

ID Construct **13ABSMC** **Map**
 Customer **UNIVERSITÄT DES SAARLANDES, Sonja Kessler**
 Name of the gene **H19**
 optimized for non-optimized

14.10.2013 10:51:20

HindIII

BsaI *NheI* *PmeI* *AflIII*

TATAGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGGAGGGGGTGGGATGGGT

1 -----+-----+-----+-----+-----+-----+
 ATATCCCTCTGGGTTTCGACCGATCGCAAATTTGAATTCGAACCCTCCCCACCCTACCCA

GGGGGTAAACGGGGAAACTGGGGAAGTGGGGAACCGAGGGGCAACCAGGGGAAGATGGG

61 -----+-----+-----+-----+-----+-----+
 CCCCCATTGCCCTTTGACCCCTTCACCCCTTGGCTCCCCGTTGGTCCCCTTCTACCC

GTGCTGGAGGAGAGCTTGTGGGAGCCAAGGAGCACCTTGGACATCTGGAGTCTGGCAGGA

121 -----+-----+-----+-----+-----+-----+
 CACGACCTCCTCTCGAACACCCTCGGTTCTCGTGGAACCTGTAGACCTCAGACCGTCTC

NheI *XhoI*

GTGATGACGGGTGGAGGGGCTAGCTCGAGGCAGGGCTGGTGGGGCCTGAGGCCAGTGAGG

181 -----+-----+-----+-----+-----+-----+
 CACTACTGCCACCTCCCCGATCGAGCTCCGTCCCGACCACCCCGACTCCGGTCACTCC

NarI

KasI

PvuII

AGTGTGGAGTAGGCGCCCAGGCATCGTGCAGACAGGGCGACATCAGCTGGGGACGATGGG

241 -----+-----+-----+-----+-----+-----+
 TCACACCTCATCCGCGGGTCCGTAGCACGTCTGTCCCGCTGTAGTCGACCCCTGCTACCC

CCTGAGCTAGGGCTGGAAAAGAAGGGGGAGCCAGGCATTCATCCCAGGTCACCTTTTGGTTAC
301 -----+-----+-----+-----+-----+-----+
GGACTCGATCCCGACCTTCTTCCCCCTCGGTCCGTAAGTAGGGCCAGTGAAAACCAATG

PvuII *PflMI*
AGGACGTGGCAGCTGGTTGGACGAGGGGAGCTGGTGGGCAGGGTTTGATCCCAGGGCCTG
361 -----+-----+-----+-----+-----+-----+
TCCTGCACCGTCGACCAACCTGCTCCCCCTCGACCACCCGTCCCAAACCTAGGGTCCCGGAC

BspMI *BspMI*
AarI *AarI*
GGCAACGGAGGTGTAGCTGGCAGCAGCGGGCAGGTGAGGACCCCATCTGCCGGGCAGGTG
421 -----+-----+-----+-----+-----+-----+
CCGTTGCCTCCACATCGACCGTCGTCGCCCGTCCACTCCTGGGGTAGACGGCCCGTCCAC

StuI
AGTCCCTTCCCTCCCCAGGCCTCGCTTCCCCAGCCTTCTGAAAGAAGGAGGTTTAGGGGA
481 -----+-----+-----+-----+-----+-----+
TCAGGGAAGGGAGGGGTCCGGAGCGAAGGGGTCGGAAGACTTTCTTCTCCAAATCCCCT

TCGAGGGCTGGCGGGGAGAAGCAGACACCCTCCAGCAGAGGGGCAGGATGGGGGCAGGA
541 -----+-----+-----+-----+-----+-----+
AGCTCCCGACCGCCCTCTTCGTCTGTGGGAGGTCGTCTCCCCGTCTACCCCCGTCT

GAGTTAGCAAAGGTGACATCTTCTCGGGGGGAGCCGAGACTGCGCAAGGCTGGGGGGTTA
601 -----+-----+-----+-----+-----+-----+
CTCAATCGTTTCCACTGTAGAAGAGCCCCCTCGGCTCTGACGCGTTCCGACCCCCAAT

ApaI
TGGGCCCGTTCCAGGCAGAAAGAGCAAGAGGGCAGGGAGGGAGCACAGGGGTGGCCAGCG
661 -----+-----+-----+-----+-----+-----+
ACCCGGGCAAGGTCCGTCTTTCTCGTTCTCCCGTCCCTCCCTCGTGTCCCCACCGGTGCG

PflMI *KpnI* *StuI*

TAGGGTCCAGCACGTGGGGTGGTACCCCAGGCCTGGGTGAGACAGGGACATGGCAGGGGA
721 -----+-----+-----+-----+-----+-----+-----+
ATCCCAGGTCGTGCACCCCACCATGGGGTCCGGACCCAGTCTGTCCCTGTACCGTCCCCT

