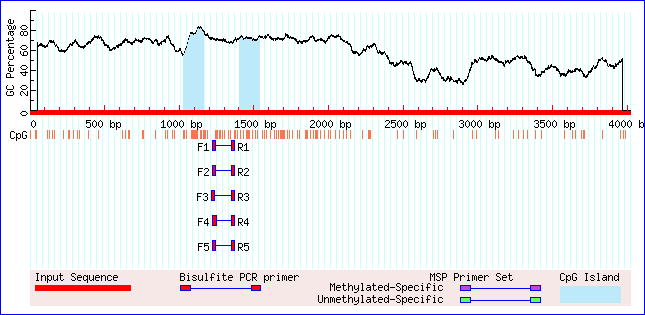
**Supplement 1:** The NY-ESO-1 gene promoter and primer sequences

**MethPrimer result**



Sequence Name:

Sequence Length: 4020

CpG island prediction results

(Criteria used: Island size > 100, GC Percent > 50.0, Obs/Exp > 0.6)

2 CpG island(s) were found in your sequence

Size (Start - End)

Island 1 131 bp (1031 - 1161)

Island 2 135 bp (1402 - 1536)

Primer picking results for bisulfite sequencing (or restriction) PCR

Primer Start Size Tm GC% 'C's Sequence

1 Left primer 1222 25 55.95 68.00 10 TTAGGGTTTTTTGGGTTATTAGTAT

Right primer 1367 25 57.74 60.00 4 AAACTTCCTACAACCTCTCTACCTC

Product size: 146, Tm: 71.0, CpGs in product: 9

2 Left primer 1221 26 56.69 69.23 10 GTTAGGGTTTTTTGGGTTATTAGTAT

Right primer 1367 25 57.74 60.00 4 AAACTTCCTACAACCTCTCTACCTC

Product size: 147, Tm: 70.9, CpGs in product: 9

3 Left primer 1217 26 59.82 65.38 9 GAATGTTAGGGTTTTTTGGGTTATTA

Right primer 1367 25 57.74 60.00 4 AAACTTCCTACAACCTCTCTACCTC

Product size: 151, Tm: 70.9, CpGs in product: 9

4 Left primer 1220 27 58.81 66.67 10 TGTTAGGGTTTTTTGGGTTATTAGTAT

Right primer 1367 25 57.74 60.00 4 AAACTTCCTACAACCTCTCTACCTC

Product size: 148, Tm: 70.8, CpGs in product: 9

5 Left primer 1223 24 54.69 66.67 9 TAGGGTTTTTTGGGTTATTAGTAT

Right primer 1367 25 57.74 60.00 4 AAACTTCCTACAACCTCTCTACCTC

Product size: 145, Tm: 71.0, CpGs in product: 9

1 GGCGACACCTCTGCACCCATCTCCCTGGGCTCCCTCGGGTGGCGGCGGGCCTGGTGTACC

||++|:|::|:||:|:::||:|:::||||:|:::|++|||||++|++||::|||||||::

1 GGCGATATTTTTGTATTTATTTTTTTGGGTTTTTTCGGGTGGCGGCGGGTTTGGTGTATT

61 AGGTCTCTGTTCTGAGACCCTGTGCTGGGGTGTTCCCAGGTTTCTAGCAGCCTGACCGTG

||||:|:||||:|||||:::||||:|||||||||:::||||||:|||:||::|||:++||

61 AGGTTTTTGTTTTGAGATTTTGTGTTGGGGTGTTTTTAGGTTTTTAGTAGTTTGATCGTG

121 GGGTGTAGGCGGATCCCAGCCCCCACCCTGCCACGCTGTGACCGCCACCCACCCAGGCCC

|||||||||++|||:::||:::::|:::||::|++:|||||:++::|:::|:::|||:::

121 GGGTGTAGGCGGATTTTAGTTTTTATTTTGTTACGTTGTGATCGTTATTTATTTAGGTTT

181 CATCCCTGTCCTGGTCCTGAACTGACATAGTCAGTATGTTGCCGGACACAGTGAACTCCT

:||:::|||::||||::||||:|||:|||||:|||||||||:++||:|:||||||:|::|

181 TATTTTTGTTTTGGTTTTGAATTGATATAGTTAGTATGTTGTCGGATATAGTGAATTTTT

241 TCAGAAGCACCCCTGGCACGGGAAGCGGTGGGGCATCCTGGGCCAGGCTCCTGCGGGCCA

|:|||||:|::::|||:|++|||||++||||||:||::||||::|||:|::||++||::|

241 TTAGAAGTATTTTTGGTACGGGAAGCGGTGGGGTATTTTGGGTTAGGTTTTTGCGGGTTA

301 GCTCTGCTTCCATGGGTGTCGCGAAAGGCATGGCGAGGTAGCTGGTGGGGGCCCAGTTAA

|:|:||:||::||||||||++++|||||:||||++||||||:|||||||||:::||||||

301 GTTTTGTTTTTATGGGTGTCGCGAAAGGTATGGCGAGGTAGTTGGTGGGGGTTTAGTTAA

361 GGCATCCTCTCCTAGGACTTGGCCTGTGGCTCCGGCCTGCTGCTTACCCCAGGCCAGCTT

||:||::|:|::|||||:||||::|||||:|:++|::||:||:|||::::|||::||:||

361 GGTATTTTTTTTTAGGATTTGGTTTGTGGTTTCGGTTTGTTGTTTATTTTAGGTTAGTTT

421 CCCCCTCCCCCACTCCCCCACCCCTCCCCCCTACCCCGGATTGCCCAGCCCATCCCCCCC

:::::|:::::|:|:::::|::::|::::::||:::++|||||:::||:::||:::::::

421 TTTTTTTTTTTATTTTTTTATTTTTTTTTTTTATTTCGGATTGTTTAGTTTATTTTTTTT

481 AGGCTGTCTCCCCAGGCACTGGCCCAGTAGCACACCCCACCCAGCTGTCTTGGTTCCCCA

|||:|||:|::::|||:|:|||:::|||||:|:|::::|:::||:|||:||||||::::|

481 AGGTTGTTTTTTTAGGTATTGGTTTAGTAGTATATTTTATTTAGTTGTTTTGGTTTTTTA

541 CTTTCCTTTGCTGCACCCCAAGCTGACTCCTCCATGCCCTTACAAGACCCCTCCCCACCC

:|||::||||:||:|::::|||:|||:|::|::|||:::|||:||||::::|::::|:::

