Table S1 Information on the 37 candidate antigens.

| No. | Ref protein | Gene description | Locus tag | Sequence | Predicted PI | Mw(kDa) | Expression in E.coli |
|-----|-------------|------------------|-----------|----------|--------------|---------|---------------------|
| 1   | rePstS      | phosphate ABC transporter substrate-binding protein | PA5369    | 41Gly-323Leu | 8.92 | 30.5 | Soluble            |
| 2   | reFlgE      | flagellar hook protein FlgE | PA1080    | 1Met-462Arg | 4.48 | 48.3 | Soluble            |
| 3   | reOprL      | peptidoglycan associated lipoprotein OprL | PA0973    | 22Cys-168Lys | 5.73 | 15.8 | Soluble            |
| 4   | reAmpDh3    | Protein AmpDh3 | PA0807    | 1Met-255Ala | 6.10 | 28.7 | Soluble            |
| 5   | reAmpC      | beta-lactamase | PA4110    | 32Asp-397Arg | 8.89 | 40.3 | Soluble            |
| 6   | reIptF      | outer membrane porin F | PA3692    | 27Asn-261Gly | 9.36 | 25.9 | Soluble            |
| 7   | rePA5505    | TonB-dependent receptor | PA5505    | 22Ala-261Phe | 6.78 | 26.03 | Soluble          |
| 8   | reIcmP      | insulin-cleaving metalloproteinase outer membrane protein | PA4370    | 48Lys-445Phe | 4.52 | 42.7 | Soluble            |
| 9   | rePcrV      | type III secretion protein PcrV | PA1706    | 28Gly-294Ile | 5.08 | 29.5 | Soluble            |
| 10  | reExoU      | type III secretion system effector cytoxin ExoU | PA1706    | 100Ser-360Asn | 8.34 | 27.4 | Soluble            |
| 11  | reOprF      | Outer membrane porin F | PA1777    | 25Gln-350Lys | 4.75 | 35.2 | Precipitated       |
| 12  | reOprI      | Major outer membrane lipoprotein | PA2853    | 25Lys-83Lys | 6.67 | 6.4 | Precipitated       |
| 13  | reEta       | Exotoxin A | PA1148    | 401Ala-638Lys | 4.68 | 25.6 | Precipitated       |
| 14  | rePlcB      | phospholipase C | PA0026    | 23Trp-326Leu | 5.10 | 34.5 | No expression      |
| 15  | rePilA      | Type IV major pilin protein PilA | PA4525    | 30Tyr-146Gly | 6.56 | 12.1 | Precipitated       |
| 16  | reAlgE      | Alginate production protein AlgE | PA3544    | 35Ser-490Phe | 4.64 | 50.9 | No expression      |
| 17  | reOprG      | outer membrane protein | PA2760    | 22Asn-425Phe | 5.12 | 44.6 | Precipitated       |
| 18  | rePopB      | Translocator protein PopB | PA1708    | 1Met-390Ile | 5.93 | 40.1 | Precipitated       |
| 19  | reFpvA      | Ferripyoverdine receptor | PA2398    | 523Asp-815Phe | 5.19 | 33.7 | Precipitated       |
| 20  | rePelC      | biosynthesis outer membrane protein | PA3062    | 27Ala-173Glu | 5.17 | 16.0 | Precipitated       |
| 21  | reAprF      | Alkaline protease secretion protein | PA1248    | 27Leu-444Phe | 5.85 | 47.4 | No expression      |
| No. | Ref protein | Gene description                          | Locus tag | Sequence           | Predicted PI | Mw(kDa) | Expression in E.coli |
|-----|-------------|-------------------------------------------|-----------|--------------------|--------------|---------|---------------------|
| 22  | rePA4974    | Probable outer membrane protein           | PA4974    | 31Asp-482Tyr       | 5.35         | 50.4    | No expression       |
| 23  | PA2462      | Haemagg_act domain-containing protein      | PA2462    | 40Asn-420Lys       | 7.35         | 39.0    | Precipitated        |
| 24  | reOprM      | Outer membrane protein OprM                | PA0427    | 65Gln-463Leu       | 5.35         | 43.4    | No expression       |
