**V region**

```
                        <---------------------------------------------------------------------FWR1--------------------------
clone1         1 GAGGTGCAGCTCGAGCAGTCAGGCCGAACCGTGACGGTGTAGCCTTCGGAGACCCTG  57
IGHV4-61*08    1 C... ... ... ... ...GC....G........G........C...GGAC.....-----.......A....................... 54
```

```
                        ----------------------------------------------------------------><---------------CDR1--------------->
clone1        58 TCCCTCATCTGCTCTGTCTCTGGGGACTCCGTCAGT  AGTGGCGGTTACTACTGGAGC 114
IGH4-61*08    55 ..............C........A..................T...G.................C  ...........T............................ 111
```

```
                        <-----------------------------------------FWR2------------------------------><-------------------------
clone1       115 TGGCTCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGC  TATGTCTATAATAG 170
IGH4-61*08   112 ......A...........................................................G  ......A........T.C..... 167
```

```
                        --------------------CDR2-------------------------------------><-------------------------------------
clone1       171 TGCGAGCACCAATTACAATCCCTCCCTCAGGGGT  CGAGTCACCATCTCAGAAGACAC 227
IGH4-61*08   168 ....G.................C.............................A...A....  ..................A.........T............ 224
```

```
                        --------------------------------------------------------------FWR3----------------------------------
clone1       228 GTCCAAGAACCAGTTCTCCTTGAATCTGAGTTCTGTGACCGCTGCGGACACGGCCGTA 285
IGH4-61*08   225 ................................................C.......G.........C..............................................G 282
```

```
                        --------------------------->
clone1       286 TATTTTTGTGCGAGG 300
IGH4-61*08   283 ........AC.................-- 296
```

**N-D region**

```
clone1       301 TATACCAGCAATG 313
IGHD6-13*01    4 ........G............------  13
```

**JH region**

```
clone1       314 ACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 360
IGHJ5*02       4 ...................................................................................... 50
```

**Supplementary Figure S4** Analysis of the VH regions of Igγ isolated from the placental trophoblasts.

**V region**

```
                         <------------------------------------------------------------------------FWR1--------------------
      clone2    30      ---------------------------------------------------------------------------CGGTGACGGTGTCCC   44
  IGHV4-61*08    1      CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT......A......CC............   58


                         -----------------------------------------------------><----------------CDR1---------------><------
      clone2    45      TCATCTGCTCTGTCTCTGGGGACTCCGTCAGT  AGTGGCGGTTACTACTGGAGC   TGG  100
  IGHV4-61*08   59      .....C........A....................T..G.................C   .........T...........................   A...  114


                         ---------------------------FWR2-------------------------------------------><--------------------------------
      clone2   101      CTCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGC  TATGTCTATAATAGTGCG  157
  IGHV4-61*08  115      ............................................................G   ....A.........T.C......G..  171


                         ----------------CDR2------------------------------------><------------------------------------------
      clone2   158      AGCACCAATTACAATCCCTCCCTCAGGGGT  CGAGTCACCATCTCAGAAGACACGTCC  214
  IGHV4-61*08  172      ..............C.........................A..A...  ..................A.......T....................   228


                         -------------------------------FWR3-------------------------------------------------------------------
      clone2   215      AAGAACCAGTTCTCCTTGAATCTGAGTTCTGTGACCGCTGCGGACACGGCCGTATATTT  273
  IGHV4-61*08  229      ............................C.......G.........C........................................G.....A  287


                         -------------------->
      clone2   274      TTGTGCGAAG  283
  IGHV4-61*08  288      C...............---   295
```

**N-D region**

```
      clone2   284   TATACCAGCAATG   296
  IGHD6-13*01    4   .........G.................-----   13
```

**JH region**

```
      clone2   297   ACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA   343
    IGHJ5*02     4   ...........................................................................   50
```

**Supplementary Figure S4** Continued.

## V region

```
                  <----------------------------------------------------FWR1-----------------------------------------------
clone3    35    --------------------------------------------------------------------------CGGTGACGGTGTCCC  49
IGHV4-59*01  1   CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT......A......CC...........  58
```

```
                  ----------------------------------------------------------><--------------CDR1----------------><-----
clone3    50    TCACCTGGAGTGTCTCAGGTGCTTCCATGAGC  ------AGT------TACTTCTGGAAC  TGG  99
IGHV4-59*01  59  ...........C...C............T.......GC..........C....T  -------.....------.......A..........G..  ......  108
```

```
                  ----------------------------------FWR2-----------------------------><--------------------------------
clone3    100   GTCCGGCAGTCCCCAGGGAAGGGACTGGAGTGGATTGGG  TATATGTTTTACACTGGG  156
IGHV4-59*01  109  A.................C..........................................  .........C..A.........G........  165
```

```
                  ---------------CDR2----------------------------------><-----------------------------------------
clone3    157   ATGAGCAACTTCAATCCCTCCCTCAAGAGC  CGAGTCACCATATCATTAGACACGTCC  213
IGHV4-59*01  166  ..GC..C...........A......C......................T  ...........................G...................  222
```

```
                  ----------------------------------------FWR3-----------------------------------------------------
clone3    214   AAGAAGCAGTTCTCCCTGAAGTTGTATTCTATGACCGCTGCGGACACGGCCGTGTATT  271
IGHV4-59*01  223  ...........C...............................C...AGC....G....................................  280
```

```
                  --------------------->
clone3    272   ATTGTGCGGGG  282
IGHV4-59*01  281  ....C............------  288
```

## N-D region

```
clone3    283   ATCCCACATGGAGACATTTTTGGTTAC  309
IGHD5-5*01  2   ---------------.........T......GC..A.............  20
```

## JH region

```
clone3    310   TTTGAAAGGTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  351
IGHJ4*02   6   .........CTAC.....................................................  47
```

**Supplementary Figure S4** Continued.