PvuII

CACAGGACAGAGGGGTCCCAGCTGCCACCTACCCACCGCAATTCATTTAGTAGCAGGC
781 -----+-----+-----+-----+-----+-----+-----+
GTGTCCCTGTCTCCCAGGGTTCGACGGTGGAGTGGGTGGCGTTAAGTAAATCATCGTCCG

StuI *XhoI*

ACAGGGGACAGCTCCGGCACGGCTTCTCAGGCCTATGCCGGAGCCTCGAGGGCTGGAGAG
841 -----+-----+-----+-----+-----+-----+-----+
TGTCCCCGTCGAGGCCGTGCCGAAAGAGTCCGGATACGGCCTCGGAGCTCCCAGCCTCTC

BbsI *AatII*

CGGGAAGACAGGCAGTGCTCGGGGAGTTGCAGCAGGACGTCACCAGGAGGGCGAAGCGGC
901 -----+-----+-----+-----+-----+-----+-----+
GCCCTTCTGTCCGTCACGAGCCCCTCAACGTCGTCCTGCAGTGGTCTCCCGCTTCGCCG

SmaI *NarI*
ApaI *PstI* *KasI*

CACGGGAGGGGGGCCCCGGGACATTCGCGCAGCAAGGAGGCTGCAGGGGCTCGGCCGCGG
961 -----+-----+-----+-----+-----+-----+-----+
GTGCCCTCCCCCGGGGCCCTGTAACGCGTCGTTCCCTCCGACGTCCCCAGCCGGACGCC

PflMI *ApaI*

GCGCCGGTCCCACGAGGCACTGCGGCCAGGGTCTGGTGGGAGAGGGCCCACAGTGGAC
1021 -----+-----+-----+-----+-----+-----+-----+
CGCGGCCAGGGTGTCTCCGTGACGCGGGTCCCAGACCACGCCTCTCCCGGGTGTACCTG

TTGGTGACGCTGTATGCCCTCACCGCTCAGCCCCTGGGGCTGGCTTGGCAGACAGTACAG
1081 -----+-----+-----+-----+-----+-----+-----+
AACCACTGCGACATACGGGAGTGGCGAGTCGGGGACCCGACCGAACCGTCTGTTCATGTC

BsaI

1141 CATCCAGGGGAGTCAAGGGCATGGGGCGAGACCAGACTAGGCGAGGCGGGCGGGGCGGAG
-----+-----+-----+-----+-----+-----+
GTAGGTCCCCTCAGTTCCCGTACCCCGCTCTGGTCTGATCCGCTCCGCCC GCCCGCCTC

SacI

1201 TGAATGAGCTCTCAGGAGGGAGGATGGTGCAGGCAGGGGTGAGGAGCGCAGCGGGCGGCG
-----+-----+-----+-----+-----+-----+
ACTTACTCGAGAGTCCTCCCTCCTACCACGTCCGTCCCCACTCCTCGCGTCGCCCCGCCG

1261 AGCGGGAGGCACTGGCCTCCAGAGCCCCTGGCCAAGGCGGGCCTCGCGGGCGGGCAGCGA
-----+-----+-----+-----+-----+-----+
TCGCCCTCCGTGACCGGAGGTCTCGGGCACCGGTTCCGCCCGGAGCGCCC GCCGCTGCCT

BsmBI *BsaI* *PvuII*

1321 GCCGGGATCGGTGCCTCAGCGTTCGGGCTGGAGACGAGGCCAGGTCTCCAGCTGGGGTGG
-----+-----+-----+-----+-----+-----+
CGGCCCTAGCCACGGAGTCGCAAGCCGACCTCTGCTCCGGTCCAGAGGTCGACCCCACC

PvuII

1381 ACGTGCCCACCAGCTGCCGAAGGCCAAGACGCCAGGTCCGGTGGACGTGACAAGCAGGAC
-----+-----+-----+-----+-----+-----+
TGCACGGGTGGTGCACGGCTTCCGGTCTGCGGTCCAGGCCACCTGCACGTTCGTCTCTG

1441 ATGACATGGTCCGGTGTGACGGCGAGGACAGAGGAGGCGCGTCCGGCCTTCTTGAACACC
-----+-----+-----+-----+-----+-----+
TACTGTACCAGGCCACACTGCCGCTCCTGTCTCTCCGCGCAGGCCGGAAGGACTTGTGG

1501 TTAGGCTGGTGGGGCTGCGGCAAGAAGCGGGTCTGTTTCTTTACTTCTCCACGGAGTCG
-----+-----+-----+-----+-----+-----+
AATCCGACCACCCCGACCCGTTCTTCGCCAGACAAAGAAATGAAGGAGGTGCCTCAGC

