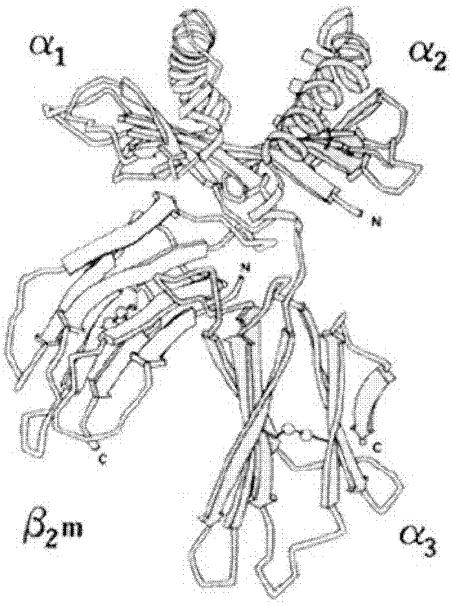

α1
α2
N
N
C
C
β2m
α3

FIG. 1

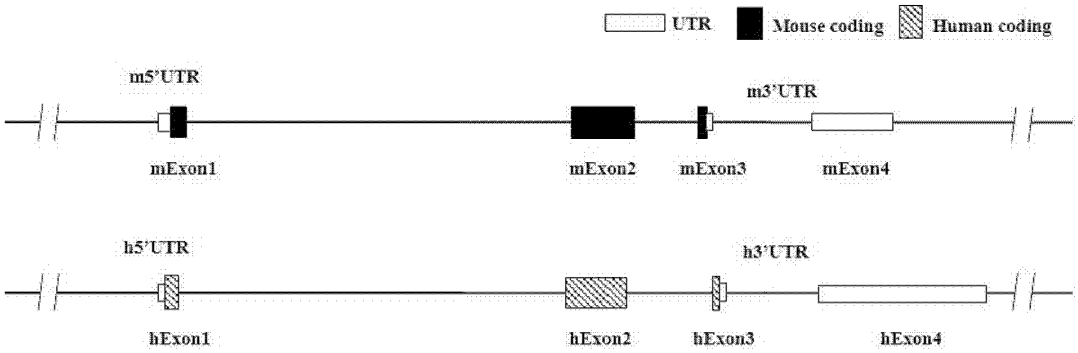

UTR
Mouse coding
Human coding
m5'UTR
m3'UTR
mExon1
mExon2
mExon3
mExon4
h5'UTR
h3'UTR
hExon1
hExon2
hExon3
hExon4

