**Supplementary Table 1: DNA sequences**

|  |  |
| --- | --- |
| **Construct** | **Accession no.** |
| **CD9 aa 1-228** | Genbank: NM\_001769.3 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgccggtcaaaggaggcaccaagtgcatcaaatacctgctgttcggatttaacttcatcttctggcttgccgggattgctgtccttgccattggactatggctccgattcgactctcagaccaagagcatcttcgagcaagaaactaataataataattccagcttctacacaggagtctatattctgatcggagccggcgccctcatgatgctggtgggcttcctgggctgctgcggggctgtgcaggagtcccagtgcatgctgggactgttcttcggcttcctcttggtgatattcgccattgaaatagctgcggccatctggggatattcccacaaggatgaggtgattaaggaagtccaggagttttacaaggacacctacaacaagctgaaaaccaaggatgagccccagcgggaaacgctgaaagccatccactatgcgttgaactgctgtggtttggctgggggcgtggaacagtttatctcagacatctgccccaagaaggacgtactcgaaaccttcaccgtgaagtcctgtcctgatgccatcaaagaggtcttcgacaataaattccacatcatcggcgcagtgggcatcggcattgccgtggtcatgatatttggcatgatcttcagtatgatcttgtgctgtgctatccgcaggaaccgcgagatggtcaagcttatcgataccgtcgacctcgag-3’ |
| **CD81 aa 1-236** | Genbank: NM\_004356.3 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggagtggagggctgcaccaagtgcatcaagtacctgctcttcgtcttcaatttcgtcttctggctggctggaggcgtgatcctgggtgtggccctgtggctccgccatgacccgcagaccaccaacctcctgtatctggagctgggagacaagcccgcgcccaacaccttctatgtaggcatctacatcctcatcgctgtgggcgctgtcatgatgttcgttggcttcctgggctgctacggggccatccaggaatcccagtgcctgctggggacgttcttcacctgcctggtcatcctgtttgcctgtgaggtggccgccggcatctggggctttgtcaacaaggaccagatcgccaaggatgtgaagcagttctatgaccaggccctacagcaggccgtggtggatgatgacgccaacaacgcgaaggctgtggtgaagaccttccacgagacgcttgactgctgtggctccagcacactgactgctttgaccacctcagtgctcaagaacaatttgtgtccctcgggcagcaacatcatcagcaacctcttcaaggaggactgccaccagaagatcgacgacctcttctccgggaagctgtacctcatcggcattgctgccatcgtggtcgctgtgatcatgatcttcgagatgatcctgagcatggtgctgtgctgtggcatccggaacagctccgtgtacaagcttatcgataccgtcgacctcgag-3’ |
| **CD82 aa 1-267** | Genbank: NM\_002231.3 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggctcagcctgtatcaaagtcaccaaatactttctcttcctcttcaacttgatcttctttatcctgggcgcagtgatcctgggcttcggggtgtggatcctggccgacaagagcagtttcatctctgtcctgcaaacctcctccagctcgcttaggatgggggcctatgtcttcatcggcgtgggggcagtcactatgctcatgggcttcctgggctgcatcggcgccgtcaacgaggtccgctgcctgctggggctgtactttgctttcctgctcctgatcctcattgcccaggtgacggccggggcactcttctacttcaacatgggcaagctgaagcaggagatgggtggcatcgtgactgagctcattcgagactacaacagcagtcgcgaggacagcctgcaggatgcctgggactacgtgcaggctcaggtgaagtgctgcggctgggtcagcttctacaactggacagacaacgctgagctcatgaatcgccctgaggtcacctacccctgttcctgcgaagtcaagggggaagaggacaacagcctttctgtgaggaagggcttctgcgaggcccccggcaacaggacccagagtggcaaccaccctgaggactggcctgtgtaccaggagggctgcatggagaaggtgcaggcgtggctgcaggagaacctgggcatcatcctcggcgtgggcgtgggtgtggccatggtcgagctcctggggatggtcctgtccatctgcttgtgccggcacgtgcattccgaagactacagcaaggtccccaagtacaagcttatcgataccgtcgacctcgag-3’ |
| **CD151 aa 1-253** | Genbank: BT007397.1 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggtgagttcaacgagaagaagacaacatgtggcaccgtttgcctcaagtacctgctgtttacctacaattgctgcttctggctggctggcctggctgtcatggcagtgggcatctggacgctggccctcaagagtgactacatcagcctgctggcctcaggcacctacctggccacagcctacatcctggtggtggcgggcactgtcgtcatggtgactggggtcttgggctgctgcgccaccttcaaggagcgtcggaacctgctgcgcctgtacttcatcctgctcctcatcatctttctgctggagatcatcgctggtatcctcgcctacgcctactaccagcagctgaacacggagctcaaggagaacctgaaggacaccatgaccaagcgctaccaccagccgggccatgaggctgtgaccagcgctgtggaccagctgcagcaggagttccactgctgtggcagcaacaactcacaggactggcgagacagtgagtggatccgctcacaggaggccggtggccgtgtggtcccagacagctgctgcaagacggtggtggctctttgtggacagcgagaccatgcctccaacatctacaaggtggagggcggctgcatcaccaagttggagaccttcatccaggagcacctgagggtcattggggctgtggggatcggcattgcctgtgtgcaggtctttggcatgatcttcacgtgctgcctgtacaggagtctcaagctggagcactacaagcttatcgataccgtcgacctcgag-3’ |
