

Fig. S3: Analysis of the 12 selected unique duplication events of *D. melanogaster*. Phylogenetic trees performed for divergence analysis between the two copies of *D. melanogaster* selected for the identification of DDSA traces and the single copy of *D.yakuba*. Parts of the alignments of the 12 selected unique duplication events shown the DDSA traces identified.

1. Phylogenetic trees generated by PHYML v2.4.4 -

- o Model of nucleotides substitution : HKY85
- o Proportion of Transition / transversion = 4.0 (default value)
- o Initial tree : BIONJ

2. Trace detection

Parameters of traces detection			
Gap size	Min. identity between the two repeats	Size of repeats	Gap coverage
≥ 5 bp and ≤ 100 bp	75%	≥ 5 bp	≥ 60 %
		≥ 3 bp	≤ 40 %

Legend
Tandem repeats
Micro-homology traces
<u>Exonic gap</u>
Selected repeats

Micro-homology traces

Exonic gap

Selected repeats

Examples of DDSA Traces

Two tandem repeats:

Exonic gap Tandem repeats selected

Donor 2851 CATGTTGGTATT-AATCTTTTAATCTACCGATAGGTCTAACTCTACAATAA

Recipient 2851 CATGCTTTTATTCAGCCTTTTAATCTACCGATAGGTCTAATC-----TGA

Micro-homology traces:

Micro-homology traces **not** selected

Donor 1421 GTCGAGGTAAAGTTAACTCTTTGTTCCGCATCTCTTGAAATTTGTTGGAGAT

Recipient 1420 -----GTTAACTCTTTGTTCCG-----AGAT

Micro-homology traces **selected**

Two tandem repeats:

Exonic gap Tandem repeats selected

Donor 2851 CATGTTGGTATT-AATCTTTTAACTACCGATAGGTCTAAATCTACAATAA

Recipient 2851 CATGCTTTTATTCAGCCTTTTAACTACCGATAGGTCTAAATC-----TGA

Detailed description: The diagram illustrates a gene conversion event. The Donor sequence (top) is CATGTTGGTATT-AATCTTTTAACTACCGATAGGTCTAAATCTACAATAA. The Recipient sequence (bottom) is CATGCTTTTATTCAGCCTTTTAACTACCGATAGGTCTAAATC-----TGA. The tandem repeats in the Donor sequence, CTAAATCTACAATAA, are highlighted in yellow and labeled 'Tandem repeats selected' with arrows. An 'Exonic gap' is indicated between the two tandem repeats in the Donor sequence. The Recipient sequence has a gap (indicated by dashes) between the two tandem repeats, suggesting a deletion or a different structure.

Exonic gap

Tandem repeats selected

Donor 2851 CATGTTGGTATT-AATCTTTTAATCTACCGATAGGTCTAAATCTACAATAA
Recipient 2851 CATGCTTTTATTCAGCCTTTTAATCTACCGATAGGTCTAATC-----TGA

Micro-homology traces:

Micro-homology traces **not** selected

Donor 1421 GTCGAGGTTAAGTTAACTCTTTGTTCCGATCTCTTGAAATTTGTTGGAGAT

Recipient 1420 -----GTAACTCTTTGTTCCG-----AGAT

Micro-homology traces **selected**

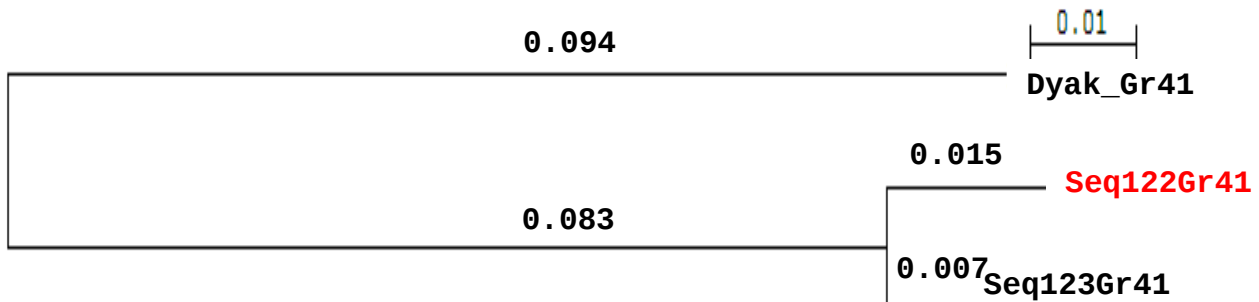
Micro-homology traces **not** selected

Donor 1421 GTCGAGGTTAA GTTAACTCTTGTTCGCATCTCTTGAAATGTTGG AGAT
Recipient 1420 ----- GTTAACTCTTGTTCGC ----- AGAT

Micro-homology traces selected

Group 41

Sequence	Sequence name	Divergence
Donor	Seq122Gr41	0.015103
Recipient	Seq123Gr41	0.007315
Single copy of <i>D. yakuba</i>	Dyak_Gr41	0.176950



Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq122Gr41	1	0	3
Seq123Gr41	1	0	1

		. . . + . . . : . . . + . . . : . . . + . . . : . . . + . . . :
Seq122Gr41	938	GACCTTTATCAATTGCCAAGGCCAAAG-----TAATAA----
Seq123Gr41	905	GGTCTCTATCAATTGTCAAGTCCAAAG GTTCTTGCGATATAAGAAAACAC
		. . . + . . . : . . . + . . . : . . . + . . . : . . . + . . . :
Seq122Gr41	971	-----TTAATTAAT----AA ATT-ATT TTAATTT-TTACATTTTT
Seq123Gr41	955	CCCTATTG TTACTTAGTT TTGCGAATTGGA CTAATTTATTAAAGTTTT

