A novel cell division protein critical for the assembly of the bacterial divisome

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Abstract

Identification of novel essential bacterial genes is important for not only the understanding of their cell biology but also the development of new antimicrobials. Here we report a previously unrecognized core component of the *Acinetobacter baumannii* divisome. Our results reveal that the protein, termed Aeg1 interacts with multiple cell division proteins, including FtsN, which is required for components of the divisome to localize to the midcell. We demonstrate that the $FtsA_{E202K}$ and $FtsB_{E65A}$ mutants effectively bypassed the need of Aeg1 by *A*. *baumannii*, so did the activation variants $FtsW_{M254I}$ and $FtsW_{S274G}$. Our results suggest that Aeg1 is a cell division protein that arrives at the division site to initiate cell division by recruiting FtsN, which activates FtsQLB and FtsA to induces the septal peptidoglycan synthase FtsWI. The discovery of the new essential cell division protein has provided a new target for the development of antibacterial agents.

Keywords: conditional gene deletion; essential gene; cell division; antibacterial targets

Introduction

Acinetobacter baumannii is a Gram-negative bacterial pathogen that causes a wide variety of nosocomial infections (1, 2), including urinary tract infections, gastrointestinal and skin/wound infections and secondary meningitis (3-6). The challenge posed by this pathogen is compounded by the emergence of isolates that are resistant to almost all of the available antibiotics, including some of the last resort for treatment of infections caused by bacterial pathogens, including colistin, tigecycline, and carbapenems (2, 7). As a result, the World Health Organization (WHO) has classified *A. baumannii* as a pathogen for which new antibiotics are urgently needed (8). Meeting this challenge requires the discovery of antimicrobials of new mechanisms of action or other mitigation strategies that enable reduction of disease burden caused by this pathogen.

Historically, the discovery of antibiotics was largely based on the search for secondary metabolites produced by soil-dwelling microbes (9, 10). The majority of clinically used antibiotic classes originate from soil bacteria, including lactams, aminoglycosides, polymyxins, and glycopeptides (11). Unfortunately, natural products discovery is now plagued by problems of so-called ‘dereplication problem’, wherein rediscovery of molecules or their close relatives (12). As a result, there has not been a novel antibiotic discovered in over 30 years using traditional methods of screening environmental samples (13). The overuse of these merely variants of existing compounds has further accelerated the problem associated with antibiotic resistance. Thus, identification of novel therapeutic targets in the pathogen may serve as an effective alternative to the problem.

A better understanding of gene function associated with *A. baumannii* pathogenesis and biology will provide us strategies to develop antibiotics with potentially novel mechanisms of action. One extensively explored avenue in this regard is the identification of previously unrecognized essential genes by methods enabled by new DNA sequencing technologies, including insertion sequencing (INSeq) (14), transposon sequencing (Tn-seq) (15)，transposon-directed insertion site sequencing (TraDIS) (16), and high-throughput insertion tracking sequencing (HITS) (17). Application of these methods has identified genes believed to be required for bacterial viability under various

conditions in such important pathogens as *Streptococcus pneumoniae* (15), *Pseudomonas aeruginosa* (18), *Vibrio cholerae* (19) and *A. baumannii* (20-22).

Similar to candidate genes identified by other methods, putative essential genes obtained by In-seq were deduced from sequencing results of surviving mutants, some of which can be false positives or negatives due to unsaturated mutant libraries or polar effects on downstream genes of the insertion sites. Using In-seq Wang et al identified 453 candidate essential genes for the growth of *A. baumannii* strain ATCC 17978 on rich medium (22). Among these, genes annotated as hypotheticals with orthologs in other taxonomically distant microorganisms are of particular interest because their potential role in cellular processes that can be explored as targets for the development of novel antimicrobials. We thus set out to determine a subgroup of the predicted essential genes by a conditional gene deletion strategy based on the arabinose inducible promoter (23). From ten genes examined, three were found to be essential for *A. baumannii* viability on rich medium. Further study revealed that one of these genes codes for a novel bacterial cell division protein.

Results

Identification of genes required for *A. baumannii* viability

Analysis of strains of *A. baumannii*, including the model strain 17978 by In-seq technologies have led to the identification of at least 453 genes potentially required for bacterial growth on rich medium (21, 22). Whereas many of these genes are involved in known cellular processes fundamental for cell viability such as DNA replication, transcription and translation, some code for proteins of unknown activity, are thus of great interest as potentially new antimicrobial targets (21). To determine the function of the candidate essential genes annotated as hypotheticals, we first confirmed their essentiality by a conditional gene deletion method. To this end, we employed a set of plasmids that allow inducible gene expression in *A. baumannii* (24). Each of the gene of interest was expressed from the arabinose-inducible promoter (23), and the corresponding gene was deleted from the chromosome by the standard allele exchange method (25) **(Fig. 1A)**. Chromosomal deletion mutants harboring the arabinose-inducible gene were tested for essentiality by spotting serially diluted cells

onto solid medium with or without arabinose (ara) **(Fig. 1A)**. If the gene of interest is essential, the bacterium should fail to grow on plates without ara.

Our initial analysis of 10 genes (**Table S1**) identified *A1S_0137*, *A1S_2249*, and *A1S_3387* (26) that met the criteria of being required for growth on LB agar (**Fig. 1B**). These genes were thus designated as *A. baumannii* essential genes (Aeg) and Aeg1 (*A1S_3387*) was chosen for detailed study.

Sequence analysis revealed that Aeg1 has orthologs in a number of Gram-negative bacteria, including *Klebsiella pneumoniae*, *Salmonella enterica* members of the *Moraxellaceae* family and some strains of *Escherichia coli*, with sequence similarity ranging from 80% to identical **(Fig. S1).** Aeg1 is predicted to harbor a single transmembrane domain composing of 23 residues close to its amino terminal end **(Fig. 1C)**. To determine the importance of the putative membrane spanning region in its function, we employed a dual inducible system with two compatible plasmids that use promoters that respond to ara and isopropyl-β-D-thiogalactopyranoside (IPTG), respectively. Strain Δ*aeg1*(P_{BAD}::Aeg1, P_{TAC}::Aeg1) was able to grow on medium containing 1% ara or 0.5 mM IPTG **(Fig. 1D)** indicating that the chromosomal deletion can be complemented by either of the constructs when expression of Aeg1 was induced. Importantly, expression of the Aeg1 mutant lacking the predicted membrane anchoring region was unable to restore the growth of the strain (**Fig. 1D**), suggesting that association with membrane is essential for its activity.

Depletion of Aeg1 caused cell filamentation in *A. baumannii*.

We next examined the morphology of *A. baumannii* lacking Aeg1 by optical and scanning electron microscopy. Cultures of strain Δ*aeg1*(P_{BAD}::Aeg1) were induced by ara for 14 h, cells diluted into fresh LB with or without ara were allowed to grow for 18 h. We found that cells of cultures grown in medium containing 1% ara exhibited a short rod cell shape similar to that of the wild-type strain (**Fig. 2A**). In medium without ara most cells of strain Δ*aeg1*(P_{BAD}::Aeg1) displayed an elongated morphology which is in sharp contrast to those of wild-type cells grew under identical conditions (**Fig. 2A**). Quantitative analysis indicated that in medium supplemented with ara, more than 95% of the cells of strain Δ*aeg1*(P_{BAD}::Aeg1) were shorter than 5 μm. Incubation in medium

without ara for 18 h caused more than 96% of the cells to become elongated with cell lengths ranging from 5 μm to over 10 μm (**Fig. 2B**). The phenotype can be partially reversed after growing the elongated cells in medium containing 1% ara for 4 h and the morphology of almost all cells were restored to that of wild-type bacteria after 8 h incubation in inducing conditions (**Fig. 2C**). These results indicate that depletion of Aeg1 causes cell elongation, which suggests that this protein is involved in cell division.

Mutations in the cell division gene *ftsA* bypasses the requirement of Aeg1

To explore the cellular process participated by Aeg1, we sought to isolate suppressor mutants that can survive in standard medium under conditions the gene is not expressed. To this end, cells of strain Δ*aeg1*(P_{BAD}::Aeg1) grown in medium supplemented with ara were exposed to the mutagen ethyl methanesulfonate (EMS), and the treated cells were plated on LB agar without ara. A few colonies were obtained from approximately $6x10^8$ cells and two independent mutants M1 and M2 were chosen for further analysis. In spotting assays using diluted cells, each of these two mutants derived from strain Δ*aeg1*(P_{BAD}::Aeg1) was able to grow on medium without ara at rates comparable to those of wild-type bacteria (**Fig. 3A)**. We then performed whole genome sequencing analysis of these two mutants, which revealed that M1 and M2 had 320 and 328 substitution mutations, respectively. In addition, 659 insertion-deletion (InDel) mutations were found in M1 and 665 such mutations were associated with M2 **(Table S3)**.

Because depletion of Aeg1 caused cell elongation, we first examined mutated genes whose functions are known to be involved in cell division. An E202K mutation caused by a G to A substitution in the first position of the codon was found in the cell division protein FtsA in both M1 and M2 (**Table S3**). We thus verified the suppression phenotype by introducing a plasmid expressing FtsA or $FtsA_{E202K}$ into strain Δ*aeg1*(P_{BAD}::Aeg1) and examined the growth of the resulting bacterial strains under different induction conditions. Expression of $FtsA_{E202K}$ allowed strain Δ*aeg1*(P_{BAD}::Aeg1) to gain the ability to grow in the absence of ara. In contrast, although the protein was expressed at a comparable level, FtsA cannot suppress the growth defect caused by Aeg1 depletion (**Fig. 3B**). Consistent with the growth phenotypes, expression of

154 $FtsA_{E202K}$ in strain Δ*aeg1*(P_{BAD}::Aeg1) under conditions in which the complementation
155 gene was not expressed displayed a morphology similar to that of wild-type bacteria
156 (**Fig. 3C**).

157 Previous studies have found that several mutations in FtsA bypassed the
158 requirement of a number of essential cell division proteins in *E. coli*, including ZipA (27),
159 FtsK (28), and FtsN (29). Among these, $FtsA_{Q286W}$ (FtsA*) was the first gain-of-function
160 mutation found in *E. coli*, which allowed the survival of mutants lacking ZipA (Δ*zipA*) or
161 FtsK (Δ*ftsK*) (27, 28, 30). Additionally, $FtsA_{I143L}$ and $FtsA_{E124A}$ weakly bypassed the
162 requirement of FtsN. These mutations also rescued the $FtsL_{L86F/E87K}$ mutant when
163 overexpressed (31). We thus examined whether similar mutations in FtsA of *A.*
164 *baumannii* can bypass the need of Aeg1 by constructing substitution FtsA mutants
165 D124A, V144L and Q285W, which correspond to E124A, I143L, and Q286W in its *E. coli*
166 counterpart, respectively (**Fig. S2**) and tested them in strain Δ*aeg1*(P_{BAD}::Aeg1).
167 Whereas $FtsA_{Q285W}$ cannot detectably suppress Aeg1 depletion, expression of $FtsA_{D124A}$
168 or $FtsA_{V144L}$ partially resecured the growth of strain Δ*aeg1*(P_{BAD}::Aeg1) in medium
169 without ara (**Fig. 3D**). Despite multiple attempts, we were unable to detect the
170 expression of these FtsA mutants by immunoblotting using antibody specific to the Flag
171 epitope fused to these alleles (**Fig. 3D, lower panels**), suggesting that the low activity
172 exhibited by these mutants may result from low protein levels.

173 The observation that mutations in genes involved in cell division bypass the need of
174 Aeg1 suggests that this protein participate in the same cellular process. We thus
175 analyzed the cellular localization of Aeg1 in *A. baumannii* by introducing a plasmid that
176 expresses Aeg1-mCherry from the P_{BAD} promoter. Fluorescence microscopy analysis
177 revealed that Aeg1 localized at the septum of dividing cells (**Fig. 3E**), which validated
178 the genetic evidence for its role in cell division.

179 **Aeg1 interacts with multiple core components of the *A. baumannii* divisome**

180 To further explore the possibility that Aeg1 is a component of the *A. baumannii*
181 divisome, we determined its interactions with known cell division proteins using the
182 Cya-based bacterial two-hybrid method (32). Among the tested proteins FtsZ, FtsA,
183 ZipA, FtsK, FtsQ, FtsL, FtsB, FtsW, FtsI, and FtsN, Aeg1 detectably interacts with ZipA,

FtsK, FtsL, FtsB, and FtsN. ZipA and FtsN appearing to have higher binding affinity with Aeg1 as indicated by the hydrolysis of X-gal by derivatives of the *E. coli* reporter strain BTH101 (32) harboring appropriate protein fusions (**Fig. 4A**). When the interactions were quantitatively determined by measuring galactosidase activity, the binding between FtsN and Aeg1 appeared the strongest among all examined protein pairs (**Fig. 4B**).

We next analyzed the localization of Aeg1 and core divisome proteins during cell division of *A. baumannii* by taking advantage of the elongated morphology of Aeg1-depleted cells, which may allow better resolution of observation via fluorescence microscopy. To this end, we coexpressed the mCherry-Aeg1 fusion with GFP fusion of ZipA, FtsK, FtsL, FtsB, or FtsN in the Δ*aeg*1 mutant from the ara- and IPTG-inducible promoter, respectively. Cultures of strains derived from Δ*aeg1*(P_{BAD}::mCherry-Aeg1) harboring the GFP fusions were induced by ara for 14 h, saturated bacterial cultures were then diluted into fresh LB broth without ara for 18 h to induce the elongation morphology. IPTG (0.5 mM) and ara (1%) were added to induce the expression of fusion proteins for 3 h before samples were processed for microscopic analysis. Consistent with results from the protein interaction experiments using the bacterial two-hybrid assay, Aeg1 colocalized with ZipA, FtsK, FtsL, FtsB, and FtsW (**Fig. 4C**). Thus, Aeg1 interacts with multiple core cell divisome proteins of *A. baumannii*.

Aeg1 is an essential core cell division protein in *A. baumannii*

The interaction map between Aeg1 and core divisome proteins prompted us to postulate that the absence of Aeg1 prevented these proteins from localizing to the midcell. To test this hypothesis, we introduced plasmids that direct the expression of GFP fusion of each of the divisome proteins into strain Δ*aeg1*(P_{BAD}::mCherry-Aeg1). Each of the resulting strains was grown in LB broth with ara overnight prior to being diluted into fresh medium without ara for 18 h to induce the elongation morphology. IPTG (0.5 mM) was then added to induce the expression of the GFP fusions. In cells not expressing Aeg1, all of the examined core division proteins displayed midcell mistargeting, this phenomenon was particularly apparent for proteins that interact with Aeg1, including ZipA, FtsK, FtsB, FtsL, and FtsN (**Fig. 5A, Table S2**). These results suggest that Aeg1 is a new member of cell division protein, which plays a role in

positioning several other core proteins at the septum of *A. baumannii*.

During the formation of the divisome, FtsN was believed to be the last protein being recruited to the septum where it converts FtsQLB and FtsA into their active forms, which subsequently activate the septal peptidoglycan synthase FtsWI (33, 34). If the interaction between Aeg1 and FtsN is critical for the ability of the latter to switch on FtsQLB and FtsA, constitutively active mutants of FtsQLB or Fts A should suppress the need of Aeg1 for cell viability. To test this hypothesis, we expressed HA-FtsB$_{E65A}$ and HA-FtsL$_{Q70K}$ of *A. baumannii* (equivalent to mutants of their *E. coli* counterparts that allow the bypass of the requirement of FtsN) (**Fig. S2**) (33, 35) in strain Δ*aeg1*(P$_{BAD}$::Aeg1) on medium without ara. Although the expression of HA-FtsB$_{E65A}$ was not detectable with the HA-specific antibody, induction of this mutant completely restored the growth of the Δ*aeg1* mutant in the absence of Aeg1 (**Fig. 5B**). In contrast, a similarly constructed plasmid that directs the expression of HA-FtsB$_{D68H}$ cannot bypass the requirement of Aeg1 under the same conditions (**Fig. 5B**). Similarly expressed HA-FtsL$_{Q70K}$ detectably rescued bacterial growth without Aeg1 at a level considerably lower than that of FtsB$_{E65A}$ (**Fig. 5C**). The low or undetectable activity exhibited by FtsL$_{Q70K}$ and FtsB$_{D68H}$ may result from the low protein levels in strain Δ*aeg1*(P$_{BAD}$::Aeg1). Nevertheless, these results support our hypothesis that Aeg1 functions upstream of FtsN, probably by functioning as its activator or recruiting factor.

It is known that expression of mutants FtsI$_{K211I}$, FtsW$_{M269I}$, and FtsW$_{E289G}$ driven by a strong promoter can bypass the need of FtsN in *E. coli* (36). The ability of FtsB$_{E65A}$ and FtsA$_{E202K}$ to suppress the growth defect of the Δ*aeg1* mutant prompted us to examine whether constitutively active alleles of FtsW or FtsI have the same effects. Overexpression of FtsW$_{M254I}$ and FtsW$_{S274G}$ of *A. baumannii* detectably rescued the growth of the strain in which Aeg1 had been depleted (**Fig. 5D**). FtsI from *A. baumannii* does not have a residue corresponding to K211 of its *E. coli* counterpart (**Fig. S2**), we thus did not test the effect of this mutation. Therefore, our results demonstrate that Aeg1 may collaborate with FtsN to activate at least a part of FtsQLB and FtsA for subsequently activation of FtsWI during cell division. Together with results that the variant FtsA$_{E202K}$ suppressed the growth defect caused by *aeg1* depletion (**Fig. 3B**),

these observations support a model in which the Aeg1-FtsN complex is involved in the activation of FtsQLB and FtsA.

Discussion

Powerful In-seq DNA sequencing technologies based on saturated transposon insertion libraries have allowed the identification of genes essential for bacterial viability under specific conditions, including commonly used rich media such as LB broth (22). Using a conditional gene deletion method, we have revealed that from 10 putative essential genes identified by this method, three previously annotated as hypotheticals are essential for *A. baumannii* viability, suggesting that assignment of essentiality to genes identified by methods of this kind need to be individually verified.

Our assignment of *aeg1* as an essential gene is consistent with a recent study which revealed its essentiality (termed *advA*) by transposon insertion sequencing, which also observed cell elongation upon the depletion of this gene (37), Our results provided at least two additional lines of evidence to support the notion that Aeg1 is a core cell division protein in *A. baumannii*. First, random suppression mutations that bypassed the requirement of Aeg1 mapped to a classic cell division gene and mutations in some cell division genes known to circumvent the need of specific cell division proteins rescued the growth defect caused by Aeg1 depletion. Second, Aeg1 interacts with at least a subset of proteins involved in cell division (**Fig. 4A-B**).

In the process of bacterial cell division, over 30 distinct proteins are assembled into a complex typically referred to as “divisome” (38). Ten of these are normally essential for both cell division and survival, and they are now mainly suggested to be the core of the divisome in various bacteria (38, 39). These essential division proteins are mostly named Fts (filamentation temperature sensitive), which stems from the fact that inactivating one of these Fts proteins causes cells to become filamentous, which eventually failed to survive (38, 40). Among these, the FtsQLB complex not only serves as a scaffold for recruitment of subsequent divisome proteins (41, 42), but also plays a an important role in regulating the activity of the divisome (33, 34). The constriction control domain (CCD) of FtsL was previously defined as a critical component for switching the conformation of FtsLB from an off to an on state in order to activate FtsWI

by enabling the interaction between $FtsI^{peri}$ and the AWI (activation of FtsWI) region of FtsL (33, 34, 43). Division obstruction caused by Aeg1 depletion can be effectively circumvented by suppression mutations ($FtsB_{E65A}$) in its CCD domain and by activation mutations (M254I and S274G) of FtsW **(Fig. 5D),** suggesting that Aeg1 functions upstream of these proteins.

In addition to FtsQLB-mediated activation of FtsI in the periplasm, the constitutively active form of FtsA (FtsA*) acting on FtsW in the cytoplasm, these two events functions synergistically to activate FtsWI for sPG synthesis (31). FtsA is a member of the actin family (44, 45), which interacts with FtsN via a unique IC domain positioned between the IA and IIA domains (46-48). Little is known about the function of the IA and IIA domains of FtsA. That the E202K mutation in the IIA domain bypasses the requirement of Aeg1 by *A. baumannii* **(Fig. 3B**) suggests that Aeg1 and FtsA work together to activate FtsW*.*

The maturation of the core divisome is facilitated by the recruitment in a nearly sequential order of the late-division proteins FtsK, FtsQ, FtsL/FtsB, FtsW, FtsI, and FtsN (49-51). Once the latest division protein, FtsN, is recruited, division-specific peptidoglycan synthesis conferred by the FtsWI complex is activated to build the septum (51, 52). More recent studies suggest that by binding to FtsA, a small amount of FtsN is recruited to the division site earlier than previously thought (33, 48, 53) where it induces a conformational switch in both FtsA and the FtsQLB subcomplex on both sides of the membrane (33). Furthermore, binding between FtsA and FtsN is regulated by ZipA (48). Our observation of strong binding of Aeg1 to ZipA and FtsN **(Fig. 4A-B)** prompted us to propose a model in which Aeg1 participates in cell division by anchoring to the division site together with ZipA where it recruits FtsN, which in turn signals to both the cytoplasmic or periplasmic branches of peptidoglycan synthesis involving FtsA and the FtsQLB complex, respectively (33) (**Fig. 6A**). The placement of Aeg1 as one of the early arrivals in the hierarchical sequential assembly of the divisome is consistent with the fact that the requirement of Aeg1 can be bypassed by constitutively active mutants of $FtsA_{E202K}$ (**Fig. 3**), FtsB ($FtsB_{E65A}$), FtsL ($FtsL_{Q70K}$) and of FtsW ($FtsW_{M254I}$ and $FtsW_{S274G}$) (**Fig. 5**).

