTTTCATCATG CGACGGGACCACCTTATGTTATTTTCATCATG *****
Restriction site	At position 417
Map to genome	Chr: 3R Start: 1439101 End: 1438713 Dir: rev [Ensembl Location View]
Overlapping genes	The mapped location overlaps: CG1427 , asl , Rga , Atu , Spec2 , CG2911
Annotated sequence output	CGACGGGACCACCTTATGTTATTTTCATCATGGTCTAGGCACTGTCACAGTAATCGATAACT TGAAATACGCAAAGAGGTCTTCGCATAGACGCCCCAGATGGCAGCCCAATAACTGTTTTT GTCTATCGATTAAGTAAACAACATTTTTACCAATCGCAAAGGCGAATAAAATGTTGT CTTTAAAGAAAACAATTCGAATATCTTTGAAATATACAGTAATCAATGCACCAAAACCTC CTCGTTGCAAACAACTAATACTACTATCGATACCAACGCTGTCTCGATAGCAGATTTTTACATCC CTAATTCCTGTGTGTTGTATTCTGTGACAGCCACAAAGTTTTTTGCGGAACATTTTTGTG GTACAATTTAAAGCCATTTCGGGCGCTAAAGAATTGTTTACTGCCCTCGATAGTGGATC NNN tag sequence NNN genomic sequence NNN restriction site

C

Tag Sequence	From 1 to 31 on the FWD strand
Alignment	CGACGGGACCACCTTATGTTATTTTCATCATG CGACGGGACCACCTTATGTTATTTTCATCATG *****
Restriction site	At position 416
Map to genome	Chr: 3R Start: 1439098 End: 1438713 Dir: rev [Ensembl Location View]
Overlapping genes	The mapped location overlaps: CG1427 , asl , Rga , Atu , Spec2 , CG2911
Annotated sequence output	CGACGGGACCACCTTATGTTATTTTCATCATGGTLAGGCACTGTCACAGTAATCGATAACT GAAATACGCAAAGAGGTCTTCGCATAGACGCCCCAGATGGCAGCCCAATAACTGTTTTTG TCTATCGATTAAGTAAACAACATTTTTACCAATCGCAAAGGCGAATAAAATGTTGTG TTTAAAGAAAACAATTCGAATATCTTTGAAATATACAGTAATCAATGCACCAAAACCTC TCGTTGCAAACAACTAATACTACTATCGATACCAACGCTGTCTCGATAGCAGATTTTTACATCC TAATTCCTGTGTGTTGTATTCTGTGACAGCCACAAAGTTTTTTGCGGAACATTTTTGTG TACAATTTAAAGCCATTTCGGGCGCTAAAGAATTGTTTACTGCCCTCGATAGTGGATC NNN tag sequence NNN genomic sequence NNN restriction site

A deletion affecting the genomic nucleotide 3 relative to the TIR was simulated for a *P{lacW}* insertion affecting *Atu* gene from *D. melanogaster* [GenBank:HM210951.1]. While Genome ARTIST still reports the coordinate 1439101 as the insertion site (A), iMapper

erroneously displays the T (underlined in red) at the coordinate 1439098 (highlighted with green) as the mapping coordinate for the simulated query sequence (C). Nevertheless, the respective T nucleotide is not intuitively positioned right next to the terminal nucleotide of the TIR (or the tag sequence, highlighted with light green by iMapper). Instead, a G nucleotide, which actually should stand for the real mapping position at 1439101 (B), is somehow confusingly depicted as the one bordering the TIR. Moreover, the deleted nucleotide is explicitly represented by Genome ARTIST, but it cannot be directly inferred from the graphics of iMapper.