

Table S2. Results of *Klebsiella pneumoniae* NTUH-K2044 transposon mutants.

Mutant	Probable interrupted gene (NTUH-K2044 ORF)	Function/probable function	Gene size (bp)	Tn insertion point
Mutants with decreased biofilm formation				
Cellular processes and signaling				
Tn4-87	KP1_0404	Putative secretion ATPase. Belongs to HlyD protein family involved in multidrug resistance.	1220	566
Tn4-97	KP1_3573	Polymyxin B resistance protein, <i>pmrD</i> . Prolongs the half-life of phosphorylated- <i>pmrA</i> , which is a two-component system regulator involved in modification of lipopolysaccharide and polymyxin B resistance.	245	32
Tn9-39	KP1_3178	Formate dehydrogenase H selenopolypeptide subunit, <i>fdhF</i> . Metabolism of formate under anaerobic conditions.	2150	572
Tn10-33	KP1_1271	Caseinolytic peptidase X homolog, <i>clpx</i> . A ATPase belonged to the AAA+ (ATPases associated with various cellular activities) family ATPases. Involves in the protein degradation.	1274	763
Tn11-19	KP1_4552	Putative LuxR family bacterial regulatory protein. Transcriptional regulator that involves in the regulation of quorum sensing.	584	469
Tn12-06	KP1_0578	Putative exonuclease.	989	639
Tn20-28	KP1_3171	CRISPR-associated helicase Cas3 domain-containing (HD-nuclease and DEXD helicase domain) protein. Unwinds DNA/DNA and DNA/RNA duplexes. Interferences with virus proliferation.	2615	2035
Surface molecules (capsule, adhesion polysaccharide, and pilin) biosynthesis				
Tn3-2	KP1_3720	Putative capsular polysaccharide export protein precursor, <i>wza</i> . Capsular polysaccharide transport.	1133	973
Tn16-47	KP1_0383	Outer membrane protein, <i>pgaA</i> . Exopolysaccharide biosynthesis	2489	511
Tn19-26	KP1_3718	Inner membrane tyrosin kinase, <i>wzc</i> . Capsular biosynthesis	2153	1347
Tn24-36	KP1_4245	Probable pilin chaperone, <i>fim</i> . Pilin biosynthesis.	668	165
Carbohydrate transport and metabolism				
Tn10-43	KP1_3030	6-phospho-beta-glucosidase A. Catalyzes the hydrolysis of 6-phospho-beta-D-glucosyl-(1,4)-D-glucose to produce D-glucose and D-glucose and 6-phosphate. Participates in glycolysis/gluconeogenesis.	1421	475

Tn12-16	KP1_2884	PTS system, cellobiose-specific IIC component, <i>celB</i> . One of subunit of the membrane permease, which is responsible for the recognition and transport of the sugar across the cytoplasmic membrane.	1280	615
Tn16-6, Tn18-57, Tn19-70	KP1_0530	Trehalose-6-phosphate hydrolase, <i>treC</i> . Catalyzes the hydrolysis of trehalose-6-phosphate to produce glucose and glucose-6-phosphate.	1655	1505
Tn23-31	KP1_5472	Probable D-galactonate transport protein, <i>dgoT</i> . Belongs to Major Facilitator Superfamily.	1337	180
Unknown function				
Tn4-96	KP1_1830	Hypothetical protein. Unknown	122	-1352
Tn8-61	KP1_2181	Hypothetical protein. Unknown	539	377
Tn9-30	KP1_3087	Hypothetical protein. Unknown	326	3
Tn14-86	KP1_3087	Hypothetical protein. Unknown	326	116
Tn10-49	KP_p012	Hypothetical protein. Unknown	995	180
Tn21-15	KP1_0662	Hypothetical protein. Unknown	2222	213
Mutants with increased biofilm formation				
Inorganic ion transport and metabolism				
Tn10-23	KP1_0420	Small multidrug resistance protein, <i>sugE</i> . Confers resistance to quaternary cation compounds.	317	-7
Transcription				
Tn24-71	KP1_3465	Cold-shock protein, <i>cspC</i> . Regulates <i>rpoS</i> -dependent stress response, through stabilization of <i>rpoS</i> transcript.	209	-706
Unknown function				
Tn10-19	KP1_2828	Conserved hypothetical protein. Unknown.	899	695
Tn10-30	KP1_2389	Conserved hypothetical protein. Unknown.	1532	1358