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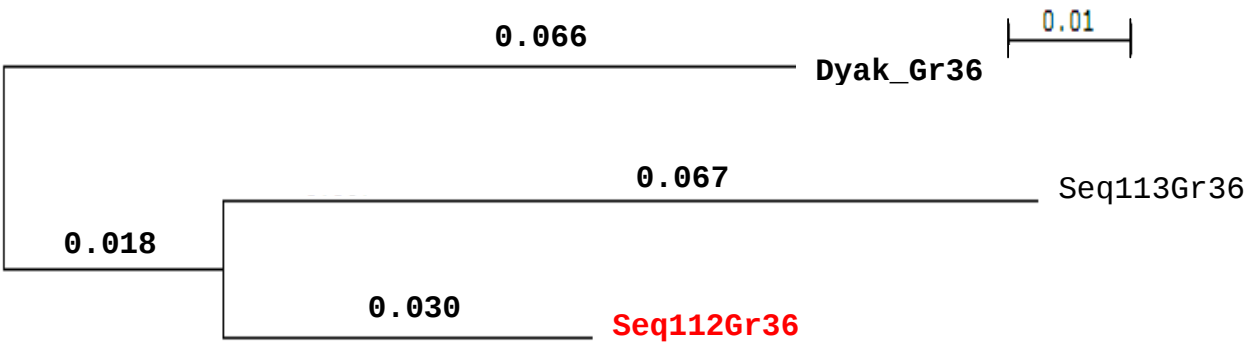
[illegible]

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		 + . . . : . . . + . . . : . . . + . . . : . . . + . . . : . . . + . . . :
Seq122Gr41	2851	CATGTTGGTATT-AATCTTTTAATCTACCGATAGGT <u>CTAATCTACAAT</u> TAA
Seq123Gr41	2851	CATGCTTTTATT CAGCCTTTTAATCTACCGATAGGT CTAATC ------TGA
		 + . . . : . . .
Seq122Gr41	2900	GATACAGTTTTCTTT
Seq123Gr41	2896	GGCACATTTTCCTTT

Group 36

Sequence	Sequence name	Divergence
Donor	Seq112Gr36	0.030138
Recipient	Seq113Gr36	0.066576
Single copy of <i>D. yakuba</i>	Dyak_Gr36	0.084232



Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq112Gr36	1	0	3
Seq113Gr36	1	4	7

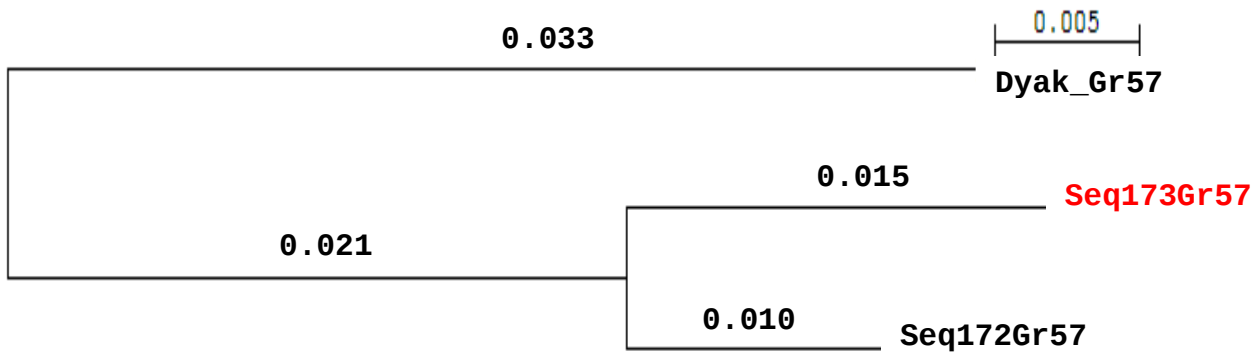
Seq112Gr36	248	GGATT+CGAATAGATTGTGCGTTGAGCAGAGGTAAACTCTGACAGCTGACC
Seq113Gr36	524	GGATCCGAATATATTGTGTGTTTAGCAGAGGTAAACTCTGACAATTGACC
Seq112Gr36	298	CTGCAACTTCTGT-----CGATGTTTGGCAGTTGCAGTTGCAGTTTG
Seq113Gr36	574	CTGCAACTTCTGTCAACTTCTGATATTTGGCAGTTGCAGTTGCAGTTTG
Seq112Gr36	340	CATTTCGAGCTTCGCTGCGCTTCGCTGAAAACAGCCTGAAACTGCTTTTG
Seq113Gr36	624	CATTTGAGCTTCGCTGCGGCTTCGCTGAAAACAGCCTGAAACTGCTTTTC
Seq112Gr36	390	AAAATCGGCATAACGCATTTTCTTTGTCTTTGCCGTTCGAAAAACAAACTG
Seq113Gr36	674	AAAAT-----AAACTG
Seq112Gr36	440	ATAAGCTTGGTCTTGATCAA--ACACTTGGGAACAGAATCTCCGTCGCTC
Seq113Gr36	685	ATAAGCTCGGTCTTGATCAAACACACTTGGAACAGAATTTCCGTCGATC
Seq112Gr36	488	GCATAAGCAATAT-----CGGTCCGATCAGCACTCG--GTGGCTTCGTG
Seq113Gr36	735	G----TCAATCTTGGAGACGGTTTCGATC-GAAAT-GTAGTG--TTCTTG

...

