Doctoral Thesis

Study on the regulation of host apoptosis and apoptotic factors by *Chlamydia* infection

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Contents

Abstract

Chlamydia pneumoniae is an obligate intracellular pathogen and can replicate solely within a membrane-bound vacuole termed an inclusion. *C. pneumoniae* can cause acute and chronic respiratory diseases, including pneumonia and bronchitis, and its chronic infection is widely considered to be a cause of atherosclerosis, asthma, Alzheimer's disease and other inflammatory processes. *Chlamydia* perturbs multiple cellular processes of the host to facilitate their survival and evade the host immune surveillance, such as host cell apoptosis. Apoptosis is an active process of cellular suicide triggered by a variety of stressors and physiological stimuli for tissue development and homeostasis of organisms. *C. pneumoniae* was reported to inhibit apoptosis induced by staurosporine (STS) and tumor necrosis factor alpha (TNF-α) in infected epithelial cells, macrophages and monocytes. But the precise mechanisms by which *C. pneumoniae* regulates host cell apoptosis remain unknown.

In our first attempt to clarify host and chlamydial factors involved in apoptosis regulation, it has been found that Apaf-1 and caspase-9 inhibitors were shown to increase and decrease *C. pneumoniae* infection, respectively. But no effects were observed by caspase-8 and -3 inhibitors or Bcl-2 over expression. These opposite effects by Apaf-1 and caspase-9 inhibitors were confirmed using *apaf-1*$^{-/-}$and *caspase-9*$^{-/-}$ mouse embryonic fibroblasts (MEFs) as host cells. Moreover caspase-9 was activated without activation by Apaf-1, and accumulated within chlamydial inclusions. The sequestration of caspase-9, which means physical disconnection from the caspase cascade, by *Chlamydia* seems to result in apoptosis repression. As an interesting observation, caspase-9 inhibitor could diminish chlamydial infection. Thus there are crucial queries remained, such as which chlamydial proteins are involved in the sequestration of caspase-9 on the chlamydial inclusions and are affected by caspase-9 inhibitor in the inclusions.

As our next attempt to clone chlamydial genes, which products can interact with human caspase-9, a screening using a yeast two-hybrid system was performed. We have constructed the genomic library including 1065 genes of *Chlamydia pneumoniae* by homologous recombination method and analyzed interaction with caspase-9. We found chlamydial proteins Cpj0056, Cpj0444, Cpj0512, Cpj0838 and Cpj0948 to positively interact with capase-9. Pull-down experiments showed that caspase-9 physically bound to the Cpj0838 product and chlamydial cells (EB). These interactions may provide a valuable clue regarding the mechanism for Apaf-1-

independent activation of caspase-9 supporting chlamydial multiplication in parallel with apoptosis repression by the caspase-9 sequestration. Using gene annotation chlamydial 47 outer membrane protein coding genes were selected for screening interaction with human aorta cDNA library. Human aorta cDNA library were individually transformed into the yeast strains AH109 carrying pGBKT7 vector cloned with chlamydial 47 outer membrane genes. Chlamydial 22 outer membrane proteins found to interact with 74 human proteins.

1. Introduction

1.1 Disease caused by *Chlamydia*

Chlamydia is an obligate intracellular parasitic bacterium firstly described as a pathogen for acute respiratory diseases (Grayston et al. 1986). Currently, 9 species of *Chlamydia* have been confirmed including *Chlamydia psittaci* (Balsamo et al. 2017). The host range is wide, and there are reports of separation from amphibians such as frogs, reptiles such as turtles, snakes, iguanas, chameleons, koalas, and horses other than humans (Bodetti et al. 2002). *Chlamydia pneumoniae* have been found by its specific antibody titers with chronic bronchitis patients and were confirmed by culture or PCR (Blasi et al. 1998). It has also considered as a cause of several chronic inflammatory diseases including atherosclerosis (Campbell & Kuo 2004), asthma (Hahn, Dodge & Golubjatnikov 1991), and Alzheimer's disease (Balin et al. 1998) (Kinoshita 2004). More than 50% tissue samples of atherosclerotic patients have been reported positive for *Chlamydia pneumoniae* (Grayston 2000), which was supported by *in vitro* experiments demonstrating that cells involved in atherogenesis are also susceptible to *Chlamydia pneumoniae* infection (Godzik et al. 1995). *Chlamydia trachomatis* is a causative microorganism of ocular conjunctivitis and if it is not treated with antibiotic, chronic infection led to the blindness of millions of people annually in developing countries (Taylor et al. 1987) through scratching of the cornea (Gambhir et al. 2007). It is also a serious cause of sexually transmitted infection (Brunham & Rey-Ladino 2005). Its chronic infection is responsible for pelvic inflammatory diseases and infertility (Sherman et al. 1990). *Chlamydophila psittaci* is a zoonotic infectious pathogen causes human psittacosis. The infection is transmitted by close contact with infected birds, especially poultry industry, and from contact with Psittaciformes (cockatoos, parrots, parakeets and lories) (Beeckman & Vanrompay 2009) (Table: 1).

1.2 Developmental cycle of *Chlamydia*

Chlamydia shows different morphology and function in infected host cell environment and external environment (Hackstadt et al. 1997). *Chlamydia* has a unique biphasic life cycle initiated by the infectious but metabolically inactive elementary bodies (EBs), with diameter approximately 0.3 μm (AbdelRahman & Belland 2005). Firstly, infectious elementary body (EB) of *Chlamydia pneumoniae* enters into the host cell by phagocytosis. Phgocytosed EBs reside within a membrane

bound vacuole named the inclusion. The inclusion membrane is actively modified to avoid fusion with late endosomes or lysosomes to ensure their survival against lysosomal degradation (Ojcius, Hellio, & Dautry-Varsat 1997; Scidmore, Fischer & Hackstadt 2003). About 2 to 3 hours after the infection, the form changes from infected type to proliferative reticulate body (RB), and the phagocytic membrane constructs inclusion body membrane by *Chlamydia* membrane protein. Growth starts in the inclusion body. RBs perform binary fissions proliferations (AbdelRahman & Belland 2005) and grows to about 1000 cells per inclusion body. In the absence of stress such as growth inhibition, RB retransforms to EB and EB is released to start the next infection (Hybiske & Stephens 2007) (Fig. 1). Antibiotics are effective for pneumonia with acute infection of *Chlamydia pneumoniae* but are considered to be ineffective for persistent infection (Yamaguchi et al. 2003). Under stressed condition (e.g. treatment with antibiotic or interferon gamma (IFNγ) induced activation host cell), *Chlamydia* can alternate some morphological changes ultimately formation of persistent body (PB) (Luis et al. 1987). Formation of persistent body (PB) allows for a chronic infection of the host cell. In the case of *Chlamydia pneumoniae*, one cycle of infection takes about 3 days, whereas, *Chlamydia trachomatis* takes about 2 days.

1.3 Pathogenicity of *Chlamydia*

1.3.1 Attachment

The very early step in the host-pathogen interaction is attachment of the pathogen to host surfaces. *Chlamydia spp.* is obligate intracellular bacterial pathogen that causes a number of diseases in human. A number of both bacterial and host factors are involved with the attachment and invasion of *Chlamydia spp.* The attachment and internalization processes vary depending on different types of hosts and tissues. The attachment starts by the low-affinity interaction of *C. pneumoniae, C. trachomatis* and *C. muridarum* with heparan sulphate proteoglaycans (HSPGs) followed by binding to host cell receptors.

Microbial factors made from polypeptides (proteins) or polysaccharides (carbohydrates or sugars) mediate the adhesion to host cell are called adhesins. Chlamydial adhesins proteins such as OmcB (also known as CT443), GroEL-1, chlamydial major outer membrane protein (MOMP), EB proteins-like glycosaminoglycans (GAGs) and polymorphic membrane protein (pmp) family from *C. trachomatis* L1 or *C. pneumoniae* mediates the adhesion. Other adhesins

lipopolysaccharides (LPS) are also involved in attachment of *Chlamydia* to host cell (Hegemann & Moelleken 2012). Surface proteins of host cell such as mannose/mannose-6-phosphate (M6P) receptor, apolipoprotein E4 receptor, epidermal growth factor receptor (EGFR), ephrin receptor A2 (EPHA2) and estrogen/protein di-sulphide isomerase (PDI) receptor have been proposed to associated with binding and adhesion of *Chlamydia spp.* (Hegemann & Moelleken 2012; Elwell, Mirrashidi & Engel 2016).

1.3.2 Type III secretion

On contact with host cells, *Chlamydia spp.* inject the pre-synthesized effectors through the type III secretion system (T3SS) to induce cytoskeletal remodeling that promote invasion and activate host signaling to establish an anti-apoptotic environment (Dai & Li 2014). The most well characterized chlamydial effector, translocated actin-recruiting phosphoprotein (TarP; also known as CT456) nucleates and bundles actin through its own globular actin (G-actin) and filamentous actin (F-actin) domains (Hackstadt 2012). T3SS effector CT694 a multidomain protein interacts with the AHNAK protein. Both CT694 and CT166 promote the depolymerization of actin and TepP (also known as CT875) phosphorylated by host tyrosine kinases, involve in the intiation of innate immune signaling (Elwell, Mirrashidi & Engel 2016). The elementary body (EB) is then endocytosed into a membrane bound vesicle termed as the inclusion.

1.3.3 Modification of host immune response

Recognition of the microbe by the innate immune system is a critical first step to remove a pathogenic microbe. The innate immune cells have certain receptors called pathogen recognition receptors (PRRs) used for recognizing the microbial conserved structures called microbe associated molecular patterns (MAMPs) (Nagarajan 2012). *Chlamydia* is an obligate intracellular bacterium and has biphasic life cycle. Chlamydial MAMPs are initially recognized by PRRs at the host cell surface but the majority of the recognition occurs intracellularly. Moreover, different effectors secreted by EBs and RBs are also recognized by different host receptors (Nagarajan 2012). Chlamydial lipopolysaccharides (LPS) and/or 60kDa heat shock protein (HSP60) are recognized by TLR4, whereas TLR2 recognizes peptidoglycan, macrophage inhibitory protein (MIP) and/or chlamydial plasmid regulated ligand. The

downstream signaling of both TLR2 and TLR4 requires the adaptor myeloid differentiation primary response protein 88 (MYD88) and tumor necrosis factor (TNF) receptor-associated factor 6 (TRAF6) for the activation of NF-κB and MAPK. In response to infection with *C. pneumoniae, C. trachomatis* and *C. muridarum* , an intracellular cytosolic receptor nucleotide-binding oligomerization domain-containing 1 (NOD1) is also activated that can causes NF-κB activation (Nagarajan 2012). To ensure their survival in the host *Chlamydia* modifies several host immune responses and in some cases, prevents clearance. TRAF3 is a signaling molecule which has a pivotal role in the production of type I interferon (IFN). Type I IFNs are induced by microbial infections and has antiviral activities. During infection with *C. pneumoniae,* an unknown protease specific to *C. pneumoniae* degrades the signaling molecule tumor necrosis factor (TNF) receptor-associated factor 3 (TRAF3) and ultimately interferon beta (IFNβ) production are suppressed (Wolf & Fields 2013).

In different manner *Chlamydia* reduce or block nuclear factor-κB (NF-κB) transcription (Bastidas et al. 2013; Hackstadt 2012) to escape cell autonomous immunity. The *C. pneumoniae* specific inclusion (Inc) protein CP0236 contains domains exposed to the host cytoplasm. The Inc protein CP0236 are shown to interact to and sequesters NF-κB activator 1 (ACT1; also known as CIKS) to the inclusion membrane, leading to the blockage of NF-κB signaling, whereas The T3SS effector ChlaDub1 (also known as CT868) binds to NF-κB inhibitor-α (IκBα) and stabilizes by impairing its ubiquitination in the cytosol (Wolf, Plano & Fields 2009). In an ex vivo tissue infection with *C. trachomatis* the level of olfactomedin 4 (a glycoprotein*) OLFM4* mRNA was increased about 100-fold compare to non-infected control. The increased level of olfactomedin 4 (OLFM4), may suppress the NOD1-mediated activation of NF-κB (Kessler et al. 2012).

1.4 Apoptosis regulation by *Chlamydia*

Apoptosis is one of the programmed cell death of the host and is induced against various stimuli from inside and outside the cell to maintain homeostasis of multi-cellular organisms. Apoptosis is characterized by apparent morphological changes thus formation of apoptotic bodies, and finally cleared from the system through phagocytosis and degradation by other cells (Kerr, Wyllie & Currie 1972). There are two types of apoptosis pathway; the death receptor mediated extrinsic pathway and the mitochondrial intrinsic pathway (Fig. 2). In mitochondrial intrinsic

pathway, when the apoptotic signal is transmitted by the ultraviolet irradiation, DNA damage, internal stress, etc., the apoptosis-promoting Bcl-2 family such as Bax and Bak is activated, and cytochrome *c* released into the cytoplasm from the mitochondria. The cytochrome *c,* Apaf-1 and procaspase-9 form an apoptosome leading to caspase-9 activation with the hydrolysis of dATP or ATP. Apoptotic pathway is initiated by the active caspase-9 mediated cleavage of caspase-3 (Salvesen & Dixit 1997). This apoptotic response is tightly regulated by Bcl-2 to prevent the release of cytochrome *c* from mitochondria (Shimizu, Narita & Tsujimoto 1999).

In order to avoid the host's immune system, many pathogenic bacteria are important to reorganize the apoptotic function (Friedrich et al. 2017) and metabolic process (Gehre et al. 2016) of host cells. The ultimate goal of all pathogen is to establish a favorable niche in the host for their own multiplication. Several pathogenic microbes both bacteria and viruses to ensure intracellular survival modulate apoptosis to escape host immune response. Bacteria like *Shigella, Salmonella*, and *Yersinia* are thought to have developed a variety of strategies to control the inflammatory and apoptotic process to establish infection, multiplication and dissemination to other hosts (Giogha et al. 2014; Gao & Kwaik 2000).

Obligate intracellular parasitic bacteria *Chlamydia* and *Rickettsia* avoid the immune system by inhibiting host cell apoptosis (Clifton et al. 1998). It is believed that by proliferating intracellularly *Chlamydia* inhibit host apoptosis; it also avoids removal of infected cells by immune cells. In case of *Chlamydia*, depending on the host and *Chlamydia* type and infection conditions, many factors that promote apoptosis have been reported, and cases in which caspase-independent apoptosis is promoted are also shown (Perfettini et al. 2002). *C. pneumoniae* was reported to inhibit apoptosis induced by staurosporine (STS) and tumor necrosis factor alpha (TNF-α) in infected epithelial cells, macrophages and monocytes (Rajalingam et al. 2001; Airenne et al. 2002; Geng et al. 2000; Fischer et al. 2001). It was reported that *C. pneumoniae* induced apoptosis in coronary artery endothelial cells (Schöier et al. 2006), whereas in many cases *C. pneumoniae* tends to suppress host apoptosis. Elucidation of host cell apoptosis controlled by *Chlamydia* is a prerequisite to understanding chlamydial strategies for persistent infection and how to overcome the diseases caused by *Chlamydia.*

The first installment reported that host cell apoptosis promoted by a variety of stimuli, such as STS and TNF-α, was inhibited by chlamydial infection. This

inhibition was accompanied with and explained by prevention of the cytochrome *c* release from mitochondria (Fischer et al. 2001; Fan et al. 1998). This prevention was later explained by specific degradation of the pro-apoptotic BH3-only proteins, such as Bik, Puma, Bim, Bad, Bmf, Noxa, and tBid (Fischer et al. 2004; Dong et al. 2005; Ying et al. 2005). Chlamydial protease– or proteasome–like activity factor (CPAF), which is a potent and promiscuous cysteine protease capable of cleaving many host proteins, was initially implicated in this degradation (Pirbhai et al. 2006). However, subsequent studies showed that the proteolysis of the reported CPAF substrates was due to enzymatic activity in cell lysates rather than in intact cells (Chen et al. 2012), (Snavely et al. 2014). Moreover, conflicting observations concerning the degradation of the pro-apoptotic BH3-only proteins were also reported (Verbeke et al. 2006), (Rajalingam et al. 2008). Thus, the involvement of BH3-only proteins and CPAF is still an important topic to be clarified. Instead of the degradation of pro-apoptotic factors, stabilization of the anti-apoptotic factor Bcl-2 has been described (Rajalingam et al. 2008; Kun et al. 2013). Along with protection from host cell apoptosis during *C. trachomatis* infection, the activation of both Raf/MEK /ERK (or MAPK/E RK) and PI3K/AKT pathways has been observed, leading to up regulation of *mcl-1* gene expression and stabilization of Bcl-2 family protein myeloid leukemia cell differentiation protein (Mcl-1). Mcl-1 protein binds to the BH3-only protein Bim and inhibits apoptosis initiation (Rajalingam et al. 2008). Recently, Bag-1 (Bcl-2-associated athanogene), which interacts with a diverse array of molecular targets including anti-apoptotic regulator Bcl-2 and heat shock proteins, was identified as another element that is potentially regulated via the MAPK/ERK pathway (Kun et al. 2013).

Two interesting sequestration models have been proposed, based on evidence suggesting that pro-apoptotic factors are mislocalized away from their conventional target sites in infected cells. In the first study, activation of the PI3K pathway by *C. trachomatis* infection, but not *C. pneumoniae*, led to phosphorylation of Bad, and the phosphorylated Bad was sequestered via 14-3-3 beta in the chlamydial inclusion membrane that expresses IncG proteins (Verbeke et al. 2006). The other observation was that protein kinase C delta (PKC-δ), which functions as a pro-apoptotic effector in the mitochondria and nucleus, was mislocalized in the immediate vicinity of chlamydial inclusions where diacylglycerol was accumulated (Tse et al. 2005). In both cases, it was not mentioned whether those factors work only to trigger apoptotic

regulation or serve any other special functions at the sequestration sites.

The engagement of downstream molecules has also been suggested. *C. pneumoniae* infection of human monocytic cells induced the expression of the cellular inhibitor of apoptosis 2 (cIAP2) by misuse of the NF-κB pathway during infection (Wahl et al. 2003). Infection with *C. trachomatis* also led to the upregulation of cIAP2 and stabilized functional heterodimers of the IAPs, thereby the ability to inhibit apoptosis may be more secure (Rajalingam et al. 2006).

1.5 Interaction with *Chlamydia* and host factors

In the early stage of infection, endocytosed inclusions of some *Chlamydia spp.* are trafficked to and aggregate at the microtubule-organizing center (MOTC). During infection with *C. trachomatis* inclusions are colocalized with host factor src-family kinases (SFKs). Four inclusion membrane proteins (Incs) in *C. trachomatis* (IncB, CT101, CT222 and CT850) are shown to contact and colocalize with active SFKs and is enriched in cholesterol (Mital et al. 2010; Kokes & Valdivia 2012). *C. psittaci* inclusion protein IncB found to interact and colocalize with host cytosolic fator Snapin, a protein that associates with host SNARE proteins (soluble N-ethylmaleimide-sensitive factor attachment protein receptor proteins) (Böcker et al. 2014). These inclusion and host factor interaction with SFKs and Snapin are involved in inclusion transport to MOTC possibly through dynein motor complex. Moreover CT850 from *C. trachomatis* also directly bind to dynein light chain 1 (DYNLT1) (Mital et al. 2015). *Chlamydia spp*. can arrest apoptotic cell death and modify immune response by activating pro-survival pathway (Bastidas et al. 2013). Human epidermal growth factor receptor (EGFR) is recruited for binding both *C. pneumoniae* adhesin protein Pmp21 and EB. This binding of Pmp21 to EGFR activates the signaling cascade and enhances the internalization of EB into host cell (Mölleken, Becker & Hegemann 2013). In *C. trachomatis* infection, fibroblast growth factor 2 (FGF2) mediated binding of EB with fibroblast growth factor receptor (FGFR) activate MEK–ERK signaling survival pathway (Kim et al. 2011)

C. pneumoniae inclusion protein Cpn1027 can binds with cytoplasmic activation/proliferation-associated protein 2 (CAPRIN2) and glycogen synthase kinase 3β (GSK3β) members of the Wnt signaling pathway associated β-catenin destruction complex (Flores & Zhong 2015), which may allows β-catenin to activate

the transcription of anti-apoptotic genes hence promote the survival of *C. pneumoniae*.

1.6 Aim of this study

Apoptosis or programmed cell death is an active process of cellular suicide triggered by a variety of stresses and physiological stimuli for tissue development and homeostasis (Steller 1995). *Chlamydia* seems to perturb multiple cellular processes of the host, such as, rearrangement of the membrane trafficking system for its intracellular multiplication, and inhibition of host cell apoptosis for persistent infection. In this study our first attempt was to clarify host factor involvement in apoptosis regulation by *Chlamydia*. We found that inhibition of Caspase-9 restricted, while Apaf-1 promoted, *Chlamydia pneumoniae* infectionin HEp-2, HeLa, and mouse epithelial fibroblast (MEF) cells. These opposite contributions to the chlamydial infection were confirmed using *caspase-9*$^{-/-}$ and *apaf-1*$^{-/-}$ MEFs. Similar phenomena also appeared in the case of infection with *Chlamydia trachomatis*. Interestingly, caspase-9 in *apaf-1*$^{-/-}$ MEFs was activated by chlamydial infection but during the infection caspase-3 was not activated. That is, caspase-9 was activated without support for multiplication and activation by Apaf-1, and the activated caspase-9 may be physically disconnected from the caspase cascade. This may be partially explained by the observation of caspase-9 accumulation within chlamydial inclusions. The sequestration of caspase-9 by *Chlamydia* seems to result in apoptosis repression, which is crucial for the chlamydial development cycle. Our next attempt was to identify chlamydial genes interact with caspase-9 using chlamydial gene library of 1033 genes and 47 chlamydial outer membrane gene interactions with human aorta cDNA library by yeast two-hybrid (Y2H) system and to explain the repression of apoptosis and pathogenicity caused by *Chlamydia pneumoniae.*

2. Materials and methods

2.1 Host cell lines, chlamydial strains, other bacteria and yeast

Apaf-1 knockout (*apaf-1*$^{-/-}$) and caspase-9 knockout (*caspase-9*$^{-/-}$) mouse epithelial fibroblasts (MEF), and Bcl-2-overexpressing HeLa cells were kind gifts from Xiaodong Wang (Univ of Texas) (Honarpour et al. 2000), Shin Yonehara (Kyoto Univ) (Ohgushi et al. 2005) and Yoshihide Tsujimoto (Osaka Univ) (Tsujimoto 1998), respectively. These cell lines and their corresponding control cells, i.e. MEFs, HeLa229 (ATCC CCL-2), and HEp2 (ATCC CCL23) were cultured in Dulbecco's modified Eagle's medium supplemented with 2 mM L-glutamine (Sigma-Aldrich), 10% heat-inactivated fetal calf serum and 50 μg/mL gentamicin at 37ºC under 5% CO_2. *Chlamydia pneumoniae* J138 and AR39, and *Chlamydia trachomatis* serovar D were used for chlamydial infection. For vector construction and protein expression *E.coli* DH5α, *E.coli* BL21(DE3) bacterial strains were used respectively. *Saccharomyces cerevisiae* (AH109) (Clontech) strain were used for *C. pneumoniae* genomic library construction and Y2H assay.

2.2 Media and culturing

E. coli strains were cultured in Luria-Bertani (LB, Nacalai tescue) broth or plated on solid media containing 1.5% bacteriological agar. Transformed *E. coli* with plasmid vector were selected on solid LB + ampicilin (Amp) (100 μg/ml) or LB + kanamycin (Kan) (25 μg/ml) supplemented medium. *Saccharomyces cerevisiae* (AH109) (Clontech) strain was cultured on YPD broth medium or plated on solid media containing 2.0% bacteriological agar. Yeast transformed with vector(s) was selected on yeast synthetic dropout (SD) medium supplemented with yeast nitrogen base (YNB w/o amino acids, Difco) and glucose (2%). SD medium without tryptophan (SD-W), SD medium without leucine (SD-L), SD medium without leucine, tryptophan (SD-LW), SD medium without tryptophan, adenine and histidine (SD-WAH) and SD medium without leucine, tryptophan, adenine and histidine (SD-LWAH) were prepared by adding required Adenine (0.4 mg/mL), Leucine (3.6 mg/mL), Histidine (10.0 mg/mL) purchased from Wako (Tokyo, Japan) and L-Tryptophane (4.0 mg/mL) from Sigma (Saint Louis, MO).

2.3 Reagents and antibodies

Apoptosis inhibitors, Hoechst 33258,4′6-diamidino-2-phenylindole (DAPI), and cell-permeant inhibitors of Apaf-1 (NS3694), caspase-8 (Z-IETD-FMK), caspase-9 (Z-LEHD-FMK), and caspase-3 (Z-EDVD-FMK) were obtained from Sigma-Aldrich (Saint Louis, MO). Fetal calf serum was from Cansera International Inc. (Etobicoke, Canada). Staurosporine (STS), gentamicin, penicillin, streptomycin, and cycloheximide were from Wako (Tokyo, Japan). Anti-Apaf-1, anti-caspase-9 and anti-caspase-3 antibodies were from Cell Signaling Technology (Danvers, MA). Anti-caspase-9 antibodies were also purchased from Calbiochem (La Jolla, CA) and Abcam (Cambridge, UK). Caspase-9, -8 and -3 Colorimetric Activity Assay kits, and ApopTag Fluorescein kit for TUNEL assays were from Chemicon (Temecula, CA). *Chlamydiaceae*-specific fluorescein isothiocyanate (FITC)-conjugated monoclonal antibody (Chlamydia-FA) was from Denka Seiken (Tokyo, Japan). For pull-down assay experiment caspase-9 was stained by anti pro-caspase-9 mouse monoclonal antibody Santa Cruze (Santa Cruze, CA) followed by alkaline phosphatase conjugated anti-mouse goat polyclonal antibody Santa Cruze (Santa Cruze, CA) and His-tagged chlamydial protein was detected by alkaline phosphatase conjugated anti-6X His-tag monoclonal antibody (Abcam, Cambridge, UK). *Chlamydia pneumoniae* J138 EB were detected by anti-*Chlamydia* Pmp mouse monoclonal antibody.

2.4 Chlamydial infection

Host cells, 2×10^4 cells per well of flat-bottomed 96-well tissue culture plates, were allowed to adhere for 24 hours prior to infection. Measurements of infection rates for *C. pneumoniae* J138 were calculated by the same method described previously (Rahman et al. 2005), or as described in the figure legend for each experiment. Briefly, the multiplicity of infection (MOI) of each chlamydial stock solution was first calculated and determined by its inclusion formation units (IFUs) against HEp-2 cells. Infection rates achieved at MOI = 0.2 in HEp-2, HeLa, and MEFs were approximately from 15% to 25% in our experiments. Infection was generally carried out at MOI = 0.2 to given host cells. After cells were fixed at 48 hours post-infection (hpi) and stained with Chlamydia-FA and DAPI, cells with inclusions only larger than 4 μm in diameter were counted as infected ones, to adjust the infectious stage and diminish staining noises. Infection rates were calculated based on cell numbers determined by DAPI staining of nuclei. Generally more than

100 infected cells were counted as a population for one sample. All data are expressed as means ± SD calculated from at least three independent experiments. An asterisk denotes $p < 0.05$ with Student's *t* test.

Amounts of infectious progenies of *C. pneumoniae* were calculated as previously described (Rahman et al. 2005). Briefly, culture supernatants of *Chlamydia* infection at 80 hpi were harvested and used for re-infection in control MEFs. The infection rates were measured at 48 hpi.

2.5 Apoptosis induction and assays

HEp-2 cells were infected with *C. pneumoniae* J138 (MOI= 0.2). At certain times during infection, apoptosis of host cells was induced with 0.5 μM STS for 4 h. After fixation with 30% and then 70% ethanol for 10 min at room temperature, cells were stained with Chlamydia-FA and 2 μM Hoechst 33258 in phosphate-buffered saline (PBS) for 45 min at 4ºC.

For the categorization of apoptotic or non-apoptotic cells in the infection cases, only cells containing inclusions larger than 4 μm in diameter were counted as infected cells. Out of more than 50 infected cells, which were selected randomly under 200 times magnification, cells showing apoptotic nuclear morphology were counted. All data are expressed as means ± SD calculated from at least three independent experiments. An asterisk denotes $p < 0.05$ with Student's *t* test. To confirm apoptotic cell death, we carried out TUNEL staining as described previously (Tse et al. 2005).

For caspase-8, -3 and -9 activity assays, cytosolic extracts were prepared and analyzed by caspase-8, -3 and -9 Colorimetric Activity Assay Kits from Chemicon (Temecula, CA), according to the manufacturer's protocol. For western blot detection of Apaf-1, caspase-3 and -9 protein, total cell extracts were prepared from *apaf-1*$^{-/-}$ and control MEFs in the lysis buffer of the caspase activity assay kit, and western blotting assays to detect caspase cleavage were performed as described previously (Murata et al. 2007).

2.6 Immunofluorescence staining

For analysis of the localization of caspase-9, host cells grown on coverglasses (with or without chlamydial infection) were fixed with 100% methanol and independently stained with anti-caspase-9 antibodies purchased from Cell Signaling,

Calbiochem and Abcam. To detect chlamydial inclusions, mouse anti-*Chlamydia spp.* monoclonal antibody RR402 (Washington Research, Seattle, WA) and rhodamine-conjugated goat anti-mouse antibody (DAKO) were used. Polyclonal antibody against IncA2 (inclusion membrane protein A2) of *C. pneumoniae* J138 was produced using recombinant IncA2 protein by the same method as described previously (Murata et al. 2007).

2.7 pCMV Vector construction and transfection

pCMV-SPORT6.1 containing the mouse *apaf-1* gene was obtained from Invitrogen (Carlsbad, CA). The pCMV control vector was prepared by removing the 0.9-kb *Hind*III-*Hind*III region containing the mouse *apaf-1* gene from the pCMV-SPORT6.1. Transfection was carried out with a Nucleofector (Lonza, Cologne, Germany) based on the manufacturer's recommended methods. The infection assays were carried out when the rates of the transient transfection were above 70%.

2.8 Construction of whole chlamydial genome library

To construct a chlamydial genomic library for Y2H screening, the pGBKT7 vector was linearized by restriction digestion with *Bam*HI Clontech Takara (Mountain View, CA). Reaction condition for linearization was total volume 25.0 µL with composition (DNA 5.0 µL, 10 x K buffer 2.5 µL, BamHI 0.5 µL (12 U/µL), H_2O 17.0 µL) and incubated at 37 ℃ over night. All protein coding DNA fragments of *Chlamydia* were individually amplified by PCR using modified method (Miura et al. 2008). *C. pneumoniae* J138 genomic DNA was used as a template. The 1072 sets of primer sequences designed for construction of whole chlamydial genome library are shown in Table: 3. The PCR cycles comprised an initial denaturation step at 95°C for 5 minutes, followed by 25 cycles of, 95°C for 30 seconds, 54°C-65°C (according to primers annealing temperature) for 30 seconds, and 72°C for 30 seconds, and 72°C for 5 minutes, finally hold on temperature 4°C. Size of some PCR products were confirmed by electrophoresis.

Yeast cells were transformed using a Lithium acetate method (Fukunaga et al. 2013). Briefly, cells of AH109 were initially grown in YPD liquid medium overnight, from which 1 mL of the cultures was added with 9 mL of fresh YPD, and incubation was carried out at 30°C for 5 hours with shaking at 250 rpm. The yeast cells were then collected by centrifugation at 2000 rpm (1000 xg) for 5 minutes at room

temperature, washed once with 1 mL of sterile Milli Q water, and suspended in approximately 100 µL of Milli Q water. The cells were next mixed with transformation solution as follows; 120 µL of 60% Polyethyleneglycol 4000 (Wako Pure Chemical Industries Ltd. Japan), 10 µL 5 mg/mL carrier DNA (Calf thymus DNA) , 20 µL 1 M Lithium acetate, 1 µL linearized pGBKT7 vector (50-100 ng) and 5 µL (50-100 ng) of the PCR product. The resulting mixture was incubated at 42°C for 1 hour. 5 µL from each transformant was spotted on SD medium without Trp (SD-W) plate and incubated at 30°C for 2 to 3 days. Cloning was confirmed by colony PCR of nine genes as examples using respective primers shown in (Table: 3) designed for chlamydial gene cloning. Colony PCR was carried out using yeast colony as template and same condition for DNA fragments amplification.

2.9 Construction of pGADT7+caspase-9 vector

To construct a bait vector, pGADT7+caspase-9, a human caspase-9 DNA fragment was amplified by PCR using human aorta cDNA library as a template and two primers, Caspase-9 for pGADT7_F (*Bam*HI site) and Caspase-9 for pGADT7_B (*Bam*HI site) (Table: 4). PCR reaction was carried in total volume 40.0 µL with composition H_2O 21.8 µL, template DNA 2.0 µL (human PACT2 aorta cDNA library 1/10 dilution), 10X Ex Taq buffer 4.0 µL, dNTP (2.5 mM) mixture 3.2 µL, Ex Taq (5 U/µL) 1.0 µL Clontech Takara (Mountain View, CA), forward primer (Caspase -9 for pGADT7 primer 10 pmol / µL) 4.0 µL, backward primer (Caspase-9 for pGADT7 primer 10 pmol / µL) 4.0 µL. The PCR cylcles comprised an initial denaturation step at 95°C for 5 minutes, followed by 25 cycles of, 95°C for 30 seconds, 62°C for 30 seconds, and 72°C for 30 seconds, and 72°C for 5 minutes, finally hold on temperature 4°C. Amplified PCR product was confirmed by electrophoresis. pGADT7 vector was linearized by *Bam*HI (Clontech TAKARA) restriction enzyme. Reaction condition using total volume 25.0 µL with composition (DNA 5.0 µL, 10 x K buffer 2.5 µL, *Bam*HI (12 U/µL) 0.5 µL, H_2O 17.0 µL) and incubate at 37°C over night. Full-length PCR product of Caspase-9 was cloned with linearized pGADT7 vector by infusion cloning method. Infusion cloning was performed using Infusion kit (TAKARA). Total reaction volume 10 µL (In-fuison HD Enzyme premix 2.0 µL, vector 2.0 µL, insert 2.0 µL, sterile Milli Q H_2O 4.0 Ml) incubated at 50 ° C for 15 minutes. Transformed using *E. coli* DH5α competent cell (TAKARA). Total 54.0 µL

(competent cell 50.0 µL, DNA 4.0 µL,) was run on 1700 V, incubated at 37°C for 30 minutes, then spread on LB + Amp plate and incubated at 37°C for 12 h.

2.10 Caspase-9 cloning into pGEX(2T-P) vector

The plasmid vector pGEX(2T-P)+caspase-9 was constructed by cloning the full-length DNA fragment of human caspase-9 into the *Bam*HI and *Sal*I sites of pGEX(2T-P)SRP1, an improved version of pGEX-2T vector (GE Healthcare Japan) which was mutated at *Pst*I site of AmpR and introduced SRP1 gene at multiple cloning site between *Bam*HI and *Eco* RI (Azuma et al. 1995). The *Bam*HI/*Sal*I digested PCR product was then cloned into *Bam*HI/*Sal*I digested pGEX(2T-P)SRP1 to generate pGEX(2T-P)Caspase-9. Full length Caspase-9 DNA fragment was amplified from human aorta cDNA library by PCR. PCR reaction solution was carried in total volume 40.0 µL with composition H_2O 21.8 µL, template DNA 2.0 µL (human PACT 2 aorta cDNA library 1/10 dilution), 10X Ex Taq buffer 4.0 µL, dNTP (2.5 mM) mixture 3.2 µL, Ex Taq (5 U/µL) 1.0 µL Clontech Takara (Mountain View, CA). Forward primer (hCaspase-9_3 primer 10 pmol / µL 4.0 µL, reverse primer (hCaspase-9_4 primer 10 pmol / µL) 4.0 µL (Table: 4). The PCR cylcles comprised an initial denaturation step at 95°C for 5 minutes, followed by 25 cycles of, 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 30 seconds, and 72°C for 5 minutes, finally hold on temperature 4°C.

Restriction enzyme treatment was carried out for insert and vector preparation as described bellow. Insert (Caspase-9) and vector (pGEX(2T-P)SRP1) were treated with restriction enzymes *Bam*HI. Restriction enzyme reaction: (For insert) total 25.0 µL (DNA (~30 ng/ µL) 19.0 µL, 10 × K buffer 2.5 µL, *Bam*HI (12 U/ µL) 0.5 µL, H_2O 3.0 µL), (For vector) total 25.0 µL (DNA (~120 ng/ µL) 5.0 µL, 10 x K buffer 2.5 µL, *Bam*HI (12 U/ µL) 0.5 µL, H_2O 17.0 µL), was incubated at 37°C over night. Insert (Caspase-9) and vector (pGEX(2T-P)SRP1) after *Bam*HI treatment were treated with restriction enzymes *Sal*I (Clontech TAKARA). Restriction enzyme reaction: (For insert) total 25.0 µL (DNA (~30 ng/ µL) 19.0 µL, 10 × H buffer 2.5 µL, *Sal*I (15 U/ µL) 0.5 µL, H_2O 3.0 µL), (For vector) total 25.0 µL (DNA (~30 ng/ µL) 19.0 µL, 10 × H buffer 2.5 µL, *Sal*I (15 U/ µL) 0.5 µL, H_2O 3.0 µL), was incubated at 37°C over night.

Restriction enzyme-treated inserts and vectors were applied to 1% agarose gel and electrophoresed (total amount 25.0 µL) at 100 V for 30 minutes. After

electrophoresis, the gel was stained with ethidium bromide (EtBr) solution for 15 minutes, and was washed with ultrapure water. Ultraviolet irradiation / photographing apparatus set TCP 20 LM (Amuzu System Science) was used to cut out the gel out of the wavelength of 312 nm and collected in a micro tube. DNA purification QIAquick Gel extraction kit (Qiagen) was used to purify insert caspase-9 and linearized vector. Ligation was performed using DNA ligation kit (TAKARA). For ligation, vector 2 μL, insert 2 μL and ligation buffer 4 μL were mixed and incubated at 16°C for 1 h. PGEX(2T-P)+caspase-9 was transformed into *E. coli* DH5α compatible cell (TAKARA) and cells were spread on LB + Amp plate and incubated at 37°C for 12 h.

2.11 Chlamydial gene clone into pET-15b vector

For tagging the production of caspase-9 interacting five *Chlamydia pneumoniae* proteins with Histidine (6X), the coding DNA fragments were cloned into pET-15b vector. DNA fragments coding for five chlamydial genes were amplified form *C. pneumoniae* J138 genomic DNA by PCR using the corresponding primers (Cpj0056 for pET-15b_F, Cpj0056 for pET-15b_B; Cpj0444 for pET-15b_F, Cpj0444 for pET-15b_B; Cpj0512 for pET-15b_F, Cpj0512 for pET-15b_B; Cpj0838 for pET-15b_F, Cpj0838 for pET-15b_B; Cpj0948 for pET-15b_F, and Cpj0948 for pET-15b_B) (Table: 4) designed for infusion cloning into pET-15b vector. pET-15b was digested with *Nde*I (Clontech TAKARA). Reactions in total volume 25.0 μL with DNA 22.0 μL, 10 x K buffer 2.5 μL and *Nde*I(10 U/ μL) 0.5 μL were incubated at 37°C over night. Full-length chlamydial five genes and linearized pET-15b vectors were cloned using infusion cloning method (Clontech Mountain View, CA). Reaction in total volume 10 μL (In-fuison HD Enzyme premix 2.0 μL, vector (~30 ng/ μL) 2.0 μL, insert (~30 ng/ μL) 2.0 μL, sterile Milli Q H_2O 4.0 μL) was incubated at 50°C for 15 minutes. After cloning vectors were transformed into *E. coli* DH5α competent cell (TAKARA) and cells were spread on LB + Amp plate and incubated at 37°C for 12 h. Primarily Cpj0444 was not cloned into pET-15b vector. After isolation all four cloned plasmid vectors were re-transformed into *E. coli* BL21 (DE3) and confirmed by colony PCR using same the primers used for infusion cloning.

2.12 Selection of chlamydial factors interacting with caspase-9

Cloned pGADT7+caspase-9 vector was isolated from *E. coli* DH5α and the insert was checked by vector and caspase-9 specific restriction enzyme digestion.

After confirmation the DNA sequence, pGADT7+caspase-9 were individually transformed into the 1033 yeast strains (Fukunaga et al. 2013). Briefly, colonies grown on SD-W plate were inoculated into 100 µL of SD-W liquid medium and incubated at 30°C for 16 to 18 hours. A single culture mixture was prepared by mixing 30 µL over night culture from each 6-8 types of yeast colony containing pGBKT7+chlamydia genes. Fresh SD-W liquid medium were added to the culture mixtures (culture 100 µL: SD-W medium 900 µL) and incubated at 30°C for 5 hours. After incubation, centrifugation was carried out at 1000 xg for 5 minutes at room temperature. After the supernatant was removed, the pellet was suspended in 100 µL of sterilized Milli Q water and centrifuged at 2000 rpm for 5 minutes at room temperature. The supernatant was removed and the pellet was suspended with 11.5 µL of sterilized Milli Q water and transferred to a 200 µL PCR tube. The transformation mixture 38.5 µL composed with 30.0 µL of 60% Polyethyleneglycol 4000 (Wako Pure Chemical Industries Ltd. Japan), 2.5 µL 5mg/mL carrier DNA (Calf thymus DNA, 5.0 µL 1M Lithium acetate and 1 µL pGADT7+Caspase-9 vector (50-100 ng) was added per reaction and incubated at 42°C for 1 hour. The culture (5 µL) was spotted on SD-LW, as control, and on SD-LWAH. The colony show positive interaction was selected on SD-LWAH.

2.13 Selection of human factors interacting with Chlamydial OMPs

Using gene annotation chlamydial 47 outer membrane protein coding genes were selected (Table: 7) for screening interaction with human aorta cDNA library. Human aorta cDNA library were individually transformed into the yeast strains AH109 containing pGBKT7 vector cloned with chlamydial 47 outer membrane protein coding genes (Fukunaga et al. 2013). Briefly, 47 chlamydial colonies containing omp/pmp protein grown on SD-W plate were inoculated into 2 mL of SD-W liquid medium and incubated at 30°C with shaking at 250 rpm for 16 to 18 hours. The 200 µL of culture was mixed with 1.8 mL SD-W liquid medium to make 2 mL and the cell was cultured at 30°C for 5 hours with shaking at 250 rpm. After incubation, centrifugation was carried out at 1000 xg for 5 minutes at room temperature. After the supernatant was removed, the pellet was suspended with 200 µL of sterilized Milli Q water and centrifuged at 2000 rpm for 5 minutes at room temperature. The supernatant was removed and the pellet was suspended with 10.5 µL of sterilized Milli Q water and transferred to a 200 µL PCR tube. The transformation

mixture composed with 30.0 µL of 60% polyethylene glycol 4000 (Wako Pure Chemical Industries Ltd. Japan), 2.5 µL 5mg/mL carrier DNA (Calf thymus DNA, 5.0 µL 1M Lithium acetate and 2 µL human pACT2 aorta cDNA library was added per reaction and incubated at 42°C for 1 hour. All transformed cells were spread on SD-LWAH or SD-LWAH+x-α-Gal. Blue colonies from SD-LWAH+x-α-Gal and all colonies from SD-LWAH were selected as positive clones.

2.14 Protein expression and purification

For GST pull-down assay, *Escherichia coli* BL21(DE3) harboring pGEX(2T-P) caspase-9, pET-15b Cpj0056, pET-15b Cpj0512, pET-15b Cpj0838 and pET-15b Cpj0948 were initially grown overnight at 37°C with shaking in LB+Amp medium. Culture solution was $1/100^{th}$ diluted with fesh liquid LB+Amp medium and cultured at 37°C at 200 rpm for 3:30 hours. Then IPTG (at final concentration 0.5mM) was added to the culture and culturing was continued at 37°C at 200 rpm for 3:30 hours and finally the cell was harvested by centrifugation at 9000 rpm, 4°C for 5 min. Proteins were purified from the harvested cell. Briefly, for GST-Caspase-9 cells were lysed using the lysis buffer (1% Triton X-100 and 1× phosphate buffered saline (PBS), pH7.4 (Sigma/Merch, Darmstadt, Germany)) by ultrasonication on ice and the supernatant was collected by centrifugation at 7,740 ×g at 4˚C for 15 minutes. GST-Casp9 was purified using Glutathione Sepharose 4B beads (Amersham/GE Healthcare, Marlborough, MA). Glutathione sepharose beads bound to GST-caspase-9 were used to interaction assay with His-tagged chlamydial MnmE protein. GST-caspase-9 proteins were purified from glutathione sepharose beads through competitive elution with 50 mM reduced glutathione in 1% lysis buffer (1% Triton X-100 and 1× phosphate buffered saline (PBS), pH7.4 (Sigma/Merch, Darmstadt, Germany)). 10 µL of 0.2 M GSH was added to the 20 µL glutathione sepharose beads bound to GST-caspase-9 suspension with 1% Triton X-100 and 1× PBS. To adjust the GSH concentration 10 µL of 1% lysis buffer (1% Triton X-100 and 1× PBS) was added to the reaction mixture. The total 40 µL reaction mixture into a 1.5 mL micro centrifuge tube was rotated at 5-10 rpm at 4°C for 20 minutes with a rotator. The supernatant (GST-caspase-9) was recovered by centrifugation at 4000 rpm for 5 minutes at 4°C. Cells with chlamydial proteins were lyses with lysis buffer (50mM NaH_2PO_4, 300mM NaCl, 10mM imidazole, pH 8.0) and purified protein by Ni-NTA spin column

(Qiagen, Venlo, Netherlands). Purified proteins were boiled at 95°C for 5 min with 3xSDS sample buffer and analyzed by 10% SDS-PAGE and western blotting.