| 25  | reExoT      | Exoenzyme T                                | PA0044    | 100Ser-457Ala      | 5.14         | 38.0    | Precipitated        |
| 26  | reExoS      | Secreted exoenzyme S                       | PA3841    | 95Met-453Ala       | 5.33         | 38.3    | Precipitated        |
| 27  | reAzu       | Azurin                                     | PA4922    | 21Ala-148Lys       | 5.92         | 13.9    | No expression       |
| 28  | rePA3931    | Uncharacterized protein                    | PA3931    | 22Glu-259Phe       | 6.43         | 26.0    | No expression       |
| 29  | reHasAp     | Heme acquisition protein HasAp             | PA3407    | 1Met-205Ala        | 4.07         | 20.9    | Precipitated        |
| 30  | reChiC      | Chitinase                                  | PA2300    | 25Gly-483Arg       | 5.17         | 50.4    | Precipitated        |
| 31  | reOprE      | Anaerobically-induced outer membrane porin OprE | PA0291 | 30Ala-460Leu      | 6.52         | 46.7    | Precipitated        |
| 32  | reOprH      | outer membrane protein H                   | PA1178    | 23Ala-200Phe       | 8.30         | 19.4    | Precipitated        |
| 33  | reOaT       | O-antigen translocase                      | PA3153    | 1Met-411Lys        | 8.71         | 45.3    | No expression       |
| 34  | reFlgG      | Flagellar basal-body rod protein FlgG     | PA1082    | 1Met-261Leu        | 4.33         | 27.7    | Precipitated        |
| 35  | reDCP       | DAO domain-containing protein             | PA0534    | 32Asp-429Phe       | 7.09         | 44.3    | Precipitated        |
| 36  | reCntO      | Metal-pseudopaline receptor CntO          | PA4837    | 31Glu-708Tyr       | 5.83         | 76.0    | No expression       |
| 37  | rePopD      | Translocator outer membrane protein PopD  | PA1709    | 138Gly-295Val      | 9.01         | 17.1    | Precipitated        |
| P. aeruginosa strain | Source                          | Serotypes | Lethal doses (CFU per mouse) | Sublethal doses (CFU per mouse) |
|---------------------|--------------------------------|-----------|-----------------------------|-------------------------------|
| XN-1                | Southwest Hospital in Chongqing, China | 1         | $1.0 \times 10^7$           | $1.3 \times 10^6$            |
| PA-464              | Southwest Hospital in Chongqing, China | 4         | $2.5 \times 10^7$           | $3.5 \times 10^6$            |
| ZNJ004              | No.422 Hospital of the Chinese People's Liberation Army | 15        | $3.5 \times 10^6$           | $5.8 \times 10^5$            |
| PA-451              | Southwest Hospital in Chongqing, China | 3         | $1.0 \times 10^7$           | $1.4 \times 10^6$            |
| Number | Location | Sequence   | Number | Location | Sequence   |
|--------|----------|------------|--------|----------|------------|
| P1     | 1-18     | DRLKALVDAAVQPVVMKAN | P27    | 183-200  | THLDVPEAAALAQYAQGYG |
| P2     | 8-25     | DAAVQPVKMANDIPGLAV | P28    | 190-207  | AALAQYAQGYGKDDRPLR |
| P3     | 15-32    | MKANDIPGLAVAILSKGE | P29    | 197-214  | QGYGKDDRPLVRGPGPLD |
| P4     | 22-39    | GLAVAILKGEHYFYSYG | P30    | 204-221  | RPLRVPGPLDAGEYGYVK |
| P5     | 29-46    | LKGEPHYFSYGLASKEDG | P31    | 211-228  | GPLDAEYGVKTSADLL |
| P6     | 36-53    | FSYGLASKEDGGTVTPET | P32    | 218-235  | YGVKTSADLLRFVDANL |
| P7     | 43-60    | KEDGRVTPETLFEIGSV | P33    | 225-242  | ADLLRFVDANLHPERLDR |
| P8     | 50-67    | TPETLFEIGSVSKFTAT | P34    | 232-249  | DANLHPERLDRPWAQALD |