541 TTTTTTTTTGTTGTATTTTAAGTTGATTTTTTTATGTTTTTATAAGATTTTTTTTTATTT

601 TGCCCCCTGTGGCATCACCCGGCCCCCTCCTCATCACTCGACCCTCCATCCCAACCACCT

||:::::|||||:||:|::++|:::::|::|:||:|:|++|:::|::||:::||::|::|

601 TGTTTTTTGTGGTATTATTCGGTTTTTTTTTTATTATTCGATTTTTTATTTTAATTATTT

661 CCCGCCACCCGCTCCCATCTTGCCCCCTTCCCCCCACCTCCTGATCCCCTCCTACACCTG

::++::|::++:|:::||:|||:::::||::::::|::|::||||::::|::||:|::||

661 TTCGTTATTCGTTTTTATTTTGTTTTTTTTTTTTTATTTTTTGATTTTTTTTTATATTTG

721 GGTCCCCCTATCTCCTGGCCCCTGCTCCCCTCCCCGCATGACCCGGTGCCCCTCACCCAA

|||:::::|||:|::|||::::||:|::::|:::++:||||::++|||::::|:|:::||

721 GGTTTTTTTATTTTTTGGTTTTTGTTTTTTTTTTCGTATGATTCGGTGTTTTTTATTTAA

781 TCACCCAGCCCCTCTCCCCCACCCCCACCCCCTCTACCTCCCAGCCCTTACCTCCTCCCC

|:|:::||::::|:|:::::|:::::|:::::|:||::|:::||:::|||::|::|::::

781 TTATTTAGTTTTTTTTTTTTATTTTTATTTTTTTTATTTTTTAGTTTTTATTTTTTTTTT

841 TCCTCGCAGCTGGCCTCTCATATCCCCACCTCCCAACCCCCACCCCCACCCCCACCCAAC

|::|++:||:|||::|:|:||||::::|::|:::||:::::|:::::|:::::|:::||:

841 TTTTCGTAGTTGGTTTTTTATATTTTTATTTTTTAATTTTTATTTTTATTTTTATTTAAT

901 CACTTACTCGCATCTCCCCCGCCTCCTCCCCCACCTGGCCCTGCCCTCCCCATCTCCCGG

:|:|||:|++:||:|::::++::|::|:::::|::|||:::||:::|::::||:|::++|

901 TATTTATTCGTATTTTTTTCGTTTTTTTTTTTATTTGGTTTTGTTTTTTTTATTTTTCGG

961 CCCCCACCTCGCCACCAGAACTGTCAGAACAGAACAGAACAGAACAGAACAGAATACAAC

:::::|::|++::|::||||:|||:||||:||||:||||:||||:||||:||||||:||:

961 TTTTTATTTCGTTATTAGAATTGTTAGAATAGAATAGAATAGAATAGAATAGAATATAAT

1021 TCAAGCAGGCGGCTCTCCGGCCCCCTGGCCCCGCATCTGCAGCATCCATTCAGCCCTGAA

|:|||:|||++|:|:|:++|:::::|||:::++:||:||:||:||::|||:||:::||||

1021 TTAAGTAGGCGGTTTTTCGGTTTTTTGGTTTCGTATTTGTAGTATTTATTTAGTTTTGAA

1081 GCCGCGCCGCCATGCGGACCCCGCGGGGCGCCTCCTCCCGGCCCCGAGGCCCTTGCTGCC

|:++++:++::|||++||:::++++|||++::|::|::++|:::++|||:::|||:||::

1081 GTCGCGTCGTTATGCGGATTTCGCGGGGCGTTTTTTTTCGGTTTCGAGGTTTTTGTTGTT

1141 CCTGCGCCCCGGGGACCTCTGCCGCCCGTGGCACCCGCCTCTCCTGGGCCGCCAGCATTG

::||++:::++||||::|:||:++::++|||:|::++::|:|::||||:++::||:||||

1141 TTTGCGTTTCGGGGATTTTTGTCGTTCGTGGTATTCGTTTTTTTTGGGTCGTTAGTATTG

1201 CCCCCTGGGCCATCAGGAATGCCAGGGCCTCCTGGGCCATCAGCATCGCCCGTCGAACCC

:::::||||::||:|||||||::||||::|::||||::||:||:||++::++|++||:::

1201 TTTTTTGGGTTATTAGGAATGTTAGGGTTTTTTGGGTTATTAGTATCGTTCGTCGAATTT

>>>>>>>>>>>>>>>>>>>>>>>>>

1261 CCTGTGCCCCGGCCTTCGGCCTGCATGGCTCCGGAGCCTCTGCCCGGCTCTCAGAGAGAA

::||||:::++|::||++|::||:||||:|:++|||::|:||::++|:|:|:||||||||

1261 TTTGTGTTTCGGTTTTCGGTTTGTATGGTTTCGGAGTTTTTGTTCGGTTTTTAGAGAGAA

1321 GGTCAGGGCCCACGAGGATGCGGAGGCAGAGAGGCTGCAGGAAGTTCCGCCCCCTGGCGT

|||:||||:::|++||||||++||||:|||||||:||:||||||||:++:::::|||++|

1321 GGTTAGGGTTTACGAGGATGCGGAGGTAGAGAGGTTGTAGGAAGTTTCGTTTTTTGGCGT

<<<<<<<<<<<<<<<<<<<<<<<<<

1381 GAGATGGGCAGCCCGGGATCCTCAGGGCGCCTGCGCACAGGGGCCCTACTTCCGGCCCTG

||||||||:||::++||||::|:||||++::||++:|:|||||:::||:||:++|:::||

1381 GAGATGGGTAGTTCGGGATTTTTAGGGCGTTTGCGTATAGGGGTTTTATTTTCGGTTTTG

1441 GGAGACCCCGAGTGAGCCCCGGAGCACGTGACCGGTTCTCACCAACCCCGCCCCTCCCCA

|||||:::++||||||:::++|||:|++|||:++|||:|:|::||:::++::::|::::|

1441 GGAGATTTCGAGTGAGTTTCGGAGTACGTGATCGGTTTTTATTAATTTCGTTTTTTTTTA

1501 AGAGAGCCCGGGCCGGAAGGTGGCCGCAATGCCAGCTTGGACCCCTCACCCCTGAGCAGC

||||||::++||:++||||||||:++:||||::||:|||||::::|:|::::||||:||:

1501 AGAGAGTTCGGGTCGGAAGGTGGTCGTAATGTTAGTTTGGATTTTTTATTTTTGAGTAGT

1561 CGGCTGTCCGCCGGACCCCTGTCCCGGGAGCCCTGCAGGGAGTCAGGCACTGCGGGGCCC

++|:|||:++:++||::::|||::++||||:::||:|||||||:|||:|:||++|||:::