Seq112Gr36	621	TTTGACGAGCGAACCGCCAAACGTATTCCATTTCGAAGGAGCAAAGTGA
Seq113Gr36	1024	TTTGACG-----
Seq112Gr36	671	AAGGCAGGAAGCTAACGCTGTATTAGCTACATTGCGCGCTTCGTTGCAAG
Seq113Gr36	1031	-----AGCTAAAGCTGTATTAGCTACATTCACCGCCTCGTTGCCAG
...		
Seq112Gr36	1371	CCTCGTTTGAGGTCACCCAAGATGCTGTAAGTACTATTAAAAATGTAATT
Seq113Gr36	1385	CCTCCTTTGAGGTCACAAAAGATGCTGTAAGT-----TTT
Seq112Gr36	1421	GTCGAGGTTAAGTTAACTCTTTGTTCCATCTCTTGAAATGTTGAGAT
Seq113Gr36	1420	-----GTTAACTCTTTGTTCC-----AGAT
...		
Seq112Gr36	1471	TAGCTAATCCCAAGCTAATAAGTCC-----
Seq113Gr36	1441	AAGCTAATTCGAAGCTAATAAGTCCAGTGATATGTTGAATAATTCAGAT
Seq112Gr36	1496	-----CAAAGGAGCGTTTCAAAGTCACACTTTTCCATCGAAACTCGAATT
Seq113Gr36	1491	AATTTCAACAGAGCGTTTCAAAGGCACACTTTTCCAGCGAAAATCGGATT
...		
Seq112Gr36	2690	TGCACGTTTGTGGTGACCAAGACCTTCCAGGACCTCACGGGTGCGTAGTG
Seq113Gr36	2687	TGCACGTTTGTGGTAACCAAGACCTTCCAGGACCTCACGGGTGCGTAGTG
Seq112Gr36	2740	CAAGCATAGAGCTAACAAAAATGAGTGGTTTAATAATATTTGATATTTTT
Seq113Gr36	2737	CAA-----CTAACTAAAATAAGTGGTGTAAATAATATTTAATATTTTT

Group 57

Sequence	Sequence name	Divergence
Donor	Seq173Gr57	0.014520
Recipient	Seq172Gr57	0.009583
Single copy of <i>D. yakuba</i>	Dyak_Gr57	0.054924



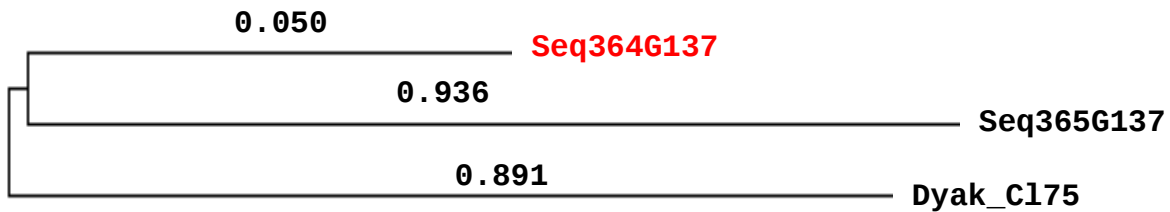
Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq173Gr57	0	0	0
Seq172Gr57	0	0	1

Seq172Gr57 946 AGTTGGATGCATGGTCCGGTGAAATAAAACGTCAATCTACATATCAAACCTC
 Seq173Gr57 931 AGTTGGTTGCATGGTCCGGTGAAATAAAACGTCAATCTACATATCAAACCTC

Seq172Gr57 996 CAT-----CCCTCTACGATGTGAACTTGGTGTCTCTAGAA
 Seq173Gr57 981 CTTAGCAGCACATACAGACTCTCTACGATGCGAACTTGGTTTCTCTAGAA

Group 75

Sequence	Sequence name	Divergence
Donor	Seq215Gr75	0.049227
Recipient	Seq216Gr75	0.093576
Single copy of <i>D. yakuba</i>	Dyak_Gr75	0.091014



0.02

Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq215Gr75	2	0	3
Seq216Gr75	0	1	6

Seq215Gr75	916	TATTTTACAATCTCGTCCACATCGATGGTGGAGCTCAGCAGTTCGTA
Seq216Gr75	916	TATGGTCATAATCTGGTGCACATCGATGGTGGAGCTCAGCAGTTCGTA
Seq215Gr75	966	TGACGT-----TCTGTG GTGTCGT AGCAGGTAGCAAGTCGTCTCCTGC
Seq216Gr75	966	TGACGT TGCCAAT CGCTGG-----AGCAGGGAGCCCGCCCTCCTCCTGT
Seq215Gr75	1010	CGTTTTTCTTAATACGCGAACAGCGCCTCACTTCGTTATAATTTGATGA
Seq216Gr75	1010	CGATTTTTCATGATCCACGAACAGCGCTTTACTTCGTTATAATTTGATGA
...		
Seq215Gr75	2895	TACCTAATTCATGACAATCTGCGAAAAGTCGATTT--GTTTTTCAGCCG
Seq216Gr75	2905	CACTTAATTCATGGCAATGCTATGTCAAGTCGATTTCTTTTTTTTGCCG
Seq215Gr75	2943	GCTTGACTTAGTTTTATTTAGCTTG-----CAACAGCTGA
Seq216Gr75	2955	GTTTCGATTTATTTTAATTTA GCTTGAAAGTTGCAA CGAACAAACAGCTGA
Seq215Gr75	2979	CGCCGATTACCGTAAGTGGATGGTTTTAAAC-ATAGTGGCAGCGCTATCT
Seq216Gr75	3005	ACCCGATTACTGTAAATCGATG---TTAATCGAAAGGGGAACGCTGTCT

