**Supplementary Table 1: DNA sequences**

|  |  |
| --- | --- |
| **Construct** | **Accession no.** |
| **CD9 aa 1-228** | Genbank: NM\_001769.3 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgccggtcaaag  gaggcaccaagtgcatcaaatacctgctgttcggatttaacttcatcttctggcttgccgggattgctgtccttgc  cattggactatggctccgattcgactctcagaccaagagcatcttcgagcaagaaactaataataataattccagc  ttctacacaggagtctatattctgatcggagccggcgccctcatgatgctggtgggcttcctgggctgctgcgggg  ctgtgcaggagtcccagtgcatgctgggactgttcttcggcttcctcttggtgatattcgccattgaaatagctgc  ggccatctggggatattcccacaaggatgaggtgattaaggaagtccaggagttttacaaggacacctacaacaagc  tgaaaaccaaggatgagccccagcgggaaacgctgaaagccatccactatgcgttgaactgctgtggtttggctggg  ggcgtggaacagtttatctcagacatctgccccaagaaggacgtactcgaaaccttcaccgtgaagtcctgtcctga  tgccatcaaagaggtcttcgacaataaattccacatcatcggcgcagtgggcatcggcattgccgtggtcatgatat  ttggcatgatcttcagtatgatcttgtgctgtgctatccgcaggaaccgcgagatggtcaagcttatcgataccgtc  gacctcgag-3’ | |
| **CD81 aa 1-236** | Genbank: NM\_004356.3 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggagtggagg  gctgcaccaagtgcatcaagtacctgctcttcgtcttcaatttcgtcttctggctggctggaggcgtgatcctggg  tgtggccctgtggctccgccatgacccgcagaccaccaacctcctgtatctggagctgggagacaagcccgcgccc  aacaccttctatgtaggcatctacatcctcatcgctgtgggcgctgtcatgatgttcgttggcttcctgggctgct  acggggccatccaggaatcccagtgcctgctggggacgttcttcacctgcctggtcatcctgtttgcctgtgaggt  ggccgccggcatctggggctttgtcaacaaggaccagatcgccaaggatgtgaagcagttctatgaccaggccctac  agcaggccgtggtggatgatgacgccaacaacgcgaaggctgtggtgaagaccttccacgagacgcttgactgctgt  ggctccagcacactgactgctttgaccacctcagtgctcaagaacaatttgtgtccctcgggcagcaacatcatcag  caacctcttcaaggaggactgccaccagaagatcgacgacctcttctccgggaagctgtacctcatcggcattgctg  ccatcgtggtcgctgtgatcatgatcttcgagatgatcctgagcatggtgctgtgctgtggcatccggaacagctcc  gtgtacaagcttatcgataccgtcgacctcgag-3’ | |
| **CD82 aa 1-267** | Genbank: NM\_002231.3 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggctcagcct  gtatcaaagtcaccaaatactttctcttcctcttcaacttgatcttctttatcctgggcgcagtgatcctgggctt  cggggtgtggatcctggccgacaagagcagtttcatctctgtcctgcaaacctcctccagctcgcttaggatgggg  gcctatgtcttcatcggcgtgggggcagtcactatgctcatgggcttcctgggctgcatcggcgccgtcaacgagg  tccgctgcctgctggggctgtactttgctttcctgctcctgatcctcattgcccaggtgacggccggggcactctt  ctacttcaacatgggcaagctgaagcaggagatgggtggcatcgtgactgagctcattcgagactacaacagcagt  cgcgaggacagcctgcaggatgcctgggactacgtgcaggctcaggtgaagtgctgcggctgggtcagcttctacaa  ctggacagacaacgctgagctcatgaatcgccctgaggtcacctacccctgttcctgcgaagtcaagggggaagagg  acaacagcctttctgtgaggaagggcttctgcgaggcccccggcaacaggacccagagtggcaaccaccctgaggac  tggcctgtgtaccaggagggctgcatggagaaggtgcaggcgtggctgcaggagaacctgggcatcatcctcggcgt  gggcgtgggtgtggccatggtcgagctcctggggatggtcctgtccatctgcttgtgccggcacgtgcattccgaag  actacagcaaggtccccaagtacaagcttatcgataccgtcgacctcgag-3’ | |