1561 CGGTTGTTCGTCGGATTTTTGTTTCGGGAGTTTTGTAGGGAGTTAGGTATTGCGGGGTTT

1621 AGCCTGTCCCATCCCCCGGGTCTCCCTCACATCGAGGAGCAAGACGGGCCTGGGAACACG

||::|||:::||::::++|||:|:::|:|:||++|||||:||||++||::||||||:|++

1621 AGTTTGTTTTATTTTTCGGGTTTTTTTTATATCGAGGAGTAAGACGGGTTTGGGAATACG

1681 GGGCCGGGACTGTGCGGCCATCGTCCCGGACCCTGCCTGCCCTGTCCGTCCTTGGGGGAG

|||:++|||:||||++|::||++|::++||:::||::||:::|||:++|::|||||||||

1681 GGGTCGGGATTGTGCGGTTATCGTTTCGGATTTTGTTTGTTTTGTTCGTTTTTGGGGGAG

1741 CGCCCAGGACAGACCCCGGGGGGCAGGCCTCTAACTGGGCTCAGCAGCCTCCGTCCCTGT

++:::||||:|||:::++|||||:|||::|:|||:||||:|:||:||::|:++|:::|||

1741 CGTTTAGGATAGATTTCGGGGGGTAGGTTTTTAATTGGGTTTAGTAGTTTTCGTTTTTGT

1801 CCTGGTCGCCCAGCTGGTGGGGTAGCTGGAACTGCATGTCTGGTGGGCGTGGCCTCGCGC

::||||++:::||:|||||||||||:|||||:||:||||:|||||||++|||::|++++:

1801 TTTGGTCGTTTAGTTGGTGGGGTAGTTGGAATTGTATGTTTGGTGGGCGTGGTTTCGCGT

1861 CAGCCAAGGTCTCCCAGGCGCCAGGTCCAGCCAAGGTGGACGGGAGGGCCCAGCGGGACC

:||::|||||:|:::|||++::||||::||::||||||||++||||||:::||++|||::

1861 TAGTTAAGGTTTTTTAGGCGTTAGGTTTAGTTAAGGTGGACGGGAGGGTTTAGCGGGATT

1921 CGGGGCCGGATCTCACTCCTGGGTTCAACGGGTTCTGTCCCTGTCCTAGTCGCCCCGCCT

++|||:++|||:|:|:|::||||||:||++||||:|||:::|||::||||++:::++::|

1921 CGGGGTCGGATTTTATTTTTGGGTTTAACGGGTTTTGTTTTTGTTTTAGTCGTTTCGTTT

1981 GGTGGGGGAGCTGGAGCTGCGTGTGGGGTGGGTTGCGGGTGGCCTCCCACCAGCCAGGGG

||||||||||:|||||:||++||||||||||||||++|||||::|:::|::||::|||||

1981 GGTGGGGGAGTTGGAGTTGCGTGTGGGGTGGGTTGCGGGTGGTTTTTTATTAGTTAGGGG

2041 CTCCCGGGCTCTAGGCCTGGCCCAGGTGGACAGGCGGGACCTGCTGGACCTGAGGCTGGG

:|::++||:|:||||::|||:::|||||||:|||++|||::||:||||::|||||:||||

2041 TTTTCGGGTTTTAGGTTTGGTTTAGGTGGATAGGCGGGATTTGTTGGATTTGAGGTTGGG

2101 TCGGGCCTGGCTCCTGGGTTCGGCAGTATCAGTCCCTGCCCTGGTCGCTCTTGCCTGGTA

|++||::|||:|::||||||++|:|||||:|||:::||:::||||++:|:|||::|||||

2101 TCGGGTTTGGTTTTTGGGTTCGGTAGTATTAGTTTTTGTTTTGGTCGTTTTTGTTTGGTA

2161 GGGAGCTGGGAGGTGACCCTGTGTCTGCTCAGTGGTGATCTATTTGTGTGTCTGGAAGGG

|||||:||||||||||:::|||||:||:|:|||||||||:|||||||||||:||||||||

2161 GGGAGTTGGGAGGTGATTTTGTGTTTGTTTAGTGGTGATTTATTTGTGTGTTTGGAAGGG

2221 GGTCAAATCCACGGGACAGGTACCTCTAGAGGCATGCAGGGGTGAGGGCGGCACGGCCCC

|||:||||::|++|||:|||||::|:||||||:|||:|||||||||||++|:|++|:::+

2221 GGTTAAATTTACGGGATAGGTATTTTTAGAGGTATGTAGGGGTGAGGGCGGTACGGTTTC

2281 GGGAGCTGAATGTCTGTGCCAGGCACACCTGTAGCAACAGGAGGTGACCAGACAGGGCCT

+||||:|||||||:||||::|||:|:|::|||||:||:|||||||||::|||:||||::|

2281 GGGAGTTGAATGTTTGTGTTAGGTATATTTGTAGTAATAGGAGGTGATTAGATAGGGTTT

2341 AGCCCTGAGGAAGGGGGAGGTACTGAAATCCAAACCACTCTCCCCCACCTTCCAAATCCA

||:::|||||||||||||||||:||||||::|||::|:|:|:::::|::||::||||::|

2341 AGTTTTGAGGAAGGGGGAGGTATTGAAATTTAAATTATTTTTTTTTATTTTTTAAATTTA

2401 GGAATCAGCAGCCTCTGCACCTGGGAAAAGCATATTGGCACTCATGTGGAAACTAAAAAC

|||||:||:||::|:||:|::|||||||||:|||||||:|:|:|||||||||:||||||+

2401 GGAATTAGTAGTTTTTGTATTTGGGAAAAGTATATTGGTATTTATGTGGAAATTAAAAAC

2461 GTTGATCTTTTGGAGGTAGAGCAGAATGATGGTTACCAGACGCTGGGAAAGGTGGGGAGG

+|||||:||||||||||||||:|||||||||||||::|||++:|||||||||||||||||

2461 GTTGATTTTTTGGAGGTAGAGTAGAATGATGGTTATTAGACGTTGGGAAAGGTGGGGAGG

2521 GTGGGGAGGTTAATGGGGACAAACATATAGTTGCATAGAAGGATTAAGTTCTAGTGTTTG

|||||||||||||||||||:|||:|||||||||:||||||||||||||||:|||||||||

2521 GTGGGGAGGTTAATGGGGATAAATATATAGTTGTATAGAAGGATTAAGTTTTAGTGTTTG

2581 ATAGCACCGTAGAGGGACTATAGGTAATTATTTATTGTATATTTCAAAATAGCTAAAAGA

||||:|:++||||||||:||||||||||||||||||||||||||:|||||||:|||||||

2581 ATAGTATCGTAGAGGGATTATAGGTAATTATTTATTGTATATTTTAAAATAGTTAAAAGA

2641 TAGGAAATGTTCCCCAAAAAAAGAAATGATAAATGCTTGAGGTGGTGGAGATCCTAAATA

|||||||||||::::||||||||||||||||||||:||||||||||||||||::||||||

2641 TAGGAAATGTTTTTTAAAAAAAGAAATGATAAATGTTTGAGGTGGTGGAGATTTTAAATA

2701 CCCCGACTTGATCATTACATCGTGTGTGCGTGTGCATGTATCAGAATATCACATGTATCC

:::++|:|||||:||||:||++||||||++||||:||||||:|||||||:|:||||||::