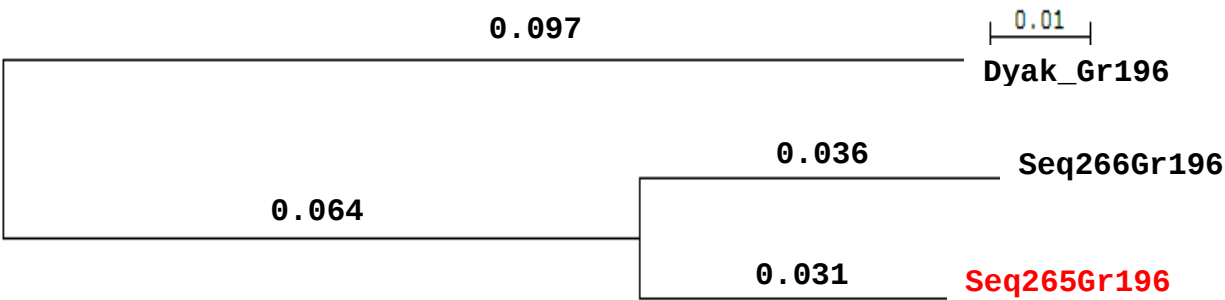
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Seq215Gr75	3789 CTCTCGTTGAAGTCGTGGGTAGCCATCGTGGAAGTTTCTGAGTTTACGC
Seq216Gr75	3356 CTTCTCGTTAAATTCGTGTGTAGCCATCGTGGAAGTTTCGGAATTCACGC
Seq215Gr75	3839 TTTCAGTTTCCGATCCCGTGC GAACGATATTTTGAACA AGCTGGGAACAT
Seq216Gr75	3406 TTTCAGTTTCTGATCCTGTGC GAACG ----- AGCTGTGAACAT
Seq215Gr75	3889 GGCTGCACGGCGGCTTTTGCAGCTTTGGCCATTTTGAGGGCCTTCAAGAT
Seq216Gr75	3444 GGCTGTCCGGCTGCTTTTGCAGATTTGCCATTTTGAGGTCCTTCAATAA
Seq215Gr75	4038 CGGCTTAAACCGACGGTTTCGTTGGTAAATTTGGGTCGTGACTCCATCA
Seq216Gr75	3593 CGGCTTAAATCCTTTCGTTTCGTTGGTAAACATGGGTCGTGACTTCATCA
Seq215Gr75	4088 GTTCGCTAATCGTACGCTTTT <u>CGACACGCGCAGATGTTTCTTGTAGACAC</u>
Seq216Gr75	3643 GCTCGGCAATTGTACGCTTTT -----
Seq215Gr75	4138 <u>AG</u> TTGTTTTGGAGGCTGGACTGCGATTTTGGCTGCTCCTCGACGACGGG
Seq216Gr75	3664 -GTTGATTTTGC GGCTGAAC TGC GATTTTGGCTGCTCCGCGACGACGGG
Seq215Gr75	4352 CAGCCTCCTCCTCGTCTTCCGAA <u>AATACT</u> ACTGTGGGATTTTAAATTGAA
Seq216Gr75	4363 CAGCCTCTTCCTCGTCTTCCGAA-----ACTGTGGGATTTAAAAATCAA
Seq215Gr75	4402 ATTATTAGTATGACTGAAT-TATTAGTTATTATGAAAGGAAGTGGCTCAA
Seq216Gr75	4407 TTCATTAGTTTGACTGAATCTAAT-CTTA-TATGA---AAGTTGCTCAA
...	
Seq215Gr75	4899 GGATCGTAATGGTTCGTTATTTTACAATCTCGTCCACATCGATGGTGGA
Seq216Gr75	4899 GGATCTTCATGGTTTGTTATGGTCATAATCTGGTGCACATCGATGGTGGA
Seq215Gr75	4949 GCTCAGCAGTTCGTACTTGACGT-----TCTGTG GTGTCGT AGCAGGTA
Seq216Gr75	4949 GCTCAGCAGTTCGTAC TTGACGTTGCC AATCGCTG G -----AGCAGGGA
Seq215Gr75	4993 GCAAGTCGTCCTCCTGCCGTTTTTTCTTAATACGCGAACAGCGCCTCACT
Seq216Gr75	4993 GCCCGCCCTCCTCCTGTGATTTTTTCATGATCCACGAACAGCGCTTTACT
...	
Seq215Gr75	7108 CCAACTTAAA-TTTATCTCGCAGGCAAAAAGTAATTGAACAATACATTTGA
Seq216Gr75	7135 CCAACTGAAATTTTATTATGCAGGCAAAAAGTAATTTAAAAATTTATTTGA

Seq215Gr75 7157 AAAAA⁺AATACAA⁺CAAAAATA⁺

Seq216Gr75 7185 AAGA-----AA⁺CAAGAATA

Group 196

Sequence	Sequence name	Divergence
Donor	Seq265Gr196	0.030586
Recipient	Seq266Gr196	0.035844
Single copy of <i>D. yakuba</i>	Dyak_Gr196	0.160251

