

**LE\_HBa0246L12\_SP6\_405980, 3.0 cM, Chromosome 6**  
**These Primers Were Designed From the SP6 BAC End**

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Primer Name	Primer Sequence (5'-3-)
CM2-F1	GATCAGTCAGGAACTCAAAGAG
CM2-R1	CCATCGAGCCGTTTATTTCTGTAC

Gc143-2\_CM2F1-R1: 471 bp;

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1      GATCAGTCAG GAACTCAAAG AGAAAATGAT GGTCACACAT TTCGAATACC TCTACATAGC
61     TGCCCCATTT TCTGTTTGCC CATATGCACA TGTCTGTATG GTTTGGGATC TCCTGACCGT
121    CGAAATGGCC CAGCCAGCAT CTTCCAGAA TCTCTTTATC TCTGATTCCCT CCAATCCGTT
181    TGCTTTTATG GAGTTCCTCC ATTGAGAAAG TGCCAGATCT CACTGTCCAT CTTTTCTGTT
241    AGTGCCTTCA GCATGCGAAG AATTCAATTA TTGGGGAGAT GTGATTGTTG TAATCTTGTT
301    TTTATCTGAA TATAATTTTC AATTTTATCT GCTGGCTTGT CTCAACCAGC ATTGAATGCT
361    GATTCTGGAA TAATAAAAAT AACGGACCTT TTGCTCCCAT GTACTGCGAC AATGGAAACA
421    AATCTGCCGA AAGCACTGAA CTTCTTTGTA CAGAAATAAA CGGCTCGATG G
    
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Gc43\_CM2F1-R1: 473 bp;

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1      GATCAGTCAG GAACTCAAAG AGAAAATGAT GGTCACACAT TTCGAATACC TAGTACATAG
61     CTGCCCCATT TTCTGTTTGC CCATATGCAC ATGTCTGTAT GGTGGGGAT CTCCTGACTG
121    TCGAAATGGC CCAGCCAGCA TCTTCCGAGA ATCTCTTTAT CTCTGATTAC TCCAATGCGT
181    TTGCTTTTAT GGAGTTCCTC CATTGAGAAA GTGCCAGATC TCACTGTCCA TCTGTTTTTG
241    TTAGTGCCTT CAGCATGCGA AGAATTGAAT TATTGGGGAG ATGTGATTGT TGTAATCTTG
301    TTTTTATCTG AATAAAAATTT CCAATTTTAT CTGCTGGCTT GTCTCAACCA GCATCGAATG
361    CTGATTCTGT AATAATAAAA ATAACGGACC TTTTGCTCCC CTGTACTGCG ACAATGGAAA
421    CAAATCTGCC GAAAGCACTG AACTTCTTTG TACAGAAATA AACGGCTCGA TGG
    
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Gc9\_CM2F1-R1: 471 bp;

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1      GATCAGTCAG GAACTCAAAG AGAAAATGAT GGTCACACAT TTCGAATACC TCTACATAGC
61     TGCCCCATTT TCTGTTTGCC CATATGCACA TGTCTGTATG GTTTGGGATC TCCTGACCGT
121    CGAAATGGCC CAGCCAGCAT CTTCCAGAA TCTCTTTATC TCTGATTCCCT CCAATCCGTT
181    TGCTTTTATG GAGTTCCTCC ATTGAGAAAG TGCCAGATCT CACTGTCCAT CTTTTCTGTT
241    AGTGCCTTCA GCATGCGAAG AATTCAATTA TTGGGGAGAT GTGATTGTTG TAATCTTGTT
301    TTTATCTGAA TATAATTTTC AATTTTATCT GCTGGCTTGT CTCAACCAGC ATTGAATGCT
361    GATTCTGGAA TAATAAAAAT AACGGACCTT TTGCTCCCAT GTACTGCGAC AATGGAAACA
421    AATCTGCCGA AAGCACTGAA CTTCTTTGTA CAGAAATAAA CGGCTCGATG G
    
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HUJ-VF\_CM2F1-R1: 471 bp;

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1      GATCAGTCAG GAACTCAAAG AGAAAATGAT GGTCACACAT TTCGAATACC TCTACATAGC
61     TGCCCCATTT TCTGTTTGCC CATATGCACA TGTCTGTATG GTTTGGGATC TCCTGACCGT
121    CGAAATGGCC CAGCCAGCAT CTTCCAGAA TCTCTTTATC TCTGATTCCCT CCAATCCGTT
181    TGCTTTTATG GAGTTCCTCC ATTGAGAAAG TGCCAGATCT CACTGTCCAT CTTTTCTGTT
241    AGTGCCTTCA GCATGCGAAG AATTCAATTA TTGGGGAGAT GTGATTGTTG TAATCTTGTT
301    TTTATCTGAA TATAATTTTC AATTTTATCT GCTGGCTTGT CTCAACCAGC ATTGAATGCT
361    GATTCTGGAA TAATAAAAAT AACGGACCTT TTGCTCCCAT GTACTGCGAC AATGGAAACA
421    AATCTGCCGA AAGCACTGAA CTTCTTTGTA CAGAAATAAA CGGCTCGATG G
    
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## **Summary**

Upon sequence alignment, Gc9, HUJBF, and Gc143-2 all matched identically. Gc43 differed by 11 SNP and two INDEL. This region is not suitable for development of a SCAR marker linked to TY-1.