| P9     | 57-74    | IGVSCTFTATLAGYALT | P35    | 239-256  | RLDRPWAQALDATHRGYY |
| P10    | 64-81    | FTATLAGYALTQDMRQLD | P36    | 246-263  | QALDATHRGYYKVGDMTQ |
| P11    | 71-88    | YALTQDMRQLDDRASQHW | P37    | 253-270  | RGYYKVGDMTQGLGWEAY |
| P12    | 78-95    | MRLDDRRSQQHPALQGSR | P38    | 260-277  | DMTQGLGWEAYDWPSLKL |
| P13    | 85-102   | SQHPALQGSRSFDGISLL | P39    | 267-284  | WEAYDWPSLKLQAGNS |
| P14    | 92-109   | QGSRSFDGISSLDLAYTA | P40    | 274-291  | ISLKRQAGNSPTMALQ |
| P15    | 99-116   | ISLDLAYTATAGGLPLQF | P41    | 281-298  | AGNSTMALQPHRIARLP |
| P16    | 106-123  | TYTAGGLPLQFPDSPVQKD | P42    | 288-305  | ALQPHRIARLPAPQALEG |
| P17    | 113-130  | PLQFPDSPVQKDQAGIRDY | P43    | 295-312  | ARLPAPQALEGQRLLNKT |
| P18    | 120-137  | VQKDQAQIRDRYYRQWQP | P44    | 302-319  | ALEGQRLNKTGSTNGFG |
| P19    | 127-144  | IRDYYRQWQPYTAPGGSQR | P45    | 309-326  | LNKTGSTNGFGAYVAFVP |
| P20    | 134-151  | WQPTYAPGQSQRQLSNPSI | P46    | 316-333  | NGFGAYVAIFVGRDLGLV |
| P21    | 141-158  | GSQRLYNSNPSIGLGFLYA | P47    | 323-340  | AFVPGRLGLVLILANRNY |
| P22    | 148-165  | NPSIGLFGYLAARSLGQP | P48    | 330-347  | LGLVILANRNPAAERVK |
| P23    | 155-172  | GYLAARSLGQFPERTMEQ | P49    | 337-354  | NRNPAAERVKIAAYL |
| P24    | 162-179  | LGQFPERTMEQQQVFPALG | P50    | 344-361  | ERVKIAAYLGSQGK |
| P25    | 169-186  | LMEQVFPALGQLEQTHLD | P51    | 351-368  | AYAILSGQGEQQGVPLK |
| P26    | 176-193  | PALGLEQTHLDVPEAAALA |
| Number | Location | Sequence           | Number | Location | Sequence           |
|--------|----------|--------------------|--------|----------|--------------------|
| Pc1    | 1-18     | GSEQEELLALLRSERIVL | Pc23   | 155-172  | AKQGIRIDAGGGIDLVDP  |
| Pc2    | 8-25     | LLALLRSERIVLHAGQP  | Pc24   | 162-179  | IDAGGIDLVDPTLGYAY   |
| Pc3    | 15-32    | SERIVLHAGQPPLSEAQV | Pc25   | 169-186  | DLVDTPLGYAVGDPWRK   |
| Pc4    | 22-39    | AHAQGPLSEAQVHLKALAW| Pc26   | 176-193  | LYGYAVGDPRWKDSPEYA  |
| Pc5    | 29-46    | LSEAQVLKALAWLLAAP  | Pc27   | 183-200  | GDPRWKDSPEYALLSNLD  |
| Pc6    | 36-53    | LKLAWLLAANPSAPPQ   | Pc28   | 190-207  | DSPEYALLSNLDTFSGLK  |
| Pc7    | 43-60    | LLAAANPSAPPQGQGLEVL | Pc29   | 197-214  | LLSNLDTFSGLSISKDFL  |
| Pc8    | 50-67    | SAPPGQGLEVLREVLQR  | Pc30   | 204-221  | TFSGKLSIKDFLSGSPKQ  |
| Pc9    | 57-74    | GLEVLERLQRARRPQAQ  | Pc31   | 211-228  | SIKDFLSGSPKQSGELKG  |
| Pc10   | 64-81    | EVLQRARRPQGAWDLREF | Pc32   | 218-235  | SGSPKQSGELKGLSDEYP  |
| Pc11   | 71-88    | RQPGAQWDLREFLVSAYF | Pc33   | 225-242  | SGELKGLSDEYPFEKDYN  |
| Pc12   | 78-95    | WDLREFLVSAYFSLHGR  | Pc34   | 232-249  | LSDEYPFEKDNPNPVGNF  |
| Pc13   | 85-102   | LVSAFSLHGRLDDEVDIG| Pc35   | 239-256  | FEKDNPNVGNFATTVSDR  |
| Pc14   | 92-109   | SLHGRLDDEVDIVGYKDVL| Pc36   | 246-263  | PVGNFATTVSDRSRPLND  |
| Pc15   | 99-116   | DEDVIGVYKDLQQTQDGK | Pc37   | 253-270  | TTVSDSRPLNDKVNKEKT |
| Pc16   | 106-123  | VYKDVLQQTQDGKRKALLD| Pc38   | 260-277  | SRPLNDKVNKTLLNLDT   |
| Pc17   | 113-130  | QTQDGKRKALDELKALT | Pc39   | 267-284  | KVNKEKTLLNDTSSRYNS  |
| Pc18   | 120-137  | RKALLDELKALKATELK  | Pc40   | 274-291  | TLLNDSRSRYNSAVEALN  |
| Pc19   | 127-144  | ELKALTAELKLYSVIQSQ | Pc41   | 281-298  | SSRYNSAVEALNRFIQKY  |
| Pc20   | 134-151  | AELKLYSVIQSAKAALS | Pc42   | 288-305  | AVEALNRFIQKYDVLRLD  |
| Pc21   | 141-158  | SVIQSAKAALSRAKQGIR| Pc43   | 295-312  | RFIQKYDVLRLDILSAI   |
| Pc22   | 148-165  | INAALSRAKQGIRIDAGGI|        |          |                    |