It is worth noting that that although homologs of Aeg1 are present in many

Gram-negative bacteria, including some recent isolate of *E. coli,* it appears to be absent in more extensively studied model strains such as K12 **(Fig. S1).** It is possible that in strain K12, its activity is conferred by a yet unidentified protein that employs a conserved mechanism in cell division. Future study aiming at elucidating the biochemical and structural basis of the activity of Aeg1 and its homologs, and their relationship with other components of the divisome may provide not only insights into the mechanism of bacterial cell division but also leads for the design of antibiotics with novel mechanism of action.

Materials and methods

Bacterial strains, growth conditions, and plasmids construction

All bacterial strains and plasmids used in this study are listed in **Table S4**. All *A. baumannii* strains were derivatives of strain ATCC17978 (54). Bacteria were grown in Luria Bertani (LB) broth or agar. Antibiotics were added to media when necessary. For *E. coli*, the concentrations used were: ampicillin, 100 μg/mL, kanamycin, 30 μg/mL, chloramphenicol, 30 μg/mL, and gentamicin, 10 μg/mL. For *A. baumannii,* kanamycin, 30 μg/mL, gentamicin, 10 μg/mL, and streptomycin, 100 μg/mL.

To construct pUT18C-Flag, two oligos with sequences coding for the Flag tag and appropriate restriction sites were mixed at a 1: 1 ratio, heated to 100°C for 5 min and allowed the mixed DNA to anneal by gradually cooling down to room temperature. The resultant DNA fragment was then inserted into *Sal*I/*Cla*I digested pUT18C (32). We introduced an *Eco*RV site into the inserted DNA fragment to facilitate the identification of plasmids carrying the intended insert. To make pJL05 that allows P_{TAC}-driven expression of HA-tagged protein, primers containing the coding sequence of the HA tag were used to amplified the promoter region of pJL02 (24), PCR product was inserted as a *Pci*I/*BamH*I fragment. This manipulation replaced the Flag tag on pJL02 with an HA tag. The integrity of all constructs was verified by sequencing analysis.

Introduction of plasmids into *A. baumannii*

Plasmids were introduced into *A. baumannii* by electroporation (55) or by triparental mating. Electrocompetent cells were prepared using a previously described protocol (56) with minor modifications. Briefly, saturated cultures of *A. baumannii* were diluted 1:100 into 50 mL LB medium to grow for 18 h at 37°C and cells were harvested by centrifugation (4000*g*) at room temperature (RT) for 5 min. Cells were washed twice with 10 mL of 10% glycerol, resuspended in 1 mL of 10% glycerol, cells aliquoted in 50 μL. were stored at -80˚C. For transformation, 1 μg of plasmid DNA was mixed with 50 μL competent cells and electroporation was performed in 0.2-cm cuvettes on a Bio-Rad Gene Pulser system (2.5 kV/cm, 25 μF, 200 Ω).

The *E. coli* MT607 harboring pRK600 (57) was used for triparental mating. Briefly, 100 μL of overnight cultures of the donor, recipient, and the helper strain were mixed

and cells were harvest by centrifugation (4000*g*) for 5 min. Mixed cells washed twice with 1 mL of sterile water were spotted onto LB agar and the mating was allowed to proceeded for 4-6 h at 37°C before plating onto selective medium.

Construction of in-frame deletion mutants of *A. baumannii*

To delete the putative essential genes, we first introduced a plasmid expressing the gene of interest into *A. baumannii* and the resulting strains were used to construct chromosomal deletion mutants using a method based on the suicide plasmid pSR47s (25). Briefly, the coding region of the gene was inserted into pJL03, which allows expression of Flag-tagged protein from the P_{BAD} promoter (24) and the resulting plasmid was introduced into *A. baumannii* by electroporation.

To construct the plasmid used for in-frame deletion of *A. baumannii* genes, 1.0 kilobase DNA fragment was amplified from the upstream and downstream of the gene to delete, respectively, digested with appropriate restriction enzymes and inserted into similarly digested pSR47s (25). The primers were designed so that in each case the gene to be deleted was replaced with an open reading frame consisting of the first and last 15 residues linked by two amino acids encoded by the sequence of the restriction enzyme used to fuse the two DNA fragments (**Table S4**). The plasmid was then introduced into the *A. baumannii* strain harboring the pJL03 derivative expressing the gene to be deleted from the P_{BAD} promoter by triparental mating. Transconjugants obtained on LB agar containing 1% ara were grown in LB broth containing 5% sucrose for 18 h prior to being streaked onto LB agar supplemented with 5% sucrose. Deletion mutants were identified by colony PCR with primers corresponding to the 5' end of the upstream fragment and the 3' of the downstream fragments.

Ethyl methanesulfonate (EMS) mutagenesis

The *A. baumannii* strain Δ*aeg1*(P_{BAD}::Aeg1) was grown in LB broth containing 1% ara to saturation, cells from 2-mL culture collected by centrifugation were washed twice with cold buffer A [60 mM K_2HPO_4, 33 mM KH_2PO_4, 7.6 mM $(NH_4)_2SO_4$, 1.7 mM sodium citrate, PH=7]. Cells resuspended in 2× buffer A supplemented with 1.4% EMS were incubated in a shaker (220 rpm) at 37°C for 15 min for 30 min, 45 min and 60 min, respectively. Treated cells harvested by centrifugation were washed twice with buffer A

prior to being plated onto LB agar supplemented with 5% glucose. Colonies appeared were purified and tested by spotting diluted cells onto LB agar with or without ara, respectively to confirm the ability to grown in the absence Aeg1. To eliminate the possibility that the ara-independent growth phenotype was due to mutations in the P_{BAD} promoter, the plasmid from each mutant candidate was rescued and the promoter region was sequenced. Only mutants harboring an intact P_{BAD} promoter were retained for further study.

Genome sequencing was performed by Suzhou Golden Wisdom Biological Technology Co., Ltd, and mutations were identified using the genome of the parent strain ATCC 17978 as reference (26).

Bacterial Two-Hybrid assays

To assess interactions between Aeg1 and *A. baumannii* Fts proteins, we employed the *Bordetella pertussis* adenylate cyclase (Cya)-based bacterial two-hybrid system (32). The coding region of Aeg1 was fused to the T25 fragment of Cya and testing Fts proteins were individually fused to the T18 fragment on pUT18C-Flag, which allows the detection of the fusion protein with the Flag-specific antibody (**Table S4**). Interaction was evaluated in the cya^- *E. coli* strain BTH101 (32) by the ability of the testing strains to hydrolyze X-Gal. Quantitative measurement of β-galactosidase activity with performed with ortho-nitrophenyl-β-galactoside (ONPG) using an established protocol (58). Testing bacterial strains were cultured in 2 mL LB broth containing 0.5 mM IPTG for 18 h, and 0.2 mL cells were harvest and resuspended in 1 mL Z-buffer (60 mM Na_2HPO_4, 40 mM $NaH_2PO_4 \cdot H_2O$, 1 mM $MgSO_4$, 10 mM KCl, and 7 mL of 2-mercaptoethanol per liter). After adding 50 μL 1% (m/v) SDS and 100 μL of chloroform, cells were lysed by 30 s vortex and 50 μL of ONPG (40 mg/mL) was added. The reaction was terminated with 500 μL of 1 M Na_2CO_3 after ONPG hydrolysis had occurred as determined the presence of the yellow color product. β-galactosidase activity is defined as in Miller units using the following equation: (OD_{420}×1000)/ [(time of incubation in min)x(volume of cell suspension in mL)x(cell density of the culture in OD_{600})]. All assays were done in triplicate.

Antibodies and immunoblotting

HA-specific antibody (1:1000) was purchased from Santa Cruz (Cat #sc-7392), and rabbit anti-ICDH (1:2000) was described previously (24). To prepare protein samples, we diluted (1:100) saturated bacterial cultures into fresh LB broth. When OD_{600} of the cultures reached 0.6, IPTG was added to a final concentration of 0.5 mM. Approximately $1x10^9$ cells were collected, resuspended in 100 μL SDS sample buffer and were boiled for 5 min. Proteins separated by SDS-PAGE were transferred onto nitrocellulose membranes, which were first blocked with 5% nonfat milk for 1 h followed by incubation with appropriate primary antibodies for 14 h. Washed membranes were incubated with the appropriate IRDye-labeled secondary antibodies and signals were detected using an Odyssey CLx system (LI-COR).

Fluorescence imaging

To determine the cellular localization of Aeg1 and its colocalization with members of the divisome, we constructed pJL03::Aeg1-mCherry, which expressed the fusion from the P_{BAD} promoter (23). GFP chimera of Fts proteins were expressed from pJL05 driven by the P_{TAC} promoter inducible by IPTG. Each of the GFP-Fts fusion was introduced into strain Δ*aeg1*(P_{BAD}::mCherry-Aeg1). All strains were maintained in media containing 1% ara to ensure their viability.

To visualize the localization of the fusions, bacterial strains were grown to saturation in LB broth containing ara and the cells washed twice with PBS were diluted to a density of approximately $5x10^6$ cells/mL. The cultures were split into two 2-mL subcultures, the one used to determine how the absence of Aeg1 impacted the cellular localization of Fts proteins received only IPTG but not ara. Cultures were incubated in a shaker for an additional 6 h, and 100 μL cells were withdrawn and fixed by incubation in 4% paraformaldehyde for 20 min at RT. After washing twice with PBS, samples were stained with Hoechst 33342 (1:5000) (Invitrogen, cat#H3570) and mounted on slides for observation with an Olympus IX-83 fluorescence microscope.

Bioinformatics analysis

Aeg1 homologs were identified using tBLASTn (59) using the Aeg1 protein (*A1S_3387*) from strain ATCC17978 (GenBank: CP000521.1) as the query sequence. Clustal omega (https://www.ebi.ac.uk/Tools/msa/clustalo/) was used to perform multiple

sequence alignments. The homology comparison of Fts proteins between *E. coli* and *A. baumannii* was also performed using Clustal omega. Jalview was used for editing and viewing sequence alignments (60). TMHMM 2.0 were used to predict protein topology (61) .

Data quantitation, statistical analyses

Student's *t*-test was used to compare the mean between two groups each with at least three independent samples.

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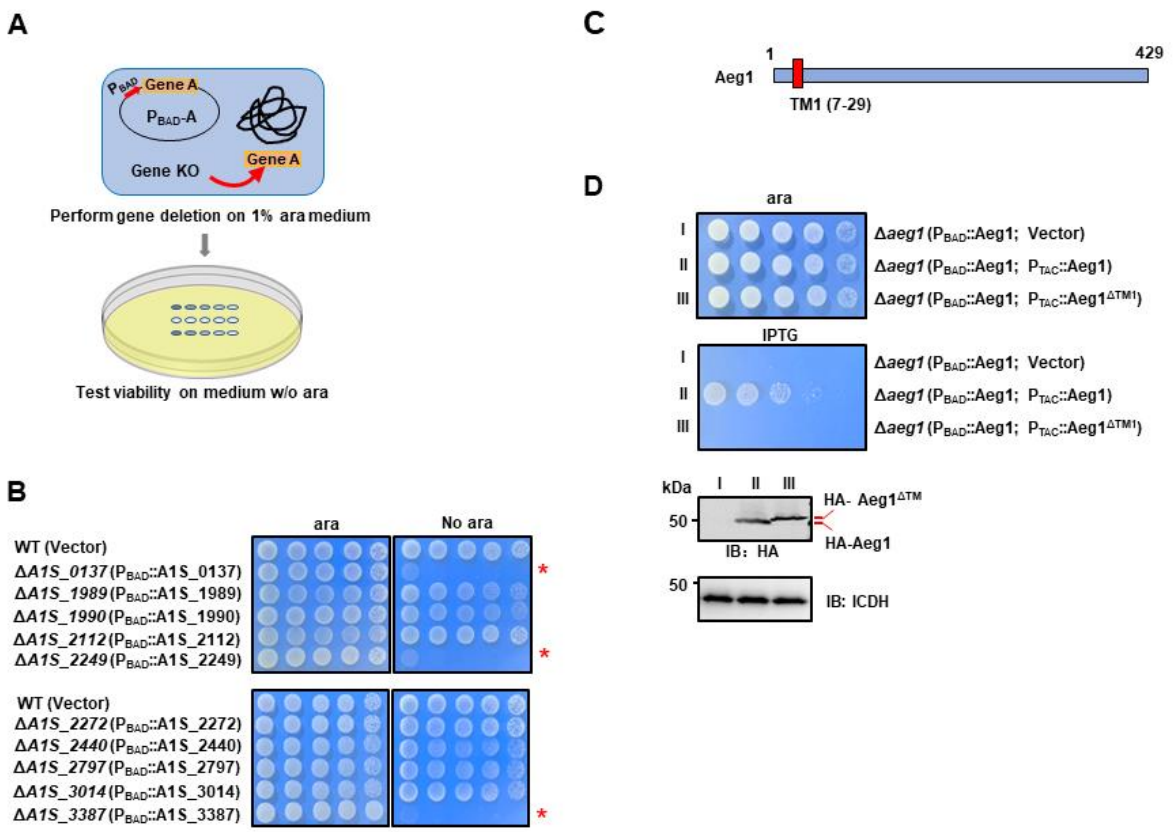


Fig. 1 Identification of *aeg1* as an essential gene for *A. baumannii* viability on rich medium

A. A diagram depicting the method for conditional deletion of potential essential genes. The gene to be examined was expressed from the arabinose-inducible promoter on a plasmid and the gene was deleted from the chromosome using the standard allele exchange method (upper panel) and strains lacking the chromosomal gene were tested for essentiality by spotting diluted cells on media with and without arabinose, respectively (lower panel).

B. Identification of *A1S_0137*, *A1S_2249,* and *A1S_3387* as *A. baumannii* essential genes. Each of the 10 genes predicted to be essential were deleted by the method described in A and the resulting bacterial strains were tested for growth by spotting serially diluted cells on medium with or without 1% arabinose. Images were acquired after incubation at 37°C for 18 h. Similar results were obtained in at least three independent experiments.

C-D. The predicted transmembrane (TM) domain in the amino terminal end of Aeg1 is required for its activity. A diagram illustrating the location of the TM domain which is

predicted to span between the 7th and the 29th residues of Aeg1 **(C)**. Cells harboring differentially regulated HA-Aeg1 and HA-Aeg1$^{\Delta TM}$ spotted onto LB agar supplemented with 0.5 mM IPTG or 1% ara, images were acquired after 18 h incubation at 37ºC **(D upper two panels)**. The expression of the Aeg1 and Aeg1$^{\Delta TM}$ were examined by immunoblotting with the HA-specific antibody. The metabolic enzyme isocitrate dehydrogenase (ICDH) was probed as a loading control **(D, lower two panels)**. Similar results were obtained in three independent experiments.

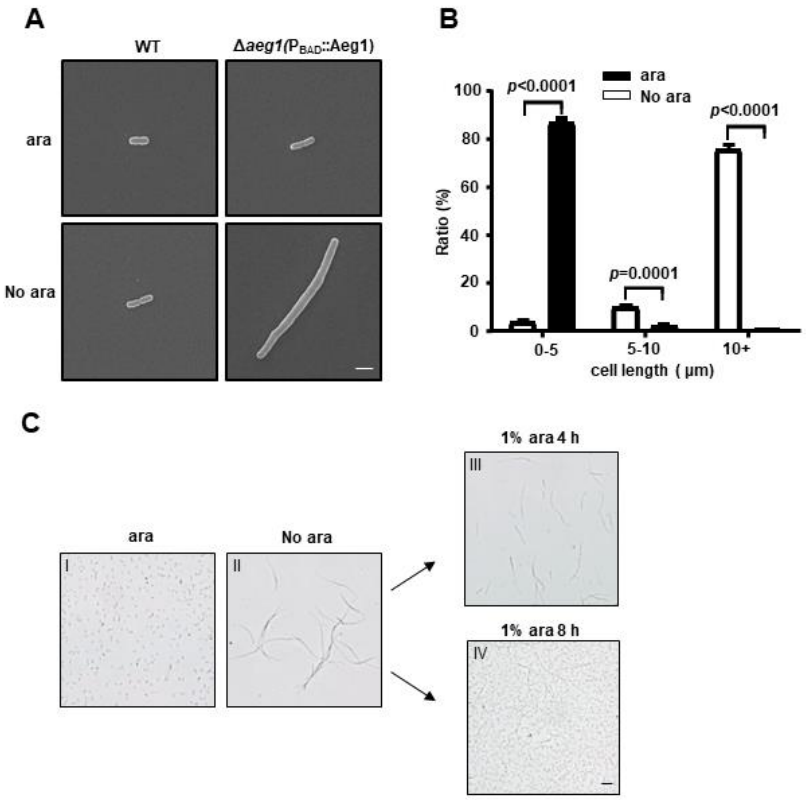


Fig. 2 Aeg1 deficiency causes cell elongation in *A. baumannii*.

A. Cell morphology of the wild-type and strain Δ*aeg1*(P_{BAD}::Aeg1) grown in medium with or without ara. The Δ*aeg1*(P_{BAD}::Aeg1) and the wild-type strains were grown in medium with or without ara for 18 h, samples were processed for scanning electron microscope imaging. Images shown are representative of three parallel cultures. Bar, 2 μm.

B-C. Expression of Aeg1 reversed the cell elongation phenotype caused by its depletion. Saturated bacterial cultures of Δ*aeg1*(P_{BAD}::Aeg1) diluted in fresh LB broth with (I) or without (II) ara were incubated for 18 h. The culture from the uninduced sample was split

into two subcultures, ara was added to one of the subcultures and the morphology of the cells was determined at 4 h (III) and 8 h (IV) post induction. Images are representative of three parallel cultures. Bar, 10 μm **(B)**. Quantitation of the cell length in samples differently expressing Aeg1. Cell length was categorized into groups of 0-5 μm, 5-10 μm, and more than 10 μm. At least 300 cells were counted for each sample **(C)**. Results shown were from the average of three independent experiments. Statistical analysis in each panel was performed by Student's *t* test.

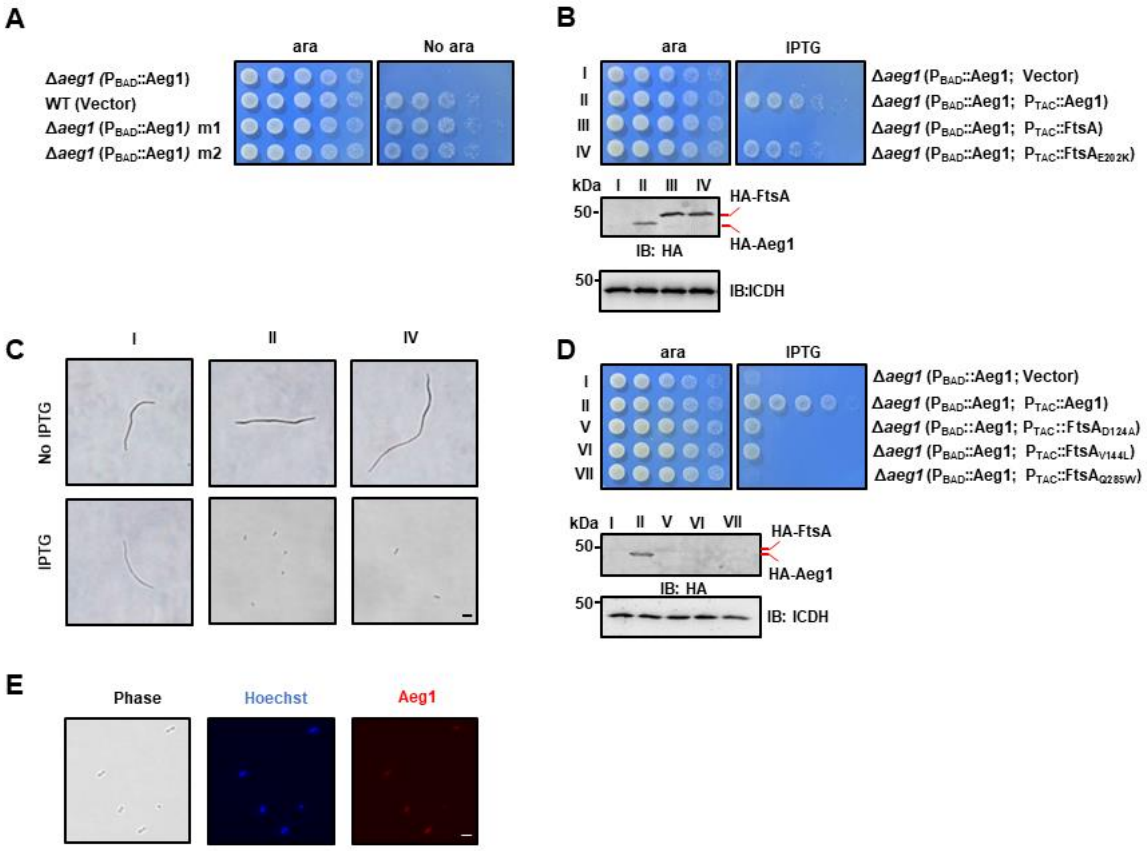


Fig. 3 Mutations in proteins involved in cell division bypass the requirement of Aeg1.