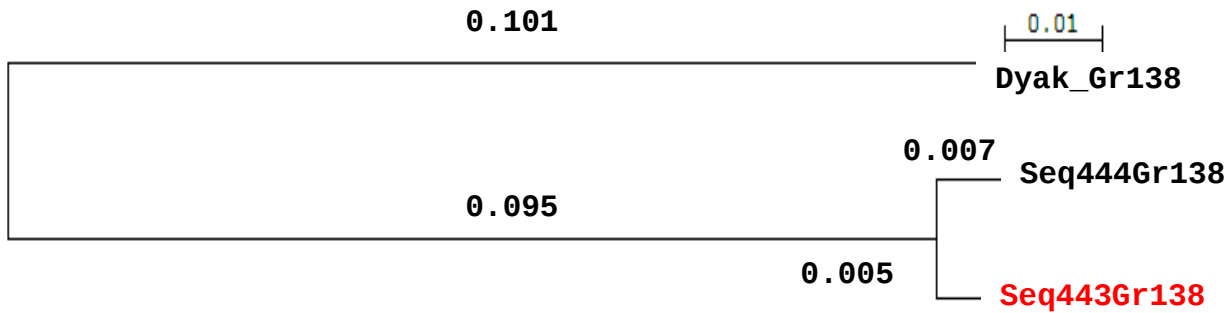


Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq265Gr196	0	0	0
Seq266Gr196	0	2	3

Seq265Gr196	2062	TCGGTTGACCGGCCAACGCCACCTTTGCCGGTTGCGCCGGGTACATTTTCG
Seq266Gr196	2350	TCGGTTGACCGGCCAACCCACCTTTGCCGCTTGCGCCGGGTACATTTTCG
Seq265Gr196	2112	TTGGTT CGGGGTTCTCAAATGGCACTAAATCGATACGTATCCGA AAAAATG
Seq266Gr196	2400	TTGATT-----CAC-----A AAAAATG
Seq265Gr196	2162	AATTCACATTTTACTTGGAACCTATTTTATTTTGTATTAA-TTACGCT
Seq266Gr196	2416	AATTCAGATTTTACTTGGAACCTATTTTATTATTGTTACTAATTTACGCT
Seq265Gr196	2261	GCTATTGGT GCTGGCGGGCT AGCTTTT
Seq266Gr196	2516	TCTATTGGT GCTG ----TTAGCTTTT

Group 138

Sequence	Sequence name	Divergence
Donor	Seq443Gr138	0.004698
Recipient	Seq444Gr138	0.007631
Single copy of <i>D. yakuba</i>	Dyak_Gr138	0.195772



Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq443Gr138	0	0	0
Seq444Gr138	0	0	2

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Seq443Gr138      747  ACTCTAACGCCCAAAACGGGCACAAAACCTCCACGCCCACACTTTTGAAA
                  |||||
Seq444Gr138      804  ACTCTAACGCCCAAAACGGGCACAAAACCTCCACGCCCA-----

Seq443Gr138      797  AATGTTTTCATATTTTATTAGTCTTGCAAATTTTCATAAATTTGTAAATG
                              |||||
Seq444Gr138      843  -----CAAAATTTTCATAAATTTGTAAATG

Seq443Gr138      847  TGGCTGAGTAACGGGTGTCTGATAGTCGGGGAGCTGGAATTCTCTCTTGT
                  |||||
Seq444Gr138      866  TGGCTGAGTAACGGGTGTCTGATAGTCAGGGAGCTGGAATTCTCTCTTGT

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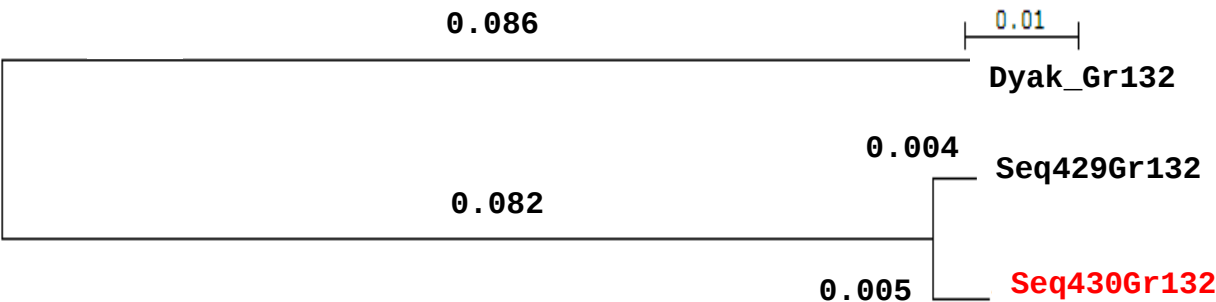
Seq443Gr138      947  CCGCAAGCTACGTACGGGTATCTGATAGTCAAAGAAATGCCTTAGGAT
                  |||||
Seq444Gr138      966  CCACAAGCTACGTACGGGTATCTGATAGTCAAAG-----

Seq443Gr138      997  TCGCATACCATACCATTTGTATATATTTATTTTATGCCGTCTATATTAAT
                  |||||
Seq444Gr138     1001  ----ATACCATACCATTTGTATATATTTATTTTATGCCGTCTATATTCAT

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Group 132

Sequence	Sequence name	Divergence
Donor	Seq430Gr132	0.004930
Recipient	Seq429Gr132	0.003779
Single copy of <i>D. yakuba</i>	Dyak_Gr132	0.168578