FIG. 2

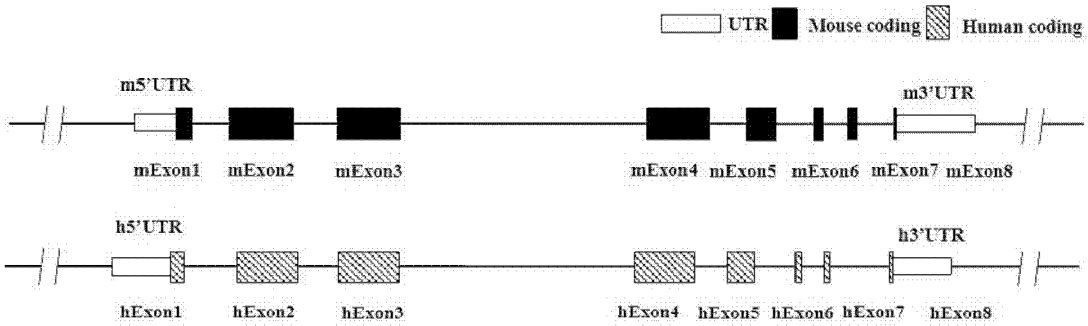


FIG. 3

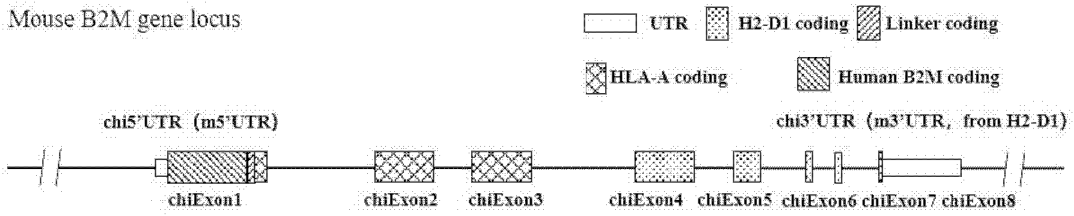


FIG. 4

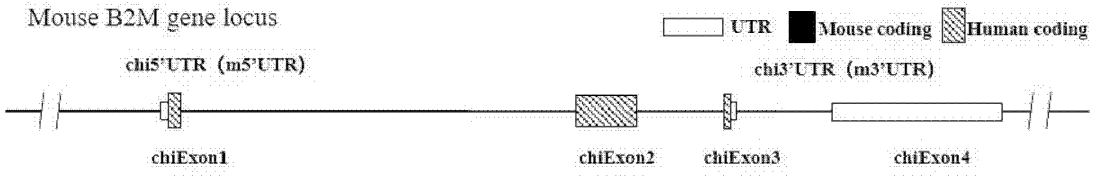


FIG. 5

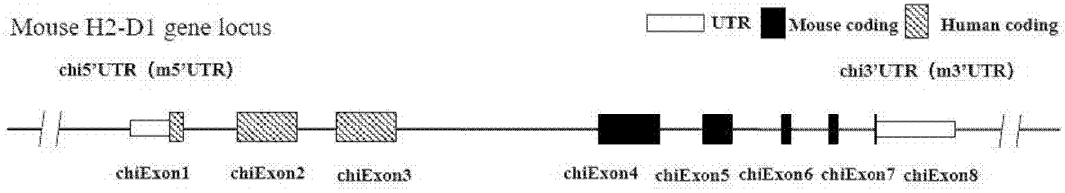


FIG. 6