A. Isolation of two suppressor mutants that gained viability in the absence of Aeg1. Cells serially diluted with water were spotted onto LB agar with or without ara. Note that the Δ*aeg1*(P_{BAD}::Aeg1) strain (top row) cannot grow on medium without ara and the wild-type strain (2nd row) can grow on both conditions. Similar results were obtained in three independent experiments.

B. The $FtsA_{E202K}$ mutant suppressed the requirement of Aeg1. Cells of strains derived from Δ*aeg1*(P_{BAD}::*aeg1*) that harbored the vector (I), pHA-Aeg1 (II), pHA-FtsA (III), or pHA-$FtsA_{E202K}$ (IV) were spotted onto LB agar containing ara (left) or IPTG (right), Images were acquired after 18 h incubation at 37°C **(b, upper panels)**. Expression of Aeg1, FtsA or $FtsA_{E202K}$ in these strains were detected by immunoblotting with the HA-specific antibody after lysates of IPTG-induced cells being resolved by SDS-PAGE. ICDH was probed as a loading control **(b, lower panels)**. Similar results were obtained in three independent experiments.

C. The suppression mutants assumed normal cell morphology. Bacterial strains derived from Δ*aeg1*(P_{BAD}::*aeg1*) grown in LB broth containing ara for 18 h were diluted into fresh medium with the inducer and the cultures were induced with IPTG for 18 h prior to being processed for imaging. Images were representatives of three parallel cultures. Bar, 2 µm.

D. Additional FtsA mutants bypassed the need of Aeg1. Mutant $FtsA_{D124A}$, $FtsA_{V144A}$, or $FtsA_{Q285A}$ expressed from the IPTG-inducible P_{TAC} was introduced into strain Δ*aeg1*(P_{BAD}::Aeg1) and serially diluted cells of resulting strains were spotted onto LB agar supplemented with ara or IPTG. Images were acquired after incubation at 37°C for 18 h **(upper panels)**. Expression of Aeg1, $FtsA_{D124A}$, $FtsA_{V144A}$, and $FtsA_{Q285A}$ in these strains. Total protein of IPTG-induced cells resolved by SDS-PAGE and proteins transferred onto nitrocellulose membranes were detected by immunoblotting with the HA-specific antibody. ICDH was probed as a loading control **(lower panels).** Similar results were obtained in three independent experiments.

E. The Aeg1-mCherry fusion localizes to division constrictions. Wild-type *A. baumannii* harboring P_{BAD}::Aeg1-mCherry grown to the mid-log phase in LB broth containing 1% ara were processed for imaging. Bar, 2 µm. Images are representative of three parallel cultures.

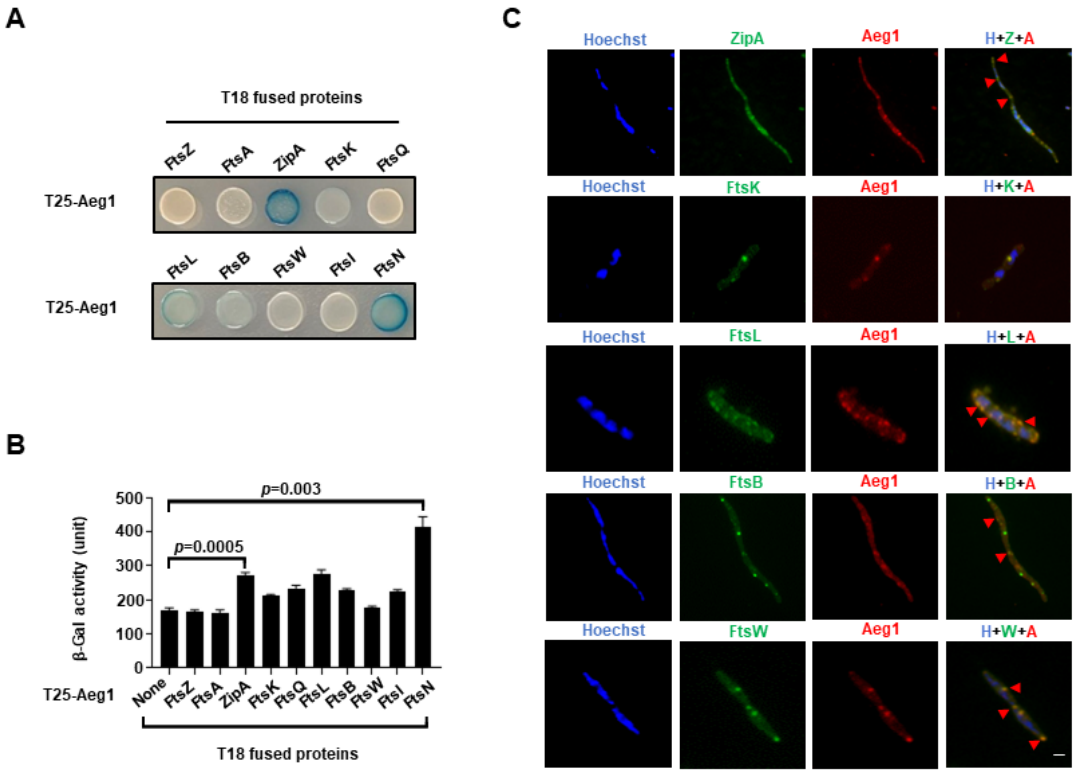


Fig. 4 Aeg1 interacts with multiple core proteins of the *A. baumannii* divisome.

A-B. Derivatives of strain *E. coli* BTH101 containing T18-Aeg1 and T25 fusion of the indicated proteins were spotted onto LB agar containing X-gal. Images were acquired after incubation for 18 h at 37°C **(A)**. Interactions determined by quantitative measurement of β-galactosidase activity **(B)**. Results shown were from three independent experiments. Statistical analysis was performed by Student's *t* test.

C. Aeg1 colocalized with a set of core divisome proteins. GFP fusion of ZipA, FtsK, FtsL, FtsB, or FtsW was expressed in strain Δ*aeg1*(pJL03::mCherry-Aeg1). Cells grown in LB broth without ara for 18 h were induced with IPTG to express the GFP fusions for 3 h prior to being processed for imaging. Red arrows indicate the sites of colocalization. Bar, 2 µm. Images are representative of three independent cultures.

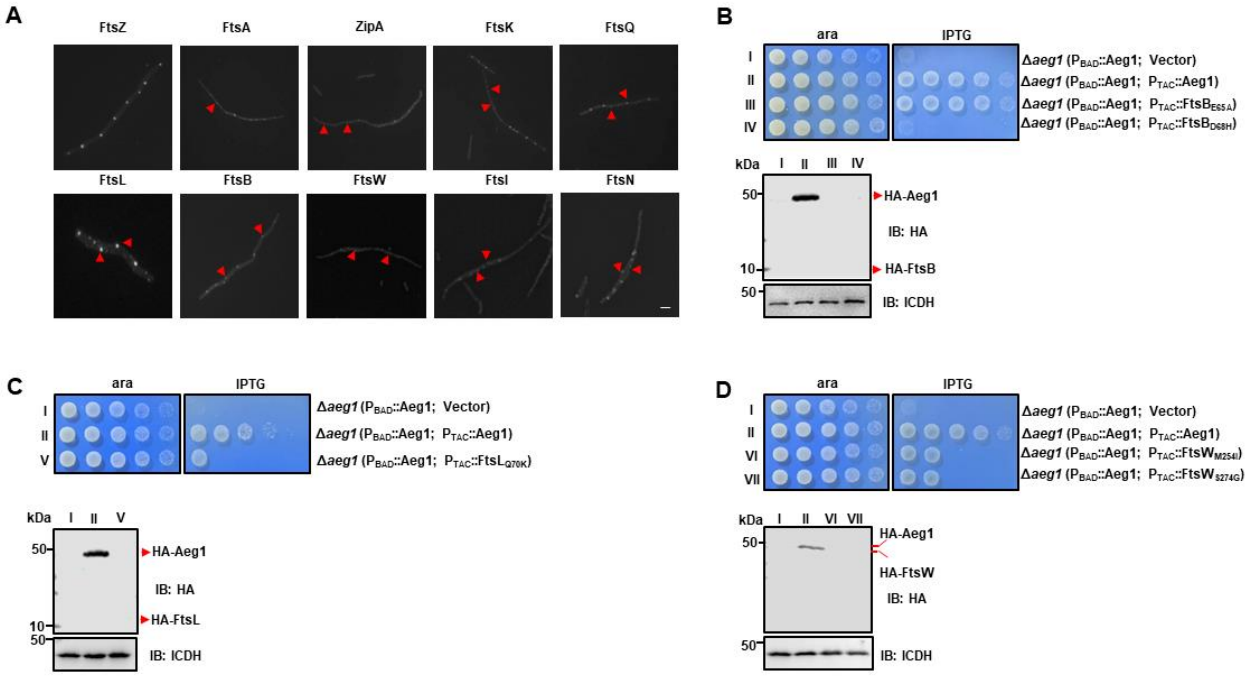
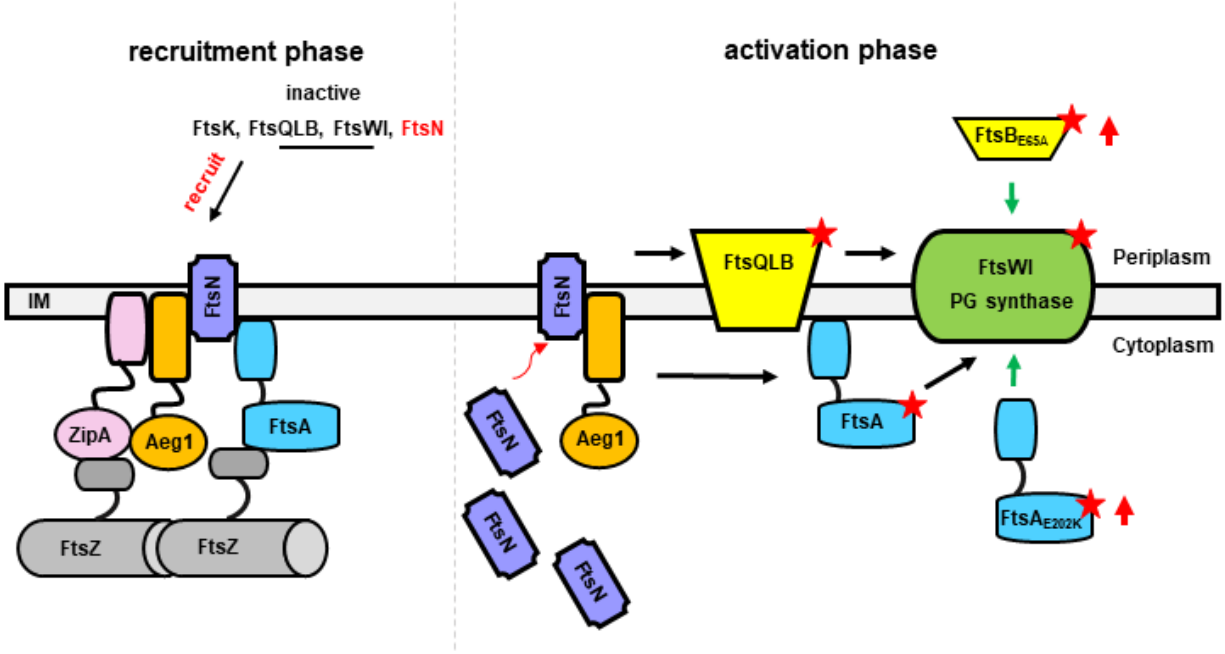


Fig. 5 Aeg1 dictates the cellular localization of core divisome proteins.

A. Aeg1 deficiency prevented core divisome proteins from localizing to the middle cell. Cells of derivatives of strain Δ*aeg1*(pJL03::mCherry-Aeg1) expressing GFP fusion of each of the divisome proteins from the P_{TAC} promoter grown in medium with ara were processed for imaging. The red arrows representative examples of the inability of fusion proteins to target to the septal ring. Bar, 2 µm. Images are representative of three parallel cultures.

B-D. A few dominant active mutants of FtsB and FtsW bypassed the need of Aeg1 by *A. baumannii.* Mutant $FtsB_{E65A}$ **(B)**, $FtsB_{D68H}$ **(B)**, $FtsL_{Q70K}$ **(C)**, $FtsW_{M254I}$ **(D)**, or $FtsW_{S274G}$ **(D)** was expressed from the IPTG-inducible promoter P_{TAC} in strain Δ*aeg1*(pJL03::Aeg1). Serially diluted cells were spotted onto LB agar containing ara or IPTG. Images were acquired after incubation at 37°C for 18 h **(B-D)**. Similar results were obtained in three independent experiments. The expression of the protein was probed with the HA-specific antibody after IPTG induction **(B-D)**. ICDH was probed as a loading control.



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721 **Fig. 6 A model for the function of Aeg1 in cell division of *A. baumannii*.** In the early
722 stages of Z-ring assembly, anchor proteins FtsA and ZipA tether FtsZ to the inner face of
723 the plasma membrane. In the initial phase of cell division, a small amount of FtsN is
724 recruited to the divisome in a FtsA-dependent manner **(left, recruitment phase)** (62).
725 The Aeg1-ZipA-FtsN complex acts as a dynamic scaffold for recruiting downstream of
726 Fts proteins. Once more FtsN is recruited to the divisome, it will activate both FtsA and
727 the FtsQLB complex, which in turn activates FtsI in the periplasm (35). Note that
728 constitutively active form of FtsA (FtsA*) acts on FtsW in the cytoplasm (31) so did the
729 hyperactive mutants $FtsA_{E202K}$ or $FtsB_{E65A}$. These mutants all bypassed the need of
730 Aeg1 **(right, activation phase)**. Constitutively active mutants were indicated by a star.
731 The red arrows next to $FtsA_{E202K}$ or $FtsB_{E65A}$ indicate overexpression of these mutants.

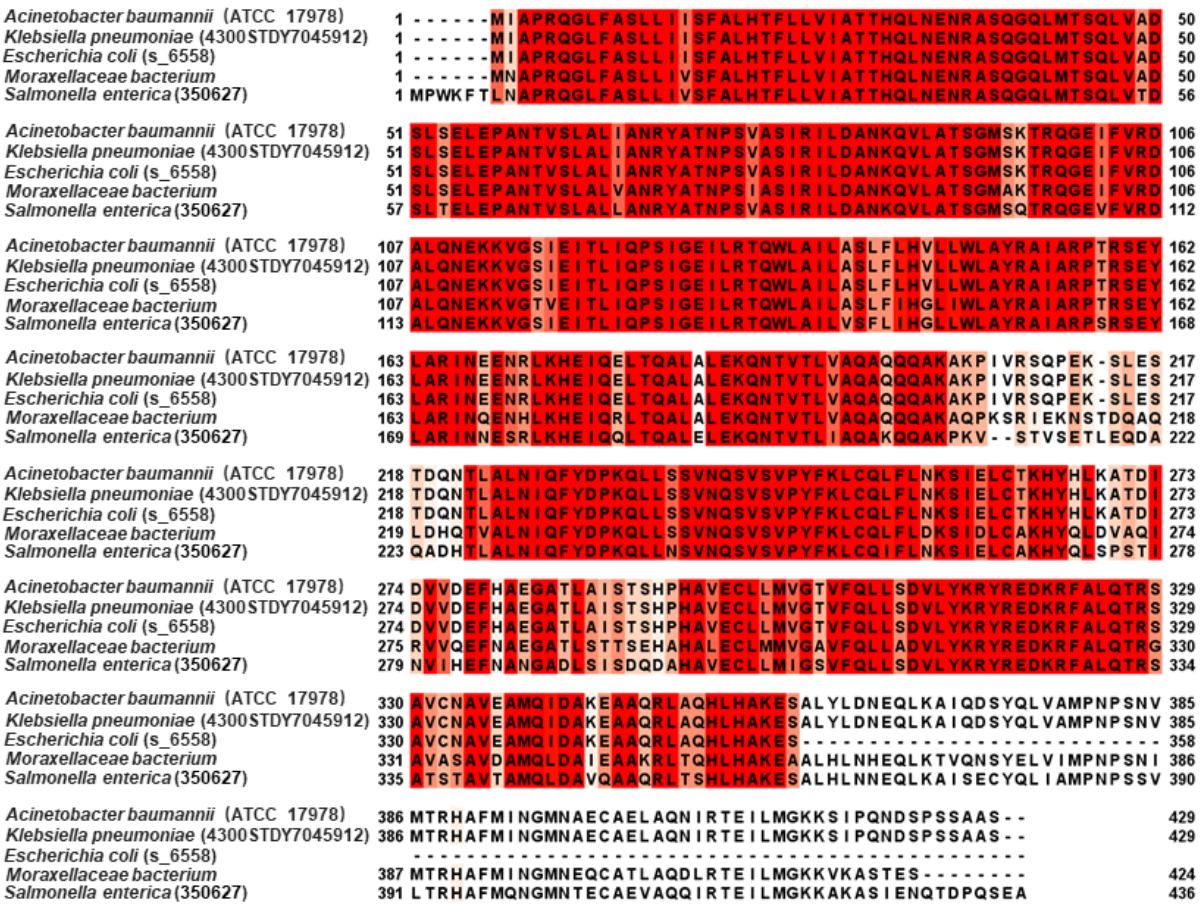

Fig. S1 Alignment of Aeg1 homologs from a few Gram-negative bacteria. Aeg1 of *A. baumannii* and its homologs from a member of the *Moraxellaceae* family, *E. coli* (strain s_6558), *Klebsiella pneumoniae* (strain 4300STDY7045912), and *Salmonella enterica* (strain 350627) were compared with Jalview. Homology from high to low was presented in dark red, orange, yellow, light yellow, or no highlight.

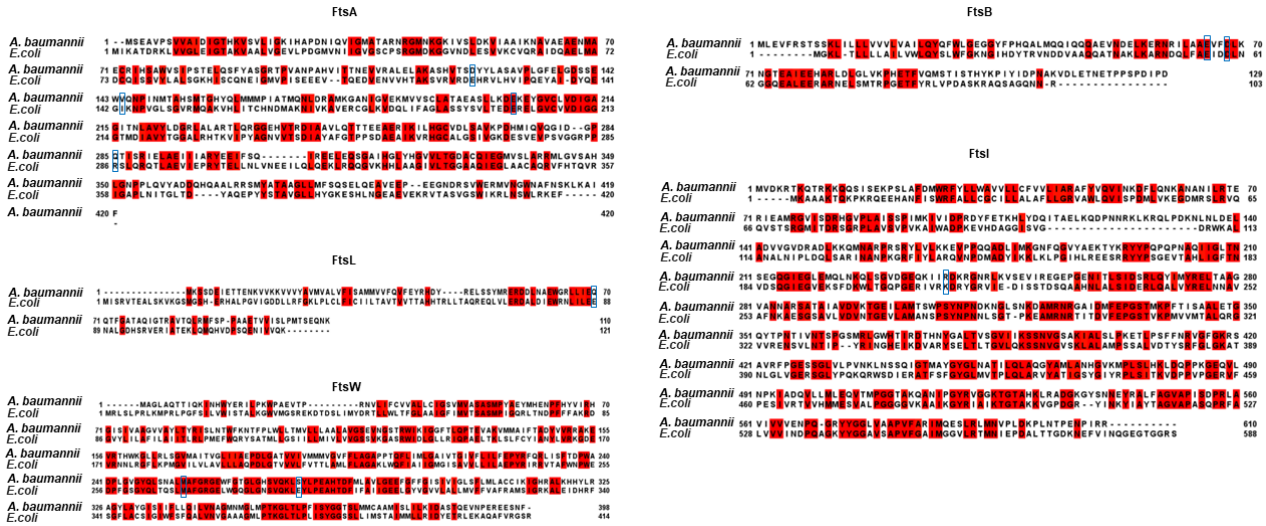

Fig. S2 Alignment of Fts proteins between *A. baumannii* and *E. coli*. The FtsA, FtsB, FtsL, FtsW, and FtsI proteins from *A. baumannii* and *E. coli* were compared using Jalview. The residues highlighted by blue boxes indicate the site of dominant active sites in *E. coli* proteins, and corresponding mutations were made in their *A. baumannii* counterparts.

Table S1 List of 10 candidate essential genes to be deleted

Gene accession no.	Size (bp)	Gene function
A1S_0137	627	hypothetical
A1S_1989	351	hypothetical
A1S_1990	285	hypothetical
A1S_2112	726	hypothetical
A1S_2249	651	hypothetical
A1S_2272	459	hypothetical
A1S_2440	735	hypothetical
A1S_2797	576	hypothetical
A1S_3014	351	hypothetical
A1S_3387	1290	hypothetical

Table S2 Localization of core divisome proteins in Aeg1 deficiency strain

Gene	Protein	No. of cells	Proteins displayed midcell mistargeting
A1S_3331	FtsZ	300	-
A1S_3332	FtsA	300	+
A1S_0798	ZipA	300	++
A1S_0876	FtsK	300	+
A1S_3333	FtsQ	300	+
A1S_3205	FtsL	300	++
A1S_1896	FtsB	300	++
A1S_0246	FtsW	300	++
A1S_ 3204	FtsI	300	++
A1S_0137	FtsN	300	++

++, indicates >50% proteins cannot be located in the middle cells.

+, indicates 5% to 50% proteins cannot be located in the middle cells.

-, indicates <5% proteins cannot be located in the middle cells.