2.15 GST pull-down assay

To clarify whether caspase-9 can bind to the chlamydial outer membrane, a pull-down experiment was carried out using recombinant caspase-9 and the EBs of *C. pneumoniae* J138. GST-Casp9 and purified EBs of *C. pneumoniae* J138 (Rahman et al. 2015) were mixed in 1% lysis buffer (1% Triton X-100, 1x PBS, 1mM $MgSO_4$, 0.01% BSA) and incubated at 37˚C for 15 min. After incubation centrifugation was carried out at 15000 rpm at 4°C for 5 min and supernatant was removed. EBs were washed with wash buffer (1% Triton X-100, 1x PBS, 1mM $MgSO_4$, 0.01% BSA) three times and collected by centrifugation at 4˚C for 5 min at 21,500 ×g. EB interacted GST-Casp9 was then analyzed by western blotting using anti-pro-caspase-9 mouse monoclonal antibody (Santa Cruz, Dallas, TX), followed by a second detection using anti-chlamydia Pmp mouse monoclonal antibody (Cp-11, HITACHI, Tokyo, Japan). In both detections, alkaline phosphatase conjugated anti-mouse IgG goat polyclonal antibody (Santa Cruz) was used as a secondary antibody and target proteins were visualized using CDP-star (Roche, Basel, Switzerland).

To confirm the interaction between Cpj0838 and caspase-9, a pull-down experiment was performed. To conduct GST pull-down experiments, GST-Casp9 and His-Cpj0838 were mixed in the pull-down buffer (1×PBS, 1 mM DTT, 0.5% triton, and 10 mM $MgSO_4$, pH 7.4) at 25˚C for 10 min, and GST-Casp9 was retrieved with glutathione beads. The beads were washed three times with the pull-down buffer. The proteins on the beads were boiled at 95°C for 5 min with 3xSDS sample buffer and analyzed by 10% SDS-PAGE and western blotting using anti pro-caspase-9 mouse monoclonal antibody (Santa Cruz) and alkaline phosphatase conjugated anti-6X His tag antibody monoclonal antibody (Abcam, Cambridge, UK).

2.16 SDS-PAGE and western blotting

Proteins were resolve by SDS-10% PAGE and then transferred onto a 0.45 μm PVDF blotting membrane (GE Healthcare life science.). Nonspecific binding sites were blocked with 1xDIG blocking buffer and membrane was then probed with the alkaline phosphatase conjugated anti-6X His tag antibody monoclonal antibody (mAb) (Abcam, Cambridge, UK) to detect the chlamydial gene product. The same

blot was used to detect caspase-9 by anti pro-caspase-9 mouse monoclonal antibody (Santa cruze) and second antibody alkaline phosphatase conjugated anti-mouse goat polyclonal antibody (Santa cruze). Immunopositive proteins were visualized by alkaline phosphatase activity using CDP star (Roche) as a substrate.

3. Results

3.1 Apoptosis regulation by *Chlamydia pneumoniae*

3.1.1 Apoptosis repression by *Chlamydia pneumoniae*

We verified the involvement of *C. pneumoniae* J138 in HEp-2 cell apoptosis. *C. pneumoniae* mediated blockage of STS-induced apoptosis was found at 48 hpi and this blockage ceased by 72 hpi (Fig. 3). Similar responses were observed using HeLa cells and MEFs (data not shown). In the absence of apoptotic stimuli, apoptotic induction by *C. pneumoniae* infection was not observed between 48 and 72 hpi, which are the middle and late stages of *C. pneumoniae* infection, respectively (Miura et al. 2008); chlamydial infection partially stimulated STS-induced apoptosis at 72 hpi. These data, combined with previous results (Rajalingam et al. 2001; Airenne et al. 2002; Geng et al. 2000; Fischer et al. 2001), indicate that *C. pneumoniae* infection at relatively low MOI represses STS-induced apoptosis of various host cell lines in the early-to-middle stages of infection, but not in the late stage.

3.1.2 Anti-apoptotic environments for chlamydial infection

The anti-apoptotic activity of chlamydial infection seems to be an advantage for escaping from the host immunosurveillance. It is also possible that this anti-apoptotic environment is also favorable for chlamydial multiplication. To verify this possibility, the susceptibility of host cells to chlamydial infection was assessed by adding anti-apoptotic agents prior to chlamydial infection (Fig.4a). The cell-permeant irreversible caspase-9 inhibitor (C9-i) decreased the infection rate to nearly half of control, and cell-permeant Apaf-1 inhibitor (Ap-i) conduced a 1.5 times higher infection rate, while caspase-8 and -3 inhibitors (C8-i, C3-i, respectively) showed no modification of infection rates. It has been reported that *C. trachomatis* and *C. psittaci* induce host apoptosis and that chlamydial infection is inhibited by Bcl-2 over expression (Perfettini et al. 2002). In contrast, no significant difference was observed in the current study in infection rates or inclusion sizes of *C. pneumoniae* J138 between the HeLa cells over expressing Bcl-2 and control cells (Fig. 4b).

3.1.3 Chlamydial infection in Apaf-1- and Caspase-9-deficient cells.

To confirm the different contributions of Apaf-1 and caspase-9 in chlamydial infection, Apaf-1 and caspase-9 knockout (*apaf-1*$^{-/-}$ and *caspase-9*$^{-/-}$, respectively) MEFs were used as host cells for infection. Consistent with the inhibitor treatment

results, *C. pneumoniae* infection rates were four times greater in *apaf-1*$^{-/-}$ MEFs than in controls, and reduced by nearly half in *caspase-9*$^{-/-}$ MEFs (Fig. 5a). Generation of infectious progenies of *C. pneumoniae* was calculated using *apaf-1*$^{-/-}$ MEFs. This result was consistent with the infection rate (Fig. 5b). Generation of infectious progenies from infected *caspase-9*$^{-/-}$ MEFs was consistent with the infection rate as well as in the case of *apaf-1*$^{-/-}$ MEFs (data not shown). To test further species specificity, *C. trachomatis* was used for infection of*apaf-1*$^{-/-}$ and *caspase-9*$^{-/-}$ MEFs (Fig. 5c). Similar outcomes of infection were observed in both MEFs. Most of phenomena observed here were confirmed using *C. pneumoniae* AR39 (data not shown). In cells infected with both chlamydiae, no morphological changes of host nuclei between infected and non-infected cells were observed (Fig. 5d).

To clarify whether or not caspase-9 functions independently from Apaf-1, and whether or not Apaf-1 is indeed a target of Ap-i, C9-i and other inhibitors were used during infection of *apaf-1*$^{-/-}$ MEFs (Fig. 6a). In agreement with the HEp-2 data (Fig. 4), C9-i decreased but Ap-i increased the *C. pneumoniae* infection rates to MEF control cells (Fig. 6a left panel). When *apaf-1*$^{-/-}$ MEFs were treated with Ap-i, the incremental increase in the *C. pneumoniae* infection rate was negated; however, C9-i still decreased the infection rate (Fig. 6a right panel). Complementation assays were performed using the *apaf-1* gene and the *apaf-1*$^{-/-}$ MEFs (Fig. 6b). The results showed that the incremental increase in infection rate was absent, but there was no further decline in the rate at the higher doses of the vector containing the *apaf-1* gene.

3.1.4 Apaf-1-independent caspase-9 activation by chlamydial infection

Caspase-9 is generally activated in apoptosomes that contain Apaf-1, but the C9-i used here, which is an antagonist of caspase-9 self-cleavage, inhibited chlamydial infection. Thus, it is possible that caspase-9 activation is required for chlamydial infection. We evaluated caspase-9 protease activities in host cell cytosolic fractions after infection of *apaf-1*$^{-/-}$ MEFs (Fig. 7a). As expected, caspase-9 protease activity was increased in the control MEFs but not in *apaf-1*$^{-/-}$ MEFs with STS treatment. In contrast, *C. pneumoniae* infection significantly increased caspase-9 protease activity in both of *apaf-1*$^{-/-}$ and control MEFs (Fig. 7a). Generally, caspase-9 activation leads to activation of caspase-3 followed by apoptosis, but apoptosis was not observed after caspase-9 activation by chlamydial infection in *apaf-1*$^{-/-}$MEFs (Fig. 4a and 5d). Surprisingly, caspase-3 activity was not significantly increased by

chlamydial infection at 48 hpi in the *apaf-1*$^{-/-}$ and control MEFs, compared to STS treatment (Fig. 7b). Caspase-3 activity in the infected *apaf-1*$^{-/-}$ MEFs was slightly higher than the background controls, which may be because activated caspase-9 activates caspase-3 when assay samples are prepared *in vitro*.

Activation of caspase-3 and -9 was analyzed by western blot. Results were consistent with the activity assays on *apaf-1*$^{-/-}$ and control MEFs cytosolic fractions (Fig. 8). The higher levels of activated capase-9 in the infected *apaf-1*$^{-/-}$ MEFs compared to the infected control MEFs (approximately 5 times) is due to a higher infection rate in the *apaf-1*$^{-/-}$ MEFs (Fig. 5a). These results indicate that there is a *de novo* mechanism for Apaf-1-independent caspase-9 activation during chlamydial infection and that the activated caspase-9 is not engaged in caspase-3 activation for host cell apoptosis.

To address how caspase-3 is not activated by infection-induced activated caspase-9, we first analyzed expression of genes encoding inhibitors of apoptosis protein IAP1, IAP2, and XIAP. DNA microarray and quantitative RT-PCR at 48 hpi (data not shown) (Miura et al. 2008) showed that expression of these genes was not increased. However, caspase-9 was colocalized with chlamydial inclusions at 48 hpi by immunofluorescence staining using a caspase-9 antibody with *apaf-1*$^{-/-}$ MEFs (Fig. 9) and all inclusions showed the presence of caspase-9. Two additional anti-caspase-9 antibodies purchased from different companies were tested and confirmed this result, and caspase-9 was not detected in the *caspase-9*$^{-/-}$ MEFs (data not shown). Moreover, as compared with localization of chlamydial inclusion membrane protein (IncA2), caspase-9 seemed to localize inside of inclusions. These data suggests the hypothesis that chlamydial infection-mediated repression of apoptosis is at least partially a result of caspase-9 sequestration in inclusions in which caspase-9 is precluded from its role (or availability) in the host apoptosis cascade. Mechanisms for caspase-9 localization and activation remain as a challenge to comprehend chlamydial developmental cycle.

3.2 Screening of chlamydial gene interacting with caspase-9

3.2.1 Chlamydial genomic library construction

Chlamydial genomic library was constructed using pGBKT7 by homologous recombination in yeast (Fig. 10). pGBKT7 vector was linearized by *Bam*HI restriction digestion (Fig. 11). Among total 1072 *Chlamydia* genes, 10 genes were previously cloned into pGBKT7 vector. The other 1062 genes were amplified by

PCR using primer designed for homologous recombination (Table: 3). We selected 149 PCR products randomly to confirm the gene fragment size by agarose-gel electrophoresis (Fig. 12 a). By first line PCR, 2 genes were not amplified and one of 2 was recovered by second line PCR (Fig. 12 b). The success rate of the first line PCR was calculated as 98.65%. So other 913 genes PCR products were used for library construction without checking by agarose-gel electrophoresis. In order to prepare a library into the pGBKT7 vector, the 1062 genes PCR products were transformed into AH109 along with linearized pGBKT7 vector and selected on SD-W (Fig. 13a-m). After construction library for 1062 genes, we found 7 genes were absent from the library. For confirmation of cloning, randomly selected nine genes were amplified by colony PCR using yeast grown on SD-W plate and the same primers used for amplification of the gene for cloning (Fig. 14). Thirty-two yeast strains were excluded from the 1065 clones because of the sensitive growth on SD-WAH as pseudo-positive clones (Table: 5). The protein coding for these thirty two genes may activate transcription of the reporter gene without activation domain by itself or via other yeast proteins. We have to check interaction of these genes with caspase-9 using different method. Eleven randomly selected strains were subjected to western blotting analysis using an anti-c-Myc mouse monoclonal antibody (Clontech Mountain View, CA). Most of the samples showed target proteins at expected sizes at detectable levels (Fig. 15). Some genes were expressed with shorter fragment(s) along with the expected size. This type of background may not critically affect the Y2H screening.

For cloning of caspase-9 into pGADT7, full-length DNA fragment of caspase-9 gene was amplified by PCR (Fig. 16a). pGADT7 vector was linearized by *Bam*HI (Fig. 16b**).** After infusion cloning and transformation colony PCR was performed to check insertion of caspase-9 using *E. coli* DH5α colony as template (Fig. 16c). pGADT7+Caspase-9 cloned plasmid vector was isolated from 3 colony and those were confirmed by colony PCR (Fig. 16d). Isolated pGADT7 and pGADT7+caspase-9 vectors were then treated by restriction enzyme (*Pst*I, *Xho*I and *Xho*I/*Eco*RI) to check insert (Fig. 16e**)**.

After confirmation by DNA sequencing pGADT7+caspase-9 vector was transformed into the chlamydial genomic library by modified method describe in materials and method section (Fig. 17).

3.2.2 Human apoptotic factor caspase-9 interact with five *C. pneumoniae* (J138) protein

From result of the Y2H screening, five chlamydial proteins interacted with bait protein caspase-9 (pGADT7+caspase-9), forming colonies on SD-LWAH plate (Fig. 18). The *Chlamydia* genes that showed positive interaction were found to be genes encoding Cpj0056 (*pgcA*), Cpj0444 (*Pmp-6*), Cpj0512 (CT425 Hypothetical protein), Cpj0838 (*mnmE*) and Cpj0948 (*glgA*) protein (Table: 6).

3.2.3 Protein preparation of GST-caspase-9 and *Chlamydia* protein

Caspase-9 was cloned into pGEX(2T-P) vector for expression and purification of GST-Caspase-9. Caspase-9 was amplified for cloning into pGEX(2T-P) vector (Fig. 19a). pGEX(2T-P) vector and insert (caspase-9 PCR product) was treated with restriction enzyme *Bam*HI (Fig. 19b) then *Bam*HI digested vector and caspase-9 DNA fragment again treated with restriction enzyme *Sal*I (Fig. 19c). After cloning and transformation colony PCR was performed to check insert using *E.coli* DH5α containing pGEX(2T-P)Caspase-9_16 colony (Fig. 19d). After checking colony PCR, pGEX(2T-P)+caspase-9 vector was isolated from *E.coli* DH5α pGEX(2T-P)+Caspase-9_16 colony (Fig. 19e). Isolated vector then checked by restriction enzyme (*Pst*I) treatment (Fig. 19f).

3.2.4 Pull-down assay

GST-Caspase-9 protein expression was induced by IPTG and partially purified using Glutathione Sepharose 4B beads described in materials and methods (Fig. 20a). Partially purified GST-Caspase-9 was resolved by 10% SDS-PAGE electrophoresis and blotted on PVDF membrane developed by CBB staining (Fig. 20 b). GST-Caspase-9 was expressed in low amount not detected by CBB staining but detected by antibody stained with anti-pro-caspase-9 mouse monoclonal antibody (Fig. 20c).

We investigated the screening of chlamydial 1033 genes with caspase-9 by Y2H assay and found chlamydial five genes interact with caspase-9 (see 3.2.2). *Chlamydia* gene Cpj0444 (*Pmp-6*) among the five is a membrane protein. Interaction of caspase-9 with *Chlamydia* EB was confirmed by pull-down assay (Fig. 21). These results support the previous observation that caspase-9 accumulates in inclusions (Rahman et al. 2015), as well as the finding of our Y2H assay.

For the expression and purification of 6x His-tagged chlamydial protein five genes were cloned into pET-15b vector. *Chlamydia pneumoniae* five genes interacting with caspase-9 amplified by PCR and confirmed by electrophoresis (Fig. 22a) and pET-15b vector was linearized by restriction enzyme *Nde*I (Fig. 22b). Full-length genes were cloned by infusion cloning method and transformed into *E. coli* DH5α. One gene Cpj0444 did not cloned in this study. Cpj0444 is an outer membrane protein. Instead of cloning and purification of the protein, we used chlamydial EBs to check the physical interaction with GST-caspase-9. Other 4 plasmid vectors cloned with chlamydial 4 genes were isolated (Fig. 22c). After confirming DNA sequence 4 vectors were re-transformed into *E. coli* BL21 (DE3) and checked by colony PCR using the infusion primers for each gene (Fig. 22d).

Among the chlamydial four proteins one (Cpj0512) is hypothetical protein and not yet well defined. Two (Cpj0056 and Cpj0948) of them are involved in glycogen synthesis pathway. The interaction of caspase-9 with these two proteins is may be the biochemical interaction that is difficult to show by *in vitro* interaction. We need to investigate these interactions in another way by enzymatic characterization. Finally we purified His–tagged chlamydial protein Cpj0838 (*mnmE*) and perfomed GST-pull-down experiment with GST fused caspase-9. Cells with chlamydial protein Cpj0838 (*mnmE*) were lyses with lysis buffer and purified protein by Ni-NTA spin column (Fig. 23a). The purified MnmE (Cpj0838) was resolved by 10% SDS-PAGE electrophoresis and blotted on PVDF membrane. After developing by CBB staining (Fig. 23b) the protein was detected by antibody stained with anti-6x His-tag mouse monoclonal antibody (Fig. 23c). The result of this pull-down experiment showed that Cpj0838 bound to GST-Caspase-9 (Fig. 24). This result indicates that Cpj0838/MnmE might function pleiotropically not only for the modification of tRNA but also for *C. pneumoniae* infection (Fig. 25).

3.3 Selection of human factors interacting with Chlamydial OMPs

3.3.1 Chlamydial 22 OMPs interact with 74 human proteins

Using gene annotation chlamydial 47 outer membrane protein coding genes were selected from chlamydial 1072 genes (Table: 7) for screening interaction with human aorta cDNA library. Firstly we transformed human aorta cDNA library into the chlamydial gene containing yeast, and about 12,400 colonies appears on SD-LW. Under this condition human aorta cDNA library were individually transformed into

the yeast strains AH109 containing 47 outer membrane genes and positive clones were selected on SD-LWAH or SD-LWAH+x-α-Gal plate. From result of the Y2H library screening, primarily maximum twenty one or less for each colony were selected for further investigation. Finally 121 clones from Y2H library screening were selected (Fig. 26 and Fig. 27(i-xxiii)). cDNA were isolated from these 121 positive yeast colonies. After analyzing DNA sequences of the 121 cDNA, 94 independent human cDNAs found to interact with 22 chlamydial outer membrane genes (Fig. 26). The 22 chlamydial (*omp/pmp*) genes were individually screened with human 94 cDNA vectors by transforming cDNAs into respective 22 (*omp/pmp*) genes containing yeast and 20 interactions were excluded because those interactions were not strong (Fig. 28). Finally chlamydial 22 outer membrane proteins found to interact with 74 human proteins (Table: 8). Sub-cellular location of proteins interacting with chlamydial outer membrane proteins are shown in Fig. 29.

4. Discussion

Modifications of host cell apoptosis by chlamydial infection have been intensively studied. However, the roles of pro- or anti-apoptotic factors in chlamydial infections are not yet elucidated. In this study, we have attempted to clarify host apoptosis regulation by *Chlamydia*, mainly *C. pneumoniae*, using exogenous apoptosis repressors, such as *bcl-2* overexpression, chemical apoptosis inhibitors, and gene knockout of apoptotic factors. Based on the results shown here, two hypotheses are proposed regarding an epistatic effect of *apaf-1* and *caspase-9* on chlamydial infection.

First, both human and mouse cells treated with an apoptosome inhibitor and *apaf-1*$^{-/-}$ MEFs are more susceptible to chlamydial infections than control cells. The *apaf-1* gene could complement the susceptible phenotype. Beyond controversy, Apaf-1 is well-known to oligomerize and activate caspase-9 through a caspase recruitment domain (CARD). Nod1 and Nod2, which also contain the CARDs, were implicated as intracellular sensors that recognize patterns of intracellular pathogens, (Werts, Girardin & Philpott 2006; Inohara & Nuñez 2003), while expression of both Nod1 and Nod2 in HEp-2 cells were not modified by chlamydial infection based on a DNA microarray analysis (data not shown). Thus, it is conceivable that the Apaf-1 functions as a host defense factor against invasion by intracellular pathogens as an inhibitor or sensor as well as a pro-apoptotic agent. In favor of this notion, a non-apoptotic role for Apaf-1 was recently proposed, in which it functions as a DNA damage regulator controlling the checkpoint kinase Chk1 and thus acts as a tumor suppressor (Zermati et al. 2007). In this case, Apaf-1 may indirectly confine *Chlamydia* to supporting host cell proliferation; however we are proposing another direct response of Apaf-1 against chlamydial infection, as described below.

In an opposite manner, human and mouse cells treated with a caspase-9 inhibitor and *caspase-9*$^{-/-}$ MEFs are more insusceptible to chlamydial infections than control cells. Interestingly, caspase-9 was activated in *Apaf-1*$^{-/-}$ MEFs by chlamydial infection, but the activated capase-9 was disconnected from the caspase cascade that activates caspase-3. Moreover, activated caspase-9 was colocalized with chlamydial inclusions. Taken together, these data suggest that *Chlamydia* require caspase-9 activation for its inclusion maturation and/or multiplication. Therefore, we herein present another model for the repression of apoptosis by chlamydial infection. That is, caspase-9 sequestration by chlamydial infection from the host apoptosis cascade

results in apoptosis repression of host cells, and Apaf-1 may compete against chlamydial utilization of caspase-9. This sequestration model is partially similar to those in which phosphorylated Bad was sequestered via 14-3-3 beta to the chlamydial inclusion membrane that contains IncG proteins (Verbeke et al. 2006) and a pro-apoptotic effector protein kinase C delta (PKC-δ) was mislocalized according to accumulation of diacylglycerol in the immediate vicinity of chlamydial inclusions (Tse et al. 2005). *Chlamydia* might develop this sequestration system to perturb multiple cellular processes of the host, such as rearrangement of the membrane trafficking system for its intracellular multiplication and inhibition of host cell apoptosis for persistent infection.

Despite a well-known role of Apaf-1 in the activation of caspase-9 as the initiation of caspase cascade in a variety of cell models, several reports demonstrated that alternative mechanisms for caspase-9 activation exist independently of Apaf-1 on the basis of certain stimuli, such as the infection of Sendai virus in *apaf-1*$^{-/-}$ MEFs (Bitzer et al. 2002) and UV irradiation in *apaf-1*$^{fog/fog}$ cells (Katoh et al. 2008). In *Chlamydia* cases, it is deemed that *Chlamydia* possesses a mechanism for Apaf-1-independent activation of caspase-9 supporting its multiplication in parallel with apoptosis repression by the caspase-9 sequestration. The hypotheses shown here may provide a valuable clue to investigate mechanisms for chlamydial infection causing varied diseases.

To identify the chlamydial factor(s) involved in the Apaf-1 independent activation and sequestration of caspase-9 in *Chlamydia* infected cells, we constructed whole chlamydial genomic library. Using caspase-9 as bait we performed Y2H assay with chlamydial genomic library including 1033 genes and found five proteins to interact with caspase-9. In molecular biology, Y2H assay is simple and efficient method for screening *in vivo* interaction of two proteins as well library screening (Makuch 2014). As with Y2H approach, false positives and false negative are unavoidable. We employed pull-down assay experiment to check the interaction *in vitro*.

The result from Y2H has confirmed by pull-down assay between Cpj0838/MnmE and caspase-9. This indicates that Cpj0838/MnmE might function pleiotropically not only for the modification of tRNA but also for *C. pneumoniae* infection. MnmE is well conserved in all three kingdoms of life and is involved in the modification of uridine bases (U34) at the first anticodon position of tRNAs.

However, no data exists regarding the localization and functions of chlamydial MnmE. *C. trachomatis* was reported to accumulate glycogen, while *Chlamydia psittaci* and *C. pneumoniae* could not (Gilkes, Smith & Sowa 1958; Moulder 1991). However, during *C. psittaci* infection, glycogen production in HeLa cells was increased (Ojcius et al. 1998), and all chlamydial genomes encode the genes necessary for both glycogen biosynthesis and catabolism (data not shown). It is possible that all *Chlamydia* species can accumulate glycogen within the chlamydial inclusion or host cytoplasm. Interestingly, *C. trachomatis* glycogen synthase, GlgA, was shown to be secreted into the host cell cytoplasm (Lu et al. 2013). The products of Cpj0948/glgA might play an important role, possibly in conjunction with caspase-9. Additionally, the glucose metabolism enzyme, phosphoglucomutase, is known to be involved in the production of polysaccharides including glycogen and the pathogenicity in bacterial pathogens (Buchanan et al. 2005). It is possible that the product of Cpj0056/pgcA is located in inclusions and caspase-9 is involved in the glycogen metabolism accompanied by two additional enzymes, GlgC (CPj0607) and GlgB (CPj0475) (Fig. 25). The hypothetical protein encoded by *C. trachomatis* CT425, which is homologous to Cpj0512, was shown to be immunogenic in humans infected with *C. trachomatis* (Barker et al. 2008). However, this protein contains a histidinol phosphatase domain, which is conserved among *Chlamydia* species and other bacteria. Further investigation is requested to predict its functions.

In conclusion, this study could serve as a clue to understanding molecular interactions between host and chlamydial factors, and to develop therapeutic agents to interfere with *Chlamydia* infection. For the development of the therapeutic agent firstly we need to confirm the important interaction between the domains of caspase-9 and chlamydial protein. In human immunodeficiency virus (HIV) infection viral glycoprotein, gp120 interact with the CD4 glycoprotein and a chemokine receptor to enter into the host cell. An HIV-1 gp120 core complexed was designed with a two-domain fragment of human CD4 and an antigen-binding fragment of a neutralizing antibody that blocks chemokine-receptor binding (Kwong et al. 1998). In our study, after finding the critically important interaction for chlamydial infection, we can design therapeutic agents in two ways. Firstly by immunizing with the chlamydial peptide and secondly by developing such agent that can interfere the caspase-9 interaction with chlamydial protein of interest.

Among five chlamydial genes interacting with caspase-9 by Y2H, Cpj0444

(*Pmp-6*) is *Chlamydia* membrane protein. From other study, chlamydial outer membrane protein OmcB (from both *C. pneumoniae* and *C. trachomatis*) binds to heparan sulphate-like structures on host cells for adhesion (Moelleken & Hegemann 2008) and *C. pneumoniae* adhesin protein Pmp21 binds to EGFR to activate the signaling cascade and enhances the internalization of EB into host cell (Mölleken et al. 2013). Chlamydial outer protein N (CopN) is a multifunctional chlamydial effector protein functioning both as the T3SS plug protein and as a secreted effector protein that causes mitotic arrest due to disruption of microtubules (Huang, Lesser & Lory 2008; Slepenkin, Luis & Peterson 2005). Considering these evidence, we selected whole 47 chlaydial outer membrane proteins and screened the interaction with human PACT2 aorta cDNA library.

From result of the Y2H library screening, our data demonstrate that the Y2H system can be used to screen for host–pathogen interacting proteins, using a bacterial protein as bait. It is possible that some of the interactions identified in our screen may be indirect i.e. transcription activated using other bridge molecule or do not occur *in vivo* during the natural course of a chlamydial infection. We tried to overcome false positive interaction or faint interaction by transforming isolated 94 cDNA. We found chlamydial 22 outer membrane proteins interact with 74 human proteins in this study (Table: 8).

There are some limitations to studying bacterial membrane proteins in the Y2H system since bacterial membrane proteins often have their own signal sequence that targets them to the outer membrane. Yeast two-hybrid systems are unable to detect protein–protein interactions for those proteins localized not at the nucleus. Moreover, in some cases, any membrane protein fused to one of the GAL4 domains will probably change its natural conformation, which could result in true interactions missed or even false interactions obtained.

From our screening, one chlamydial omp/pmp protein interacts with several human proteins and vice-versa. Moreover, it has been shown that Snapin and dynein intermediate chain (DIC) interact with *C. psittaci in vitro* and *in vivo* via IncB, but not with *C. trachomatis* and *C. pneumoniae* (Böcker et al. 2014). Here using Y2H, we found that Snapin interact with three different pmp protein of *C. pneumoniae* and dynein, cytoplasmic 1, heavy chain 1 (DYHC1) interact with *C. pneumoniae* conserved outer membrane lipoprotein protein. Three different pmp and omcA (pmp_2_2, pmp_11 and omcA) found to interact with galectin 1 (beta-galactoside-

binding lectin precursor 1-LGALS1). Though galectins are shown to interact with cell surface glycans of pathogenic microorganism and activate innate immune response, some pathogens modulate the recognition roles of galectin for their attachment and entry into the host (Vasta 2009).

C. pneumoniae was firstly described as a pathogen for acute respiratory diseases (Grayston et al. 1986). It has also considered as a cause of several chronic inflammatory diseases including atherosclerosis (Campbell & Kuo 2004). *Chlamydia pneumoniae* pmp_2_2 also interacts with the host zinc finger protein 496 (ZNF496) and may associate with inflammation and atherosclerosis through Jarid2/JJM and Notch signaling pathway (Liu et al. 2012). Our Y2H screening results need to clarify by further investigation with *in vitro* or *in vivo* interaction assay to exclude the false positive interactions. From the literature review we know that, some chlamydial outer membrane proteins are considered as virulence factors or involved in host cell cycle arrest. Some outer membrane proteins are also associated with the attachment to host cell. In our Y2H screening results, most of the host proteins interact with outer membrane proteins are intracellular proteins and some of them are secreted extracellular matrix proteins. The interaction between chlamydial outer membrane proteins and host extracellular matrix proteins may indicate that host cell can consider the inclusion as it is outside the cell. After confirmation the true interactions we can explain the inclusion-cytoskeleton network of *Chlamydia* into the host cells.

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6. Abbreviations

Amp, Ampicilin; kDa, kilo Dalton; OLFM4, Olfactomedin 4 (a glycoprotein); CARD, Caspase recruitment domain; Chk1, Checkpoint kinase; cIAP2, Cellular inhibitor of apoptosis 2; CopN, Chlamydial outer protein N; CPAF, Chlamydial protease or proteasome-like activity factor; DIC, Dynein intermediate chain; DYHC1, Dynein, cytoplasmic 1, heavy chain 1; DYNLT1, Dynein light chain 1; EB, Elementary body; EGFR, Epidermal growth factor receptor; EPHA2, Ephrin receptor A2; EtBr., Ethidium bromide; GAGs, Glycosaminoglycans; HSPGs, Heparan sulphate proteoglaycans; IFN-β, Interferon beta; IFN-γ, Interferon gamma; IFU, Inclusion formation unit; Inc, Inclusion; IκB-α, NF-κB inhibitor-α; Kan, Kanamycin; kbp, Kilo base pair; LGALS1, Beta-galactoside-binding lectin precursor 1; LPS, Lipopolysaccharide; M6P, Mannose/Mannose-6-phosphate; MAMP, Microbe associated molecular pattern; Mcl-1, Myeloid leukemia cell differentiation protein; MEF, Mouse embryonic fibroblast; MIP, Macrophage inhibitory protein; MOI, Multiplicity of infection; MOMP, Major outer membrane protein; MOTC, Microtubule-organizing center; MYD88, Myeloid differentiation primary response protein 88; NF-κB, Nuclear factor-Kappa B; NOD1, Nucleotide-binding oligomerization domain-containing 1; PB, Persistent body; PBS, Phosphate-buffered saline; PDI, Estrogen/protein di-sulphide isomerase; PRR, Pathogen recognition receptor; RB, Reticulate body; RNA pol, RNA polymerase; SD, Synthetic dropout; SFKs, Src family kinases; SNARE, Soluble N-ethylmaleimide-sensitive factor attachment protein receptor protein; STS, Staurosporine; T3SS, Type III secretion system; TNF, Tumor necrosis factor; TRAF3, TNF receptor-associated factor 3; TRAF6, TNF receptor-associated factor 6; Y2H, Yeast two-hybrid; ZNF, Zinc finger protein; λ-*Hind*III, λ-phage genome DNA digested by *Hind*III;

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8. List of tables

Table: 1 *Chlamydiaceae* family (species that cause disease in human)

Species	Disease	Persistent infection	Features
Chlamydia trachomatis	Trachoma, NGU, MPC, PID, Infant pneumonia	Conjunctivitis	Reduction of pro-inflammatory or cytotoxic responses
Chlamydia pneumoniae	Pharyngitis, Bronchitis, Pneumonia	Atherosclerosis	Low stimulation of NO synthesis in macrophage and monocyte.
Chlamydia psittaci	Psittacosis	No persistent diseases for human	Causing sporadic zoonotic disease Psittacosis

Table: 2 List of cells and strains

Host cells	HeLa229 (AT CC CCL- 2)
	HEp2 (ATCC CCL23)
	Bcl-2-ove rexpress ing HeLa cells
	mouse embryonic fibroblasts (MEF)
	Apaf-1 knockout and Caspase-9 knockout mouse embryonic fibroblasts (MEFs)
Strains	*Chlamydia pneumoniae* J138 and AR39
	C. trachomatis serovar D
	Saccharomyces cerevisiae (AH109)
	E.coli DH5α
	E.coli BL21(DE3)

Table: 3 List of primer for chlamydial genomic library construction

Gene name	Primer name	Forward Primer	Primer name	Backward Primer
CPj0001	CPj0001_F	AGGCCGAATTCCCGGGGATCATGCTAGGCAAAATTATTCG	CPj0001_B	CCGCTGCAGGTCGACGGATCCTAATTTTTGTCAGAATGATG
CPj0002	CPj0002_F	AGGCCGAATTCCCGGGGATCATGGAGCAATTTCATTTGGA	CPj0002_B	CCGCTGCAGGTCGACGGATCTTACTTGATTACCGCAGGAA
CPj0003	CPj0003_F	AGGCCGAATTCCCGGGGATCATGTATCGATATAGTGCTTTA	CPj0003_B	CCGCTGCAGGTCGACGGATCTCATGATTGACCTCCTAGAA
CPj0004	CPj0004_F	AGGCCGAATTCCCGGGGATCATGAGTGCTGTTTATGCAGA	CPj0004_B	CCGCTGCAGGTCGACGGATCCTAGCCCTTATCTAATTCTA
CPj0005	CPj0005_F	AGGCCGAATTCCCGGGGATCATGCGATTTTCGCTCTGCGG	CPj0005_B	CCGCTGCAGGTCGACGGATCCTAAAAACGAAATTTGCTTC
CPj0006	CPj0006_F	AGGCCGAATTCCCGGGGATCTTGCAGGAACCTCTTCGAAG	CPj0006_B	CCGCTGCAGGTCGACGGATCTCATAGGGATTCCAGGGTTC
CPj0007	CPj0007_F	AGGCCGAATTCCCGGGGATCATTTTTTCCTTTCTTGTCGTG	CPj0007_B	CCGCTGCAGGTCGACGGATCTTATTCACTGGGAGCTTGAA
CPj0008	CPj0008_F	AGGCCGAATTCCCGGGGATCGTGATTTCGGGACTTCTATT	CPj0008_B	CCGCTGCAGGTCGACGGATCCTATAACCATTTGAAACGCC
CPj0009	CPj0009_F	AGGCCGAATTCCCGGGGATCATGTGGCTGGATCGTTATGC	CPj0009_B	CCGCTGCAGGTCGACGGATCTTAGAAGCCTTTGACTCGCT
CPj0010	CPj0010_F	AGGCCGAATTCCCGGGGATCATGCTCTTACTGATTTCAGG	CPj0010_B	CCGCTGCAGGTCGACGGATCCTAGGAATGGTCCTCGCGAG
CPj0011	CPj0011_F	AGGCCGAATTCCCGGGGATCATGACTGCAGCACCAGCTAT	CPj0011_B	CCGCTGCAGGTCGACGGATCTTAGAAAAAAAACTCTAATTCC
CPj0012	CPj0012_F	AGGCCGAATTCCCGGGGATCATGTACCAGGAGAATCTAAG	CPj0012_B	CCGCTGCAGGTCGACGGATCTTAGATTTTCTTCTTCAGCT
CPj0013	CPj0013_F	AGGCCGAATTCCCGGGGATCATGAAGATTCCACTCCGCTT	CPj0013_B	CCGCTGCAGGTCGACGGATCTTACAAATGGAGTGTACTCT
CPj0014	CPj0014_F	AGGCCGAATTCCCGGGGATCATGAAGTCTTCTTTCCCCAA	CPj0014_B	CCGCTGCAGGTCGACGGATCTTAATGAAAGAGTTTTTGCG
CPj0015	CPj0015_F	AGGCCGAATTCCCGGGGATCTTGCTCTTCAGCAAAAACTT	CPj0015_B	CCGCTGCAGGTCGACGGATCTTAGAATTGGTATTTTGCTC
CPj0016 A	CPj0016 A_F	AGGCCGAATTCCCGGGGATCATGAGATCGTCTTTTTCCTT	CPj0016 A_B	CCGCTGCAGGTCGACGGATCTCAGATTGTCAGGTTTCTTA
CPj0016 B	CPj0016 B_F	AGGCCGAATTCCCGGGGATCTTGAAAGATGGAGTGACTGT	CPj0016 B_B	CCGCTGCAGGTCGACGGATCTTAGTCCAAGTTAAGGTAGC
CPj0017	CPj0017_F	AGGCCGAATTCCCGGGGATCATGGGTATCAAGGGAACTGG	CPj0017_B	CCGCTGCAGGTCGACGGATCTTAAAATCCGAATCTTCCTC
CPj0018	CPj0018_F	AGGCCGAATTCCCGGGGATCATGAAGACTTCAGTTTCTATG	CPj0018_B	CCGCTGCAGGTCGACGGATCTTATAATGAGGTCCCCAGAT
CPj0019	CPj0019_F	AGGCCGAATTCCCGGGGATCATTGTCATCACAAATTTATCTA	CPj0019_B	CCGCTGCAGGTCGACGGATCTTAAAATCGGTATTTACCCC
CPj0020	CPj0020_F	AGGCCGAATTCCCGGGGATCATGAAACGTTGCTTCTTATTT	CPj0020_B	CCGCTGCAGGTCGACGGATCTTAGAAGGGAGGTTTTTTAG
CPj0021	CPj0021_F	AGGCCGAATTCCCGGGGATCATGGGACTATTCCATCTAAC	CPj0021_B	CCGCTGCAGGTCGACGGATCTTACTCCACAATTTTTATGAG
CPj0022	CPj0022_F	AGGCCGAATTCCCGGGGATCATGTCCCTTCCTTTAGTTTT	CPj0022_B	CCGCTGCAGGTCGACGGATCTTAGATGGAATAGTCCCATA
CPj0023	CPj0023_F	AGGCCGAATTCCCGGGGATCATGAGCATAGTATTAGATAAAA	CPj0023_B	CCGCTGCAGGTCGACGGATCTTACAACAATTGCTTATGACC
CPj0024	CPj0024_F	AGGCCGAATTCCCGGGGATCATGATTGCCTCTATCTATTC	CPj0024_B	CCGCTGCAGGTCGACGGATCTTAGGCATGGGGATGGGCTT
CPj0025	CPj0025_F	AGGCCGAATTCCCGGGGATCATGAGTTCTAGAGAGTTAATT	CPj0025_B	CCGCTGCAGGTCGACGGATCCTATTTATTTAGAAGAGGATTT
CPj0026	CPj0026_F	AGGCCGAATTCCCGGGGATCATGTCCCATCTTATTCCTAG	CPj0026_B	CCGCTGCAGGTCGACGGATCTTATGGGTCTGTCGGTTGCT
CPj0027	CPj0027_F	AGGCCGAATTCCCGGGGATCGTGGACTCTACAACCAATAG	CPj0027_B	CCGCTGCAGGTCGACGGATCCTATTTTAGCTTGGGAAAAG
CPj0028	CPj0028_F	AGGCCGAATTCCCGGGGATCATGTTTCTTCAGTTTTTTCATC	CPj0028_B	CCGCTGCAGGTCGACGGATCTTATAGGGGGTAGATTTTCC
CPj0029	CPj0029_F	AGGCCGAATTCCCGGGGATCATGAACGATGGGTTGCGATT	CPj0029_B	CCGCTGCAGGTCGACGGATCTTATGGCTTAGTCTTGTTTC
CPj0030	CPj0030_F	AGGCCGAATTCCCGGGGATCATGTACTTCTATAAGTATGTTA	CPj0030_B	CCGCTGCAGGTCGACGGATCTCAAAAAATACATGAATAGCTA
CPj0031	CPj0031_F	AGGCCGAATTCCCGGGGATCATGCCCAGTGTTAAAGTTCG	CPj0031_B	CCGCTGCAGGTCGACGGATCTTAACGACTACGATACTTAG
CPj0032	CPj0032_F	AGGCCGAATTCCCGGGGATCATGGATTATTATTCAATTTTAGG	CPj0032_B	CCGCTGCAGGTCGACGGATCTTATACTGTGAAGTCAGAAAA
CPj0033	CPj0033_F	AGGCCGAATTCCCGGGGATCATGGGAGTAGTACAAAATCA	CPj0033_B	CCGCTGCAGGTCGACGGATCCTAGAATTCTGCGAGACTTT
CPj0034	CPj0034_F	AGGCCGAATTCCCGGGGATCATGGCGGAAATATCGACTCC	CPj0034_B	CCGCTGCAGGTCGACGGATCTTAATTCAAAAAGAGAGCCC
CPj0035	CPj0035_F	AGGCCGAATTCCCGGGGATCATGTGGAATCGTTGTCAGGT	CPj0035_B	CCGCTGCAGGTCGACGGATCTTATAGGGTTTCGATGAAGC
CPj0036	CPj0036_F	AGGCCGAATTCCCGGGGATCATGAAAAAACCTGACAACGA	CPj0036_B	CCGCTGCAGGTCGACGGATCTCATTCATTATACACCTCCT
CPj0037	CPj0037_F	AGGCCGAATTCCCGGGGATCATGAATGAGCCTACTCGCAC	CPj0037_B	CCGCTGCAGGTCGACGGATCTTATAGTTCTCCAAAACCGG
CPj0038	CPj0038_F	AGGCCGAATTCCCGGGGATCATGGATACACAGTCCTCTAT	CPj0038_B	CCGCTGCAGGTCGACGGATCTTATGATGTGATTTTGTTGTTT
CPj0039	CPj0039_F	AGGCCGAATTCCCGGGGATCATGGGCAGCGGATACGCTAA	CPj0039_B	CCGCTGCAGGTCGACGGATCCTAGAAAGGCATTGTGGAAC
CPj0040	CPj0040_F	AGGCCGAATTCCCGGGGATCATGACTCTACAACCCTACCA	CPj0040_B	CCGCTGCAGGTCGACGGATCTTATTGTCTTAAAATTCCTGAA
CPj0041	CPj0041_F	AGGCCGAATTCCCGGGGATCGTGCTTTTACTGATTTCAGG	CPj0041_B	CCGCTGCAGGTCGACGGATCTCAGTAGAGCTCTTGCTCTC
CPj0042	CPj0042_F	AGGCCGAATTCCCGGGGATCATGGAGGAGGTGTCTGAGTA	CPj0042_B	CCGCTGCAGGTCGACGGATCTCAATGTTTCTTTTTACTCTTT
CPj0043	CPj0043_F	AGGCCGAATTCCCGGGGATCATGCAAGTACCTCTATCACC	CPj0043_B	CCGCTGCAGGTCGACGGATCCTATATGTACATGCTTCCGT
CPj0044	CPj0044_F	AGGCCGAATTCCCGGGGATCGTGAGCTTGATAAAAGAAGA	CPj0044_B	CCGCTGCAGGTCGACGGATCCTATTCTGGAATCTCCATCG
CPj0045	CPj0045_F	AGGCCGAATTCCCGGGGATCGTGCTTTTACTGATTTCAGG	CPj0045_B	CCGCTGCAGGTCGACGGATCTTATGAATCCGAGGGTCCAA
CPj0047	CPj0047_F	AGGCCGAATTCCCGGGGATCGTGACTATAGTGGGATTTTT	CPj0047_B	CCGCTGCAGGTCGACGGATCTCACAACCATTTATGAGAGG
CPj0048	CPj0048_F	AGGCCGAATTCCCGGGGATCATGAAAGAACTTAGACATGAA	CPj0048_B	CCGCTGCAGGTCGACGGATCCTAAGTTCCTCCTATAGAGG
CPj0049	CPj0049_F	AGGCCGAATTCCCGGGGATCATGCTACATCAACCTTACTA	CPj0049_B	CCGCTGCAGGTCGACGGATCTTACGTGGCGTTTGATTTCC
CPj0050	CPj0050_F	AGGCCGAATTCCCGGGGATCATGAGATATGCAAAGCATCA	CPj0050_B	CCGCTGCAGGTCGACGGATCTTACGCCAAGGTGTTATTTA
CPj0051	CPj0051_F	AGGCCGAATTCCCGGGGATCATGGGAAACCATGAGACCTA	CPj0051_B	CCGCTGCAGGTCGACGGATCTCAAAACCCCCTTTCTCCAT
CPj0052	CPj0052_F	AGGCCGAATTCCCGGGGATCATGCTATCCGTCTGTTACTC	CPj0052_B	CCGCTGCAGGTCGACGGATCTTATGAGGAGTGGCAGTGTA
CPj0053	CPj0053_F	AGGCCGAATTCCCGGGGATCATGGCAACAAAAACCAAAAC	CPj0053_B	CCGCTGCAGGTCGACGGATCTCAGAGTAACAGACGGATAG
CPj0054	CPj0054_F	AGGCCGAATTCCCGGGGATCATGCATCCCCCTATAGACAT	CPj0054_B	CCGCTGCAGGTCGACGGATCTTACACGTCCATTGTGTTTT
CPj0055	CPj0055_F	AGGCCGAATTCCCGGGGATCATGAGGTCTGCTCTACACCT	CPj0055_B	CCGCTGCAGGTCGACGGATCTTAAATTACTGGAATCCCTAC
CPj0056	CPj0056_F	AGGCCGAATTCCCGGGGATCATGAAAGAAGTAGAACAACG	CPj0056_B	CCGCTGCAGGTCGACGGATCTCACAAATTGGAAAATTTCTC
CPj0057	CPj0057_F	AGGCCGAATTCCCGGGGATCATGAGTTTTGTTCCTTATTCT	CPj0057_B	CCGCTGCAGGTCGACGGATCTTATTTAGATGATATTATTTCAG
CPj0058	CPj0058_F	AGGCCGAATTCCCGGGGATCGTGCGTCTATTTTCTTACGA	CPj0058_B	CCGCTGCAGGTCGACGGATCTTATTCACTGTCATCTGTCA
CPj0059	CPj0059_F	AGGCCGAATTCCCGGGGATCATGACTGTATTTTGTGAATTG	CPj0059_B	CCGCTGCAGGTCGACGGATCTTAGCTTGCTCCAGTATGAC
CPj0060	CPj0060_F	AGGCCGAATTCCCGGGGATCATGCCATCCTATTGTCAAAA	CPj0060_B	CCGCTGCAGGTCGACGGATCTTACATCCCCACAAATACAT
CPj0061	CPj0061_F	AGGCCGAATTCCCGGGGATCATGGATTTAAAGTTAGATGAAG	CPj0061_B	CCGCTGCAGGTCGACGGATCTTAATGAGTTTGGGACTCCC