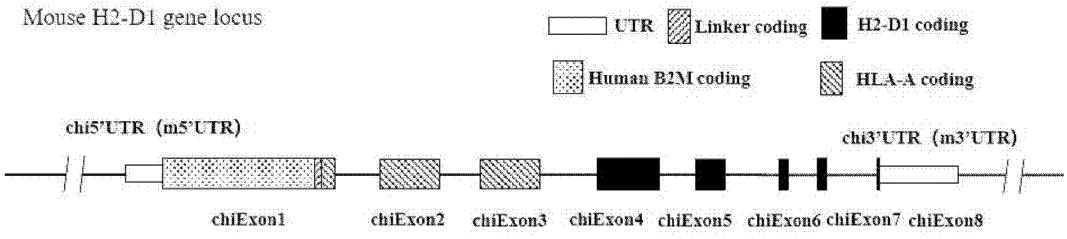


FIG. 7

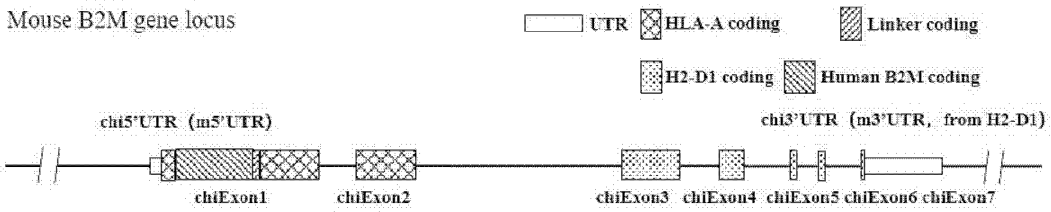


FIG. 8

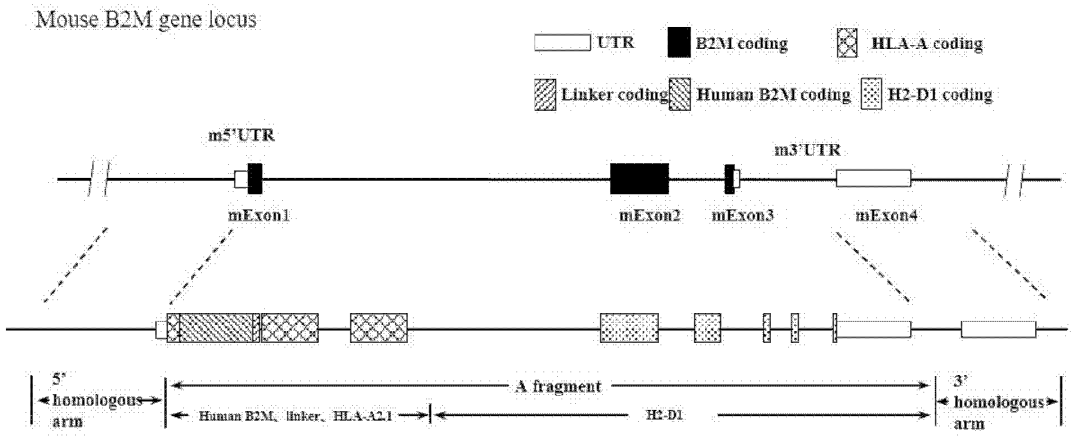
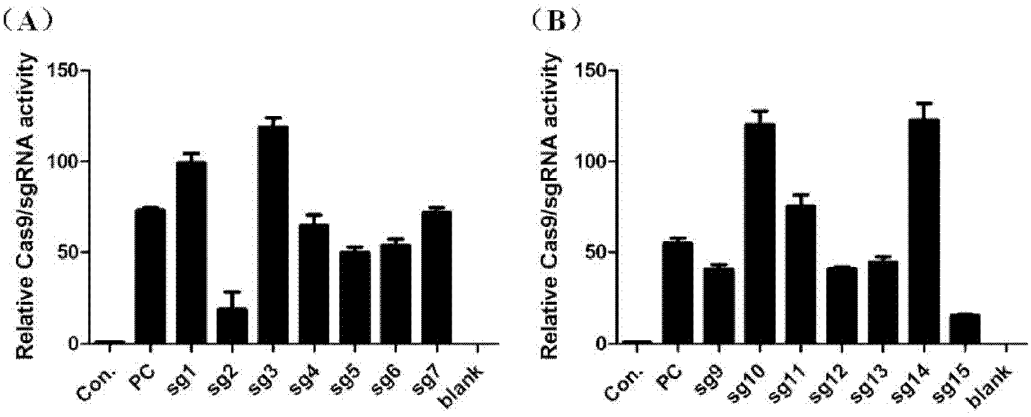
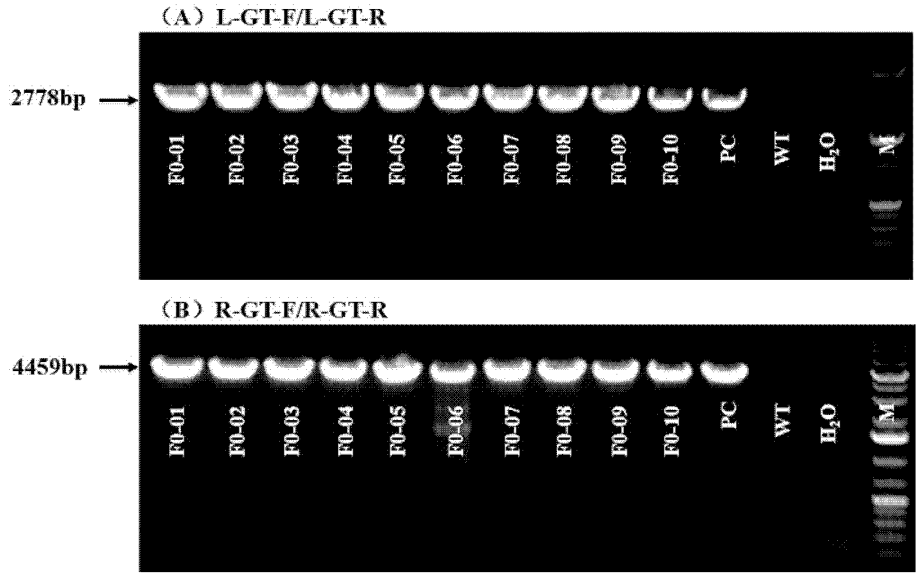