2701 TTTCGATTTGATTATTATATCGTGTGTGCGTGTGTATGTATTAGAATATTATATGTATTT

2761 CATAAATATGCAGAGTTATCATACATCAGTTAAAAATGTTTTTACTTACAGAAAAGAAAA

:|||||||||:||||||||:|||:||:|||||||||||||||||:|||:|||||||||||

2761 TATAAATATGTAGAGTTATTATATATTAGTTAAAAATGTTTTTATTTATAGAAAAGAAAA

2821 ATTCACCCAAGCTCTTGCGTGTACCTCCAGTTTATTATTTTCACTGCTGTATTTCATTAC

|||:|:::|||:|:|||++||||::|::|||||||||||||:|:||:|||||||:||||:

2821 ATTTATTTAAGTTTTTGCGTGTATTTTTAGTTTATTATTTTTATTGTTGTATTTTATTAT

2881 ATATATTTCATTAAATGATGAATTTTAAAAACCAGAGAACACAACTTGTTAACACCTGGA

||||||||:||||||||||||||||||||||::||||||:|:||:|||||||:|::||||

2881 ATATATTTTATTAAATGATGAATTTTAAAAATTAGAGAATATAATTTGTTAATATTTGGA

2941 ATAGCTGAAAATCAGACATAACCCGGTTAGTGATTGCCATCCTTCCTGTCGTCCTCTGCT

||||:|||||||:|||:||||::++|||||||||||::||::||::|||++|::|:||:|

2941 ATAGTTGAAAATTAGATATAATTCGGTTAGTGATTGTTATTTTTTTTGTCGTTTTTTGTT

3001 CAGTCTCCCCATTCTCAGACAGAGGCAGGCTAAAGTTCTTACCTTCAACAGGTCAGGGAA

:|||:|::::|||:|:|||:|||||:|||:|||||||:|||::||:||:||||:||||||

3001 TAGTTTTTTTATTTTTAGATAGAGGTAGGTTAAAGTTTTTATTTTTAATAGGTTAGGGAA

3061 GGGAGAGTAAAGTGCATGTGACCCTGTCTTAGGAAGCAGGAAGACAGAGGGAGGGTCTCC

||||||||||||||:||||||:::|||:||||||||:|||||||:|||||||||||:|:+

3061 GGGAGAGTAAAGTGTATGTGATTTTGTTTTAGGAAGTAGGAAGATAGAGGGAGGGTTTTC

3121 GGGTCCCCATTATTTTCCCGGCCTATTATCCTCAGATCAAGTCAAGAAAGGAAGTCCTAA

+|||::::||||||||::++|::||||||::|:||||:||||:||||||||||||::|||

3121 GGGTTTTTATTATTTTTTCGGTTTATTATTTTTAGATTAAGTTAAGAAAGGAAGTTTTAA

3181 CTGATTGAGAGATTCCTGGAGATACTGCCACTGTCCTGGAAGTCTCAGCCAGCCACTGGA

:|||||||||||||::||||||||:||::|:|||::|||||||:|:||::||::|:||||

3181 TTGATTGAGAGATTTTTGGAGATATTGTTATTGTTTTGGAAGTTTTAGTTAGTTATTGGA

3241 CCGGAAATCTCCATCAATATTTCAGCCAGAGCAACGTCTGCCACTAGATGGCATCAAACT

:++|||||:|::||:|||||||:||::||||:||++|:||::|:|||||||:||:|||:|

3241 TCGGAAATTTTTATTAATATTTTAGTTAGAGTAACGTTTGTTATTAGATGGTATTAAATT

3301 CCAGCCGGGAGCAGGACAGATTTGGATGGTCCAGCGGGCTTGCCTCATTCATTTCATTAA

::||:++||||:||||:|||||||||||||::||++||:|||::|:|||:||||:|||||

3301 TTAGTCGGGAGTAGGATAGATTTGGATGGTTTAGCGGGTTTGTTTTATTTATTTTATTAA

3361 CCCCACAGTAACACATTTTCACATTGTATGCGATTGGATTTCTTGGAAACTACCTATTAC

::::|:|||||:|:|||||:|:||||||||++|||||||||:|||||||:||::|||||:

3361 TTTTATAGTAATATATTTTTATATTGTATGCGATTGGATTTTTTGGAAATTATTTATTAT

3421 ATTACGGCAGAGTTTTATAGTCCTCTAATTTATCCATTCTGCTGATGATGGGCAGGCATT

||||++|:|||||||||||||::|:||||||||::|||:||:||||||||||:|||:|||

3421 ATTACGGTAGAGTTTTATAGTTTTTTAATTTATTTATTTTGTTGATGATGGGTAGGTATT

3481 TGGATAGTTTCCAGCCCTTGGCTATGAACATGCTTGTACAGGTCTCTTGAAGCACATGTC

||||||||||::||:::||||:||||||:|||:|||||:||||:|:||||||:|:||||:

3481 TGGATAGTTTTTAGTTTTTGGTTATGAATATGTTTGTATAGGTTTTTTGAAGTATATGTT

3541 CAAGTTTTTTTTTGGAATTGCTGTATCACAGCCAATACATATCTCGAAATTTACTAGATA

:|||||||||||||||||||:|||||:|:||::||||:||||:|++|||||||:||||||

3541 TAAGTTTTTTTTTGGAATTGTTGTATTATAGTTAATATATATTTCGAAATTTATTAGATA

3601 ATGCCATGTTTTCCCAAGTGGTTTGAGCCAATTTTCGCTTCCACCATAATGTGTCAGCGT

|||::|||||||:::||||||||||||::||||||++:||::|::|||||||||:||++|

3601 ATGTTATGTTTTTTTAAGTGGTTTGAGTTAATTTTCGTTTTTATTATAATGTGTTAGCGT

3661 ACATACACATAGCTCAACATTCTCATCAATATTGACGGTACTAATCCGTTCTCGCATTGC

|:|||:|:||||:|:||:|||:|:||:||||||||++|||:||||:++||:|++:||||:

3661 ATATATATATAGTTTAATATTTTTATTAATATTGACGGTATTAATTCGTTTTCGTATTGT

3721 TATAAAGGACTACCTAAGACTGAGTAATTTATAAAGAAAAGAGGTTTAATTGACTCACAG

|||||||||:||::|||||:|||||||||||||||||||||||||||||||||:|:|:||

3721 TATAAAGGATTATTTAAGATTGAGTAATTTATAAAGAAAAGAGGTTTAATTGATTTATAG

3781 TTCTGCAGGCTCTACAGGAAGCATGGCTGGGGAGGCCTCAGGAAAGTTACAATCATAGCG

||:||:|||:|:||:||||||:||||:||||||||::|:||||||||||:|||:||||++

3781 TTTTGTAGGTTTTATAGGAAGTATGGTTGGGGAGGTTTTAGGAAAGTTATAATTATAGCG

3841 GAAGGCAAAGAGGAAGGAGGCACATCTTATATGGCCAGAGAAGGAGAAAGAGAAAGTGAA

|||||:||||||||||||||:|:||:||||||||::||||||||||||||||||||||||

3841 GAAGGTAAAGAGGAAGGAGGTATATTTTATATGGTTAGAGAAGGAGAAAGAGAAAGTGAA

3901 GGGGGAGGTGCTATACACTTTTAAACAACCACATCTTGTGAGAGCTCAACATCACGAGAA

||||||||||:||||:|:|||||||:||::|:||:|||||||||:|:||:||:|++||||

3901 GGGGGAGGTGTTATATATTTTTAAATAATTATATTTTGTGAGAGTTTAATATTACGAGAA

3961 TAGCAAGGGGGAAATCGACCCCCATGATCCAATCGCCTCCCACCAGTCCCCTCCTCCAAC

|||:|||||||||||++|:::::|||||::|||++::|:::|::|||::::|::|::||:

3961 TAGTAAGGGGGAAATCGATTTTTATGATTTAATCGTTTTTTATTAGTTTTTTTTTTTAAT

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\* Explanations \*

\*----------------------------------------------------------------\*

\* Upper row: Original sequence \*

\* Lower row: Bisulfite modified sequence \*

\* (For display, assume all CpG sites are methylated) \*

\* ++ CpG sites \*

\* :::: Non-CpG 'C' converted to 'T' \*

\* >>>>>> Left primer \*

\* <<<<<< Right primer \*

\* \*

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

MethPrimer v1.1 beta  
  
Li Lab, PUMCH

</br

**NY-ESO-1 promoter sequence (hg38\_dna range=chrX:154617933-154621952)**

**4020 base pairs**

[Graphic map](http://rna.lundberg.gu.se/cgi-bin/cutter2/cutter#GraphicMap) | [Table by enzyme name](http://rna.lundberg.gu.se/cgi-bin/cutter2/cutter#TableByEnzyme)   
 BsoBI   
 FriOI BcoI   
 BcgI BstXI BanII Eco88I SexAI BsaI   
ggcgacacctctgcacccatctccctgggctccctcgggtggcggcgggcctggtgtaccaggtctctgttctga base pairs  
ccgctgtggagacgtgggtagagggacccgagggagcccaccgccgcccggaccacatggtccagagacaagact 1 to 75  
 BsgI Eco24I Eco31I   
 AvaI   
 Ama87I   
   
 MflI   
 BamHI   
 BsaI DsaI BstX2I   
gaccctgtgctggggtgttcccaggtttctagcagcctgaccgtggggtgtaggcggatcccagcccccaccctg base pairs  
ctgggacacgaccccacaagggtccaaagatcgtcggactggcaccccacatccgcctagggtcgggggtgggac 76 to 150  
 Eco31I BstDSI BstI   
 XhoII   
 BstYI   
   
   
 AspI   
 DraIII DraII XcmI AtsI   
ccacgctgtgaccgccacccacccaggccccatccctgtcctggtcctgaactgacatagtcagtatgttgccgg base pairs  
ggtgcgacactggcggtgggtgggtccggggtagggacaggaccaggacttgactgtatcagtcatacaacggcc 151 to 225  
 EcoO109I Tth111I   
   
   
   
   
   
 Asp700I EcoNI   
acacagtgaactccttcagaagcacccctggcacgggaagcggtggggcatcctgggccaggctcctgcgggcca base pairs  
tgtgtcacttgaggaagtcttcgtggggaccgtgcccttcgccaccccgtaggacccggtccgaggacgcccggt 226 to 300  
 XmnI Eco57I   
   
   
   
 BssT1I ApaI BssT1I  
 NcoI DsaI Bsp120I BlnI  
 Bsp19I Bsp68I DraII Eco24I EcoNI  
gctctgcttccatgggtgtcgcgaaaggcatggcgaggtagctggtgggggcccagttaaggcatcctctcctag base pairs  
cgagacgaaggtacccacagcgctttccgtaccgctccatcgaccacccccgggtcaattccgtaggagaggatc 301 to 375  
 Eco130I NruI EcoO109I Eco130I  
 StyI BstDSI PspOMI FriOI StyI  
 ErhI EcoT14I BanII AvrII  
   
   
 EcoT14I   
 ErhI   
gacttggcctgtggctccggcctgctgcttaccccaggccagcttccccctcccccactcccccacccctccccc base pairs  
ctgaaccggacaccgaggccggacgacgaatggggtccggtcgaagggggagggggtgagggggtggggaggggg 376 to 450  
   
   
   
   
 AccB7I   
 PflMI MspA1I  
 Esp1396I NspBII  
ctaccccggattgcccagcccatcccccccaggctgtctccccaggcactggcccagtagcacaccccacccagc base pairs  
gatggggcctaacgggtcgggtagggggggtccgacagaggggtccgtgaccgggtcatcgtgtggggtgggtcg 451 to 525  
 AlwNI PvuII  
 Van91I   
   
   
   
   
 BsgI BseRI   
tgtcttggttccccactttcctttgctgcaccccaagctgactcctccatgcccttacaagacccctccccaccc base pairs  
acagaaccaaggggtgaaaggaaacgacgtggggttcgactgaggaggtacgggaatgttctggggaggggtggg 526 to 600  
   
   
   
   
   
 AccBSI  
 BseRI BsrBI  
tgccccctgtggcatcacccggccccctcctcatcactcgaccctccatcccaaccacctcccgccacccgctcc base pairs  
acgggggacaccgtagtgggccgggggaggagtagtgagctgggaggtagggttggtggagggcggtgggcgagg 601 to 675  
 BstD102I  
   
   
   
   
 PpuMI   
 DraII   
catcttgcccccttccccccacctcctgatcccctcctacacctgggtccccctatctcctggcccctgctcccc base pairs  
gtagaacgggggaaggggggtggaggactaggggaggatgtggacccagggggatagaggaccggggacgagggg 676 to 750  
 EcoO109I   
 Psp5II   
   
   
   
 AccB1I   
 Eco64I   
tccccgcatgacccggtgcccctcacccaatcacccagcccctctcccccacccccaccccctctacctcccagc base pairs  
aggggcgtactgggccacggggagtgggttagtgggtcggggagagggggtgggggtgggggagatggagggtcg 751 to 825  
 BanI   
 BshNI   
   
   
   
 PvuII   
 BseRI BseRI   
ccttacctcctcccctcctcgcagctggcctctcatatccccacctcccaacccccacccccacccccacccaac base pairs  
ggaatggaggaggggaggagcgtcgaccggagagtataggggtggagggttgggggtgggggtgggggtgggttg 826 to 900  
 NspBII   
 MspA1I   
   