Table S4 Bacterial strains, plasmids and primers used in this study

Strains or plasmids	Source	Identifier
A. baumannii		
ATCC 17978	(54)	N/A
17978Δ*A1S_0137*	This study	N/A
17978Δ*A1S_1989*	This study	N/A
17978Δ*A1S_1990*	This study	N/A
17978Δ*A1S_2112*	This study	N/A
17978Δ*A1S_2249*	This study	N/A
17978Δ*A1S_2272*	This study	N/A
17978Δ*A1S_2440*	This study	N/A
17978Δ*A1S_2797*	This study	N/A
17978Δ*A1S_3014*	This study	N/A
17978Δ*A1S_3387*	This study	N/A
E. coli		
DH5α	(63)	N/A
BTH101	(32)	N/A
MT607 (pRK600)	(57)	N/A
Plasmids		
pJL03	(24)	N/A
pJL05	This study	N/A
pSR47s	(25)	N/A
pJL03::A1S_0137 (P_{BAD}::A1S_0137)	This study	N/A
pJL03::A1S_1989 (P_{BAD}::A1S_1989)	This study	N/A
pJL03::A1S_1990 (P_{BAD}::A1S_1990)	This study	N/A
pJL03::A1S_2112 (P_{BAD}::A1S_2112)	This study	N/A
pJL03::A1S_2249 (P_{BAD}::A1S_2249)	This study	N/A
pJL03::A1S_2272 (P_{BAD}::A1S_2272)	This study	N/A
pJL03::A1S_2440 (P_{BAD}::A1S_2440)	This study	N/A
pJL03::A1S_2797 (P_{BAD}::A1S_2797)	This study	N/A

pJL03::A1S_3014 (P_{BAD}::A1S_3014)	This study	N/A
pJL03::Aeg1 (P_{BAD}::A1S_3387)	This study	N/A
pJL03::mCherry-Aeg1 (P_{BAD}::mCherry-Aeg1)	This study	N/A
pJL05::Aeg1 (P_{TAC}::Aeg1)	This study	N/A
pJL05::Aeg1$^{\Delta TM}$ (P_{TAC}::Aeg1$^{\Delta TM}$)	This study	N/A
pJL05::FtsA (P_{TAC}::FtsA)	This study	N/A
pJL05::FtsA$_{E202K}$ (P_{TAC}::FtsA$_{E202K}$)	This study	N/A
pJL05::FtsA$_{D124A}$ (P_{TAC}::FtsA$_{D124A}$)	This study	N/A
pJL05::FtsA$_{V144L}$ (P_{TAC}::FtsA$_{V144L}$)	This study	N/A
pJL05::FtsA$_{Q285W}$ (P_{TAC}::FtsA$_{Q285W}$)	This study	N/A
pJL05::FtsL$_{Q70K}$ (P_{TAC}::FtsL$_{Q70K}$)	This study	N/A
pJL05::FtsB$_{E65A}$ (P_{TAC}::FtsB$_{E65A}$)	This study	N/A
pJL05::FtsB$_{D68H}$ (P_{TAC}::FtsB$_{D68H}$)	This study	N/A
pJL05::FtsW$_{M254I}$ (P_{TAC}::FtsW$_{M254I}$)	This study	N/A
pJL05::FtsW$^{M}{}_{254I}$ (P_{TAC}::FtsW$_{M254I}$)	This study	N/A
pJL05::FtsW$_{S274G}$ (P_{TAC}::FtsW$_{S274G}$)	This study	N/A
pJL05::eGFP-FtsZ (P_{TAC}::eGFP-FtsZ)	This study	N/A
pJL05::eGFP-FtsA (P_{TAC}::eGFP-FtsA)	This study	N/A
pJL05::eGFP-ZipA (P_{TAC}::eGFP-ZipA)	This study	N/A
pJL05::eGFP-FtsK (P_{TAC}::eGFP-FtsK)	This study	N/A
pJL05::eGFP-FsQ (P_{TAC}::eGFP-FtsQ)	This study	N/A
pJL05::eGFP-FtsL (P_{TAC}::eGFP-FtsL)	This study	N/A
pJL05::eGFP-FtsB (P_{TAC}::eGFP-FtsB)	This study	N/A
pJL05::eGFP-FtsW (P_{TAC}::eGFP-FtsW)	This study	N/A
pJL05::eGFP-FtsI (P_{TAC}::eGFP-FtsI)	This study	N/A
pJL05::eGFP-FtsN (P_{TAC}::eGFP-FtsN)	This study	N/A
pKT25	(64)	N/A
pUT18C-Flag	This study	N/A
pKT25::Aeg1	This study	N/A
pUT18C -Flag::FtsZ	This study	N/A

pUT18C -Flag::FtsA	This study	N/A
pUT18C-Flag::ZipA	This study	N/A
pUT18C-Flag::FtsK	This study	N/A
pUT18C-Flag::FtsQ	This study	N/A
pUT18C-Flag::FtsL	This study	N/A
pUT18C-Flag::FtsB	This study	N/A
pUT18C-Flag::FtsW	This study	N/A
pUT18C-Flag::FtsI	This study	N/A
pUT18C-Flag::FtsN	This study	N/A

761

Primers	**Sequence (Restriction enzyme sites are underlined)**	**Note**
pCL1001	ctgggatccgtgtttggcaaaacgcaa	*A1S_0137 5*F *BamH*I
pCL1002	ctggtcgacttatttgcgtttaatcac	*A1S_0137* 3R *Sal*I
pCL1003	ctggagctcaaacacttgatcaacgcg	*A1S_0137* up 5F *Sac*I KO
pCL1004	ctgggatcccttgttaggtctttcagatacacc	*A1S_0137* up 3R *BamH*I KO
pCL1005	ctgggatcctttgcagcatagcggtattga	*A1S_0137* down 5F *BamH*I KO
pCL1006	ctggtcgacgaaattgattttcataccaaccgag	*A1S_0137* down 3R *Sal*I KO
pCL1007	ctggcggccgcgcaataggctcatgatacaactgac	*A1S_1989 5*F*Not*I
pCL1008	ttcagggcccgctggttagattggcttggg	*A1S_1989* 3R *Apa*I
pCL1009	aacggggcccgatactgaactcatccggtc	*A1S_1989* up 5F *Apa*I KO
pCL1010	ctgggatcctgcacaaggtggtattgctgcaatt	*A1S_1989* up 3R *BamH*I KO
pCL1011	ctgggatccgtgaaaactgtactcgtt	*A1S_1989* down 5F *BamH*I KO
pCL1012	ctggtcgacctaccaatataagacatg	*A1S_1989* down 3R *Sal*I KO
pCL1013	ctgggatccatgacgcaatcaactctttatc	*A1S_1990 5*F *BamH*I
pCL1014	ctggtcgacttatttcaaagaaatgcatcgattaaatt	*A1S_1990* 3R *Sal*I
pCL1015	ctggagctcgaacgtacataccagagatgtattc	*A1S_1990* up 5F *Sac*I KO
pCL1016	ctgggatccatggtgataagaagcttgcac	*A1S_1990* up 3R *BamH*I KO
pCL1017	ctgggatccgcggatctggttttacaatttaatc	*A1S_1990* down 5F *BamH*I KO
pCL1018	ctgctcgagggccactcgctattgtgg	*A1S_1990* down 3R *Xho*I KO

pCL1019	ctggatccatggtattaatatttgctgc	*A1S_2112* 5F *BamH*I
pCL1020	ctggtcgactcatactcgcaaagacaa	*A1S_2112* 3R *Sal*I
pCL1021	ctggagctcagtcgagtctctaattgaaaaatacg	*A1S_2112* up 5F *Sac*I KO
pCL1022	ctggatccagaaaccagaacactgcac	*A1S_2112* up 3R *BamH*I KO
pCL1023	ctggatccatattttactcaaagattctccggc	*A1S_2112* down 5F *BamH*I KO
pCL1024	ctggtcgacagcttactttttcgattaattggtattaattc	*A1S_2112* down 3R *Sal*I KO
pCL1025	ctggatccatgattgggcagcaaaga	*A1S_2249* 5F *BamH*I
pCL1026	ctggtcgacctactcattgttatcttg	*A1S_2249* 3R *Sal*I
pCL1027	ctggagctcttaaagaaacttcgaaatcgtcct	*A1S_2249* up 5F *Sac*I KO
pCL1028	ctggatccgtctattcctaaagttgccagtata	*A1S_2249* up 3R *BamH*I KO
pCL1029	ctggatcccttaagaaaagattgtggcaac	*A1S_2249* down 5F *BamH*I KO
pCL1030	ctggtcgactgcaatgaagtgttattcatcctt	*A1S_2249* down 3R *Sal*I KO
pCL1031	ctggatccatgaaactcgcagaagca	*A1S_2272* 5F *BamH*I
pCL1032	ctggtcgacttaattgattagatcaatt	*A1S_2272* 3R *Sal*I
pCL1033	ctggcggccgcgcagtgaactgtcaccataac	*A1S_2272* up 5F *Not*I KO
pCL1034	tcagggccctttttgttgattgcttcgaagtaaaag	*A1S_2272* up 3R *Apa*I KO
pCL1035	acggggcccgtaaaaattcaggctgctaactg	*A1S_2272* down 5F *Apa*I KO
pCL1036	ctggatccatggctgaatggtaacttgaattt	*A1S_2272* down 3R *BamH*I KO
pCL1037	ctggatccatggtggagttacccttc	*A1S_2440* 5F *BamH*I
pCL1038	ctggtcgacttagataacttggtactg	*A1S_2440* 3R *Sal*I
pCL1039	ctgctggcggccgctgcagattttattgcaacaggt	*A1S_2440* up 5F *Not*I KO
pCL1040	tcagggcccgcgaacattcaaggcttgt	*A1S_2440* up 3R *Apa*I KO
pCL1041	acggggccccaggatattcaagcacttgct	*A1S_2440* down 5F *Apa*I KO
pCL1042	ctggatcctcgtgtggctcaatttgagt	*A1S_2440* down 3R *BamH*I KO
pCL1043	ctggatccatgaccgcgaaaactttatatg	*A1S_2797* 5F *BamH*I
pCL1044	ctggtcgacttataaagttttcggttcacctaca	*A1S_2797* 3R *Sal*I
pCL1045	ctggagctcttgacagctttatttgttagccaac	*A1S_2797* up 5F *Sac*I KO
pCL1046	ctggatccaggaacaggctgaagcg	*A1S_2797* up 3R *BamH*I KO
pCL1047	ctggatcccgtaagcatttgaaagaaagtgtag	*A1S_2797* down 5F *BamH*I KO
pCL1048	ctggtcgacatcatctttttaggtaagttaactgttaaa	*A1S_2797* down 3R *Sal*I KO

	gtc	
pCL1049	ctggatccatggaatataaaggaagttgtca	*A1S_3014* 5F *BamH*I
pCL1050	ctggtcgacttaaacagaacgcccatc	*A1S_3014* 3R *Sal*I
pCL1051	ctggatccgcgcgcttaactgcgagac	*A1S_3014* up 5F *Sac*I KO
pCL1052	ctggaattcggcaaactttacctgaccacaatgaca	*A1S_3014* up 3R *EcoR*I KO
pCL1053	ctggaattcttagaaaagataaaaataaattattttgat gggcgttctg	*A1S_3014* down 5F *EcoR*I KO
pCL1054	ctggtcgacaccatgagcgagatatgcaccc	*A1S_3014* down 3R *Sal*I KO
pCL1055	ctggatccatgattgcgcctagacaagg	*aeg1* 5F *BamH*I
pCL1056	ctggtcgacttaagatgctgcactactcgg	*aeg1* 3R *Sal*I
pCL1057	ctggagctcacggaaactttgctggaa	*aeg1* up 5F *Sac*I KO
pCL1058	ctggatccaatgatcagtaggctagc	*aeg1* up 3R *BamH*I KO
pCL1059	ctggatcctcaattcctcaaaatgac	*aeg1* down 5F *BamH*I KO
pCL1060	ctggtcgacaaaaatttctaaatctgcg	*aeg1* down 3R *Sal*I KO
pCL1061	ctggatccatggcctcatttgaatttatag	*ftsZ* 5F *BamH*I
pCL1062	ctggtcgacttacttacgttgctgatttttca	*ftsZ* 3R *Sal*I
pCL1063	ctggatccatgagtgaagctgttccct	*ftsA* 5F *BamH*I
pCL1064	ctggtcgacctaaaaaatggctttaagtttgc	*ftsA* 3R *Sal*I
pCL1065	ctggatccatggaaatcaatacgattattg	*zipA* 5F *BamH*I
pCL1066	ctggtcgacctaggctgttgcctgtgctg	*zipA* 3R *Sal*I
pCL1067	ctggatccatgactgcggtgtcaagt	*ftsK* 5F *BamH*I
pCL1068	ctgctcgagttaaactaaaatatcgcgctt	*ftsK* 3R *Xho*I
pCL1069	ctggatccatggcacaacttccggca	*ftsQ* 5F *BamH*I
pCL1070	ctggtcgacttatggctttgcttttgtaccacct	*ftsQ* 3R *Sal*I
pCL1071	ctggatccatgaaaagcagtgatgaaatc	*ftsL* 5F *BamH*I
pCL1072	ctggtcgacttacttattttgctctgaggt	*ftsL* 3R *Sal*I
pCL1073	ctggatccatgttagaagtatttcgttc	*ftsB* 5F *BamH*I
pCL1074	ctggtcgacttaatctgggatgtctggtga	*ftsB* 3R *Sal*I
pCL1075	ctggatccatggcaggcttagctcag	*ftsW* 5F *BamH*I
pCL1076	ctggtcgacttagaagtttgattcttccctctcag	*ftsW* 3R *Sal*I

pCL1077	ctgggatccatggtagataagcgaacaaag	*ftsI* 5F *BamH*I
pCL1078	ctggtcgacttacctgcgaataggattttc	*ftsI* 3R *Sal*I
pCL1079	ctgggatccatgcaccagctcaatgaaaacc	*aeg1*$^{\Delta tm}$ 5F *BamH*I
pCL1080	ctgggtaccttaagatgctgcactactcgg	*aeg1* 3R *Kpn*I
pCL1081	ctgggatccatggtgagcaagggcgag	*mCherry* 5F *BamH*I
pCL1082	ctgagatctcttgtacagctcgtccatgc	*mCherry 3*R *Bgl*II
pCL1083	ctgggatccatggtgagcaagggcg	*gfp* 5F *BamH*I
pCL1084	ctgagatctcttgtacagctcgtccatgcc	*gfp 3*R *Bgl*II
pCL1085	ccacgaccaaaagctattaacgcatttgataactgataacct	*ftsW*^{M254I} 5F
pCL1086	aggttatcagttatcaaatgcgttaatagcttttggtcgtgg	*ftsW*^{M254I} 3R
pCL1087	gtatgcgcttctggtaaatagccaagcttttgaacactatgccc	*ftsW*^{S274G} 5F
pCL1088	gggcatagtgttcaaaagcttggctatttaccagaagcgcatac	*ftsW*^{S274G} 3R
pCL1089	gtcgcaccaaatgtttgtttctcaatcaataaacgcccc	*ftsL*^{Q70K} 5F
pCL1090	ggggcgtttattgattgagaaacaaacatttggtgcgac	*ftsL*^{Q70K} 3R
pCL1091	gcactcgctagataataggcagaagtcacatggcttg	*ftsA*^{D124A} 5F
pCL1092	caagccatgtgacttctgcctattatctagcgagtgc	*ftsA*^{D124A} 3R
pCL1093	catattgattgggttttgaagccattcagatgagtcacctta	*ftsA*^{V144L} 5F
pCL1094	taggtgactcatctgaatggcttcaaaacccaatcaatatg	*ftsA*^{V144L} 3R
pCL1095	caactcaattcggctaatcgtccacggaccatcaatacctgtac	*ftsA*^{Q285W} 5F
pCL1096	gtacagggtattgatggtccgtggacgattagccgaattgagttg	*ftsA*^{Q285W} 3R
pCL1097	cattctttaggtcgaaaactgcagctgccaaaatacg	*ftsB*^{E65A} 5F

	gttt	
pCL1098	aaaccgtattttggcagctgcagttttcgacctaaaga atg	*ftsB*^{E65A} 3R
pCL1099	cgtaccattctttaggtggaaaacttcagctgccaa	*ftsB*^{D68H} 5F
pCL1100	ttggcagctgaagttttccacctaaagaatggtacg	*ftsB*^{D68H} 3R
pCL1101	ctgacatgtcgagaaaaggccatc	pJL05 5F *Pci*I
pCL1102	cagggatccagcgtaatctggaacatcgtatgggtac atgggcagtcctcgg	pJL05 3R *BamH*I
pCL1103	tcgagggactacaaagacgatgacgacaagggatc cgatatcggtaccgagctcgaattcgtcgacat	pUT18C-Flag 5F
pCL1104	cgatgtcgacgaattcgagctcggtaccgatatcgga tcccttgtcgtcatcgtctttgtagtccc	pUT18C-Flag 3R

Table S3 Substitution mutations and insertion-deletion (InDel) mutations of M1 and M2 compared with *A. baumannii* strain ATCC 17978 genome sequence

Type	Chr	Start	END	Ref	Obs	Gene accession no.	M1	M2
SNV	CP00052	101398	101398	A	G	A1S_0081(dist=614)	hom	-
SNV	CP00052	101410	101410	T	C	A1S_0081(dist=626)	hom	-
SNV	CP00052	101515	101515	T	C	A1S_0081(dist=731)	hom	hom
SNV	CP00052	101587	101587	C	T	A1S_0081(dist=803)	hom	hom
SNV	CP00052	101642	101642	G	A	A1S_0081(dist=858)	hom	hom
SNV	CP00052	101665	101665	C	T	A1S_0081(dist=881)	hom	hom
SNV	CP00052	101677	101677	A	C	A1S_0081(dist=893)	-	hom
SNV	CP00052	101678	101678	C	T	A1S_0081(dist=894)	-	hom
SNV	CP00052	101680	101680	G	A	A1S_0081(dist=896)	-	hom
SNV	CP00052	102413	102413	A	G	A1S_0081(dist=1629)	hom	hom
SNV	CP00052	102444	102444	C	A	A1S_0081(dist=1660)	hom	hom
SNV	CP00052	102445	102445	G	C	A1S_0081(dist=1661)	hom	hom
SNV	CP00052	154871	154871	G	A	A1S_0129	-	het
SNV	CP00052	156961	156961	G	A	A1S_0131(dist=38);A	hom	hom
SNV	CP00052	165413	165413	C	T	A1S_0140	-	het
SNV	CP00052	202345	202345	G	A	A1S_0180	-	het
SNV	CP00052	225739	225739	C	T	A1S_0202	-	het
SNV	CP00052	230437	230437	T	C	A1S_0207(dist=79);A	het	het
SNV	CP00052	230448	230448	C	T	A1S_0207(dist=68);A	het	het
SNV	CP00052	230450	230450	T	C	A1S_0207(dist=66);A	het	het
SNV	CP00052	230466	230466	A	G	A1S_0207(dist=50);A	het	het
SNV	CP00052	230470	230470	G	A	A1S_0207(dist=46);A	het	het
SNV	CP00052	230487	230487	G	A	A1S_0207(dist=29);A	het	het
SNV	CP00052	230509	230509	C	A	A1S_0207(dist=7);A1	het	het
SNV	CP00052	230581	230581	G	A	A1S_0207	het	het
SNV	CP00052	230593	230593	C	T	A1S_0207	het	het
SNV	CP00052	230605	230605	G	A	A1S_0207	het	het
SNV	CP00052	230614	230614	T	A	A1S_0207	het	het
SNV	CP00052	230728	230728	C	T	A1S_0207	het	het
SNV	CP00052	230736	230736	C	A	A1S_0207	het	het
SNV	CP00052	230743	230743	T	C	A1S_0207	het	het
SNV	CP00052	230755	230755	A	G	A1S_0207	het	het
SNV	CP00052	230797	230797	T	C	A1S_0207	het	het
SNV	CP00052	230806	230806	A	T	A1S_0207	het	het
SNV	CP00052	230812	230812	C	T	A1S_0207	het	het
SNV	CP00052	230815	230815	C	T	A1S_0207	het	het
SNV	CP00052	230827	230827	T	C	A1S_0207	het	het
SNV	CP00052	230841	230841	T	C	A1S_0207	het	het
SNV	CP00052	230872	230872	C	T	A1S_0207	het	het
SNV	CP00052	230881	230881	C	T	A1S_0207	het	het
SNV	CP00052	232099	232099	G	A	A1S_0208,A1S_0209	het	het
SNV	CP00052	232103	232103	G	A	A1S_0208,A1S_0209	het	het
SNV	CP00052	232120	232120	C	T	A1S_0208,A1S_0209	het	het
SNV	CP00052	232176	232176	C	T	A1S_0208,A1S_0209	het	het
SNV	CP00052	232180	232180	A	C	A1S_0208,A1S_0209	het	het
SNV	CP00052	232845	232845	C	T	A1S_0209	het	het
SNV	CP00052	232887	232887	T	A	A1S_0209	het	het
SNV	CP00052	232908	232908	G	A	A1S_0209	het	het
SNV	CP00052	232948	232948	A	G	A1S_0209	het	het
SNV	CP00052	233013	233013	T	G	A1S_0209	het	het
SNV	CP00052	233022	233022	T	C	A1S_0209	het	het
SNV	CP00052	233099	233099	T	C	A1S_0209	het	het