CPj0062	CPj0062_F	AGGCCGAATTCCCGGGGATCATGATGAGCTCTAAGCGTAC	CPj0062_B	CCGCTGCAGGTCGACGGATCCTATGGAGTAGGAGTTGGAG
CPj0063	CPj0063_F	AGGCCGAATTCCCGGGGATCATGTATGCGAATTGTAAGCA	CPj0063_B	CCGCTGCAGGTCGACGGATCTTATAATAAAACAATATTAGACG
CPj0064	CPj0064_F	AGGCCGAATTCCCGGGGATCATGACTAAAATTCAATGTAGTG	CPj0064_B	CCGCTGCAGGTCGACGGATCTTAAAAAGCAAGTAAATACGAC
CPj0065	CPj0065_F	AGGCCGAATTCCCGGGGATCATGACAGATTTTCCTACTCA	CPj0065_B	CCGCTGCAGGTCGACGGATCCTATTCCTGAGGCTCTTCTT
CPj0066	CPj0066_F	AGGCCGAATTCCCGGGGATCATGGCAAATCCCACACAATC	CPj0066_B	CCGCTGCAGGTCGACGGATCCTATCGATGAGGTCTACGAT
CPj0067	CPj0067_F	AGGCCGAATTCCCGGGGATCATGGCAGTAGAAGGAAGAGT	CPj0067_B	CCGCTGCAGGTCGACGGATCTTAGCCCCAAAATTGATCTT
CPj0068	CPj0068_F	AGGCCGAATTCCCGGGGATCATGATTAAGAAATTTTTTATTTAT	CPj0068_B	CCGCTGCAGGTCGACGGATCTTATTTTTTTAATAGCATAAGAG
CPj0069	CPj0069_F	AGGCCGAATTCCCGGGGATCATGTTTGGTACCTTGGTCTC	CPj0069_B	CCGCTGCAGGTCGACGGATCTTAGCGGCGGGATCTATGGT
CPj0071	CPj0071_F	AGGCCGAATTCCCGGGGATCTTGGAATTTATCTGTCCTCT	CPj0071_B	CCGCTGCAGGTCGACGGATCTTATGTTTGAGGCGGCTTTA
CPj0072	CPj0072_F	AGGCCGAATTCCCGGGGATCATGTCTACTCCACTATCTTC	CPj0072_B	CCGCTGCAGGTCGACGGATCTCAATGATTTGATTCAATGATA
CPj0073	CPj0073_F	AGGCCGAATTCCCGGGGATCATGGCGAAAAAAGAAGATAC	CPj0073_B	CCGCTGCAGGTCGACGGATCTTAACGATGTCTGTAGACAA
CPj0074	CPj0074_F	AGGCCGAATTCCCGGGGATCATGTCAAAAGAAACTTTTCAAC	CPj0074_B	CCGCTGCAGGTCGACGGATCTTAAGCATTGATCTTTGAAATC
CPj0075	CPj0075_F	AGGCCGAATTCCCGGGGATCATGAAACAACAACACAATCG	CPj0075_B	CCGCTGCAGGTCGACGGATCTTAACCGAACAAAAAGGTTG
CPj0076	CPj0076_F	AGGCCGAATTCCCGGGGATCATGTATAAATGGTATGTCGTT	CPj0076_B	CCGCTGCAGGTCGACGGATCCTACTCACTTTCTTGCCCTG
CPj0077	CPj0077_F	AGGCCGAATTCCCGGGGATCATGTCGGTAAAAAAGGTAATC	CPj0077_B	CCGCTGCAGGTCGACGGATCTTATTCTACGTCTATACCCA
CPj0078	CPj0078_F	AGGCCGAATTCCCGGGGATCATGACAAAACATGGAAAACG	CPj0078_B	CCGCTGCAGGTCGACGGATCTTAAGATGCCATTAATTCTCT
CPj0079	CPj0079_F	AGGCCGAATTCCCGGGGATCATGAAACAAGAAAAAACATTAC	CPj0079_B	CCGCTGCAGGTCGACGGATCTTAGTTCTTTCCTGCCTTTT
CPj0080	CPj0080_F	AGGCCGAATTCCCGGGGATCGTGACAACAGAAAGTTTGGA	CPj0080_B	CCGCTGCAGGTCGACGGATCTTACAGTCCCTTAAATGAGG
CPj0081	CPj0081_F	AGGCCGAATTCCCGGGGATCATGTTGAAGTGCCCTGAACG	CPj0081_B	CCGCTGCAGGTCGACGGATCTTAAGCGTCTACGACCATAG
CPj0082	CPj0082_F	AGGCCGAATTCCCGGGGATCATGTTCGGAGAAAATTCTCG	CPj0082_B	CCGCTGCAGGTCGACGGATCTTAACAAACACACTCTGTTTC
CPj0083	CPj0083_F	AGGCCGAATTCCCGGGGATCATGTCTAACCAATTTGATCAA	CPj0083_B	CCGCTGCAGGTCGACGGATCTTACGCACCTTCTGCAGCAA
CPj0084	CPj0084_F	AGGCCGAATTCCCGGGGATCATGGACTATAAATCGCAACT	CPj0084_B	CCGCTGCAGGTCGACGGATCTTAAGAAATAAGATCGCTTTC
CPj0085	CPj0085_F	AGGCCGAATTCCCGGGGATCATGAAATTTTTTATTCTTTTTATT	CPj0085_B	CCGCTGCAGGTCGACGGATCTTATTTGTTTTCGTTTTGCAG
CPj0086	CPj0086_F	AGGCCGAATTCCCGGGGATCATGGCGAATCTTAATGCCGA	CPj0086_B	CCGCTGCAGGTCGACGGATCTCAAGATCCTTGAAAAATCAT
CPj0087	CPj0087_F	AGGCCGAATTCCCGGGGATCATGACTCAATATTATTTTTTATC	CPj0087_B	CCGCTGCAGGTCGACGGATCTTACCATTTGATTGCCTTTTC
CPj0088	CPj0088_F	AGGCCGAATTCCCGGGGATCATGGTAACAGTTTCAGAACA	CPj0088_B	CCGCTGCAGGTCGACGGATCTTACGCCATTTGTACCATTG
CPj0089	CPj0089_F	AGGCCGAATTCCCGGGGATCATGCAAACAATCTACACAAAA	CPj0089_B	CCGCTGCAGGTCGACGGATCTTACTTGGACAGACATGCTT
CPj0090	CPj0090_F	AGGCCGAATTCCCGGGGATCATGTCTGTCCAAGTAAAGCT	CPj0090_B	CCGCTGCAGGTCGACGGATCTTAAACGCACTCATCCCCCC
CPj0091	CPj0091_F	AGGCCGAATTCCCGGGGATCGTGCGTTTAAATATACATAAG	CPj0091_B	CCGCTGCAGGTCGACGGATCTCAAACTATTGAATTATTATCTAA
CPj0092	CPj0092_F	AGGCCGAATTCCCGGGGATCATGATTGATATGTCTGTTGTT	CPj0092_B	CCGCTGCAGGTCGACGGATCTTAGAGTAGTAGTAGCGCAA
CPj0093	CPj0093_F	AGGCCGAATTCCCGGGGATCATGCAGCGATTGGGATTGTC	CPj0093_B	CCGCTGCAGGTCGACGGATCTTAAGGAGAATCCAGAGAGA
CPj0094	CPj0094_F	AGGCCGAATTCCCGGGGATCATGACAACAGAAGATTTTCC	CPj0094_B	CCGCTGCAGGTCGACGGATCCTAAGCAAACGATGCAAGCT
CPj0095	CPj0095_F	AGGCCGAATTCCCGGGGATCTTGGAGCGCTATGATATTGT	CPj0095_B	CCGCTGCAGGTCGACGGATCTTAAAGCTGAAATTCTTCGG
CPj0096	CPj0096_F	AGGCCGAATTCCCGGGGATCATGAAATCACTTCCTGTATAT	CPj0096_B	CCGCTGCAGGTCGACGGATCTTAAGAATCGAGTTCTTCATT
CPj0097	CPj0097_F	AGGCCGAATTCCCGGGGATCATGATCACACGCACTAAAAT	CPj0097_B	CCGCTGCAGGTCGACGGATCCTAGGTTTCAGGAAATTCCG
CPj0100	CPj0100_F	AGGCCGAATTCCCGGGGATCTTGGATTTGGAAACGATGAT	CPj0100_B	CCGCTGCAGGTCGACGGATCCTACCACTCTTTTTTATATAAT
CPj0101	CPj0101_F	AGGCCGAATTCCCGGGGATCATGCCCTTTGATATTACTTAT	CPj0101_B	CCGCTGCAGGTCGACGGATCTCATCGTTTCCAAATCCAAG
CPj0102	CPj0102_F	AGGCCGAATTCCCGGGGATCATGGATGCGCTTATCTTATC	CPj0102_B	CCGCTGCAGGTCGACGGATCCTATTTCACTTCAAATTCTGT
CPj0103	CPj0103_F	AGGCCGAATTCCCGGGGATCATGGAACTTTCTCTAACAAG	CPj0103_B	CCGCTGCAGGTCGACGGATCTCAATATATAGAGGGAAAATTA
CPj0104	CPj0104_F	AGGCCGAATTCCCGGGGATCATGAGAATGCTCCAGATTTC	CPj0104_B	CCGCTGCAGGTCGACGGATCTTATGAAGCTTCTTTAATTCC
CPj0105	CPj0105_F	AGGCCGAATTCCCGGGGATCATGAAAGTCAAAATTAATGATC	CPj0105_B	CCGCTGCAGGTCGACGGATCCTAAGTATATAAAACAGCTTTT
CPj0106	CPj0106_F	AGGCCGAATTCCCGGGGATCATGAAGAAAACAATGGTCATT	CPj0106_B	CCGCTGCAGGTCGACGGATCCTATAGGATAGTTGCGGCCG
CPj0107	CPj0107_F	AGGCCGAATTCCCGGGGATCATGGTTTCTCCTCTATCTCT	CPj0107_B	CCGCTGCAGGTCGACGGATCTTATAAGTGACTTTTCTTCTTC
CPj0108	CPj0108_F	AGGCCGAATTCCCGGGGATCATGAGCATTTTTAATGAAGAAG	CPj0108_B	CCGCTGCAGGTCGACGGATCTTACAGGTGGGGGGCTTTTT
CPj0109	CPj0109_F	AGGCCGAATTCCCGGGGATCATGACAGCAGATGAGGTAGG	CPj0109_B	CCGCTGCAGGTCGACGGATCCTAAGAATCTATAGAACTAACT
CPj0110	CPj0110_F	AGGCCGAATTCCCGGGGATCATGAAACAACACTATTCTCTA	CPj0110_B	CCGCTGCAGGTCGACGGATCTTATTTCTTGTGGTTTTTCTC
CPj0111	CPj0111_F	AGGCCGAATTCCCGGGGATCATGAAAAAGCAAGGAAAAACA	CPj0111_B	CCGCTGCAGGTCGACGGATCTCATTGTGTCTTAGAGTCAG
CPj0112	CPj0112_F	AGGCCGAATTCCCGGGGATCATGAAAAAAAATACCCACCC	CPj0112_B	CCGCTGCAGGTCGACGGATCTTATTTCTTTTTCTTAGTTACAA
CPj0113	CPj0113_F	AGGCCGAATTCCCGGGGATCATGAAGAAAAAAGTTGCCGA	CPj0113_B	CCGCTGCAGGTCGACGGATCTTAATTTCCATGTTCGAGTAA
CPj0114	CPj0114_F	AGGCCGAATTCCCGGGGATCATGGAAATTAAAAAGGCGATT	CPj0114_B	CCGCTGCAGGTCGACGGATCTCAAGAATAAGCCCCCGAGG
CPj0115	CPj0115_F	AGGCCGAATTCCCGGGGATCATGATTAATTCTTTATCGCAAA	CPj0115_B	CCGCTGCAGGTCGACGGATCTTAACGCCACTGATTTCCTC
CPj0116	CPj0116_F	AGGCCGAATTCCCGGGGATCGTGGCGTTAAAAATTCGTTT	CPj0116_B	CCGCTGCAGGTCGACGGATCCTACTTAGTTGCATCTTTTG
CPj0117	CPj0117_F	AGGCCGAATTCCCGGGGATCATGAAGATCGATATACTTTCT	CPj0117_B	CCGCTGCAGGTCGACGGATCCTATTTCATCCTATGCCACG
CPj0118	CPj0118_F	AGGCCGAATTCCCGGGGATCATGGTGAATTTACTCAAAGAA	CPj0118_B	CCGCTGCAGGTCGACGGATCCTATTTCTTTGAAGATCTAGG
CPj0119	CPj0119_F	AGGCCGAATTCCCGGGGATCATGAATACTTCTATTTCTGAAA	CPj0119_B	CCGCTGCAGGTCGACGGATCTCATACAATAGCACACATTTG
CPj0120	CPj0120_F	AGGCCGAATTCCCGGGGATCATGAATAAGATCCTAGTTGAC	CPj0120_B	CCGCTGCAGGTCGACGGATCTCATAATATGTTCCTATGTTC
CPj0121	CPj0121_F	AGGCCGAATTCCCGGGGATCATGATTAAAAAAGATCGTTTCA	CPj0121_B	CCGCTGCAGGTCGACGGATCTTACTTTACATCACTCCAAG
CPj0122	CPj0122_F	AGGCCGAATTCCCGGGGATCATGCCACAAAAAGTCCTGAT	CPj0122_B	CCGCTGCAGGTCGACGGATCCTACTCTACAGTAGTAAATAA
CPj0123	CPj0123_F	AGGCCGAATTCCCGGGGATCATGGAGAAAATCTGCGGATA	CPj0123_B	CCGCTGCAGGTCGACGGATCTTACAGATCTGCATAATTTTTC
CPj0124	CPj0124_F	AGGCCGAATTCCCGGGGATCGTGCTTGGCATTCTTTTGAT	CPj0124_B	CCGCTGCAGGTCGACGGATCCTAACTATTCTCTAAACTCAT
CPj0125	CPj0125_F	AGGCCGAATTCCCGGGGATCATGTCAGAAGTGAAGCCTTT	CPj0125_B	CCGCTGCAGGTCGACGGATCCTAGTCCTGTTCTTTCTTTC
CPj0126	CPj0126_F	AGGCCGAATTCCCGGGGATCTTGGTATTCTCATACTATTGC	CPj0126_B	CCGCTGCAGGTCGACGGATCCTATCTCCTAGACAGCCTTG
CPj0127	CPj0127_F	AGGCCGAATTCCCGGGGATCATGTTCCCCAGCGCAAATCA	CPj0127_B	CCGCTGCAGGTCGACGGATCTTATTCGTTAGAAGACGATAC
CPj0128	CPj0128_F	AGGCCGAATTCCCGGGGATCATGTTAAGGAATCAGGTACT	CPj0128_B	CCGCTGCAGGTCGACGGATCTCAGCAGTCCGCTTTCGAAA
CPj0130	CPj0130_F	AGGCCGAATTCCCGGGGATCATGGTCAAGTGTTCTTCAAT	CPj0130_B	CCGCTGCAGGTCGACGGATCCTAAATTAGGCAATCGAAATC

CPj0131	CPj0131_F	AGGCCGAATTCCCGGGGATCATGGAGAATGCTATGTCATC	CPj0131_B	CCGCTGCAGGTCGACGGATCTTACCTCACTAAAAATTGTTTT
CPj0132	CPj0132_F	AGGCCGAATTCCCGGGGATCATGATCGAGTTTGCTTTTGT	CPj0132_B	CCGCTGCAGGTCGACGGATCTTAAAGAGAGGCTACGTCTT
CPj0133	CPj0133_F	AGGCCGAATTCCCGGGGATCATGTTTAAACTGCTAAAAAATC	CPj0133_B	CCGCTGCAGGTCGACGGATCTTAATGAAAGAAGAGTCCTC
CPj0134	CPj0134_F	AGGCCGAATTCCCGGGGATCATGGCAGCGAAAAATATTAAA	CPj0134_B	CCGCTGCAGGTCGACGGATCCTAGTAGTCCATTCCTGCGC
CPj0135	CPj0135_F	AGGCCGAATTCCCGGGGATCATGTCTGATCAAGCAACGAC	CPj0135_B	CCGCTGCAGGTCGACGGATCTTATTTTAGGACGGCCATGA
CPj0136	CPj0136_F	AGGCCGAATTCCCGGGGATCATGACTACTGAACTGAAAAC	CPj0136_B	CCGCTGCAGGTCGACGGATCTCAATCTTCTGAAAGCAAGG
CPj0137	CPj0137_F	AGGCCGAATTCCCGGGGATCATGAATGTTGCGGATCTCCT	CPj0137_B	CCGCTGCAGGTCGACGGATCTTAGAAGGGGTTGGCCGTAT
CPj0138	CPj0138_F	AGGCCGAATTCCCGGGGATCATGTTGAACTGCTCAAATCA	CPj0138_B	CCGCTGCAGGTCGACGGATCTTAGAAAAATCTTTGAGCCG
CPj0139	CPj0139_F	AGGCCGAATTCCCGGGGATCATTATGAAAATTCCTTATGCAC	CPj0139_B	CCGCTGCAGGTCGACGGATCTTAGTTTAGCAATAGATTGTC
CPj0140	CPj0140_F	AGGCCGAATTCCCGGGGATCATGAGCTTAGAAAAAGAACTC	CPj0140_B	CCGCTGCAGGTCGACGGATCTTATTCTTCGTAGGGGACTA
CPj0141	CPj0141_F	AGGCCGAATTCCCGGGGATCGTGGAAAAAGATCTTCATCT	CPj0141_B	CCGCTGCAGGTCGACGGATCTCATACAGAATATTTTTTGCTG
CPj0142	CPj0142_F	AGGCCGAATTCCCGGGGATCTTGGAAAAATTTCACTTCAAAA	CPj0142_B	CCGCTGCAGGTCGACGGATCCTATGTTACAAAATATTCCCA
CPj0143	CPj0143_F	AGGCCGAATTCCCGGGGATCATGAATACTTCACTAAAAAGAC	CPj0143_B	CCGCTGCAGGTCGACGGATCTTATTTCCAAACTTCTTCGG
CPj0144	CPj0144_F	AGGCCGAATTCCCGGGGATCATGGAGAAATTTTCCGATGC	CPj0144_B	CCGCTGCAGGTCGACGGATCCTAAGAAGGAGTTTCCACTT
CPj0145	CPj0145_F	AGGCCGAATTCCCGGGGATCATGTTTGTAGGTGGCCTTGT	CPj0145_B	CCGCTGCAGGTCGACGGATCTTATCTTTCAGACTCCATTAA
CPj0146	CPj0146_F	AGGCCGAATTCCCGGGGATCATGAGCAGTTCGGAAGTTGT	CPj0146_B	CCGCTGCAGGTCGACGGATCTCAATCATCTGACATCTGAT
CPj0147	CPj0147_F	AGGCCGAATTCCCGGGGATCATGGCTGTTCAATCTATAAAA	CPj0147_B	CCGCTGCAGGTCGACGGATCCTAACTTCCCGCCCCTGAAT
CPj0148	CPj0148_F	AGGCCGAATTCCCGGGGATCATGGAAAGTGAGAAAGATATA	CPj0148_B	CCGCTGCAGGTCGACGGATCTTAATTGATATTTTTAGCGCAC
CPj0149	CPj0149_F	AGGCCGAATTCCCGGGGATCATGAAGGAAGAGAATTCACA	CPj0149_B	CCGCTGCAGGTCGACGGATCTTATTCTAAATGAATTAGATTTG
CPj0150	CPj0150_F	AGGCCGAATTCCCGGGGATCATGGCTTCTTCTTCAAACAA	CPj0150_B	CCGCTGCAGGTCGACGGATCCTAAGCAGCCTCTTCTCTAC
CPj0151	CPj0151_F	AGGCCGAATTCCCGGGGATCATGGCAGACATTTTAGTCAT	CPj0151_B	CCGCTGCAGGTCGACGGATCTTAGCTGGTCTTTTCGCTGG
CPj0152	CPj0152_F	AGGCCGAATTCCCGGGGATCATGCGTAAAGTTGCTTTTTTA	CPj0152_B	CCGCTGCAGGTCGACGGATCTTAAAGTGTTCGTTGGAAGT
CPj0153	CPj0153_F	AGGCCGAATTCCCGGGGATCATGCGATATGACCCCAACTT	CPj0153_B	CCGCTGCAGGTCGACGGATCTCATAGGACAAAATTCACTAG
CPj0154	CPj0154_F	AGGCCGAATTCCCGGGGATCATGATGCTACGAGGTGTCCA	CPj0154_B	CCGCTGCAGGTCGACGGATCTTAACTATTTTTGTACAAGGGA
CPj0155	CPj0155_F	AGGCCGAATTCCCGGGGATCTTGAGTTTTGGAGTGCCTTT	CPj0155_B	CCGCTGCAGGTCGACGGATCTCAATTTGGATTTATGTTTTCT
CPj0156	CPj0156_F	AGGCCGAATTCCCGGGGATCATGATGCACAATATTGTGGT	CPj0156_B	CCGCTGCAGGTCGACGGATCTTACTCATCTCTAATAAACAAG
CPj0157	CPj0157_F	AGGCCGAATTCCCGGGGATCATGAACATATACCAATTTTCTC	CPj0157_B	CCGCTGCAGGTCGACGGATCTTAAGGAGTTTCAACTTTCAT
CPj0158	CPj0158_F	AGGCCGAATTCCCGGGGATCTTGCTCTTAGAGGACTTAGA	CPj0158_B	CCGCTGCAGGTCGACGGATCTTAATTGTCTTTGATAAATCCA
CPj0159	CPj0159_F	AGGCCGAATTCCCGGGGATCATGACTCCCTCTGGGTTTTC	CPj0159_B	CCGCTGCAGGTCGACGGATCCTACCCTTTAGAAGTTTGGA
CPj0160	CPj0160_F	AGGCCGAATTCCCGGGGATCGTGGAACTTCTCTCGTTAAA	CPj0160_B	CCGCTGCAGGTCGACGGATCTCAGAGTAGAGGCGAATGCG
CPj0161	CPj0161_F	AGGCCGAATTCCCGGGGATCTTGATTACAGGCGTGGTATT	CPj0161_B	CCGCTGCAGGTCGACGGATCTTATTCCCCAGAAGTTAATTC
CPj0162	CPj0162_F	AGGCCGAATTCCCGGGGATCATGAAACTTTATAGCATCTCT	CPj0162_B	CCGCTGCAGGTCGACGGATCTTAAACCTCCTTATTGGGTT
CPj0163	CPj0163_F	AGGCCGAATTCCCGGGGATCTTGCGAGCAGGAGGTAGTCT	CPj0163_B	CCGCTGCAGGTCGACGGATCTTACTTGTTAGTACAAAGCAA
CPj0164	CPj0164_F	AGGCCGAATTCCCGGGGATCATGACTAGAAGTACTATTGAA	CPj0164_B	CCGCTGCAGGTCGACGGATCTCATAAATAAAAGTACATTTTAG
CPj0165	CPj0165_F	AGGCCGAATTCCCGGGGATCATGAATTGGGTTCCAAAAAC	CPj0165_B	CCGCTGCAGGTCGACGGATCTTAAGTGCAGAACACATCAG
CPj0166	CPj0166_F	AGGCCGAATTCCCGGGGATCATGTCTGAAAGTATTAACAGA	CPj0166_B	CCGCTGCAGGTCGACGGATCTTAAAGAGTACTGTCCGTTT
CPj0167	CPj0167_F	AGGCCGAATTCCCGGGGATCTTGTGGTCGCATTTCCCAAG	CPj0167_B	CCGCTGCAGGTCGACGGATCTTAATGTATAGGGCTAATCG
CPj0168	CPj0168_F	AGGCCGAATTCCCGGGGATCTTGGCCTTTAATGAGTCAGT	CPj0168_B	CCGCTGCAGGTCGACGGATCTTAAGAACAAAATATATCGGC
CPj0169	CPj0169_F	AGGCCGAATTCCCGGGGATCATGAAAAATGTTGGTTCAGAG	CPj0169_B	CCGCTGCAGGTCGACGGATCTTATATAGCTCTATTTATAATATA
CPj0170	CPj0170_F	AGGCCGAATTCCCGGGGATCATGTCTTATGATACGTTATTCA	CPj0170_B	CCGCTGCAGGTCGACGGATCTTATCCTAACTGGCAAGTAA
CPj0171	CPj0171_F	AGGCCGAATTCCCGGGGATCTTGAACACCATATTTATTCTAG	CPj0171_B	CCGCTGCAGGTCGACGGATCCTATTCCCATTCTATAGTTG
CPj0173	CPj0173_F	AGGCCGAATTCCCGGGGATCATGGACTTTAGCGTATTTCC	CPj0173_B	CCGCTGCAGGTCGACGGATCTTAAGATATACGACGACAGC
CPj0174	CPj0174_F	AGGCCGAATTCCCGGGGATCATGATTATGACTACTATATCTA	CPj0174_B	CCGCTGCAGGTCGACGGATCTCATAACCAGGTACTAGGAG
CPj0175	CPj0175_F	AGGCCGAATTCCCGGGGATCATGGAGCAACCCAATTGTGT	CPj0175_B	CCGCTGCAGGTCGACGGATCTCATCGTTTCAGAGCTTCCT
CPj0176	CPj0176_F	AGGCCGAATTCCCGGGGATCATGGATGAATCCGATGGAGA	CPj0176_B	CCGCTGCAGGTCGACGGATCTTATACAGTAATTATAAAGACAG
CPj0177	CPj0177_F	AGGCCGAATTCCCGGGGATCATGAAACAGCCCATGTCTCT	CPj0177_B	CCGCTGCAGGTCGACGGATCTTAGGGCTGAGGAGGAACTT
CPj0178	CPj0178_F	AGGCCGAATTCCCGGGGATCGTGAAAGAATACTTAGATTTTC	CPj0178_B	CCGCTGCAGGTCGACGGATCTTAGTCCAAGTACACCCACA
CPj0179	CPj0179_F	AGGCCGAATTCCCGGGGATCTTGCAAGCAGGCCGCTCTG	CPj0179_B	CCGCTGCAGGTCGACGGATCTCAATCTAACTTCTCCTCAT
CPj0181	CPj0181_F	AGGCCGAATTCCCGGGGATCGTGCATGAATTGTTTAAAATAG	CPj0181_B	CCGCTGCAGGTCGACGGATCCTAATAAACAGATTTTCTTAGC
CPj0182	CPj0182_F	AGGCCGAATTCCCGGGGATCATGAAAAAAGTCTTAATCGCT	CPj0182_B	CCGCTGCAGGTCGACGGATCTTAGAATTCTTTAAAAAAAGAATT
CPj0183	CPj0183_F	AGGCCGAATTCCCGGGGATCATGGACTTAAAACAAATAGAAA	CPj0183_B	CCGCTGCAGGTCGACGGATCTCATGATGCATCTTTAGCTA
CPj0184	CPj0184_F	AGGCCGAATTCCCGGGGATCATGGTGTTAAGTAGCCAATT	CPj0184_B	CCGCTGCAGGTCGACGGATCTTAGACGCGTTGAATATACT
CPj0185	CPj0185_F	AGGCCGAATTCCCGGGGATCATGGGGGCAGATCTTACCTG	CPj0185_B	CCGCTGCAGGTCGACGGATCCTACTTAACACCATAATTTTCT
CPj0186	CPj0186_F	AGGCCGAATTCCCGGGGATCATGTCATCTCCTGTAAATAAC	CPj0186_B	CCGCTGCAGGTCGACGGATCTTACTGACCATCTCCTGTTG
CPj0187	CPj0187_F	AGGCCGAATTCCCGGGGATCATGCATTCAAAATTTCTTTCTC	CPj0187_B	CCGCTGCAGGTCGACGGATCTTATTTTATCTTAATGCATGAAA
CPj0188	CPj0188_F	AGGCCGAATTCCCGGGGATCATGTTTCGAAAACTTTTCCC	CPj0188_B	CCGCTGCAGGTCGACGGATCTCATTTGATTCGCCTAGCAA
CPj0189	CPj0189_F	AGGCCGAATTCCCGGGGATCATAATCAATCTATCAGCAGAG	CPj0189_B	CCGCTGCAGGTCGACGGATCCTATTTATTTTCTATAGAATCAA
CPj0190	CPj0190_F	AGGCCGAATTCCCGGGGATCATGAGAAAACGTCACTCTTT	CPj0190_B	CCGCTGCAGGTCGACGGATCTTAGAATCCTGACCAGTGGC
CPj0191	CPj0191_F	AGGCCGAATTCCCGGGGATCATGACAATTAGAGTCCGAAA	CPj0191_B	CCGCTGCAGGTCGACGGATCCTATTGAGCAGAGTGGATAT
CPj0192	CPj0192_F	AGGCCGAATTCCCGGGGATCGTGGATCATTGGCTAGCTAT	CPj0192_B	CCGCTGCAGGTCGACGGATCCTAATTGTCATAGCTCCTTC
CPj0193	CPj0193_F	AGGCCGAATTCCCGGGGATCATGAAAAAAAAAGTAACTATAGA	CPj0193_B	CCGCTGCAGGTCGACGGATCTTAATCCAAGAAAACTTGCAG
CPj0194	CPj0194_F	AGGCCGAATTCCCGGGGATCATGCTCACCCTAGGCTTGGA	CPj0194_B	CCGCTGCAGGTCGACGGATCCTACGGAGAGGCTAAGGAGA
CPj0195	CPj0195_F	AGGCCGAATTCCCGGGGATCATGCGCAAGATATCAGTGGG	CPj0195_B	CCGCTGCAGGTCGACGGATCCTAATTTTCCTTAGCATAACG
CPj0196	CPj0196_F	AGGCCGAATTCCCGGGGATCATGCTCCGTTTCTTCGCTGT	CPj0196_B	CCGCTGCAGGTCGACGGATCCTATAGTTTTTCTATAAAACGA
CPj0197	CPj0197_F	AGGCCGAATTCCCGGGGATCATGTTTTCACGATGGATCAC	CPj0197_B	CCGCTGCAGGTCGACGGATCCTAGGGGAAATAGGTATATT

CPj0198	CPj0198_F	AGGCCGAATTCCCGGGGATCATGAAGATGCATAGGCTTAA	CPj0198_B	CCGCTGCAGGTCGACGGATCCTAACTTAAGATATCGATATTT
CPj0199	CPj0199_F	AGGCCGAATTCCCGGGGATCGTGTTCTCATACATAAAAAAC	CPj0199_B	CCGCTGCAGGTCGACGGATCTTATTTTCTTTTTTTTTCCTTTC
CPj0200	CPj0200_F	AGGCCGAATTCCCGGGGATCATGGAAAACCTATCCTCAGC	CPj0200_B	CCGCTGCAGGTCGACGGATCTTATCCATGAGATCCCTCTT
CPj0201	CPj0201_F	AGGCCGAATTCCCGGGGATCATGGATAACTACTTACTAAATA	CPj0201_B	CCGCTGCAGGTCGACGGATCTCATAAACCACCTTGCATAC
CPj0202	CPj0202_F	AGGCCGAATTCCCGGGGATCATGACAACTCTACTAAGTATA	CPj0202_B	CCGCTGCAGGTCGACGGATCTTACTTTGAGGCGACTTGTA
CPj0203	CPj0203_F	AGGCCGAATTCCCGGGGATCATGAATACCTATACCTTCTC	CPj0203_B	CCGCTGCAGGTCGACGGATCTTATATTTCCTTCATGATGGG
CPj0204	CPj0204_F	AGGCCGAATTCCCGGGGATCATGGGCTACCAAATCTTCAC	CPj0204_B	CCGCTGCAGGTCGACGGATCTTAAGTATTTCTATAGAATGTTT
CPj0205	CPj0205_F	AGGCCGAATTCCCGGGGATCTTGCTAAAGTTCTTTCTAGTA	CPj0205_B	CCGCTGCAGGTCGACGGATCTTAAGAACATAACGGTGATG
CPj0206	CPj0206_F	AGGCCGAATTCCCGGGGATCATGGATATTTCCCATATCCT	CPj0206_B	CCGCTGCAGGTCGACGGATCTCACGGTTCTATGGGGAAGT
CPj0207	CPj0207_F	AGGCCGAATTCCCGGGGATCGTGAACAAAAAAAAACGTTTCT	CPj0207_B	CCGCTGCAGGTCGACGGATCCTAAATGAGTCCGAGGGCTT
CPj0208	CPj0208_F	AGGCCGAATTCCCGGGGATCATGCATCCTTTATACGTTGA	CPj0208_B	CCGCTGCAGGTCGACGGATCTTAATACGTAGTATCAGGGA
CPj0209	CPj0209_F	AGGCCGAATTCCCGGGGATCATGGAAACTTATAGCTTTTCT	CPj0209_B	CCGCTGCAGGTCGACGGATCTCAAGGGCGATACCACAAAC
CPj0210	CPj0210_F	AGGCCGAATTCCCGGGGATCATGCTAGTAGAGTTAGAGGC	CPj0210_B	CCGCTGCAGGTCGACGGATCTTATTCTGTGTCTTTCCGCG
CPj0211	CPj0211_F	AGGCCGAATTCCCGGGGATCATGTCTTATCCTGATATTTCC	CPj0211_B	CCGCTGCAGGTCGACGGATCCTATAATAAAGATTTTGCCTC
CPj0212	CPj0212_F	AGGCCGAATTCCCGGGGATCGTGGTTGTGTCTATTTATTC	CPj0212_B	CCGCTGCAGGTCGACGGATCTTATGCCTCTAGAAGGATAT
CPj0214	CPj0214_F	AGGCCGAATTCCCGGGGATCGTGGTGGTTGTCGCTTTATT	CPj0214_B	CCGCTGCAGGTCGACGGATCCTAAGTTTCTTCTGTCACTA
CPj0215	CPj0215_F	AGGCCGAATTCCCGGGGATCATGTCTAGCGCTATTGCCCG	CPj0215_B	CCGCTGCAGGTCGACGGATCTTAATCCAAGAAATCATCGTG
CPj0216	CPj0216_F	AGGCCGAATTCCCGGGGATCATGAATCCTGTGACATTTGA	CPj0216_B	CCGCTGCAGGTCGACGGATCTTAAACAAAGACACTATCGC
CPj0217	CPj0217_F	AGGCCGAATTCCCGGGGATCTTGAAAGGATTTTTATCTGTGA	CPj0217_B	CCGCTGCAGGTCGACGGATCTTAAGAGGAACGACGATCTA
CPj0218	CPj0218_F	AGGCCGAATTCCCGGGGATCTTGTCTAAAAAAGTGTTTTTCG	CPj0218_B	CCGCTGCAGGTCGACGGATCTTAAGCTAAGAAATTAACAGC
CPj0219	CPj0219_F	AGGCCGAATTCCCGGGGATCTTGGCACTCAAATTCCATCT	CPj0219_B	CCGCTGCAGGTCGACGGATCTTAGATTTCATCTTTTAAGATG
CPj0220	CPj0220_F	AGGCCGAATTCCCGGGGATCATGTCGAAGGAAAGCATTAG	CPj0220_B	CCGCTGCAGGTCGACGGATCTTATACAATGATCTCTCTTAC
CPj0221	CPj0221_F	AGGCCGAATTCCCGGGGATCATGGTAAACAGATACAAGAG	CPj0221_B	CCGCTGCAGGTCGACGGATCCTAAATAGGATGAAAATCACT
CPj0222	CPj0222_F	AGGCCGAATTCCCGGGGATCTTGCGAGAATTAAATGCTTTT	CPj0222_B	CCGCTGCAGGTCGACGGATCTCATGATAAAAGTAGATGATAA
CPj0223	CPj0223_F	AGGCCGAATTCCCGGGGATCATGCTAATAGGCAGATACAG	CPj0223_B	CCGCTGCAGGTCGACGGATCTTATTTGCAGAACCCAATAAC
CPj0224	CPj0224_F	AGGCCGAATTCCCGGGGATCATGAAGCCAAATAGTATTATTT	CPj0224_B	CCGCTGCAGGTCGACGGATCTCAAACCACTTGTTTTTTCC
CPj0225	CPj0225_F	AGGCCGAATTCCCGGGGATCATGACTAAAAATGCTATAAATTC	CPj0225_B	CCGCTGCAGGTCGACGGATCTTACTTTCTTTTAGCTACTTC
CPj0226	CPj0226_F	AGGCCGAATTCCCGGGGATCATGCCATACTATGCAAACAC	CPj0226_B	CCGCTGCAGGTCGACGGATCTTAAGAATAAAATAGGAAAGTTG
CPj0227	CPj0227_F	AGGCCGAATTCCCGGGGATCATGATTAATTTTATCCGTAGCT	CPj0227_B	CCGCTGCAGGTCGACGGATCCTATCCTCTATATTTTTTTGTA
CPj0228	CPj0228_F	AGGCCGAATTCCCGGGGATCTTGAATAAAAAGATCCTAGTTC	CPj0228_B	CCGCTGCAGGTCGACGGATCTTAATCATCATGATCTCCTTC
CPj0229	CPj0229_F	AGGCCGAATTCCCGGGGATCATGGATAAAGAAACACTAGAA	CPj0229_B	CCGCTGCAGGTCGACGGATCTTAGAGTTTGCGTTTAGTTC
CPj0230	CPj0230_F	AGGCCGAATTCCCGGGGATCATGAGTTCACAGCCTCTGGT	CPj0230_B	CCGCTGCAGGTCGACGGATCTTACGTGCCTAACCCCTCCC
CPj0231	CPj0231_F	AGGCCGAATTCCCGGGGATCATGTTACAAGCTCATCGTCT	CPj0231_B	CCGCTGCAGGTCGACGGATCTCATGTATATAAGTGCTTTTTT
CPj0232	CPj0232_F	AGGCCGAATTCCCGGGGATCATGCGTCGTTTTCTGTTTCT	CPj0232_B	CCGCTGCAGGTCGACGGATCTTAATGAGAAGAACAGAGTTC
CPj0233	CPj0233_F	AGGCCGAATTCCCGGGGATCATGTTTTTGGGCAAAGTTCT	CPj0233_B	CCGCTGCAGGTCGACGGATCTTAACTCTGTCCTTTGTTCT
CPj0234	CPj0234_F	AGGCCGAATTCCCGGGGATCATGTTGCAGAGTTGCAAAAA	CPj0234_B	CCGCTGCAGGTCGACGGATCTTACAGACTTACTTTCTTTTTC
CPj0235	CPj0235_F	AGGCCGAATTCCCGGGGATCATGAAGCCGGAAGAGTCTGA	CPj0235_B	CCGCTGCAGGTCGACGGATCTTAAAAATATGCATTTGAAAGG
CPj0236	CPj0236_F	AGGCCGAATTCCCGGGGATCATGCCTTTCAAATGCATATTT	CPj0236_B	CCGCTGCAGGTCGACGGATCTTAGACATGGCTTGCATCCT
CPj0237	CPj0237_F	AGGCCGAATTCCCGGGGATCATGTCTAAGCCATCTAGTTG	CPj0237_B	CCGCTGCAGGTCGACGGATCTTACAAGGTTAGTTTTTTAGG
CPj0238	CPj0238_F	AGGCCGAATTCCCGGGGATCATGACGAATGTTGTTCAGGA	CPj0238_B	CCGCTGCAGGTCGACGGATCCTATAAAGGTCTCCAGCTTC
CPj0240	CPj0240_F	AGGCCGAATTCCCGGGGATCTTGGTTTATTTTATGGTGTTTT	CPj0240_B	CCGCTGCAGGTCGACGGATCTTAGCCGTAGATAGTATCGT
CPj0241	CPj0241_F	AGGCCGAATTCCCGGGGATCATGTCTGCCATGATTTCTCT	CPj0241_B	CCGCTGCAGGTCGACGGATCTTAGCGATAATAAGGAGCAG
CPj0242	CPj0242_F	AGGCCGAATTCCCGGGGATCATGGCTTGTTCTATTTTTTTTA	CPj0242_B	CCGCTGCAGGTCGACGGATCTTAAGGTTTGATTAATCCAGA
CPj0243	CPj0243_F	AGGCCGAATTCCCGGGGATCATGGCTTGTTCTATTGGTTA	CPj0243_B	CCGCTGCAGGTCGACGGATCTTACCAATTTATAATAGCAGTT
CPj0244	CPj0244_F	AGGCCGAATTCCCGGGGATCGTGACTAAGGGCTCTGTTTT	CPj0244_B	CCGCTGCAGGTCGACGGATCCTATTTATAAATGCATTTCAAAA
CPj0245	CPj0245_F	AGGCCGAATTCCCGGGGATCATGAAACACTACCTATCATTT	CPj0245_B	CCGCTGCAGGTCGACGGATCTTACAGAAAGGCTTTTCTTTT
CPj0246	CPj0246_F	AGGCCGAATTCCCGGGGATCGTGGCAAAAAGTACAATACA	CPj0246_B	CCGCTGCAGGTCGACGGATCTTAACGCTTAGAGAATTGGA
CPj0247	CPj0247_F	AGGCCGAATTCCCGGGGATCATGGAAAAAAGAAAAGACACA	CPj0247_B	CCGCTGCAGGTCGACGGATCTTAAATATCTAATAAAATTGGCT
CPj0248	CPj0248_F	AGGCCGAATTCCCGGGGATCATGTCCTTACTTATAGAAGC	CPj0248_B	CCGCTGCAGGTCGACGGATCTTAAGAGTTATGAAAAAATAGC
CPj0249	CPj0249_F	AGGCCGAATTCCCGGGGATCATGAAGTTCGAATTTTCAGTA	CPj0249_B	CCGCTGCAGGTCGACGGATCCTAATCTGCTTTTAAAATTTCT
CPj0250	CPj0250_F	AGGCCGAATTCCCGGGGATCATGGCAAGCAAGAATCGGGA	CPj0250_B	CCGCTGCAGGTCGACGGATCTTACCTAGCTTCTTTGAAAAT
CPj0251	CPj0251_F	AGGCCGAATTCCCGGGGATCATGACAACAAAAAGTTTAGATT	CPj0251_B	CCGCTGCAGGTCGACGGATCCTAAGCTTTGCTAGTTTTTAG
CPj0253	CPj0253_F	AGGCCGAATTCCCGGGGATCATGTCGAGTTCGATACCCAC	CPj0253_B	CCGCTGCAGGTCGACGGATCTCACTGTACTTTGTGTTGAC
CPj0254	CPj0254_F	AGGCCGAATTCCCGGGGATCATGAAAACTCTGGGGGTCAA	CPj0254_B	CCGCTGCAGGTCGACGGATCTTAATCTACCTCCACAAAATT
CPj0255	CPj0255_F	AGGCCGAATTCCCGGGGATCATGAAAAACAATATTAATAATAAT	CPj0255_B	CCGCTGCAGGTCGACGGATCCTACCCTCTATCGTCCGGAT
CPj0256	CPj0256_F	AGGCCGAATTCCCGGGGATCATGTCAAATCCTACACCGAA	CPj0256_B	CCGCTGCAGGTCGACGGATCTTATTCAACGTAAGGCAAGG
CPj0257	CPj0257_F	AGGCCGAATTCCCGGGGATCATGAAAAGAAGAAACCTACAA	CPj0257_B	CCGCTGCAGGTCGACGGATCTTAATCTACCTCCGCAAAAT
CPj0259	CPj0259_F	AGGCCGAATTCCCGGGGATCATGACAACAACAAATAATCAAG	CPj0259_B	CCGCTGCAGGTCGACGGATCTTAGGATATAGGTTCCTGCA
CPj0260	CPj0260_F	AGGCCGAATTCCCGGGGATCGTGTCAAAAAAAATTAATAGAAA	CPj0260_B	CCGCTGCAGGTCGACGGATCTTAATCTTCCTCAACTGGAG
CPj0261	CPj0261_F	AGGCCGAATTCCCGGGGATCATGTCCACTTTACTTTTAAATC	CPj0261_B	CCGCTGCAGGTCGACGGATCTCAAATTTTTTGTGATTTGGAT
CPj0262	CPj0262_F	AGGCCGAATTCCCGGGGATCATGAATAAAAGATTAAAGATAATT	CPj0262_B	CCGCTGCAGGTCGACGGATCTTAGAAAATTTTAGTGGTCAG
CPj0263	CPj0263_F	AGGCCGAATTCCCGGGGATCATGTCTCACGGTCCACGTCC	CPj0263_B	CCGCTGCAGGTCGACGGATCTTAAGTTCGTCTACCATTGA
CPj0264	CPj0264_F	AGGCCGAATTCCCGGGGATCATGAAGCGTTATGTTGTGGG	CPj0264_B	CCGCTGCAGGTCGACGGATCTCACTCTGGATTCGACCATT
CPj0265	CPj0265_F	AGGCCGAATTCCCGGGGATCGTGAGATTAAATTATTTTTTAAAT	CPj0265_B	CCGCTGCAGGTCGACGGATCTCATCTACTCAAACTCCAAA
CPj0266	CPj0266_F	AGGCCGAATTCCCGGGGATCATGGCGTTAGATGAAATTAAT	CPj0266_B	CCGCTGCAGGTCGACGGATCTTATTTCTCTGGTGTTAGGC