   
   
   
 BseRI   
cacttactcgcatctcccccgcctcctcccccacctggccctgccctccccatctcccggcccccacctcgccac base pairs  
gtgaatgagcgtagagggggcggaggagggggtggaccgggacgggaggggtagagggccgggggtggagcggtg 901 to 975  
   
   
   
   
   
   
   
cagaactgtcagaacagaacagaacagaacagaacagaatacaactcaagcaggcggctctccggccccctggcc base pairs  
gtcttgacagtcttgtcttgtcttgtcttgtcttgtcttatgttgagttcgtccgccgagaggccgggggaccgg 976 to 1050  
   
   
   
   
 Cfr42I BanI NarI EheI  
 PstI NspBII SstII Msp17I HaeII  
 BstSFI Eco57I DsaI Sfr303I BshNI Hsp92I  
ccgcatctgcagcatccattcagccctgaagccgcgccgccatgcggaccccgcggggcgcctcctcccggcccc base pairs  
ggcgtagacgtcgtaggtaagtcgggacttcggcgcggcggtacgcctggggcgccccgcggaggagggccgggg 1051 to 1125  
 SfcI BstDSI KspI AccB1I BbiII  
 MspA1I KasI Hin1I BsaHI  
 SacII Eco64I AcyI BstH2I  
   
 Bsp143II BcgI Ama87I DraII AccB1I   
 BsoBI EcoO109I XmaI BcoI PpuMI Eco64I   
 BseRI DraII AvaI Cfr9I Psp5II DsaI   
gaggcccttgctgcccctgcgccccggggacctctgccgcccgtggcacccgcctctcctgggccgccagcattg base pairs  
ctccgggaacgacggggacgcggggcccctggagacggcgggcaccgtgggcggagaggacccggcggtcgtaac 1126 to 1200  
 BbeI Eco88I BsoBI PspALI BstDSI   
 AvaI BcoI PspAI SmaI BanI   
 Ama87I Eco88I EcoO109I BshNI   
   
 EcoO109I   
 Mva1269I   
 BsrDI BsaMI SfiI   
ccccctgggccatcaggaatgccagggcctcctgggccatcagcat**cg**cc**cg**t**cg**aaccccctgtgccc**cg**gcct base pairs  
gggggacccggtagtccttacggtcccggaggacccggtagtcgta**gc**gggca**gc**ttgggggacacggg**gc**cgga 1201 to 1275  
 BglI BsmI BglI   
 DraII   
   
   
 BsaWI ApaI BssSI   
 BseAI Kpn2I Bsp120I BsiI   
 BglI MroI AccIII DraII Eco24I   
t**cg**gcctgcatggctc**cg**gagcctctgcc**cg**gctctcagagagaaggtcagggccca**cg**aggatg**cg**gaggcaga base pairs  
a**gc**cggacgtaccgag**gc**ctcggagacgg**gc**cgagagtctctcttccagtcccgggt**gc**tcctac**gc**ctccgtct 1276 to 1350  
 Bsp13I EcoO109I MslI   
 BsiMI PspOMI FriOI   
 BspEI BanII   
   
 Ama87I BstX2I Bsu36I AccB1I Hsp92I  
 PstI XmaI BcoI BamHI CvnI BanI AcyI HaeII  
 BstSFI AvaI Cfr9I XhoII Bse21I Msp17I BstH2I  
gaggctgcaggaagttccgccccctggcgtgagatgggcagcccgggatcctcagggcgcctgcgcacaggggcc base pairs  
ctccgacgtccttcaaggcgggggaccgcactctacccgtcgggccctaggagtcccgcggacgcgtgtccccgg 1351 to 1425  
 SfcI BsoBI PspALI AocI KasI BshNI BbiII  
 PspAI SmaI MflI Eco81I Hin1I BsaHI  
 Eco88I BstI BstYI Eco64I NarI EheI  
   
 Acc16I PspOMI Ama87I PmaCI AgeI Bse118I   
 AviII ApaI FriOI BsaI FriOI BsiHKAI PinAI   
 DraII BanII AvaI BcoI BanII Alw21I PmlI BssAI   
ctacttccggccctgggagaccccgagtgagccccggagcacgtgaccggttctcaccaaccccgcccctcccca base pairs  
gatgaaggccgggaccctctggggctcactcggggcctcgtgcactggccaagagtggttggggcggggaggggt 1426 to 1500  
 BbeI EcoO109I BsoBI Eco24I Bbv12I BbrPI BsaWI   
 Bsp143II Eco24I Eco31I AspHI Eco72I Cfr10I   
 FspI Bsp120I Eco88I BsaAI BsrFI   
   
 Ama87I FriOI NgoAIV   
 XmaI BcoI PspALI NgoMI   
 AvaI Cfr9I SmaI BsrDI BsrFI Cfr10I   
agagagcccgggccggaaggtggccgcaatgccagcttggacccctcacccctgagcagccggctgtccgccgga base pairs  
tctctcgggcccggccttccaccggcgttacggtcgaacctggggagtggggactcgtcggccgacaggcggcct 1501 to 1575  
 BsoBI BanII CfrI BssAI NaeI   
 PspAI Eco24I EaeI Bse118I   
 Eco88I SrfI MroNI   
   
 PspAI SmaI SfcI ApaI Ama87I BsaI   
 BsoBI PspALI SbfI Bsp120I XmaI BcoI   
 PshAI Eco88I BanII Sse8387I AlwNI DraII Eco24I AvaI Cfr9I   
cccctgtcccgggagccctgcagggagtcaggcactgcggggcccagcctgtcccatcccccgggtctccctcac base pairs  
ggggacagggccctcgggacgtccctcagtccgtgacgccccgggtcggacagggtagggggcccagagggagtg 1576 to 1650  
 AvaI Cfr9I BstSFI EcoO109I BsoBI PspALI   
 XmaI BcoI FriOI PstI PspOMI FriOI PspAI SmaI   
 Ama87I Eco24I BanII Eco88I Eco31I  
   
   
   
 BseRI CfrI   
atcgaggagcaagacgggcctgggaacacggggccgggactgtgcggccatcgtcccggaccctgcctgccctgt base pairs  
tagctcctcgttctgcccggacccttgtgccccggccctgacacgccggtagcagggcctgggacggacgggaca 1651 to 1725  
 EaeI   
   
   
   
 EcoT14I Ama87I SseBI BanII   
 BssT1I Bsp143II XmaI BcoI StuI Bsp1720I   
 Eco130I BstH2I AvaI Cfr9I AatI Bpu1102I   
ccgtccttgggggagcgcccaggacagaccccggggggcaggcctctaactgggctcagcagcctccgtccctgt base pairs  
ggcaggaaccccctcgcgggtcctgtctggggccccccgtccggagattgacccgagtcgtcggaggcagggaca 1726 to 1800  
 StyI HaeII BsoBI PspALI BlpI FriOI   
 ErhI PspAI SmaI Pme55I CelII   
 Eco88I Eco147I Eco24I   
   