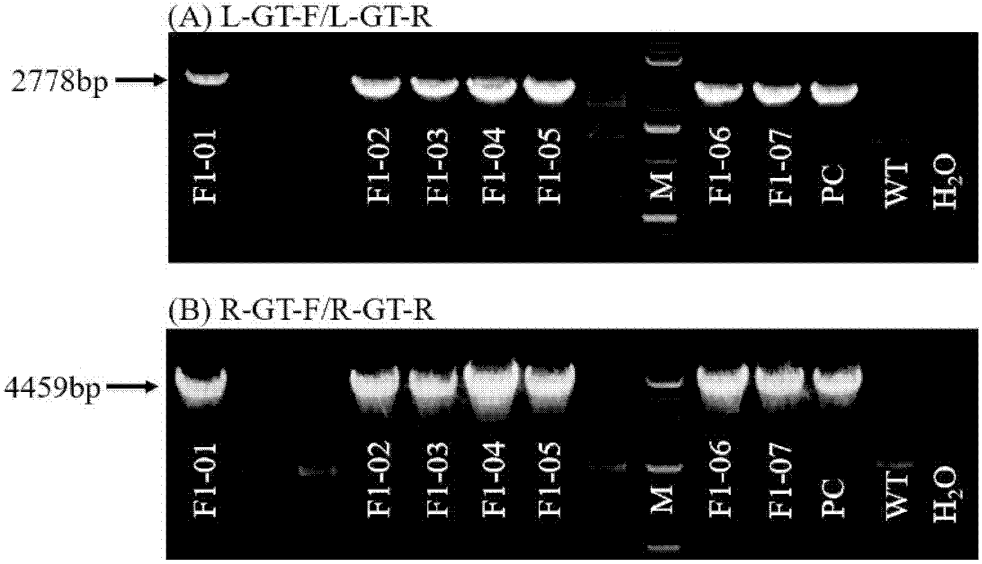
FIG. 9



FIGS. 10A-10B



FIGS. 11A-11B



FIGS. 12A-12B

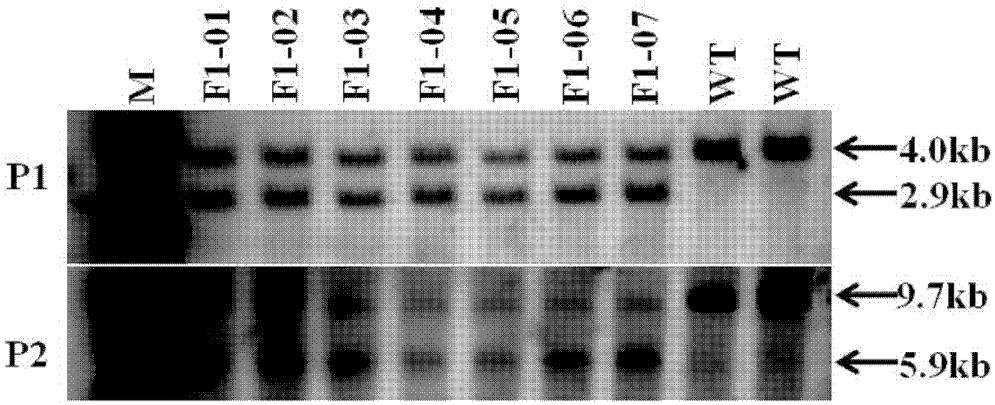
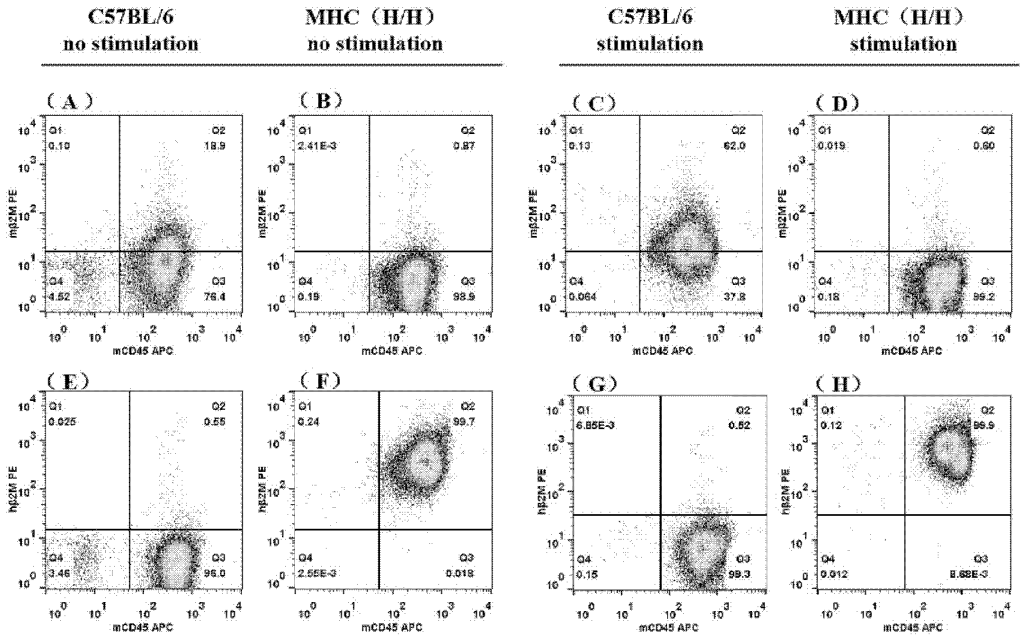
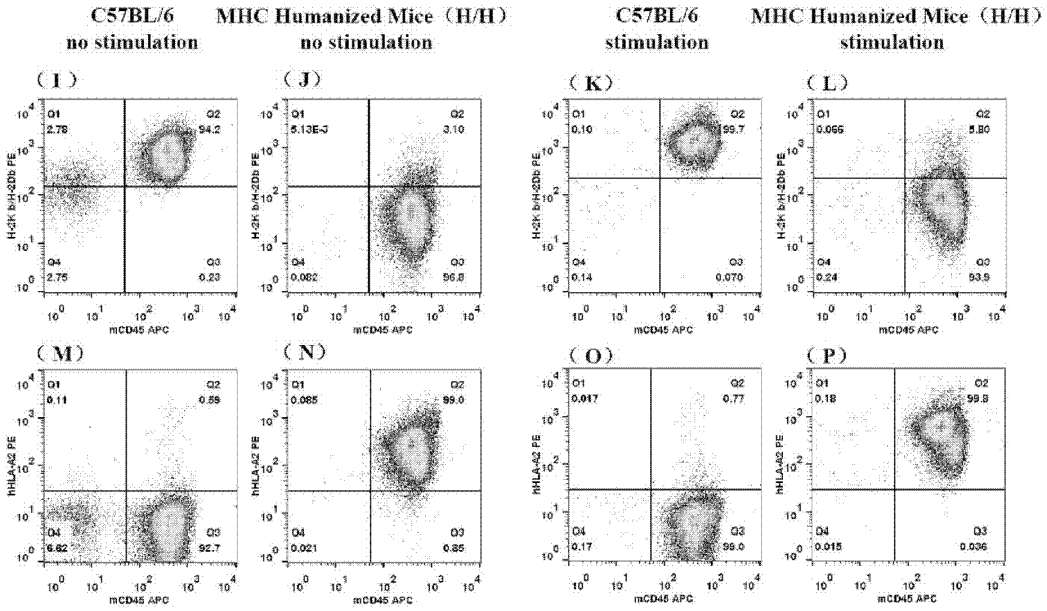