CPj0267	CPj0267_F	AGGCCGAATTCCCGGGGATCGTGTCAATAATGTCATTGAAT	CPj0267_B	CCGCTGCAGGTCGACGGATCCTATTCCAACAGCGCCTTTT
CPj0268	CPj0268_F	AGGCCGAATTCCCGGGGATCATGTCTCAATGTCAGAGTAG	CPj0268_B	CCGCTGCAGGTCGACGGATCCTTATCCTATAAGATCCTCATT
CPj0269	CPj0269_F	AGGCCGAATTCCCGGGGATCATGACTATCGATATGCATTG	CPj0269_B	CCGCTGCAGGTCGACGGATCCTATAATTTCACGTCTGTTAT
CPj0270	CPj0270_F	AGGCCGAATTCCCGGGGATCGTGCCTGATAAAAAAGCACA	CPj0270_B	CCGCTGCAGGTCGACGGATCCTACTCAATATAATAAGGGG
CPj0271	CPj0271_F	AGGCCGAATTCCCGGGGATCATGACAGACTACTCTTTCTT	CPj0271_B	CCGCTGCAGGTCGACGGATCTCAGCCCCGGGCAGGATCT
CPj0272	CPj0272_F	AGGCCGAATTCCCGGGGATCATGCACCTAGAAGAAGAGAA	CPj0272_B	CCGCTGCAGGTCGACGGATCCTAATTGGATAGATCCTGCC
CPj0273	CPj0273_F	AGGCCGAATTCCCGGGGATCGTGTTTATCGTGATTGAGGG	CPj0273_B	CCGCTGCAGGTCGACGGATCCTAGGTGCATAACCCAAGTT
CPj0274	CPj0274_F	AGGCCGAATTCCCGGGGATCATGTTCAATAAAGATGAAATTAT	CPj0274_B	CCGCTGCAGGTCGACGGATCCTACCTTAGGCTTACTGTAT
CPj0275	CPj0275_F	AGGCCGAATTCCCGGGGATCATGGACCCAAAAGAAAAAAAT	CPj0275_B	CCGCTGCAGGTCGACGGATCCTAAATATCTAAATTATTTATCC
CPj0276	CPj0276_F	AGGCCGAATTCCCGGGGATCATGTTCTTAAAGCGAAAAAAAA	CPj0276_B	CCGCTGCAGGTCGACGGATCCTATCCTAACAAAAACTGTAT
CPj0277	CPj0277_F	AGGCCGAATTCCCGGGGATCATGATAATTAATGTTAGAGCC	CPj0277_B	CCGCTGCAGGTCGACGGATCCTAAACATATACAACGGTAG
CPj0278	CPj0278_F	AGGCCGAATTCCCGGGGATCATGAAAAAAAAATTATCATTACTT	CPj0278_B	CCGCTGCAGGTCGACGGATCCTAACCATTGTCTTGAGTCA
CPj0279	CPj0279_F	AGGCCGAATTCCCGGGGATCATGCAATCCGATCTTATTCA	CPj0279_B	CCGCTGCAGGTCGACGGATCTCATAGAATCCCTCTATACT
CPj0280	CPj0280_F	AGGCCGAATTCCCGGGGATCGTGTCAGAACAACATTCTCC	CPj0280_B	CCGCTGCAGGTCGACGGATCCTAATAAAATTCTTTAATAACGA
CPj0281	CPj0281_F	AGGCCGAATTCCCGGGGATCATGTTGAATATTCATGATATTCT	CPj0281_B	CCGCTGCAGGTCGACGGATCTTAAGCGATTGTAATATTAGG
CPj0282	CPj0282_F	AGGCCGAATTCCCGGGGATCATGCACTCCCACTCAAAACC	CPj0282_B	CCGCTGCAGGTCGACGGATCTTAGCTCTTTTTAGATAAGCG
CPj0283	CPj0283_F	AGGCCGAATTCCCGGGGATCGTGAAGCTTCTTATAAAATTTG	CPj0283_B	CCGCTGCAGGTCGACGGATCCTAATCTAAAAGCATTTTTGG
CPj0284	CPj0284_F	AGGCCGAATTCCCGGGGATCATGAACATACCCGCTCCCCA	CPj0284_B	CCGCTGCAGGTCGACGGATCTTATAAGATCTTGGAAGTATGA
CPj0285	CPj0285_F	AGGCCGAATTCCCGGGGATCTTGTTTAATTTATTTTTTTTCACT	CPj0285_B	CCGCTGCAGGTCGACGGATCCTAAAAATCAAATAAGTGTTGT
CPj0286	CPj0286_F	AGGCCGAATTCCCGGGGATCATGGATTCCAGGACGAGTCA	CPj0286_B	CCGCTGCAGGTCGACGGATCCTAATTAAAAAAGAGAAAGTTTA
CPj0287	CPj0287_F	AGGCCGAATTCCCGGGGATCATGATTAGATCACCATTACC	CPj0287_B	CCGCTGCAGGTCGACGGATCCTAGTTTCTCTTCATTTCGG
CPj0288	CPj0288_F	AGGCCGAATTCCCGGGGATCATGTCTTGTTTTAATCTTACAT	CPj0288_B	CCGCTGCAGGTCGACGGATCTTAAACAATAAAATTTTTAGCAC
CPj0289	CPj0289_F	AGGCCGAATTCCCGGGGATCATGAAAAAACAACGCTCTCA	CPj0289_B	CCGCTGCAGGTCGACGGATCTTAGTTTGCTAAACTGACTA
CPj0290	CPj0290_F	AGGCCGAATTCCCGGGGATCATGAATAAAAAACACGCCAG	CPj0290_B	CCGCTGCAGGTCGACGGATCTTATAGAATTTCGTGATTGTAA
CPj0291	CPj0291_F	AGGCCGAATTCCCGGGGATCATGTCAGCACCTATACCAAC	CPj0291_B	CCGCTGCAGGTCGACGGATCTTATCTTGTTGTACGGACAG
CPj0292	CPj0292_F	AGGCCGAATTCCCGGGGATCATGACCTCACCGATCCCCTT	CPj0292_B	CCGCTGCAGGTCGACGGATCTTAAGAAGCCGGTAGAGGCG
CPj0293	CPj0293_F	AGGCCGAATTCCCGGGGATCATGCAGAGAGTTTTGCGACT	CPj0293_B	CCGCTGCAGGTCGACGGATCTTAGATAGATAAGAAAGATATTA
CPj0294	CPj0294_F	AGGCCGAATTCCCGGGGATCATGAATTTGATCGATCGCGC	CPj0294_B	CCGCTGCAGGTCGACGGATCTTAAGGTTCTCTGAACTTGA
CPj0295	CPj0295_F	AGGCCGAATTCCCGGGGATCATGAGTTTAGAAGATGATGTA	CPj0295_B	CCGCTGCAGGTCGACGGATCTTATTGTTCAGCTTGACGTT
CPj0296	CPj0296_F	AGGCCGAATTCCCGGGGATCATGGATATAACATTAGTAGGC	CPj0296_B	CCGCTGCAGGTCGACGGATCTTAGTAAGTCAATCCCCCAT
CPj0297	CPj0297_F	AGGCCGAATTCCCGGGGATCATGAAAAAACGTTATGCTTTTT	CPj0297_B	CCGCTGCAGGTCGACGGATCTCATACCTCTGATAGGAATT
CPj0298	CPj0298_F	AGGCCGAATTCCCGGGGATCATGTGGTTCTCTGTGAATAA	CPj0298_B	CCGCTGCAGGTCGACGGATCTTAGACCTGCTTTAAAACTAC
CPj0299	CPj0299_F	AGGCCGAATTCCCGGGGATCATGACAAGATATCCAGATTAC	CPj0299_B	CCGCTGCAGGTCGACGGATCCTAATAGGAGTGTCGTCCAG
CPj0300	CPj0300_F	AGGCCGAATTCCCGGGGATCATGCTCATCATGCGAAATAAA	CPj0300_B	CCGCTGCAGGTCGACGGATCCTAGAACATGCCCCCTAAAG
CPj0301	CPj0301_F	AGGCCGAATTCCCGGGGATCATGAAAAAATTATTATTTTCTACA	CPj0301_B	CCGCTGCAGGTCGACGGATCCTAGTTTTGTTTTTTGAAAGAT
CPj0302	CPj0302_F	AGGCCGAATTCCCGGGGATCATGTCCGAAGCACCAGTCTA	CPj0302_B	CCGCTGCAGGTCGACGGATCTTAGATCTCTGAAGGAATCT
CPj0303	CPj0303_F	AGGCCGAATTCCCGGGGATCATGGACGTTTCTCGTAAAAT	CPj0303_B	CCGCTGCAGGTCGACGGATCTTAAATATATAAAGAACGTACTC
CPj0304	CPj0304_F	AGGCCGAATTCCCGGGGATCATGGATAGTTCAGCACCTTA	CPj0304_B	CCGCTGCAGGTCGACGGATCTTAGGCATAGACTCCTTCCT
CPj0305	CPj0305_F	AGGCCGAATTCCCGGGGATCATGCCTAAACATAAAACATTAG	CPj0305_B	CCGCTGCAGGTCGACGGATCTTACCTCATGACTTTTTCAAT
CPj0306	CPj0306_F	AGGCCGAATTCCCGGGGATCGTGATCTCCTTATTGAAAATG	CPj0306_B	CCGCTGCAGGTCGACGGATCCTAGTTTAATAGTAGGACAG
CPj0307	CPj0307_F	AGGCCGAATTCCCGGGGATCGTGGAAGATTTTTCGAGTTT	CPj0307_B	CCGCTGCAGGTCGACGGATCTTAATTTCCTTCTCCAGAGC
CPj0308	CPj0308_F	AGGCCGAATTCCCGGGGATCATGGCTACAGTAGCACAAAC	CPj0308_B	CCGCTGCAGGTCGACGGATCTTATTTAGAGGAGTACCGAT
CPj0309	CPj0309_F	AGGCCGAATTCCCGGGGATCATGCGAGCATGGGAAGAATT	CPj0309_B	CCGCTGCAGGTCGACGGATCCTAAATAATCATCTCTTCGC
CPj0310	CPj0310_F	AGGCCGAATTCCCGGGGATCATGAATAAACGCACTTTGCT	CPj0310_B	CCGCTGCAGGTCGACGGATCTTATCGATGTTTTTTATTATTTAA
CPj0311	CPj0311_F	AGGCCGAATTCCCGGGGATCATGCGAGCTGAGATGGCTGT	CPj0311_B	CCGCTGCAGGTCGACGGATCCTATATGTGTGAACGGTGCC
CPj0312	CPj0312_F	AGGCCGAATTCCCGGGGATCATGGCAAGAAACATCAAATAT	CPj0312_B	CCGCTGCAGGTCGACGGATCCTAATTTCCTTCAGGATTTTC
CPj0313	CPj0313_F	AGGCCGAATTCCCGGGGATCATGGAAATCATTCATATAGGA	CPj0313_B	CCGCTGCAGGTCGACGGATCTTAGGCTAATGCGATTGCAG
CPj0314	CPj0314_F	AGGCCGAATTCCCGGGGATCATGATTCATTCCCGGTTAAT	CPj0314_B	CCGCTGCAGGTCGACGGATCTTAGCCTAAGAATCTTTCAG
CPj0315	CPj0315_F	AGGCCGAATTCCCGGGGATCATGCCAAAACAAGCTGAATA	CPj0315_B	CCGCTGCAGGTCGACGGATCCTATTTTCCTTTTTTCTTTCTC
CPj0316	CPj0316_F	AGGCCGAATTCCCGGGGATCATGAATAAAAATCTTGTAGCTA	CPj0316_B	CCGCTGCAGGTCGACGGATCTTAATCTTCAATTTCAGGTTTT
CPj0317	CPj0317_F	AGGCCGAATTCCCGGGGATCATGGAGAAAGTAAAGTTGAC	CPj0317_B	CCGCTGCAGGTCGACGGATCTTATAGTTTTTGTGGATGATAG
CPj0318	CPj0318_F	AGGCCGAATTCCCGGGGATCATGACAGAAAATAGACGTATT	CPj0318_B	CCGCTGCAGGTCGACGGATCTTAACTCTTTTCTTTCTCTTG
CPj0319	CPj0319_F	AGGCCGAATTCCCGGGGATCATGGATCTTGCAGTAGAATT	CPj0319_B	CCGCTGCAGGTCGACGGATCCTATAGGCTATTTCCATGGG
CPj0320	CPj0320_F	AGGCCGAATTCCCGGGGATCATGGAAATAGCCTATAGTTTA	CPj0320_B	CCGCTGCAGGTCGACGGATCCTATGCTGTTCCTTCATAAT
CPj0321	CPj0321_F	AGGCCGAATTCCCGGGGATCATGAGTCATACTGAATGTGG	CPj0321_B	CCGCTGCAGGTCGACGGATCTTAATTATGAAGGAACAGCAT
CPj0322	CPj0322_F	AGGCCGAATTCCCGGGGATCATGGGTGAAAAAACAGAAAAG	CPj0322_B	CCGCTGCAGGTCGACGGATCTTATAAATGATCAGGTTGGTT
CPj0323	CPj0323_F	AGGCCGAATTCCCGGGGATCATGAATAAGCTACTCAATTTC	CPj0323_B	CCGCTGCAGGTCGACGGATCTTAGAAAATCTGAATTCTTCC
CPj0324	CPj0324_F	AGGCCGAATTCCCGGGGATCATGGCAGCATCAGGAGGCAC	CPj0324_B	CCGCTGCAGGTCGACGGATCTCATGACCAAGGATAGGGTT
CPj0325	CPj0325_F	AGGCCGAATTCCCGGGGATCATGCAAAACCAATACGAGCA	CPj0325_B	CCGCTGCAGGTCGACGGATCTCACGCGACGTAGTAGATTC
CPj0326	CPj0326_F	AGGCCGAATTCCCGGGGATCGTGAATGTTTTAAAATACACAA	CPj0326_B	CCGCTGCAGGTCGACGGATCTTACAGTCCTGTAAGGATCT
CPj0327	CPj0327_F	AGGCCGAATTCCCGGGGATCATGTCAAGAAAGTGCCCACT	CPj0327_B	CCGCTGCAGGTCGACGGATCTTAAAAATTTTTACTTTTAGCTC
CPj0328	CPj0328_F	AGGCCGAATTCCCGGGGATCATGTCTTTCTTAAGGCGTCA	CPj0328_B	CCGCTGCAGGTCGACGGATCTTAAATATAAAAAGTTTCTTTATT
CPj0329	CPj0329_F	AGGCCGAATTCCCGGGGATCATGAATAAAAGACAAAAAGATAA	CPj0329_B	CCGCTGCAGGTCGACGGATCTCACGCTGCTTCTTGCTCTT
CPj0330	CPj0330_F	AGGCCGAATTCCCGGGGATCATGCGTATAATTCGTTTTGAT	CPj0330_B	CCGCTGCAGGTCGACGGATCCTAGGCCTCTTCATCCTTTT
CPj0331	CPj0331_F	AGGCCGAATTCCCGGGGATCATGGCAGTTTCAGGTGGCGG	CPj0331_B	CCGCTGCAGGTCGACGGATCCTAAATATCCGTAGATAATTTT

CPj0332	CPj0332_F	AGGCCGAATTCCCGGGGATCGTGATCCCTCTAGCTCGACA	CPj0332_B	CCGCTGCAGGTCGACGGATCTTAAAAATCTAAAAAACAAAAAAA
CPj0333	CPj0333_F	AGGCCGAATTCCCGGGGATCATGGGGAAGCCTAAGAAGAG	CPj0333_B	CCGCTGCAGGTCGACGGATCCTAAAGACGGATAGAGTACT
CPj0334	CPj0334_F	AGGCCGAATTCCCGGGGATCATGTCTGTCCACATAACACC	CPj0334_B	CCGCTGCAGGTCGACGGATCTCAGTAACATACCAATCTCC
CPj0335	CPj0335_F	AGGCCGAATTCCCGGGGATCATGTTACTGAGAGGGATTCC	CPj0335_B	CCGCTGCAGGTCGACGGATCCTAAGAAAAATTTTGGTAACAT
CPj0336	CPj0336_F	AGGCCGAATTCCCGGGGATCATGGCGATGTTACCAAAATT	CPj0336_B	CCGCTGCAGGTCGACGGATCCTATGAAGAGGCGCCATCAT
CPj0337	CPj0337_F	AGGCCGAATTCCCGGGGATCATGGCACAAAAAGAAATTGTT	CPj0337_B	CCGCTGCAGGTCGACGGATCTCAATGATGGCGCCTCTTCA
CPj0338	CPj0338_F	AGGCCGAATTCCCGGGGATCATGAAATTCGTTGTATCCCG	CPj0338_B	CCGCTGCAGGTCGACGGATCTTAATCATCATGTAGCCTCA
CPj0342	CPj0342_F	AGGCCGAATTCCCGGGGATCATGAAGAAATTTTTATTAACTATA	CPj0342_B	CCGCTGCAGGTCGACGGATCTTATTTTTCTAACTTTTCAGGA
CPj0343	CPj0343_F	AGGCCGAATTCCCGGGGATCATGACAATAATCTATTTTATTCT	CPj0343_B	CCGCTGCAGGTCGACGGATCTTAACCAAAAAAACGAAATAAAT
CPj0344	CPj0344_F	AGGCCGAATTCCCGGGGATCTTGAAACATTTAGCCGTTCT	CPj0344_B	CCGCTGCAGGTCGACGGATCTTATATTTCTTGAGCAAGAGC
CPj0345	CPj0345_F	AGGCCGAATTCCCGGGGATCATGGCTTTGGGACCTTCTCC	CPj0345_B	CCGCTGCAGGTCGACGGATCCTAATATTGAGAACTTTTCTCA
CPj0346	CPj0346_F	AGGCCGAATTCCCGGGGATCATGCTCAGTTGTGTTTTTTC	CPj0346_B	CCGCTGCAGGTCGACGGATCTTAGACTTCCTTTTTTTTATTTG
CPj0347	CPj0347_F	AGGCCGAATTCCCGGGGATCTTGAATGTCAAAGATGAGAC	CPj0347_B	CCGCTGCAGGTCGACGGATCTCAGCACGATCCAAATTGTT
CPj0348	CPj0348_F	AGGCCGAATTCCCGGGGATCATGGATGCGAAAATGGGATA	CPj0348_B	CCGCTGCAGGTCGACGGATCTCATCTTTGACATTCAAGAG
CPj0350	CPj0350_F	AGGCCGAATTCCCGGGGATCATGGCCGTAGAACAATCACA	CPj0350_B	CCGCTGCAGGTCGACGGATCTTAAACGAAAGGAGAGGTAA
CPj0351	CPj0351_F	AGGCCGAATTCCCGGGGATCATGACAAAAACCGAAGAAAAA	CPj0351_B	CCGCTGCAGGTCGACGGATCCTATGAAGAAGCAGGAGCTG
CPj0352	CPj0352_F	AGGCCGAATTCCCGGGGATCATGAAGTGTAGTCCTTTAAC	CPj0352_B	CCGCTGCAGGTCGACGGATCTTATAGGGAAGATCGTATAG
CPj0353	CPj0353_F	AGGCCGAATTCCCGGGGATCTTGAGATTTAGAAATATAAAAAAA	CPj0353_B	CCGCTGCAGGTCGACGGATCTTATATCGTAAATTTAACAAAAAT
CPj0354	CPj0354_F	AGGCCGAATTCCCGGGGATCATGAGTAATATAACCTCGCC	CPj0354_B	CCGCTGCAGGTCGACGGATCCTAACCTATCAGCAGGGAGG
CPj0355	CPj0355_F	AGGCCGAATTCCCGGGGATCATGAGCATGACGATCGTTCC	CPj0355_B	CCGCTGCAGGTCGACGGATCTTAGTCTTTAAAGAAGATACTC
CPj0356	CPj0356_F	AGGCCGAATTCCCGGGGATCGTGCAATTATTTCAATATATGAA	CPj0356_B	CCGCTGCAGGTCGACGGATCTCACTCCCTATCTAAATGGT
CPj0357	CPj0357_F	AGGCCGAATTCCCGGGGATCATGGTTAATATACAGCCTGT	CPj0357_B	CCGCTGCAGGTCGACGGATCTCAAGAGAGCTTGTGAGAAA
CPj0358	CPj0358_F	AGGCCGAATTCCCGGGGATCGTGCTCTCCGTTAGTATGAA	CPj0358_B	CCGCTGCAGGTCGACGGATCTCAAACCCCAATGCTTTCAT
CPj0359	CPj0359_F	AGGCCGAATTCCCGGGGATCTTGAAAGAATATAAGATAGAGAA	CPj0359_B	CCGCTGCAGGTCGACGGATCTTAATCTAATTTTAGAACTTCAA
CPj0360	CPj0360_F	AGGCCGAATTCCCGGGGATCATGGGGAAAAATCTTGTCTT	CPj0360_B	CCGCTGCAGGTCGACGGATCTTACTTCACTCTTTCTGTAG
CPj0361	CPj0361_F	AGGCCGAATTCCCGGGGATCATGCAATCCTGGTTACAATC	CPj0361_B	CCGCTGCAGGTCGACGGATCCTAATTTAAATATAGAACAAGC
CPj0362	CPj0362_F	AGGCCGAATTCCCGGGGATCGTGAAAACACAGCAAACTCA	CPj0362_B	CCGCTGCAGGTCGACGGATCTTATCGAAATGCAGAGAGTG
CPj0363	CPj0363_F	AGGCCGAATTCCCGGGGATCGTGTCTGGGAAGAAAGATGG	CPj0363_B	CCGCTGCAGGTCGACGGATCTTAAGGAACTAAAACCTCATC
CPj0364	CPj0364_F	AGGCCGAATTCCCGGGGATCATGGCCAAGCTAGTCATTAC	CPj0364_B	CCGCTGCAGGTCGACGGATCTTAGAAAGTAACTTTGACACA
CPj0365	CPj0365_F	AGGCCGAATTCCCGGGGATCATGGCTACAATCTCACCCAT	CPj0365_B	CCGCTGCAGGTCGACGGATCCTAAGAGAGATCCTCAATAC
CPj0366	CPj0366_F	AGGCCGAATTCCCGGGGATCATGGGATATCTTCCAGTATC	CPj0366_B	CCGCTGCAGGTCGACGGATCCTATAATTGCGCCTGGGATT
CPj0367	CPj0367_F	AGGCCGAATTCCCGGGGATCATGACTAAAACCACTTCAATC	CPj0367_B	CCGCTGCAGGTCGACGGATCTCATTTATTCGTCCAGTCTC
CPj0368	CPj0368_F	AGGCCGAATTCCCGGGGATCGTGAATGCCGCTCAGCACC	CPj0368_B	CCGCTGCAGGTCGACGGATCCTACGTACGGATGTGGTAAA
CPj0369	CPj0369_F	AGGCCGAATTCCCGGGGATCATGACAGATTCTAATCCCCT	CPj0369_B	CCGCTGCAGGTCGACGGATCCTAGGGAGTCGTTAGATCGA
CPj0370	CPj0370_F	AGGCCGAATTCCCGGGGATCATGTCCACCACAGAACCCAA	CPj0370_B	CCGCTGCAGGTCGACGGATCTTAGGGTGTGATGAGGGGAT
CPj0371	CPj0371_F	AGGCCGAATTCCCGGGGATCATGCCCGTGTCCTCAGCCC	CPj0371_B	CCGCTGCAGGTCGACGGATCCTAAGAAATACTTTTAGAAGAG
CPj0372	CPj0372_F	AGGCCGAATTCCCGGGGATCATGTCTTCTCCAGTAGTCAC	CPj0372_B	CCGCTGCAGGTCGACGGATCCTAATTTGAAATCGGTGTATT
CPj0373	CPj0373_F	AGGCCGAATTCCCGGGGATCATGACACTCATTACCCCTGC	CPj0373_B	CCGCTGCAGGTCGACGGATCTCATACTGTCAACTTAGTTTC
CPj0374	CPj0374_F	AGGCCGAATTCCCGGGGATCATGACTCTATCCTTCCACAC	CPj0374_B	CCGCTGCAGGTCGACGGATCTTAATCTCTGGGTAGGAGAA
CPj0375	CPj0375_F	AGGCCGAATTCCCGGGGATCATGAAATTAGGCGCATCAAC	CPj0375_B	CCGCTGCAGGTCGACGGATCTTAGTGAGTTTTTCTTTGGG
CPj0376	CPj0376_F	AGGCCGAATTCCCGGGGATCATGAAAACTAAAATGAACTCTA	CPj0376_B	CCGCTGCAGGTCGACGGATCTTAACCTCTTTTCTTATCATG
CPj0377	CPj0377_F	AGGCCGAATTCCCGGGGATCATGACTACAGAAGTACGCAT	CPj0377_B	CCGCTGCAGGTCGACGGATCTTACAAGTCGAGTAATGAGG
CPj0378	CPj0378_F	AGGCCGAATTCCCGGGGATCATGGATTCCGAGTTTGTGGG	CPj0378_B	CCGCTGCAGGTCGACGGATCTTACCTTAAAGAAAAGAGGG
CPj0379	CPj0379_F	AGGCCGAATTCCCGGGGATCATGAAAAGCGAACGTCTTAA	CPj0379_B	CCGCTGCAGGTCGACGGATCTTACCATTCATTAGCATCGG
CPj0380	CPj0380_F	AGGCCGAATTCCCGGGGATCATGAATGGTAAGGCTCCCCT	CPj0380_B	CCGCTGCAGGTCGACGGATCTTAGAAGGAATATCCCATAAT
CPj0381	CPj0381_F	AGGCCGAATTCCCGGGGATCATGACAGCACCCACAGAATC	CPj0381_B	CCGCTGCAGGTCGACGGATCTTAGCGACGACGACGCCTAG
CPj0382	CPj0382_F	AGGCCGAATTCCCGGGGATCGTGACTTTATATCTTCTTCC	CPj0382_B	CCGCTGCAGGTCGACGGATCTTAATTCGGGATGTGGAAAA
CPj0383	CPj0383_F	AGGCCGAATTCCCGGGGATCATGCAAAAATCCTTAACGAG	CPj0383_B	CCGCTGCAGGTCGACGGATCTCACAGGTTAACCATTCTAA
CPj0384	CPj0384_F	AGGCCGAATTCCCGGGGATCATGATTGGAGCGCAAAAAAA	CPj0384_B	CCGCTGCAGGTCGACGGATCTTATCGAGACATCATTTTGAT
CPj0385	CPj0385_F	AGGCCGAATTCCCGGGGATCGTGGTTTTATTTCATGCTCA	CPj0385_B	CCGCTGCAGGTCGACGGATCCTACTTAGAAAGACTATTTTC
CPj0386	CPj0386_F	AGGCCGAATTCCCGGGGATCATGTTTGGGCATTTTGCTGG	CPj0386_B	CCGCTGCAGGTCGACGGATCTTAAAAAGGAACATCTTCACA
CPj0387	CPj0387_F	AGGCCGAATTCCCGGGGATCATGTCCAGGCAAAATGCTGA	CPj0387_B	CCGCTGCAGGTCGACGGATCTTAAGCACGAATACCTGTAG
CPj0388	CPj0388_F	AGGCCGAATTCCCGGGGATCATGGAAAAAGTTTCTTCTTATC	CPj0388_B	CCGCTGCAGGTCGACGGATCTCAGGTAACCTCTTTCGCAT
CPj0389	CPj0389_F	AGGCCGAATTCCCGGGGATCGTGAAACTATTGAAAAACGTA	CPj0389_B	CCGCTGCAGGTCGACGGATCTTACCTGATCTCTCCGTCCA
CPj0390	CPj0390_F	AGGCCGAATTCCCGGGGATCATGACGCATCAAGTAGCTGT	CPj0390_B	CCGCTGCAGGTCGACGGATCTCACTGTCCTTCTCCTAAAC
CPj0391	CPj0391_F	AGGCCGAATTCCCGGGGATCTTGTATAAACAAGAAAAGCCT	CPj0391_B	CCGCTGCAGGTCGACGGATCTCAAGGTCCTCGCATGAATG
CPj0392	CPj0392_F	AGGCCGAATTCCCGGGGATCATGAGCATAAAAGAAGATAAGT	CPj0392_B	CCGCTGCAGGTCGACGGATCTTAGACACAAGGTACGGTGA
CPj0393	CPj0393_F	AGGCCGAATTCCCGGGGATCATGATCAAATCCTGGTGGGT	CPj0393_B	CCGCTGCAGGTCGACGGATCTCAGTCCTTATTTTCTGATTG
CPj0394	CPj0394_F	AGGCCGAATTCCCGGGGATCATGATTCCTACCATGTTAATG	CPj0394_B	CCGCTGCAGGTCGACGGATCTTAGTCATACAATTTCCTTATA
CPj0395	CPj0395_F	AGGCCGAATTCCCGGGGATCATGACTAATTCTGCTCTCTT	CPj0395_B	CCGCTGCAGGTCGACGGATCCTATGAGAGTAAGTTTTTAATC
CPj0396	CPj0396_F	AGGCCGAATTCCCGGGGATCATGATCTATTTGGATAACAATG	CPj0396_B	CCGCTGCAGGTCGACGGATCTTAGGAATTTTTCAAACGTTC
CPj0397	CPj0397_F	AGGCCGAATTCCCGGGGATCGTGGATTTTGATTATTTTGGT	CPj0397_B	CCGCTGCAGGTCGACGGATCCTATTGTATTCGGACTAATAC
CPj0398	CPj0398_F	AGGCCGAATTCCCGGGGATCATGCAAATAGAAAATAGTAGTA	CPj0398_B	CCGCTGCAGGTCGACGGATCTCAAGGTTGAGAAAGGGATT
CPj0399	CPj0399_F	AGGCCGAATTCCCGGGGATCATGCGAAAAATGTTGGTATTA	CPj0399_B	CCGCTGCAGGTCGACGGATCCTACGAGTAGTTAGCACAAA
CPj0400	CPj0400_F	AGGCCGAATTCCCGGGGATCATGTCCAAGTTTATTCTTCTC	CPj0400_B	CCGCTGCAGGTCGACGGATCTTACTTTATTCCCAAAAATAGC

CPj0401	CPj0401_F	AGGCCGAATTCCCGGGGATCATGCGAGATCACGCTTTTTC	CPj0401_B	CCGCTGCAGGTCGACGGATCCTATGTAGATTCATTTTTCTC
CPj0402	CPj0402_F	AGGCCGAATTCCCGGGGATCATGACAAAGATAGCTTTTTCT	CPj0402_B	CCGCTGCAGGTCGACGGATCCTATACTCCTATTGATTCTC
CPj0403	CPj0403_F	AGGCCGAATTCCCGGGGATCATGCAATTATCAAATGATAAAAG	CPj0403_B	CCGCTGCAGGTCGACGGATCCTAGGGAGTGAGCATGGAGG
CPj0404	CPj0404_F	AGGCCGAATTCCCGGGGATCATGAGCTTATTATCAGGACA	CPj0404_B	CCGCTGCAGGTCGACGGATCTCAAAACATAACCTCCTCTT
CPj0405	CPj0405_F	AGGCCGAATTCCCGGGGATCTTGGGTTTCACTGATTACTT	CPj0405_B	CCGCTGCAGGTCGACGGATCTTATAAAGGGATTGCGGGTT
CPj0406	CPj0406_F	AGGCCGAATTCCCGGGGATCATGCTAAAGATTGATCTAACA	CPj0406_B	CCGCTGCAGGTCGACGGATCTTATGAGTCTTTAGGGAACA
CPj0407	CPj0407_F	AGGCCGAATTCCCGGGGATCATGGAAAAGTTACTAGTGAC	CPj0407_B	CCGCTGCAGGTCGACGGATCCTAAAGACTCATAAGGTCGT
CPj0408	CPj0408_F	AGGCCGAATTCCCGGGGATCATGTTTTTTAATCTTTTTTCTTTA	CPj0408_B	CCGCTGCAGGTCGACGGATCCTAATCTTGATTCGTCTGTT
CPj0409	CPj0409_F	AGGCCGAATTCCCGGGGATCATGACGACATGGACATTAAA	CPj0409_B	CCGCTGCAGGTCGACGGATCCTACTCATTACGTTTTTCTTG
CPj0410	CPj0410_F	AGGCCGAATTCCCGGGGATCATGGATGTTCTTATTTTCTATG	CPj0410_B	CCGCTGCAGGTCGACGGATCTCATGTCGGTTGATGTAATA
CPj0411	CPj0411_F	AGGCCGAATTCCCGGGGATCATGATACTGACTGCTGCCTT	CPj0411_B	CCGCTGCAGGTCGACGGATCTTAGGTGTATTGACAGCATT
CPj0412	CPj0412_F	AGGCCGAATTCCCGGGGATCATGAATGCTGTCAATACACC	CPj0412_B	CCGCTGCAGGTCGACGGATCCTACGGACATGGCAATAACA
CPj0413	CPj0413_F	AGGCCGAATTCCCGGGGATCATGAAACTACTTCTGAAAGC	CPj0413_B	CCGCTGCAGGTCGACGGATCCTAAGTTGTTATTGCCATGT
CPj0414	CPj0414_F	AGGCCGAATTCCCGGGGATCATGGAACTTCTTCCACACGA	CPj0414_B	CCGCTGCAGGTCGACGGATCTTATGCCTCAGGACCGCTTT
CPj0415	CPj0415_F	AGGCCGAATTCCCGGGGATCTTGACTCTAATTTTTGTTATTAT	CPj0415_B	CCGCTGCAGGTCGACGGATCTTAATTCATCTTCGTAAAGAAT
CPj0416	CPj0416_F	AGGCCGAATTCCCGGGGATCATGGCTACCATGACAAAGAA	CPj0416_B	CCGCTGCAGGTCGACGGATCTTAAGAATGCTTATTCGGAG
CPj0417	CPj0417_F	AGGCCGAATTCCCGGGGATCATGAAGCTTACCAAATATTTAA	CPj0417_B	CCGCTGCAGGTCGACGGATCCTAATTTGCTTGTATCTGTG
CPj0418	CPj0418_F	AGGCCGAATTCCCGGGGATCATGGATTTAAAAGAGTTACTC	CPj0418_B	CCGCTGCAGGTCGACGGATCTTAGACATAGGAAGCGAGTA
CPj0419	CPj0419_F	AGGCCGAATTCCCGGGGATCATGAGCTACCGTAAACGTTC	CPj0419_B	CCGCTGCAGGTCGACGGATCTCACCTCGTTCCCCCTTGTT
CPj0420	CPj0420_F	AGGCCGAATTCCCGGGGATCATGAACAAAAGTCGTTTTTTAC	CPj0420_B	CCGCTGCAGGTCGACGGATCTTACGGTAGCTCATAGGATA
CPj0421	CPj0421_F	AGGCCGAATTCCCGGGGATCATGTCCGAACGTGCGCATAT	CPj0421_B	CCGCTGCAGGTCGACGGATCTCATTGGGAAGCTTTTTCAA
CPj0422	CPj0422_F	AGGCCGAATTCCCGGGGATCATGGTAGAAATTTTTAATTATAG	CPj0422_B	CCGCTGCAGGTCGACGGATCTTATCCTTGAACAAATTGAAAG
CPj0423	CPj0423_F	AGGCCGAATTCCCGGGGATCATGTTGGATAATGAATGGAAA	CPj0423_B	CCGCTGCAGGTCGACGGATCTTAACGAACTAACGCAGCAT
CPj0424	CPj0424_F	AGGCCGAATTCCCGGGGATCATGTTAACCTGTAACGAGTG	CPj0424_B	CCGCTGCAGGTCGACGGATCTTAACCAACAATATGATTTTTAC
CPj0425	CPj0425_F	AGGCCGAATTCCCGGGGATCATGTTCCGTAGAACAGGAAA	CPj0425_B	CCGCTGCAGGTCGACGGATCCTATAAGTCTCTTTCTCTCT
CPj0426	CPj0426_F	AGGCCGAATTCCCGGGGATCATGGTACTTTTTTCGTTGCT	CPj0426_B	CCGCTGCAGGTCGACGGATCTTACTGATCATTCTGAGAGA
CPj0427	CPj0427_F	AGGCCGAATTCCCGGGGATCATGCTCAAAAAATTCATAAATTC	CPj0427_B	CCGCTGCAGGTCGACGGATCCTAGACTCCCCTTTTTCTAT
CPj0428	CPj0428_F	AGGCCGAATTCCCGGGGATCATGTCTAAAGGCTCTTCAAA	CPj0428_B	CCGCTGCAGGTCGACGGATCTCATTCGCCTGTTTTCTTTT
CPj0429	CPj0429_F	AGGCCGAATTCCCGGGGATCATGACAAGTAAAAAGTCCTAT	CPj0429_B	CCGCTGCAGGTCGACGGATCCTACCTTTTTCTCTTTTTAGA
CPj0430	CPj0430_F	AGGCCGAATTCCCGGGGATCATGTGGTTAGGTGCGTATAC	CPj0430_B	CCGCTGCAGGTCGACGGATCCTAGAGAGAGCGACGCTGC
CPj0431	CPj0431_F	AGGCCGAATTCCCGGGGATCATGACTACATTACCTAAGTAC	CPj0431_B	CCGCTGCAGGTCGACGGATCCTAAACAATTTCAATTCGAGA
CPj0432	CPj0432_F	AGGCCGAATTCCCGGGGATCATGGATCCAGCTAGTCCGGT	CPj0432_B	CCGCTGCAGGTCGACGGATCTCAGCTTTCATGCGCTACCT
CPj0433	CPj0433_F	AGGCCGAATTCCCGGGGATCATGTGGTATTCTGATTATCAT	CPj0433_B	CCGCTGCAGGTCGACGGATCTTACTCTTCATCCATCAAAG
CPj0434	CPj0434_F	AGGCCGAATTCCCGGGGATCTTGTTATCGTTCTTCTATAAG	CPj0434_B	CCGCTGCAGGTCGACGGATCTCACCTTACGACTCCCTGTT
CPj0435	CPj0435_F	AGGCCGAATTCCCGGGGATCATGATGAGTCGGTTGCGTTT	CPj0435_B	CCGCTGCAGGTCGACGGATCCTAGGCTGGCATATAGGTCA
CPj0436	CPj0436_F	AGGCCGAATTCCCGGGGATCATGAAAGTTCGTATCGTAGA	CPj0436_B	CCGCTGCAGGTCGACGGATCTCATAACCCCTCACCACAAA
CPj0437	CPj0437_F	AGGCCGAATTCCCGGGGATCATGTTTGAGACGTTCACTAA	CPj0437_B	CCGCTGCAGGTCGACGGATCCTATGATTCCAAGTGAGGGC
CPj0438	CPj0438_F	AGGCCGAATTCCCGGGGATCATGCAACAAACTGTAATTGTA	CPj0438_B	CCGCTGCAGGTCGACGGATCCTAGCCCTCACTTGGAATCA
CPj0439	CPj0439_F	AGGCCGAATTCCCGGGGATCGTGTCTAGTACTTTAAACGG	CPj0439_B	CCGCTGCAGGTCGACGGATCCTAGTTTTGATTTGTCTTTTC
CPj0440	CPj0440_F	AGGCCGAATTCCCGGGGATCATGGCAACTTCCGTAGCCCC	CPj0440_B	CCGCTGCAGGTCGACGGATCTCAGCAATCGAACAAAATTAC
CPj0441	CPj0441_F	AGGCCGAATTCCCGGGGATCATGTTCAAACTGCTCTTCCA	CPj0441_B	CCGCTGCAGGTCGACGGATCTTAGAAGTTCATTACAGCGG
CPj0442	CPj0442_F	AGGCCGAATTCCCGGGGATCATGGGATTCAAAAATATCTGC	CPj0442_B	CCGCTGCAGGTCGACGGATCTTAGTCGAAATAAGACTCGC
CPj0443	CPj0443_F	AGGCCGAATTCCCGGGGATCATGAGCCAACCCCCTATAAA	CPj0443_B	CCGCTGCAGGTCGACGGATCTTATTTGTTCTTTCTGTGTTTC
CPj0444	CPj0444_F	AGGCCGAATTCCCGGGGATCATGAAATATTCTTTACCTTGG	CPj0444_B	CCGCTGCAGGTCGACGGATCTTAGAAAGAATAACGAGTTCC
CPj0445	CPj0445_F	AGGCCGAATTCCCGGGGATCATGAAGTCCTCTGTCTCTTG	CPj0445_B	CCGCTGCAGGTCGACGGATCCTAGAAACAAAACTTAGAGC
CPj0446	CPj0446_F	AGGCCGAATTCCCGGGGATCATGAAAATACCCTTGCACAA	CPj0446_B	CCGCTGCAGGTCGACGGATCCTAGAATGAGTATCTTAGCC
CPj0447	CPj0447_F	AGGCCGAATTCCCGGGGATCATGAAATCCTCTCTTCATTG	CPj0447_B	CCGCTGCAGGTCGACGGATCTTAGAACTGGAACTTACCTC
CPj0448	CPj0448_F	AGGCCGAATTCCCGGGGATCATGGAAATGATGAGCCCATT	CPj0448_B	CCGCTGCAGGTCGACGGATCTTATCCCCAGATCTCTTTAG
CPj0449	CPj0449_F	AGGCCGAATTCCCGGGGATCATGAAATCGCAATTTTCCTG	CPj0449_B	CCGCTGCAGGTCGACGGATCCTAGAATTGGAACTTACCCC
CPj0450	CPj0450_F	AGGCCGAATTCCCGGGGATCATGAAGACTTCGATTCCTTG	CPj0450_B	CCGCTGCAGGTCGACGGATCCTAGAATCGGAGTTTGGTAC
CPj0451	CPj0451_F	AGGCCGAATTCCCGGGGATCATGACCATACTTCGAAATTTT	CPj0451_B	CCGCTGCAGGTCGACGGATCTTATGGCGTAGAAGTGATCT
CPj0452	CPj0452_F	AGGCCGAATTCCCGGGGATCATGAAAACGTCTATTCGTAAG	CPj0452_B	CCGCTGCAGGTCGACGGATCTTAAAATCGTAATTTGCTTCC
CPj0453	CPj0453_F	AGGCCGAATTCCCGGGGATCATGCCTCTTTCTTTCAAATC	CPj0453_B	CCGCTGCAGGTCGACGGATCTTAAAATGTGGATTTTAGTCC
CPj0456	CPj0456_F	AGGCCGAATTCCCGGGGATCATGACTCATTGCTTACATGG	CPj0456_B	CCGCTGCAGGTCGACGGATCCTAGGTTTTATCTTTAGAGTC
CPj0457	CPj0457_F	AGGCCGAATTCCCGGGGATCATGGCTTCTTGTTTATCTGC	CPj0457_B	CCGCTGCAGGTCGACGGATCCTAGATTCCCCTGAGGATCT
CPj0458	CPj0458_F	AGGCCGAATTCCCGGGGATCTTGTTTGTTTCTAATTTTATTTTT	CPj0458_B	CCGCTGCAGGTCGACGGATCCTAACTGCCTTCATTTTGCG
CPj0459	CPj0459_F	AGGCCGAATTCCCGGGGATCTTGAGAGAAGAAGGTAGTGT	CPj0459_B	CCGCTGCAGGTCGACGGATCTTACTCATCTTCGTGCATGT
CPj0460	CPj0460_F	AGGCCGAATTCCCGGGGATCGTGATACAACATCTTCTAAAC	CPj0460_B	CCGCTGCAGGTCGACGGATCCTACCTTCTTCTCTCAACTT
CPj0461	CPj0461_F	AGGCCGAATTCCCGGGGATCGTGGCTTGTCCAAGTATTTC	CPj0461_B	CCGCTGCAGGTCGACGGATCCTAGGGATCTTGGACTTCCT
CPj0462	CPj0462_F	AGGCCGAATTCCCGGGGATCATGGCATGCTATATTTCTATT	CPj0462_B	CCGCTGCAGGTCGACGGATCTTAGTCATCTGTATTGTTCTC
CPj0463	CPj0463_F	AGGCCGAATTCCCGGGGATCATGATGAAACAAGGAGTCGG	CPj0463_B	CCGCTGCAGGTCGACGGATCTTAAGAGTCTTCAAGATCCG
CPj0464	CPj0464_F	AGGCCGAATTCCCGGGGATCTTGTTCTCTGAGGGGACAGC	CPj0464_B	CCGCTGCAGGTCGACGGATCCTACGAAAGCATTCGAGGTC
CPj0465	CPj0465_F	AGGCCGAATTCCCGGGGATCATGAGTTATTACTTTTCTCTTT	CPj0465_B	CCGCTGCAGGTCGACGGATCTCAAAAAAAAGGAGCTGAAG
CPj0466	CPj0466_F	AGGCCGAATTCCCGGGGATCATGCGCTTTTTTTGCTTCGG	CPj0466_B	CCGCTGCAGGTCGACGGATCTTAAAATCTCATTCTACTCGC
CPj0467	CPj0467_F	AGGCCGAATTCCCGGGGATCATGTTCGGGATGACTCCTGC	CPj0467_B	CCGCTGCAGGTCGACGGATCTTAGAATTTTAAGGTACTTCC