| **CD151 aa 1-253** | Genbank: BT007397.1 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggtgagttca  acgagaagaagacaacatgtggcaccgtttgcctcaagtacctgctgtttacctacaattgctgcttctggctggc  tggcctggctgtcatggcagtgggcatctggacgctggccctcaagagtgactacatcagcctgctggcctcaggc  acctacctggccacagcctacatcctggtggtggcgggcactgtcgtcatggtgactggggtcttgggctgctgcg  ccaccttcaaggagcgtcggaacctgctgcgcctgtacttcatcctgctcctcatcatctttctgctggagatcat  cgctggtatcctcgcctacgcctactaccagcagctgaacacggagctcaaggagaacctgaaggacaccatgacc  aagcgctaccaccagccgggccatgaggctgtgaccagcgctgtggaccagctgcagcaggagttccactgctgtgg  cagcaacaactcacaggactggcgagacagtgagtggatccgctcacaggaggccggtggccgtgtggtcccagaca  gctgctgcaagacggtggtggctctttgtggacagcgagaccatgcctccaacatctacaaggtggagggcggctgc  atcaccaagttggagaccttcatccaggagcacctgagggtcattggggctgtggggatcggcattgcctgtgtgca  ggtctttggcatgatcttcacgtgctgcctgtacaggagtctcaagctggagcactacaagcttatcgataccgtcg  acctcgag-3’ | |
| **CLDN1 aa 1-211** | Genbank: NM\_021101.5 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatggccaacgcgg  ggctgcagctgttgggcttcattctcgccttcctgggatggatcggcgccatcgtcagcactgccctgccccagtg  gaggatttactcctatgccggcgacaacatcgtgaccgcccaggccatgtacgaggggctgtggatgtcctgcgtg  tcgcagagcaccgggcagatccagtgcaaagtctttgactccttgctgaatctgagcagcacattgcaagcaaccc  gtgccttgatggtggttggcatcctcctgggagtgatagcaatctttgtggccaccgttggcatgaagtgtatgaag  tgcttggaagacgatgaggtgcagaagatgaggatggctgtcattgggggtgcgatatttcttcttgcaggtctggc  tattttagttgccacagcatggtatggcaatagaatcgttcaagaattttatgaccctatgaccccagtcaatgcca  ggtacgaatttggtcaggctctcttcactggctgggctgctgcttctctctgccttctgggaggtgccctactttgc  tgttcctgtccccgaaaaacaacctcttacccaacaccaaggccctatccaaaacctgcaccttccagcgggaaaga  ctacgtgaagcttatcgataccgtcgacctcgag-3’ | |
| **CD9ΔLEL-V5-6xHis ΔLEL aa 113-194** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgccggtcaaag  gaggcaccaagtgcatcaaatacctgctgttcggatttaacttcatcttctggcttgccgggattgctgtccttgc  cattggactatggctccgattcgactctcagaccaagagcatcttcgagcaagaaactaataataataattccagc  ttctacacaggagtctatattctgatcggagccggcgccctcatgatgctggtgggcttcctgggctgctgcggggc  tgtgcaggagtcccagtgcatgctgggactgttcttcggcttcctcttggtgatattcgccattgaaatagctgcgg  ccatctggggatattcccacaaggatgaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctc  ctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggaatcatcggcgcagt  gggcatcggcattgccgtggtcatgatatttggcatgatcttcagtatgatcttgtgctgtgctatccgcaggaacc  gcgagatggtcaagcttatcgataccgtcgacctcgag-3’ | |
