

Supplemental information S8

Sequences of the 170 bp segments upstream the start codon of the 32 genes used for the Gibbs Sampling analysis. (The start codon is shown in bold letter).

Gene	Sequence
<i>omp25a</i> (BAB1_0722, BAB_RS19375)	CTCGACAGATTATCTCCACACAATGGGGCATTTCGTGCCGCAATTACCCTCGATATGTCACCCCTGTC AGCGCGGCATGGGCGGTTTACTCCCGATGCTGCCCCGCCGATAAGGGACCGCGCAAAACGTAATTT GTGTAAGGAGAATGCC ATG CGCACTCTTAAGTCTCTC
<i>omp25d</i> (BAB1_0115, BAB_RS16480)	TAAATTTCAAGTTAATCAAATATATATCAACTTTTTGTATAAATGAAAATCAAGACAATTCATTATTG TTGCTCATTACTACATACATTTCGACCAGATCATCACTATATGCTAGCCGCATTGCAACGCCATTCTT ATTAGGAGTTTTCA ATG ACGTTCAAAAATCTACTT
BAB1_0358, BAB_RS17640	CTTGGTCCACGTGTAACCCATAAGCCTCAACAGCCAGATACTCTGCTTATCGTGGATAAAAGTGGGT TGGCAGGGATTGTTCCGTGAAGGATATATTAACCGCGAATTTCCGGTGTAAAGAAAACTTTTTCGGTT CGGCGGACAGGGAAT TTG GATTTCGGCGCATGTGTT
BAB1_0589, BAB_RS18735	CTCACAAACGTCGAACCCAGCCGTGCATCAAGCAGCGGCCCATGCAAATTCAACTGTTACCCGCGC ACCGACCACCCCGGTCTGGTCGCATTTTCGTTAACCTTAAACGTTGTATCTCTATCCCTCTCCCATCA TCAATCTGGTTTTTCAT ATG CAAACGACCCTTACCCGC
BAB1_2147, BAB_RS26155	GCGGTCGCGCCAAGGCGGGGATTGACCTTTTCGCCTTTTTTGGCCTAAAAATCCAAAACCTTGCA TTCGGAAGAGAAATTGCCGGACGTTGATTTTGATCCTGTCCGCTTTGACTTGACCCCCAGCCGGATCGTT CGGATATTTCCGGG ATG GCTGGATCAGTTAAGGGT
<i>htpX</i> (BAB1_1821, BAB_RS24585)	CGTCGTTATTTTCGCTCATCGATAACATTCCAATTCTCGGCTTTGCCACAAATATTGAAGCGAAGCTT TTTCATACCCATCATATAGGCAGAAAGGCTTGCCGTGCAAAACCGTTTGACGGGCAATTGCCAGATT TGGAGACCGCCACGG ATG AATATGACGAAAACCTGCC
<i>moxR</i> (BAB1_1573, BAB_RS23420)	CTTCCTTGCCGCCGGGGGTGCTTTTATCATCCGACTCGGTTATTCCTGCGCAAATAGACTTAAAGCC ATGAAATAGTCACCCTTTCACGGCTTGTCACTATTATATAGCGATTATGAAGCAGTTCGCCCAGAG CATTGCGAGGTCCATAT ATG AGCGTTGCCGTTACGCCT
<i>clpB</i> (BAB1_1868, BAB_RS24840)	TTTTTATTTGGATTTTCCGATGCCTGCCGGTCTTGCCGAAAGAGGGCAATATTTCCCATATGCACTTTTG AGAAGAGCCCGCCCTTGTGGGGGGTTCGTCACCCAACATCTCTCGGTGCCGCGGGACGGACCGAGAG GCAAACGGAGACATT ATG AATATCGAAAAATATACA
BAB2_1107, BAB_RS31625	GATCACCTATAAACCTCTGGGATGATGTTGAAATGCAGTTGCATCAACATGATCCCGGGCATTTTTTG CTTATGAATAACAGAATACTCGTACCTCCCTTTTGAAATGACCGCGAATTGATGTGGTAAATGACAG AGGCGGGGTTGAGAT ATG CCTAATTGGCCAATCAG
<i>s7</i> (BAB1_0505, BAB_RS18325)	TCCTGTGCGTGGTCATAGTAATAAAGAAGGTAGCAAGACTCAGCAAAATGACAATGGCTTTCCATC GCGGGCGGCCGCTTTGGCGCGAATTATCCGGTTAGGCTATCTGTTGGACTTGAAGCGACCATTTTTTT CATTTTCAGGGCATGAAAATCTGTACCTCTATT
BAB1_1022, BAB_RS20820	TTCGTGGGGTTATCATCACAGGCAAGGGCTGATGGAGGCTGGCGCCCATCATATCCTGGAAAAGCCT TCCGATCTTCATGCTCTATTGCTGGAAATGGAAGAATTCTGAGCCTCGCCCTTTGAAATCCGTGACAC GGGACTGGATAATTC ATG CGTGACATTTTGAGCGAT

