

Supplementary Material For:

# Simplified DGS procedure for large-scale genome structural study

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**Table S1. Ditag sequences generated by using the revised DGS protocol**

No. of bases	Sequence
30 bases	CTGCAGCAGACATAATCTATTTACCTGCAG
32 bases	CTGCAGAGGAGACAGGTGGCATGCGCCTGCAG CTGCAGAGGATCGAGAGGATCAAGCCCTGCAG CTGCAGTCTGAGATCGACCTGCAACGCTGCAG
35 bases	CTGCAGAAATGGACTTCTAGTCCTTCTCTGCAG CTGCAGATTCACCTGTGGGTTTCTCATGAACTGCAG CTGCAGGGCGCAGAAGGTGGCAGACTGGAGCTGCAG CTGCAGGGGAGACAGTTGCCGGGTGTGCTGCTGCAG CTGCAGGGTACGTTTCATATCTCTCCAGAGCTGCAG CTGCAGGGTTGTCTATGGTGGGGGGAGGGCTGCAG CTGCAGTGAGCTACCATCTGTCCCACTCGCTGCAG CTGCAGTGAGCTGTGATCTGGTCCCTTCTCTGCAG CTGCAGAACATTAGAAGTGAACATGGCTTACTGCAG CTGCAGAAGGGCAGAGCACAATCTTGCTGCTGCAG CTGCAGAATAAAGGAACCTTCCCTCTGCCCTGCAG CTGCAGAATATTATTACCTCCGTGACTTCTCTGCAG CTGCAGACCAGGCACGTAATCTCAGCTCACTGCAG CTGCAGAGTCTTTTGGAGCTAACCTCAAACCTGCAG CTGCAGATCAGCCCTGGTTAATCTTCCACCTGCAG CTGCAGCCACATGGTGTATATTCTATTGTCTGCAG CTGCAGCCTCCACCTCCTGATCATGGCTCACTGCAG CTGCAGCCTGTCTTGAGTCCCTGTGCTTTCTGCAG CTGCAGCGAGCTATGGTCGCCAGTCCAGTCTGCAG CTGCAGCTCCTGACCTCGGCCCTGGTTACTGCAG CTGCAGCTCTCATGGTGCCAGACTCCCGCTCTGCAG
36 bases	CTGCAGGAGTCTGAACAGTGGGAAGCTTTTCTGCAG CTGCAGGCAATGGTGACACAGAATGCTTCTCTGCAG CTGCAGGGGGGACCGGTCTCCAATAAAACTGCAG CTGCAGGGGTGGTCTGCCGTTAATGGTTTCTGCAG CTGCAGTCAGGGCTGTAGGAGAAGTCGGGGCTGCAG CTGCAGTCCCAACCCTGCACTGAACACTAGCTGCAG CTGCAGTCTCAGCCTTCCAACACTTACCCTGCAG CTGCAGTGCCCAGAGGCTCCTGCTTCTTCTGCAG CTGCAGTGGCCGATCAGCCCTAATAGACATCTGCAG CTGCAGTGGCGATGGGGTCCCTGGAGTCACCTGCAG CTGCAGTGGCGTATCTCCCTCACTGAGGGCTGCAG CTGCAGTGGGCCATGATCTCCTTGTCTTCTGCAG CTGCAGTTAGTAAATGTGGCACTGCTATGGCTGCAG CTGCAGTTTTTTAGCTTGAGAACCACAGCTGCAG

**Table S1 (continued). Ditag sequences generated by using the revised DGS protocol**

No. of bases	Sequence
37 bases	CTGCAGAGCTCCTAAGTTTGCTCCTCCCAGGCTGCAG
	CTGCAGAGTTCAAGTGAGAAATCATAACTACTGCAG
	CTGCAGATCGGAAAAGCTCGTATGCCGTCTTCTGCAG
	CTGCAGATCTGCTGCTTTAGGCCTACTGGGCTGCAG
	CTGCAGCCCCGAGCCCGAGGGACTCTGCGCCTGCAG
	CTGCAGCCTCAACTTCCCCTCTTAAAGGGAAGTGCAG
	CTGCAGCGGGTTTCAGAGGCCTCATTGTCAACTGCAG
	CTGCAGCGTCTGCTTGACTCTTCCCAGAGGCTGCAG
	CTGCAGCTATGCAGCCATGACTCAAAGCAAAGTGCAG
	CTGCAGCTGGGATTACAGACGGGGAGGCTCCTGCAG
	CTGCAGGAGCAAGAGAGCATGGCTTGTACTGCAG
	CTGCAGGCATTTCTGTAATCTCCAGCCCTGCTGCAG
	CTGCAGGCTTCTGGAGAAGCAAACAGGCTCCCTGCAG
	CTGCAGGAAACCCCGAGCAGCCATGGAGACTGCAG
	CTGCAGGGAGGCTGAAATCTTAGCATTGACTGCAG
	CTGCAGTTACGTTAAAGGCACTAAGGCAAAGTGCAG
	CTGCAGTACATCATAATACATCACCACGGGCTGCAG
	CTGCAGTATGACTCATAACTCCCATGCTCACTGCAG
	CTGCAGTATCCAGAGTGCCTTACAGCTTACTGCAG
	CTGCAGTGAGACAGAGTTACTGTTGCCAGGCTGCAG
CTGCAGTGACACGCTGGCACACCGAACTAGTGCAG	
CTGCAGTGCACTGGTACCATAAAAAAAAAATCCTGCAG	
CTGCAGTGCCGGCTGTGTATGATGACAGTGGCTGCAG	
CTGCAGTGTGAGCTTGAAGCTGTCTCCAGGCTGCAG	
CTGCAGTGTGAGTGCCTGTCTCACTTTGCTGCAG	
CTGCAGTTGTGGCCTGGGTGCAATGGCTCACTGCAG	
38 bases	CTGCAGATTAATGAAGATTTGCCAGCCTCCTCTGCAG
	CTGCAGCACATCAACGCTTACTCAAAACATTCTGCAG
	CTGCAGCCCAGCTCAGGGTACGTGTATGTTCACTGCAG
	CTGCAGCTAAGGCGTGATCCTCAGTGTCTTCTCTGCAG
	CTGCAGCTTGGTTGGGATGTCTGCGTCCCCTGCAG
	CTGCAGGAGGCAGTATGGCCGCACACATACTGCAG
	CTGCAGGCCATGCCCTCAGATATTAGTTACCTCTGCAG
	CTGCAGGTAGAAGGGCCTAATGCCAGGAGCTCTGCAG
	CTGCAGGTCTCAGGGCGGGTGGTGGGAGGCTGCAG
	CTGCAGGTGCGCACGTGCCTCCTAACAAAATGCTGCAG
	CTGCAGTAACAATAGTACCGGCCCGTACCAGGCTGCAG
	CTGCAGTCCAGCCTGGGTGGGCTCTTTCTAACTGCAG
CTGCAGTTGTTGGCCTTTTGGCGCGCTTGGGCTGCAG	
39 bases	CTGCAGCCACAGAGCCCGTATCATAGTCACTGCAG
	CTGCAGTCTTCCCTACACGACTCTTCCGATCTGCAG
44 bases	CTGCAGTCCCAAGGACGTCCAGGTAAAATGATAGCCCTGCAG