SNV	CP00052	233123	233123	T	C	A1S_0209	het	het
SNV	CP00052	233159	233159	C	T	A1S_0210	het	het
SNV	CP00052	233162	233162	A	T	A1S_0210	het	het
SNV	CP00052	233165	233165	G	A	A1S_0210	het	het
SNV	CP00052	233186	233186	G	A	A1S_0210	het	het
SNV	CP00052	233216	233216	C	A	A1S_0210	het	het
SNV	CP00052	233258	233258	C	A	A1S_0210	het	het
SNV	CP00052	233259	233259	G	A	A1S_0210	het	het
SNV	CP00052	233288	233288	G	T	A1S_0210	het	het
SNV	CP00052	233318	233318	C	A	A1S_0210	het	het
SNV	CP00052	233354	233354	T	C	A1S_0210	het	het
SNV	CP00052	233360	233360	G	A	A1S_0210	het	het
SNV	CP00052	233381	233381	C	T	A1S_0210	het	het
SNV	CP00052	233382	233382	C	A	A1S_0210	het	het
SNV	CP00052	233399	233399	A	G	A1S_0210	het	het
SNV	CP00052	233417	233417	C	T	A1S_0210	het	het
SNV	CP00052	233420	233420	G	A	A1S_0210	het	het
SNV	CP00052	233435	233435	C	T	A1S_0210	het	het
SNV	CP00052	233456	233456	C	G	A1S_0210	het	het
SNV	CP00052	233457	233457	T	C	A1S_0210	het	het
SNV	CP00052	233483	233483	A	G	A1S_0210	het	het
SNV	CP00052	233492	233492	T	A	A1S_0210	het	het
SNV	CP00052	233495	233495	G	A	A1S_0210	het	het
SNV	CP00052	233534	233534	A	G	A1S_0210	het	het
SNV	CP00052	233537	233537	G	A	A1S_0210	het	het
SNV	CP00052	233555	233555	G	T	A1S_0210	het	het
SNV	CP00052	233579	233579	C	T	A1S_0210	het	het
SNV	CP00052	233588	233588	A	G	A1S_0210	het	het
SNV	CP00052	233594	233594	C	A	A1S_0210	het	het
SNV	CP00052	233609	233609	C	A	A1S_0210	het	het
SNV	CP00052	233612	233612	A	T	A1S_0210	het	het
SNV	CP00052	233615	233615	C	T	A1S_0210	het	het
SNV	CP00052	233642	233642	G	A	A1S_0210	het	het
SNV	CP00052	233660	233660	T	A	A1S_0210	het	het
SNV	CP00052	233732	233732	T	C	A1S_0210	het	het
SNV	CP00052	233753	233753	A	G	A1S_0210	het	het
SNV	CP00052	233777	233777	C	A	A1S_0210	het	het
SNV	CP00052	233789	233789	A	G	A1S_0210	het	het
SNV	CP00052	233816	233816	G	C	A1S_0210	het	het
SNV	CP00052	233849	233849	G	A	A1S_0210	het	het
SNV	CP00052	233855	233855	A	G	A1S_0210	het	het
SNV	CP00052	233899	233899	A	T	A1S_0210	het	het
SNV	CP00052	233924	233924	T	C	A1S_0210	het	het
SNV	CP00052	233927	233927	C	T	A1S_0210	het	het
SNV	CP00052	233968	233968	A	G	A1S_0210	het	het
SNV	CP00052	233969	233969	G	A	A1S_0210	het	het
SNV	CP00052	233975	233975	T	A	A1S_0210	het	het
SNV	CP00052	234041	234041	G	A	A1S_0210	het	het
SNV	CP00052	234053	234053	T	G	A1S_0210	het	het
SNV	CP00052	234056	234056	A	G	A1S_0210	het	het
SNV	CP00052	234069	234069	A	C	A1S_0210	het	het
SNV	CP00052	234121	234121	C	A	A1S_0210	het	het
SNV	CP00052	234140	234140	T	A	A1S_0210	het	het
SNV	CP00052	234182	234182	T	C	A1S_0210	het	het
SNV	CP00052	234230	234230	C	T	A1S_0210	het	het
SNV	CP00052	234245	234245	C	T	A1S_0211,A1S_0212	het	het
SNV	CP00052	234246	234246	A	G	A1S_0211,A1S_0212	het	het
SNV	CP00052	234262	234262	C	T	A1S_0211	het	het

SNV	CP00052	234327	234327	T	C	A1S_0211	het	het
SNV	CP00052	234334	234334	A	C	A1S_0211	-	het
SNV	CP00052	234372	234372	C	A	A1S_0211	het	het
SNV	CP00052	273249	273249	G	A	A1S_0246	-	het
SNV	CP00052	289905	289905	C	T	A1S_0264	-	het
SNV	CP00052	459328	459328	A	T	A1S_0421,A1S_0422	hom	hom
SNV	CP00052	521304	521304	G	A	A1S_0480	het	-
SNV	CP00052	645133	645133	C	T	A1S_3504	het	-
SNV	CP00052	686510	686510	C	A	A1S_0628	hom	hom
SNV	CP00052	763287	763287	G	A	A1S_0649	-	hom
SNV	CP00052	763567	763567	C	T	A1S_0649	hom	hom
SNV	CP00052	791352	791352	T	C	A1S_0666	hom	hom
SNV	CP00052	791353	791353	C	T	A1S_0666	hom	hom
SNV	CP00052	791357	791357	G	C	A1S_0666	hom	hom
SNV	CP00052	792584	792584	C	T	A1S_0666,A1S_0667	-	hom
SNV	CP00052	806621	806621	T	G	A1S_0677(dist=5990)	het	het
SNV	CP00052	860357	860357	C	T	A1S_0729	-	hom
SNV	CP00052	877431	877431	G	A	A1S_0742	het	het
SNV	CP00052	877440	877440	C	T	A1S_0742	het	het
SNV	CP00052	877443	877443	T	C	A1S_0742	het	het
SNV	CP00052	877451	877451	C	A	A1S_0742	hom	hom
SNV	CP00052	877517	877517	T	C	A1S_0742	het	het
SNV	CP00052	877518	877518	T	A	A1S_0742	het	het
SNV	CP00052	877554	877554	G	A	A1S_0742	het	het
SNV	CP00052	877617	877617	C	T	A1S_0742	het	het
SNV	CP00052	877650	877650	T	A	A1S_0742	het	het
SNV	CP00052	877653	877653	C	T	A1S_0742	het	het
SNV	CP00052	877656	877656	G	A	A1S_0742	het	het
SNV	CP00052	877659	877659	T	G	A1S_0742	het	het
SNV	CP00052	877661	877661	G	C	A1S_0742	het	het
SNV	CP00052	877668	877668	G	A	A1S_0742	het	het
SNV	CP00052	877671	877671	C	T	A1S_0742	het	het
SNV	CP00052	877675	877675	T	C	A1S_0742	het	het
SNV	CP00052	877677	877677	G	A	A1S_0742	het	het
SNV	CP00052	877678	877678	A	G	A1S_0742	het	het
SNV	CP00052	877679	877679	A	G	A1S_0742	het	het
SNV	CP00052	877681	877681	G	C	A1S_0742	het	het
SNV	CP00052	877683	877683	C	G	A1S_0742	het	het
SNV	CP00052	877683	877683	C	T	A1S_0742	het	het
SNV	CP00052	877685	877685	A	G	A1S_0742	het	het
SNV	CP00052	877686	877686	T	C	A1S_0742	het	het
SNV	CP00052	877689	877689	T	C	A1S_0742	het	het
SNV	CP00052	877692	877692	G	C	A1S_0742	het	het
SNV	CP00052	877695	877695	C	T	A1S_0742	het	het
SNV	CP00052	877701	877701	G	A	A1S_0742	het	het
SNV	CP00052	877704	877704	C	T	A1S_0742	het	het
SNV	CP00052	877707	877707	C	T	A1S_0742	het	het
SNV	CP00052	877710	877710	C	T	A1S_0742	-	het
SNV	CP00052	877722	877722	C	A	A1S_0742	-	het
SNV	CP00052	877722	877722	C	G	A1S_0742	het	-
SNV	CP00052	877759	877759	G	A	A1S_0742	het	het
SNV	CP00052	877760	877760	T	C	A1S_0742	het	het
SNV	CP00052	877762	877762	A	T	A1S_0742	het	het
SNV	CP00052	877766	877766	C	A	A1S_0742	het	het
SNV	CP00052	877831	877831	A	G	A1S_0742	het	het
SNV	CP00052	877878	877878	G	A	A1S_0742	het	het
SNV	CP00052	877908	877908	C	T	A1S_0742	-	het
SNV	CP00052	1074992	1074992	C	A	A1S_0924(dist=105);	hom	hom

SNV	CP00052´	1076891	1076891	G	T	A1S_0927	hom	hom
SNV	CP00052´	1093717	1093717	G	A	A1S_0942,A1S_0943	hom	hom
SNV	CP00052´	1147577	1147577	C	A	A1S_0990	het	het
SNV	CP00052´	1147579	1147579	C	T	A1S_0990	het	het
SNV	CP00052´	1147595	1147595	T	C	A1S_0990	het	het
SNV	CP00052´	1147597	1147597	A	G	A1S_0990	het	het
SNV	CP00052´	1148509	1148509	T	C	A1S_0990	het	het
SNV	CP00052´	1148510	1148510	C	A	A1S_0990	het	het
SNV	CP00052´	1148515	1148515	A	C	A1S_0990	het	het
SNV	CP00052´	1148518	1148518	C	T	A1S_0990	het	het
SNV	CP00052´	1148521	1148521	T	G	A1S_0990	het	het
SNV	CP00052´	1148527	1148527	A	T	A1S_0990	het	het
SNV	CP00052´	1148532	1148532	G	A	A1S_0990	het	het
SNV	CP00052´	1148533	1148533	T	A	A1S_0990	het	het
SNV	CP00052´	1148540	1148540	C	A	A1S_0990	het	het
SNV	CP00052´	1148542	1148542	A	T	A1S_0990	het	het
SNV	CP00052´	1148545	1148545	A	T	A1S_0990	het	het
SNV	CP00052´	1148546	1148546	C	T	A1S_0990	het	het
SNV	CP00052´	1148548	1148548	C	A	A1S_0990	het	het
SNV	CP00052´	1148560	1148560	G	A	A1S_0990	het	het
SNV	CP00052´	1148569	1148569	T	C	A1S_0990	het	het
SNV	CP00052´	1148578	1148578	C	T	A1S_0990	het	het
SNV	CP00052´	1148581	1148581	A	C	A1S_0990	het	het
SNV	CP00052´	1148582	1148582	G	A	A1S_0990	het	het
SNV	CP00052´	1148593	1148593	T	C	A1S_0990	het	het
SNV	CP00052´	1148596	1148596	T	A	A1S_0990	het	het
SNV	CP00052´	1148600	1148600	G	C	A1S_0990	het	het
SNV	CP00052´	1148614	1148614	C	T	A1S_0990	het	het
SNV	CP00052´	1148638	1148638	G	C	A1S_0990	het	-
SNV	CP00052´	1148644	1148644	A	T	A1S_0990	het	-
SNV	CP00052´	1148650	1148650	A	G	A1S_0990	het	-
SNV	CP00052´	1148653	1148653	A	G	A1S_0990	het	-
SNV	CP00052´	1151791	1151791	A	T	A1S_0993	hom	hom
SNV	CP00052´	1175602	1175602	T	G	A1S_1016	hom	hom
SNV	CP00052´	1250326	1250326	C	T	A1S_1073	het	het
SNV	CP00052´	1261971	1261971	G	T	A1S_1081(dist=28);A	hom	hom
SNV	CP00052´	1334078	1334078	A	C	A1S_3603	hom	-
SNV	CP00052´	1334126	1334126	C	A	A1S_3603	hom	hom
SNV	CP00052´	1334207	1334207	T	A	A1S_3604	hom	hom
SNV	CP00052´	1334272	1334272	A	T	A1S_3604	hom	hom
SNV	CP00052´	1334329	1334329	T	G	A1S_3604	hom	hom
SNV	CP00052´	1334365	1334365	T	A	A1S_3604	hom	hom
SNV	CP00052´	1405425	1405425	G	C	A1S_1200	hom	hom
SNV	CP00052´	1405545	1405545	C	T	A1S_1200	het	het
SNV	CP00052´	1405547	1405547	A	C	A1S_1200	het	het
SNV	CP00052´	1405569	1405569	C	A	A1S_1200	het	het
SNV	CP00052´	1405848	1405848	C	T	A1S_1200	het	-
SNV	CP00052´	1405860	1405860	T	C	A1S_1200	het	-
SNV	CP00052´	1405875	1405875	C	A	A1S_1200	het	het
SNV	CP00052´	1405931	1405931	C	T	A1S_1200	het	het
SNV	CP00052´	1405962	1405962	A	G	A1S_1200	het	het
SNV	CP00052´	1405965	1405965	C	G	A1S_1200	het	het
SNV	CP00052´	1406031	1406031	T	C	A1S_1200	het	het
SNV	CP00052´	1406034	1406034	A	G	A1S_1200	het	het
SNV	CP00052´	1406055	1406055	G	A	A1S_1200	het	het
SNV	CP00052´	1406094	1406094	G	A	A1S_1200	het	het
SNV	CP00052´	1406347	1406347	A	T	A1S_1201	hom	hom
SNV	CP00052´	1406359	1406359	T	C	A1S_1201	hom	hom

SNV	CP00052´	1406477	1406477	G	A	A1S_1201	-	het
SNV	CP00052´	1406519	1406519	G	A	A1S_1201	het	het
SNV	CP00052´	1406537	1406537	T	C	A1S_1201	het	het
SNV	CP00052´	1406570	1406570	C	A	A1S_1201	het	het
SNV	CP00052´	1406615	1406615	G	A	A1S_1201	het	het
SNV	CP00052´	1406630	1406630	C	T	A1S_1201	het	het
SNV	CP00052´	1406681	1406681	A	G	A1S_1201	het	het
SNV	CP00052´	1441387	1441387	A	T	A1S_1230,A1S_1231	hom	hom
SNV	CP00052´	1510161	1510161	C	T	A1S_1286	-	hom
SNV	CP00052´	1512001	1512001	C	T	A1S_1288	het	het
SNV	CP00052´	1512056	1512056	G	A	A1S_1288	het	het
SNV	CP00052´	1512079	1512079	C	T	A1S_1288	het	het
SNV	CP00052´	1512091	1512091	A	C	A1S_1288	het	het
SNV	CP00052´	1512092	1512092	C	T	A1S_1288	het	het
SNV	CP00052´	1512094	1512094	G	A	A1S_1288	het	het
SNV	CP00052´	1512098	1512098	T	C	A1S_1288	het	het
SNV	CP00052´	1512184	1512184	G	C	A1S_1288	het	het
SNV	CP00052´	1527164	1527164	A	C	A1S_1302	hom	hom
SNV	CP00052´	1552490	1552490	G	A	A1S_1324	hom	-
SNV	CP00052´	1558646	1558646	G	A	A1S_1331(dist=123);,	hom	-
SNV	CP00052´	1559203	1559203	G	A	A1S_1332	hom	-
SNV	CP00052´	1561979	1561979	G	T	A1S_1333	hom	hom
SNV	CP00052´	1585215	1585215	G	A	A1S_1353	hom	-
SNV	CP00052´	1601651	1601651	T	A	A1S_1367,A1S_1368	hom	hom
SNV	CP00052´	1601654	1601654	A	T	A1S_1367,A1S_1368	hom	hom
SNV	CP00052´	1670026	1670026	C	T	A1S_1429	hom	-
SNV	CP00052´	1699087	1699087	T	C	A1S_1458,A1S_1459	hom	hom
SNV	CP00052´	1699138	1699138	G	A	A1S_1458,A1S_1459	hom	hom
SNV	CP00052´	1699153	1699153	C	T	A1S_1458,A1S_1459	hom	hom
SNV	CP00052´	1699228	1699228	A	G	A1S_1458	hom	hom
SNV	CP00052´	1699246	1699246	C	T	A1S_1458	hom	hom
SNV	CP00052´	1699288	1699288	C	T	A1S_1458	hom	hom
SNV	CP00052´	1699447	1699447	C	T	A1S_1458	hom	het
SNV	CP00052´	1699521	1699521	C	T	A1S_1458	het	het
SNV	CP00052´	1699778	1699778	G	C	A1S_1459	-	hom
SNV	CP00052´	1699781	1699781	T	C	A1S_1459	-	hom
SNV	CP00052´	1699812	1699812	G	A	A1S_1459	-	hom
SNV	CP00052´	1699868	1699868	G	T	A1S_1459	-	hom
SNV	CP00052´	1699883	1699883	A	G	A1S_1459	hom	hom
SNV	CP00052´	1699895	1699895	G	A	A1S_1459	hom	hom
SNV	CP00052´	1699988	1699988	C	T	A1S_1459	hom	hom
SNV	CP00052´	1736140	1736140	C	T	A1S_1490(dist=143);,	hom	hom
SNV	CP00052´	1782907	1782907	T	C	A1S_1530(dist=91);A	hom	hom
SNV	CP00052´	1792081	1792081	G	A	A1S_1540	-	hom
SNV	CP00052´	1799260	1799260	A	C	A1S_1546	hom	hom
SNV	CP00052´	1862343	1862343	G	A	A1S_3704	hom	hom
SNV	CP00052´	1870450	1870450	A	G	A1S_1607	hom	hom
SNV	CP00052´	1904060	1904060	A	T	A1S_1638	hom	hom
SNV	CP00052´	2148769	2148769	C	T	A1S_1847	hom	-
SNV	CP00052´	2157019	2157019	G	C	A1S_1854	hom	hom
SNV	CP00052´	2192708	2192708	G	A	A1S_1891	hom	hom
SNV	CP00052´	2192711	2192711	C	T	A1S_1891	hom	hom
SNV	CP00052´	2193096	2193096	C	T	A1S_1891	hom	hom
SNV	CP00052´	2193191	2193191	A	G	A1S_1891	hom	hom
SNV	CP00052´	2193320	2193320	G	A	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2193335	2193335	A	T	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2193341	2193341	T	C	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2193344	2193344	C	T	A1S_1890,A1S_1891	hom	hom

SNV	CP00052´	2193346	2193346	A	G	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2193347	2193347	G	A	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2193350	2193350	G	C	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2193368	2193368	A	G	A1S_1890,A1S_1891	hom	hom
SNV	CP00052´	2243186	2243186	A	C	A1S_1936,A1S_1939	hom	hom
SNV	CP00052´	2243187	2243187	C	A	A1S_1936,A1S_1939	hom	hom
SNV	CP00052´	2286491	2286491	A	G	A1S_1973	hom	hom
SNV	CP00052´	2322896	2322896	A	T	A1S_2007	hom	hom
SNV	CP00052´	2404500	2404500	T	C	A1S_3780	hom	hom
SNV	CP00052´	2452857	2452857	G	T	A1S_2101	hom	hom
SNV	CP00052´	2452858	2452858	T	G	A1S_2101	hom	hom
SNV	CP00052´	2460574	2460574	C	T	A1S_2107,A1S_2108	hom	hom
SNV	CP00052´	2460583	2460583	G	T	A1S_2107,A1S_2108	hom	hom
SNV	CP00052´	2460585	2460585	T	G	A1S_2107,A1S_2108	hom	hom
SNV	CP00052´	2582274	2582274	A	T	A1S_2218,A1S_3796	hom	hom
SNV	CP00052´	2745350	2745350	C	T	A1S_2369	hom	hom
SNV	CP00052´	2814760	2814760	A	T	A1S_2429	hom	hom
SNV	CP00052´	2896159	2896159	T	A	A1S_2498	hom	hom
SNV	CP00052´	2906685	2906685	T	C	A1S_2506	hom	hom
SNV	CP00052´	2906686	2906686	C	A	A1S_2506	hom	hom
SNV	CP00052´	2950285	2950285	T	C	A1S_2554,A1S_2555	hom	hom
SNV	CP00052´	2950324	2950324	A	G	A1S_2554,A1S_2555	hom	hom
SNV	CP00052´	2950336	2950336	A	G	A1S_2554,A1S_2555	hom	hom
SNV	CP00052´	2950342	2950342	T	A	A1S_2554,A1S_2555	hom	hom
SNV	CP00052´	2950835	2950835	A	G	A1S_2554	hom	hom
SNV	CP00052´	2950838	2950838	G	A	A1S_2554	hom	hom
SNV	CP00052´	2950843	2950843	G	A	A1S_2554	hom	hom
SNV	CP00052´	3098204	3098204	G	A	A1S_2671	hom	hom
SNV	CP00052´	3128967	3128967	T	C	A1S_2696	het	het
SNV	CP00052´	3128991	3128991	G	A	A1S_2696	het	het
SNV	CP00052´	3128992	3128992	T	C	A1S_2696	het	het
SNV	CP00052´	3129000	3129000	T	C	A1S_2696	het	het
SNV	CP00052´	3129006	3129006	G	A	A1S_2696	het	het
SNV	CP00052´	3129024	3129024	T	C	A1S_2696	het	het
SNV	CP00052´	3129105	3129105	G	A	A1S_2696	het	het
SNV	CP00052´	3129117	3129117	A	G	A1S_2696	het	het
SNV	CP00052´	3129141	3129141	T	C	A1S_2696	het	het
SNV	CP00052´	3130125	3130125	G	A	A1S_2697	hom	hom
SNV	CP00052´	3220250	3220250	G	A	A1S_2778	-	hom
SNV	CP00052´	3309200	3309200	A	G	A1S_2860,A1S_2861	hom	hom
SNV	CP00052´	3309201	3309201	G	C	A1S_2860,A1S_2861	hom	hom
SNV	CP00052´	3309219	3309219	A	G	A1S_2860,A1S_2861	hom	hom
SNV	CP00052´	3309221	3309221	A	C	A1S_2860,A1S_2861	hom	hom
SNV	CP00052´	3357559	3357559	G	A	A1S_2905	-	hom
SNV	CP00052´	3379249	3379249	A	T	A1S_2914,A1S_2915	hom	hom
SNV	CP00052´	3379250	3379250	T	A	A1S_2914,A1S_2915	hom	hom
SNV	CP00052´	3430417	3430417	C	A	A1S_2946,A1S_2947	hom	hom
SNV	CP00052´	3430419	3430419	A	T	A1S_2946,A1S_2947	hom	hom
SNV	CP00052´	3430428	3430428	G	T	A1S_2946,A1S_2947	hom	hom
SNV	CP00052´	3430430	3430430	A	T	A1S_2946,A1S_2947	hom	hom
SNV	CP00052´	3430432	3430432	T	G	A1S_2946,A1S_2947	hom	hom
SNV	CP00052´	3500309	3500309	T	C	A1S_3013,A1S_3014	het	-
SNV	CP00052´	3500531	3500531	C	T	A1S_3013,A1S_3014	het	-
SNV	CP00052´	3631552	3631552	C	T	A1S_3144	hom	hom
SNV	CP00052´	3631553	3631553	A	C	A1S_3144	hom	hom
SNV	CP00052´	3723224	3723224	C	T	A1S_3229	-	hom
SNV	CP00052´	3734861	3734861	C	T	A1S_3244	-	hom
SNV	CP00052´	3735486	3735486	G	A	A1S_3244	hom	-