BAB1_1620, BAB_RS23635	AGGGACGCCCCGTGCGCCAATTGTCCGCATAAGCCAAAAAATACACGATCTGGCCCAGGCGATGACA AAGCGCGCACACTTTATACTGCTGCCATTAATTGACTAGAATTCAAAGGCCTCCTAATGAATGACCA TTCCAAGGGGGGGCTTTATGAAGTGTTATCTTATTAAT
<i>fabG</i> (BAB1_2043, BAB_RS25660)	GCTCGATCCTTATTGCCGCGCTTACGATCACCCCAATCTCTACGTGGTCGATGCGTCGTTCTGCCAA CATCGGCAGCGGTCAATCCGGCGCTGACCATCGCCGCGCAAGCCTTGCGCGTCGCAGACCGTATCA AGCGGGAGGGTTTTGCATGAGCCGTCAAAGACCTGTA
<i>fabF</i> (BAB1_0872, BAB_RS20090)	CGTTGGCGCAATTTCCTGCTGAAAGGCGAAGCCTTCGCCCCGCTGGATGCTTCGAAAAAGCCTGC CAGTGGCGCGGTCAGCGAAGCCATTGTCACCACCATCGGGGCAACCCGCGCTGAAGGCGCAGCAA AGCTGGTGAGAGCATAAGATGACGAAATATACAGACCAT
BAB1_0320, BAB_RS17460	TTAATTTACTCTTACGTCAATGTAACCTTTGCGAAGACAGTGAAACTCGACCACACTAAACAGCGAG GGGCTATCCGGGGGCGGATGGCTGGGAGATGGGCGGGCGCCCTAGCGGCCTGCACAAAGGACGGA GCGATCCGGGGAGAAGACATGGCAAAAAAGGTGACTGGG
<i>cfa</i> (BAB1_0476, BAB_RS18195)	TGTTGCTTTGGCATTCTTCCAGGGCCGGTTGATTGACGGAAAACTGCCTGGAAATTTGACGGCAGA GGGGCTTCTTTTGATAATGCCGCTGCCGGGCAGCAGCATGGATGTATGCACCTGCTTCGTTCCCAA AGAGGAGATGGGGCCGATGTATGGAATGCTGCGTACA
BAB1_1357, BAB_RS22425	GTTTACCGTTCTCAATCGCGGTGTGACGCTTGGCACGCGCACCAAGGACGATGTGGATATGGATGAG TTGCAAAGCCTGATGGCAGGCGGGCAGGAGCTTGCCGATCTTACCGCTGAACTGGGCGGGCGAGTA TAACCGGAGAACATGGAATGGGCGGACAGTTGAAGGTT
<i>nirK</i> (BAB2_0943, BAB_RS30770)	AATATAATTTAACTATCTGATTTTATTATGGAAATATTTCCATATCGAGCGCCTTATATTGATTGCGGT CAAGGAAGCGCCATGCGGCATCGCCTAGAAAGGAGGGGACAGAGCCAATGGCTCTTGGTCCTATCG CAAAGGAGAGAAACGATGGCCGACCAGATACAAGTC
<i>norC</i> (BAB2_0955, BAB_RS30825)	CTGCATCTTTGCCTATTTCGCAAAGAAGGGTTCTGCGCGACCGATAGAATGGAAGCATCCCGCGGGG CCGGCGAGGGGAATTGCCCGGCCGCAATTTCTCGGGGGATTGGCTGCCGAGCGATGGTTCCGGCC AATGAAAGGACGAAGGGATGGCAGAACGCCTAACCAAG
<i>nosZ</i> (BAB2_0928, BAB_RS30695)	CGAAAAATTTGCAGCCCCGAATGCACCTCTCGCAGCGGCTGCCGAACGTGGCGGCGGTCCAGCCAG GCCTATCATCTCGGTCAAGGGAAAGCCGGTGAAACACCCGTCAATCCCGTCCCCGGCCCTGATTT TTTCAAAGGAGAAAAAGTATGACTGAAGAAACCAGGAAA
BAB2_0863, BAB_RS30420	TACCTACGCAATTCGCAAGCCGCACTGGAAAAACGCCGAAGGGTCGGCCGATTTTGAGCCGTTCAA CTGGGAAAAGGAAGGCCGGATGCCGGGTCCCAGCAAGCCGACGGCTGAAAAGCCCGTCCTGCAA AAGCTATGGAGACATCTTAATGTCAAGCTCATCAGATGCG
BAB1_0383, BAB_RS17760	GGCCCATGCGCGTGAAATCTATTTGCAGGCTGGCCGCTCCCATGCCATGCCGCCGCCAACGTTACC GGCGTGACGGACGAGGAACGCCAGCTTCTGGCCTCCTGGTATCAATCCGTGACGACAGGCCCAAAA GAGGGGACCAAGACCGAATGACAAAGCTTCTCATCCG
<i>hPr-K</i> (BAB1_2094, BAB_RS25910)	CGATCAGCCGGCAGATCATCGAGGCGCATGGCGGCGCGCTGACGGCGGAAAAATATTACCGATCCGG ATAAGCCGATATTTCAAGGGTGCCCGCTTATCGTTGATCTTCCGGCCAGCGCATGACCGTGAAA AGTGGATATCTGAACCTGTGACGCCCCGAGGAGGAAAGA
BAB1_2091,	CGGGTTAAACGATTAAAAAAATTTCAAAAATTTTAAATCGATTAAATATTTGAATTTTCTCAATTAA