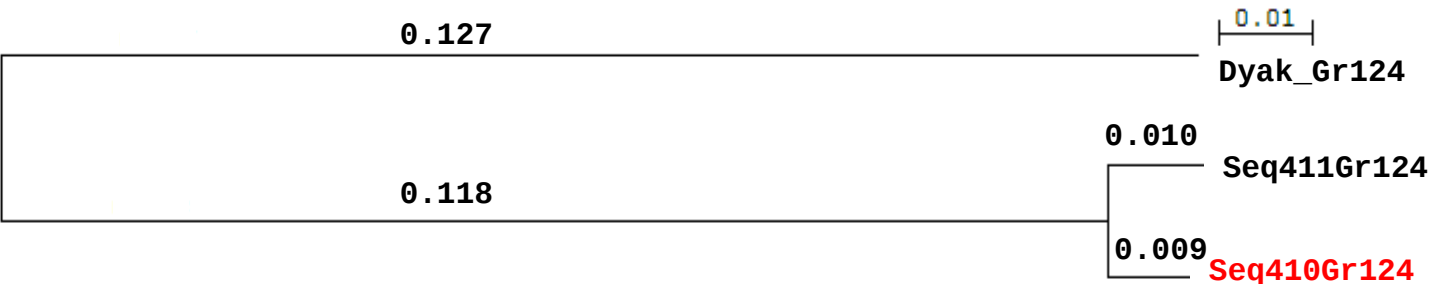
Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq430Gr132	0	0	0
Seq429Gr132	1	0	4

Seq429Gr132	808	AGCATGAATTTGAAAATCTAAGTATATTTCCCAACGCTGAAATCTTAAAG
Seq430Gr132	779	CGCATGAGTTAGAAAATCTCTGTATATTTGCAACGCTGAAGTCTTAAAA
Seq429Gr132	858	A-----ATGCCAATTAACAGACAATATTCCTAAGTATTTCTAACTCTG
Seq430Gr132	829	AATTATATGCCAATGAAAACAGAAAATATTTCAAAGTATTTCTAACTCTG
Seq429Gr132	903	AAAATTTTCGTTTCATCTTATCTTTTCGACAAAGTTTTGTC-----
Seq430Gr132	879	AAAATTTTCGTTAATCTTATCTTTTCGACAAAGTTTTGGCTATATTGGCCGT
Seq429Gr132	941	CTGTTAATAGTGATCCTTTACTGCGCTGCAAACCTGGGACTGAAATTGAA
Seq430Gr132	929	CTGTTAATAGTGATCCTTAACGTGCTTCAAACCTGGGACTGAAATT-AA
Seq429Gr132	991	TACATG-----TAAGGTTATAATAAATTTAATTATTTTGTAC
Seq430Gr132	978	TACATGCAGCAATACAATACAAAGTTATAATAAATTTAATTATTTTGTAC
...		
Seq429Gr132	1378	CGAAAATGTGCACAAAAA-----TCCCTTACCATTCCCGTTATCAG
Seq430Gr132	1378	CGAAAATGTGCACCAAAAAAACGGTCCCTTACCATTCCCGTTATCAG
...		

Seq429Gr132	4572	AAATACCACCCTCTGTCTCCTCATTCCCCTGATTTCCACTTTAACTGAAA
Seq430Gr132	4575	AAATACCACCCTCTGTCTCCTCATTCCCCTGATTTCCACTTTAACTGAAA
Seq429Gr132	4622	CTTGAAAATAA-----ATAAAAGCACTAAAGTGAGCGGCCGGAAGTTG
Seq430Gr132	4625	CTTGAAAATAAATAAAAGCATAAAAGCACTAAAGTGAGCGGCCGGAAGTTG

Group 124

Sequence	Sequence name	Divergence
Donor	Seq410Gr124	0.009006
Recipient	Seq411Gr124	0.010251
Single copy of <i>D. yakuba</i>	Dyak_Gr124	0.244970



Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq410Gr124	1	0	1
Seq411Gr124	0	1	1

Seq410Gr124	914	AACAAGCGAGAATCCTACAGT-----CGACTATCAGATACACGTTT
Seq411Gr124	932	AACAAGAGAGAATGCTATGGT CGAGTTACC CGACTATCAGATACCAGTTA
Seq410Gr124	955	TTCAGCTAGTGGGAATGCGAAATTTTCATACTTTTTC TGGGATATCAATA
Seq411Gr124	982	CTCAGTTAGGGGGAATGG-----GAATA
Seq410Gr124	1005	GATATTGAAGAATAGAATGAGAAAAATTGTTTCAAATTATTCAAAAAGTAG
Seq411Gr124	1005	GATATTGGGGAATAGAATGAGAAAAATTGTTTCAAATTATTCAAAAAGTAG

Group 104

Sequence	Sequence name	Divergence
Donor	Seq292Gr104	0.026581
Recipient	Seq293Gr104	0.029648
Single copy of <i>D. yakuba</i>	Dyak_Gr104	0.378039

0.203

0.02

Dyak_Gr104

0.030

Seq293Gr104

0.175

0.027

Seq292Gr104

Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq292Gr104	1	0	2
Seq293Gr104	0	0	2

Seq292Gr104 1494 GATCCTAGCAATAGCCGGCCAAGCCACTGACCATTTCTCCGTGTTACGCG
Seq293Gr104 1494 GATCCTAGCAATAGCCAGCCAAGCCACTGACCTTTTTTCCCGTGTTACGCG

Seq292Gr104 1544 CTTACAAAATGCAAAAATGT-----GGGGGCC
Seq293Gr104 1544 GTTACAAAATGCAAAAATGTGGTGATAGTTCAGCTGCAGTGGAAAGGGGCC

Seq292Gr104 1570 TTAAAGT-----ATCGGACGAAGAGGCT--GCCGCATCGTTCC
Seq293Gr104 1594 TTGAGGTACATCAATCGCAATCCGACAAAGAGGCTGCGCCGCATCGTTCC

Seq292Gr104 1606 GATTCTGAGAGAGCACAGGGATCAGGCACGCCGACAGCGTCAGCAATAAA
Seq293Gr104 1644 GATTCTGAGAGAGCACAGGGATCAGGCACGCCGACAGCGTCAGCAATAAA