CPj0468	CPj0468_F	AGGCCGAATTCCCGGGGATCATGATTTTTTATGACAAACTCTA	CPj0468_B	CCGCTGCAGGTCGACGGATCCTAGGGCAGAAAATATACCA
CPj0469	CPj0469_F	AGGCCGAATTCCCGGGGATCATGTGTACCTCCTTAGTCAT	CPj0469_B	CCGCTGCAGGTCGACGGATCTCATCTAAGTTCATGGCTTC
CPj0470	CPj0470_F	AGGCCGAATTCCCGGGGATCATCTCTCTGAACCTCGAAAG	CPj0470_B	CCGCTGCAGGTCGACGGATCTTAAAATGTGCAATGACTCTC
CPj0471	CPj0471_F	AGGCCGAATTCCCGGGGATCGTGCAAAATAACAGATCCCT	CPj0471_B	CCGCTGCAGGTCGACGGATCTTAAAACTTAAAGGTCGTTCC
CPj0472	CPj0472_F	AGGCCGAATTCCCGGGGATCATGGCATCAGGAATCGGAGG	CPj0472_B	CCGCTGCAGGTCGACGGATCCTAAGCATTCGACTCTCCAC
CPj0473	CPj0473_F	AGGCCGAATTCCCGGGGATCATGGCAGTTGGTGGCGTAGG	CPj0473_B	CCGCTGCAGGTCGACGGATCCTACTGTCCCTCTGGAGCAA
CPj0474	CPj0474_F	AGGCCGAATTCCCGGGGATCATGTCTACATCACCAATTAG	CPj0474_B	CCGCTGCAGGTCGACGGATCCTAAGCAGCTCCATCTATAT
CPj0475	CPj0475_F	AGGCCGAATTCCCGGGGATCATGGTTGATAAACTGATCCA	CPj0475_B	CCGCTGCAGGTCGACGGATCTTAGAAAAAAGTAACTAAATAGA
CPj0476	CPj0476_F	AGGCCGAATTCCCGGGGATCATGATAGATATAATGCAACATT	CPj0476_B	CCGCTGCAGGTCGACGGATCCTATTTATGAAAACAATCCCA
CPj0477	CPj0477_F	AGGCCGAATTCCCGGGGATCATGACGGTTGCGGAAGTCAA	CPj0477_B	CCGCTGCAGGTCGACGGATCTCATACAATCTCCCCAATCA
CPj0478	CPj0478_F	AGGCCGAATTCCCGGGGATCTTGGACACTATAGATACGCC	CPj0478_B	CCGCTGCAGGTCGACGGATCCTAATCCCCGAAAGAACTCT
CPj0479	CPj0479_F	AGGCCGAATTCCCGGGGATCATGGTAAGAGATATTCAGAG	CPj0479_B	CCGCTGCAGGTCGACGGATCCTATAGTGTCCAAAGGACCT
CPj0480	CPj0480_F	AGGCCGAATTCCCGGGGATCATGTTAGGTTCTTTGCCATG	CPj0480_B	CCGCTGCAGGTCGACGGATCTTAGTTATCTCTGCGTGATC
CPj0481	CPj0481_F	AGGCCGAATTCCCGGGGATCATGGCAACCTCTGTTCCTGT	CPj0481_B	CCGCTGCAGGTCGACGGATCCTAGTCTCCCAGAGATTCCC
CPj0482	CPj0482_F	AGGCCGAATTCCCGGGGATCATGATAAAACAAATAGGCCG	CPj0482_B	CCGCTGCAGGTCGACGGATCCTATTCGTAAGCAACTTCAG
CPj0483	CPj0483_F	AGGCCGAATTCCCGGGGATCTTGATTAAAAAACGAGCAATTT	CPj0483_B	CCGCTGCAGGTCGACGGATCCTAGGGATTTGAGCTGTCCG
CPj0484	CPj0484_F	AGGCCGAATTCCCGGGGATCTTGCATGAGGTACTTATTCT	CPj0484_B	CCGCTGCAGGTCGACGGATCTCAAGAAATCGCATGAGCCC
CPj0485	CPj0485_F	AGGCCGAATTCCCGGGGATCATGATAAAACAAGCGTGTAAA	CPj0485_B	CCGCTGCAGGTCGACGGATCTTATTCATTCGTAGGGGCGG
CPj0486	CPj0486_F	AGGCCGAATTCCCGGGGATCATGAATTTTTCATTATTTTTATTT	CPj0486_B	CCGCTGCAGGTCGACGGATCCTAAGTTTGCGTTTTGACTT
CPj0487	CPj0487_F	AGGCCGAATTCCCGGGGATCTTGTTCGGCTCGGAGTCCCT	CPj0487_B	CCGCTGCAGGTCGACGGATCTTATTTGAAAATAGAGAAAAGAG
CPj0488	CPj0488_F	AGGCCGAATTCCCGGGGATCATGACAGTATTCAAACAAATTA	CPj0488_B	CCGCTGCAGGTCGACGGATCTTAGGCTATAGCACCTAAAG
CPj0489	CPj0489_F	AGGCCGAATTCCCGGGGATCATGCAGATTCCAAGAAGCAT	CPj0489_B	CCGCTGCAGGTCGACGGATCTCATATGATCCCTCGATCTT
CPj0490	CPj0490_F	AGGCCGAATTCCCGGGGATCATGTATAACCTACTCCACGC	CPj0490_B	CCGCTGCAGGTCGACGGATCCTAAACGATAACAAAACCATC
CPj0491	CPj0491_F	AGGCCGAATTCCCGGGGATCATGAAGACAGCTTTTCACTC	CPj0491_B	CCGCTGCAGGTCGACGGATCTTAGAATCCATAGGTAAGAC
CPj0492	CPj0492_F	AGGCCGAATTCCCGGGGATCTTGATCTTTCCGATCTGTGA	CPj0492_B	CCGCTGCAGGTCGACGGATCTCAGAGTTTTAGGTCTCTGC
CPj0493	CPj0493_F	AGGCCGAATTCCCGGGGATCTTGCGAACTTACACACGCAG	CPj0493_B	CCGCTGCAGGTCGACGGATCTTAGCTGTCTTTCCAATGGA
CPj0494	CPj0494_F	AGGCCGAATTCCCGGGGATCATGATAAGGGTCAATCCTTA	CPj0494_B	CCGCTGCAGGTCGACGGATCTTATTTGAAATGGGCTTCTG
CPj0495	CPj0495_F	AGGCCGAATTCCCGGGGATCATGCGTAGAAATCCCCACTT	CPj0495_B	CCGCTGCAGGTCGACGGATCTCATGCAAGAACCATCGTTT
CPj0496	CPj0496_F	AGGCCGAATTCCCGGGGATCATGACAATTCTACGTAAACTC	CPj0496_B	CCGCTGCAGGTCGACGGATCCTAACTCACAGCTACGTTTT
CPj0497	CPj0497_F	AGGCCGAATTCCCGGGGATCTTGGATGATTCATGGATCTT	CPj0497_B	CCGCTGCAGGTCGACGGATCCTATACGTCTATATGCAAAG
CPj0498	CPj0498_F	AGGCCGAATTCCCGGGGATCATGAATAGAAGAAAAGCAAGA	CPj0498_B	CCGCTGCAGGTCGACGGATCTCATCCAAAACAACCCTCTG
CPj0499	CPj0499_F	AGGCCGAATTCCCGGGGATCATGTCGTCAGTAAATCAAAG	CPj0499_B	CCGCTGCAGGTCGACGGATCTTATAACTCCGTCTCTTCCT
CPj0500	CPj0500_F	AGGCCGAATTCCCGGGGATCATGAAAACGTCTCAACTCTT	CPj0500_B	CCGCTGCAGGTCGACGGATCCTAGGCTAAGTGATTCTGAC
CPj0501	CPj0501_F	AGGCCGAATTCCCGGGGATCATGGCTAGATCCAAAGTCTC	CPj0501_B	CCGCTGCAGGTCGACGGATCTCATAACGTCTCCTTAGAGG
CPj0502	CPj0502_F	AGGCCGAATTCCCGGGGATCATGACAGATACCCCACCTGA	CPj0502_B	CCGCTGCAGGTCGACGGATCCTATTCTTTATTTTCTTTGGGA
CPj0503	CPj0503_F	AGGCCGAATTCCCGGGGATCATGAGTGAACACAAAAAATCA	CPj0503_B	CCGCTGCAGGTCGACGGATCTTACTTATCGTCGTTATCAAT
CPj0504	CPj0504_F	AGGCCGAATTCCCGGGGATCTTGTTGAAAAAACCAAAAAGAA	CPj0504_B	CCGCTGCAGGTCGACGGATCTTACGAGGCTCTTTTTTTCG
CPj0505	CPj0505_F	AGGCCGAATTCCCGGGGATCGTGCTACAAGAACATTTTTTT	CPj0505_B	CCGCTGCAGGTCGACGGATCTTAAGATAAAACTTTTCCCGA
CPj0506	CPj0506_F	AGGCCGAATTCCCGGGGATCATGAAAAAATACTTTATTACAGG	CPj0506_B	CCGCTGCAGGTCGACGGATCTTAGCTGCCTTGATCTTGGT
CPj0507	CPj0507_F	AGGCCGAATTCCCGGGGATCATGACACGAATGAGTAAACA	CPj0507_B	CCGCTGCAGGTCGACGGATCTTAACCTATTTTCGGGATAAA
CPj0508	CPj0508_F	AGGCCGAATTCCCGGGGATCATGTCTCGACATCGTAGTTA	CPj0508_B	CCGCTGCAGGTCGACGGATCTTATTTTAAAATAGGGGTCTTA
CPj0509	CPj0509_F	AGGCCGAATTCCCGGGGATCGTGACGCAAGAAAAGATCAA	CPj0509_B	CCGCTGCAGGTCGACGGATCTTAAGCTGTTAGCAAAGCAT
CPj0510	CPj0510_F	AGGCCGAATTCCCGGGGATCATGCTCCATATTCTTTTAGC	CPj0510_B	CCGCTGCAGGTCGACGGATCTTAGGAGATATTGAATTTACG
CPj0511	CPj0511_F	AGGCCGAATTCCCGGGGATCATGAGTGATATCCAAAAAGAA	CPj0511_B	CCGCTGCAGGTCGACGGATCTCAATCCCCGTCTTTGTTTA
CPj0512	CPj0512_F	AGGCCGAATTCCCGGGGATCATGCGACGATCTGTTTGTTA	CPj0512_B	CCGCTGCAGGTCGACGGATCTTAATTTAAATCCACCCAGAT
CPj0513	CPj0513_F	AGGCCGAATTCCCGGGGATCATGACGACGTGCCTCCCACA	CPj0513_B	CCGCTGCAGGTCGACGGATCTTATACATGGCTGGAGTTGG
CPj0514	CPj0514_F	AGGCCGAATTCCCGGGGATCATGTCTAACCAACTCCAGCC	CPj0514_B	CCGCTGCAGGTCGACGGATCTTACAGTCGGGCTTGTTGGT
CPj0515	CPj0515_F	AGGCCGAATTCCCGGGGATCATGGAACCCTCTACCAACAA	CPj0515_B	CCGCTGCAGGTCGACGGATCTTATTGTTTCTCTAGTAGCC
CPj0516	CPj0516_F	AGGCCGAATTCCCGGGGATCATGGTGGCAAGGGGGCTCT	CPj0516_B	CCGCTGCAGGTCGACGGATCCTAAACTAAAATGGTAAACCT
CPj0517	CPj0517_F	AGGCCGAATTCCCGGGGATCATGTCATCACTACTGAGCTG	CPj0517_B	CCGCTGCAGGTCGACGGATCTCACAGAGCCCCCTTGCCA
CPj0518	CPj0518_F	AGGCCGAATTCCCGGGGATCATGATGACGTATCCTGTACC	CPj0518_B	CCGCTGCAGGTCGACGGATCTTAAGAAGATTTTTTGCGGC
CPj0519	CPj0519_F	AGGCCGAATTCCCGGGGATCATGGCATTTTATTCTCCTTC	CPj0519_B	CCGCTGCAGGTCGACGGATCTTATAAATCTCTAGTTACAGAG
CPj0520	CPj0520_F	AGGCCGAATTCCCGGGGATCATGGCAGACGGGGAAGTTCA	CPj0520_B	CCGCTGCAGGTCGACGGATCTTAGAGATCGTTGAAGGAGA
CPj0521	CPj0521_F	AGGCCGAATTCCCGGGGATCGTGGTTTCGTTGTTGCATAA	CPj0521_B	CCGCTGCAGGTCGACGGATCCTAAACTAAAGCTTCTAAATC
CPj0522	CPj0522_F	AGGCCGAATTCCCGGGGATCATGACCCTCTACTTAGGATT	CPj0522_B	CCGCTGCAGGTCGACGGATCTCACGGAGATGTCCTGGACT
CPj0523	CPj0523_F	AGGCCGAATTCCCGGGGATCATGGCTTCTTCAGCTACTCC	CPj0523_B	CCGCTGCAGGTCGACGGATCTTATCGATCCGAGAAAATTG
CPj0524	CPj0524_F	AGGCCGAATTCCCGGGGATCATGTCAGGACCCTCACGTAC	CPj0524_B	CCGCTGCAGGTCGACGGATCTTACTCCTCAGAACGACTTT
CPj0525	CPj0525_F	AGGCCGAATTCCCGGGGATCATGCATGACGCACTTCTAAG	CPj0525_B	CCGCTGCAGGTCGACGGATCTTATACAGCTGCGCGACGAC
CPj0526	CPj0526_F	AGGCCGAATTCCCGGGGATCATGCCTTCCCCGATGATTTC	CPj0526_B	CCGCTGCAGGTCGACGGATCTCAAAGTAGACCAGCTTTGG
CPj0527	CPj0527_F	AGGCCGAATTCCCGGGGATCATATTTGAGTTCCGATTCCC	CPj0527_B	CCGCTGCAGGTCGACGGATCTTAGCCCATCGTAACAGACT
CPj0528	CPj0528_F	AGGCCGAATTCCCGGGGATCATGAAATTATGGATGAAGATCT	CPj0528_B	CCGCTGCAGGTCGACGGATCCTATGTAGTTTCAACGCTTT
CPj0529	CPj0529_F	AGGCCGAATTCCCGGGGATCATGAAAAAACGGTTTCCTTC	CPj0529_B	CCGCTGCAGGTCGACGGATCTTAGTTACCCCTGTTTTTTATG
CPj0530	CPj0530_F	AGGCCGAATTCCCGGGGATCATGGATTGCATAGGGAAACA	CPj0530_B	CCGCTGCAGGTCGACGGATCCTAATTAACCCAACGTTGAC
CPj0531	CPj0531_F	AGGCCGAATTCCCGGGGATCATGGATTATAAATTGCTCGAT	CPj0531_B	CCGCTGCAGGTCGACGGATCCTATGCAATCCATTGAACAA
CPj0532	CPj0532_F	AGGCCGAATTCCCGGGGATCATGTTTTCAGGAATTATTCAAG	CPj0532_B	CCGCTGCAGGTCGACGGATCCTAATCTTTCCCTGATGAGG

CPj0533	CPj0533_F	AGGCCGAATTCCCGGGGATCATGCAGTGTCCTTTTTGCAA	CPj0533_B	CCGCTGCAGGTCGACGGATCCTATTTTTCCATATCTGGAG
CPj0534	CPj0534_F	AGGCCGAATTCCCGGGGATCGTGCCGTTATCAGATGACGA	CPj0534_B	CCGCTGCAGGTCGACGGATCTTAATTTCCAGATAGGAGTC
CPj0535	CPj0535_F	AGGCCGAATTCCCGGGGATCATGGCAACTCGTTTTCGTAG	CPj0535_B	CCGCTGCAGGTCGACGGATCTTATCTCTTTTTTTCAGTTTGT
CPj0536	CPj0536_F	AGGCCGAATTCCCGGGGATCATGAACCGTCTTCTATCGCT	CPj0536_B	CCGCTGCAGGTCGACGGATCTTATTCTGTAGAAAGAGAAGT
CPj0537	CPj0537_F	AGGCCGAATTCCCGGGGATCATGGATAACTATCTCCTCGG	CPj0537_B	CCGCTGCAGGTCGACGGATCTTAATCTTTATTACGAAACACT
CPj0538	CPj0538_F	AGGCCGAATTCCCGGGGATCATGTTCAGGAACAACCACAA	CPj0538_B	CCGCTGCAGGTCGACGGATCCTAATCTTTGTCGTCGAGGA
CPj0539	CPj0539_F	AGGCCGAATTCCCGGGGATCATGAAGCAGATGCGTCTTTG	CPj0539_B	CCGCTGCAGGTCGACGGATCCTAGAAACTAAGGGAGAGGC
CPj0540	CPj0540_F	AGGCCGAATTCCCGGGGATCATGAAGTGGCTACCAGCTAC	CPj0540_B	CCGCTGCAGGTCGACGGATCCTAGAATACAAACCGGATCC
CPj0541	CPj0541_F	AGGCCGAATTCCCGGGGATCATGCATAAAGTAATAGTTTTCAT	CPj0541_B	CCGCTGCAGGTCGACGGATCTCATAAACTAGAAAAAGTCGT
CPj0542	CPj0542_F	AGGCCGAATTCCCGGGGATCATGACAATACGAATTCTTGC	CPj0542_B	CCGCTGCAGGTCGACGGATCTTAGTGAGGAGAGCATGAAA
CPj0543	CPj0543_F	AGGCCGAATTCCCGGGGATCATGCTCTCCTCACTAATCCG	CPj0543_B	CCGCTGCAGGTCGACGGATCCTATACATTTGTATTGATTTCA
CPj0544	CPj0544_F	AGGCCGAATTCCCGGGGATCATGTTTGTAGATCAAATTACCT	CPj0544_B	CCGCTGCAGGTCGACGGATCTTATACAGCGAGTCTTTGTG
CPj0545	CPj0545_F	AGGCCGAATTCCCGGGGATCATGGCACATAAGAAAGGACA	CPj0545_B	CCGCTGCAGGTCGACGGATCCTAAAGTTGCTCAGGAACAA
CPj0546	CPj0546_F	AGGCCGAATTCCCGGGGATCATGGAGCCCTACGCAGTAAT	CPj0546_B	CCGCTGCAGGTCGACGGATCTTATATCAATATCTCACGGAT
CPj0547	CPj0547_F	AGGCCGAATTCCCGGGGATCATGGATAGAGACAATGAGGT	CPj0547_B	CCGCTGCAGGTCGACGGATCTTAGTCACAGTATTCCATCA
CPj0548	CPj0548_F	AGGCCGAATTCCCGGGGATCATGTACCTACAAGAAAAGTTT	CPj0548_B	CCGCTGCAGGTCGACGGATCCTAATAGACGTCAACAACGT
CPj0549	CPj0549_F	AGGCCGAATTCCCGGGGATCATGAAGCAGCAAAAGCAAAA	CPj0549_B	CCGCTGCAGGTCGACGGATCTTAAGCCGCTTTGATTTTAAT
CPj0550	CPj0550_F	AGGCCGAATTCCCGGGGATCATGAGCAATCAAGAATTCGA	CPj0550_B	CCGCTGCAGGTCGACGGATCTTACTTCTTAACAATCTCTTC
CPj0551	CPj0551_F	AGGCCGAATTCCCGGGGATCATGTCAAGGCGGCACTCCG	CPj0551_B	CCGCTGCAGGTCGACGGATCTTATTTTCTCCGTAATTTAACT
CPj0552	CPj0552_F	AGGCCGAATTCCCGGGGATCATGCCCACCATTAATCAATT	CPj0552_B	CCGCTGCAGGTCGACGGATCTTACTTAGGCCGCTTTGCGC
CPj0553	CPj0553_F	AGGCCGAATTCCCGGGGATCATGTGGCGCGTTGTCCTCAG	CPj0553_B	CCGCTGCAGGTCGACGGATCTTAGGTTTCTCCTAATGAAG
CPj0554	CPj0554_F	AGGCCGAATTCCCGGGGATCATGTACGAAGGAAAATCACG	CPj0554_B	CCGCTGCAGGTCGACGGATCCTAAGACGAGGTAAGGTACT
CPj0555	CPj0555_F	AGGCCGAATTCCCGGGGATCATGAAAAAACTTGTCCGTCT	CPj0555_B	CCGCTGCAGGTCGACGGATCTTATTTTCTACACTGTTGTAAT
CPj0556	CPj0556_F	AGGCCGAATTCCCGGGGATCATGTCATCAAATCTACATCC	CPj0556_B	CCGCTGCAGGTCGACGGATCCTAAACGCGAGCTATTTTAC
CPj0557	CPj0557_F	AGGCCGAATTCCCGGGGATCATGTCCAAACTCATCAGACG	CPj0557_B	CCGCTGCAGGTCGACGGATCTTAATACACGTGGGTATTTTC
CPj0558	CPj0558_F	AGGCCGAATTCCCGGGGATCATGAAGAAAGCTGTTTTAATTG	CPj0558_B	CCGCTGCAGGTCGACGGATCTTACTGTTTGCATCTGCCAT
CPj0559	CPj0559_F	AGGCCGAATTCCCGGGGATCATGAAATTATTTTACTTTTGTAAC	CPj0559_B	CCGCTGCAGGTCGACGGATCCTATAAGTTCGTATTATAACAC
CPj0560	CPj0560_F	AGGCCGAATTCCCGGGGATCATGAATTGGGAAAATGTCCG	CPj0560_B	CCGCTGCAGGTCGACGGATCTTAGAGATCGAAAGTAGCCT
CPj0561	CPj0561_F	AGGCCGAATTCCCGGGGATCATGGCGTGCGAACAACATGA	CPj0561_B	CCGCTGCAGGTCGACGGATCTTAGTTAGATTCAGGAAAAATT
CPj0562	CPj0562_F	AGGCCGAATTCCCGGGGATCATGTCAATAGCTATTGCAAG	CPj0562_B	CCGCTGCAGGTCGACGGATCCTAATTATCGAAATGTCTTCG
CPj0563	CPj0563_F	AGGCCGAATTCCCGGGGATCATGACAAATTCAGATAATGCT	CPj0563_B	CCGCTGCAGGTCGACGGATCTTAGTCTGAAAATCTAGGTTC
CPj0564	CPj0564_F	AGGCCGAATTCCCGGGGATCATGAAACAGAAGGTTAAGCG	CPj0564_B	CCGCTGCAGGTCGACGGATCTTATTTTGAGCGATTTTCTTTA
CPj0565	CPj0565_F	AGGCCGAATTCCCGGGGATCATGAAATTTCCTCGCATATC	CPj0565_B	CCGCTGCAGGTCGACGGATCCTAGGCAAAAGTATAGCTCT
CPj0566	CPj0566_F	AGGCCGAATTCCCGGGGATCTTGTCTTTAGCTACCAACAA	CPj0566_B	CCGCTGCAGGTCGACGGATCCTATTTCCCCCCTCGTCTTG
CPj0567	CPj0567_F	AGGCCGAATTCCCGGGGATCGTGCTTAATTCAAATAAGTTTA	CPj0567_B	CCGCTGCAGGTCGACGGATCTCATCCAATAAACTCTTTAGA
CPj0568	CPj0568_F	AGGCCGAATTCCCGGGGATCATGATTATCACTATTGATGGG	CPj0568_B	CCGCTGCAGGTCGACGGATCTCATAGCTCGTTTCGAAATA
CPj0569	CPj0569_F	AGGCCGAATTCCCGGGGATCATGATTTTCCGCATTTGTAAA	CPj0569_B	CCGCTGCAGGTCGACGGATCTTAGGGGACGTCTCCTTTGC
CPj0570	CPj0570_F	AGGCCGAATTCCCGGGGATCATGTCGACATTACTTTCTATC	CPj0570_B	CCGCTGCAGGTCGACGGATCTTACAACCTCTCCAAAGTCT
CPj0571	CPj0571_F	AGGCCGAATTCCCGGGGATCATGCAGATTGCTCAAGTATT	CPj0571_B	CCGCTGCAGGTCGACGGATCCTACAGGGATGCATCTCTTA
CPj0572	CPj0572_F	AGGCCGAATTCCCGGGGATCATGGCAGCTCCTATCAACCA	CPj0572_B	CCGCTGCAGGTCGACGGATCCTATTTTCTTCGTGGACTTG
CPj0573	CPj0573_F	AGGCCGAATTCCCGGGGATCATGGCAGGGCATAGTAAGTG	CPj0573_B	CCGCTGCAGGTCGACGGATCTTAGGACATGTTGTGGTAGA
CPj0574	CPj0574_F	AGGCCGAATTCCCGGGGATCATGGTTGAAACAGTACTTCA	CPj0574_B	CCGCTGCAGGTCGACGGATCCTATGCCCTGCCATATCCTC
CPj0575	CPj0575_F	AGGCCGAATTCCCGGGGATCATGACAGCAGAAAAGCAAAA	CPj0575_B	CCGCTGCAGGTCGACGGATCCTATAGATCCTTTTCCATAG
CPj0576	CPj0576_F	AGGCCGAATTCCCGGGGATCATTTCTGAACAGATTGTAAGT	CPj0576_B	CCGCTGCAGGTCGACGGATCTCATGAAACTTCTCCAAACT
CPj0577	CPj0577_F	AGGCCGAATTCCCGGGGATCATGAGTCAAAAAAATAAAAACTC	CPj0577_B	CCGCTGCAGGTCGACGGATCTTATTTTACAATATGTTTGGAAA
CPj0578	CPj0578_F	AGGCCGAATTCCCGGGGATCATAGTGCTTATCTCTATTTCT	CPj0578_B	CCGCTGCAGGTCGACGGATCTTAATCATAGGAACATGTGAT
CPj0579	CPj0579_F	AGGCCGAATTCCCGGGGATCATGATTAAGTCTTCTCTAATAC	CPj0579_B	CCGCTGCAGGTCGACGGATCTCATAGGAGGGCTTGGGCAA
CPj0580	CPj0580_F	AGGCCGAATTCCCGGGGATCATGACTAAAGTAGCTCTTCT	CPj0580_B	CCGCTGCAGGTCGACGGATCTTATCCTTCGTTTGACGTGC
CPj0581	CPj0581_F	AGGCCGAATTCCCGGGGATCATGTATTTAGAGGATTATGAC	CPj0581_B	CCGCTGCAGGTCGACGGATCCTACAATAACTTCTGTTGTG
CPj0582	CPj0582_F	AGGCCGAATTCCCGGGGATCATGATTTTACGGATCTCCAC	CPj0582_B	CCGCTGCAGGTCGACGGATCTTATGCGGAGGAAAGAGCCT
CPj0583	CPj0583_F	AGGCCGAATTCCCGGGGATCATGAATGAAAGAACCCTCTT	CPj0583_B	CCGCTGCAGGTCGACGGATCTCAGGGACGTTCATAAATAC
CPj0584	CPj0584_F	AGGCCGAATTCCCGGGGATCATGAACGTCCCTGATTCCAA	CPj0584_B	CCGCTGCAGGTCGACGGATCCTAGCTAGCGGCTCTTTCTT
CPj0585	CPj0585_F	AGGCCGAATTCCCGGGGATCATGGCAACACCCGCTCAAAA	CPj0585_B	CCGCTGCAGGTCGACGGATCTTATCCTTGAAATTGCTCTTG
CPj0586	CPj0586_F	AGGCCGAATTCCCGGGGATCATGGCGATTAAAAATATACTTG	CPj0586_B	CCGCTGCAGGTCGACGGATCTCAAGCTAAAGCGAGCATGT
CPj0587	CPj0587_F	AGGCCGAATTCCCGGGGATCATGAGACCTCATCGTAAACA	CPj0587_B	CCGCTGCAGGTCGACGGATCTCAGATGCAGAATCCTGGCT
CPj0588	CPj0588_F	AGGCCGAATTCCCGGGGATCATGTCCTTATTGAACCTTCC	CPj0588_B	CCGCTGCAGGTCGACGGATCCTATAAGTTTAAAGAAATAAAGT
CPj0589	CPj0589_F	AGGCCGAATTCCCGGGGATCATGCAGATCTGTGTTACCGG	CPj0589_B	CCGCTGCAGGTCGACGGATCTCAGTAGGGATGGACTACTT
CPj0590	CPj0590_F	AGGCCGAATTCCCGGGGATCTTGGGATTCGCTTGTCGATA	CPj0590_B	CCGCTGCAGGTCGACGGATCCTAAGAGAAGGTAATTGTAC
CPj0591	CPj0591_F	AGGCCGAATTCCCGGGGATCATGCGTTGCACTGCCTACTG	CPj0591_B	CCGCTGCAGGTCGACGGATCTTAAATGACATTGAAAACATCT
CPj0592	CPj0592_F	AGGCCGAATTCCCGGGGATCATGTCATTTAAACGTTTCTTG	CPj0592_B	CCGCTGCAGGTCGACGGATCTCATTCAGAAAAATGGCTTG
CPj0593	CPj0593_F	AGGCCGAATTCCCGGGGATCATGGCTTTCAAAAGAAAAACT	CPj0593_B	CCGCTGCAGGTCGACGGATCCTAAGACTGCTTTGCAGGAA
CPj0594	CPj0594_F	AGGCCGAATTCCCGGGGATCATGCGGATTCCAATAACTCT	CPj0594_B	CCGCTGCAGGTCGACGGATCTCATGAATTGATAGTCCCTT
CPj0595	CPj0595_F	AGGCCGAATTCCCGGGGATCATGAAACAATTACTTTTCTGTG	CPj0595_B	CCGCTGCAGGTCGACGGATCCTATCCTGCAGCATTTAGCC
CPj0596	CPj0596_F	AGGCCGAATTCCCGGGGATCATGGCTGATGACACCCTCAT	CPj0596_B	CCGCTGCAGGTCGACGGATCTTAGTAGCTATTCTCAAATTTC
CPj0597	CPj0597_F	AGGCCGAATTCCCGGGGATCATGCAGAAGCATCCTTCCTT	CPj0597_B	CCGCTGCAGGTCGACGGATCTTAAGAGTCTTGCAGACGGG

CPj0598	CPj0598_F	AGGCCGAATTCCCGGGGATCGTGCTTAAGTACATCCTAAA	CPj0598_B	CCGCTGCAGGTCGACGGATCTTATATCCTCCTTCCCTCTA
CPj0599	CPj0599_F	AGGCCGAATTCCCGGGGATCATGTATAAAAGATGTGTGCTA	CPj0599_B	CCGCTGCAGGTCGACGGATCTTAGGATGTACTTAAGCACG
CPj0600	CPj0600_F	AGGCCGAATTCCCGGGGATCATGAAGATTAAAAAATCTTTTCA	CPj0600_B	CCGCTGCAGGTCGACGGATCTTAGAGGCAAGGACTCATAG
CPj0601	CPj0601_F	AGGCCGAATTCCCGGGGATCATGGACGAAATAACACCTAA	CPj0601_B	CCGCTGCAGGTCGACGGATCTTACTCGCGTTGTTGAGGAA
CPj0602	CPj0602_F	AGGCCGAATTCCCGGGGATCATGAAACCTTTAGGTTTTCAG	CPj0602_B	CCGCTGCAGGTCGACGGATCTTAGTATTTATATTCAACACCA
CPj0603	CPj0603_F	AGGCCGAATTCCCGGGGATCATGCAATGTTTGGTCTCCCT	CPj0603_B	CCGCTGCAGGTCGACGGATCTTATCGAATCCCTGTGTGTT
CPj0604	CPj0604_F	AGGCCGAATTCCCGGGGATCGTGAAGATAAAATTTTCTTGGA	CPj0604_B	CCGCTGCAGGTCGACGGATCTTAGGGAAGACGATACCGCT
CPj0605	CPj0605_F	AGGCCGAATTCCCGGGGATCGTGAGAATTTTAGCAGGTAA	CPj0605_B	CCGCTGCAGGTCGACGGATCTTAAGGGTCCTTTTCCACAA
CPj0606	CPj0606_F	AGGCCGAATTCCCGGGGATCATGCATATTTATGGTTTGGC	CPj0606_B	CCGCTGCAGGTCGACGGATCTCACATCACCTCTTGAGGAA
CPj0607	CPj0607_F	AGGCCGAATTCCCGGGGATCATGATAGAAAACGATTTTCCG	CPj0607_B	CCGCTGCAGGTCGACGGATCCTAGAAGATATAGTTGTCAG
CPj0608	CPj0608_F	AGGCCGAATTCCCGGGGATCATGATGAACTACGAAGATGC	CPj0608_B	CCGCTGCAGGTCGACGGATCTTAAGATTCAATTTCTAGAATTT
CPj0609	CPj0609_F	AGGCCGAATTCCCGGGGATCATGCTAATACGCCTGTTTCT	CPj0609_B	CCGCTGCAGGTCGACGGATCTCACTCAGTAGATTGTGTTG
CPj0610	CPj0610_F	AGGCCGAATTCCCGGGGATCATGAAAGAAGAGCGTTCTTC	CPj0610_B	CCGCTGCAGGTCGACGGATCCTATTCTTTGAGTGACAACA
CPj0611	CPj0611_F	AGGCCGAATTCCCGGGGATCATGTTAAAATTATTAAAAGTTTCC	CPj0611_B	CCGCTGCAGGTCGACGGATCTCATAATGCTCCCTTTAAAG
CPj0612	CPj0612_F	AGGCCGAATTCCCGGGGATCATGAAGAAACTGTTTGTATTAG	CPj0612_B	CCGCTGCAGGTCGACGGATCTTAACATTCTGCCCAATTTTT
CPj0613	CPj0613_F	AGGCCGAATTCCCGGGGATCATGAAAACGTTGTGGCACTT	CPj0613_B	CCGCTGCAGGTCGACGGATCCTACAGTGCCAAGTAGGGAG
CPj0614	CPj0614_F	AGGCCGAATTCCCGGGGATCATGCAGTCATCAGAAGTGAA	CPj0614_B	CCGCTGCAGGTCGACGGATCCTACAGAACAGCCATTTCTT
CPj0615	CPj0615_F	AGGCCGAATTCCCGGGGATCATGAGACAATTTTGCAACCT	CPj0615_B	CCGCTGCAGGTCGACGGATCTTAGCGGAGAAACTGTTTTT
CPj0616	CPj0616_F	AGGCCGAATTCCCGGGGATCATGGACAAATCTACTGGTGT	CPj0616_B	CCGCTGCAGGTCGACGGATCCTAGCTGATACATTCAAAAG
CPj0617	CPj0617_F	AGGCCGAATTCCCGGGGATCATGTGGACTCACCCAATTGC	CPj0617_B	CCGCTGCAGGTCGACGGATCTTAGTGGTGGGCATGTTTTT
CPj0618	CPj0618_F	AGGCCGAATTCCCGGGGATCATGCCCACCACTAACTGTAT	CPj0618_B	CCGCTGCAGGTCGACGGATCTTAGTTTAGTACTGTAGTTGC
CPj0619	CPj0619_F	AGGCCGAATTCCCGGGGATCATGGAACAAACGCTATCCAT	CPj0619_B	CCGCTGCAGGTCGACGGATCCTAAACGAGAGGTTTCGAAG
CPj0620	CPj0620_F	AGGCCGAATTCCCGGGGATCATGTACGACTATATTCGTGG	CPj0620_B	CCGCTGCAGGTCGACGGATCCTAGTCCTTGTTCACTCCTG
CPj0621	CPj0621_F	AGGCCGAATTCCCGGGGATCGTGTCAGAACTGATTATAGG	CPj0621_B	CCGCTGCAGGTCGACGGATCTTATCTCACTCCACAAAGAG
CPj0622	CPj0622_F	AGGCCGAATTCCCGGGGATCGTGCGGCTCTTATCTATACT	CPj0622_B	CCGCTGCAGGTCGACGGATCTTAACTCCCTAAAGATTTAGA
CPj0623	CPj0623_F	AGGCCGAATTCCCGGGGATCGTGTATTTTACAAGAGACCC	CPj0623_B	CCGCTGCAGGTCGACGGATCCTATTCTTCTTCTGTAGCAG
CPj0624	CPj0624_F	AGGCCGAATTCCCGGGGATCATGAAAGTTGTAATTAATGGTT	CPj0624_B	CCGCTGCAGGTCGACGGATCTTATTTAGAGTTTTTTTCTACATA
CPj0625	CPj0625_F	AGGCCGAATTCCCGGGGATCATGCAACACGCTAGAAAAAA	CPj0625_B	CCGCTGCAGGTCGACGGATCTTAGCTAGCTAAAAACTCTAT
CPj0626	CPj0626_F	AGGCCGAATTCCCGGGGATCATGTCAGATAACGCACACAA	CPj0626_B	CCGCTGCAGGTCGACGGATCCTATCCCTTTATATTTTTAGC
CPj0627	CPj0627_F	AGGCCGAATTCCCGGGGATCTTGGTTAAAAATCAAGCGCA	CPj0627_B	CCGCTGCAGGTCGACGGATCCTACACTCTGCGCCTTTTTC
CPj0628	CPj0628_F	AGGCCGAATTCCCGGGGATCATGCCACGCATCATTGGAAT	CPj0628_B	CCGCTGCAGGTCGACGGATCTTATTTCTTCTTACCTGCGA
CPj0629	CPj0629_F	AGGCCGAATTCCCGGGGATCATGACCACATTGAGACAATT	CPj0629_B	CCGCTGCAGGTCGACGGATCTCAATGTCTTCCTTTCGTCC
CPj0630	CPj0630_F	AGGCCGAATTCCCGGGGATCATGATTAAGTTAGAATCATTATT	CPj0630_B	CCGCTGCAGGTCGACGGATCTTAAGTAATGCCTAGCAAATT
CPj0631	CPj0631_F	AGGCCGAATTCCCGGGGATCATGTCGCTATCAAAGAATTC	CPj0631_B	CCGCTGCAGGTCGACGGATCTTAATCATTTATAGCCGCTC
CPj0632	CPj0632_F	AGGCCGAATTCCCGGGGATCATGGAAAGTTCGTTATGTAAA	CPj0632_B	CCGCTGCAGGTCGACGGATCTTAAAACTGTAAACCACCCT
CPj0633	CPj0633_F	AGGCCGAATTCCCGGGGATCATGTCTCGTAAGGCTCGAGA	CPj0633_B	CCGCTGCAGGTCGACGGATCCTATTTTTTGCCTGTTTTCG
CPj0634	CPj0634_F	AGGCCGAATTCCCGGGGATCATGGGCATGACAAGTGATTC	CPj0634_B	CCGCTGCAGGTCGACGGATCTTACCACACCAAACAGAGCA
CPj0635	CPj0635_F	AGGCCGAATTCCCGGGGATCATGAGTAGATTAAAAAAATTCTA	CPj0635_B	CCGCTGCAGGTCGACGGATCTTATTGAGCTTTCTTAAATCG
CPj0636	CPj0636_F	AGGCCGAATTCCCGGGGATCATGAAAAAGCAAAACATTCGT	CPj0636_B	CCGCTGCAGGTCGACGGATCTTAGCCTTTCTTTCCCCTCA
CPj0637	CPj0637_F	AGGCCGAATTCCCGGGGATCATGATTCAGCAAGAAAGTCA	CPj0637_B	CCGCTGCAGGTCGACGGATCTTAAATTACCTCAGGAGCTA
CPj0638	CPj0638_F	AGGCCGAATTCCCGGGGATCATGGCTAGTGAACCAAGAGG	CPj0638_B	CCGCTGCAGGTCGACGGATCCTAACTTACCACGCCAACAT
CPj0639	CPj0639_F	AGGCCGAATTCCCGGGGATCATGGCTGCTAAAAAGGATTT	CPj0639_B	CCGCTGCAGGTCGACGGATCCTAGCCATGGACTTTACCTT
CPj0640	CPj0640_F	AGGCCGAATTCCCGGGGATCATGTTAATGCCTAAACGAAC	CPj0640_B	CCGCTGCAGGTCGACGGATCTTATACCCTTTCCACTCGCT
CPj0641	CPj0641_F	AGGCCGAATTCCCGGGGATCATGGGTCAGAAAGGTTGTCC	CPj0641_B	CCGCTGCAGGTCGACGGATCTTAAGCAGCTGCAGAGGGTG
CPj0642	CPj0642_F	AGGCCGAATTCCCGGGGATCATGTTTAAAGCGACCGCCCG	CPj0642_B	CCGCTGCAGGTCGACGGATCTTACCGTTCCTTCTCACCAA
CPj0643	CPj0643_F	AGGCCGAATTCCCGGGGATCATGAGTAGATCGTTAAGAAAA	CPj0643_B	CCGCTGCAGGTCGACGGATCTTACCCTTTCTTCACAGGAT
CPj0644	CPj0644_F	AGGCCGAATTCCCGGGGATCATGTTTAAAAAATTTAAACCAGT	CPj0644_B	CCGCTGCAGGTCGACGGATCTTATTTCCTACGATCTTTAAC
CPj0645	CPj0645_F	AGGCCGAATTCCCGGGGATCATGAAAGATCCTTATGATGTA	CPj0645_B	CCGCTGCAGGTCGACGGATCTTATCCGACAGAGTGCCCTT
CPj0646	CPj0646_F	AGGCCGAATTCCCGGGGATCATGGTTTTATTATCAAAATTTGA	CPj0646_B	CCGCTGCAGGTCGACGGATCTTAATCTTTCGTTTCAGAAAC
CPj0647	CPj0647_F	AGGCCGAATTCCCGGGGATCATGCGGTCTCATATTAGTGT	CPj0647_B	CCGCTGCAGGTCGACGGATCCTAAGTTCTAGAAGAATGTTT
CPj0648	CPj0648_F	AGGCCGAATTCCCGGGGATCATGGCGACTAACGCAATTAG	CPj0648_B	CCGCTGCAGGTCGACGGATCTTATTTGCCAGACTTTGTTTT
CPj0649	CPj0649_F	AGGCCGAATTCCCGGGGATCTTGAATCTTAAGGTTGTCTAT	CPj0649_B	CCGCTGCAGGTCGACGGATCTTAATTATTTAAAGTAAAAACTAT
CPj0650	CPj0650_F	AGGCCGAATTCCCGGGGATCATGGCGAGCATTCACCCAAC	CPj0650_B	CCGCTGCAGGTCGACGGATCTTAAGATTCAATCAAAACTCCT
CPj0651	CPj0651_F	AGGCCGAATTCCCGGGGATCATGAATCAACCCTCTGTCAT	CPj0651_B	CCGCTGCAGGTCGACGGATCTTATATGGATTCCTTATCTAC
CPj0652	CPj0652_F	AGGCCGAATTCCCGGGGATCATGTTAGAACGAACTCAAAG	CPj0652_B	CCGCTGCAGGTCGACGGATCTTATAGTTCTAATGCTTCCAA
CPj0653	CPj0653_F	AGGCCGAATTCCCGGGGATCGTGCTACGAATCTTTTGCTT	CPj0653_B	CCGCTGCAGGTCGACGGATCTTATCGAATTTCTTTTTTTAGCA
CPj0654	CPj0654_F	AGGCCGAATTCCCGGGGATCATGCTTAAGAAAAAACCCGT	CPj0654_B	CCGCTGCAGGTCGACGGATCTTATTTCAGTTCAAGCCTTG
CPj0655	CPj0655_F	AGGCCGAATTCCCGGGGATCATGAGTTTATTAAAAGATACGG	CPj0655_B	CCGCTGCAGGTCGACGGATCTTACAATTCCATAAAGGGATT
CPj0656	CPj0656_F	AGGCCGAATTCCCGGGGATCTTGTTTGATATCCTTCTGAC	CPj0656_B	CCGCTGCAGGTCGACGGATCCTAGTCTTTATTCTCCATAG
CPj0657	CPj0657_F	AGGCCGAATTCCCGGGGATCATGGGTAGATACAGAAGAGT	CPj0657_B	CCGCTGCAGGTCGACGGATCCTAGCGCTTCTCTATAATAA
CPj0658	CPj0658_F	AGGCCGAATTCCCGGGGATCATGGATATTTCTGGAGCAGT	CPj0658_B	CCGCTGCAGGTCGACGGATCTTACTCTTCTGTATCTACCC
CPj0659	CPj0659_F	AGGCCGAATTCCCGGGGATCATGGTAAAGATCATATCAAGT	CPj0659_B	CCGCTGCAGGTCGACGGATCTTAAGCGTGCTTATTGATAAG
CPj0660	CPj0660_F	AGGCCGAATTCCCGGGGATCATGAGAGTAGTTCTTCATTG	CPj0660_B	CCGCTGCAGGTCGACGGATCTTAAACCGTAGGATTCTTTTG
CPj0661	CPj0661_F	AGGCCGAATTCCCGGGGATCATGAACAGACGGTGGAATTT	CPj0661_B	CCGCTGCAGGTCGACGGATCTCATTCACCTTGATTTCCTT
CPj0662	CPj0662_F	AGGCCGAATTCCCGGGGATCATGAAATACAGAACACACCG	CPj0662_B	CCGCTGCAGGTCGACGGATCTCAAAAAGCTACCTTAATACT