 PflMI EcoT14I   
 MspA1I BssT1I   
 NspBII NspI Eco130I BsaI  
cctggtcgcccagctggtggggtagctggaactgcatgtctggtgggcgtggcctcgcgccagccaaggtctccc base pairs  
ggaccagcgggtcgaccaccccatcgaccttgacgtacagaccacccgcaccggagcgcggtcggttccagaggg 1801 to 1875  
 PvuII AccB7I StyI Eco31I  
 Esp1396I ErhI   
 Van91I   
   
 BanI NarI EheI StyI ApaI DraII XmaI BcoI XhoII   
 KasI Msp17I HaeII BssT1I Bsp120I NspBII AvaI Eco88I BstYI   
 BshNI AcyI BstH2I EcoT14I DraII Eco24I PpuMI PspAI SmaI   
aggcgccaggtccagccaaggtggacgggagggcccagcgggacccggggccggatctcactcctgggttcaacg base pairs  
tccgcggtccaggtcggttccacctgccctcccgggtcgccctgggccccggcctagagtgaggacccaagttgc 1876 to 1950  
 Hin1I BsaHI Eco130I EcoO109I MspA1I BsoBI PspALI   
 Eco64I Hsp92I Bsp143II PspOMI FriOI Psp5II Cfr9I BstX2I   
 AccB1I BbiII BbeI ErhI BanII EcoO109I Ama87I MflI   
   
   
   
 GsuI   
ggttctgtccctgtcctagtcgccccgcctggtgggggagctggagctgcgtgtggggtgggttgcgggtggcct base pairs  
ccaagacagggacaggatcagcggggcggaccaccccctcgacctcgacgcacaccccacccaacgcccaccgga 1951 to 2025  
 BpmI   
   
   
   
 BsoBI PspALI StuI Bse21I   
 FriOI Ama87I FriOI EcoNI PpuMI CvnI   
 BanII PspAI SmaI Pme55I DraII BspMI AocI   
cccaccagccaggggctcccgggctctaggcctggcccaggtggacaggcgggacctgctggacctgaggctggg base pairs  
gggtggtcggtccccgagggcccgagatccggaccgggtccacctgtccgccctggacgacctggactccgaccc 2026 to 2100  
 Eco24I BcoI BanII SseBI EcoO109I Bsu36I   
 AvaI Eco88I AatI Eco147I Psp5II Eco81I   
 XmaI Cfr9I Eco24I   
   
 Eco91I  
 BstPI  
 AlwNI PspEI  
tcgggcctggctcctgggttcggcagtatcagtccctgccctggtcgctcttgcctggtagggagctgggaggtg base pairs  
agcccggaccgaggacccaagccgtcatagtcagggacgggaccagcgagaacggaccatccctcgaccctccac 2101 to 2175  
 EcoO65I  
 BstEII  
   
   
 AccB1I   
 AhdI Asp718I   
 AspEI DsaI Acc65I   
accctgtgtctgctcagtggtgatctatttgtgtgtctggaagggggtcaaatccacgggacaggtacctctaga base pairs  
tgggacacagacgagtcaccactagataaacacacagaccttcccccagtttaggtgccctgtccatggagatct 2176 to 2250  
 EclHKI BstDSI Eco64I   
 Eam1105I BanI KpnI   
 BshNI XbaI   
   
 Ama87I Eco91I  
 BbuI XmaI BcoI BstPI  
 SphI AvaI Cfr9I BstSFI PspEI  
ggcatgcaggggtgagggcggcacggccccgggagctgaatgtctgtgccaggcacacctgtagcaacaggaggt base pairs  
ccgtacgtccccactcccgccgtgccggggccctcgacttacagacacggtccgtgtggacatcgttgtcctcca 2251 to 2325  
 PaeI BsoBI PspALI SfcI EcoO65I  
 NspI PspAI SmaI BstEII  
 Eco88I   
   
 Bse21I   
 CvnI   
 DraII AocI   
gaccagacagggcctagccctgaggaagggggaggtactgaaatccaaaccactctcccccaccttccaaatcca base pairs  
ctggtctgtcccggatcgggactccttccccctccatgactttaggtttggtgagagggggtggaaggtttaggt 2326 to 2400  
 EcoO109I Bsu36I   
 Eco81I   
 EcoNI   
   
   
   
 AlwNI BsgI MslI Psp1406I   
ggaatcagcagcctctgcacctgggaaaagcatattggcactcatgtggaaactaaaaacgttgatcttttggag base pairs  
ccttagtcgtcggagacgtggacccttttcgtataaccgtgagtacacctttgatttttgcaactagaaaacctc 2401 to 2475  
   
   
   
   
 Eco91I AccB7I   
 BstPI PflMI   
 PspEI Esp1396I   
gtagagcagaatgatggttaccagacgctgggaaaggtggggagggtggggaggttaatggggacaaacatatag base pairs  
catctcgtcttactaccaatggtctgcgaccctttccacccctcccacccctccaattacccctgtttgtatatc 2476 to 2550  
 EcoO65I AlwNI   
 BstEII Van91I   
   
   
   
   
 BstSFI   
ttgcatagaaggattaagttctagtgtttgatagcaccgtagagggactataggtaattatttattgtatatttc base pairs  
aacgtatcttcctaattcaagatcacaaactatcgtggcatctccctgatatccattaataaataacatataaag 2551 to 2625  
 SfcI   
   
   
   
   
 MflI   
 BstX2I   
aaaatagctaaaagataggaaatgttccccaaaaaaagaaatgataaatgcttgaggtggtggagatcctaaata base pairs  
ttttatcgattttctatcctttacaaggggtttttttctttactatttacgaactccaccacctctaggatttat 2626 to 2700  
 XhoII   
 BstYI   
   
   
   
 Ksp22I NspI   
 FbaI NspI AflIII MslI   
ccccgacttgatcattacatcgtgtgtgcgtgtgcatgtatcagaatatcacatgtatcccataaatatgcagag base pairs  
ggggctgaactagtaatgtagcacacacgcacacgtacatagtcttatagtgtacatagggtatttatacgtctc 2701 to 2775  
 BclI BspLU11I   
   
   
   
   
   
 AcsI   
ttatcatacatcagttaaaaatgtttttacttacagaaaagaaaaattcacccaagctcttgcgtgtacctccag base pairs  
aatagtatgtagtcaatttttacaaaaatgaatgtcttttctttttaagtgggttcgagaacgcacatggaggtc 2776 to 2850  
 ApoI   
   
   
   
   
   