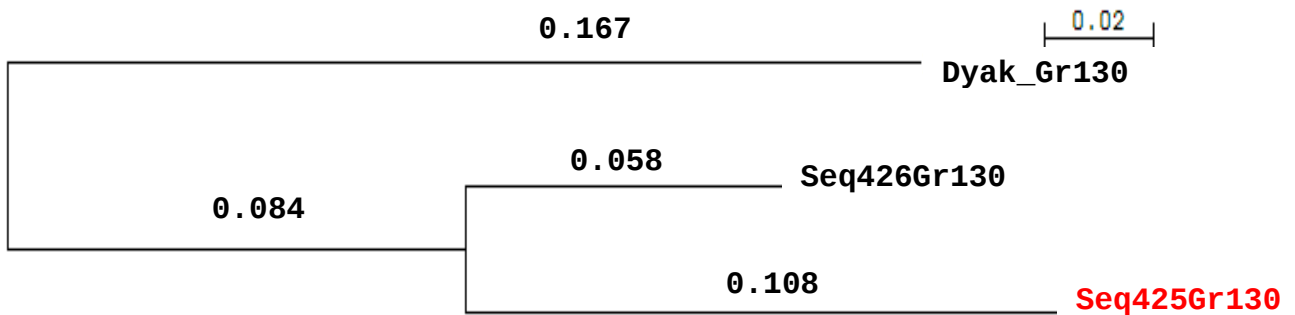
Seq292Gr104 1656 GGGAAACTTGTGATAGGCACGAGAATTC AATTGGATTCTGTTTATTTAATG
Seq293Gr104 1694 GTGAAACTTGTGAT-----AATTGGATTGTTTATTTTATG

Seq292Gr104 1706 CAAGAAATAAAAAAGATCATAATAATTGAATTGGTTTTATTTAAAT TAAAA
Seq293Gr104 1730 CAAGAAATAAAAAAG-----AATGCAA

Seq292Gr104 1756 AATAACGACTATATATGATTTGCTTTCTACAGCACT 1791
Seq293Gr104 1752 AATAACCACTATATTTAATTTGCTTTCTACAGCACT 1787

Group 130

Sequence	Sequence name	Divergence
Donor	Seq425Gr130	0.108003
Recipient	Seq426Gr130	0.057939
Single copy of <i>D. yakuba</i>	Dyak_Gr130	0.250179

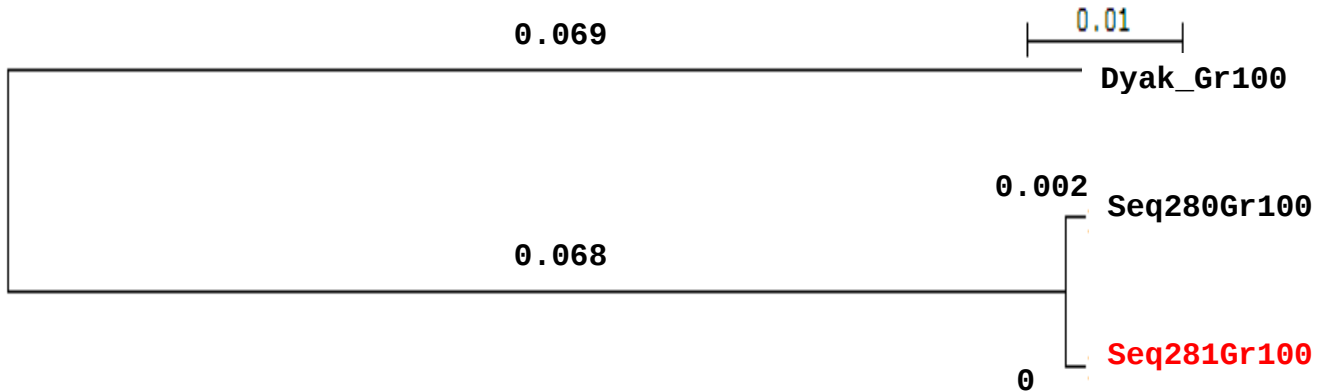


Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq425Gr130	0	1	1
Seq426Gr130	0	0	0

Seq425Gr130	1451	AATGAAAAAAGGAAGTACACCTAAGGAGGGTTTCGTATGATCAGAATGCAA
Seq426Gr130	1451	AATGAAAAAAGGAAGTAAACCTGAGGAGGGTTTCGTATGATCAGAATGCAA
Seq425Gr130	1501	AAAGCTATATTAATAGGCCAAT-----CTGAGTTCAAGAT
Seq426Gr130	1501	AAAGCTATATAAATAGGCCAATCTGACAAAGTATATACTGAGTTCAAGAT
Seq425Gr130	1536	CAAAGTTTTAGATATTAACCCCTTTAAATGCCAATTGCCCGAAGAAGTTG
Seq426Gr130	1551	CAAAGTTTTAGACATTAACCCCTTTAAATGCCAATTGCCCGAAGAAGTTG

Group 100

Sequence	Sequence name	Divergence
Donor	Seq281Gr100	0.000000
Recipient	Seq280Gr100	0.002456
Single copy of <i>D. yakuba</i>	Dyak_Gr100	0.214202