FIG. 13



FIGS. 14A-14H



FIGS. 14I-14P

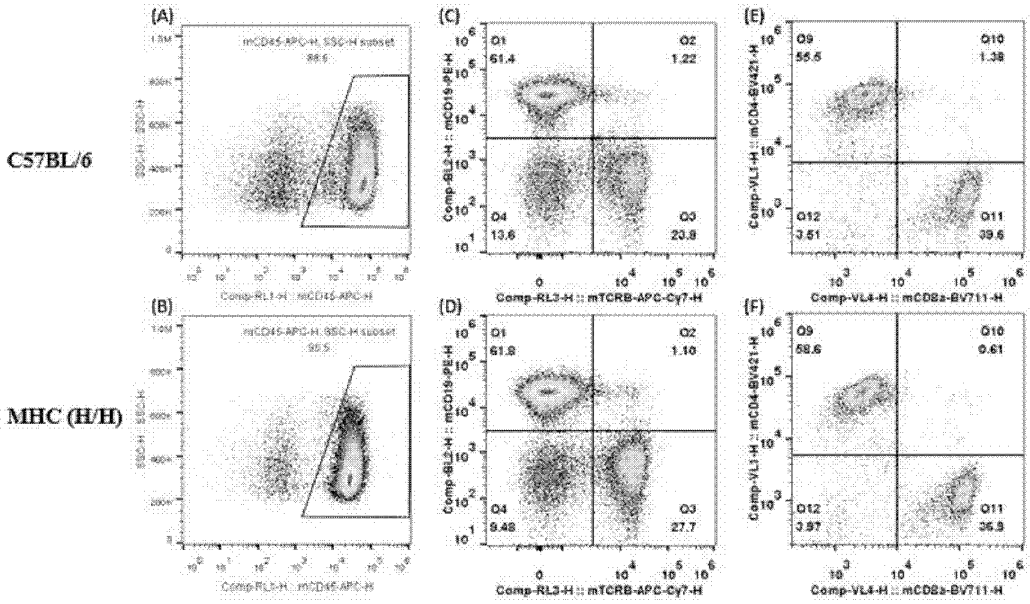


FIG. 15A-15F

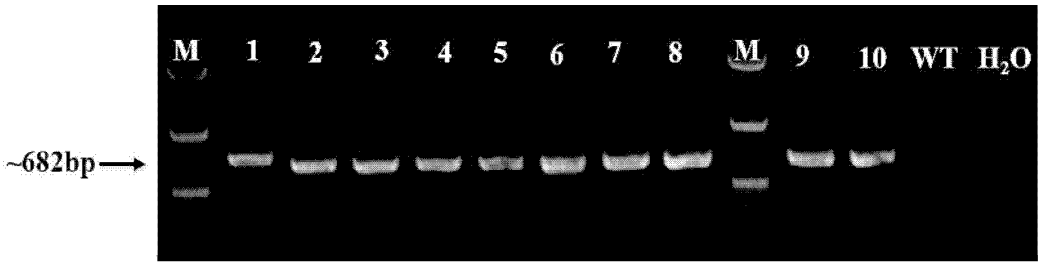


FIG. 16

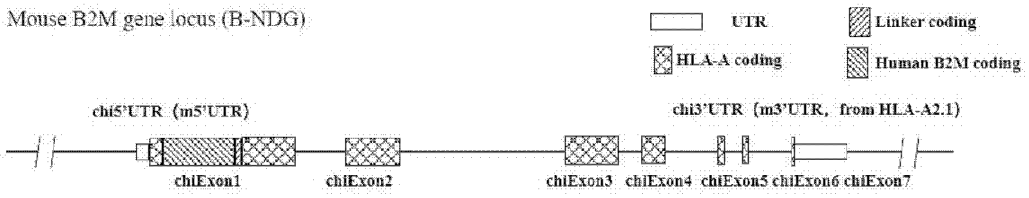

Mouse B2M gene locus (B-NDG)
UTR
Linker coding
HLA-A coding
Human B2M coding
chi5'UTR (m5'UTR)
chi3'UTR (m3'UTR, from HLA-A2.1)
chiExon1
chiExon2
chiExon3
chiExon4
chiExon5
chiExon6
chiExon7

FIG. 17

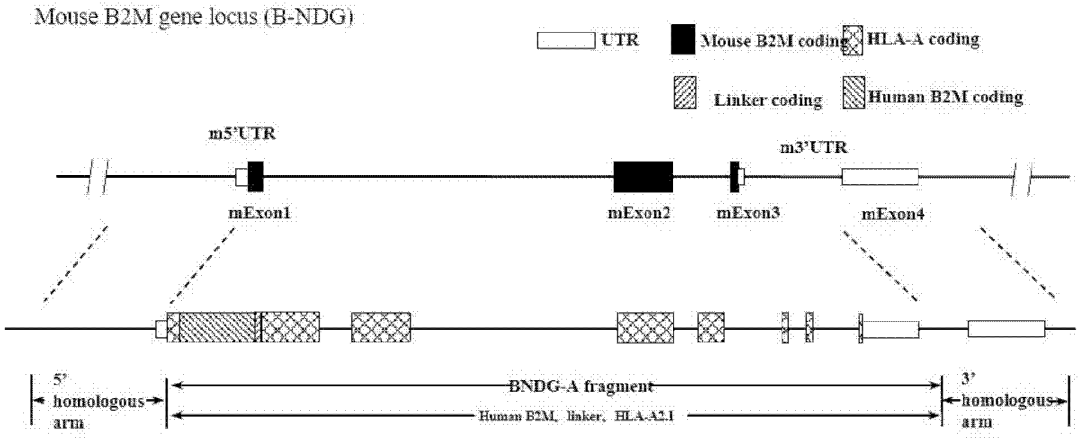
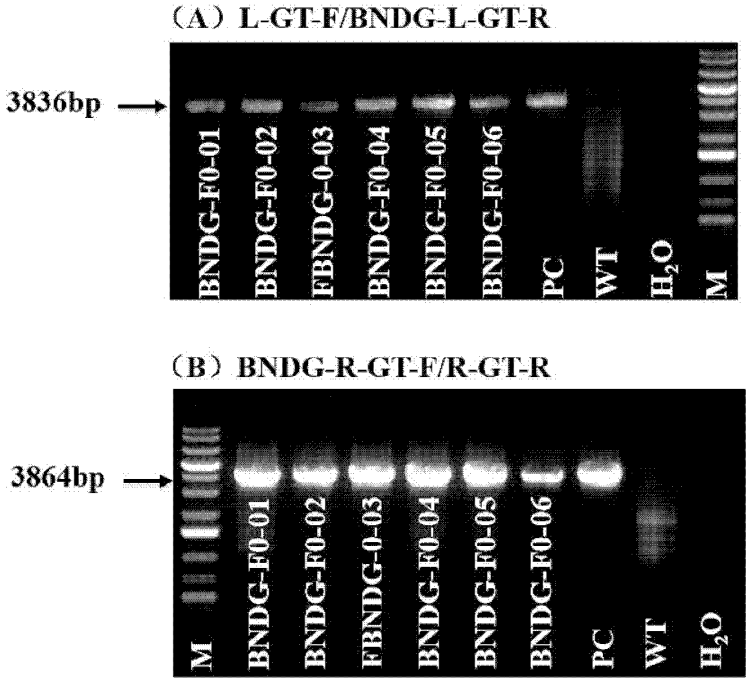
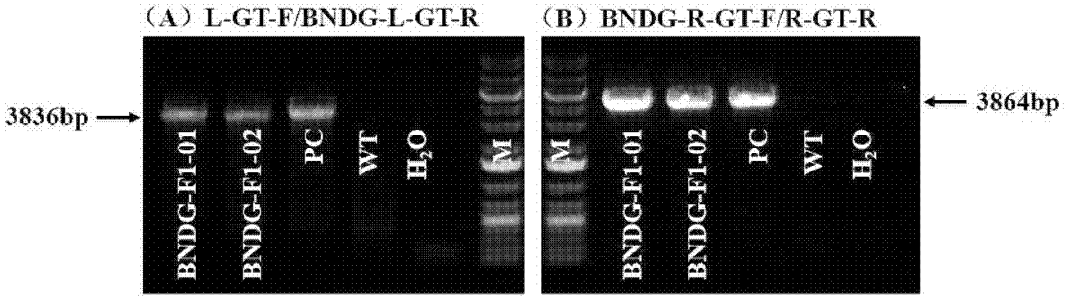