SNV	CP00052	3742196	3742196	C	A	A1S_3252(dist=720);	hom	hom
SNV	CP00052	3794200	3794200	C	T	A1S_3300	hom	hom
SNV	CP00052	3812367	3812367	C	T	A1S_3316	-	hom
SNV	CP00052	3826366	3826366	C	T	A1S_3327	-	hom
SNV	CP00052	3834335	3834335	C	T	A1S_3332	hom	hom
SNV	CP00052	3837626	3837626	C	T	A1S_3335	-	hom
SNV	P3	2735	2735	T	A	NONE(dist=NONE),N	hom	hom
SNV	P3	6574	6574	G	A	NONE(dist=NONE),N	hom	-
INDEL	CP00052	24320	24320	-	A	A1S_0017(dist=694)	hom	hom
INDEL	CP00052	25695	25695	T	-	A1S_0018	hom	hom
INDEL	CP00052	30365	30365	-	T	A1S_0020,A1S_0023	hom	hom
INDEL	CP00052	43501	43501	-	T	A1S_0035,A1S_0036	hom	hom
INDEL	CP00052	48200	48200	T	-	A1S_0041	hom	hom
INDEL	CP00052	65812	65812	T	-	A1S_0056	hom	hom
INDEL	CP00052	65840	65840	-	T	A1S_0056	hom	hom
INDEL	CP00052	74349	74349	T	-	A1S_3484	hom	hom
INDEL	CP00052	74647	74647	-	A	A1S_0063,A1S_0064	hom	hom
INDEL	CP00052	89649	89649	-	A	A1S_0076(dist=634);	hom	hom
INDEL	CP00052	89766	89766	T	-	A1S_0076(dist=517);	hom	hom
INDEL	CP00052	89779	89779	C	-	A1S_0076(dist=504);	hom	hom
INDEL	CP00052	89811	89811	T	-	A1S_0076(dist=472);	hom	hom
INDEL	CP00052	96263	96263	-	T	A1S_0078	hom	hom
INDEL	CP00052	96688	96688	-	TTG	A1S_0079(dist=339);	hom	hom
INDEL	CP00052	101768	101768	C	-	A1S_0081(dist=984)	hom	hom
INDEL	CP00052	101775	101775	G	-	A1S_0081(dist=991)	hom	hom
INDEL	CP00052	101797	101797	G	-	A1S_0081(dist=1013)	hom	hom
INDEL	CP00052	102300	102300	T	-	A1S_0081(dist=1516)	hom	hom
INDEL	CP00052	102351	102351	T	-	A1S_0081(dist=1567)	hom	hom
INDEL	CP00052	102393	102393	C	-	A1S_0081(dist=1609)	hom	hom
INDEL	CP00052	102434	102434	C	-	A1S_0081(dist=1650)	hom	hom
INDEL	CP00052	102455	102455	-	C	A1S_0081(dist=1671)	hom	hom
INDEL	CP00052	105457	105457	-	A	A1S_0086(dist=808)	hom	hom
INDEL	CP00052	107640	107640	T	-	A1S_0087,A1S_0088	hom	hom
INDEL	CP00052	107655	107655	T	-	A1S_0087,A1S_0088	hom	hom
INDEL	CP00052	122902	122902	-	A	A1S_0103(dist=316)	hom	hom
INDEL	CP00052	149266	149266	-	A	A1S_0122,A1S_0123	hom	hom
INDEL	CP00052	160497	160497	-	A	A1S_0136(dist=22);A	hom	hom
INDEL	CP00052	162598	162598	-	T	A1S_0137(dist=741)	hom	hom
INDEL	CP00052	163696	163696	-	GT	A1S_0140(dist=598)	hom	hom
INDEL	CP00052	178760	178760	-	CAC	A1S_0156,A1S_0157	hom	hom
INDEL	CP00052	178762	178762	-	G	A1S_0156,A1S_0157	hom	hom
INDEL	CP00052	178766	178766	-	C	A1S_0156,A1S_0157	hom	hom
INDEL	CP00052	183535	183535	-	A	A1S_0163	hom	hom
INDEL	CP00052	188771	188771	G	-	A1S_0170	hom	hom
INDEL	CP00052	193299	193299	A	-	A1S_0173(dist=473)	het	het
INDEL	CP00052	198673	198673	-	C	A1S_0176,A1S_0177	hom	hom
INDEL	CP00052	219217	219217	G	-	A1S_0193(dist=1852)	hom	hom
INDEL	CP00052	219260	219260	C	-	A1S_0193(dist=1895)	hom	hom
INDEL	CP00052	221520	221520	A	-	A1S_0199(dist=238);	hom	hom
INDEL	CP00052	221545	221545	A	-	A1S_0199(dist=213);	hom	hom
INDEL	CP00052	227227	227227	T	-	A1S_0203	hom	hom
INDEL	CP00052	227244	227244	A	-	A1S_0203	hom	hom
INDEL	CP00052	227247	227247	T	-	A1S_0203	hom	hom
INDEL	CP00052	227260	227260	T	-	A1S_0203	hom	hom
INDEL	CP00052	227262	227262	T	-	A1S_0203	hom	hom
INDEL	CP00052	227297	227297	G	-	A1S_0203	hom	hom
INDEL	CP00052	233080	233080	-	A	A1S_0209	hom	hom
INDEL	CP00052	233990	233993	AAGT	-	A1S_0210	het	het

INDEL	CP00052	233996	233996	-	TGG	A1S_0210	-	het
INDEL	CP00052	245274	245274	-	A	A1S_0217,A1S_0219	hom	hom
INDEL	CP00052	259143	259143	-	T	A1S_0233	hom	hom
INDEL	CP00052	259453	259453	T	-	A1S_0234	hom	hom
INDEL	CP00052	273651	273651	T	-	A1S_0247	hom	hom
INDEL	CP00052	283998	283998	T	-	A1S_0256,A1S_0257	hom	hom
INDEL	CP00052	284025	284025	-	A	A1S_0256,A1S_0257	hom	hom
INDEL	CP00052	284627	284627	-	T	A1S_0259	hom	hom
INDEL	CP00052	290089	290089	-	AA	A1S_0264	hom	hom
INDEL	CP00052	309686	309686	-	A	A1S_0287	hom	hom
INDEL	CP00052	314746	314746	A	-	A1S_0290,A1S_3493	hom	hom
INDEL	CP00052	320541	320541	-	TA	A1S_0293(dist=959)	hom	hom
INDEL	CP00052	334524	334524	T	-	A1S_0308(dist=974)	hom	hom
INDEL	CP00052	341418	341418	-	TC	A1S_0315,A1S_3494	hom	hom
INDEL	CP00052	363779	363779	-	A	A1S_0338(dist=835)	hom	hom
INDEL	CP00052	381104	381104	-	A	A1S_0350,A1S_0351	hom	hom
INDEL	CP00052	386228	386228	T	-	A1S_0354	hom	hom
INDEL	CP00052	387449	387449	-	A	A1S_0356	hom	hom
INDEL	CP00052	410869	410869	-	A	A1S_0374	hom	hom
INDEL	CP00052	412748	412748	-	A	A1S_0375(dist=978);	hom	hom
INDEL	CP00052	413441	413441	A	-	A1S_0378	hom	hom
INDEL	CP00052	413449	413449	C	-	A1S_0378	hom	hom
INDEL	CP00052	439900	439900	-	T	A1S_0406(dist=428)	hom	hom
INDEL	CP00052	459327	459327	C	-	A1S_0421,A1S_0422	hom	hom
INDEL	CP00052	497792	497792	-	A	A1S_0459,A1S_0460	hom	hom
INDEL	CP00052	519936	519936	T	-	A1S_0479(dist=151);	hom	hom
INDEL	CP00052	520271	520271	A	-	A1S_0479(dist=486);	hom	hom
INDEL	CP00052	530075	530075	-	TT	A1S_0485	hom	hom
INDEL	CP00052	531846	531846	-	T	A1S_0489(dist=846)	hom	hom
INDEL	CP00052	532569	532569	-	T	A1S_0489(dist=123)	hom	hom
INDEL	CP00052	532624	532624	-	T	A1S_0489(dist=68)	hom	hom
INDEL	CP00052	532632	532632	-	G	A1S_0489(dist=60)	hom	hom
INDEL	CP00052	536626	536626	-	A	A1S_0491(dist=160);	hom	hom
INDEL	CP00052	541071	541071	-	G	A1S_0494	hom	hom
INDEL	CP00052	542467	542467	-	C	A1S_0497	hom	hom
INDEL	CP00052	553615	553615	T	-	A1S_0509	hom	hom
INDEL	CP00052	570643	570643	-	A	A1S_0528,A1S_0529	hom	hom
INDEL	CP00052	574329	574329	A	-	A1S_0533,A1S_0534	hom	hom
INDEL	CP00052	578045	578045	-	A	A1S_0538	hom	hom
INDEL	CP00052	581818	581818	T	-	A1S_0542	hom	hom
INDEL	CP00052	593371	593371	G	-	A1S_0550(dist=309);	hom	hom
INDEL	CP00052	602227	602227	A	-	A1S_3503	hom	hom
INDEL	CP00052	604620	604620	A	-	A1S_0557	hom	hom
INDEL	CP00052	617566	617566	-	A	A1S_0568,A1S_0569	hom	hom
INDEL	CP00052	627158	627158	-	A	A1S_0579(dist=742);	hom	hom
INDEL	CP00052	634460	634460	-	T	A1S_0585,A1S_0586	hom	hom
INDEL	CP00052	634468	634468	-	G	A1S_0585,A1S_0586	hom	hom
INDEL	CP00052	634955	634955	T	-	A1S_0585	hom	hom
INDEL	CP00052	647766	647766	-	T	A1S_0600,A1S_0601	hom	hom
INDEL	CP00052	653327	653327	A	-	A1S_0606(dist=923)	hom	hom
INDEL	CP00052	662825	662825	-	A	A1S_0612,A1S_0613	hom	hom
INDEL	CP00052	674210	674210	-	AGC	A1S_0622(dist=117);	-	hom
INDEL	CP00052	674212	674212	-	CTT(	A1S_0622(dist=119);	-	hom
INDEL	CP00052	677009	677009	A	-	A1S_0623(dist=59);A	hom	hom
INDEL	CP00052	680045	680045	A	-	A1S_0626	hom	hom
INDEL	CP00052	680052	680052	A	-	A1S_0626	hom	hom
INDEL	CP00052	680059	680059	A	-	A1S_0626	hom	hom
INDEL	CP00052	686423	686423	T	-	A1S_0628	hom	hom

INDEL	CP00052	687962	687962	-	T	A1S_3514	hom	hom
INDEL	CP00052	690243	690243	-	T	A1S_3517	hom	hom
INDEL	CP00052	690900	690900	-	T	A1S_3515,A1S_3516	hom	hom
INDEL	CP00052	697315	697315	-	A	A1S_0629	hom	hom
INDEL	CP00052	718436	718436	-	A	A1S_0634(dist=79);A	hom	hom
INDEL	CP00052	721531	721531	-	A	A1S_0635(dist=197);	hom	hom
INDEL	CP00052	721731	721731	A	-	A1S_0635	hom	hom
INDEL	CP00052	723865	723865	-	T	A1S_0637	hom	hom
INDEL	CP00052	728741	728741	-	T	A1S_0639(dist=572);	hom	hom
INDEL	CP00052	729262	729262	-	T	A1S_3531	hom	hom
INDEL	CP00052	732413	732413	-	A	A1S_0640(dist=46);A	hom	hom
INDEL	CP00052	745848	745848	T	-	A1S_3540(dist=3);A1	hom	hom
INDEL	CP00052	754682	754682	-	T	A1S_0647,A1S_3546	hom	hom
INDEL	CP00052	754688	754688	-	T	A1S_0647,A1S_3546	hom	hom
INDEL	CP00052	756675	756675	A	-	A1S_0647	hom	hom
INDEL	CP00052	756679	756679	-	T	A1S_0647	hom	hom
INDEL	CP00052	756687	756688	AC	-	A1S_0647	hom	hom
INDEL	CP00052	767895	767895	-	T	A1S_0650,A1S_3553	hom	hom
INDEL	CP00052	778263	778263	-	A	A1S_0654,A1S_0655	hom	hom
INDEL	CP00052	791347	791347	-	T	A1S_0666	hom	hom
INDEL	CP00052	791359	791359	-	G	A1S_0666	hom	hom
INDEL	CP00052	791364	791364	-	C	A1S_0666	hom	hom
INDEL	CP00052	793101	793101	-	A	A1S_0669	hom	hom
INDEL	CP00052	794057	794057	C	-	A1S_0670,A1S_0671	hom	hom
INDEL	CP00052	797536	797536	-	G	A1S_0673	hom	hom
INDEL	CP00052	800617	800617	-	A	A1S_0677	hom	hom
INDEL	CP00052	833980	833980	T	-	A1S_0701	hom	hom
INDEL	CP00052	835153	835153	-	A	A1S_0703	hom	hom
INDEL	CP00052	861171	861171	A	-	A1S_0729,A1S_0730	hom	hom
INDEL	CP00052	871610	871610	-	A	A1S_0739(dist=878);	hom	hom
INDEL	CP00052	874441	874447	AACT	-	A1S_0741	hom	hom
INDEL	CP00052	877730	877730	-	GGC	A1S_0742	-	het
INDEL	CP00052	877733	877734	TA	-	A1S_0742	het	het
INDEL	CP00052	877740	877740	A	-	A1S_0742	-	het
INDEL	CP00052	877754	877754	-	CT	A1S_0742	het	het
INDEL	CP00052	877756	877756	-	CAA	A1S_0742	het	het
INDEL	CP00052	892094	892094	-	A	A1S_0751,A1S_0752	hom	hom
INDEL	CP00052	897781	897781	T	-	A1S_0756	hom	hom
INDEL	CP00052	897792	897792	A	-	A1S_0756	hom	hom
INDEL	CP00052	897810	897810	T	-	A1S_0756	hom	hom
INDEL	CP00052	916774	916774	-	A	A1S_3566	hom	hom
INDEL	CP00052	921301	921301	-	A	A1S_0776,A1S_3567	hom	hom
INDEL	CP00052	932685	932685	-	AAA	A1S_0786	hom	hom
INDEL	CP00052	940301	940301	A	-	A1S_0793(dist=493)	hom	hom
INDEL	CP00052	940312	940312	A	-	A1S_0793(dist=482)	hom	hom
INDEL	CP00052	950884	950884	-	A	A1S_0800,A1S_0801	hom	hom
INDEL	CP00052	951587	951587	-	T	A1S_0801,A1S_0802	hom	hom
INDEL	CP00052	952236	952236	A	-	A1S_0801	hom	hom
INDEL	CP00052	971409	971409	-	T	A1S_3571	hom	hom
INDEL	CP00052	974124	974124	T	-	A1S_0827	hom	hom
INDEL	CP00052	975787	975787	G	-	A1S_0829(dist=158);	hom	hom
INDEL	CP00052	981923	981923	T	-	A1S_0838,A1S_0839	hom	hom
INDEL	CP00052	996562	996562	-	G	A1S_0853	hom	hom
INDEL	CP00052	996565	996567	ATG	-	A1S_0853	hom	hom
INDEL	CP00052	1000113	1000113	-	T	A1S_0859	hom	hom
INDEL	CP00052	1004793	1004793	-	T	A1S_0864	hom	hom
INDEL	CP00052	1010211	1010211	-	GGA	A1S_0869(dist=12);A	hom	hom
INDEL	CP00052	1023287	1023287	-	A	A1S_0880,A1S_0881	hom	hom

INDEL	CP00052´	1026221	1026221	-	T	A1S_0883,A1S_0885	hom	hom
INDEL	CP00052´	1046531	1046531	G	-	A1S_0903	hom	hom
INDEL	CP00052´	1074988	1074988	-	GT	A1S_0924(dist=101);,	hom	hom
INDEL	CP00052´	1074990	1074990	-	C	A1S_0924(dist=103);,	hom	hom
INDEL	CP00052´	1074994	1074995	GA	-	A1S_0924(dist=107);,	hom	hom
INDEL	CP00052´	1074998	1074998	A	-	A1S_0925	hom	hom
INDEL	CP00052´	1075276	1075276	T	-	A1S_0926	hom	hom
INDEL	CP00052´	1076890	1076890	C	-	A1S_0927	hom	hom
INDEL	CP00052´	1081426	1081426	-	T	A1S_0930	hom	hom
INDEL	CP00052´	1093718	1093718	-	G	A1S_0942,A1S_0943	hom	hom
INDEL	CP00052´	1093724	1093726	ACG	-	A1S_0942,A1S_0943	hom	hom
INDEL	CP00052´	1093727	1093727	-	A	A1S_0942,A1S_0943	hom	hom
INDEL	CP00052´	1093734	1093734	T	-	A1S_0942,A1S_0943	hom	hom
INDEL	CP00052´	1094504	1094504	T	-	A1S_0944	hom	hom
INDEL	CP00052´	1094794	1094794	-	T	A1S_0944,A1S_0945	hom	hom
INDEL	CP00052´	1098670	1098670	-	A	A1S_0950	hom	hom
INDEL	CP00052´	1100655	1100655	-	A	A1S_0952	hom	hom
INDEL	CP00052´	1108352	1108352	-	T	A1S_0960	hom	hom
INDEL	CP00052´	1114043	1114043	-	A	A1S_3582(dist=168);,	hom	hom
INDEL	CP00052´	1117207	1117207	T	-	A1S_3583,A1S_3584	hom	hom
INDEL	CP00052´	1130114	1130114	A	-	A1S_0974,A1S_0975	hom	hom
INDEL	CP00052´	1138269	1138269	-	T	A1S_0980	hom	hom
INDEL	CP00052´	1139921	1139921	-	T	A1S_0982,A1S_3587	hom	hom
INDEL	CP00052´	1148563	1148563	A	-	A1S_0990	het	het
INDEL	CP00052´	1148566	1148566	-	A	A1S_0990	het	het
INDEL	CP00052´	1148598	1148598	-	GCT	A1S_0990	het	het
INDEL	CP00052´	1148603	1148605	TTA	-	A1S_0990	het	het
INDEL	CP00052´	1149141	1149141	A	-	A1S_0990	hom	hom
INDEL	CP00052´	1149209	1149209	A	-	A1S_0990	hom	hom
INDEL	CP00052´	1149220	1149220	C	-	A1S_0990	hom	hom
INDEL	CP00052´	1162771	1162771	-	A	A1S_1003	hom	hom
INDEL	CP00052´	1166807	1166807	T	-	A1S_1007	hom	hom
INDEL	CP00052´	1169650	1169650	-	T	A1S_1009	hom	hom
INDEL	CP00052´	1170586	1170586	-	A	A1S_1009,A1S_1010	hom	hom
INDEL	CP00052´	1175601	1175601	A	-	A1S_1016	hom	hom
INDEL	CP00052´	1175616	1175616	-	A	A1S_1016	hom	hom
INDEL	CP00052´	1175756	1175756	C	-	A1S_1017,A1S_3589	hom	hom
INDEL	CP00052´	1190456	1190456	T	-	A1S_1031	hom	hom
INDEL	CP00052´	1224646	1224646	T	-	A1S_1059	hom	hom
INDEL	CP00052´	1225336	1225336	A	-	A1S_1060	hom	hom
INDEL	CP00052´	1233498	1233498	A	-	A1S_1068(dist=162);,	hom	hom
INDEL	CP00052´	1233531	1233531	A	-	A1S_1068(dist=195);,	hom	hom
INDEL	CP00052´	1233565	1233565	T	-	A1S_1068(dist=229);,	hom	hom
INDEL	CP00052´	1233581	1233581	T	-	A1S_1069	hom	hom
INDEL	CP00052´	1239202	1239202	A	-	A1S_1072(dist=331);,	hom	hom
INDEL	CP00052´	1262155	1262155	-	G	A1S_1081,A1S_3598	hom	hom
INDEL	CP00052´	1273970	1273970	G	-	A1S_1091	hom	hom
INDEL	CP00052´	1295648	1295648	T	-	A1S_1107(dist=61);A	hom	hom
INDEL	CP00052´	1295652	1295652	T	-	A1S_1107(dist=65);A	hom	hom
INDEL	CP00052´	1301307	1301307	-	A	A1S_1111,A1S_1112	hom	hom
INDEL	CP00052´	1311332	1311332	-	A	A1S_1121	hom	hom
INDEL	CP00052´	1317959	1317959	T	-	A1S_1126	hom	hom
INDEL	CP00052´	1324684	1324684	-	C	A1S_1133	hom	hom
INDEL	CP00052´	1326075	1326075	-	T	A1S_1135(dist=709);,	hom	hom
INDEL	CP00052´	1327040	1327040	T	-	A1S_1135	hom	hom
INDEL	CP00052´	1327085	1327085	T	-	A1S_1136(dist=262);,	hom	hom
INDEL	CP00052´	1359463	1359463	A	-	A1S_1164,A1S_1165	hom	hom
INDEL	CP00052´	1364748	1364748	A	-	A1S_1169,A1S_1170	hom	hom