| **CD81ΔLEL-V5-6xHis ΔLEL aa 119-200** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggagtggagg  gctgcaccaagtgcatcaagtacctgctcttcgtcttcaatttcgtcttctggctggctggaggcgtgatcctggg  tgtggccctgtggctccgccatgacccgcagaccaccaacctcctgtatctggagctgggagacaagcccgcgccc  aacaccttctatgtaggcatctacatcctcatcgctgtgggcgctgtcatgatgttcgttggcttcctgggctgcta  cggggccatccaggaatcccagtgcctgctggggacgttcttcacctgcctggtcatcctgtttgcctgtgaggtgg  ccgccggcatctggggctttgtcaacaaggaccaggaattcggaaagggcccgcggttcgaaggtaagcctatccct  aaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggaaagct  gtacctcatcggcattgctgccatcgtggtcgctgtgatcatgatcttcgagatgatcctgagcatggtgctgtgct  gtggcatccggaacagctccgtgtacaagcttatcgataccgtcgacctcgag-3’ | |
| **CD82ΔLEL-V5-6xHis ΔLEL aa 115-142** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggctcagcct  gtatcaaagtcaccaaatactttctcttcctcttcaacttgatcttctttatcctgggcgcagtgatcctgggctt  cggggtgtggatcctggccgacaagagcagtttcatctctgtcctgcaaacctcctccagctcgcttaggatgggg  gcctatgtcttcatcggcgtgggggcagtcactatgctcatgggcttcctgggctgcatcggcgccgtcaacgagg  tccgctgcctgctggggctgtactttgctttcctgctcctgatcctcattgcccaggtgacggccggggcactcttc  tacttcaacatgggcaagctgaagcaggaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctct  cctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggagtgcaggcgtggc  tgcaggagaacctgggcatcatcctcggcgtgggcgtgggtgtggccatggtcgagctcctggggatggtcctgtcc  atctgcttgtgccggcacgtgcattccgaagactacagcaaggtccccaagtacaagcttatcgataccgtcgacct  cgag-3’ | |
| **CD151ΔLEL-V5-6xHis ΔLEL aa 122-219** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggtgagttca  acgagaagaagacaacatgtggcaccgtttgcctcaagtacctgctgtttacctacaattgctgcttctggctggc  tggcctggctgtcatggcagtgggcatctggacgctggccctcaagagtgactacatcagcctgctggcctcaggc  acctacctggccacagcctacatcctggtggtggcgggcactgtcgtcatggtgactggggtcttgggctgctgcgc  caccttcaaggagcgtcggaacctgctgcgcctgtacttcatcctgctcctcatcatctttctgctggagatcatcg  ctggtatcctcgcctacgcctactaccagcagctgaacacggaattcggaaagggcccgcggttcgaaggtaagcct  atccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggagg  actgagggtcattggggctgtggggatcggcattgcctgtgtgcaggtctttggcatgatcttcacgtgctgcctgt  acaggagtctcaagctggagcactacaagcttatcgataccgtcgacctcgag-3’ | |
| **CLDN1ΔEC1-V5-6xHis ΔEC1 aa 34-76** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatggccaacgcgg  ggctgcagctgttgggcttcattctcgccttcctgggatggatcggcgccatcgtcagcactgccctgccccagtg  gaggatttacgaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattct  acgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggattgcaagcaacccgtgccttgatggtgg  ttggcatcctcctgggagtgatagcaatctttgtggccaccgttggcatgaagtgtatgaagtgcttggaagacgat  gaggtgcagaagatgaggatggctgtcattgggggtgcgatatttcttcttgcaggtctggctattttagttgccac  agcatggtatggcaatagaatcgttcaagaattttatgaccctatgaccccagtcaatgccaggtacgaatttggtc  aggctctcttcactggctgggctgctgcttctctctgccttctgggaggtgccctactttgctgttcctgtccccga  aaaacaacctcttacccaacaccaaggccctatccaaaacctgcaccttccagcgggaaagactacgtgaagcttat  cgataccgtcgacctcgag-3’ | |