Mouse B2M gene locus (B-NDG)
UTR
Mouse B2M coding
HLA-A coding
Linker coding
Human B2M coding
m5'UTR
m3'UTR
mExon1
mExon2
mExon3
mExon4
5' homologous arm
BNDG-A fragment
Human B2M, linker, HLA-A2.1
3' homologous arm

FIG. 18



FIGS. 19A-19B



FIGS. 20A-20B

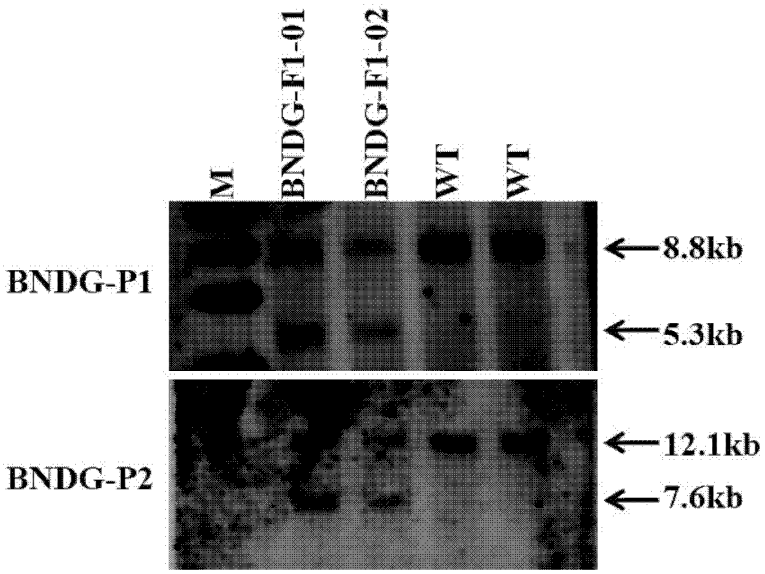
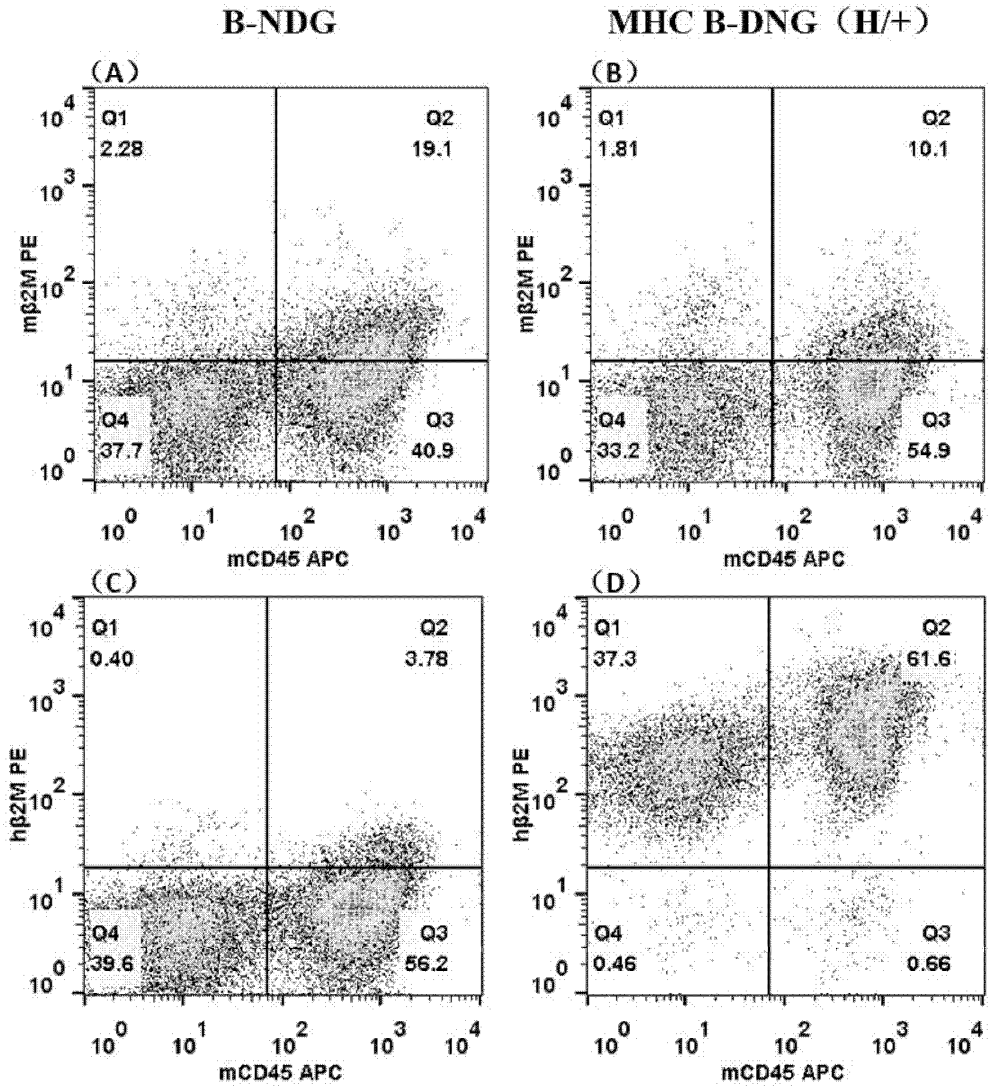
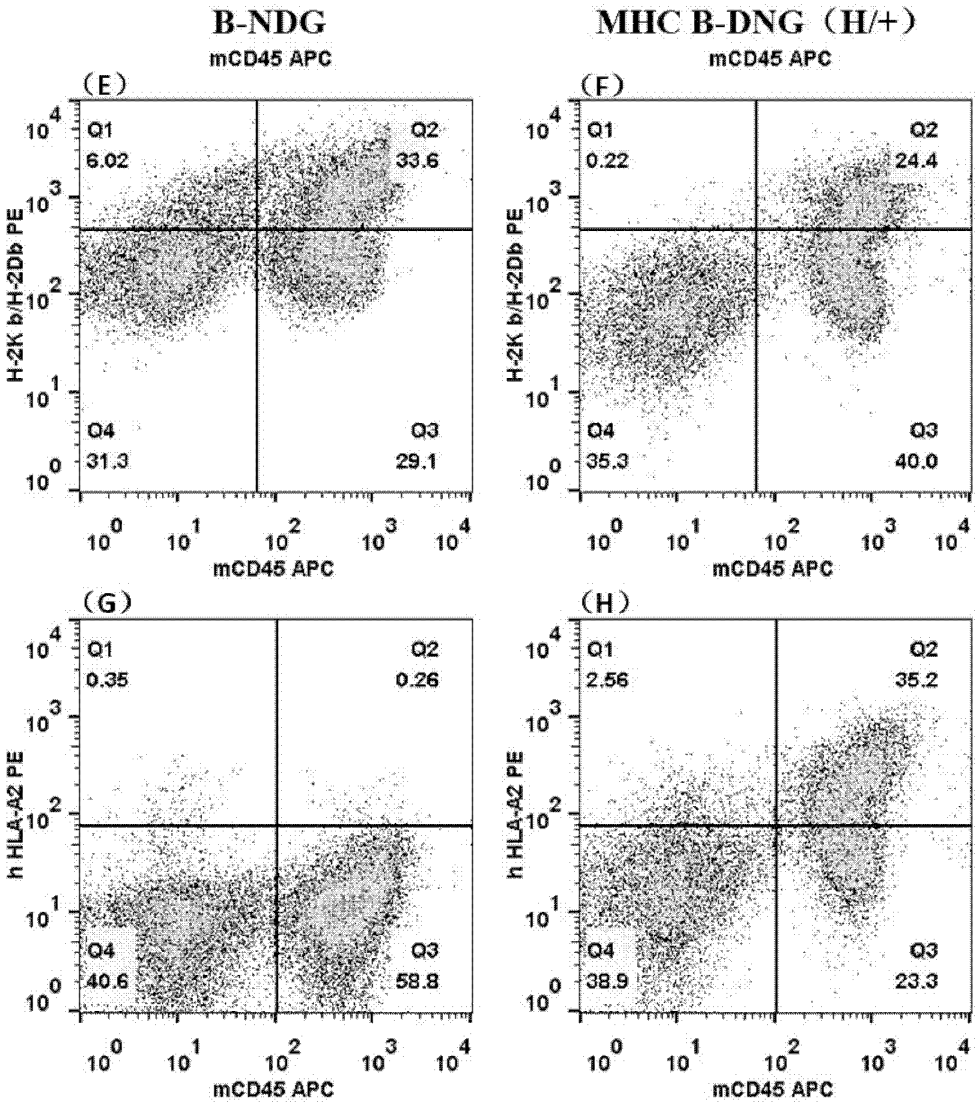