INDEL	CP00052´	1365457	1365457	-	A	A1S_1169	hom	hom
INDEL	CP00052´	1379989	1379989	-	A	A1S_3623	hom	hom
INDEL	CP00052´	1385135	1385135	-	A	A1S_1182	hom	hom
INDEL	CP00052´	1385755	1385755	C	-	A1S_1181,A1S_1182	hom	hom
INDEL	CP00052´	1385814	1385814	A	-	A1S_1181,A1S_1182	hom	hom
INDEL	CP00052´	1385826	1385826	A	-	A1S_1181,A1S_1182	hom	hom
INDEL	CP00052´	1385833	1385833	T	-	A1S_1181,A1S_1182	hom	hom
INDEL	CP00052´	1392723	1392723	-	A	A1S_1189	hom	hom
INDEL	CP00052´	1394196	1394196	-	TA	A1S_1189,A1S_1190	hom	hom
INDEL	CP00052´	1396861	1396861	-	T	A1S_1191	hom	hom
INDEL	CP00052´	1399957	1399957	-	T	A1S_1195	hom	hom
INDEL	CP00052´	1402909	1402909	T	-	A1S_1197	hom	hom
INDEL	CP00052´	1406256	1406256	G	-	A1S_1200,A1S_1202	hom	hom
INDEL	CP00052´	1406322	1406322	G	-	A1S_1201	hom	hom
INDEL	CP00052´	1406521	1406521	-	TA	A1S_1201	het	het
INDEL	CP00052´	1406524	1406525	GC	-	A1S_1201	het	het
INDEL	CP00052´	1412365	1412365	-	A	A1S_1206	hom	hom
INDEL	CP00052´	1440298	1440298	A	-	A1S_1230(dist=253);,	hom	hom
INDEL	CP00052´	1441368	1441368	-	TA	A1S_1230	hom	hom
INDEL	CP00052´	1445838	1445838	A	-	A1S_3636	hom	hom
INDEL	CP00052´	1459044	1459044	A	-	A1S_1246,A1S_1247	hom	hom
INDEL	CP00052´	1459141	1459141	G	-	A1S_1246,A1S_1247	hom	hom
INDEL	CP00052´	1459145	1459145	A	-	A1S_1247	hom	hom
INDEL	CP00052´	1459153	1459153	-	T	A1S_1247	hom	hom
INDEL	CP00052´	1463979	1463979	T	-	A1S_1252	hom	hom
INDEL	CP00052´	1479862	1479862	-	T	A1S_1262,A1S_1263	hom	hom
INDEL	CP00052´	1483282	1483282	-	T	A1S_1266(dist=339);,	hom	hom
INDEL	CP00052´	1497862	1497862	-	A	A1S_1276	hom	hom
INDEL	CP00052´	1500489	1500489	-	T	A1S_1277	hom	hom
INDEL	CP00052´	1504043	1504043	A	-	A1S_1281,A1S_3644	hom	hom
INDEL	CP00052´	1510446	1510446	-	TA	A1S_1287	hom	hom
INDEL	CP00052´	1511568	1511568	-	A	A1S_1287,A1S_1288	hom	hom
INDEL	CP00052´	1512867	1512867	-	G	A1S_1288	hom	hom
INDEL	CP00052´	1517488	1517488	-	T	A1S_1291	hom	hom
INDEL	CP00052´	1519789	1519789	A	-	A1S_1293	hom	hom
INDEL	CP00052´	1519906	1519906	-	A	A1S_1293	hom	hom
INDEL	CP00052´	1523594	1523594	-	A	A1S_1298	hom	hom
INDEL	CP00052´	1523776	1523776	-	A	A1S_1299,A1S_1300	hom	hom
INDEL	CP00052´	1530218	1530218	-	A	A1S_1302	hom	hom
INDEL	CP00052´	1540013	1540013	-	T	A1S_1311	hom	hom
INDEL	CP00052´	1546034	1546034	-	T	A1S_1318(dist=140);,	hom	hom
INDEL	CP00052´	1546927	1546927	-	T	A1S_1319,A1S_1320	hom	hom
INDEL	CP00052´	1547655	1547655	-	T	A1S_1319,A1S_1320	hom	hom
INDEL	CP00052´	1555587	1555587	-	A	A1S_1328	hom	hom
INDEL	CP00052´	1562167	1562167	-	T	A1S_3650	hom	hom
INDEL	CP00052´	1574856	1574856	T	-	A1S_1345	hom	hom
INDEL	CP00052´	1577832	1577832	-	A	A1S_3651,A1S_3652	hom	hom
INDEL	CP00052´	1578541	1578541	-	A	A1S_3652(dist=187);,	hom	hom
INDEL	CP00052´	1593564	1593564	-	A	A1S_1360	hom	hom
INDEL	CP00052´	1593620	1593620	-	A	A1S_1361,A1S_1362	hom	hom
INDEL	CP00052´	1593645	1593645	G	-	A1S_1361,A1S_1362	hom	hom
INDEL	CP00052´	1593684	1593684	G	-	A1S_1361,A1S_1362	hom	hom
INDEL	CP00052´	1601643	1601643	A	-	A1S_1367	hom	hom
INDEL	CP00052´	1601662	1601662	A	-	A1S_1367,A1S_1368	hom	hom
INDEL	CP00052´	1601665	1601665	A	-	A1S_1367,A1S_1368	hom	hom
INDEL	CP00052´	1601679	1601679	C	-	A1S_1367,A1S_1368	hom	hom
INDEL	CP00052´	1602213	1602213	A	-	A1S_1369	hom	hom
INDEL	CP00052´	1602222	1602222	T	-	A1S_1369	hom	hom

INDEL	CP00052	1603464	1603464	-	T	A1S_1370	hom	hom
INDEL	CP00052	1620424	1620424	-	G	A1S_3656,A1S_3657	hom	hom
INDEL	CP00052	1623786	1623786	-	T	A1S_1384	hom	hom
INDEL	CP00052	1640776	1640776	A	-	A1S_1396	hom	hom
INDEL	CP00052	1643298	1643298	-	A	A1S_1400(dist=59);A	hom	hom
INDEL	CP00052	1647152	1647152	A	-	A1S_1404	hom	hom
INDEL	CP00052	1647404	1647404	T	-	A1S_1405	hom	hom
INDEL	CP00052	1653405	1653405	-	A	A1S_1411	hom	hom
INDEL	CP00052	1670836	1670836	-	A	A1S_1431	hom	hom
INDEL	CP00052	1676914	1676914	-	T	A1S_1435	hom	hom
INDEL	CP00052	1677481	1677481	-	A	A1S_1436	hom	hom
INDEL	CP00052	1679288	1679288	A	-	A1S_1438	hom	hom
INDEL	CP00052	1686799	1686799	-	C	A1S_1445	hom	hom
INDEL	CP00052	1698830	1698830	-	C	A1S_1458,A1S_1459	hom	hom
INDEL	CP00052	1699192	1699192	-	T	A1S_1458	hom	hom
INDEL	CP00052	1699195	1699195	-	CT	A1S_1458	hom	hom
INDEL	CP00052	1699240	1699241	GC	-	A1S_1458	hom	hom
INDEL	CP00052	1699243	1699243	-	TA	A1S_1458	hom	hom
INDEL	CP00052	1699448	1699448	-	ATG	A1S_1458	hom	hom
INDEL	CP00052	1699612	1699612	-	G	A1S_1458	hom	hom
INDEL	CP00052	1700004	1700004	-	A	A1S_1459	hom	hom
INDEL	CP00052	1700007	1700007	-	T	A1S_1459	hom	hom
INDEL	CP00052	1712118	1712118	G	-	A1S_1467(dist=93);A	hom	hom
INDEL	CP00052	1712136	1712136	A	-	A1S_1467(dist=111);	hom	hom
INDEL	CP00052	1715290	1715290	-	A	A1S_1471,A1S_1472	hom	hom
INDEL	CP00052	1727912	1727912	A	-	A1S_1482,A1S_3672	hom	hom
INDEL	CP00052	1743318	1743318	-	A	A1S_1496,A1S_1497	hom	hom
INDEL	CP00052	1743356	1743356	-	A	A1S_1496,A1S_1497	hom	hom
INDEL	CP00052	1746068	1746068	-	T	A1S_3674	hom	hom
INDEL	CP00052	1758690	1758690	-	T	A1S_1509,A1S_1510	hom	hom
INDEL	CP00052	1765230	1765230	-	T	A1S_1516	hom	hom
INDEL	CP00052	1768046	1768046	-	T	A1S_3679,A1S_3680	hom	hom
INDEL	CP00052	1770673	1770673	A	-	A1S_1520	hom	hom
INDEL	CP00052	1773734	1773734	-	T	A1S_1524,A1S_1525	hom	hom
INDEL	CP00052	1781384	1781384	-	T	A1S_1530	hom	hom
INDEL	CP00052	1783978	1783978	-	AC	A1S_1531(dist=57);A	hom	hom
INDEL	CP00052	1783989	1783989	-	A	A1S_1531(dist=68);A	hom	hom
INDEL	CP00052	1783995	1783995	-	T	A1S_1531(dist=74);A	hom	hom
INDEL	CP00052	1794865	1794865	-	A	A1S_3681	hom	hom
INDEL	CP00052	1796669	1796669	-	T	A1S_1544(dist=81);A	hom	hom
INDEL	CP00052	1801169	1801169	T	-	A1S_1547	hom	hom
INDEL	CP00052	1827586	1827586	-	C	A1S_1579(dist=51);A	hom	hom
INDEL	CP00052	1829271	1829271	-	T	A1S_1580(dist=122);	hom	hom
INDEL	CP00052	1836840	1836840	-	G	A1S_1585	hom	hom
INDEL	CP00052	1844009	1844009	G	-	A1S_1587	hom	hom
INDEL	CP00052	1851242	1851242	-	A	A1S_3701	hom	hom
INDEL	CP00052	1852725	1852725	-	A	A1S_1596	hom	hom
INDEL	CP00052	1863395	1863395	-	A	A1S_1601,A1S_3706	hom	hom
INDEL	CP00052	1870384	1870384	-	T	A1S_1607	hom	hom
INDEL	CP00052	1885755	1885755	-	A	A1S_1618(dist=37);A	hom	hom
INDEL	CP00052	1889553	1889553	A	-	A1S_1622,A1S_3710	hom	hom
INDEL	CP00052	1894895	1894895	T	-	A1S_1625	hom	hom
INDEL	CP00052	1894903	1894904	TT	-	A1S_1625	hom	hom
INDEL	CP00052	1894907	1894907	G	-	A1S_1625	hom	hom
INDEL	CP00052	1899622	1899622	-	T	A1S_1633	hom	hom
INDEL	CP00052	1902836	1902836	T	-	A1S_1638(dist=365);	hom	hom
INDEL	CP00052	1918340	1918340	T	-	A1S_1650	hom	hom
INDEL	CP00052	1951892	1951892	T	-	A1S_1676	hom	hom

INDEL	CP00052´	1955409	1955409	-	T	A1S_3713(dist=370);,	hom	hom
INDEL	CP00052´	1956154	1956154	-	A	A1S_1681(dist=566);,	hom	hom
INDEL	CP00052´	1956573	1956573	-	A	A1S_1681(dist=147);,	hom	hom
INDEL	CP00052´	1973873	1973873	-	A	A1S_1697	hom	hom
INDEL	CP00052´	1981008	1981008	T	-	A1S_1702	hom	hom
INDEL	CP00052´	1981011	1981011	T	-	A1S_1702	hom	hom
INDEL	CP00052´	1983441	1983441	-	C	A1S_1706	hom	hom
INDEL	CP00052´	1994816	1994816	-	T	A1S_1716,A1S_1717	hom	hom
INDEL	CP00052´	2007245	2007245	T	-	A1S_1726	hom	hom
INDEL	CP00052´	2007252	2007252	-	T	A1S_1726	hom	hom
INDEL	CP00052´	2008427	2008427	-	T	A1S_1726,A1S_1727	hom	hom
INDEL	CP00052´	2008804	2008804	-	T	A1S_1727(dist=532);,	hom	hom
INDEL	CP00052´	2008812	2008812	-	T	A1S_1727(dist=524);,	hom	hom
INDEL	CP00052´	2016885	2016885	-	A	A1S_1733,A1S_1734	hom	hom
INDEL	CP00052´	2019813	2019813	T	-	A1S_1735,A1S_1736	hom	hom
INDEL	CP00052´	2020298	2020298	-	T	A1S_1736(dist=240);,	hom	hom
INDEL	CP00052´	2024976	2024976	A	-	A1S_1740	hom	hom
INDEL	CP00052´	2040253	2040253	A	-	A1S_1752	hom	hom
INDEL	CP00052´	2064898	2064898	-	T	A1S_1772	hom	hom
INDEL	CP00052´	2070123	2070123	-	T	A1S_1776	hom	hom
INDEL	CP00052´	2074018	2074018	-	A	A1S_1778	hom	hom
INDEL	CP00052´	2093586	2093586	A	-	A1S_1796	hom	hom
INDEL	CP00052´	2093591	2093591	C	-	A1S_1796	hom	hom
INDEL	CP00052´	2093645	2093645	G	-	A1S_1797(dist=145);,	hom	hom
INDEL	CP00052´	2093653	2093653	A	-	A1S_1797(dist=137);,	hom	hom
INDEL	CP00052´	2093670	2093670	T	-	A1S_1797(dist=120);,	hom	hom
INDEL	CP00052´	2093675	2093675	G	-	A1S_1797(dist=115);,	hom	hom
INDEL	CP00052´	2098001	2098001	A	-	A1S_1800,A1S_1801	hom	hom
INDEL	CP00052´	2115125	2115125	-	T	A1S_1814	hom	hom
INDEL	CP00052´	2117684	2117684	-	A	A1S_1816	hom	hom
INDEL	CP00052´	2119092	2119092	-	G	A1S_1816(dist=37);A	hom	hom
INDEL	CP00052´	2140266	2140266	-	A	A1S_1838	hom	hom
INDEL	CP00052´	2146241	2146241	A	-	A1S_1843	hom	hom
INDEL	CP00052´	2149784	2149785	AA	-	A1S_1849	hom	hom
INDEL	CP00052´	2149786	2149786	-	CG	A1S_1849	hom	hom
INDEL	CP00052´	2163574	2163574	-	T	A1S_1859	hom	hom
INDEL	CP00052´	2164808	2164808	-	T	A1S_1861	hom	hom
INDEL	CP00052´	2171390	2171390	-	A	A1S_1868	hom	hom
INDEL	CP00052´	2175506	2175506	C	-	A1S_1873	hom	hom
INDEL	CP00052´	2175509	2175510	AA	-	A1S_1873	hom	hom
INDEL	CP00052´	2180550	2180550	-	T	A1S_1878,A1S_1879	hom	hom
INDEL	CP00052´	2189257	2189257	-	A	A1S_1888	hom	hom
INDEL	CP00052´	2193174	2193174	-	CG	A1S_1891	hom	hom
INDEL	CP00052´	2193176	2193177	TT	-	A1S_1891	hom	hom
INDEL	CP00052´	2210832	2210832	A	-	A1S_1908(dist=178);,	hom	hom
INDEL	CP00052´	2216129	2216129	-	T	A1S_1913,A1S_3745	hom	hom
INDEL	CP00052´	2257166	2257166	-	G	A1S_1949,A1S_3746	hom	hom
INDEL	CP00052´	2257555	2257555	-	A	A1S_1949,A1S_3746	hom	hom
INDEL	CP00052´	2264546	2264546	G	-	A1S_1953,A1S_1954	hom	hom
INDEL	CP00052´	2264552	2264552	T	-	A1S_1953,A1S_1954	hom	hom
INDEL	CP00052´	2264569	2264569	-	T	A1S_1954	hom	hom
INDEL	CP00052´	2264583	2264583	-	T	A1S_1954	hom	hom
INDEL	CP00052´	2273675	2273675	T	-	A1S_1961	hom	hom
INDEL	CP00052´	2275273	2275273	-	G	A1S_1963,A1S_1964	hom	hom
INDEL	CP00052´	2275287	2275287	T	-	A1S_1963,A1S_1964	hom	hom
INDEL	CP00052´	2289728	2289728	-	AA	A1S_1976,A1S_1977	hom	hom
INDEL	CP00052´	2310851	2310851	-	T	A1S_3751	hom	hom
INDEL	CP00052´	2317612	2317612	T	-	A1S_2004	hom	hom

INDEL	CP00052´	2317648	2317648	T	-	A1S_2004	hom	hom
INDEL	CP00052´	2317670	2317670	T	-	A1S_2004	hom	hom
INDEL	CP00052´	2317680	2317680	A	-	A1S_2004	hom	hom
INDEL	CP00052´	2338087	2338087	-	A	A1S_2017,A1S_3756	hom	hom
INDEL	CP00052´	2344491	2344491	-	T	A1S_2018(dist=81);A	hom	hom
INDEL	CP00052´	2344541	2344541	T	-	A1S_3759	hom	hom
INDEL	CP00052´	2353947	2353947	-	T	A1S_2026	hom	hom
INDEL	CP00052´	2368961	2368961	-	G	A1S_2036	hom	hom
INDEL	CP00052´	2385229	2385229	-	T	A1S_2044	hom	hom
INDEL	CP00052´	2385603	2385603	-	T	A1S_2045	hom	hom
INDEL	CP00052´	2387862	2387862	T	-	A1S_2049	hom	hom
INDEL	CP00052´	2396780	2396780	-	AGG	A1S_2056	hom	hom
INDEL	CP00052´	2415823	2415823	-	T	A1S_2071(dist=83);A	hom	hom
INDEL	CP00052´	2415856	2415856	-	T	A1S_2071(dist=116);,	hom	hom
INDEL	CP00052´	2415884	2415884	-	A	A1S_2071,A1S_2072	hom	hom
INDEL	CP00052´	2416382	2416382	-	T	A1S_3783	hom	hom
INDEL	CP00052´	2423218	2423218	-	T	A1S_2077	hom	hom
INDEL	CP00052´	2430520	2430520	-	T	A1S_2080	hom	hom
INDEL	CP00052´	2452196	2452196	T	-	A1S_2099	hom	hom
INDEL	CP00052´	2458779	2458779	-	A	A1S_2105	hom	hom
INDEL	CP00052´	2460560	2460560	A	-	A1S_2107,A1S_2108	hom	hom
INDEL	CP00052´	2460569	2460569	-	CA	A1S_2107,A1S_2108	hom	hom
INDEL	CP00052´	2460573	2460573	A	-	A1S_2107,A1S_2108	hom	hom
INDEL	CP00052´	2460578	2460579	GT	-	A1S_2107,A1S_2108	hom	hom
INDEL	CP00052´	2465057	2465057	-	A	A1S_2112	hom	hom
INDEL	CP00052´	2468830	2468830	-	T	A1S_2115	hom	hom
INDEL	CP00052´	2480118	2480118	-	A	A1S_2127	hom	hom
INDEL	CP00052´	2480962	2480962	-	A	A1S_2128	hom	hom
INDEL	CP00052´	2482776	2482776	A	-	A1S_2130	hom	hom
INDEL	CP00052´	2486279	2486279	-	A	A1S_2131	hom	hom
INDEL	CP00052´	2491306	2491306	T	-	A1S_2133	hom	hom
INDEL	CP00052´	2501430	2501430	-	C	A1S_2142,A1S_3789	hom	hom
INDEL	CP00052´	2504757	2504757	-	T	A1S_2145	hom	hom
INDEL	CP00052´	2510563	2510563	T	-	A1S_2151	hom	hom
INDEL	CP00052´	2516007	2516007	-	T	A1S_2158,A1S_3791	hom	hom
INDEL	CP00052´	2535678	2535678	-	A	A1S_2174,A1S_2175	hom	hom
INDEL	CP00052´	2536275	2536275	-	A	A1S_2174	hom	hom
INDEL	CP00052´	2549620	2549620	A	-	A1S_2187	hom	hom
INDEL	CP00052´	2552509	2552509	-	AA	A1S_2190	hom	hom
INDEL	CP00052´	2559780	2559780	T	-	A1S_2198,A1S_3793	hom	hom
INDEL	CP00052´	2580169	2580169	A	-	A1S_2216	hom	hom
INDEL	CP00052´	2590156	2590156	-	T	A1S_2224,A1S_2225	hom	hom
INDEL	CP00052´	2591282	2591282	-	T	A1S_2225,A1S_3797	hom	hom
INDEL	CP00052´	2599367	2599367	-	T	A1S_2233,A1S_2235	hom	hom
INDEL	CP00052´	2599406	2599406	-	A	A1S_2234	hom	hom
INDEL	CP00052´	2599409	2599409	-	A	A1S_2234	hom	hom
INDEL	CP00052´	2599434	2599434	T	-	A1S_2234	hom	hom
INDEL	CP00052´	2622738	2622738	-	T	A1S_2260,A1S_2261	hom	hom
INDEL	CP00052´	2634116	2634116	-	A	A1S_2273	hom	hom
INDEL	CP00052´	2645327	2645327	-	A	A1S_2281,A1S_2282	hom	hom
INDEL	CP00052´	2652055	2652055	-	C	A1S_2287	hom	hom
INDEL	CP00052´	2652067	2652067	C	-	A1S_2287	hom	hom
INDEL	CP00052´	2673797	2673797	-	A	A1S_2306,A1S_2307	hom	hom
INDEL	CP00052´	2673817	2673817	T	-	A1S_2306,A1S_2307	hom	hom
INDEL	CP00052´	2678352	2678352	-	T	A1S_2311(dist=222);,	hom	hom
INDEL	CP00052´	2690029	2690029	-	T	A1S_2322,A1S_2323	hom	hom
INDEL	CP00052´	2696114	2696114	-	A	A1S_2327,A1S_2328	hom	hom
INDEL	CP00052´	2699733	2699733	-	A	A1S_2330	hom	hom

