

Supplementary Figure S1. Chemical solid phase synthesis and quality inspection of pBD114. (A) The signal cleavage site of pBD114's precursor protein was determined by SignalP-5.0 to be between the 22nd and 23rd amino acids. The purity of pBD114 synthesized by chemical solid phase was higher than 95% (C) by HPLC (B).

Table S1. Minimum inhibitory concentration value of pBD114 against various indicator bacteria.

|  |  |
| --- | --- |
| Item | PBD114, μg/mL |
| *Staphylococcus aureus* ATCC 29213 | >256 |
| *Staphylococcus aureus* ATCC 43300 | >256 |
| *Enterococcus faecalis* ATCC 29212 | 128 |
| *Escherichia coli* ATCC 25922 | >256 |
| *Pseudomonas aeruginosa* ATCC 27853 | >256 |
| *Salmonella typhimurium* ATCC 13311 | 128 |
| *Klebsiella pneumoniae* ATCC 13883 | >256 |

Table S2. The results about the comparison of clean reads with reference genome.

|  |  |  |  |
| --- | --- | --- | --- |
| Sample | Total Clean Reads (M) | Total Mapping (%) | Uniquely Mapping (%) |
| MOCK-1 | 23.83 | 90.18 | 68.90 |
| MOCK-2 | 23.83 | 90.01 | 69.11 |
| MOCK-3 | 23.82 | 89.59 | 69.41 |
| MOCK-4 | 22.15 | 89.44 | 69.17 |
| LPS-1 | 23.83 | 90.19 | 69.10 |
| LPS-2 | 23.83 | 90.42 | 68.89 |
| LPS-3 | 23.81 | 90.69 | 69.02 |
| LPS-4 | 23.83 | 90.51 | 68.85 |
| PBD114-1 | 23.70 | 89.81 | 69.28 |
| PBD114-2 | 23.67 | 88.51 | 69.34 |
| PBD114-3 | 23.66 | 89.53 | 69.10 |
| PBD114-4 | 23.69 | 88.57 | 69.70 |
| PBD114LPS-1 | 23.86 | 89.70 | 69.20 |
| PBD114LPS-2 | 23.85 | 90.30 | 69.09 |
| PBD114LPS-3 | 22.84 | 89.93 | 69.60 |
| PBD114LPS-4 | 21.20 | 91.61 | 69.16 |

Table S5. The primer sequences

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genes | ACCESSION | Primer sequence | Product size | Tm/℃ |
| *β-actin* | NM\_001272041.1 | AAGCGAGGTATCCTGACCCT | 456 | 60 |
| GATGTCGCGCACAATCTCAC |
| *IL-10* | NM\_010548.2 | GCAGAGAAGCATGGCCCAGAA | 181 | 60 |
| TGGCCTTGTAGACACCTTGGTCTT |
| *TGF-β* | NM\_011577.2 | CGAACCCCCATTGCTGTCCC | 294 | 60 |
| CGTTTGGGGCTGATCCCGT |
| *CD4* | NM\_013488.3 | CCAACAGCGCCAGGCA | 295 | 60 |
| AGTGTCTGAAACGCAGAGGG |
| *IL2Rb* | NM\_008368.4 | GCAGGGAACATCTCGACACAA | 277 | 60 |
| CAGTGTCGCAGGTTCGACTT |
| *TLR-4* | NM\_021297.3 | CGCTGCCACCAGTTACAGAT | 263 | 60 |
| CTTCAAGGGGTTGAAGCTCAG |
| *MyD88* | NM\_010851 | AGCAGAACCAGGAGTCCGAGAAG | 148 | 60 |
| GGGCAGTAGCAGATAAAGGCATCG |
| *RELA* | NM\_009045 | AGACCCAGGAGTGTTCACAGACC | 141 | 60 |
| GTCACCAGGCGAGTTATAGCTTCAG |
| *P38* | NM\_011951 | CTGGCTCGGCACACTGATGATG | 120 | 60 |
| GCCCACGGACCAAATATCCACTG |
| *JNK9* | NM\_207692 | ACTATCGGGCTCCAGAAGTCATCC | 103 | 60 |
| ATCACACAACCTTTCACCAGCTCTC |
| *JUN* | *NM\_010591* | CTTCTACGACGATGCCCTCAACG | 105 | 60 |
| GCCAGGTTCAAGGTCATGCTCTG |
| *FOS* | NM\_010234 | AAGACCGTGTCAGGAGGCAGAG | 115 | 60 |
| CAGCCATCTTATTCCGTTCCCTTCG |
| *TNFα* | NM\_013693.3 | TGTAGCCCACGTCGTAGCAA | 216 | 60 |
| TGTAGCCCACGTCGTAGCAA |
| *IL-1β* | NM\_008361.4 | TGCCACCTTTTGACAGTGATG | 220 | 60 |
| AAGGTCCACGGGAAAGACAC |
| *Icam1* | NM\_010493.3 | CTGGGCTTGGAGACTCAGTG | 175 | 60 |
| CCACACTCTCCGGAAACGAA |
| *Ptgs2* | NM\_011198.5 | CATCCCCTTCCTGCGAAGTT | 178 | 60 |
| CATGGGAGTTGGGCAGTCAT |
| *Csf2* | NM\_009969.4 | CTGGCCCCATGTATAGCTGA | 170 | 60 |
| CTGGCCCCATGTATAGCTGA |
| *Cxcl2* | NM\_009140.2 | CTGGCCCCATGTATAGCTGA | 184 | 60 |
| CTGGCCCCATGTATAGCTGA |
| *Cxcl10* | NM\_021274.2 | GAGAGACATCCCGAGCCAAC | 228 | 60 |
| TCAACACGTGGGCAGGATAG |
| *Ccl2* | NM\_011333.3 | AGGTGTCCCAAAGAAGCTGT | 163 | 60 |
| AGGTGTCCCAAAGAAGCTGT |