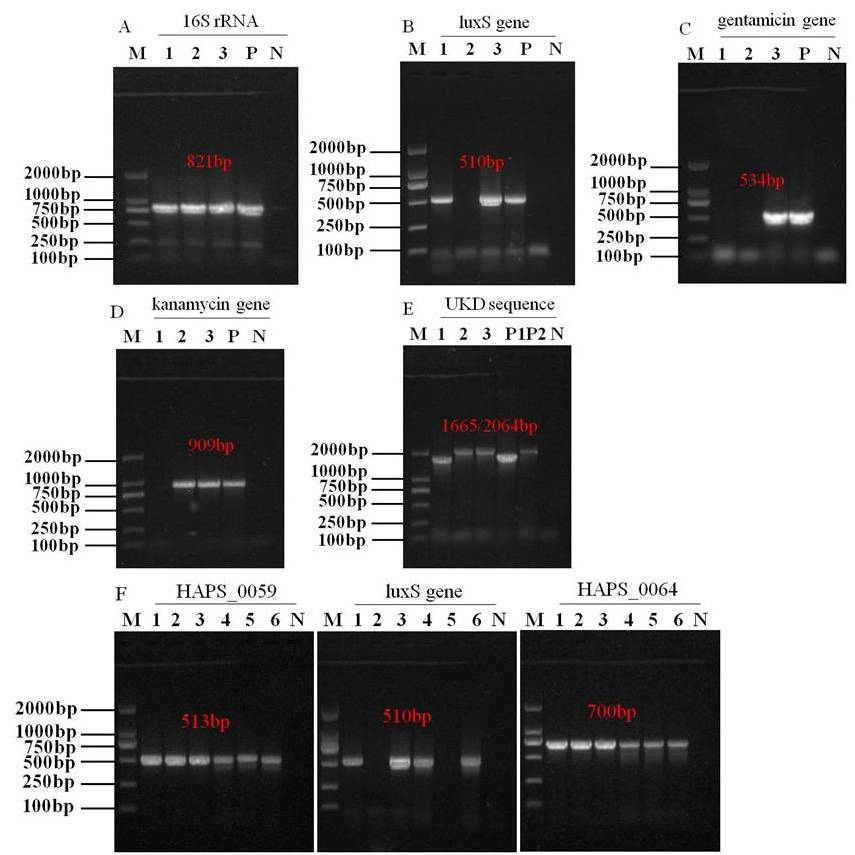
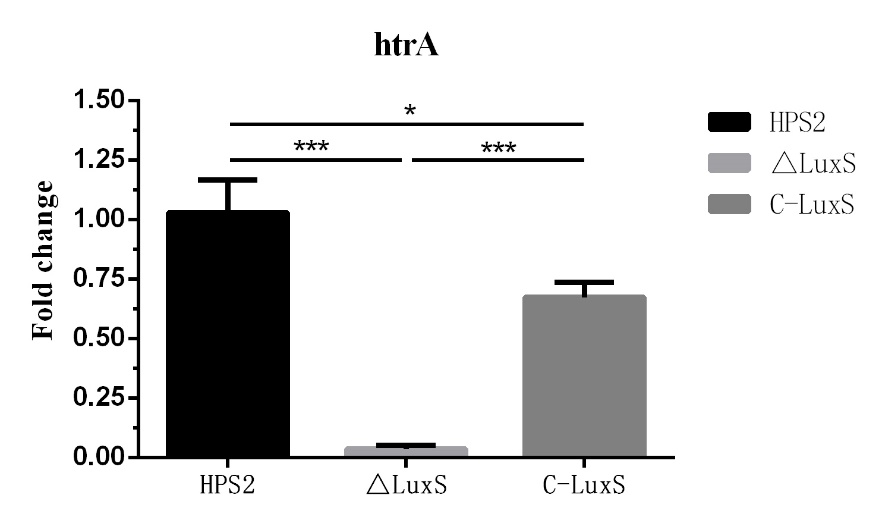
Supplementary data:

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**Figure 1.** Construction and verification of *luxS* mutant strain and the complemented strain. (A-E) Identification results of the wild-type HPS2, deletion mutant ΔluxS and complemented strain C-luxS. The 16S rRNA, *luxS* gene, gentamicin gene, kanamycin resistance cassette sequence and UKD sequence were amplified, respectively. 1 to 3 represent genomes of the HPS2, ΔluxS and C-luxS strains, respectively, P: positive control, N: negative control. (F) RT-PCR identification of the HAPS\_0059, *luxS* gene and HAPS\_0064 from cDNAs of the HPS2, ΔluxS, and C-luxS strains. Amplification with the genomic DNA (gDNA) of the strains was used as the control. 1 to 3 represented cDNA genomes of the HPS2, ΔluxS and C-luxS strains, respectively, 4 to 6 represented genomes DNA (gDNA) of the HPS2, ΔluxS and C-luxS strains, respectively, which were positive controls, N: negative control.