INDEL	CP00052	2702705	2702705	A	-	A1S_2333,A1S_2334	hom	hom
INDEL	CP00052	2702764	2702764	-	T	A1S_2333,A1S_2334	hom	hom
INDEL	CP00052	2705885	2705885	T	-	A1S_2337(dist=65);A	hom	hom
INDEL	CP00052	2705907	2705907	-	A	A1S_2337(dist=43);A	hom	hom
INDEL	CP00052	2712647	2712647	-	A	A1S_2339,A1S_2340	hom	hom
INDEL	CP00052	2712658	2712658	-	A	A1S_2339,A1S_2340	hom	hom
INDEL	CP00052	2713634	2713634	-	A	A1S_2341	hom	hom
INDEL	CP00052	2713958	2713958	A	-	A1S_2340,A1S_2341	hom	hom
INDEL	CP00052	2715597	2715597	-	A	A1S_2347(dist=602);A	hom	hom
INDEL	CP00052	2720582	2720582	-	C	A1S_2352	hom	hom
INDEL	CP00052	2722082	2722082	T	-	A1S_2352,A1S_2353	hom	hom
INDEL	CP00052	2722091	2722091	A	-	A1S_2352,A1S_2353	hom	hom
INDEL	CP00052	2729685	2729685	C	-	A1S_2357,A1S_2358	hom	hom
INDEL	CP00052	2736404	2736404	-	T	A1S_2364	hom	hom
INDEL	CP00052	2752844	2752844	A	-	A1S_2376,A1S_2377	hom	hom
INDEL	CP00052	2753432	2753432	A	-	A1S_2378	hom	hom
INDEL	CP00052	2759434	2759434	-	G	A1S_2382	hom	hom
INDEL	CP00052	2762708	2762708	A	-	A1S_2384,A1S_2385	hom	hom
INDEL	CP00052	2769104	2769104	-	A	A1S_2389,A1S_2390	hom	hom
INDEL	CP00052	2780770	2780770	-	T	A1S_2397,A1S_3804	hom	hom
INDEL	CP00052	2784979	2784979	T	-	A1S_2399,A1S_3805	hom	hom
INDEL	CP00052	2789804	2789804	-	T	A1S_2404(dist=184);A	hom	hom
INDEL	CP00052	2791909	2791909	-	C	A1S_2407	hom	hom
INDEL	CP00052	2791913	2791913	-	C	A1S_2407	hom	hom
INDEL	CP00052	2791922	2791922	-	T	A1S_2407	hom	hom
INDEL	CP00052	2792261	2792261	A	-	A1S_2408	hom	hom
INDEL	CP00052	2794605	2794605	-	T	A1S_2410(dist=10);A	hom	hom
INDEL	CP00052	2801576	2801576	A	-	A1S_2416,A1S_2417	hom	hom
INDEL	CP00052	2801607	2801607	-	A	A1S_2418	hom	hom
INDEL	CP00052	2802818	2802818	-	A	A1S_2418(dist=123);A	hom	hom
INDEL	CP00052	2803166	2803166	A	-	A1S_2418,A1S_2420	hom	hom
INDEL	CP00052	2809364	2809364	T	-	A1S_2424	hom	hom
INDEL	CP00052	2809618	2809618	-	A	A1S_2425	hom	hom
INDEL	CP00052	2813631	2813631	-	T	A1S_2428	hom	hom
INDEL	CP00052	2814759	2814759	C	-	A1S_2429	hom	hom
INDEL	CP00052	2815708	2815708	-	A	A1S_2429,A1S_2430	hom	hom
INDEL	CP00052	2822256	2822256	A	-	A1S_2438	hom	hom
INDEL	CP00052	2836258	2836258	A	-	A1S_3809	hom	hom
INDEL	CP00052	2836267	2836267	-	AT	A1S_3809	hom	hom
INDEL	CP00052	2857829	2857829	-	A	A1S_2465,A1S_2466	hom	hom
INDEL	CP00052	2862299	2862299	T	-	A1S_2470	hom	hom
INDEL	CP00052	2862328	2862328	-	A	A1S_2470	hom	hom
INDEL	CP00052	2874169	2874169	A	-	A1S_2477(dist=40);A	hom	hom
INDEL	CP00052	2885181	2885181	-	T	A1S_2486	hom	hom
INDEL	CP00052	2906690	2906690	-	A	A1S_2506	hom	hom
INDEL	CP00052	2906714	2906714	A	-	A1S_2506	hom	hom
INDEL	CP00052	2906736	2906736	A	-	A1S_2508(dist=26);A	hom	hom
INDEL	CP00052	2915497	2915497	-	A	A1S_2514(dist=90);A	hom	hom
INDEL	CP00052	2923178	2923178	-	T	A1S_2523	hom	hom
INDEL	CP00052	2930417	2930417	-	A	A1S_2529,A1S_2530	hom	hom
INDEL	CP00052	2931464	2931464	T	-	A1S_2531	hom	hom
INDEL	CP00052	2931518	2931518	-	A	A1S_2532,A1S_2533	hom	hom
INDEL	CP00052	2931649	2931649	-	A	A1S_3813	hom	hom
INDEL	CP00052	2938716	2938716	-	A	A1S_2540	hom	hom
INDEL	CP00052	2950382	2950382	-	G	A1S_2554,A1S_2555	hom	hom
INDEL	CP00052	2950384	2950384	-	TAG	A1S_2554,A1S_2555	hom	hom
INDEL	CP00052	2950442	2950442	A	-	A1S_2554,A1S_2555	hom	hom
INDEL	CP00052	2950848	2950848	-	A	A1S_2554	hom	hom

INDEL	CP00052	2962493	2962493	-	T	A1S_2564	hom	hom
INDEL	CP00052	2966320	2966320	-	T	A1S_2566,A1S_2567	hom	hom
INDEL	CP00052	2972698	2972698	-	A	A1S_2573,A1S_2574	hom	hom
INDEL	CP00052	2978693	2978693	-	A	A1S_2576(dist=94);A	hom	hom
INDEL	CP00052	2978701	2978701	-	C	A1S_2576(dist=102);	hom	hom
INDEL	CP00052	2978726	2978726	-	A	A1S_2577	hom	hom
INDEL	CP00052	3002180	3002180	-	GCT	A1S_2593	hom	hom
INDEL	CP00052	3023410	3023410	T	-	A1S_2613	hom	hom
INDEL	CP00052	3029280	3029280	-	A	A1S_2618	hom	hom
INDEL	CP00052	3034743	3034743	-	A	A1S_2624(dist=229);	hom	hom
INDEL	CP00052	3041681	3041681	-	CA	A1S_2627(dist=110);	hom	hom
INDEL	CP00052	3066681	3066681	-	T	A1S_2649	hom	hom
INDEL	CP00052	3066692	3066692	T	-	A1S_2649	hom	hom
INDEL	CP00052	3066717	3066717	G	-	A1S_2649	hom	hom
INDEL	CP00052	3086712	3086712	G	-	A1S_2661,A1S_2662	hom	hom
INDEL	CP00052	3086725	3086725	-	T	A1S_2661,A1S_2662	hom	hom
INDEL	CP00052	3094402	3094402	-	A	A1S_2668	hom	hom
INDEL	CP00052	3094421	3094421	A	-	A1S_2668	hom	hom
INDEL	CP00052	3117504	3117504	-	A	A1S_2691	hom	hom
INDEL	CP00052	3154175	3154175	-	T	A1S_2717	hom	hom
INDEL	CP00052	3164749	3164750	TC	-	A1S_2726(dist=207);	hom	hom
INDEL	CP00052	3164782	3164782	T	-	A1S_2727	hom	hom
INDEL	CP00052	3171015	3171015	-	A	A1S_2733	hom	hom
INDEL	CP00052	3171186	3171186	-	A	A1S_2734,A1S_2735	hom	hom
INDEL	CP00052	3178241	3178241	-	T	A1S_2739(dist=176);	hom	hom
INDEL	CP00052	3180221	3180221	-	T	A1S_2740,A1S_2741	hom	hom
INDEL	CP00052	3183305	3183305	T	-	A1S_2742	hom	hom
INDEL	CP00052	3183322	3183322	A	-	A1S_2743(dist=81);A	hom	hom
INDEL	CP00052	3183357	3183357	-	A	A1S_2743(dist=46);A	hom	hom
INDEL	CP00052	3183362	3183362	-	T	A1S_2743(dist=41);A	hom	hom
INDEL	CP00052	3203809	3203810	AC	-	A1S_2762	hom	hom
INDEL	CP00052	3279646	3279646	-	T	A1S_2833,A1S_2834	hom	hom
INDEL	CP00052	3291393	3291393	T	-	A1S_2842,A1S_2843	hom	hom
INDEL	CP00052	3291442	3291442	T	-	A1S_2844	hom	hom
INDEL	CP00052	3295632	3295632	-	T	A1S_2848	hom	hom
INDEL	CP00052	3302359	3302359	T	-	A1S_2853	hom	hom
INDEL	CP00052	3302415	3302415	A	-	A1S_2854(dist=151);	hom	hom
INDEL	CP00052	3309204	3309205	TC	-	A1S_2860,A1S_2861	hom	hom
INDEL	CP00052	3309207	3309207	-	TC	A1S_2860,A1S_2861	hom	hom
INDEL	CP00052	3309210	3309211	CT	-	A1S_2860,A1S_2861	hom	hom
INDEL	CP00052	3309215	3309217	AAG	-	A1S_2860,A1S_2861	hom	hom
INDEL	CP00052	3309224	3309233	ACGT	-	A1S_2860,A1S_2861	hom	hom
INDEL	CP00052	3314113	3314113	-	A	A1S_2864,A1S_2865	hom	hom
INDEL	CP00052	3316753	3316753	-	T	A1S_2868	hom	hom
INDEL	CP00052	3334492	3334492	A	-	A1S_2884	hom	hom
INDEL	CP00052	3378697	3378697	A	-	A1S_2915	hom	hom
INDEL	CP00052	3378700	3378700	A	-	A1S_2916(dist=82);A	hom	hom
INDEL	CP00052	3379262	3379262	T	-	A1S_2915,A1S_2916	hom	hom
INDEL	CP00052	3379275	3379275	T	-	A1S_2915,A1S_2916	hom	hom
INDEL	CP00052	3387351	3387351	A	-	A1S_2925,A1S_2926	hom	hom
INDEL	CP00052	3417123	3417123	-	T	A1S_3852,A1S_3853	hom	hom
INDEL	CP00052	3430415	3430415	-	CCA	A1S_2946,A1S_2947	hom	hom
INDEL	CP00052	3430422	3430423	CT	-	A1S_2946,A1S_2947	hom	hom
INDEL	CP00052	3430425	3430426	GT	-	A1S_2946,A1S_2947	hom	hom
INDEL	CP00052	3431037	3431037	A	-	A1S_2948,A1S_2949	hom	hom
INDEL	CP00052	3431044	3431044	A	-	A1S_2948,A1S_2949	hom	hom
INDEL	CP00052	3435875	3435875	-	A	A1S_2952(dist=135)	hom	hom
INDEL	CP00052	3441296	3441296	T	-	A1S_2955(dist=375)	-	hom

INDEL	CP00052	3441456	3441458	CTG	-	A1S_2955,A1S_2956	hom	hom
INDEL	CP00052	3441564	3441564	-	A	A1S_2955,A1S_2956	hom	hom
INDEL	CP00052	3444420	3444420	-	A	A1S_2956,A1S_3865	hom	hom
INDEL	CP00052	3450859	3450859	-	T	A1S_3867,A1S_3868	hom	hom
INDEL	CP00052	3451365	3451365	-	A	A1S_3867	hom	hom
INDEL	CP00052	3454245	3454245	-	T	A1S_2962(dist=624);	hom	hom
INDEL	CP00052	3458778	3458778	-	T	A1S_2967	hom	hom
INDEL	CP00052	3460446	3460446	T	-	A1S_2969(dist=38);A	hom	hom
INDEL	CP00052	3465510	3465510	-	A	A1S_2972	hom	hom
INDEL	CP00052	3468391	3468396	GTGA	-	A1S_2977,A1S_3873	hom	hom
INDEL	CP00052	3471234	3471234	-	A	A1S_2981	hom	hom
INDEL	CP00052	3477223	3477223	-	T	A1S_2988	hom	hom
INDEL	CP00052	3477643	3477643	-	A	A1S_3874	hom	hom
INDEL	CP00052	3500513	3500513	A	-	A1S_3013,A1S_3014	het	het
INDEL	CP00052	3506094	3506094	-	T	A1S_3016(dist=25)	hom	hom
INDEL	CP00052	3506102	3506102	-	CA	A1S_3016(dist=17)	hom	hom
INDEL	CP00052	3515366	3515366	-	A	A1S_3028	hom	hom
INDEL	CP00052	3528080	3528080	-	A	A1S_3043(dist=215);	hom	hom
INDEL	CP00052	3534889	3534889	-	T	A1S_3046	hom	hom
INDEL	CP00052	3551583	3551583	T	-	A1S_3064	hom	hom
INDEL	CP00052	3564937	3564937	-	C	A1S_3086	hom	hom
INDEL	CP00052	3566939	3566939	-	A	A1S_3088,A1S_3089	hom	hom
INDEL	CP00052	3569404	3569404	-	T	A1S_3090,A1S_3091	hom	hom
INDEL	CP00052	3573425	3573425	A	-	A1S_3094	hom	hom
INDEL	CP00052	3578696	3578696	-	C	A1S_3098	hom	hom
INDEL	CP00052	3579286	3579286	-	C	A1S_3100	hom	hom
INDEL	CP00052	3585646	3585646	-	AC	A1S_3105(dist=3);A1	hom	hom
INDEL	CP00052	3610075	3610075	-	T	A1S_3124,A1S_3125	hom	hom
INDEL	CP00052	3610089	3610089	-	A	A1S_3124,A1S_3125	hom	hom
INDEL	CP00052	3619058	3619058	G	-	A1S_3131,A1S_3132	hom	hom
INDEL	CP00052	3619067	3619067	G	-	A1S_3131,A1S_3132	hom	hom
INDEL	CP00052	3619095	3619095	T	-	A1S_3133	hom	hom
INDEL	CP00052	3621363	3621363	-	A	A1S_3134(dist=636);	hom	hom
INDEL	CP00052	3623239	3623239	-	A	A1S_3135(dist=44);A	hom	hom
INDEL	CP00052	3623426	3623426	-	T	A1S_3135(dist=231);	hom	hom
INDEL	CP00052	3631574	3631574	A	-	A1S_3144	hom	hom
INDEL	CP00052	3631581	3631581	T	-	A1S_3144	hom	hom
INDEL	CP00052	3631587	3631587	T	-	A1S_3145(dist=401);	hom	hom
INDEL	CP00052	3642286	3642286	T	-	A1S_3157	hom	hom
INDEL	CP00052	3662076	3662076	T	-	A1S_3176	hom	hom
INDEL	CP00052	3683961	3683961	G	-	A1S_3196	hom	hom
INDEL	CP00052	3686886	3686886	-	T	A1S_3201	hom	hom
INDEL	CP00052	3688793	3688793	-	T	A1S_3202(dist=2);A1	hom	hom
INDEL	CP00052	3695605	3695605	A	-	A1S_3209	hom	hom
INDEL	CP00052	3695672	3695672	T	-	A1S_3210(dist=113);	hom	hom
INDEL	CP00052	3700055	3700061	CTAA	-	A1S_3212,A1S_3884	hom	hom
INDEL	CP00052	3721551	3721551	T	-	A1S_3228	hom	hom
INDEL	CP00052	3727512	3727512	-	C	A1S_3234(dist=302);	hom	hom
INDEL	CP00052	3739293	3739293	-	T	A1S_3247,A1S_3248	hom	hom
INDEL	CP00052	3750131	3750131	-	A	A1S_3891(dist=254);	hom	hom
INDEL	CP00052	3758233	3758233	-	T	A1S_3894	hom	hom
INDEL	CP00052	3758338	3758338	T	-	A1S_3269,A1S_3894	hom	hom
INDEL	CP00052	3812401	3812401	-	T	A1S_3316	hom	hom
INDEL	CP00052	3823261	3823261	-	T	A1S_3324	hom	hom
INDEL	CP00052	3823319	3823319	-	T	A1S_3325(dist=122);	hom	hom
INDEL	CP00052	3846455	3846455	-	T	A1S_3343	hom	hom
INDEL	CP00052	3850367	3850367	A	-	A1S_3347	hom	hom
INDEL	CP00052	3850372	3850372	A	-	A1S_3347	hom	hom

INDEL	CP00052	3860370	3860370	A	-	A1S_3359	hom	hom
INDEL	CP00052	3860388	3860388	A	-	A1S_3359	hom	hom
INDEL	CP00052	3860393	3860393	T	-	A1S_3359	hom	hom
INDEL	CP00052	3864405	3864405	-	T	A1S_3362(dist=541);	hom	hom
INDEL	CP00052	3869954	3869954	-	GAT	A1S_3363	hom	hom
INDEL	CP00052	3870893	3870893	-	AA	A1S_3364	hom	hom
INDEL	CP00052	3874842	3874842	T	-	A1S_3365,A1S_3904	hom	hom
INDEL	CP00052	3874876	3874876	T	-	A1S_3366	hom	hom
INDEL	CP00052	3883587	3883587	-	G	A1S_3374	hom	hom
INDEL	CP00052	3886969	3886969	C	-	A1S_3377(dist=201);	hom	hom
INDEL	CP00052	3890925	3890925	-	T	A1S_3382	hom	hom
INDEL	CP00052	3892977	3892977	-	A	A1S_3382(dist=648);	hom	hom
INDEL	CP00052	3894443	3894443	A	-	A1S_3384,A1S_3385	hom	hom
INDEL	CP00052	3901577	3901577	A	-	A1S_3393	hom	hom
INDEL	CP00052	3901585	3901585	A	-	A1S_3393	hom	hom
INDEL	CP00052	3901594	3901594	A	-	A1S_3394,A1S_3395	hom	hom
INDEL	CP00052	3901649	3901649	A	-	A1S_3394,A1S_3395	hom	hom
INDEL	CP00052	3903148	3903148	C	-	A1S_3395	hom	hom
INDEL	CP00052	3910391	3910391	-	T	A1S_3401	hom	hom
INDEL	CP00052	3916901	3916901	A	-	A1S_3407	hom	hom
INDEL	CP00052	3921206	3921206	-	A	A1S_3410	hom	hom
INDEL	CP00052	3928909	3928909	-	T	A1S_3417,A1S_3418	hom	hom
INDEL	CP00052	3939776	3939776	-	T	A1S_3428	hom	hom
INDEL	CP00052	3940122	3940122	-	TCC	A1S_3428	hom	hom
INDEL	CP00052	3944373	3944373	-	T	A1S_3432	hom	hom
INDEL	CP00052	3944498	3944498	-	A	A1S_3433,A1S_3434	hom	hom
INDEL	CP00052	3944507	3944507	-	C	A1S_3433,A1S_3434	hom	hom
INDEL	CP00052	3957377	3957377	-	T	A1S_3446	hom	hom
INDEL	CP00052	3957489	3957489	-	TA	A1S_3446	hom	hom
INDEL	CP00052	3957498	3957498	-	A	A1S_3446	hom	hom
INDEL	CP00052	3964609	3964609	-	A	A1S_3450	hom	hom
INDEL	CP00052	8118	8118	-	T	A1S_3466(dist=433);	hom	hom
INDEL	P3	28	28	A	-	NONE(dist=NONE),N	hom	hom
INDEL	P3	36	36	C	-	NONE(dist=NONE),N	hom	hom
INDEL	P3	8080	8080	A	-	NONE(dist=NONE),N	hom	hom