| **CLDN1 aa 1-211** | Genbank: NM\_021101.5 |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatggccaacgcggggctgcagctgttgggcttcattctcgccttcctgggatggatcggcgccatcgtcagcactgccctgccccagtggaggatttactcctatgccggcgacaacatcgtgaccgcccaggccatgtacgaggggctgtggatgtcctgcgtgtcgcagagcaccgggcagatccagtgcaaagtctttgactccttgctgaatctgagcagcacattgcaagcaacccgtgccttgatggtggttggcatcctcctgggagtgatagcaatctttgtggccaccgttggcatgaagtgtatgaagtgcttggaagacgatgaggtgcagaagatgaggatggctgtcattgggggtgcgatatttcttcttgcaggtctggctattttagttgccacagcatggtatggcaatagaatcgttcaagaattttatgaccctatgaccccagtcaatgccaggtacgaatttggtcaggctctcttcactggctgggctgctgcttctctctgccttctgggaggtgccctactttgctgttcctgtccccgaaaaacaacctcttacccaacaccaaggccctatccaaaacctgcaccttccagcgggaaagactacgtgaagcttatcgataccgtcgacctcgag-3’ |
| **CD9ΔLEL-V5-6xHis ΔLEL aa 113-194** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgccggtcaaaggaggcaccaagtgcatcaaatacctgctgttcggatttaacttcatcttctggcttgccgggattgctgtccttgccattggactatggctccgattcgactctcagaccaagagcatcttcgagcaagaaactaataataataattccagcttctacacaggagtctatattctgatcggagccggcgccctcatgatgctggtgggcttcctgggctgctgcggggctgtgcaggagtcccagtgcatgctgggactgttcttcggcttcctcttggtgatattcgccattgaaatagctgcggccatctggggatattcccacaaggatgaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggaatcatcggcgcagtgggcatcggcattgccgtggtcatgatatttggcatgatcttcagtatgatcttgtgctgtgctatccgcaggaaccgcgagatggtcaagcttatcgataccgtcgacctcgag-3’ |
| **CD81ΔLEL-V5-6xHis ΔLEL aa 119-200** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggagtggagggctgcaccaagtgcatcaagtacctgctcttcgtcttcaatttcgtcttctggctggctggaggcgtgatcctgggtgtggccctgtggctccgccatgacccgcagaccaccaacctcctgtatctggagctgggagacaagcccgcgcccaacaccttctatgtaggcatctacatcctcatcgctgtgggcgctgtcatgatgttcgttggcttcctgggctgctacggggccatccaggaatcccagtgcctgctggggacgttcttcacctgcctggtcatcctgtttgcctgtgaggtggccgccggcatctggggctttgtcaacaaggaccaggaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggaaagctgtacctcatcggcattgctgccatcgtggtcgctgtgatcatgatcttcgagatgatcctgagcatggtgctgtgctgtggcatccggaacagctccgtgtacaagcttatcgataccgtcgacctcgag-3’ |
| **CD82ΔLEL-V5-6xHis ΔLEL aa 115-142**  | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggctcagcctgtatcaaagtcaccaaatactttctcttcctcttcaacttgatcttctttatcctgggcgcagtgatcctgggcttcggggtgtggatcctggccgacaagagcagtttcatctctgtcctgcaaacctcctccagctcgcttaggatgggggcctatgtcttcatcggcgtgggggcagtcactatgctcatgggcttcctgggctgcatcggcgccgtcaacgaggtccgctgcctgctggggctgtactttgctttcctgctcctgatcctcattgcccaggtgacggccggggcactcttctacttcaacatgggcaagctgaagcaggaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggagtgcaggcgtggctgcaggagaacctgggcatcatcctcggcgtgggcgtgggtgtggccatggtcgagctcctggggatggtcctgtccatctgcttgtgccggcacgtgcattccgaagactacagcaaggtccccaagtacaagcttatcgataccgtcgacctcgag-3’ |