GCACACTATGGCTGCCCTCTGGGCTCCCAGAACCACAAACATGAAAGAAATGGTGCTACC
1561 -----+-----+-----+-----+-----+-----+
CGTGTGATACCGACGGGAGACCCGAGGGTCTTGGGTGTTGTACTTTCTTTACCACGATGG

CAGCTCAAGCCTGGGCCTTTGAATCCGGACACAAAACCCTCTAGCTTGAAATGAATATG
1621 -----+-----+-----+-----+-----+-----+
GTCGAGTTCGGACCCGAAACTTAGGCCTGTGTTTTGGGAGATCGAACCTTTACTTATAC

CTGCACTTTACAACCACTGCACTACCTGACTCAGGAATCGGCTCTGGAAGGTGAAGCTAG
1681 -----+-----+-----+-----+-----+-----+
GACGTGAAATGTTGGTGACGTGATGGACTGAGTCCTTAGCCGAGACCTTCCACTTCGATC

AGGAACCAGACCTCATCAGCCCAACATCAAAGACACCATCGGAACAGCAGCGCCCGCAGC
1741 -----+-----+-----+-----+-----+-----+
TCCTTGGTCTGGAGTAGTCGGGTTGTAGTTTCTGTGGTAGCCTTGTCTCGTCGGGGCGTCC

HincII

ACCCACCCCGCACCGGCGACTCCATCTTCATGGCCACCCCTGCGGCGGACGGTTGACCA
1801 -----+-----+-----+-----+-----+-----+
TGGGTGGGGCGTGCCGCTGAGGTAGAAGTACCGGTGGGGGACGCCGCTGCCAACTGGT

SacI

CCAGCCACCACATCATCCCAGAGCTGAGCTCCTCCAGCGGGATGACGCCGTCCCCACCAC
1861 -----+-----+-----+-----+-----+-----+
GGTCGGTGGTGTAGTAGGGTCTCGACTCGAGGAGGTCGCCCTACTGCGGCAGGGGTGGTG

CTCCCTCTTCTTCTTTTCATCCTTCTGTCTCTTTGTTTCTGAGCTTTCCTGTCTTTCCT
1921 -----+-----+-----+-----+-----+-----+
GAGGGAGAAGAAGAAAAAGTAGGAAGACAGAGAAACAAAGACTCGAAAGGACAGAAAGGA

TTTTTCTGAGAGATTCAAAGCCTCCACGACTCTGTTTCCCCGTCCCTTCTGAATTTAAT
1981 -----+-----+-----+-----+-----+-----+
AAAAAGACTCTCTAAGTTTCGGAGGTGCTGAGACAAAGGGGCAGGGAAGACTTAAATTA

BsmBI

TTGCACTAAGTCATTTGCACTGGTTGGAGTTGTGGAGACGGCCTTGAGTCTCAGTACGAG
2041 -----+-----+-----+-----+-----+-----+
AACGTGATTCAGTAAACGTGACCAACCTCAACACCTCTGCCGGAACCTCAGAGTCATGCTC

ApaI EagI

TGTGCGTGAGTGTGAGCCACCTTGGCAAGTGCCTGTGCAGGGCCCGCCGCCCTCCATCT
2101 -----+-----+-----+-----+-----+-----+
ACACGCACTCACACTCGGTGGAACCGTTCACGGACACGTCCCAGGGCCGGCGGGAGGTAGA

NarI

KasI

StuI

GGGCCGGGTGACTGGGCGCCGGCTGTGTGCCCGAGGCCTCACCCCTGCCCTCGCCTAGTCT
2161 -----+-----+-----+-----+-----+-----+
CCCGGCCCACTGACCCGCGGCCGACACACGGGCTCCGGAGTGGGACGGGAGCGGATCAGA

GGAAGCTCCGACCGACATCACGGAGCAGCCTTCAAGCATTCATTACGCCCCATCTCGCT
2221 -----+-----+-----+-----+-----+-----+
CCTTCGAGGCTGGCTGTAGTGCCCTCGTCGGAAGTTCGTAAGGTAATGCGGGGTAGAGCGA

CTGTGCCCCCTCCCACCAGGGCTTCAGCAGGAGCCCTGGACTCATCATCAATAAACACTG
2281 -----+-----+-----+-----+-----+-----+
GACACGGGGAGGGGTGGTCCCAGTTCGTCCTCGGGACCTGAGTAGTAGTTATTTGTGAC

XbaI

ApaI

PmeI

BclI

TTACAGCAAAAAAAAAAAAAAAAAAATCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGA
2341 -----+-----+-----+-----+-----+-----+
AATGTCGTTTTTTTTTTTTTTTTTTAGATCTCCCAGGCAAATTTGGGCGACTAGTCGGAGCT

CTGT
2401 ----
GACA