**Figure 2.** Quantitative results of *htrA* gene in HPS2, ΔluxS, and C-luxS strains. The assay was performed in triplicate for three times. Bars represent the mean ± standard deviation of three independent experiments. Statistical analyses were performed using the two-way ANOVA. \* p<0.05 and \*\*\* p<0.001 represent increasing degrees of significant differences, respectively.

**Table 1. The nucleotide and protein homology of *luxS* genes between *H. parasuis* with several different *Pasteuriaceae* strains.**

|  |  |  |  |
| --- | --- | --- | --- |
| Strain | Strain | Nucleotide homology (%) | Protein homology (%) |
| *H. parasuis* | *A. pleuropneumoniae* | 78 | 83 |
| *Pasteurella multocida* | 69 | 73 |
| *H. influenzae* | 71 | 74 |

Sequence results：

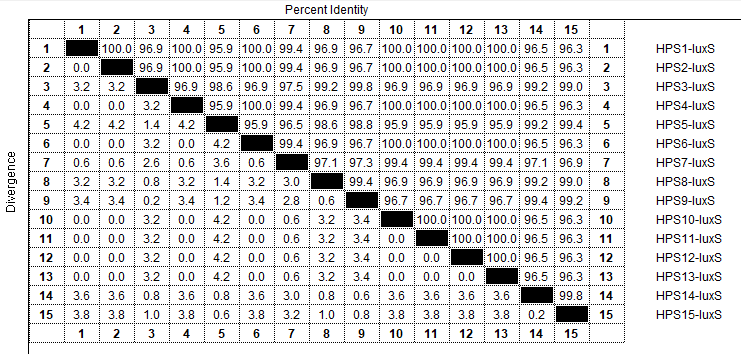
1. Promotor and *luxS* gene sequence

ATACAGAATTTTGATTGAACTGACTAGAAAGCAAGCGGTTAGATTGGCGTAAAAATTTGCAAATTATTTCGAATAACTTACCGCTTGTATGAAAACTCAGGCTTAAATAGGCTATAATCCCTACATAATTTTATTTATTGGAGAACTGTTATGCCTTTACTAGATAGCTTTAAAGTTGACCACACCAAAATGAATGCCCCAGCAGTGCGTGTTGCAAAAACCATGACAACCCCGAAGGGCAATACGATTACTGTATTTGATTTACGTTTTGTCCGTCCAAACATTGAGATTTTATCGCCTCGTGGTATTCATACCATGGAACATTTATTTGCTGGTTTTATGCGTGATCATCTCAATAGCGATACCGTTGAAATTATTGATATTTCCCCGATGGGTTGCCGTACGGGATTTTATATGTCGTTAATTGGTTCACCTTCGGCTGAAGAAGTGGCAAAAGCGTGGGAAGCCTCTATGCGTGATGCGTTAGAAAAAGTGCCTGATGAGTCTAAAATTCCTGAATTAAACGAATATCAATGTGGCTCTTATAAAGAACACTCTTTAGCTGATGCACACGAAATTGCGCGTAATGTGTTAAAACAACCGATTGGTATTAACCGTAACGAAGATTTAGCATTAGATGAGAAATTGCTAAATCCATAG