BAB_RS25895	TCTGTTTCTGACTGCCATCCCCATGAAAGCCAAACCAGGGGGACGCATTTTTTAGTTAGTCAAACA GACGGCGGAGACATC AT GAAAGAGACCGGCATCCAC
<i>vjbR</i> (BAB2_0118, BAB_RS26915)	AATTAAGTAATTGCCGGTTGCCAACGACTATATTTTTTTAAGTCACTAATAAGCGATTGAAGGCCTC TGAGGGGAGGCGATTCTCTCGCAAGCAGTTATAGAGATACCAGAGCGAAGCCCGCATGGTTTCATC ACCAAGGATATTTCCA AT GAGTCTTGATCTCGTTCAT
<i>exoR</i> (BAB1_0891, BAB_RS20180)	GAGCAGAAAAAATTCTGCCCGTTTGCTGTGCGCTCCGCCGAAGCGAGCTGAGCTTTTTTCCGTCAA GATCGGGTCTCACTGTTGACGAAAAGCAGGCGCAACCTGCCTTTCATGATCTTTCCGTTCATATGA AAGACCGGCGTTGT GAT GCGTAGTCGCAGTTTTTCA
<i>ompR</i> (BAB2_0762, BAB_RS29960)	AACGCCTATGCGGGGAAATCAGCCAGTAGGCTGATTTCTGATCCGGCTTCGATGGAAAATGCGCCA AAACAAATAGTTAGAGCAGTTCGCGCGTTTCTGTAAAAATAGGAAACGCTACAATACCCACCCCAA CGGCAATGGAACAGCAAA TTG AAAGAAGACGCCCACATT
<i>motB</i> (BAB2_1103, BAB_RS31605)	TCTGGAAGCATTGCAGGCCCATGGGGTGCTTTTGCCCTCCGGTTGCCGCTTTTCAGAGACGGCATCG AACGAACTTTCTTTTCTTTGGCGAACGGATGCTCGAAACGCGCATCGCGCCGCTTCTTGAAGAAC TGAAGGCTGCGGTGAA AT GAAACATTGAGCCCGAAACG
<i>malK</i> (BAB1_0241, BAB_RS17050)	TCGATTATACGGCCGAGTTCACCATCGATTGGCGCGGCATGTGCGCGCTTGCCGTGGTGATGATTGTT CCGGCGCTGGCGCTCACCTTCGTCATCCAGAAACACCTCGTTTCCGGCCTGACTTTCGGCGCGGTTA AAGGTTGAAATTGTA AT TGGCACAGCTTCCATCAAA
BAB1_1601, BAB_RS23550	TTCGTTGCTTAACAGAAGGACGCTGTCGTTTCGTTCAAGGCAAATGACGACTATTGGGGCGGACGCC CGAAGATCGACGATCTGGTCTTCGCGATCACGACCGATCCTGCTGTTGCGCGCGAGAAGCTCAAGGC CGGCGAATGCCAGCTT AT GTCTATCCGGCTCCGGCG
BAB1_1397, BAB_RS22600	AATATCTTTATTCCATAGAAACATGGGAAAAGCTGTTCTCGTCCGCTGAAAATTGCGCTAAACCACC ATCGTCAATAGCTGGGTTTGAGGAGACTTCGCTATTACAAGTTCGCTGCAAGAGGCGGATAGTCTA ATTGAGGAGACTTCCCG T GTTGGACTGGGAAAATGTA
BAB1_0666, BAB_RS19125	TCTGCCGCATTATCTCTTTTTTGAGATACACCCCGCTTGCTCCATTGCGGTGGCAAGACTATGGTGC AACGCCTCACGCATAATCCGATGAAGCCCGAAGGGGGCTTTGCTGCGTGGGGTCCCGTCTATCTGTT TCAGGAGTTCAGAA T GCTGAAGGGCTCAATTACCG