CPj0663	CPj0663_F	AGGCCGAATTCCCGGGGATCGTGACTGTAACTCTCCCCAA	CPj0663_B	CCGCTGCAGGTCGACGGATCTTACAACGGTGTGTTCTGTA
CPj0664	CPj0664_F	AGGCCGAATTCCCGGGGATCATGAAAAAATTGATTGCTTTGAT	CPj0664_B	CCGCTGCAGGTCGACGGATCTCAAACCCACCCTTCATAAT
CPj0665	CPj0665_F	AGGCCGAATTCCCGGGGATCATGAACGTTTGGACTAAATTT	CPj0665_B	CCGCTGCAGGTCGACGGATCCTAGGCTTTACTACGAGTGT
CPj0666	CPj0666_F	AGGCCGAATTCCCGGGGATCTTGACCTGGATACCCCTTCA	CPj0666_B	CCGCTGCAGGTCGACGGATCTCAAACAGTAATTACACGCA
CPj0667	CPj0667_F	AGGCCGAATTCCCGGGGATCATGAAGAAGTTAATTCTATATTT	CPj0667_B	CCGCTGCAGGTCGACGGATCCTATAGATCTTGAAAAGATTTT
CPj0668	CPj0668_F	AGGCCGAATTCCCGGGGATCATGAAATTTCTATTATACGTTC	CPj0668_B	CCGCTGCAGGTCGACGGATCTTAGGAAGTATGCTTAGATAT
CPj0669	CPj0669_F	AGGCCGAATTCCCGGGGATCATGAGATTGTTTTCTTTAGGC	CPj0669_B	CCGCTGCAGGTCGACGGATCTCAAAAAAGGTCATAGTATAC
CPj0670	CPj0670_F	AGGCCGAATTCCCGGGGATCATGACCTTTTTTGAAGGAGA	CPj0670_B	CCGCTGCAGGTCGACGGATCTTAGGAATGTTGGCCATTGA
CPj0671	CPj0671_F	AGGCCGAATTCCCGGGGATCATGAGTTTAGATTTTTTCGAG	CPj0671_B	CCGCTGCAGGTCGACGGATCCTAGTGATCGTTATTAAAGC
CPj0672	CPj0672_F	AGGCCGAATTCCCGGGGATCATGAAAAGACCTTTTTTTACCT	CPj0672_B	CCGCTGCAGGTCGACGGATCTTAGATTTTAGAATAGTGTTTTA
CPj0673	CPj0673_F	AGGCCGAATTCCCGGGGATCGTGTCTATTGCCTTAAACCG	CPj0673_B	CCGCTGCAGGTCGACGGATCCTACTTTAAAGTGGCAATCT
CPj0674	CPj0674_F	AGGCCGAATTCCCGGGGATCATGGTTCCTTTTCGTCAGCA	CPj0674_B	CCGCTGCAGGTCGACGGATCCTAGATTTTTTGAAAATGAGAA
CPj0675	CPj0675_F	AGGCCGAATTCCCGGGGATCATGATTTTAGATTTTCAATTTTC	CPj0675_B	CCGCTGCAGGTCGACGGATCTTACGGACGACGTTGCCATA
CPj0676	CPj0676_F	AGGCCGAATTCCCGGGGATCATGGGAACTCCTATATCTGG	CPj0676_B	CCGCTGCAGGTCGACGGATCCTAGTCTTTGGGCTCTATTG
CPj0677	CPj0677_F	AGGCCGAATTCCCGGGGATCATGGGAATCAATCCTTCGGG	CPj0677_B	CCGCTGCAGGTCGACGGATCTTATTCAAAAAGATCCCCGA
CPj0678	CPj0678_F	AGGCCGAATTCCCGGGGATCATGTCTGTTAATCCATCAGG	CPj0678_B	CCGCTGCAGGTCGACGGATCTTAATCTTCGTCAGACCAGC
CPj0679	CPj0679_F	AGGCCGAATTCCCGGGGATCATGGATAAGCTAACAGTACA	CPj0679_B	CCGCTGCAGGTCGACGGATCTTAGCTTTTGGATGGAGATA
CPj0680	CPj0680_F	AGGCCGAATTCCCGGGGATCATGCTTCCATTAATCATTTTTG	CPj0680_B	CCGCTGCAGGTCGACGGATCTTAATGGAACAAAGCTCTTAA
CPj0681	CPj0681_F	AGGCCGAATTCCCGGGGATCATGCAAACCCTTGCTCGTCT	CPj0681_B	CCGCTGCAGGTCGACGGATCTTACTTTTCTTCTAGGGTCA
CPj0682	CPj0682_F	AGGCCGAATTCCCGGGGATCATGGCTTCTAATCCCATTTT	CPj0682_B	CCGCTGCAGGTCGACGGATCTTAGTCGTCATACAGCCAAC
CPj0683	CPj0683_F	AGGCCGAATTCCCGGGGATCATGACGACTAATTTTCCCCA	CPj0683_B	CCGCTGCAGGTCGACGGATCTCAATGGATACAACGGTATG
CPj0684	CPj0684_F	AGGCCGAATTCCCGGGGATCGTGACTGAGGAAATCAGTAA	CPj0684_B	CCGCTGCAGGTCGACGGATCTTAAGATAGACTCTCACTGA
CPj0686	CPj0686_F	AGGCCGAATTCCCGGGGATCATGATGCGTGGGGGGAGGTT	CPj0686_B	CCGCTGCAGGTCGACGGATCTCAAACATGGTTGTAGAAGT
CPj0687	CPj0687_F	AGGCCGAATTCCCGGGGATCATGCAAAAGCTAGTCCATAA	CPj0687_B	CCGCTGCAGGTCGACGGATCTTATCCTTTTTTGCCAAAACG
CPj0688	CPj0688_F	AGGCCGAATTCCCGGGGATCATGCTCATAGTTCTTGCTTT	CPj0688_B	CCGCTGCAGGTCGACGGATCTTATCTTTTTGGAAGTTGTTTT
CPj0689	CPj0689_F	AGGCCGAATTCCCGGGGATCGTGAAGAATTTAAAAGAAGATT	CPj0689_B	CCGCTGCAGGTCGACGGATCTCATCTACGAATCTTATCTAA
CPj0690	CPj0690_F	AGGCCGAATTCCCGGGGATCGTGTTAGTTTCAATAGAGAC	CPj0690_B	CCGCTGCAGGTCGACGGATCCTAGGAGGTTTGATTTAGCT
CPj0691	CPj0691_F	AGGCCGAATTCCCGGGGATCATGTTAAAAATAAAGCACTTACA	CPj0691_B	CCGCTGCAGGTCGACGGATCTTATCTCCACGCAACACGCT
CPj0692	CPj0692_F	AGGCCGAATTCCCGGGGATCATGGGCGAATCAGTAAAGGT	CPj0692_B	CCGCTGCAGGTCGACGGATCCTAACCCACGCTATTTTCTA
CPj0693	CPj0693_F	AGGCCGAATTCCCGGGGATCATGGAAGAAGCTGCGAAACA	CPj0693_B	CCGCTGCAGGTCGACGGATCTTAAGAAATAGTATCTAAACGC
CPj0694	CPj0694_F	AGGCCGAATTCCCGGGGATCATGAAACGACCGAAAAAATTT	CPj0694_B	CCGCTGCAGGTCGACGGATCCTATCCCCTTAAAAAAGATTC
CPj0695	CPj0695_F	AGGCCGAATTCCCGGGGATCATGAAAAAACTCTTAAAGTCG	CPj0695_B	CCGCTGCAGGTCGACGGATCTTAGAATCTGAACTGACCAG
CPj0696	CPj0696_F	AGGCCGAATTCCCGGGGATCTTGGAATCCCAATCCTGCAA	CPj0696_B	CCGCTGCAGGTCGACGGATCTTAGTTTGCCTCGCCATCAA
CPj0697	CPj0697_F	AGGCCGAATTCCCGGGGATCATGAGCGACTTTTCTATGGA	CPj0697_B	CCGCTGCAGGTCGACGGATCTTAGGCTCCTATTTTCCATA
CPj0698	CPj0698_F	AGGCCGAATTCCCGGGGATCATGGCTAAGCAAACTAGACG	CPj0698_B	CCGCTGCAGGTCGACGGATCTCAGTGTCTTGGAGAACAGA
CPj0699	CPj0699_F	AGGCCGAATTCCCGGGGATCATGTCTGTTCTCCAAGACAC	CPj0699_B	CCGCTGCAGGTCGACGGATCTTATATTGAAGCTATTTCAGC
CPj0700	CPj0700_F	AGGCCGAATTCCCGGGGATCATGGTTCACTCACCTACCCA	CPj0700_B	CCGCTGCAGGTCGACGGATCTTAGGAAGGGTCATCTGGAT
CPj0701	CPj0701_F	AGGCCGAATTCCCGGGGATCATGACCCTTCCTAATGATTT	CPj0701_B	CCGCTGCAGGTCGACGGATCTCAGAAACTCTCAGGAGATA
CPj0702	CPj0702_F	AGGCCGAATTCCCGGGGATCGTGAAAACTGTGATATTGAAC	CPj0702_B	CCGCTGCAGGTCGACGGATCCTACTGAGCTTCTATTTCTA
CPj0703	CPj0703_F	AGGCCGAATTCCCGGGGATCATGGATTGTCGTGGTGGCAT	CPj0703_B	CCGCTGCAGGTCGACGGATCTCACCGGATTCTTTTTAAGC
CPj0704	CPj0704_F	AGGCCGAATTCCCGGGGATCATGGCAGTAGCAGCCGATTC	CPj0704_B	CCGCTGCAGGTCGACGGATCTTATACCTCTAAAACGCGAA
CPj0705	CPj0705_F	AGGCCGAATTCCCGGGGATCATGGAATTAAAGAAAACAGCA	CPj0705_B	CCGCTGCAGGTCGACGGATCTTATAAACGTGCTTCTTCGA
CPj0706	CPj0706_F	AGGCCGAATTCCCGGGGATCGTGGCAAAATATCCACTAGA	CPj0706_B	CCGCTGCAGGTCGACGGATCCTAGCTTCCCCCTGATTCAC
CPj0707	CPj0707_F	AGGCCGAATTCCCGGGGATCATGGATCAGTTAACAACGGA	CPj0707_B	CCGCTGCAGGTCGACGGATCTTACCGGAAAATGGCGCGCA
CPj0708	CPj0708_F	AGGCCGAATTCCCGGGGATCATGATAGACCCTGTAGAATG	CPj0708_B	CCGCTGCAGGTCGACGGATCTTAACCTAATTGCGTTGTCA
CPj0709	CPj0709_F	AGGCCGAATTCCCGGGGATCATGGCAGATTTGGAAGTATT	CPj0709_B	CCGCTGCAGGTCGACGGATCCTAGCCCAAAGGACCTGCAC
CPj0710	CPj0710_F	AGGCCGAATTCCCGGGGATCATGGCTACAAATAAAAGTTGC	CPj0710_B	CCGCTGCAGGTCGACGGATCTTAACTTCCTTTAACTGCTC
CPj0711	CPj0711_F	AGGCCGAATTCCCGGGGATCATGTTTAATATGGAAAATACAG	CPj0711_B	CCGCTGCAGGTCGACGGATCTTATATCATCTTGCGGTTGA
CPj0712	CPj0712_F	AGGCCGAATTCCCGGGGATCATGGCAGTACGATTAATTGT	CPj0712_B	CCGCTGCAGGTCGACGGATCTTATTTATTGTAGTCTATTTTATA
CPj0713	CPj0713_F	AGGCCGAATTCCCGGGGATCATGTTGGAAAAATTAATAAAAAAT	CPj0713_B	CCGCTGCAGGTCGACGGATCTTACTGTTTACCTAGGCCAA
CPj0714	CPj0714_F	AGGCCGAATTCCCGGGGATCATGGTGTTAGGAGTTGTTGG	CPj0714_B	CCGCTGCAGGTCGACGGATCTCAATAGCTTAGAACGGAAG
CPj0715	CPj0715_F	AGGCCGAATTCCCGGGGATCATGGCGGCATACACAGAAGC	CPj0715_B	CCGCTGCAGGTCGACGGATCTTAAAAATCAGTAATAAGGTTAT
CPj0716	CPj0716_F	AGGCCGAATTCCCGGGGATCATGCGTGACGTTTCAGAGCT	CPj0716_B	CCGCTGCAGGTCGACGGATCTTAAATTAAGGTTTGTTGTTTC
CPj0717	CPj0717_F	AGGCCGAATTCCCGGGGATCATGGAACCACGTCACATTTA	CPj0717_B	CCGCTGCAGGTCGACGGATCTTACTGCTCTTTATAGACAG
CPj0718	CPj0718_F	AGGCCGAATTCCCGGGGATCATGTCGTTTACCTATTTCCT	CPj0718_B	CCGCTGCAGGTCGACGGATCTTAGATATTTTGGGCGCAAT
CPj0719	CPj0719_F	AGGCCGAATTCCCGGGGATCATGAAAACTGTGACTTCCTT	CPj0719_B	CCGCTGCAGGTCGACGGATCTTATTGTTCTTTTAAAATCGATT
CPj0720	CPj0720_F	AGGCCGAATTCCCGGGGATCATGAAAGAATTTTTAGCCTATA	CPj0720_B	CCGCTGCAGGTCGACGGATCCTACTTTTCTTCCATAATTTC
CPj0721	CPj0721_F	AGGCCGAATTCCCGGGGATCATGTTCAATAACAAAATGATCC	CPj0721_B	CCGCTGCAGGTCGACGGATCTCATGCTGAGACCATATCAA
CPj0722	CPj0722_F	AGGCCGAATTCCCGGGGATCATGACAAAATTTCTATACTGC	CPj0722_B	CCGCTGCAGGTCGACGGATCTTAATTCCTGAATAAAGATAAAT
CPj0723	CPj0723_F	AGGCCGAATTCCCGGGGATCATGCCTATACTTTCTGTGTG	CPj0723_B	CCGCTGCAGGTCGACGGATCTTAGTATGAGAACGAGTCTC
CPj0724	CPj0724_F	AGGCCGAATTCCCGGGGATCATGCTTCTAGGGTTTTTGTG	CPj0724_B	CCGCTGCAGGTCGACGGATCCTAATGGATCTCACAAAAGT
CPj0725	CPj0725_F	AGGCCGAATTCCCGGGGATCATGTTTTTCGCTCCTCTTCT	CPj0725_B	CCGCTGCAGGTCGACGGATCCTAATCTAGTAGAGGTTCGT
CPj0726	CPj0726_F	AGGCCGAATTCCCGGGGATCATGATTTATAGCACTTCTATTT	CPj0726_B	CCGCTGCAGGTCGACGGATCCTATCCTGTCAGGCTTCGTG
CPj0727	CPj0727_F	AGGCCGAATTCCCGGGGATCATGTCTACCTTTTCTATCCA	CPj0727_B	CCGCTGCAGGTCGACGGATCTTAGTTGGAATAGATGGCAC
CPj0728	CPj0728_F	AGGCCGAATTCCCGGGGATCATGGTTAATCCTATTGGTCC	CPj0728_B	CCGCTGCAGGTCGACGGATCTTATTGGAGATAACCAGAATA

CPj0729	CPj0729_F	AGGCCGAATTCCCGGGGATCATGAAAAAACAGGTATATCAAT	CPj0729_B	CCGCTGCAGGTCGACGGATCTTAAAACGCTGAAATTATACC
CPj0730	CPj0730_F	AGGCCGAATTCCCGGGGATCATGAGCAGAAAAGACAATGA	CPj0730_B	CCGCTGCAGGTCGACGGATCTTAATTTTGAGTGTCTTGCAT
CPj0731	CPj0731_F	AGGCCGAATTCCCGGGGATCTTGTCTTTTCTGCTCATTAAA	CPj0731_B	CCGCTGCAGGTCGACGGATCTTATGAAATGATACTTATGCTT
CPj0732	CPj0732_F	AGGCCGAATTCCCGGGGATCATGAAAGTACTTCCTCCTCC	CPj0732_B	CCGCTGCAGGTCGACGGATCCTAACTATCTCTGTTTTTTGA
CPj0733	CPj0733_F	AGGCCGAATTCCCGGGGATCATGGCTCGATATTGTGGCCC	CPj0733_B	CCGCTGCAGGTCGACGGATCTTATGTTCTATGAGATAGGAA
CPj0734	CPj0734_F	AGGCCGAATTCCCGGGGATCATGGAAAAAAAATATTATGCACT	CPj0734_B	CCGCTGCAGGTCGACGGATCTTAAATCAAACAACAACTTGC
CPj0735	CPj0735_F	AGGCCGAATTCCCGGGGATCATGTTGATGATGCTTATGATG	CPj0735_B	CCGCTGCAGGTCGACGGATCTTACTTAGAGTTGACCATATA
CPj0736	CPj0736_F	AGGCCGAATTCCCGGGGATCATGACTGTTTCGGTTAAAAAA	CPj0736_B	CCGCTGCAGGTCGACGGATCTTATGCATGAGGAAACACTA
CPj0737	CPj0737_F	AGGCCGAATTCCCGGGGATCATGAATGCCACCAAACATTG	CPj0737_B	CCGCTGCAGGTCGACGGATCTTAAACGGCTTCACAGGGAC
CPj0738	CPj0738_F	AGGCCGAATTCCCGGGGATCGTGAAGCCGTTTAATATTTTT	CPj0738_B	CCGCTGCAGGTCGACGGATCCTAATGATAGGCCTGACATT
CPj0739	CPj0739_F	AGGCCGAATTCCCGGGGATCATGAGCTATAGCCTACGCAA	CPj0739_B	CCGCTGCAGGTCGACGGATCTCAATCCCAAAGCAATCCAA
CPj0740	CPj0740_F	AGGCCGAATTCCCGGGGATCATGAGTTTTTTTAATCACATAC	CPj0740_B	CCGCTGCAGGTCGACGGATCCTATAGCTCATAAGCTTGAA
CPj0742	CPj0742_F	AGGCCGAATTCCCGGGGATCATGAATAGTAAATCTGCGCA	CPj0742_B	CCGCTGCAGGTCGACGGATCTTATAGAGGAATCCAGTTTTT
CPj0743	CPj0743_F	AGGCCGAATTCCCGGGGATCATGAAAATTACAGTCAATCGG	CPj0743_B	CCGCTGCAGGTCGACGGATCTCAATCTTGATGGGGAGTTA
CPj0744	CPj0744_F	AGGCCGAATTCCCGGGGATCATGAGTTCTTTAACACTAAGT	CPj0744_B	CCGCTGCAGGTCGACGGATCTTAAAATTCAAATCCCTGATG
CPj0745	CPj0745_F	AGGCCGAATTCCCGGGGATCGTGGATTCCTGCTTCGACGA	CPj0745_B	CCGCTGCAGGTCGACGGATCTTACAAAAATTTCTCTTGTGAT
CPj0746	CPj0746_F	AGGCCGAATTCCCGGGGATCATGTTGGGCAAAGAAGAAGA	CPj0746_B	CCGCTGCAGGTCGACGGATCTTAGGTCGTTGGTTCTTTTC
CPj0748	CPj0748_F	AGGCCGAATTCCCGGGGATCGTGTTACATGCTTTAGATAC	CPj0748_B	CCGCTGCAGGTCGACGGATCTTAAAAAGATCCTAAACTCGA
CPj0749	CPj0749_F	AGGCCGAATTCCCGGGGATCATGACTTATCTAGCCTCGTC	CPj0749_B	CCGCTGCAGGTCGACGGATCTTAAATGACTTGACCAGGAC
CPj0750	CPj0750_F	AGGCCGAATTCCCGGGGATCATGATCGGTGATAAAATCATA	CPj0750_B	CCGCTGCAGGTCGACGGATCTTACTCTTCGTTTGGATGCG
CPj0751	CPj0751_F	AGGCCGAATTCCCGGGGATCATGTTTCGTTGCATATTGTTT	CPj0751_B	CCGCTGCAGGTCGACGGATCCTAAGAGGCAACTCGGTCCT
CPj0752	CPj0752_F	AGGCCGAATTCCCGGGGATCTTGCACACAGAATTTGCTCC	CPj0752_B	CCGCTGCAGGTCGACGGATCCTAGTAATTAGACTTCTTAATT
CPj0753	CPj0753_F	AGGCCGAATTCCCGGGGATCATGGCAACAGCACATCTTGG	CPj0753_B	CCGCTGCAGGTCGACGGATCCTATCCTATTTTAGCATAATCT
CPj0754	CPj0754_F	AGGCCGAATTCCCGGGGATCATGGCACCTAAAAAACCGAA	CPj0754_B	CCGCTGCAGGTCGACGGATCTCACGATGCTCTCGCGTTAA
CPj0755	CPj0755_F	AGGCCGAATTCCCGGGGATCATGTTATTGGTAAGGAAATGG	CPj0755_B	CCGCTGCAGGTCGACGGATCTCAACTCTGAAGCACTTCTT
CPj0756	CPj0756_F	AGGCCGAATTCCCGGGGATCTTGTTCATGAATACACAGAAT	CPj0756_B	CCGCTGCAGGTCGACGGATCCTATTTGGATTTCAAACTCTT
CPj0757	CPj0757_F	AGGCCGAATTCCCGGGGATCGTGATTGCTATAGAACGTTA	CPj0757_B	CCGCTGCAGGTCGACGGATCTTAAGCAGACAAAACGGGGC
CPj0758	CPj0758_F	AGGCCGAATTCCCGGGGATCATGTCCGAGCCCCGTTTTGT	CPj0758_B	CCGCTGCAGGTCGACGGATCTTAGATGGGTGCACAGGCTT
CPj0759	CPj0759_F	AGGCCGAATTCCCGGGGATCATGTGTAAAAATAGAGGGGT	CPj0759_B	CCGCTGCAGGTCGACGGATCTCATAAGGATATATTTTTGGTG
CPj0760	CPj0760_F	AGGCCGAATTCCCGGGGATCATGAAAATCACCACAGTCAA	CPj0760_B	CCGCTGCAGGTCGACGGATCTCAGGAGGTTGGTGCGGGA
CPj0761	CPj0761_F	AGGCCGAATTCCCGGGGATCATGACATCCTGGATAGAATT	CPj0761_B	CCGCTGCAGGTCGACGGATCCTACTTACAAGAACAAGGCT
CPj0762	CPj0762_F	AGGCCGAATTCCCGGGGATCATGAATTTACCTGATAGAAAAA	CPj0762_B	CCGCTGCAGGTCGACGGATCTTAAGCTTCTACTGTTTGAG
CPj0763	CPj0763_F	AGGCCGAATTCCCGGGGATCATGACTGATCCTAAAATAGAG	CPj0763_B	CCGCTGCAGGTCGACGGATCCTAACATAAATAGATTTGGGA
CPj0764	CPj0764_F	AGGCCGAATTCCCGGGGATCATGGATATAAAAAAACTCTTTTG	CPj0764_B	CCGCTGCAGGTCGACGGATCCTAGTTGAGCAAAGGTTTGC
CPj0765	CPj0765_F	AGGCCGAATTCCCGGGGATCATGAAAAAATGGATTTCTATTTT	CPj0765_B	CCGCTGCAGGTCGACGGATCTTATATCCATCGACTTATAGC
CPj0766	CPj0766_F	AGGCCGAATTCCCGGGGATCATGAATTTCAAGCTGCCTGT	CPj0766_B	CCGCTGCAGGTCGACGGATCCTAAGAGCTTAATGTAAATTG
CPj0767	CPj0767_F	AGGCCGAATTCCCGGGGATCATGCTATCTTATTTGTTAAGAA	CPj0767_B	CCGCTGCAGGTCGACGGATCTTATAAATATTGGAGCAGCC
CPj0768	CPj0768_F	AGGCCGAATTCCCGGGGATCATGGCTGCTCCAATATTTAT	CPj0768_B	CCGCTGCAGGTCGACGGATCTCAGCATTTAACAAAGGTCT
CPj0769	CPj0769_F	AGGCCGAATTCCCGGGGATCATGAAAAAGTCCTTAATTATAGT	CPj0769_B	CCGCTGCAGGTCGACGGATCTTACGAAGAAGCCGACGACT
CPj0770	CPj0770_F	AGGCCGAATTCCCGGGGATCGTGGAAAAACTTGAGTTTGT	CPj0770_B	CCGCTGCAGGTCGACGGATCTTAAACAAAGTAGGATTGATAA
CPj0771	CPj0771_F	AGGCCGAATTCCCGGGGATCATGTTTCAGCAAAAGCAGAA	CPj0771_B	CCGCTGCAGGTCGACGGATCCTAGAACTGCCTATCTCTAA
CPj0772	CPj0772_F	AGGCCGAATTCCCGGGGATCATGACATGTATCTCAGAACT	CPj0772_B	CCGCTGCAGGTCGACGGATCCTAACGCACTTGAATCATAT
CPj0773	CPj0773_F	AGGCCGAATTCCCGGGGATCATGCAGAATGCTACTATAGA	CPj0773_B	CCGCTGCAGGTCGACGGATCTCATGGGAGCTTCCAATTAA
CPj0774	CPj0774_F	AGGCCGAATTCCCGGGGATCATGAATGAAGGTATCCACTC	CPj0774_B	CCGCTGCAGGTCGACGGATCCTACTCACTAGGGACTAGTG
CPj0775	CPj0775_F	AGGCCGAATTCCCGGGGATCATGAAAATTGTGATTGCTAGT	CPj0775_B	CCGCTGCAGGTCGACGGATCCTAGTCCCTAGTGAGTAGGT
CPj0776	CPj0776_F	AGGCCGAATTCCCGGGGATCATGAAGAAAATTTTTTACTCTTT	CPj0776_B	CCGCTGCAGGTCGACGGATCTTAGGATTCTGCATACTCTG
CPj0777	CPj0777_F	AGGCCGAATTCCCGGGGATCGTGGTTTGGGTATTTAAAAG	CPj0777_B	CCGCTGCAGGTCGACGGATCTTATGTTTTCGTCCTTGAGC
CPj0778	CPj0778_F	AGGCCGAATTCCCGGGGATCATGACACTCTCCCTAGTTGG	CPj0778_B	CCGCTGCAGGTCGACGGATCCTAGTCTATAGTCCCGAAAT
CPj0779	CPj0779_F	AGGCCGAATTCCCGGGGATCATGAAATTTACAGTTGCTTTAT	CPj0779_B	CCGCTGCAGGTCGACGGATCCTAGAAAGGCTGATTGAAAG
CPj0780	CPj0780_F	AGGCCGAATTCCCGGGGATCATGCACGCTAAGCTAAGCTT	CPj0780_B	CCGCTGCAGGTCGACGGATCTTATTGCTTATTTCTTTGTAAAC
CPj0781	CPj0781_F	AGGCCGAATTCCCGGGGATCATGAATATACATTCCCTATGG	CPj0781_B	CCGCTGCAGGTCGACGGATCTTAGCGTGCATGAATCTTAA
CPj0782	CPj0782_F	AGGCCGAATTCCCGGGGATCATGTTACGGCAACTATGCTT	CPj0782_B	CCGCTGCAGGTCGACGGATCTCATAGTGTTCTCTTTATCG
CPj0783	CPj0783_F	AGGCCGAATTCCCGGGGATCATGATGAAGTATCTTCCCTA	CPj0783_B	CCGCTGCAGGTCGACGGATCTTAGGATTCATTACTGACCA
CPj0784	CPj0784_F	AGGCCGAATTCCCGGGGATCATGAAATACCGCTTCACGGA	CPj0784_B	CCGCTGCAGGTCGACGGATCTCAATTCTGTAGGGCTACGT
CPj0785	CPj0785_F	AGGCCGAATTCCCGGGGATCATGGTACACTTCTCTCATAA	CPj0785_B	CCGCTGCAGGTCGACGGATCTCATAAGTTTGTATTGCGGT
CPj0786	CPj0786_F	AGGCCGAATTCCCGGGGATCTTGAATAAATTCAAAACATATTTA	CPj0786_B	CCGCTGCAGGTCGACGGATCCTACCTTACAAATCGACTTA
CPj0787	CPj0787_F	AGGCCGAATTCCCGGGGATCGTGGATTTGGCTGATGCTCA	CPj0787_B	CCGCTGCAGGTCGACGGATCTTAACCGTGCAGAAAGCGTA
CPj0788	CPj0788_F	AGGCCGAATTCCCGGGGATCATGTCACGACATGAAATCTG	CPj0788_B	CCGCTGCAGGTCGACGGATCCTATGCCACACTATACAAAT
CPj0789	CPj0789_F	AGGCCGAATTCCCGGGGATCATGGATGAGAATCGAAAAGT	CPj0789_B	CCGCTGCAGGTCGACGGATCCTATATGGGTAGACGGATAT
CPj0790	CPj0790_F	AGGCCGAATTCCCGGGGATCATGGAGAATCTAGAGACTTT	CPj0790_B	CCGCTGCAGGTCGACGGATCTTATTTTTTCTTTTTAAAAAGAGC
CPj0791	CPj0791_F	AGGCCGAATTCCCGGGGATCATGTCACGTTTGGATATTTTT	CPj0791_B	CCGCTGCAGGTCGACGGATCCTAGAAAAATTCTTTAGGGAG
CPj0792	CPj0792_F	AGGCCGAATTCCCGGGGATCATGAAACATACCTTTACCAAG	CPj0792_B	CCGCTGCAGGTCGACGGATCTTATGAAAATGAAAGGATGGT
CPj0793	CPj0793_F	AGGCCGAATTCCCGGGGATCATGATCCCTTTTACTAAAACA	CPj0793_B	CCGCTGCAGGTCGACGGATCTCATGATTCTAATACCTTTAAT
CPj0794	CPj0794_F	AGGCCGAATTCCCGGGGATCGTGAGTCTATATCAAAAATGG	CPj0794_B	CCGCTGCAGGTCGACGGATCTCAATCTTTCATTTGGTTATC
CPj0795	CPj0795_F	AGGCCGAATTCCCGGGGATCATGAAAGATTTGGGGACTCT	CPj0795_B	CCGCTGCAGGTCGACGGATCTTAGAATCCTAAGGCATACC

CPj0796	CPj0796_F	AGGCCGAATTCCCGGGGATCTTGCAGCCATGTCTGAATAT	CPj0796_B	CCGCTGCAGGTCGACGGATCTTAGAAGCTAAGATTATAGCT
CPj0797	CPj0797_F	AGGCCGAATTCCCGGGGATCATGAGTAAGAAGATAAAGGTT	CPj0797_B	CCGCTGCAGGTCGACGGATCTTATTTATGTATATGGAACAGA
CPj0798	CPj0798_F	AGGCCGAATTCCCGGGGATCATGAAAAAGACATGTTGCCA	CPj0798_B	CCGCTGCAGGTCGACGGATCCTAATCATCAAGGTAGATAAA
CPj0799	CPj0799_F	AGGCCGAATTCCCGGGGATCATGGCAGCTATAAAACAAATT	CPj0799_B	CCGCTGCAGGTCGACGGATCTTATTCTGATTGGACTCCAA
CPj0800	CPj0800_F	AGGCCGAATTCCCGGGGATCATGTTTGAAGCTGTCATTGC	CPj0800_B	CCGCTGCAGGTCGACGGATCCTATTCCTCAGAATCCTCGT
CPj0801	CPj0801_F	AGGCCGAATTCCCGGGGATCATGACATTCCAACTTCATGC	CPj0801_B	CCGCTGCAGGTCGACGGATCTTAGAACAAATAGAGAAGCTG
CPj0802	CPj0802_F	AGGCCGAATTCCCGGGGATCATGAATAAAAAAAAGCGCGTA	CPj0802_B	CCGCTGCAGGTCGACGGATCTTATTTAAGCAATGAGCGCC
CPj0803	CPj0803_F	AGGCCGAATTCCCGGGGATCATGGCAGCAAAGACAAAAAC	CPj0803_B	CCGCTGCAGGTCGACGGATCCTATTGAAGTGCTTTAGTTAG
CPj0804	CPj0804_F	AGGCCGAATTCCCGGGGATCATGGGGAATCTAAAAACGCT	CPj0804_B	CCGCTGCAGGTCGACGGATCTCATACCTTTGTATCGGGAA
CPj0805	CPj0805_F	AGGCCGAATTCCCGGGGATCATGAAGACCATCGCTGTAAA	CPj0805_B	CCGCTGCAGGTCGACGGATCCTAAATATCTCTTAATAAAATTAG
CPj0806	CPj0806_F	AGGCCGAATTCCCGGGGATCATGATTCAAGTAACTTGTGAT	CPj0806_B	CCGCTGCAGGTCGACGGATCCTACAATAATGCAGTTAAACT
CPj0807	CPj0807_F	AGGCCGAATTCCCGGGGATCATGTCGCTTTTTCTAGTTTTT	CPj0807_B	CCGCTGCAGGTCGACGGATCTTAAGAAACAATGTAGCCCT
CPj0808	CPj0808_F	AGGCCGAATTCCCGGGGATCATGACATCAGGAGTTAGTGG	CPj0808_B	CCGCTGCAGGTCGACGGATCTTAATTAAAGATAGCAGATGTT
CPj0809	CPj0809_F	AGGCCGAATTCCCGGGGATCATGTCTATTTCATCTTCTTCA	CPj0809_B	CCGCTGCAGGTCGACGGATCTTATGCTGCGCCAGCGATGG
CPj0810	CPj0810_F	AGGCCGAATTCCCGGGGATCATGAATAAAAAGCCCAAGAAA	CPj0810_B	CCGCTGCAGGTCGACGGATCTTACTCAGCGCCTTTAACCA
CPj0811	CPj0811_F	AGGCCGAATTCCCGGGGATCATGAGCAAGCCCTCTCCTCG	CPj0811_B	CCGCTGCAGGTCGACGGATCCTAACGTTTCTTTCCGCTTT
CPj0812	CPj0812_F	AGGCCGAATTCCCGGGGATCATGTCTACAAGAAGGCCTAT	CPj0812_B	CCGCTGCAGGTCGACGGATCTTATCCTTCCATAAAATCAGA
CPj0813	CPj0813_F	AGGCCGAATTCCCGGGGATCATGTCACACGATCGTATTTT	CPj0813_B	CCGCTGCAGGTCGACGGATCTTATAAACAAACTAACTCTGAG
CPj0814	CPj0814_F	AGGCCGAATTCCCGGGGATCATGCTGTGTTATTCACCGAA	CPj0814_B	CCGCTGCAGGTCGACGGATCCTATGATCCCCCACGATTGG
CPj0815	CPj0815_F	AGGCCGAATTCCCGGGGATCATGGTTTTTTTCCGTAATTCT	CPj0815_B	CCGCTGCAGGTCGACGGATCCTAGCAGCCATCGTATTCTT
CPj0816	CPj0816_F	AGGCCGAATTCCCGGGGATCATGGCTGCTAGTATTTTATC	CPj0816_B	CCGCTGCAGGTCGACGGATCCTAATCACAGCGCTTGGTAA
CPj0817	CPj0817_F	AGGCCGAATTCCCGGGGATCATGCCTCGATATCGGTATAC	CPj0817_B	CCGCTGCAGGTCGACGGATCTTATAATGTTTGGATATTGCTT
CPj0818	CPj0818_F	AGGCCGAATTCCCGGGGATCATGAAAAGACAAAAGAGAAAG	CPj0818_B	CCGCTGCAGGTCGACGGATCTTACTTCTTATTTGAACTTTGT
CPj0819	CPj0819_F	AGGCCGAATTCCCGGGGATCATGGGGTCTCGACGTAAACT	CPj0819_B	CCGCTGCAGGTCGACGGATCCTATAGAGTTACACATAGGC
CPj0821	CPj0821_F	AGGCCGAATTCCCGGGGATCATGCAACCTTTTATCTTTACT	CPj0821_B	CCGCTGCAGGTCGACGGATCTTATAATTTAATACTCTTTGAAG
CPj0822	CPj0822_F	AGGCCGAATTCCCGGGGATCATGGCAGACGAGACCCCGAA	CPj0822_B	CCGCTGCAGGTCGACGGATCTTAAGAAGGTTTATTAGAAGTA
CPj0823	CPj0823_F	AGGCCGAATTCCCGGGGATCATGGGAATCTCTCTACCAGA	CPj0823_B	CCGCTGCAGGTCGACGGATCTTAGAGTACTTGAGGGTTGG
CPj0824	CPj0824_F	AGGCCGAATTCCCGGGGATCGTGTTAGCATTTTTCGCAAC	CPj0824_B	CCGCTGCAGGTCGACGGATCTTATTTCCATTTATAGAAGTTTT
CPj0826	CPj0826_F	AGGCCGAATTCCCGGGGATCATGAAGTTTTTTAGCTTAATTTT	CPj0826_B	CCGCTGCAGGTCGACGGATCTTATTCTTTCTTATCCTGATC
CPj0827	CPj0827_F	AGGCCGAATTCCCGGGGATCGTGACTGCCAACACTTTTGG	CPj0827_B	CCGCTGCAGGTCGACGGATCTTATTTCACTAAGACTTTCATG
CPj0828	CPj0828_F	AGGCCGAATTCCCGGGGATCATGGTTCGTCGATCTATTTC	CPj0828_B	CCGCTGCAGGTCGACGGATCCTAAGCACCCTCAATTTCAT
CPj0829	CPj0829_F	AGGCCGAATTCCCGGGGATCGTGCCAACTTTGGCGAAATC	CPj0829_B	CCGCTGCAGGTCGACGGATCCTAAGAATAACACTTAAATAAG
CPj0830	CPj0830_F	AGGCCGAATTCCCGGGGATCTTGATAGCTTTGCTTTATAATA	CPj0830_B	CCGCTGCAGGTCGACGGATCTCAAGCAGCACTTGATTTTA
CPj0831	CPj0831_F	AGGCCGAATTCCCGGGGATCGTGCTTATAAGAAAATCTGAA	CPj0831_B	CCGCTGCAGGTCGACGGATCTTAAGCCGCGGGATGGACTG
CPj0832	CPj0832_F	AGGCCGAATTCCCGGGGATCATGAAATGTAGACCAACTTTA	CPj0832_B	CCGCTGCAGGTCGACGGATCTTAAGCTGACGCTTTGTCTT
CPj0833	CPj0833_F	AGGCCGAATTCCCGGGGATCATGACCCAAGAATTTGATTG	CPj0833_B	CCGCTGCAGGTCGACGGATCTCATGACTTAGGAGGGAAGT
CPj0834	CPj0834_F	AGGCCGAATTCCCGGGGATCATGCCATTTGCTAAAGAGAC	CPj0834_B	CCGCTGCAGGTCGACGGATCTTAAAGAGGAAGTTTACGGT
CPj0835	CPj0835_F	AGGCCGAATTCCCGGGGATCATGGTTTTAGAAGCATTAGC	CPj0835_B	CCGCTGCAGGTCGACGGATCTTAGGAATCCTCAGGGGGAA
CPj0836	CPj0836_F	AGGCCGAATTCCCGGGGATCATGAAAAAAAACGCATCTCAT	CPj0836_B	CCGCTGCAGGTCGACGGATCTTAATTCACTAACTTTAAAACAA
CPj0837	CPj0837_F	AGGCCGAATTCCCGGGGATCATGAAGCAATTTATTCTCAGA	CPj0837_B	CCGCTGCAGGTCGACGGATCCTAAGTACGGGTACTATTTG
CPj0838	CPj0838_F	AGGCCGAATTCCCGGGGATCATGCTAAAGCACGATACCAT	CPj0838_B	CCGCTGCAGGTCGACGGATCCTATTTTCCAATGCAAAATTTA
CPj0839	CPj0839_F	AGGCCGAATTCCCGGGGATCGTGCAGAAGCCCCAATATAT	CPj0839_B	CCGCTGCAGGTCGACGGATCTTAAATTTCTTCTCTCTGAGA
CPj0840	CPj0840_F	AGGCCGAATTCCCGGGGATCATGTGGTTAGTCATCTTGTG	CPj0840_B	CCGCTGCAGGTCGACGGATCTTAAGCGGCAAGCAGAGCAT
CPj0841	CPj0841_F	AGGCCGAATTCCCGGGGATCATGTTAGGTTTTCTTAAACGC	CPj0841_B	CCGCTGCAGGTCGACGGATCTTAATCTTGATCTTCAGAATC
CPj0844	CPj0844_F	AGGCCGAATTCCCGGGGATCATGCTAAAAATAGCCATCTTA	CPj0844_B	CCGCTGCAGGTCGACGGATCTTAATTATGTCTTTTTGGTTTTT
CPj0845	CPj0845_F	AGGCCGAATTCCCGGGGATCATGACAACAATTGCCATAGA	CPj0845_B	CCGCTGCAGGTCGACGGATCCTACTTCCAAAAGCCTTTTT
CPj0846	CPj0846_F	AGGCCGAATTCCCGGGGATCATGAATAAAAAAAATCTAACTATT	CPj0846_B	CCGCTGCAGGTCGACGGATCCTAAGCGATAGCTTCTGGGG
CPj0847	CPj0847_F	AGGCCGAATTCCCGGGGATCATGACACTGGTACCCTATGT	CPj0847_B	CCGCTGCAGGTCGACGGATCCTAAGTGCTACTTGTATCCT
CPj0848	CPj0848_F	AGGCCGAATTCCCGGGGATCGTGCCACGTAGTCTCTCCAA	CPj0848_B	CCGCTGCAGGTCGACGGATCTTATGCAGAAGGAGTTGAAG
CPj0849	CPj0849_F	AGGCCGAATTCCCGGGGATCATGCTTAATTTTCGCAAGTTA	CPj0849_B	CCGCTGCAGGTCGACGGATCTCATATCTGCAGCAATTCCA
CPj0850	CPj0850_F	AGGCCGAATTCCCGGGGATCATGAGTCCACATCGCAATCT	CPj0850_B	CCGCTGCAGGTCGACGGATCCTATACCAAATTCCCTTTAC
CPj0851	CPj0851_F	AGGCCGAATTCCCGGGGATCATGGTATGGAGCACCAACAT	CPj0851_B	CCGCTGCAGGTCGACGGATCTTATTTTTCTTTTAATTCTGATTT
CPj0852	CPj0852_F	AGGCCGAATTCCCGGGGATCGTGACGCTACAACCGAGCTA	CPj0852_B	CCGCTGCAGGTCGACGGATCCTAAGATTTAATCCTTCTCG
CPj0853	CPj0853_F	AGGCCGAATTCCCGGGGATCATGCATCCGAAAATAGAAAAA	CPj0853_B	CCGCTGCAGGTCGACGGATCTTAGTTTTTAAATCCAGAAATTA
CPj0854	CPj0854_F	AGGCCGAATTCCCGGGGATCATGAATAGCAAGATGCTAAAA	CPj0854_B	CCGCTGCAGGTCGACGGATCCTAAAACTGCAGACCTGACG
CPj0855	CPj0855_F	AGGCCGAATTCCCGGGGATCATGAAACAACACATCGGCTA	CPj0855_B	CCGCTGCAGGTCGACGGATCTTATAGGAACTCTTCTTTTGT
CPj0856	CPj0856_F	AGGCCGAATTCCCGGGGATCATGACTGAATCGGTATATTC	CPj0856_B	CCGCTGCAGGTCGACGGATCTCATGAGGCCTCAAAAAATG
CPj0857	CPj0857_F	AGGCCGAATTCCCGGGGATCATGAGAGATCGACTTGGGAG	CPj0857_B	CCGCTGCAGGTCGACGGATCTTACGTTCCTATCTCTTGAT
CPj0858	CPj0858_F	AGGCCGAATTCCCGGGGATCATGAATCATCTAAATAAAGAAAA	CPj0858_B	CCGCTGCAGGTCGACGGATCTCATGAGTCTGCTAATGCCT
CPj0859	CPj0859_F	AGGCCGAATTCCCGGGGATCGTGACAACACCACAATCTCC	CPj0859_B	CCGCTGCAGGTCGACGGATCTCATGCTGTCAAAACAGAAA
CPj0860	CPj0860_F	AGGCCGAATTCCCGGGGATCGTGTTTTTTCAAAATTTGGCA	CPj0860_B	CCGCTGCAGGTCGACGGATCTTAAAGTTTATATTTCAGCACT
CPj0861	CPj0861_F	AGGCCGAATTCCCGGGGATCATGACCCTACCTCTAGAACC	CPj0861_B	CCGCTGCAGGTCGACGGATCCTACGGGTGAGAAAGATTTA
CPj0862	CPj0862_F	AGGCCGAATTCCCGGGGATCATGGAAAAACCACAAAATCG	CPj0862_B	CCGCTGCAGGTCGACGGATCTCATGAGGAACTTCCAAGTA
CPj0863	CPj0863_F	AGGCCGAATTCCCGGGGATCATGGCTCTTCTTATTTTATTAC	CPj0863_B	CCGCTGCAGGTCGACGGATCTTAACCAAAAAATTCTGGGTG
CPj0864	CPj0864_F	AGGCCGAATTCCCGGGGATCGTGACAAAAGTTCGTCTTAA	CPj0864_B	CCGCTGCAGGTCGACGGATCTTAGTCAGACAATTTCATGTA

