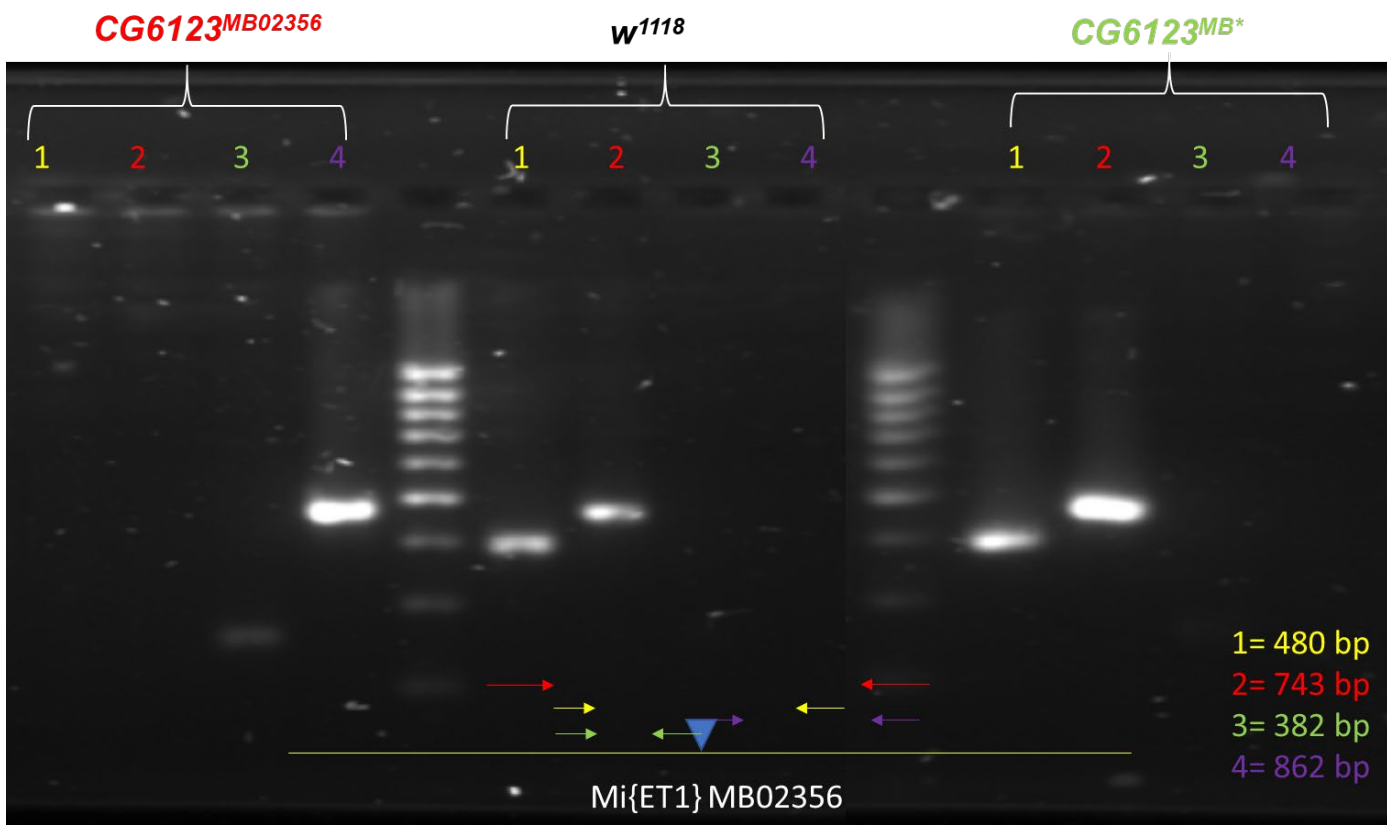


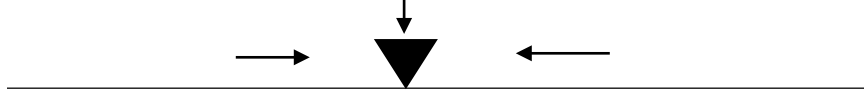
Supplemental Fig S1. Principal component analysis reveals a bias in the data according to the date of the sequencing run.



