

LE_HBa0037109_T7_80657, 5.0cM, Chromosome 6
 These primers were designed from the T7 BAC End

Christopher Martin and Douglas Maxwell, University of Wisconsin-Madison
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Primer Name	Sequence (5'-3')
CM5-F1	GTTACTTGATGCTTAATTATTGATGTC
CM5-R1	GCAGTGCAGTCATGAAAGCCAC

Gc43 Partial Sequence_CM5F1: 498 bp;

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1      TTCCACAACC ATAACCTCAA GGTTCTCTAC TTCGTGAATG CCTTCTCTCC ACTGCTTCCA
61     CAACCATTAC CTCAAGGTTT TCTACTTCTC AACTTTATTC AAACCTCAAGA TATTTTCCCA
121    CGTAACACAA CGGGGGAAAA GAGCTTCTAT GTTTTGTAAT ATTGCAGTAT TAACCATCAG
181    AAGCATATAG CTTATACAGA AGGGTTCACT ATCCAGCTTA ATTGCACCAT TTTAGAAAAA
241    GAACCGCTCC TATTTTTGTT AATTGCCTGG TTACCATTAT AAACAGCAAA ACACAAAGGA
301    CTTGAGAGAG ATGTCACAAG AACAGAATTA CTAGCAGCAA AATTAACACA GTTATAGAAA
361    CAAACATATG TTTCCCTGAA GGGAAATAAA GAGGAAAAAG AAAATCAATA TACATATGTT
421    ATAAAGCAAA ACAGTCATGA TTTGTCATCA AAAAAAAAAAT TAACATACCA CAACCAGTGG
481    CTTTCATGAC TGCCTGCTC
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HUJ-VF Sequence_CM5F1-R1: 554 bp;

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1      GTTACTTGAT GCTTAATTAT TGATGTCTAC AATCCGTAGC TGGGGGATTA CCCAACAGGA
61     AGAAAATCAA TTTTCATGGT GAGCATTTTG TGAATGCCTT CTCTCCTCTG CTTCCACAAC
121    CATTACCTCA AGGTTCTCTA CTTCTTACAC TTATTCAAAC TCAAGATATT ATCCACATA
181    ACACAAAGGG GGAAAAGAGC TTCTATGTTT TGTAATATTG CAGTATTACC CATCAGAAGC
241    ATATAGCTTA TACACAAGGG TTTACTATCC AGCTTAATTG CACCATTTTA GAATAAGAAC
301    CACTCCTATT TTTGGTAATT GCCTGGTTAC CATTTTAAAC AGCAAAACAC AAAGGACTTG
361    AGAGAGATGT CACAAGAACA GAATTACTAG CAGCACAATC AACACAGTTA TAGAAACAAA
421    CATATGTTTC CCTGAAGGGA AATAAAGAGG AAAAAGAAAA TCAATATACA TATGGTATGA
481    AGCAAAACAG TCATGATTTG TCATCAAGAA AAAAATTATC ATACCACAAC CAGTGGCTTT
541    CATGACTGCA CTGC
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Gc9 Sequence_CM5F1-R1: 554 bp;

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1      GTTACTTGAT GCTTAATTAT TGATGTCTAC AATCCGTAGC TGGGGGATTA CCCAACAGGA
61     AGAAAATCAA TTTTCATGGT GAGCATTTTG TGAATGCCTT CTCTCCTCTG CTTCCACAAC
121    CATTACCTCA AGGTTCTCTA CTTCTTACAC TTATTCAAAC TCAAGATATT ATCCACATA
181    ACACAAAGGG GGAAAAGAGC TTCTATGTTT TGTAATATTG CAGTATTACC CATCAGAAGC
241    ATATAGCTTA TACACAAGGG TTTACTATCC AGCTTAATTG CACCATTTTA GAATAAGAAC
301    CACTCCTATT TTTGGTAATT GCCTGGTTAC CATTTTAAAC AGCAAAACAC AAAGGACTTG
361    AGAGAGATGT CACAAGAACA GAATTACTAG CAGCACAATC AACACAGTTA TAGAAACAAA
421    CATATGTTTC CCTGAAGGGA AATAAAGAGG AAAAAGAAAA TCAATATACA TATGGTATGA
481    AGCAAAACAG TCATGATTTG TCATCAAGAA AAAAATTATC ATACCACAAC CAGTGGCTTT
541    CATGACTGCA CTGC
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Gc143-2 Sequence_CM5F1-R1: 554 bp;

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1      GTTACTTGAT GCTTAATTAT TGATGTCTAC AATCCGTAGC TGGGGGATTA CCCAACAGGA
61     AGAAAATCAA TTTTCATGGT GAGCATTTTG TGAATGCCTT CTCTCCTCTG CTTCCACAAC
121    CATTACCTCA AGGTTCTCTA CTTCTTACAC TTATTCAAAC TCAAGATATT ATCCACATA
181    ACACAAAGGG GGAAAAGAGC TTCTATGTTT TGTAATATTG CAGTATTACC CATCAGAAGC
241    ATATAGCTTA TACACAAGGG TTTACTATCC AGCTTAATTG CACCATTTTA GAATAAGAAC
301    CACTCCTATT TTTGGTAATT GCCTGGTTAC CATTTTAAAC AGCAAAACAC AAAGGACTTG
361    AGAGAGATGT CACAAGAACA GAATTACTAG CAGCACAATC AACACAGTTA TAGAAACAAA
421    CATATGTTTC CCTGAAGGGA AATAAAGAGG AAAAAGAAAA TCAATATACA TATGGTATGA
481    AGCAAAACAG TCATGATTTG TCATCAAGAA AAAAATTATC ATACCACAAC CAGTGGCTTT
541    CATGACTGCA CTGC
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Heinz 1706 Sequence_CM5F1-R1: 554 bp (Downloaded from SGN website
<http://www.sgn.cornell.edu/>;

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1      GTTACTTGAT GCTTAATTAT TGATGTCTAC AATCCGTAGC TGGGGGATTA CCCAACAGGA
61     AGAAAATCAA TTTTCATGGT GAGCATTTTG TGAATGCCTT CTCTCCTCTG CTTCCACAAC
121    CATTACCTCA AGGTTCTCTA CTTCTTACAC TTATTCAAAC TCAAGATATT ATCCACATA
181    ACACAAAGGG GGAAAAGAGC TTCTATGTTT TGTAATATTG CAGTATTACC CATCAGAAGC
241    ATATAGCTTA TACACAAGGG TTTACTATCC AGCTTAATTG CACCATTTTA GAATAAGAAC
301    CACTCCTATT TTTGGTAATT GCCTGGTTAC CATTTTAAAC AGCAAAACAC AAAGGACTTG
361    AGAGAGATGT CACAAGAACA GAATTACTAG CAGCACAATC AACACAGTTA TAGAAACAAA
421    CATATGTTTC CCTGAAGGGA AATAAAGAGG AAAAAGAAAA TCAATATACA TATGGTATGA
481    AGCAAAACAG TCATGATTTG TCATCAAGAA AAAAATTATC ATACCACAAC CAGTGGCTTT
541    CATGACTGCA CTGC
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Summary

Complete sequence was obtained for Gc143-2, HUI-VF, and Gc9, and partial sequence was obtained for Gc43 through standard sequencing methods in our laboratory. Complete sequence was obtained for Heinz 1706 from the SGN website <http://www.sgn.cornell.edu/>. Upon alignment Gc143-2, Gc9, Heinz 1706, and HUI-VF all matched exactly. Gc43 differed by over a dozen SNP and an INDEL of roughly 30 base pairs.