| **CLDN1ΔEC2-V5-6xHis ΔEC2 aa 140-163** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatggccaacgcgg  ggctgcagctgttgggcttcattctcgccttcctgggatggatcggcgccatcgtcagcactgccctgccccagtg  gaggatttactcctatgccggcgacaacatcgtgaccgcccaggccatgtacgaggggctgtggatgtcctgcgtg  tcgcagagcaccgggcagatccagtgcaaagtctttgactccttgctgaatctgagcagcacattgcaagcaaccc  gtgccttgatggtggttggcatcctcctgggagtgatagcaatctttgtggccaccgttggcatgaagtgtatgaa  gtgcttggaagacgatgaggtgcagaagatgaggatggctgtcattgggggtgcgatatttcttcttgcaggtctgg  ctattttagttgccacagcatgggaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctc  ggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggagctctcttcactggctg  ggctgctgcttctctctgccttctgggaggtgccctactttgctgttcctgtccccgaaaaacaacctcttacccaa  caccaaggccctatccaaaacctgcaccttccagcgggaaagactacgtgaagcttatcgataccgtcgacctcgag-3’ | |
| **IgK-leader-FLAG-V5-6xHis-PDGFR** | Synthetic construct |
| 5`-gagctccaccgcggtggcggccgccaccatggagacagacacactcctgctatgggtactgctgctctgggttccaggttc  cactggtgacgattacaaggatgacgacgataagagcccgggcggatccgaattcggaaagggcccgcggttcgaaggt  aagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcaatgctgtgggc  caggacacgcaggaggtcatcgtggtgccacactccttgccctttaaggtggtggtgatctcagccatcctggccctggtggt  gctcaccatcatctcccttatcatcctcatcatgctttggcagaagaagccacgtaagcttatcgataccgtcgacctcgag-3´ | |
| **PD-1 aa 62-86** | GenBank: EF064716.1 |
| 5´-gaattcagcttcgtgctgaactggtaccgcatgagccccagcaaccagaccgacaagctggccgccttccccgaggac  cgcgatatc-3´ | |
| **CD20 aa 162-191** | GenBank: FN555175.1 |
| 5´-gaattcatcaacatctacaactgcgagcccgccaaccccagcgagaagaacagccccagcacccagtactgctacagcatc  cagagcctgttcctggatatc-3´ | |
| **HIV-1 Rev 1-116** | Synthetic construct |
| 5´-atggccggcaggagcggcgactccgacgaggagctgctgaagacagtgcgcctgattaagttcc  tgtaccagagcaatccccccccaagcccagaaggcacacggcaggcccggcggaacagacgcc  gccgctggcgcgaaaggcagcgccagatccgcagcatcagcgaatggattctgagcacctacct  ggggcggccagccgaacccgtgccactgcagctgccacccctggaaaggctgacactggattgt  aatgaggattgcgggacatctgggacccagggagtggggtctcctcagatcctggtggaatcccc  agccgtgctggagagcgggaccaaggagatgggtaagcctatccctaaccctctcctcggtctcg  attctacgta-3´ | |

**Supplementary Table 2: Primer list**

|  |  |
| --- | --- |
| **No.** | **Sequence 5`🡪3´** |
| 01 | TTTTTCTCGAGATGGTGAGCAAGGGCGAGG |
| 02 | TTTTTGGGCCCATCTTGTACAGCTCGTCCATG |
| 03 | TTTTTTGGATCCATGGCGGTGGAAGGAGGAATG |
| 04 | TTTTTCTGCAGCTTATCTCTAAACACA |
| 05 | TTTTTGATATCGGAGGAGGAGGAAAAAATGTGCTGG |
| 06 | TTTTTTAAGCTTCATCACCTCGTAGCCACTTCT |
| 07 | TTTTTGAATTCATGGTGAGCAAGGGCGAGGA |
| 08 | TTTTTGATATCCTTTCTGAGTCCGGACTTGT |
| 12 | TTTTTGAATTCATTGAAGAATCGCAAAACC |
| 13 | TTTTTGATATCTTTTATATACCACAGCCAAT |
| 14 | TTTTGAATTCGGCGGCatggtgagcaagggcgaggaggata |
| 15 | TTTTCATATGATTAAGGTACCGGGCCCatcttgtacagc |
| 16 | TTTTTAAGCTTGCCACCATGGCCGGCAGGAGCGGCG |
| 17 | TTTTTCTCGAGAACTCCTTGGTCCCGCTCTCCA |
| 18 | TTTTTGAATTCCTGACGGTACAGGCCAGAC |
| 19 | TTTTTGATATCGTTAAACCAATTCCACAAAC |