Supplemental Fig S2. Agarose gel showing genotyping strategy used for determining the presence of *Minos* insertion in the *CG6123* genomic region as well as its precise excision in the rescued line. Yellow and red denote the oligos used for PCR amplification flanking the *Minos* insertion whereas green and purple arrows denote the oligos used for checking the presence of the *Minos* insertion in the original *CG6123*^{MB02356} mutant.

X:18,337,903 w¹¹¹⁸,CG6123^{MB02356}

insertion site



>gnl|dmel|X type=golden_path_region; loc=X:1..23542271; ID=X; dbxref=GB:AE014298, GB:AE014298, REFSEQ:NC_004354; MD5=f7228bbf9f8fa0af457bc2fb7e396e4d; length=23542271; release=r6.30; species=Dmel; Length = 23542271

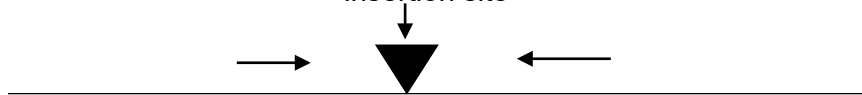
HSP # = 1 , Score = 860.835 bits (434) , Expect = 0
Identities = 587 / 632 (92.9%) , Positives = 587 / 632 (92.9%) , Gaps = 11 / 632 (1.7%)
Strand = Plus / Minus

GBrowse	Subject FASTA
Query: 21	ATGTGGTGGAA-CTTTTGCATACTAGGCTCCAAGGGA--GGGGGGCTGATGATGAAAACA 77
Subject: 18338392	ATGTGGTGGAACTTTTGCATACTAGGCTCCAAGGAATGGGGGGCTGATGATGAAAACA 18338333
Query: 78	TATCGAATCGAATTTAAAGCTAACAAGGTCCTACTCTAAAAGCTGNNNNNNNNNNNNNNN 137
Subject: 18338332	TATCGAATCGAATTTAAAGCTAACAAGGTCCTACTCTAAAAGCTGAAAAAAAAAAAAAAC 18338273
Query: 138	-TACCGATGGGACAAAACGACAAGCCGAACTTAATTATGCGATTTTATGGGGGTATTTG 196
Subject: 18338272	ATACCGATGGCACAAAACGACAAGCCGAGACTTAATTATGCGATTTTATGTGGGTATTTG 18338213
Query: 197	CACAAAATAAATGTATTGATTGCCCCCTCTGCGAGTCTCAAGTTTTCCCTGGAACTTT 256
Subject: 18338212	CACAGAAAATAAATGTATTGATTGCCCGCTCTGCGAGTCTCAAGTTTTCACTGGAACTTT 18338153
Query: 257	CAACTTTGATCAAAAGCAGCTGCGCGATGAAAATCCGCTCCGGCATTAAAGGGGCTTTTC 316
Subject: 18338152	CAACTTTGATCAAAAGCAGCTGCGCGATGATAATCCGCTCCGGCATTAAAGGGGCTTTTC 18338093
Query: 317	CAGTAAATGTTTAAATTAATAAACAARAATCAAACTGACGCGGGCGGAACACCCACATCCGT 376
Subject: 18338092	CAGTAAATGTTTAAATTAGATAAACAARAATCAAACTGACGCGGGCGGAGCACCCACATCCGT 18338033
Query: 377	CGACCCGACGACCCGACGACCCGGAAGCCATGGGGTTCGCATACCCATCCGTATCCGTAT 436
Subject: 18338032	CGACCCGACGACCCGACGACCCGGAAGCCATGTGGTTCGCATACGCATCCGTATCCGTAT 18337973
Query: 437	CCGCATCTGTATTCCCATCCGGATCCGTATTCGGTTGCGTACCAGGGGATGGCATCGTAT 496
Subject: 18337972	CCGCATCTGTATTTCGCATCCGGATCCGTATTCGGTTGCGTACCAGGTGATGGCATCGTAT 18337913
Query: 497	GGATGTACATATGTAATGCATTAATTGCGGCACCCCAACTTCGTTAA--TAACAATTA 554
Subject: 18337912	GGATGTACATATGTAGATGCATTAATTGCGGCACCCCAACTTCGTTAAATAACAATTA 18337853
Query: 555	ATTAATGGCTGTGGGGAGTGACCGAGCATTATGAATGAT-AATCATGCATG-TTCACTGC 612
Subject: 18337852	ATTAATGGCTGTGGGGAGTGACCGAGCATTATGAATGATAAATCATGCATGTTTCACTGC 18337793
Query: 613	TGA-TATTT-CCAATGA-TCTATGTATATTTA 641
Subject: 18337792	TGATTATTTCCCAATGATTCTATGTATATTTA 18337761

Supplemental Fig S3. Top panel shows the presence of the *Minos* insertion in the *CG6123* genomic region. Black flanking arrows denote the oligos used for Sanger based sequencing. Lower panel shows the snapshot of nucleotide blast of *w*¹¹¹⁸ control line. The transparent red box denotes the location of the *Minos* insertion in the original mutant of *CG6123*.

