**Table.1: The table of primers and sequence information**

| Transcript Name | Primer Sequence (5'-3') |
|---|---|
| ZNF81 | Forward primer: TGATACAGAAGACTTGAGATT<br>Reverse primer: TCACAAAGTATTCACATTACC |
| Exonic LINC00478 | Forward primer: TCAAGTTCAGTGTTTGGTTAA<br>Reverse primer: GGCAGAATCGTGAATAGC |
| Intronic LINC00478 | Forward primer: AACAGGTCACAATGGTGGAATG<br>Reverse primer: TGAAGCAACTGAAGATCCACAA |
| Beta-2-microglobulin | Forward primer: CGGGCATTCCTGAAGCTGA<br>Reverse primer: TGGAGTACGCTGGATAGCCT |
| Beta-actin | Forward primer: GTGCGCCGTTCCGAAAGT<br>Reverse primer: ATCATCCATGGTGAGCTGGCG |
| Synthetic RNA Spike-in (100 bp from Isopenicillin N-CoA synthetase) | Spike-in Forward primer: TACTGCATCCCGCTCTAC<br>Spike-in Reverse primer: CGCTCATCAAGTCGTTCA<br>Spike-in RNA sequence: UUGGGCAGAAACCGGGCCCCAACGGUGACCGCACCUACU ACUGCAUCCCGCUCUACCACGGAACGGGGGGCAUCGCGGCCAUGAACGACUUGAUGAGCGG |

**Table 1. Primer and spike-in RNA sequences.**

Specific primers used for qPCR analysis of transferred/control transcripts. Primers were designed using Beacon Designer™ (PREMIER Biosoft International, Palo Alto, USA). Primer efficiency was measured using cDNA gradient method. Efficiency in the chosen temperature profile was between 98.7% and 99.2%.

**Table.2: Putatively transferred transcripts.**

| | Gene | logFC | logCPM | LR | PValue | FDR |
|---|---|---|---|---|---|---|
| 1 | MUC4 | 4,962 | 1,84E+00 | 2,76E+01 | 1,50E-07 | 1,64E-04 |
| 2 | MUC3A | 4,09E+00 | 3,69E+00 | 2,73E+01 | 1,72E-07 | 1,64E-04 |
| 3 | MUC16 | 3,59E+00 | 3,57E+00 | 2,20E+01 | 2,68E-06 | 1,12E-03 |
| 4 | MUC12 | 3,40E+00 | 2,98E+00 | 1,93E+01 | 1,12E-05 | 3,41E-03 |
| 5 | ZNF81 | 4,43E+00 | -2,96E-01 | 1,75E+01 | 2,93E-05 | 6,97E-03 |
| 6 | RRAGB | 4,22E+00 | -7,88E-02 | 1,69E+01 | 3,87E-05 | 8,32E-03 |
| 7 | MT-TW | 2,84E+00 | 3,89E+00 | 1,48E+01 | 1,21E-04 | 2,13E-02 |
| 8 | Z95704,5 | 3,72E+00 | 1,20E-01 | 1,42E+01 | 1,67E-04 | 2,48E-02 |
| 9 | MT-TS1 | 2,67E+00 | 5,02E+00 | 1,31E+01 | 2,91E-04 | 3,29E-02 |
| 10 | ITGAE | 3,54E+00 | 9,15E-02 | 1,29E+01 | 3,30E-04 | 3,48E-02 |
| 11 | RP11-357C3,3 | 2,98E+00 | 1,85E+00 | 1,29E+01 | 3,33E-04 | 3,48E-02 |
| 12 | TMEM154 | 3,45E+00 | 4,12E-01 | 1,28E+01 | 3,40E-04 | 3,48E-02 |
| 13 | CASP14 | 3,35E+00 | 4,68E-01 | 1,22E+01 | 4,87E-04 | 4,33E-02 |
| 14 | ZNF765 | 3,31E+00 | 5,09E-01 | 1,20E+01 | 5,26E-04 | 4,45E-02 |
| 15 | LINC00478 | 3,38E+00 | -1,14E-01 | 1,18E+01 | 5,87E-04 | 4,69E-02 |
| 16 | MT-TQ | 2,56E+00 | 7,00E+00 | 1,16E+01 | 6,63E-04 | 4,85E-02 |
| 17 | ANKRD44 | 3,22E+00 | 7,80E-01 | 1,15E+01 | 6,78E-04 | 4,85E-02 |
| 18 | ZBED3-AS1 | 3,29E+00 | -1,13E-01 | 1,15E+01 | 6,98E-04 | 4,85E-02 |

**Table.2: Putatively transferred transcripts.**

The 18 putatively transferred transcripts identified using glmLRT function of edgeR package. RNA sequencing was carried out using RNA affinity precipitated from endometrial cells co-incubated for 24 hours with EU labeled trophoblast spheroids. Endometrial cells co-incubated with a similar number of unlabeled trophoblast spheroids were used as a negative control.

**Table 3: Sequences of transfered transcripts**

| Transcript | Sanger Sequence |
|---|---|
| ZNF81 | TGATACAGAAGACTTGAGATTCTGGATTGGAGCTTGATGCCACAATTTTGGATGAGAAATTTGGAGGTCCTGGAATAGG |
| Exonic LINC00478 | TCAAGTTCAGTGTTTGGTTAAAATACATACTCAGTAAATGGTAGCTATTATTGTCTTAGTTTAAGTTATTGCAAGCATTAAAATTAAATGTTTAGCTACAGACTCAATCCAGTTTTAATGTCATTGTGTTAATAAGGCCTCTTAACATTGAAGCAACAAAGA |
| Intronic LINC00478 | AACAGGTCACAATGGTGGAATGTCGTCAGCTAAGGCAGGACCTGGCTATTTGCACTTCTTTTGTGGATCTTCAGTTGCTTCA |

**Table.3: Sequences of transferred transcripts.**

Expression of transferred transcripts were quantified using qPCR. Products of qPCR were purified using column purification (MinElute PCR Purification Kit, Qiagen, No 28004) and sequenced using Sanger method.