M
BNDG-F1-01
BNDG-F1-02
WT
WT
BNDG-P1
8.8kb
5.3kb
BNDG-P2
12.1kb
7.6kb

FIG. 21


B-NDG
MHC B-DNG（H/+）
（A）
Q1
2.28
Q2
19.1
Q4
37.7
Q3
40.9
mβ2M PE
mCD45 APC
（B）
Q1
1.81
Q2
10.1
Q4
33.2
Q3
54.9
mβ2M PE
mCD45 APC
（C）
Q1
0.40
Q2
3.78
Q4
39.6
Q3
56.2
hβ2M PE
mCD45 APC
（D）
Q1
37.3
Q2
61.6
Q4
0.46
Q3
0.66
hβ2M PE
mCD45 APC

FIGS. 22A-22D


B-NDG
MHC B-DNG（H/+）
mCD45 APC
（E）
（F）
（G）
（H）
H-2K b/H-2Db PE
h HLA-A2 PE
Q1
Q2
Q3
Q4
6.02
33.6
31.3
29.1
0.22
24.4
35.3
40.0
0.35
0.26
40.6
58.8
2.56
35.2
38.9
23.3

FIGS. 22E-22H

Score	Expect	Method	Identities	Positives	Gaps
166 bits(421)	7e-60	Compositional matrix adjust.	81/119(68%)	98/119(82%)	0/119(0%)

```
MOUSE   1    MARSVTLVFLVLVSLTGLYAIQKTPQIQVYSRHPPENGKPNILNCYVTQFHPPHIEIQML  60
             M+RSV L  L L+SL+GL AIQ+TP+IQVYSRHP ENGK N LNCYV+ FHP  IE+ +L
HUMAN   1    MSRSVALAVLALLSLSGLEAIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLL  60

MOUSE   61   KNGKKIPKVEMSDMSFSKDWSFYILAHTEFTPTETDTYACRVKHASMAEPKTVYWDRDM  119
             KNG++I KVE SD+SFSKDWSFY+L +TEFTPTE D YACRV H ++++PK V WDRDM
HUMAN   61   KNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRDM  119
```