X:18,337,903 w¹¹¹⁸,CG6123^{MB02356}

insertion site



>gnl|dmel|X type=golden_path_region; loc=X:1..23542271; ID=X; dbxref=GB:AE014298, GB:AE014298, REFSEQ:NC_004354; MD5=f7228bbf9f8fa0af457bc2fb7e396e4d; length=23542271; release=r6.30; species=Dmel; Length = 23542271

HSP # = 1 , Score = 448.505 bits (226) , Expect = 1.18976e-124
Identities = 431 / 511 (84.3%) , Positives = 431 / 511 (84.3%) , Gaps = 4 / 511 (0.8%)
Strand = Plus / Minus

GBrowse	Subject FASTA
Query: 23	ATGTGGTGGAA-CTTTTGCATACTAGGCTCCAAGGGA--GGGGGGCTGATGATGAAAACA 79
Subject: 18338392	ATGTGGTGGAAACTTTTGCATACTAGGCTCCAAGGAATGGGGGGCTGATGATGAAAACA 18338333
Query: 80	TATCGAATCGAATTTAAAGCTACAAGGTCCACTCTAAAAGCTGNNNNNNNNNNNNNNNN 139
Subject: 18338332	TATCGAATCGAATTTAAAGCTACAAGGTCCACTCTAAAAGCTGAAAAAAAAAAAAAAAAAC 18338273
Query: 140	-TACCGATGGGGCAAACAACAGCCGAAAATTATTTATGCGATTTTTTGTGGGTATTG 198
Subject: 18338272	ATACCGATGGCACAACAACAGCCGAGACTTAATTATGCGATTTTATGTGGGTATTG 18338213
Query: 199	CCNNNNNNNTTGTGTTTATTGNNNNNNNNTGCGAGTCTCAAGTTTTCCCTGGAACTT 258
Subject: 18338212	CACAGAAATAATTGTATTGATTGCCGCTCTGCGAGTCTCAAGTTTTCACTGGAACTT 18338153
Query: 259	CAACTTTTATCAAAAACAGCTGCGCGATGAAAATNNNNNNNGGCATTAAGGGGTTTTC 318
Subject: 18338152	CAACTTTGATCAAAAACAGCTGCGCGATGATAATCCGCTCCGGCATTAAAGGGGCTTTTC 18338093
Query: 319	CCCTAAATGTTTAATTAATNNNNNNNTCAAATCTGACGCGGGGAGCACCCCCCTCGT 378
Subject: 18338092	CAGTAAATGTTTAATTAGATAAACAATCAAATCTGACGCGGGGAGCACCCACATCCGT 18338033
Query: 379	CGACCCACGACCCACGACCCGGAAGCCATGGGGTTCGCATACGCATCCGTATCCGTAT 438
Subject: 18338032	CGACCCGACGACCCGACCCGGAAGCCATGTGGTTCGCATACGCATCCGTATCCGTAT 18337973
Query: 439	CCCCATCTGTATCCCATCCGGATCCGTATTCGGTTGGGTACCAGGGGATGGCATCCTAT 498
Subject: 18337972	CCGCATCTGTATCCCATCCGGATCCGTATTCGGTTGCGTACCAGGTGATGGCATCCTAT 18337913
Query: 499	GGAGGTACATATGTAGATGCATTAATTGCGG 529
Subject: 18337912	GGATGTACATATGTAGATGCATTAATTGCGG 18337882

Supplemental Fig S4. Top panel shows the presence of the *Minos* insertion in the *CG6123* genomic region. Black flanking arrows denote the oligos used for Sanger based sequencing. Lower panel shows the snapshot of nucleotide blast of rescued *CG6123 Minos* insertion line. The transparent red box denotes the location of the original *Minos* insertion.