2. UKD sequence (*luxS* upstream sequence, kanamycin resistance cassette sequence and *luxS* downstream sequence)

ATGCTTACGTCCTGATAAAGCTCATACTTTGTCCGAGCATCAAGCGGTGGAAATTCCAACGCAACCGCATCGGAAATACCCCTTGTAACGACTGAAAGCGAACAGCACAGCCGAGATAGACAAACACCACACTCATCAATGCCACAATCAGCATTAATATCAGAGAAGTGCCTTTTTCTTGCCACAACTGTTGAGCAGAATAAGTGTTTACCCAGTCCACCAACTCGCCCATATACTGAAACAAAATCCCTTCAATAATGCCTATAAATGCAACAAAAATGATTAACGCCACAAAATAGCTTCTCATTCCTTTGGTACTTTCAAAAATAAAAGGAATAACCTTTGCTCGAGGCGTATTCGGCATATCTTCTGGATAAGGATTAATGCGATTTTCAAACCAATCAAATAATTTATTTAACACGGGCTCTCCTTATAAGTATGGTGGGTAAAAATTGCAAGGTAATAAAATGTAGTGGACACACTCAGTGTGCCCCCTACCATTTGAAAAGAAACTATTGTTAGTTCCGTAGCAATAACAATTAACCAATTCTGATTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGGGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGCAATGAACGATTCTCCAATAAATAAAATTATGTAGGGATTATAGCCTATTTAAGCCTGAGTTTTCATACAAGCGGTAAGTTATTCGAAATAATTTGCAAATTTTTACGCCAATCTAACCGCTTGCTTTCTAGTCAGTTTGGTGAAAATTCTGTATAATCGCCCGTCTTTTGTGATCTTCATCACAATTTTGGATTTCGTCAGATGAGCTTTAGCTCATCATTTTTTATTCTCGGTGGGCGAGCCCCACCCTACAATTAAGTTATTTCAATGCAACAATTAGATACTCAAAAACTGCGTAATATCGCAATCATTGCTCACGTTGACCACGGCAAAACCACGCTGGTTGATAAATTATTAAAACTTTCAGGCACATTAGACACTTCTCGTGGTGATGTAGATGAACGTGTAATGGACTCCAACGACCTTGAGAAAGAGCGTGGCATTACCATTCTTGCGAAAAATACCGCAATTAACTGGAACGGCTATCGTATCAATATCGTAGATACCCCAGGACACGCAGACTTCGGTGGTTAAAGTGAAGCCGG

**Table 2. The nucleotide homology of *luxS* genes between different serotype of *H. parasuis* strains.**



The detail sequences of *luxS* gene in different reference strains:

>Actinobacillus pleuropneumoniae L20 serotype 5b

ATGCCTTTATTAGATAGCTTTAAAGTGGATCACACTCGTATGAACGCACCGGCAGTGCGTGTTGCAAAAACGATGACGACGCCGAAGGGCGATACGATTACCGTATTCGATTTACGTTTTTGCCGTCCGAATATTGATATTTTACCGGTGCGTGGTATCCACACGATGGAACACTTATTTGCCGGCTTTATGCGTGATCATTTAAATAGTGAAAGTGTAGAAATTATTGATATTTCGCCGATGGGTTGCCGTACCGGTTTCTATATGTCGTTAATCGGTGCGCCAAGCGAAGCGGATGTGGTTTCGGCGTGGACAAAATCGATGGAAGATGCTTTAAATAAAGTACCGGACGTGTCAAAAATTCCGGAATTAAACGAATATCAATGCGGCTCTTATAAAGAGCATTCGCTTGAAGAAGCGCATCAAATCGCTCGTGATGTGTTAGCCAAGGGTATCGGCGTAAACCGTAACGAAGATTTAGCGCTTGATGAGAAATTATTAAATCCATAA

>Actinobacillus pleuropneumoniae serovar 3 str. JL03

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>Actinobacillus pleuropneumoniae strain KL 16

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>Actinobacillus pleuropneumoniae serovar 8 MIDG2331

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>Actinobacillus pleuropneumoniae serovar 7 str. AP76

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>Bacillus anthracis ames

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>Bacillus cereus NC7401

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>Bibersteinia trehalosi USDA-ARS-USMARC-190

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>Bifidobacterium longum strain BG7

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>Borrelia burgdorferi B31

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>Campylobacter jejuni strain CJM1cam

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>Campylobacter jejuni subsp. jejuni S3

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>Clostridium acetobutylicum DSM 1731

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>Enterococcus faecalis strain W11

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>Escherichia coli CFT073

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>Escherichia coli str. K-12 substr. MC4100

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>Haemophilus influenzae strain 723

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>Haemophilus influenzae strain C486

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>Haemophilus parasuis SH0165

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>Haemophilus parasuis ZJ0906

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>Haemophilus] parasuis strain SH03

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>Haemophilus] parasuis strain CL120103

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>Haemophilus] parasuis strain SC1401

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>Haemophilus] parasuis strain KL0318

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>Haemophilus pittmaniae strain NCTC13334

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>Helicobacter pylori 26695

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>Neisseria meningitidis strain B6116/77

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>Streptococcus pneumoniae strain K15-115

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>Streptococcus pyogenes M1 GAS

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>Vibrio albensis strain NCIMB 41

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