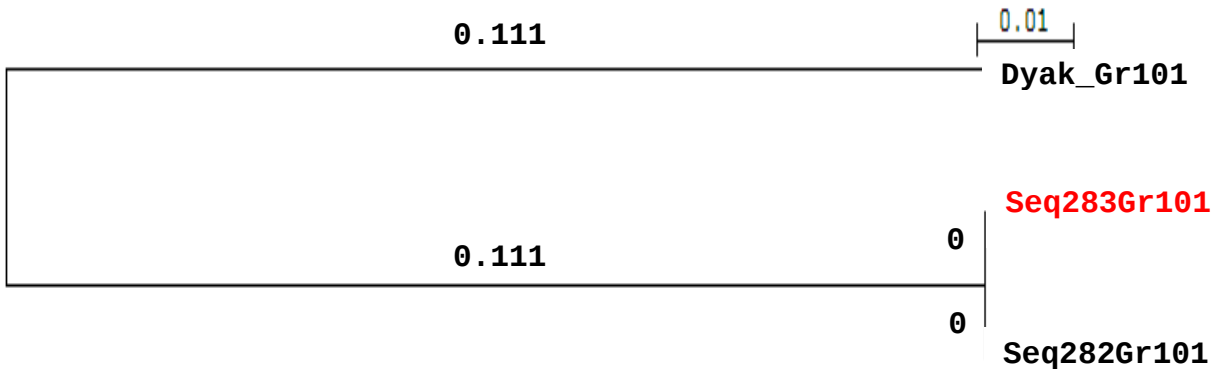


Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq281Gr100	1	0	2
Seq280Gr100	0	1	1

Seq280Gr100	977	CTGTGGATCTTTTCATTTCATCGGAT-----CTGCGACCATTT
Seq281Gr100	964	C--TGGATCTCTTATTCTTCCGATCTGCGGTTTCTACTGCTGCGACCATTT
...		
Seq280Gr100	1412	GCAAATTTTGTCAAAGTTTGGCCAAAACAAAGGGAGCGTTTTTGT--C
Seq281Gr100	1412	GCAAACGTGTCA-----GCCAAAGAAAAGATGTTATTTTTGGCC
...		
Seq280Gr100	1460	AGAACAAAAAACCCGCAAGTTTGTCAATTGTTT--ATTGTGCCCAATTGT
Seq281Gr100	1453	A-AACAAAAA-----TTCGCTATTTTTCGTATTG-GCACAATTGT

Group 101

Sequence	Sequence name	Divergence
Donor	Seq283Gr101	0.000000
Recipient	Seq282Gr101	0.000000
Single copy of <i>D. yakuba</i>	Dyak_Gr101	0.221992



Gap location	No. of gaps with tandem repeats	No. of gaps with micro-homology traces	Total no. of gaps
Seq283Gr101	1	1	2
Seq282Gr101	1	4	7

Seq282Gr101	1408	AAATAACAAAGCTTGGCAGTGGCAAAAGCATAATAATGAAAACTAAAAC
Seq283Gr101	1438	AAAT-ACAAAGCCTAGCACTGGCAATAGCATAATAATGAAAACTATAAC
Seq282Gr101	1725	ATATAGATTTAAATCGATCGTCGACCCGTTCTCAATTTATTTCTTTTAAA
Seq283Gr101	1739	ATATA-ATATATATCGATCGTCAACCCGTGCTCAATTTATTTCTTTTAAA
Seq282Gr101	1775	AACATTACAAATTTAGTCAAATGCTAGATCAACATAATTTTCTATGTTTA
Seq283Gr101	1788	AACATTACAAATTTAGTCAAATGCTAAATCAACATAGTTTTCTATGTTTG
Seq282Gr101	1825	AAGTTAATTGGCCGGCTACATTAAATTTTAACATTACGTATGGACT----
Seq283Gr101	1838	GAGTTAACTGGCCGTCTACATTAAATTTAAACATTACGTATGGACTAAAC
Seq282Gr101	1871	-----GGACTTAAACAATTGTGATCGATTAAATATATAGAA
Seq283Gr101	1888	CATACGTGCTTCGGGATTAAACAATTGTGATCAATTAAGCTATAGAA
Seq282Gr101	1908	AAATAACAAAGCTTGGCAGTGGCAAAAGCATAATAATGAAAACTAAAAC
Seq283Gr101	1938	AAAT-ACAAAGCCTAGCACTGGCAATAGCATAATAATGAAAACTATAAC
Seq282Gr101	1958	TGGTGGGTGCCATGGCTGTGGGTGTTGATGTCGGTAACGGTGTGGGTGG
Seq283Gr101	1987	TGGTGGGTGTCAT-----TTCGGTGG

Seq282Gr101	2008	CTGTGGGGAAATCCTTATTTCGATCTTCTCTAGATGATTACACGCT----
Seq283Gr101	2008	CTGTGGAAAAATCCTGATTTCGATCTTCTCTACATGATTGCCATGCT <u>GTGA</u>
Seq282Gr101	2054	---GCGATATATTTCCGCTGGCCACGCGACTTTTGAGGCGCTGTTTGGA
Seq283Gr101	2058	<u>TTCA</u> GGGATATCTGTCCGCTGGCCACGCGACTTTTGAGGCGCTGTTTGGA
Seq282Gr101	2100	TAAATGGGACTTAGGAATTTATGAGATTTTAAATATATGGGCAAATCGGG
Seq283Gr101	2108	TAAATGGGATTTAGGAATTTATGAGATTTTAAATATATGGACAAATCGGG
Seq282Gr101	2150	TTGGTTGG--GTTCAATTGTCTGACCTTGTTGAAAGCATCGCGCATCAAAC
Seq283Gr101	2158	TTGAATGGGTGTTCAATTGTCTGACCTTGTTGAAGACATCGCGCATCAAAC

[illegible]