| **CD151ΔLEL-V5-6xHis ΔLEL aa 122-219** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatgggtgagttcaacgagaagaagacaacatgtggcaccgtttgcctcaagtacctgctgtttacctacaattgctgcttctggctggctggcctggctgtcatggcagtgggcatctggacgctggccctcaagagtgactacatcagcctgctggcctcaggcacctacctggccacagcctacatcctggtggtggcgggcactgtcgtcatggtgactggggtcttgggctgctgcgccaccttcaaggagcgtcggaacctgctgcgcctgtacttcatcctgctcctcatcatctttctgctggagatcatcgctggtatcctcgcctacgcctactaccagcagctgaacacggaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggactgagggtcattggggctgtggggatcggcattgcctgtgtgcaggtctttggcatgatcttcacgtgctgcctgtacaggagtctcaagctggagcactacaagcttatcgataccgtcgacctcgag-3’ |
| **CLDN1ΔEC1-V5-6xHis ΔEC1 aa 34-76** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatggccaacgcggggctgcagctgttgggcttcattctcgccttcctgggatggatcggcgccatcgtcagcactgccctgccccagtggaggatttacgaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggattgcaagcaacccgtgccttgatggtggttggcatcctcctgggagtgatagcaatctttgtggccaccgttggcatgaagtgtatgaagtgcttggaagacgatgaggtgcagaagatgaggatggctgtcattgggggtgcgatatttcttcttgcaggtctggctattttagttgccacagcatggtatggcaatagaatcgttcaagaattttatgaccctatgaccccagtcaatgccaggtacgaatttggtcaggctctcttcactggctgggctgctgcttctctctgccttctgggaggtgccctactttgctgttcctgtccccgaaaaacaacctcttacccaacaccaaggccctatccaaaacctgcaccttccagcgggaaagactacgtgaagcttatcgataccgtcgacctcgag-3’ |
| **CLDN1ΔEC2-V5-6xHis ΔEC2 aa 140-163** | Synthetic construct |
| 5’-gctagcgcggccgccaccatggattacaaggatgacgacgataagagcccgggcggatccatggccaacgcggggctgcagctgttgggcttcattctcgccttcctgggatggatcggcgccatcgtcagcactgccctgccccagtggaggatttactcctatgccggcgacaacatcgtgaccgcccaggccatgtacgaggggctgtggatgtcctgcgtgtcgcagagcaccgggcagatccagtgcaaagtctttgactccttgctgaatctgagcagcacattgcaagcaacccgtgccttgatggtggttggcatcctcctgggagtgatagcaatctttgtggccaccgttggcatgaagtgtatgaagtgcttggaagacgatgaggtgcagaagatgaggatggctgtcattgggggtgcgatatttcttcttgcaggtctggctattttagttgccacagcatgggaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcggaggaggaggagctctcttcactggctgggctgctgcttctctctgccttctgggaggtgccctactttgctgttcctgtccccgaaaaacaacctcttacccaacaccaaggccctatccaaaacctgcaccttccagcgggaaagactacgtgaagcttatcgataccgtcgacctcgag-3’ |
| **IgK-leader-FLAG-V5-6xHis-PDGFR** | Synthetic construct |
| 5`-gagctccaccgcggtggcggccgccaccatggagacagacacactcctgctatgggtactgctgctctgggttccaggttccactggtgacgattacaaggatgacgacgataagagcccgggcggatccgaattcggaaagggcccgcggttcgaaggtaagcctatccctaaccctctcctcggtctcgattctacgcgtaccggtcatcatcaccatcaccatgatatcaatgctgtgggccaggacacgcaggaggtcatcgtggtgccacactccttgccctttaaggtggtggtgatctcagccatcctggccctggtggtgctcaccatcatctcccttatcatcctcatcatgctttggcagaagaagccacgtaagcttatcgataccgtcgacctcgag-3´ |
| **PD-1 aa 62-86** | GenBank: EF064716.1 |
| 5´-gaattcagcttcgtgctgaactggtaccgcatgagccccagcaaccagaccgacaagctggccgccttccccgaggaccgcgatatc-3´ |
| **CD20 aa 162-191** | GenBank: FN555175.1 |
| 5´-gaattcatcaacatctacaactgcgagcccgccaaccccagcgagaagaacagccccagcacccagtactgctacagcatccagagcctgttcctggatatc-3´ |
| **HIV-1 Rev 1-116** | Synthetic construct |
| 5´-atggccggcaggagcggcgactccgacgaggagctgctgaagacagtgcgcctgattaagttcctgtaccagagcaatccccccccaagcccagaaggcacacggcaggcccggcggaacagacgccgccgctggcgcgaaaggcagcgccagatccgcagcatcagcgaatggattctgagcacctacctggggcggccagccgaacccgtgccactgcagctgccacccctggaaaggctgacactggattgtaatgaggattgcgggacatctgggacccagggagtggggtctcctcagatcctggtggaatccccagccgtgctggagagcgggaccaaggagatgggtaagcctatccctaaccctctcctcggtctcgattctacgta-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 |