CPj0865	CPj0865_F	AGGCCGAATTCCCGGGGATCATGGGATATGTTTTCTATGTG	CPj0865_B	CCGCTGCAGGTCGACGGATCTTAGCTACTAAATCGAATCG
CPj0866	CPj0866_F	AGGCCGAATTCCCGGGGATCATGAAAGTTATTTATTACGAAAT	CPj0866_B	CCGCTGCAGGTCGACGGATCTTAGATGTTCCCTCGATTCG
CPj0867	CPj0867_F	AGGCCGAATTCCCGGGGATCATGAGATATCATAAATATTTTCG	CPj0867_B	CCGCTGCAGGTCGACGGATCTTAGTACTTAGCAAAGCGAT
CPj0868	CPj0868_F	AGGCCGAATTCCCGGGGATCGTGTTCTCCCGTTTGTTTTT	CPj0868_B	CCGCTGCAGGTCGACGGATCCTAACTTTTCAGCAAACGGA
CPj0869	CPj0869_F	AGGCCGAATTCCCGGGGATCATGACTCAGGATCCACATGA	CPj0869_B	CCGCTGCAGGTCGACGGATCTTATAATAATTTCATTAATGATGA
CPj0870	CPj0870_F	AGGCCGAATTCCCGGGGATCATGTTGGATATAAAAATTATACG	CPj0870_B	CCGCTGCAGGTCGACGGATCTCACTGGTCTTTGGGAAGAA
CPj0871	CPj0871_F	AGGCCGAATTCCCGGGGATCATGGAAGATTTCTCTGAGCA	CPj0871_B	CCGCTGCAGGTCGACGGATCTCAATTCCTTATGGGCTCGA
CPj0872	CPj0872_F	AGGCCGAATTCCCGGGGATCATGATAGAAACTCGAGAAGA	CPj0872_B	CCGCTGCAGGTCGACGGATCTTATTGTACCCGATTGTTAC
CPj0873	CPj0873_F	AGGCCGAATTCCCGGGGATCATGAAAACATTGAAAGGACAT	CPj0873_B	CCGCTGCAGGTCGACGGATCCTAGATTTGAGTGAATAACG
CPj0874	CPj0874_F	AGGCCGAATTCCCGGGGATCATGTTAAAAATTCTTAAAATCAAA	CPj0874_B	CCGCTGCAGGTCGACGGATCCTACAGATTGATGCTGACAG
CPj0875	CPj0875_F	AGGCCGAATTCCCGGGGATCATGAAAAGAGTCATTTATAAAAC	CPj0875_B	CCGCTGCAGGTCGACGGATCTTAAGTTATCACTATATCCAC
CPj0876	CPj0876_F	AGGCCGAATTCCCGGGGATCATGTTATATTTTATAGAACAGC	CPj0876_B	CCGCTGCAGGTCGACGGATCTTAAGCATCTAGATTACGCA
CPj0877	CPj0877_F	AGGCCGAATTCCCGGGGATCATGCAATTATTGTCCCCAGC	CPj0877_B	CCGCTGCAGGTCGACGGATCCTAACTTTTCTCGTAAGTTC
CPj0878	CPj0878_F	AGGCCGAATTCCCGGGGATCATGTCCACGGTAACTACGGA	CPj0878_B	CCGCTGCAGGTCGACGGATCTTATTCCTCTTCAGGAATAAA
CPj0879	CPj0879_F	AGGCCGAATTCCCGGGGATCATGCAAGGTTTTTTCCCTTT	CPj0879_B	CCGCTGCAGGTCGACGGATCTTACCGTGGACATGCAACCT
CPj0880	CPj0880_F	AGGCCGAATTCCCGGGGATCATGATAAGAGAAAGAAAAAAGA	CPj0880_B	CCGCTGCAGGTCGACGGATCCTAACCTTCCAGAGGATTCT
CPj0883	CPj0883_F	AGGCCGAATTCCCGGGGATCATGACTTGGCCTTCAGGCCT	CPj0883_B	CCGCTGCAGGTCGACGGATCCTAGCTTCCAAAATCATCAA
CPj0884	CPj0884_F	AGGCCGAATTCCCGGGGATCATGCTTTCTCGTATAGTGAC	CPj0884_B	CCGCTGCAGGTCGACGGATCTTATGATTTGTTATCGTTAGG
CPj0885	CPj0885_F	AGGCCGAATTCCCGGGGATCATGTCTACCATGCAAAATTG	CPj0885_B	CCGCTGCAGGTCGACGGATCCTAGAGATCGATCTCTCTTT
CPj0886	CPj0886_F	AGGCCGAATTCCCGGGGATCATGGCGCTAAAAGATACGGC	CPj0886_B	CCGCTGCAGGTCGACGGATCTTATTTTCTAAATCCGCGTG
CPj0887	CPj0887_F	AGGCCGAATTCCCGGGGATCATGAAGAAGCTATATCACCC	CPj0887_B	CCGCTGCAGGTCGACGGATCTTACACACCGAGGAAACGCT
CPj0888	CPj0888_F	AGGCCGAATTCCCGGGGATCGTGAAGAGAGCAATCATTAT	CPj0888_B	CCGCTGCAGGTCGACGGATCCTACAGAGAACTCTGGGGTT
CPj0889	CPj0889_F	AGGCCGAATTCCCGGGGATCATGTTCAACGTCAACTTTAAA	CPj0889_B	CCGCTGCAGGTCGACGGATCTTATATAGAAGCTGAGAAACA
CPj0890	CPj0890_F	AGGCCGAATTCCCGGGGATCATGTCTGCTTTTTTTGATCTT	CPj0890_B	CCGCTGCAGGTCGACGGATCTTAAAGTTGACGTTGAACATA
CPj0891	CPj0891_F	AGGCCGAATTCCCGGGGATCATGGCAATGGATTTCAACCC	CPj0891_B	CCGCTGCAGGTCGACGGATCTTATGAAGCGTTGATTAAGAA
CPj0892	CPj0892_F	AGGCCGAATTCCCGGGGATCATGTTAAGCAATACTATTCGC	CPj0892_B	CCGCTGCAGGTCGACGGATCCTAAATTAACTGGGTTGAAAT
CPj0893	CPj0893_F	AGGCCGAATTCCCGGGGATCATGATCAATAAAGAATTAGATAT	CPj0893_B	CCGCTGCAGGTCGACGGATCCTATTGAGAGAGAATCCTCT
CPj0894	CPj0894_F	AGGCCGAATTCCCGGGGATCATGTTAGAACGTTATTCTGG	CPj0894_B	CCGCTGCAGGTCGACGGATCTCAATAGTCACTGTCGGAAG
CPj0895	CPj0895_F	AGGCCGAATTCCCGGGGATCATGGTTCGTGTAAGTACTAG	CPj0895_B	CCGCTGCAGGTCGACGGATCCTATTTAGAAACTCGGGATT
CPj0896	CPj0896_F	AGGCCGAATTCCCGGGGATCATGGAAGCTAAGAAAATCAAA	CPj0896_B	CCGCTGCAGGTCGACGGATCCTAAACACCTTCTTCTAAAAT
CPj0897	CPj0897_F	AGGCCGAATTCCCGGGGATCATGCAAGAAAAGCCCCGACA	CPj0897_B	CCGCTGCAGGTCGACGGATCCTATAACTTCTGACAGTCCC
CPj0898	CPj0898_F	AGGCCGAATTCCCGGGGATCATGTCCGAACAGGAAAAATT	CPj0898_B	CCGCTGCAGGTCGACGGATCTCAGAGCGTAGAAATCTCAT
CPj0899	CPj0899_F	AGGCCGAATTCCCGGGGATCATGCGAGCTATGTTGCTTGA	CPj0899_B	CCGCTGCAGGTCGACGGATCTTAAAAACAAGCTAATAAGGAT
CPj0900	CPj0900_F	AGGCCGAATTCCCGGGGATCATGATCCCCTTAATTCCAAT	CPj0900_B	CCGCTGCAGGTCGACGGATCCTATCTCCATAAGACAGCCG
CPj0901	CPj0901_F	AGGCCGAATTCCCGGGGATCATGTGTCAGCGCATTCTTAT	CPj0901_B	CCGCTGCAGGTCGACGGATCTTACCTCACTGCCTGCATTT
CPj0902	CPj0902_F	AGGCCGAATTCCCGGGGATCATGAATCGTAGAGACATGGT	CPj0902_B	CCGCTGCAGGTCGACGGATCTCAACGTATGCGCAACTGAT
CPj0903	CPj0903_F	AGGCCGAATTCCCGGGGATCATGAAATGGTTTGTTATTTCCT	CPj0903_B	CCGCTGCAGGTCGACGGATCTCACGAGAAAAAGCTTCCTT
CPj0904	CPj0904_F	AGGCCGAATTCCCGGGGATCATGATGAAGAAAATTCGAAAAG	CPj0904_B	CCGCTGCAGGTCGACGGATCCTATAAGCATTCACAAATGAA
CPj0905	CPj0905_F	AGGCCGAATTCCCGGGGATCATGAAGGGAACTCCTCAGTA	CPj0905_B	CCGCTGCAGGTCGACGGATCTTATCTTTTAACTAAATCTTGTT
CPj0906	CPj0906_F	AGGCCGAATTCCCGGGGATCATGGAAGAGTTTGTAGCATA	CPj0906_B	CCGCTGCAGGTCGACGGATCTTAATGGTGGTTACTACATTC
CPj0907	CPj0907_F	AGGCCGAATTCCCGGGGATCATGACTGCTGTTCTTATTCT	CPj0907_B	CCGCTGCAGGTCGACGGATCCTAATCTGAAAGCGGAGGCT
CPj0908	CPj0908_F	AGGCCGAATTCCCGGGGATCATGATAAGACGTTTTTTCAAAA	CPj0908_B	CCGCTGCAGGTCGACGGATCTCATAGAGCTTTTAATAATAAG
CPj0909	CPj0909_F	AGGCCGAATTCCCGGGGATCATGAATTTATCAGCTAAAGAAT	CPj0909_B	CCGCTGCAGGTCGACGGATCCTATAACTTACTTAAACATTCC
CPj0910	CPj0910_F	AGGCCGAATTCCCGGGGATCATGCTTCCTTTTGAATTCGA	CPj0910_B	CCGCTGCAGGTCGACGGATCTCAGCTGTACAGTAAGTAGT
CPj0911	CPj0911_F	AGGCCGAATTCCCGGGGATCATGAATTTATGTAAAAGAATTTC	CPj0911_B	CCGCTGCAGGTCGACGGATCCTAAAGACTACTTACTGTAC
CPj0912	CPj0912_F	AGGCCGAATTCCCGGGGATCATGGATAATTCAGACAACAG	CPj0912_B	CCGCTGCAGGTCGACGGATCTCATAGCAATTGCTGAATCT
CPj0913	CPj0913_F	AGGCCGAATTCCCGGGGATCATGAGAAGAAACTGTATATATG	CPj0913_B	CCGCTGCAGGTCGACGGATCCTATCGAATAATAGAAGGATG
CPj0914	CPj0914_F	AGGCCGAATTCCCGGGGATCTTGAATTTTGTATCGACTCTG	CPj0914_B	CCGCTGCAGGTCGACGGATCTTAAACGATATTCCAGTAATAT
CPj0915	CPj0915_F	AGGCCGAATTCCCGGGGATCATGGATTCATTTTGTTTTGATC	CPj0915_B	CCGCTGCAGGTCGACGGATCTTAAGAAGCTAAAAGCTTGG
CPj0916	CPj0916_F	AGGCCGAATTCCCGGGGATCATGAGTAAAAAACGCGTAGT	CPj0916_B	CCGCTGCAGGTCGACGGATCCTAGGGTACATACCTCGAGA
CPj0917	CPj0917_F	AGGCCGAATTCCCGGGGATCATGATGAAGACAAAATATGAGT	CPj0917_B	CCGCTGCAGGTCGACGGATCTCAAGAAGAGAAAAGATAGTT
CPj0918	CPj0918_F	AGGCCGAATTCCCGGGGATCATGTCTAAAAAACCATTATATGT	CPj0918_B	CCGCTGCAGGTCGACGGATCTTAATTCACTTCAGCAGTGT
CPj0919	CPj0919_F	AGGCCGAATTCCCGGGGATCATGAAATACTCACTGAACTTT	CPj0919_B	CCGCTGCAGGTCGACGGATCCTATGACGTATAGGCCAAGA
CPj0920	CPj0920_F	AGGCCGAATTCCCGGGGATCATGCACTCCGAGTTGCCTAA	CPj0920_B	CCGCTGCAGGTCGACGGATCTCATAGAGCAATAAGCTTATC
CPj0921	CPj0921_F	AGGCCGAATTCCCGGGGATCATGCTAATCAAGCTATGGCG	CPj0921_B	CCGCTGCAGGTCGACGGATCTTATGCGTAAGGAACTTCTA
CPj0922	CPj0922_F	AGGCCGAATTCCCGGGGATCATGCACGATCAACGGAATAG	CPj0922_B	CCGCTGCAGGTCGACGGATCTTACCCAAATAATGAAACAGC
CPj0923	CPj0923_F	AGGCCGAATTCCCGGGGATCTTGACTACCAGTGATGTTAT	CPj0923_B	CCGCTGCAGGTCGACGGATCTTAATGCTGGCAAAGCTCTC
CPj0924	CPj0924_F	AGGCCGAATTCCCGGGGATCATGGGCTATATTGAATCGTC	CPj0924_B	CCGCTGCAGGTCGACGGATCTTAGAAAAAAGTAGTCATAGG
CPj0925	CPj0925_F	AGGCCGAATTCCCGGGGATCATGGAAAACTCTCAAAATTTTC	CPj0925_B	CCGCTGCAGGTCGACGGATCCTACGATGACTTCGGCGTAT
CPj0926	CPj0926_F	AGGCCGAATTCCCGGGGATCATGAAATTTTGGTTGCAAGG	CPj0926_B	CCGCTGCAGGTCGACGGATCTTAACGTAGTTTAAGAGCAG
CPj0927	CPj0927_F	AGGCCGAATTCCCGGGGATCATGATCCCATCCCCTACCCC	CPj0927_B	CCGCTGCAGGTCGACGGATCTTAATCAGGTTGCTGAGACT
CPj0928	CPj0928_F	AGGCCGAATTCCCGGGGATCTTGAATCTTTCAAACAGGTC	CPj0928_B	CCGCTGCAGGTCGACGGATCTTAATTTTTTCTAGAGAGACTC
CPj0929	CPj0929_F	AGGCCGAATTCCCGGGGATCATGGCTCCAATTCACGGAAG	CPj0929_B	CCGCTGCAGGTCGACGGATCCTAAGAGAGCTTTTTCAAAAT
CPj0930	CPj0930_F	AGGCCGAATTCCCGGGGATCATGAGCGAGCTCGCCCCCT	CPj0930_B	CCGCTGCAGGTCGACGGATCTCAAAAAAGAGCTTGGCGGT
CPj0931	CPj0931_F	AGGCCGAATTCCCGGGGATCATGACGGCGAGAGCAGAATA	CPj0931_B	CCGCTGCAGGTCGACGGATCTTAATTCGTCTTCTCTGCAT

CPj0932	CPj0932_F	AGGCCGAATTCCCGGGGATCATGGCATTTTCTCATATCGA	CPj0932_B	CCGCTGCAGGTCGACGGATCTTAAAGGGGCTTAACTTTAG
CPj0933	CPj0933_F	AGGCCGAATTCCCGGGGATCGTGATCCTGTTACAAAATATC	CPj0933_B	CCGCTGCAGGTCGACGGATCCTACGACTGGTGGCGAATGT
CPj0934	CPj0934_F	AGGCCGAATTCCCGGGGATCGTGCACCCACTCACCTTACC	CPj0934_B	CCGCTGCAGGTCGACGGATCCTAACGAGGTGCGGTCACAC
CPj0935	CPj0935_F	AGGCCGAATTCCCGGGGATCGTGAAACGGACTTATCAACC	CPj0935_B	CCGCTGCAGGTCGACGGATCTTATAAATCGACTAGGGAATG
CPj0936	CPj0936_F	AGGCCGAATTCCCGGGGATCATGAAAGTTAGTTCATCTGTT	CPj0936_B	CCGCTGCAGGTCGACGGATCTTATTTTTTACGTGCAGGTC
CPj0937	CPj0937_F	AGGCCGAATTCCCGGGGATCATGGCGAAAAAATCATCAGT	CPj0937_B	CCGCTGCAGGTCGACGGATCCTACCAACTAGCCTTAATAA
CPj0938	CPj0938_F	AGGCCGAATTCCCGGGGATCATGCTCCCTATTTCGATTTT	CPj0938_B	CCGCTGCAGGTCGACGGATCTTATTTTGATGCTTCTTTCAAA
CPj0939	CPj0939_F	AGGCCGAATTCCCGGGGATCATGGAAAAACAAAATTTAAAATTA	CPj0939_B	CCGCTGCAGGTCGACGGATCCTACCCTTCAGAATTCTCAA
CPj0940	CPj0940_F	AGGCCGAATTCCCGGGGATCATGCGCATTGAGGATTTTTC	CPj0940_B	CCGCTGCAGGTCGACGGATCTTAATCAGATTTGTTGAAGTC
CPj0941	CPj0941_F	AGGCCGAATTCCCGGGGATCATGACGGAAAAAAAACCTAC	CPj0941_B	CCGCTGCAGGTCGACGGATCCTAGAATAATGTCAGTTGTTG
CPj0942	CPj0942_F	AGGCCGAATTCCCGGGGATCATGTATACGGAAGAGAGCTT	CPj0942_B	CCGCTGCAGGTCGACGGATCTTAAGGAATGAGCTCACTTT
CPj0943	CPj0943_F	AGGCCGAATTCCCGGGGATCATGAAATCTTTTAAGTTTTTGTT	CPj0943_B	CCGCTGCAGGTCGACGGATCTTACATCACCTCATTTTGTG
CPj0944	CPj0944_F	AGGCCGAATTCCCGGGGATCATGATGCACCGTTATTTTATT	CPj0944_B	CCGCTGCAGGTCGACGGATCCTAATTCTTTGTTTCTAAAGG
CPj0945	CPj0945_F	AGGCCGAATTCCCGGGGATCATGCGTATCGCACTATCTCT	CPj0945_B	CCGCTGCAGGTCGACGGATCTTATGCTATAGCTGGATCTT
CPj0946	CPj0946_F	AGGCCGAATTCCCGGGGATCATGATTGCGACTATCTTACG	CPj0946_B	CCGCTGCAGGTCGACGGATCTTATACAGCTACAGATTCCC
CPj0947	CPj0947_F	AGGCCGAATTCCCGGGGATCGTGGGGCTACCTAATTACAT	CPj0947_B	CCGCTGCAGGTCGACGGATCTCAATCTTTACTCTCATGATT
CPj0948	CPj0948_F	AGGCCGAATTCCCGGGGATCATGAGAATCGTACAAGTCGC	CPj0948_B	CCGCTGCAGGTCGACGGATCTCATGAGAGTAAAGATTGATA
CPj0949	CPj0949_F	AGGCCGAATTCCCGGGGATCATGGAGCTTGTAGTTACAAG	CPj0949_B	CCGCTGCAGGTCGACGGATCTTATCTTCTAGAGACGGTTA
CPj0950	CPj0950_F	AGGCCGAATTCCCGGGGATCATGGCTAAGCTCATTGTAGC	CPj0950_B	CCGCTGCAGGTCGACGGATCTTAAAATTTCGAACACCACTC
CPj0951	CPj0951_F	AGGCCGAATTCCCGGGGATCATGGGAAAAAAAGAAAATCAAC	CPj0951_B	CCGCTGCAGGTCGACGGATCTTATTCGGGTAGAGAGGCGA
CPj0952	CPj0952_F	AGGCCGAATTCCCGGGGATCATGAATAAGCCTGTTCATAAT	CPj0952_B	CCGCTGCAGGTCGACGGATCTTAATCTTCTCCAACAAAAGG
CPj0953	CPj0953_F	AGGCCGAATTCCCGGGGATCATGAAACAACAGCTACTTTTA	CPj0953_B	CCGCTGCAGGTCGACGGATCTTAGCCTTCTTGATTTTCCT
CPj0954	CPj0954_F	AGGCCGAATTCCCGGGGATCATGCAATACTTTTCTCCCGC	CPj0954_B	CCGCTGCAGGTCGACGGATCCTAATGCTGTTCCTGAAGAA
CPj0956	CPj0956_F	AGGCCGAATTCCCGGGGATCATGATCCTGCCTCCATACTC	CPj0956_B	CCGCTGCAGGTCGACGGATCTTACCTGAAAAAACAGTAGAG
CPj0957	CPj0957_F	AGGCCGAATTCCCGGGGATCATGTTTTGGAAACTTTTATGTC	CPj0957_B	CCGCTGCAGGTCGACGGATCTTAAGAGGTCTTCTGAGTGC
CPj0958	CPj0958_F	AGGCCGAATTCCCGGGGATCATGCAGTTTTCTAGGTATTTA	CPj0958_B	CCGCTGCAGGTCGACGGATCTTACAATTCCTCGTATAGATT
CPj0959	CPj0959_F	AGGCCGAATTCCCGGGGATCATGGAAAATGAAATTTTACTCAA	CPj0959_B	CCGCTGCAGGTCGACGGATCCTATAAATCTATACTTTCCCC
CPj0961	CPj0961_F	AGGCCGAATTCCCGGGGATCATGGCGGTACCACGCAATCG	CPj0961_B	CCGCTGCAGGTCGACGGATCTTATTTCTTTTCTACAGTCATA
CPj0962	CPj0962_F	AGGCCGAATTCCCGGGGATCATGGAAGTGCAAATTGGCAT	CPj0962_B	CCGCTGCAGGTCGACGGATCCTAAATCAAATTAGACAAAATG
CPj0963	CPj0963_F	AGGCCGAATTCCCGGGGATCATGGTAGCGAAAAAAACAGT	CPj0963_B	CCGCTGCAGGTCGACGGATCCTAGAAAATAATACGGATACC
CPj0964	CPj0964_F	AGGCCGAATTCCCGGGGATCATGCATATGTCTAACCCCAT	CPj0964_B	CCGCTGCAGGTCGACGGATCTTATAGTTCGATGATCTTTAAT
CPj0965	CPj0965_F	AGGCCGAATTCCCGGGGATCATGATCCCTTCTGGCCTAGT	CPj0965_B	CCGCTGCAGGTCGACGGATCTCATACAGCGGGAAGTGTGT
CPj0966	CPj0966_F	AGGCCGAATTCCCGGGGATCATGGTCTGCGAAAACAATAT	CPj0966_B	CCGCTGCAGGTCGACGGATCCTACTTTTGAGAATGAGAATC
CPj0967	CPj0967_F	AGGCCGAATTCCCGGGGATCATGCAACAAAGTGTCAGAAA	CPj0967_B	CCGCTGCAGGTCGACGGATCCTACTCTCTACTACCTGTAC
CPj0968	CPj0968_F	AGGCCGAATTCCCGGGGATCATGTGCGGGATATTTGGATA	CPj0968_B	CCGCTGCAGGTCGACGGATCTTACTCTACAGTAACAGACT
CPj0969	CPj0969_F	AGGCCGAATTCCCGGGGATCATGTCAAATAAAGTTCTAGGT	CPj0969_B	CCGCTGCAGGTCGACGGATCTTAAAGCTCATGATAAATGCT
CPj0970	CPj0970_F	AGGCCGAATTCCCGGGGATCATGGGACTATATGATCGTGA	CPj0970_B	CCGCTGCAGGTCGACGGATCTTAGTCTCGGTTTCCTGAAG
CPj0971	CPj0971_F	AGGCCGAATTCCCGGGGATCATGTTCAAATTCTTTAGAAACAA	CPj0971_B	CCGCTGCAGGTCGACGGATCTTAGATCTTTTCTACTTCAGG
CPj0972	CPj0972_F	AGGCCGAATTCCCGGGGATCATGCATCTTCATGAGTACCA	CPj0972_B	CCGCTGCAGGTCGACGGATCCTACATACTCAGTTCTACAG
CPj0973	CPj0973_F	AGGCCGAATTCCCGGGGATCATGTTCCACTCACTAAGTAA	CPj0973_B	CCGCTGCAGGTCGACGGATCTTAGAGTTCTTTTGCCCGTA
CPj0975	CPj0975_F	AGGCCGAATTCCCGGGGATCTTGTTCCCATTAGTTTTACTC	CPj0975_B	CCGCTGCAGGTCGACGGATCCTAGAACAGTTCGATTTGTG
CPj0976	CPj0976_F	AGGCCGAATTCCCGGGGATCTTGATGCTTGTCTATTGTTTT	CPj0976_B	CCGCTGCAGGTCGACGGATCTTAAAAATATACGGAACTCGC
CPj0977	CPj0977_F	AGGCCGAATTCCCGGGGATCATGGAAGTTTATAGTTTTTCC	CPj0977_B	CCGCTGCAGGTCGACGGATCTCATTTTTGATTCCTTAAGAAG
CPj0978	CPj0978_F	AGGCCGAATTCCCGGGGATCATGATAACTAAGCAATTGCG	CPj0978_B	CCGCTGCAGGTCGACGGATCTTATTCTTCAGGTTTCAGGG
CPj0980	CPj0980_F	AGGCCGAATTCCCGGGGATCATGAATCTAGATTCGAAACAT	CPj0980_B	CCGCTGCAGGTCGACGGATCTCACTCTTTTATTTTAGGAAG
CPj0981	CPj0981_F	AGGCCGAATTCCCGGGGATCATGAAAGCTGGTGATACGTA	CPj0981_B	CCGCTGCAGGTCGACGGATCTCAAATTGCTGGTACTATGG
CPj0982	CPj0982_F	AGGCCGAATTCCCGGGGATCATGAACCTCCCTGTTTCCCT	CPj0982_B	CCGCTGCAGGTCGACGGATCTTAGTCTTGTTTTTCTAAAGAC
CPj0983	CPj0983_F	AGGCCGAATTCCCGGGGATCATGGCGGGATTAGATCTAGA	CPj0983_B	CCGCTGCAGGTCGACGGATCCTAGCTCTTTTTTCTATAGAT
CPj0984	CPj0984_F	AGGCCGAATTCCCGGGGATCATGGTCGAAGTTGAAGAAAA	CPj0984_B	CCGCTGCAGGTCGACGGATCTTATTGACAAGATTCGCAAC
CPj0985	CPj0985_F	AGGCCGAATTCCCGGGGATCATGGAAGCAGATATTTTAGAT	CPj0985_B	CCGCTGCAGGTCGACGGATCTTACCAACTTAAATTACCAGC
CPj0987	CPj0987_F	AGGCCGAATTCCCGGGGATCATGTTTGCATATCGTACCCT	CPj0987_B	CCGCTGCAGGTCGACGGATCTTATCCCTTATCAACCGAAG
CPj0988	CPj0988_F	AGGCCGAATTCCCGGGGATCATGAAAGAAGCTGCGCCTAT	CPj0988_B	CCGCTGCAGGTCGACGGATCTTATTTTTCAGAGACAGGGG
CPj0989	CPj0989_F	AGGCCGAATTCCCGGGGATCATGGCCACATTGAGTCCTGA	CPj0989_B	CCGCTGCAGGTCGACGGATCTCAGATTGATAAAGAATTTTCA
CPj0990	CPj0990_F	AGGCCGAATTCCCGGGGATCGTGGCATTAAATTTTAAGATTA	CPj0990_B	CCGCTGCAGGTCGACGGATCTTATTGGTTTTCATCTTGGG
CPj0991	CPj0991_F	AGGCCGAATTCCCGGGGATCATGCCCAAGATGAAAACCAA	CPj0991_B	CCGCTGCAGGTCGACGGATCTTAAACAAGCATCATTCGCT
CPj0992	CPj0992_F	AGGCCGAATTCCCGGGGATCATGGTAAGAGCAACAGGTTC	CPj0992_B	CCGCTGCAGGTCGACGGATCCTAAACTGTGGCTTCCAAAG
CPj0993	CPj0993_F	AGGCCGAATTCCCGGGGATCATGGAAATGAAAGAAGAGATT	CPj0993_B	CCGCTGCAGGTCGACGGATCTTAAGAGAATTGTTGTAAAAAC
CPj0994	CPj0994_F	AGGCCGAATTCCCGGGGATCATGAAAAGGTCTCGACGTAA	CPj0994_B	CCGCTGCAGGTCGACGGATCTTACAAATTATGCTTATGCGA
CPj0995	CPj0995_F	AGGCCGAATTCCCGGGGATCATGTTGATTTGGAAACGCCA	CPj0995_B	CCGCTGCAGGTCGACGGATCTCACTGAAGTTTCGCATAAG
CPj0996	CPj0996_F	AGGCCGAATTCCCGGGGATCATGCCTATTTTATGGAAAGTT	CPj0996_B	CCGCTGCAGGTCGACGGATCTTAAGCATACCCTCGACTTT
CPj0997	CPj0997_F	AGGCCGAATTCCCGGGGATCATGGTACTAAGCTCAGATTT	CPj0997_B	CCGCTGCAGGTCGACGGATCCTAATCTATCACTACTACTC
CPj0998	CPj0998_F	AGGCCGAATTCCCGGGGATCATGTCGAAAGATAAGAAAATGA	CPj0998_B	CCGCTGCAGGTCGACGGATCCTACGTAGCATTAAACCCCA
CPj0999	CPj0999_F	AGGCCGAATTCCCGGGGATCATGAATTTTCAAACTATTTCTAT	CPj0999_B	CCGCTGCAGGTCGACGGATCTTATTCTAGAGTTGCTTTATG
CPj1000	CPj1000_F	AGGCCGAATTCCCGGGGATCATGTCTTTGGATAAAGGAAC	CPj1000_B	CCGCTGCAGGTCGACGGATCCTACTTACGTAGATTCAATC
CPj1001	CPj1001_F	AGGCCGAATTCCCGGGGATCATCAATATGGAAAAAGATATTTT	CPj1001_B	CCGCTGCAGGTCGACGGATCTTATTTTTCACTTTTCTCTCTG

CPj1002	CPj1002_F	AGGCCGAATTCCCGGGGATCGTGAAAAATAAAATTGTTACATT	CPj1002_B	CCGCTGCAGGTCGACGGATCCTAGTTCTCTTGAGAGAGCG
CPj1003	CPj1003_F	AGGCCGAATTCCCGGGGATCATGAGGGTGATTTTCCCCGA	CPj1003_B	CCGCTGCAGGTCGACGGATCCTAGAATCTCAAAGAAGTAG
CPj1004	CPj1004_F	AGGCCGAATTCCCGGGGATCATGTCGATACAACCCGTCTC	CPj1004_B	CCGCTGCAGGTCGACGGATCTTAGTCAGAGGGTGAGTTCG
CPj1005	CPj1005_F	AGGCCGAATTCCCGGGGATCATGTGGATCATAGACCCTCT	CPj1005_B	CCGCTGCAGGTCGACGGATCTTAGATGTTAGCAATTAGGC
CPj1006	CPj1006_F	AGGCCGAATTCCCGGGGATCATGTCTATAACCACCTTAGG	CPj1006_B	CCGCTGCAGGTCGACGGATCTTATCCTAGGGGTTTATTCA
CPj1007	CPj1007_F	AGGCCGAATTCCCGGGGATCGTGTCTGGGAATGAGTGCAA	CPj1007_B	CCGCTGCAGGTCGACGGATCTTAAGACTCATCTAAAGAGTC
CPj1008	CPj1008_F	AGGCCGAATTCCCGGGGATCATGTTGAAACCGATGTACGT	CPj1008_B	CCGCTGCAGGTCGACGGATCTTACAGAGACAGGCTACGAG
CPj1009	CPj1009_F	AGGCCGAATTCCCGGGGATCATGAAAAGAAACGACCCTTG	CPj1009_B	CCGCTGCAGGTCGACGGATCTCAGTCATTTAGAAGAGTTAG
CPj1010	CPj1010_F	AGGCCGAATTCCCGGGGATCATGCTCATCTTACTCAATCT	CPj1010_B	CCGCTGCAGGTCGACGGATCTCACCCGATGTAAAAGCCTA
CPj1012	CPj1012_F	AGGCCGAATTCCCGGGGATCATGAAAAAAAAATTTATTTTCTAC	CPj1012_B	CCGCTGCAGGTCGACGGATCTTACACACTCTGTTCTTCTG
CPj1013	CPj1013_F	AGGCCGAATTCCCGGGGATCATGCGACAAGAAAAGGATAG	CPj1013_B	CCGCTGCAGGTCGACGGATCCTAATGGTTTCCCACCATAT
CPj1014	CPj1014_F	AGGCCGAATTCCCGGGGATCGTGAAAGTCCCTTGGGCATT	CPj1014_B	CCGCTGCAGGTCGACGGATCTTAGACTAAATGACGAGTTG
CPj1015	CPj1015_F	AGGCCGAATTCCCGGGGATCATGCTGAAACTACAATTGTG	CPj1015_B	CCGCTGCAGGTCGACGGATCTTAAATGAAAAAATTGAGGCTC
CPj1016	CPj1016_F	AGGCCGAATTCCCGGGGATCATGAAAAAAGGGAAATTAGGA	CPj1016_B	CCGCTGCAGGTCGACGGATCTTACAAAGCAGAAGTCGTTG
CPj1017	CPj1017_F	AGGCCGAATTCCCGGGGATCATGAGAAAACTTATTTTATGCAA	CPj1017_B	CCGCTGCAGGTCGACGGATCCTAAGAACAACGGAGTTCTT
CPj1018	CPj1018_F	AGGCCGAATTCCCGGGGATCATGTCGTATTTCAATTACCAA	CPj1018_B	CCGCTGCAGGTCGACGGATCTTAAGAGCCTTTTCGAATATT
CPj1019	CPj1019_F	AGGCCGAATTCCCGGGGATCATGACTGTATCTTACCAATC	CPj1019_B	CCGCTGCAGGTCGACGGATCCTACTGATACAGACTGCGAG
CPj1020	CPj1020_F	AGGCCGAATTCCCGGGGATCATGTCCTCTTGGTTATCTCA	CPj1020_B	CCGCTGCAGGTCGACGGATCTTATCCTCTTAAGGAGTGGA
CPj1021	CPj1021_F	AGGCCGAATTCCCGGGGATCATGTCACATTTAAATTATTTACT	CPj1021_B	CCGCTGCAGGTCGACGGATCTTATTTATGTTTTCGAATATCTA
CPj1022	CPj1022_F	AGGCCGAATTCCCGGGGATCATGAATATGCCTGTTCCTTC	CPj1022_B	CCGCTGCAGGTCGACGGATCTTAGGGGCGTAGGTTGTAAA
CPj1023	CPj1023_F	AGGCCGAATTCCCGGGGATCATGAAGAAAGTCGTAACACT	CPj1023_B	CCGCTGCAGGTCGACGGATCCTAATCGCATTCATAAAAAATT
CPj1024	CPj1024_F	AGGCCGAATTCCCGGGGATCATGCCCTCGACTCAGTTTCA	CPj1024_B	CCGCTGCAGGTCGACGGATCTTAGAGATTCCTGGGGTGAT
CPj1025	CPj1025_F	AGGCCGAATTCCCGGGGATCATGGAAAGAAAAAGATTTATAGA	CPj1025_B	CCGCTGCAGGTCGACGGATCTTACCTAAACTTGATGTTAAAA
CPj1026	CPj1026_F	AGGCCGAATTCCCGGGGATCATGTTTTTCATTGCAGTACG	CPj1026_B	CCGCTGCAGGTCGACGGATCTTACGAAACCAGGCTGTAGA
CPj1027	CPj1027_F	AGGCCGAATTCCCGGGGATCATGCCAGGTTCTGTGTCATC	CPj1027_B	CCGCTGCAGGTCGACGGATCTTAAAGAGGTCCCTTAGGGA
CPj1028	CPj1028_F	AGGCCGAATTCCCGGGGATCATGGCATTCAAAGAGGTCGT	CPj1028_B	CCGCTGCAGGTCGACGGATCTTATAACGAAGACACGCTAG
CPj1029	CPj1029_F	AGGCCGAATTCCCGGGGATCATGAGACAATCATTCGATGA	CPj1029_B	CCGCTGCAGGTCGACGGATCCTATTTAACAAGGGCTTTCT
CPj1030	CPj1030_F	AGGCCGAATTCCCGGGGATCATGCGTATAGCCGTTTTAGG	CPj1030_B	CCGCTGCAGGTCGACGGATCTTAAATAGTAAATAGAAATTCTTT
CPj1031	CPj1031_F	AGGCCGAATTCCCGGGGATCATGACCTCAAGGACTAAATC	CPj1031_B	CCGCTGCAGGTCGACGGATCTCAACCTGTTGAGAATAGGA
CPj1032	CPj1032_F	AGGCCGAATTCCCGGGGATCATGGCTTACGGAACTCGTTA	CPj1032_B	CCGCTGCAGGTCGACGGATCTTAATTTACCTTAGCTGGTTC
CPj1033	CPj1033_F	AGGCCGAATTCCCGGGGATCATGATATCCTTTCGTTTTCTT	CPj1033_B	CCGCTGCAGGTCGACGGATCTTATAAGGAAAGATTTGCACG
CPj1034	CPj1034_F	AGGCCGAATTCCCGGGGATCATGAAAACCTGGTTGTTCTT	CPj1034_B	CCGCTGCAGGTCGACGGATCTTATTCGTGCATTTGGTGGC
CPj1035	CPj1035_F	AGGCCGAATTCCCGGGGATCATGTTATGCGCCACTGTTAG	CPj1035_B	CCGCTGCAGGTCGACGGATCTTATACTTTTGCCATGAAGTT
CPj1036	CPj1036_F	AGGCCGAATTCCCGGGGATCATGCTCCAAACTATGATGTC	CPj1036_B	CCGCTGCAGGTCGACGGATCCTAACAGTGGCGCATAACAT
CPj1037	CPj1037_F	AGGCCGAATTCCCGGGGATCATGAAAAATAGCTTTGGCTC	CPj1037_B	CCGCTGCAGGTCGACGGATCTCATAGTTTGGAGCATCGTT
CPj1038	CPj1038_F	AGGCCGAATTCCCGGGGATCATGACAATTATTCTATGTGGT	CPj1038_B	CCGCTGCAGGTCGACGGATCTCATGACTTTAACAAGGTAAT
CPj1039	CPj1039_F	AGGCCGAATTCCCGGGGATCATGCTTACTTATAAAGTTTCAC	CPj1039_B	CCGCTGCAGGTCGACGGATCTTAGCCAAAGCTTTCCCGAG
CPj1040	CPj1040_F	AGGCCGAATTCCCGGGGATCATGTCTACAACCACAGTAAA	CPj1040_B	CCGCTGCAGGTCGACGGATCCTAGAACTTTGTAAAAGTCG
CPj1041	CPj1041_F	AGGCCGAATTCCCGGGGATCATGGACAAGCAATCATCAGG	CPj1041_B	CCGCTGCAGGTCGACGGATCTTACTGTGGTTGTAGACATA
CPj1042	CPj1042_F	AGGCCGAATTCCCGGGGATCATGCAACGTATCATCATTGT	CPj1042_B	CCGCTGCAGGTCGACGGATCCTAATGCAGATTGAGTGAAG
CPj1043	CPj1043_F	AGGCCGAATTCCCGGGGATCATGTTATGCCAACAATTCCT	CPj1043_B	CCGCTGCAGGTCGACGGATCCTACAATGATGATACGTTGC
CPj1044	CPj1044_F	AGGCCGAATTCCCGGGGATCATGCGTGAAGAAACTGTATC	CPj1044_B	CCGCTGCAGGTCGACGGATCTTAGGAATTGTTGGCATAAC
CPj1045	CPj1045_F	AGGCCGAATTCCCGGGGATCATGAATACATCCCACAGAAA	CPj1045_B	CCGCTGCAGGTCGACGGATCCTAAGGTTGATTTATCAGAG
CPj1046	CPj1046_F	AGGCCGAATTCCCGGGGATCGTGCACTACTGCGAGAGAAC	CPj1046_B	CCGCTGCAGGTCGACGGATCTCATTGGCAAAGTACCTCAA
CPj1047	CPj1047_F	AGGCCGAATTCCCGGGGATCATGCACGTTGGAGTGATTGG	CPj1047_B	CCGCTGCAGGTCGACGGATCTTAATGATCCGTTGTCTTTTT
CPj1048	CPj1048_F	AGGCCGAATTCCCGGGGATCATGCGAATCGCTGTTTTAGG	CPj1048_B	CCGCTGCAGGTCGACGGATCCTATCTTAGACACATTTCCC
CPj1049	CPj1049_F	AGGCCGAATTCCCGGGGATCGTGTCTAAGATAGTTTATAAAT	CPj1049_B	CCGCTGCAGGTCGACGGATCCTACGTGGCGACTATAGCTT
CPj1050	CPj1050_F	AGGCCGAATTCCCGGGGATCATGCATTTACTTACAGCAAC	CPj1050_B	CCGCTGCAGGTCGACGGATCTTAAGAATAGGAGAACACAG
CPj1051	CPj1051_F	AGGCCGAATTCCCGGGGATCATGACTCCGAAATCGATTCA	CPj1051_B	CCGCTGCAGGTCGACGGATCTTATTTATTTTTTCTTATAATCCG
CPj1052	CPj1052_F	AGGCCGAATTCCCGGGGATCATGAAATATAATTCAAGAGAAAA	CPj1052_B	CCGCTGCAGGTCGACGGATCTCAATCTTTGCAAAATTCAAG
CPj1053	CPj1053_F	AGGCCGAATTCCCGGGGATCTTGAATTTTGCAAAGATTGATC	CPj1053_B	CCGCTGCAGGTCGACGGATCTTAGAATGCAGACTTGACGC
CPj1055	CPj1055_F	AGGCCGAATTCCCGGGGATCGTGCTTTTCTTGATTTCAGG	CPj1055_B	CCGCTGCAGGTCGACGGATCCTATCTCCTCAACTCGAGAT
CPj1056	CPj1056_F	AGGCCGAATTCCCGGGGATCATGATGCTTCGTGTCATAGA	CPj1056_B	CCGCTGCAGGTCGACGGATCTCACGATTTTAATCGAATGAA
CPj1057	CPj1057_F	AGGCCGAATTCCCGGGGATCATGCCTGAGCCTCTATATAC	CPj1057_B	CCGCTGCAGGTCGACGGATCCTATAGAGAGATTAGATAACG
CPj1058	CPj1058_F	AGGCCGAATTCCCGGGGATCATGAAATTATATCAGACCTTG	CPj1058_B	CCGCTGCAGGTCGACGGATCCTATAATAAGGAAAATAGAGG
CPj1059	CPj1059_F	AGGCCGAATTCCCGGGGATCGTGACAAGAAGTTCTCCTGC	CPj1059_B	CCGCTGCAGGTCGACGGATCTTAACCCGCTTGCATCTTAT
CPj1060	CPj1060_F	AGGCCGAATTCCCGGGGATCATGACTTCGTCTTCTTGCCC	CPj1060_B	CCGCTGCAGGTCGACGGATCTTAAACTCTGACGTCTCCAA
CPj1061	CPj1061_F	AGGCCGAATTCCCGGGGATCATGGTAGAAATCCATCACAA	CPj1061_B	CCGCTGCAGGTCGACGGATCTTAGTGATGTGGATGTATAG
CPj1062	CPj1062_F	AGGCCGAATTCCCGGGGATCATGTCATCGCCTCCACAGGC	CPj1062_B	CCGCTGCAGGTCGACGGATCTTAGCCTTTTATAAGTTTACAA
CPj1063	CPj1063_F	AGGCCGAATTCCCGGGGATCATGACAAGGCAGAGTTATGT	CPj1063_B	CCGCTGCAGGTCGACGGATCTTATACATTAAAATTTTTAGCGA
CPj1064	CPj1064_F	AGGCCGAATTCCCGGGGATCATGAGATTTTTTTGTCTATTTTT	CPj1064_B	CCGCTGCAGGTCGACGGATCCTAAGCGTCCACTACCTTTT
CPj1065	CPj1065_F	AGGCCGAATTCCCGGGGATCTTGTTCTACTTCTCAATACC	CPj1065_B	CCGCTGCAGGTCGACGGATCCTAAGGAAGTCCTGTATTGA
CPj1066	CPj1066_F	AGGCCGAATTCCCGGGGATCATGACAGTGTTGTTTTACGC	CPj1066_B	CCGCTGCAGGTCGACGGATCCTAGGATTCATCTGCTTCAA
CPj1067	CPj1067_F	AGGCCGAATTCCCGGGGATCATGATTAGACGTTTAGAATATT	CPj1067_B	CCGCTGCAGGTCGACGGATCTTAAGAAACTAGTTCTTCTTTA
CPj1068	CPj1068_F	AGGCCGAATTCCCGGGGATCATGCCGCCACCATTTGTTGT	CPj1068_B	CCGCTGCAGGTCGACGGATCTTATTTCCCCGAACAAATTTC