FIG. 23

Score	Expect	Method	Identities	Positives	Gaps
169 bits(428)	7e-61	Compositional matrix adjust.	75/100(75%)	85/100(85%)	0/100(0%)

```
RAT     20   AIQKTPQIQVYSRHPPENGKPNFLNCYVSQFHPPQIEIELLKNGKKIPNIEMSDLSFSKD  79
             AIQ+TP+IQVYSRHP ENGK NFLNCYVS FHP  IE++LLKNG++I  +E SDLSFSKD
HUMAN   20   AIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKD  79

RAT     80   WSFYILAHTEFTPTETDVYACRVKHVTLKEPKTVTWDRDM  119
             WSFY+L +TEFTPTE D YACRV HVTL +PK V WDRDM
HUMAN   80   WSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRDM  119
```

FIG. 24

FIG. 25

Score	Expect	Method	Identities	Positives	Gaps
486 bits(1251)	6e-178	Compositional matrix adjust.	240/362(66%)	281/362(77%)	5/362(1%)

```
MOUSE  4    MAPRTLLLLLAAALAPTQTRAGPHSMRYFETAVSRPGLEEPRYISVGYVDNKEFVRFDSD  63
            MAPRTL+LLL+ ALA TQT AG HSMRYF T+VSRPG  EPR+I+VGYVD+ +FVRFDSD
HUMAN  1    MAPRTLVLLLSGALALTQTWAGSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSD  60

MOUSE  64   AENPRYEPRAPWMEQEGPEYWERETQKAKGQEQWFRVSLRNLLGYYNQSAGGSHTLQQMS  123
            A + R EPRAPW+EQEGPEYW+ ET+K K   Q  RV L  L GYYNQS  GSHT+Q+M
HUMAN  61   AASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMY  120

MOUSE  124  GCDLGSDWRLLRGYLQFAYEGRDYIALNEDLKTWTAADMAAQITRRKWEQSGAAEHYKAY  183
            GCD+GSDWR LRGY Q+AY+G+DYIAL EDL++WTAADMAAQ T+ KWE +  AE  +AY
HUMAN  121  GCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAY  180

MOUSE  184  LEGECVEWLHRYLKNGNATLLRTDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLTWQL  243
            LEG CVEWL RYL+NG  TL RTD+PK H+THH  S  E TLRCWAL FYPA+ITLTWQ
HUMAN  181  LEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQR  240

MOUSE  244  NGEELTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVYHEGLPEPLTLRWEPPPS  303
            +GE+ TQD ELVETRPAGDGTFQKWA+VVVP G+EQ YTC V HEGLP+PLTLRWEP
HUMAN  241  DGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWEPSSQ  300

MOUSE  304  TDSYMV-IVAVLGVLGAMAIIGAVVAFVMKRRRNTGGKGGDYALAPGS---QSSEMSLRD  359
                +V I+A L + GA+ I GAVVA VM RR+++  KGG Y+ A  S   Q S++SL
HUMAN  301  PTIPIVGIIAGLVLFGAV-ITGAVVAAVMWRRKSSDRKGGSYSQAASSDSAQGSDVSLTA  359

MOUSE  360  CK  361
            CK
HUMAN  360  CK  361
```

FIG. 26

Score	Expect	Method	Identities	Positives	Gaps
458 bits(1178)	9e-167	Compositional matrix adjust.	240/365(66%)	279/365(76%)	5/365(1%)

```
MOUSE   1    MGAMAPRTLLLLLAAALAPTQTRAGPHSMRYFETAVSRPGLEEPRYISVGYVDNKEFVRF  60
             M  MAPRTLLLLL+ ALA TQT AG HSMRYF T+VSRPG  EPR+I+VGYVD+ +FVRF
HUMAN   1    MAVMAPRTLLLLLSGALALTQTWAGSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRF  60

MOUSE   61   DSDAENPRYEPRAPWMEQEGPEYWERETQKAKGQEQWFRVSLRNLLGYYNQSAGGSHTLQ  120
             DSDA + + EPRAPW+EQEGPEYW++ET+  K   Q  R +L  L GYYNQS  GSHT+Q
HUMAN   61   DSDAASQKMEPRAPWIEQEGPEYWDQETRNMKAHSQTDRANLGTLRGYYNQSEDGSHTIQ  120

MOUSE   121  QMSGCDLGSDWRLLRGYLQFAYEGRDYIALNEDLKTWTAADMAAQITRRKWEQSGAAEHY  180
              M GCD+G D R LRGY Q AY+G+DYIALNEDL++WTAADMAAQIT+RKWE   AAE
HUMAN   121  IMYGCDVGPDGRFLRGYRQDAYDGKDYIALNEDLRSWTAADMAAQITKRKWEAVHAAEQR  180

MOUSE   181  KAYLEGECVEWLHRYLKNGNATLLRTDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLT  240
             + YLEG CV+ L RYL+NG  TL RTD PK H+THHP S  E TLRCWALGFYPA+ITLT
HUMAN   181  RVYLEGRCVDGLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLT  240

MOUSE   241  WQLNGEELTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVYHEGLPEPLTLRWE-  299
             WQ +GE+ TQD ELVETRPAGDGTFQKWA+VVVP G+EQ YTC V HEGLP+PLTLRWE
HUMAN   241  WQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEL  300

MOUSE   300  PPPSTDSYMVIVAVLGVLGAMAIIGAVVAFVMKRRRNTGGKGGDYALAPGS---QSSEMS  356
                 T   + I+A L +LGA+ I GAVVA VM RR+++  KGG Y  A  S   Q S++S
HUMAN   301  SSQPTIPIVGIIAGLVLLGAV-ITGAVVAAVMWRRKSSDRKGGSYTQAASSDSAQGSDVS  359

MOUSE   357  LRDCK  361
             L  CK
HUMAN   360  LTACK  364
```