GsuI AcsI DraI   
tttattattttcactgctgtatttcattacatatatttcattaaatgatgaattttaaaaaccagagaacacaac base pairs  
aaataataaaagtgacgacataaagtaatgtatataaagtaatttactacttaaaatttttggtctcttgtgttg 2851 to 2925  
BpmI ApoI   
   
   
   
 BsaBI   
 HincII MamI   
 HindII BsrBRI   
ttgttaacacctggaatagctgaaaatcagacataacccggttagtgattgccatccttcctgtcgtcctctgct base pairs  
aacaattgtggaccttatcgacttttagtctgtattgggccaatcactaacggtaggaaggacagcaggagacga 2926 to 3000  
 HpaI Bsh1365I   
 Bse8I   
   
   
   
   
 EcoNI   
cagtctccccattctcagacagaggcaggctaaagttcttaccttcaacaggtcagggaagggagagtaaagtgc base pairs  
gtcagaggggtaagagtctgtctccgtccgatttcaagaatggaagttgtccagtcccttccctctcatttcacg 3001 to 3075  
   
   
   
   
 PpuMI   
 AspI BbsI DraII   
 NspI AtsI Bbv16II BsaI   
atgtgaccctgtcttaggaagcaggaagacagagggagggtctccgggtccccattattttcccggcctattatc base pairs  
tacactgggacagaatccttcgtccttctgtctccctcccagaggcccaggggtaataaaagggccggataatag 3076 to 3150  
 Tth111I BpuAI Eco31I   
 EcoNI BpiI EcoO109I   
 Psp5II   
   
   
   
 GsuI BstXI   
ctcagatcaagtcaagaaaggaagtcctaactgattgagagattcctggagatactgccactgtcctggaagtct base pairs  
gagtctagttcagttctttccttcaggattgactaactctctaaggacctctatgacggtgacaggaccttcaga 3151 to 3225  
 BpmI   
   
   
   
 AccB7I   
 PflMI Van91I   
 Esp1396I SspI Esp1396I   
cagccagccactggaccggaaatctccatcaatatttcagccagagcaacgtctgccactagatggcatcaaact base pairs  
gtcggtcggtgacctggcctttagaggtagttataaagtcggtctcgttgcagacggtgatctaccgtagtttga 3226 to 3300  
 AlwNI PflMI   
 Van91I AccB7I   
 BsaWI   
   
   
   
 GsuI NspBII   
ccagccgggagcaggacagatttggatggtccagcgggcttgcctcattcatttcattaaccccacagtaacaca base pairs  
ggtcggccctcgtcctgtctaaacctaccaggtcgcccgaacggagtaagtaaagtaattggggtgtcattgtgt 3301 to 3375  
 BpmI MspA1I   
   
   
   
   
   
   
ttttcacattgtatgcgattggatttcttggaaactacctattacattacggcagagttttatagtcctctaatt base pairs  
aaaagtgtaacatacgctaacctaaagaacctttgatggataatgtaatgccgtctcaaaatatcaggagattaa 3376 to 3450  
   
   
   
   
 EcoT14I   
 BssT1I AccB7I SspBI   
 Eco130I NspI   
tatccattctgctgatgatgggcaggcatttggatagtttccagcccttggctatgaacatgcttgtacaggtct base pairs  
ataggtaagacgactactacccgtccgtaaacctatcaaaggtcgggaaccgatacttgtacgaacatgtccaga 3451 to 3525  
 StyI PflMI BsrGI   
 ErhI Van91I Bsp1407I   
 Esp1396I   
   
   
 NspI   
 BsaI AflIII AcsI   
cttgaagcacatgtccaagtttttttttggaattgctgtatcacagccaatacatatctcgaaatttactagata base pairs  
gaacttcgtgtacaggttcaaaaaaaaaccttaacgacatagtgtcggttatgtatagagctttaaatgatctat 3526 to 3600  
 Eco31I BspLU11I ApoI   
   
   
   
   
   
 MslI   
atgccatgttttcccaagtggtttgagccaattttcgcttccaccataatgtgtcagcgtacatacacatagctc base pairs  
tacggtacaaaagggttcaccaaactcggttaaaagcgaaggtggtattacacagtcgcatgtatgtgtatcgag 3601 to 3675  
   
   
   
   
   
   
 SspI BsrDI   
aacattctcatcaatattgacggtactaatccgttctcgcattgctataaaggactacctaagactgagtaattt base pairs  
ttgtaagagtagttataactgccatgattaggcaagagcgtaacgatatttcctgatggattctgactcattaaa 3676 to 3750  
   
   
   
   
 Eco147I   
 PstI Pme55I Bse21I  
 BstSFI BstSFI AatI Bsu36I  
ataaagaaaagaggtttaattgactcacagttctgcaggctctacaggaagcatggctggggaggcctcaggaaa base pairs  
tatttcttttctccaaattaactgagtgtcaagacgtccgagatgtccttcgtaccgacccctccggagtccttt 3751 to 3825  
 SfcI SfcI StuI CvnI   
 SseBI Eco81I  
 AocI   
   
 BalI   
 MluNI   
 CfrI   
gttacaatcatagcggaaggcaaagaggaaggaggcacatcttatatggccagagaaggagaaagagaaagtgaa base pairs  
caatgttagtatcgccttccgtttctccttcctccgtgtagaatataccggtctcttcctctttctctttcactt 3826 to 3900  
 EaeI   
 MscI   
   
   
 Eco24I AspHI   
 Alw21I SstI BsiI   
 DraI EcoICRI Bbv12I   
gggggaggtgctatacacttttaaacaaccacatcttgtgagagctcaacatcacgagaatagcaagggggaaat base pairs  
ccccctccacgatatgtgaaaatttgttggtgtagaacactctcgagttgtagtgctcttatcgttcccccttta 3901 to 3975  
 Ecl136II BsiHKAI   
 BanII SacI BssSI   
 FriOI Psp124BI   
   
   
   
 BseRI   
cgacccccatgatccaatcgcctcccaccagtcccctcctccaac base pairs  
gctgggggtactaggttagcggagggtggtcaggggaggaggttg 3976 to 4020

**Primer Sequences**

|  |  |  |
| --- | --- | --- |
| **Primer** | **Primer sequence** | **QTY** |
| MethPrimer - hu NY-ESO-1 promoter\_FW1 | TTAGGGTTTTTTGGGTTATTAGTAT | 1 |
| MethPrimer - hu NY-ESO-1 promoter\_Rev1 | AAACTTCCTACAACCTCTCTACCTC | 1 |
| MethPrimer - hu NY-ESO-1 promoter\_FW2 | GTTAGGGTTTTTTGGGTTATTAGTAT | 1 |
| MethPrimer - hu NY-ESO-1 promoter\_Rev2 | AAACTTCCTACAACCTCTCTACCTC | 1 |