CPj1069	CPj1069_F	AGGCCGAATTCCCGGGGATCATGCAAGAACACATACATAAA	CPj1069_B	CCGCTGCAGGTCGACGGATCTTAAAAAATAGAAAACAACGATC
CPj1070	CPj1070_F	AGGCCGAATTCCCGGGGATCATGACATTTCCATGTGGAAA	CPj1070_B	CCGCTGCAGGTCGACGGATCTCACAGCCATCGGTTCGGTC
CPj1071	CPj1071_F	AGGCCGAATTCCCGGGGATCATGGTTTGCCCAAATAATTC	CPj1071_B	CCGCTGCAGGTCGACGGATCTTATTCTTTGTTTATTTTTATCC
CPj1072	CPj1072_F	AGGCCGAATTCCCGGGGATCATGTTGAAAATCCAGAAAAAAA	CPj1072_B	CCGCTGCAGGTCGACGGATCTTAATTCATTTTCGGAAGAGC
CPj1073	CPj1073_F	AGGCCGAATTCCCGGGGATCATGAGACGTTATCTTTTCATG	CPj1073_B	CCGCTGCAGGTCGACGGATCCTACCCTTTGCTCTTTACAT
CPJ_RS05595	CPJ_RS05595_F	AGGCCGAATTCCCGGGGATCCTGAAAAATTTTAAGTTTAAAAG	CPJ_RS05595_B	CCGCTGCAGGTCGACGGATCCTAGGAATGGTCCTCGCGAG
CPJ_RS00515	CPJ_RS00515_F	AGGCCGAATTCCCGGGGATCGTGGGCAAAAAATTCCATCA	CPJ_RS00515_B	CCGCTGCAGGTCGACGGATCTCAGGGCCCCTTCGACTTCA
CPJ_RS05590	CPJ_RS05590_F	AGGCCGAATTCCCGGGGATCGTGCTCGTTGGTATCTGTCC	CPJ_RS05590_B	CCGCTGCAGGTCGACGGATCCTAAAAAATACCTACCGTTC
CPJ_RS01765	CPJ_RS01765_F	AGGCCGAATTCCCGGGGATCATGAAAATCTGCTCTCTGAA	CPJ_RS01765_B	CCGCTGCAGGTCGACGGATCTTAGATAATTTGCTCAGAAAC
CPJ_RS00895	CPJ_RS00895_F	AGGCCGAATTCCCGGGGATCATGGAAGAAGCCTTAACTTT	CPJ_RS00895_B	CCGCTGCAGGTCGACGGATCTTAATAATTTAAGGTTGGTTGA
CPJ_RS01245	CPJ_RS01245_F	AGGCCGAATTCCCGGGGATCATGGCAACACTGATAAATTTC	CPJ_RS01245_B	CCGCTGCAGGTCGACGGATCTTAGAGGATGTCCATTTTATA
CPJ_RS04280	CPJ_RS04280_F	AGGCCGAATTCCCGGGGATCATGTTGCTCACTTCGTATCT	CPJ_RS04280_B	CCGCTGCAGGTCGACGGATCTTATTTAAAGCTGATCATAAGC
CPJ_RS05245	CPJ_RS05245_F	AGGCCGAATTCCCGGGGATCATGATACAGTTTTCTTTTTTCTT	CPJ_RS05245_B	CCGCTGCAGGTCGACGGATCCTATAAAAATGCTTGTTGTAAT
CPJ_RS05585	CPJ_RS05585_F	AGGCCGAATTCCCGGGGATCATGCCCGTTCCTATAGATAA	CPJ_RS05585_B	CCGCTGCAGGTCGACGGATCTTACCAAAAAAATATTGGATTAA
CPJ_RS04255	CPJ_RS04255_F	AGGCCGAATTCCCGGGGATCATGTGTAACTCTATAGCTATG	CPJ_RS04255_B	CCGCTGCAGGTCGACGGATCTTATTTCCCAACCGCAAATT
CPJ_RS00980	CPJ_RS00980_F	AGGCCGAATTCCCGGGGATCATGAAACGAAGATCATGGCT	CPJ_RS00980_B	CCGCTGCAGGTCGACGGATCTCAGAACACGCTTTTCGTCA
CPJ_RS04370	CPJ_RS04370_F	AGGCCGAATTCCCGGGGATCATGAACTATGACCAATACGA	CPJ_RS04370_B	CCGCTGCAGGTCGACGGATCTTAAATAAATGGGGTCCATTC
CPJ_RS04995	CPJ_RS04995_F	AGGCCGAATTCCCGGGGATCATGGACTGTGTCGATAATTT	CPJ_RS04995_B	CCGCTGCAGGTCGACGGATCTTATAAATACTCAAAGGGATTA
CPJ_RS01310	CPJ_RS01310_F	AGGCCGAATTCCCGGGGATCGTGATCAATTCCGCTATTTA	CPJ_RS01310_B	CCGCTGCAGGTCGACGGATCTTAGTTACCAAAAGGCAAAG
CPJ_RS00935	CPJ_RS00935_F	AGGCCGAATTCCCGGGGATCATGAATGGCTTATCTAATCC	CPJ_RS00935_B	CCGCTGCAGGTCGACGGATCTTAAGAGGATCGCTTTTTTTTC
CPJ_RS01870	CPJ_RS01870_F	AGGCCGAATTCCCGGGGATCATGTCTACATCTCCAATTGG	CPJ_RS01870_B	CCGCTGCAGGTCGACGGATCTCACTCTAAAGCATTGCTTA
CPJ_RS00520	CPJ_RS00520_F	AGGCCGAATTCCCGGGGATCATGTGCTTAATAGATTGCTTG	CPJ_RS00520_B	CCGCTGCAGGTCGACGGATCCTATCTCAAGATTTCTCGTT
CPJ_RS00355	CPJ_RS00355_F	AGGCCGAATTCCCGGGGATCATGCTTGCTGTTTCATCAAA	CPJ_RS00355_B	CCGCTGCAGGTCGACGGATCCTACTCATATTTAATCTTGGT
CPJ_RS00070	CPJ_RS00070_F	AGGCCGAATTCCCGGGGATCATGTATTCTCCAGATGTTTG	CPJ_RS00070_B	CCGCTGCAGGTCGACGGATCCTAAAATTTGATTTTGCTACC
CPJ_RS05510	CPJ_RS05510_F	AGGCCGAATTCCCGGGGATCATGGAAGAGGTCCCCTTCGA	CPJ_RS05510_B	CCGCTGCAGGTCGACGGATCCTACCGAACTACAGCTTGTT
CPJ_RS01340	CPJ_RS01340_F	AGGCCGAATTCCCGGGGATCATGTTGTGCGGGAGCACAGT	CPJ_RS01340_B	CCGCTGCAGGTCGACGGATCCTACACCTTATCCCCCGCAA
CPJ_RS04970	CPJ_RS04970_F	AGGCCGAATTCCCGGGGATCATGTCTTACAAGATTACACTT	CPJ_RS04970_B	CCGCTGCAGGTCGACGGATCCTACTTACAAAAACAGCCCG
CPJ_RS04360	CPJ_RS04360_F	AGGCCGAATTCCCGGGGATCATGCTCTGCTTGCCGCTTAA	CPJ_RS04360_B	CCGCTGCAGGTCGACGGATCCTAACATATGTCGTTTAATTCA
CPJ_RS04610	CPJ_RS04610_F	AGGCCGAATTCCCGGGGATCTTGGAAAAAGCAAAAAACTTTA	CPJ_RS04610_B	CCGCTGCAGGTCGACGGATCTTATAGCAGACATTTCTCGA
CPJ_RS01805	CPJ_RS01805_F	AGGCCGAATTCCCGGGGATCATGAAAAAGCAAAGTACCAG	CPJ_RS01805_B	CCGCTGCAGGTCGACGGATCTTAACAAAATTCAAAACATAAAAA
CPJ_RS03530	CPJ_RS03530_F	AGGCCGAATTCCCGGGGATCGTGATGTTTGACTTTATGTTA	CPJ_RS03530_B	CCGCTGCAGGTCGACGGATCTCAGTGAGAGTCTATCTTAA
CPJ_RS03095	CPJ_RS03095_F	AGGCCGAATTCCCGGGGATCATGAAAAAATTAATGTTAGCCC	CPJ_RS03095_B	CCGCTGCAGGTCGACGGATCCTATTCAGCAGTATTCTCTT
CPJ_RS00100	CPJ_RS00100_F	AGGCCGAATTCCCGGGGATCATGAGATTGCTGTTGTCTTG	CPJ_RS00100_B	CCGCTGCAGGTCGACGGATCTTAGCGTGCGATCTCCCTAT
CPJ_RS01105	CPJ_RS01105_F	AGGCCGAATTCCCGGGGATCTTGGTAGTTTTCTCTAGGGT	CPJ_RS01105_B	CCGCTGCAGGTCGACGGATCTCAACTCTCGAAAACAGAAA
CPJ_RS03540	CPJ_RS03540_F	AGGCCGAATTCCCGGGGATCATGCTTACAGATCAACGTAA	CPJ_RS03540_B	CCGCTGCAGGTCGACGGATCTTACTTAAGGGTTTTAAAAAAG
CPJ_RS05575	CPJ_RS05575_F	AGGCCGAATTCCCGGGGATCGGAAGAGTGGCAGAGTGGTC	CPJ_RS05575_B	CCGCTGCAGGTCGACGGATCCGGAAGAGAAGGGATTCGAAC

Table: 4 Lists of primers used for cloning and sequencing

Primer for Caspase-9 cloning

Forward primer name	Forward primer	Backward primer name	Backward primer
Caspase-9 for pGADT7_F (*Bam*HI site)	CATCGATACGGGATCATGGACG AAGCGGATCGGC	Caspase-9 for pGADT7_B (*Bam*HI site)	CGAGCTCGATGGATCGGGGCCCTGGCC TTATGAT
hCasp9_3(pGEX(2T-P)) (*Bam*HI, *Sal*I site)	TTTGGATCCCATATGGACGAAG CGGATCGGCG	hCasp9_4(pGEX(2T-P))(*Bam*HI, *Sal*I site)	AAAGTCGACGGGGCCCTGGCCTTATGA TG

Infusion primer of Chlamydial 5 gene into pET-15b Vector (NdeI restriction site)

Forward primer name	Forward primer	Backward primer name	Backward primer
Cpj0056 for pET-15 b_F	CGCGCGGCAGCCATATGAAAGA AGTAGAACAACGTA	Cpj0056 for pET-15 b_B	GGATCCTCGAGCATA TCACAAATTGGAAAATTTCTCTT
Cpj0444 for pET-15 b_F	CGCGCGGCAGCCATATGAAATA TTCTTTACCTTGGC	Cpj0444 for pET-15 b_B	GGATCCTCGAGCATATTAGAAAGAATA ACGAGTTCCA
Cpj0512 for pET-15 b_F	CGCGCGGCAGCCATATGCGACG ATCTGTTTGTTAC	Cpj0512 for pET-15 b_B	GGATCCTCGAGCATATTAATTTAAATC CACCCAGATTG
Cpj0838 for pET-15 b_F	CGCGCGGCAGCCATATGCTAAA GCACGATACCATT	Cpj0838 for pET-15 b_B	GGATCCTCGAGCATACTATTTTCCAAT GCAAAATTTAC
Cpj0948 for pET-15 b_F	CGCGCGGCAGCCATATGAGAAT CGTACAAGTCGC	Cpj0948 for pET-15 b_B	GGATCCTCGAGCATATCATGAGAGTAA AGATTGATAAA

T7 Sequencing primer for pGBKT7 and pGADT7

Forward primer name	Forward primer	Backward primer name	Backward primer
For pGBKT7(YAY003)	TAATACGACTCACTATAGGGC	For pGBKT7 (YAY004)	TTTCGTTTTAAAACCTAAGAGTC
For pGADT7(YAY003)	TAATACGACTCACTATAGGGC	pGADT7 (YAY005)	AGATGGTGCACGATGCACAG

pET-15 b vector Sequencing Primer

Forward primer name	Forward primer	Backward primer name	Backward primer
pET-15 b sequencing _F	GGCAGCAGCCATCATCATC	pET-15 b sequencing_B	AGCAGCCAACTCAGCTTCC

pACT2 cDNA library sequencing primer

Forward primer name	Forward primer	Backward primer name	Backward primer
pACT2 sequencing_F	CTATTCGATGATGAAGATACCC	pACT2 sequencing_B	GTGAACTTGCGGGGTTTTTCA

Table: 5 Pseudo positives containing pGBKT7+ *C. pneumoniae* genes

Gene ID	Protein name
CPJ0004	(Pet112) Glu tRNA Gln amidotransferase (B subunit)
CPJ0061	Pts IIA protein with HTH DNA-Binding domain
CPJ0066	hypothetical protein
CPJ0139	hypothetical protein
CPJ0148	Serine/Threonine protein kinase
CPJ0206	hypothetical protein
CPJ0257	hypothetical protein
CPJ0259	hypothetical protein
CPJ0284	hypothetical protein
CPJ0379	hypothetical protein
CPJ0381	hypothetical protein
CPJ0405	hypothetical protein
CPJ0412	hypothetical protein
CPJ0421	ribosomal RNA small subunit methyltransferase H
CPJ0423	hypothetical protein
CPJ0436	lipoate--protein ligase A
CPJ0502	nucleotide exchange factor GrpE
CPJ0519	diaminopimelate epimerase
CPJ0526	GutQ/KpsF family sugar-phosphate isomerase
CPJ0604	amino acid ABC transporter substrate-binding protein
CPJ0623	hypothetical protein
CPJ0671	hypothetical protein
CPJ0690	Fe-S cluster assembly protein SufD
CPJ0704	type III secretion system protein
CPJ0707	EscN/YscN/HrcN family type III secretion system ATPase
CPJ0712	EscD/YscD/HrpQ family type III secretion system inner membrane ring protein
CPJ0834	hypothetical protein
CPJ0872	riboflavin biosynthesis protein RibBA
CPJ0887	hypothetical protein
CPJ1057	hypothetical protein
CPJ_RS04370	hypothetical protein
CPJ_RS04995	hypothetical protein

Table: 6 *C. pneumoniae* five proteins interact with human caspase-9

Gene ID	Protein name
Cpj0056	Phosphomanomutase
Cpj0444	polymorphic outer membrane protein G/I family
Cpj0512	CT425 Hypothetical protein
Cpj0838	Thiophene/ furan oxidation protein (tRNA modification GTPase MnmE)
Cpj0948	Glycogen synthase

Table: 7 *C. pneumoniae* 47 outer membrane proteins selected for human cDNA library screening

Gene ID	Protein name	Colony no.	Fig. 27 plate no.
CPj0005	pmp_1	0	
CPj0013A	pmp_2_1	0	
CPj0013B	pmp_2_2	10	xviii
CPj0014	pmp_3_1	0	xix (up)
CPj0015	pmp_3_2	1	xv
CPj0016 A	pmp_4_1	1	xxv
CPj0016 B	pmp_4_1_2	21	xxii
CPj0017	pmp_4_2	0	
CPj0018	pmp_5_1	1	xxvi
CPj0019	pmp_5_2	5	xi
CPj0020	Omp	0	
CPj0021	Omp	0	
CPj0030	gcp_1	10	xix (bottom)
CPj0218	hypothetical protein	1	iv
CPj0278	conserved outer membrane lipoprotein protein	6	ii
CPj0300	omp	0	xxviii
CPj0301	ompH-like outer membrane protein	2	ix
CPj0342	Omp	0	
CPj0444	pmp_6	7	i
CPj0445	pmp_7	2	vii
CPj0446	pmp_8	0	
CPj0447	pmp_9	0	
CPj0449	pmp_10	2	viii
CPj0450	pmp_11	7	xxiii
CPj0451	pmp_12	0	
CPj0452	pmp_13	0	
CPj0453	pmp_14	0	
CPj0461	hypothetical protein	0	
CPj0464	hypothetical protein	0	xvi
CPj0466	pmp_15	0	
CPj0467	pmp_16	1	xx(up)
CPj0468	pmp_17.1	0	xvii
CPj0469	pmp_17.2	0	
CPj0470	pmp_17.3	0	xii
CPj0471	pmp_18	0	xiv
CPj0539	pmp_19	5	xiii
CPj0540	pmp_20	5	xxi
CPj0557	omcB	4	x
CPj0558	omcA	9	xxiv
CPj0695	ompA	0	
CPj0818	prepilin-type N-terminal cleavage/ methylation domain-containing protein	0	
CPj0854	OmpB	0	xx(bottom)
CPj0905	murC_ddlA	6	xxvii
CPj0963	pmp_21	7	vi
CPj1034	hypothetical protein	1	iii
CPj1072	hypothetical	7	v
CPj1073	outer membrane protein	0	

Table: 8 Chlamydial 22 outer membrane proteins found to interact with 74 human proteins

Chlamydial outer membrane protein		Interacting Human protein
protein ID	gene ID	
pmp_2_2	CPj0013B	ZNF496
pmp_2_2	CPj0013B	CCDC80
pmp_2_2	CPj0013B	FBLN5
pmp_2_2	CPj0013B	LGALS1
pmp_2_2	CPj0013B	EFEMP2
pmp_2_2	CPj0013B	ACTA2
pmp_2_2	CPj0013B	FLNA
pmp_2_2	CPj0013B	COL1A1
pmp_3_2	CPj0015	SNAPIN
pmp_4_1	CPj0016A	DNAJB1
pmp_4_1_2	CPj0016B	MT2A
pmp_4_1_2	CPj0016B	ACTA2
pmp_4_1_2	CPj0016B	IFI 30
pmp_4_1_2	CPj0016B	KTN1
pmp_4_1_2	CPj0016B	COL18A1
pmp_4_1_2	CPj0016B	COL1A2
pmp_4_1_2	CPj0016B	CTGF
pmp_4_1_2	CPj0016B	ITGB3BP
pmp_4_1_2	CPj0016B	ACTA2
pmp_4_1_2	CPj0016B	SLC2A4
pmp_4_1_2	CPj0016B	CNOT2
pmp_4_1_2	CPj0016B	COL1A1
pmp_5_1	CPj0018	PDLIM3
pmp_5_2	CPj0019	MT2A
pmp_5_2	CPj0019	MT2A
pmp_5_2	CPj0019	FLNA
pmp_5_2	CPj0019	ELN
gcp_1	CPj0030	STAT6
gcp_1	CPj0030	HMCN1
hypothetical protein	CPj0218	FLNA
conserved om-lipoprotein	CPj0278	FHL2
conserved om-lipoprotein	CPj0278	DYHC1
conserved om-lipoprotein	CPj0278	SPEG
conserved om-lipoprotein	CPj0278	PRKRA
conserved om-lipoprotein	CPj0278	LPP
conserved om-lipoprotein	CPj0278	FLNA
ompH-like outer membrane	CPj0301	FLNA
pmp_6	CPj0444	FLNA
pmp_6	CPj0444	MT2A
pmp_7	CPj0445	FLNA
pmp_7	CPj0445	SNAPIN
pmp_10	CPj0449	SPAG9
pmp_10	CPj0449	PSMC2
pmp_11	CPj0450	FN1
pmp_11	CPj0450	LGALS1
pmp_11	CPj0450	GSTP1
pmp_11	CPj0450	RPL41
pmp_11	CPj0450	FN1
pmp_11	CPj0450	POMP
pmp_16	CPj0467	SNAPIN

pmp_19	CPj0539	ACTA2
pmp_19	CPj0539	FN1
pmp_19	CPj0539	PPIE
pmp_19	CPj0539	UPF3A
pmp_19	CPj0539	POMP
pmp_20	CPj0540	SERPING1
pmp_20	CPj0540	ACTA2
pmp_20	CPj0540	COL1A2
omcB	CPj0557	POLD2
omcB	CPj0557	PDCD6
omcA	CPj0558	AQP1
omcA	CPj0558	NFE2L1
omcA	CPj0558	FLNA
omcA	CPj0558	FBLN5
omcA	CPj0558	LGALS1
omcA	CPj0558	FLNA
omcA	CPj0558	ACTA2
murC_ddlA	CPj0905	AP1M1
pmp_21	CPj0963	CRTAP
pmp_21	CPj0963	GNG12
pmp_21	CPj0963	IFI35
Hypothetical	CPj1072	CD59
Hypothetical	CPj1072	COL3A1
hypothetical	CPj1072	FBLN5

9. Figures

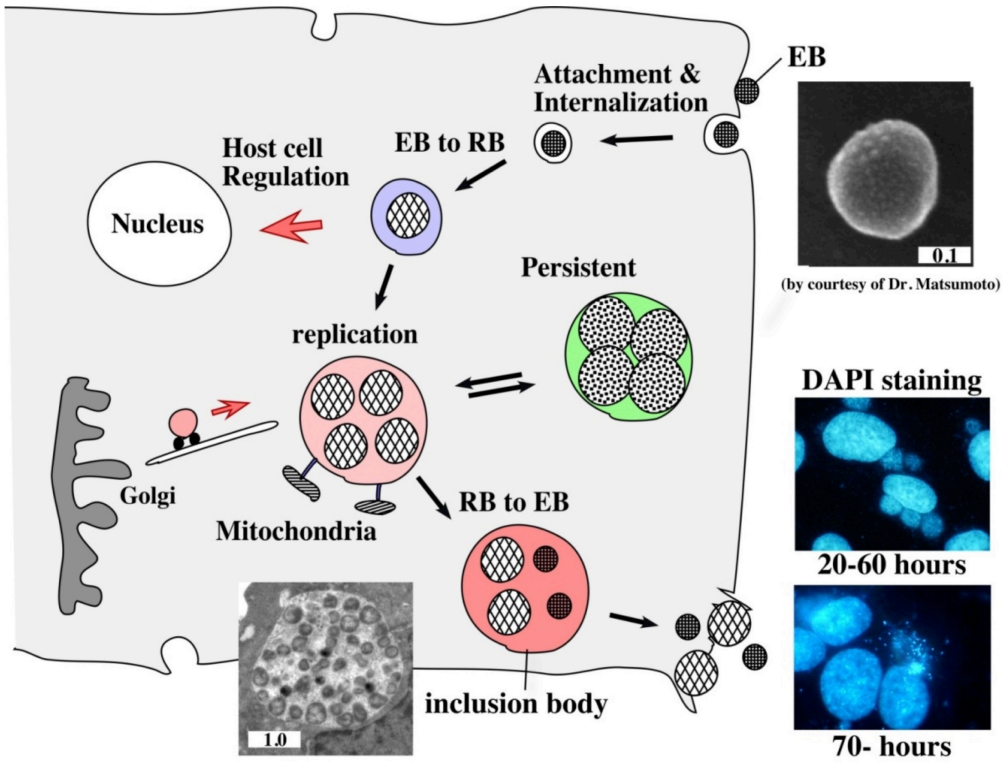

Fig. 1 Developmental cycle of *C. pneumonioae*

C. pneumonioae elementary body (EB) attach to the host cell and internalized by pagocytosis within a vesicle. About 2 to 3 hours after the infection, the form changes from infected type EB to proliferative reticulate body (RB). Under stressed condition (e.g. treatment with antibiotic or interferon gamma (IFN-γ) induced activation host cell), *Chlamydia* can alternate some morphological changes ultimately formation of persistent body (PB). Within 72 hrs, a RB re-differentiate into an EB and released for next infection.

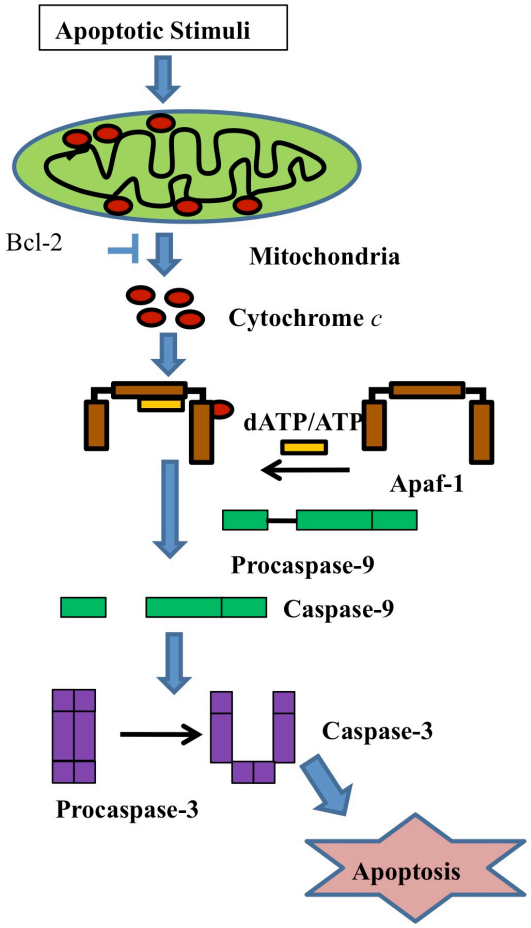

Fig. 2 Host apoptosis (Intrinsic Pathway)

Apoptotic signal was initiated by the ultraviolet irradiation, DNA damage, internal stress, etc., causes release of cytochrome *c* into the cytoplasm from the mitochondria. The cytochrome *c* and Apaf-1, inactive caspase-9 forms an apoptosome, and caspase-9 are activated. Apoptosis is induced by activation of inactive caspase-3 by this activated caspase-9. This apoptotic response is tightly regulated by Bcl-2 to prevent the release of cytochrome *c* from mitochondria.

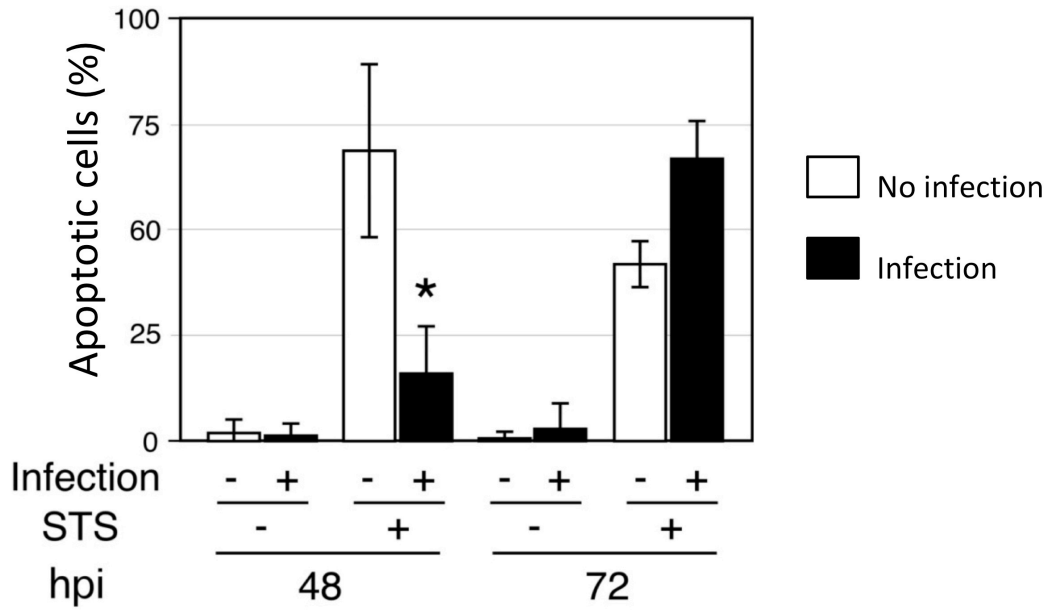

Fig. 3 *Chlamydophila pneumoniae* regulates host apoptosis under apoptotic stimulation using STS

HEp-2 cells were infected with *C. pneumoniae* J138 (MOI = 0.2), and STS (final concentration, 0.5 μM) was added at 44 and 68 h post-infection (hpi). Four hours later (shown as 48 and 72 hpi, respectively), cells were stained with Hoechst 33258. Only cells containing inclusions larger than 4 μm in diameter were counted as infected cells, and the infected cells were categorized into either apoptotic or non-apoptotic cells. Cells with smaller inclusions or without any inclusions were eliminated from the cell counting. All data are expressed as mean ± SD calculated from at least three independent experiments. An asterisk denotes $p < 0.05$ using Student's *t* test. Open column indicate no infection and black column indicate infection.

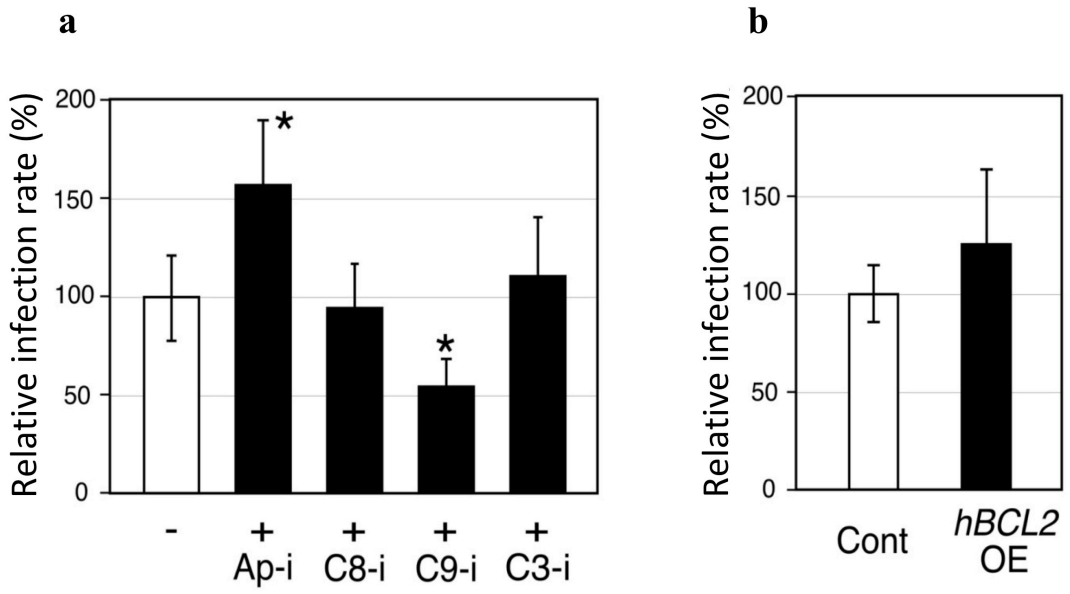

Fig. 4 Apaf-1 and caspase-9 inhibitors show opposing contributions to *C. pneumoniae* infection

a) HEp-2 cells treated with 50 μM of anti-apoptotic agents for 24 h were infected with *C. pneumoniae* J138 (MOI = 0.2). The infected cells were fixed and stained at 48 hpi. Cells with inclusions larger than 4 μm in diameter were counted as infected ones, and relative infection rates were calculated on the basis of the standard experiment without any inhibitors shown as " - ". Ap-i, C8-i, C9-i, and C3-i indicate cell-permeant inhibitors of Apaf-1 (NS3694), caspase-8 (Z-IETD-FMK), caspase-9 (Z-LEHD-FMK), and caspase-3 (Z-EDVD-FMK), respectively.

b) Bcl-2-overexpressing HeLa cells (hBCL2 OE) and control cells (Cont) (Tsujimoto 1998) were used for chlamydial infection (MOI = 0.2). Infection rates were calculated at 48 hpi. All data are expressed as mean ± SD from at least three independent experiments. Asterisks denote $p < 0.05$ using Student's *t* test.

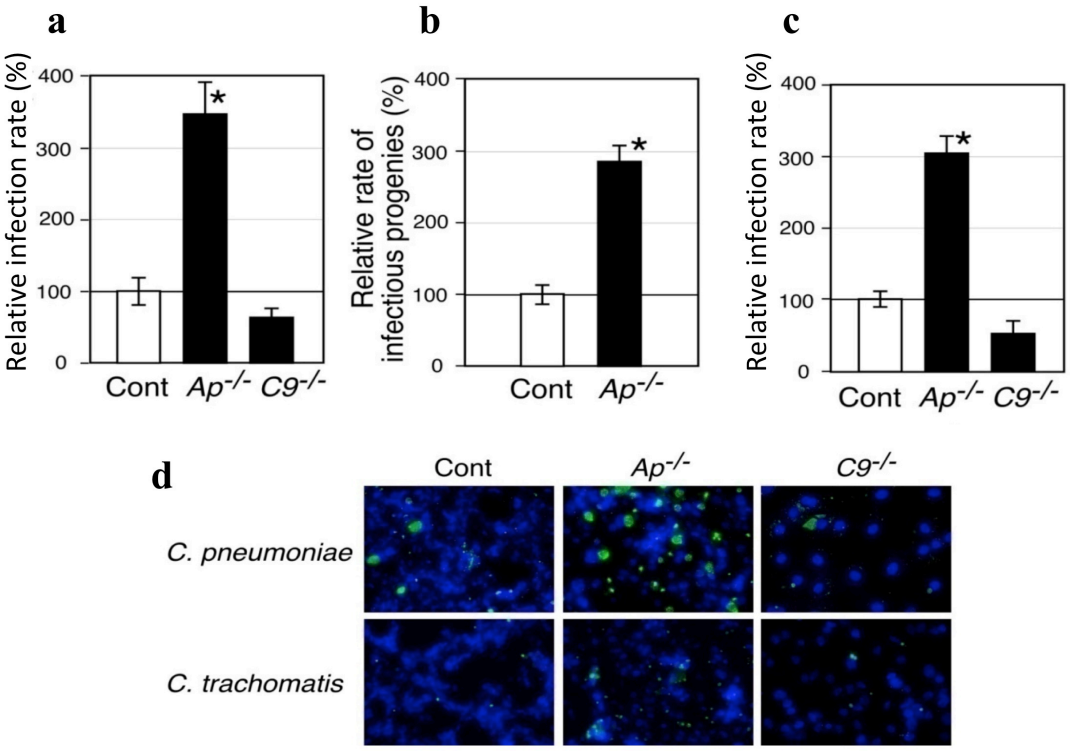

Fig. 5 Apaf-1 and caspase-9 show epistatic effects on chlamydial infection

a) *Apaf-1*$^{-/-}$ and *caspase-9*$^{-/-}$ MEFs (indicated as *Ap*$^{-/-}$ and *C9*$^{-/-}$, respectively), and control MEFs (Cont) were subjected to *C. pneumoniae* infection (MOI = 0.2). Infection rates were calculated using host cells with inclusions larger than 4 μm in diameter.

b) Generation of infectious progenies of *C. pneumoniae* was calculated using Apaf-1-deficient MEFs. After centrifugation of infection medium at 80 hpi, the supernatants were used for re-infection in control MEFs (Cont). The infection rates were measured at 48 hpi.

c) *C. trachomatis* was used to infect Apaf-1- and caspase-9-deficient MEFs (MOI = 0.2), and control MEFs (Cont). Infection rates were assessed at 20 hpi as for *C. pneumoniae*. All data are expressed as mean ± SD from at least three independent experiments. Asterisks denote $p < 0.05$ using Student's *t* test.

d) Samples at 48 hpi were fixed and stained with Hoechst (blue) and an anti-chlamydia antibody, RR402, (green) and viewed under fluorescence microscope. d) Upper pictures shows *C. pneumoniae* infection and bottom pictures shows *C. trachomatis* infection.

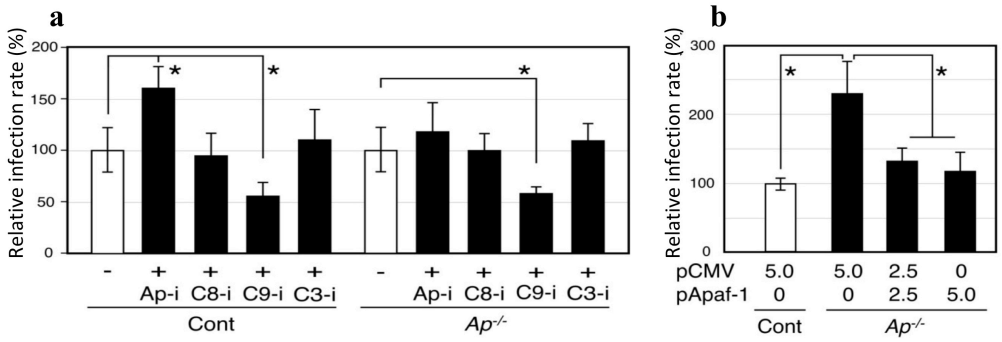

Fig. 6 Independent contributions of caspase-9 and Apaf-1 in *C. pneumoniae* infection are confirmed using apoptosis inhibitors and *apaf- 1* gene complementation

a) Effects of apoptosis inhibitors at 50 μM were assayed on *C. pneumoniae* infection in MEF cells (left panel) and *Apaf-1* deficient cells (right panel, shown as $Ap^{-/-}$). The inhibitors were added from 24 to 48 hpi and infected cells were counted at 48 hpi. Relative infection rates were calculated on the basis of the standard experiment shown as " -".

b) The pApaf-1 plasmid, consisting of the mouse *apaf -1* gene in pCMV-sport 6.1 was transiently transfected into $Apaf^{1-}$ MEFs. After *C. pneumoniae* infection (MOI = 0.2), infection rates were calculated at 48 hpi. All data are expressed as mean ± SD from at least three independent experiments. Asterisks denote $p < 0.05$ using Student's *t* test

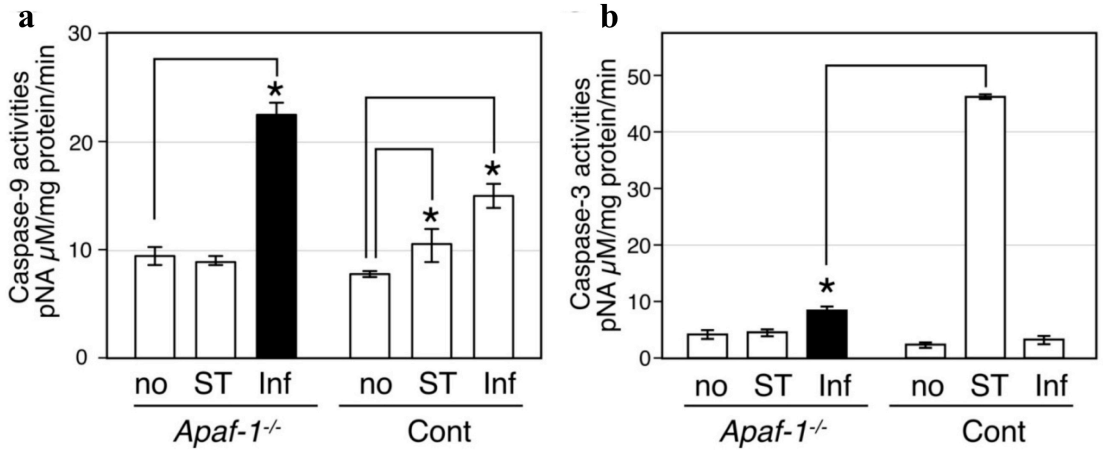

Fig. 7 Caspase-9, but not caspase-3, is activated by *C. pneumoniae* infection in a manner independent from Apaf-1

a) Caspase-9 and b) Caspase-3 activities were measured using a colorimetric activity assay. Activities are calculated as released amounts of the chromophore *p*-nitroaniline (pNA) per mg protein in cytosolic fractions prepared from *apaf-1*$^{-/-}$ and control MEFs. Mock, STS treatment, and *C. pneumoniae* infection samples are indicated as no, ST and Inf, respectively, in each panel. All data are expressed as mean ± SD from at least three independent experiments. Asterisks denote $p < 0.05$ using Student's *t* test.

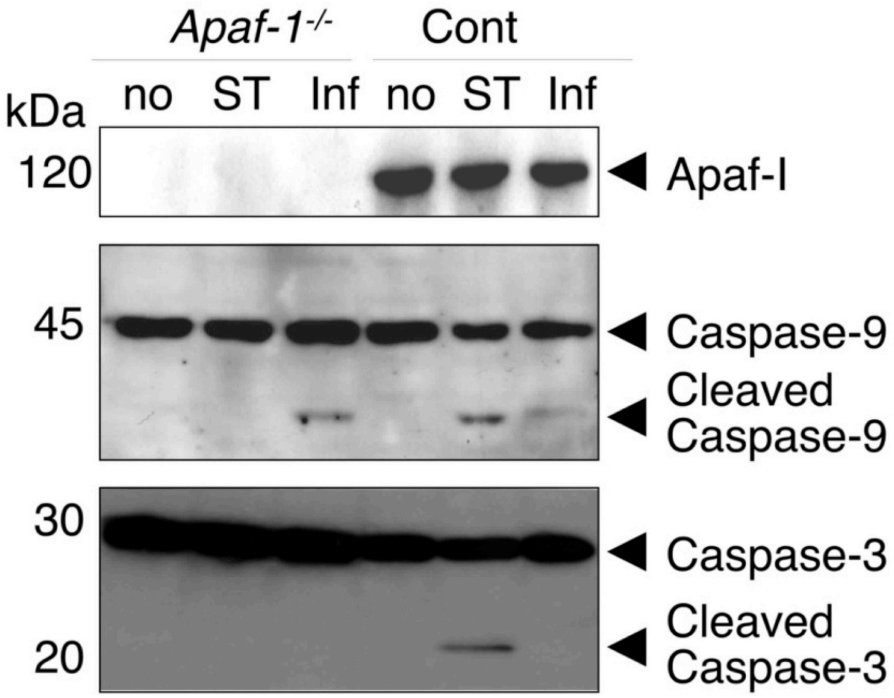

Fig. 8 Caspase-9, but not caspase-3, is proteolytically activated by *C. pneumoniae* infection in a manner independent from Apaf-1

Amounts of Apaf-1 protein, caspase-3 and -9 were analyzed by western blot detection using 30 μg total protein prepared from *Apaf-1*$^{-/-}$ and control MEFs with STS treatment or chlamydial infection. The data shown here are representative of three independent experiments. Strength of each signal was analyzed using ImageJ

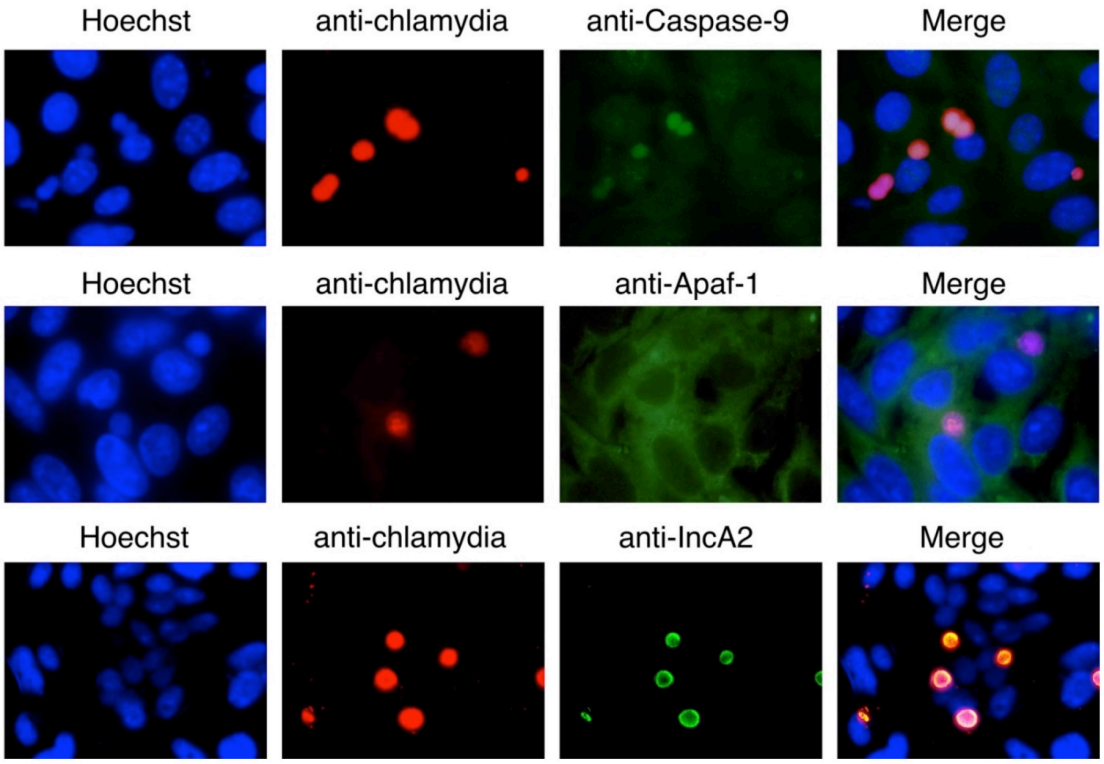

Fig. 9 Caspase-9, but not Apaf- 1, is co-localized with inclusions of *C. pneumoniae*

Apaf-1$^{-/-}$ MEFs (top) and HEp-2 cells (middle and bottom) were infected by *C. pneumoniae* and observed at 48 hpi by immunofluorescence staining using Hoechst 33258 (shown as Hoechst in blue), an anti-chlamydial specific monoclonal antibody, RR402, (anti-chlamydia in red), and anti-caspase-9, anti-Apaf-1 and IncA2 specific antibodies (in green). Merged images are shown as Merge in both experiments.

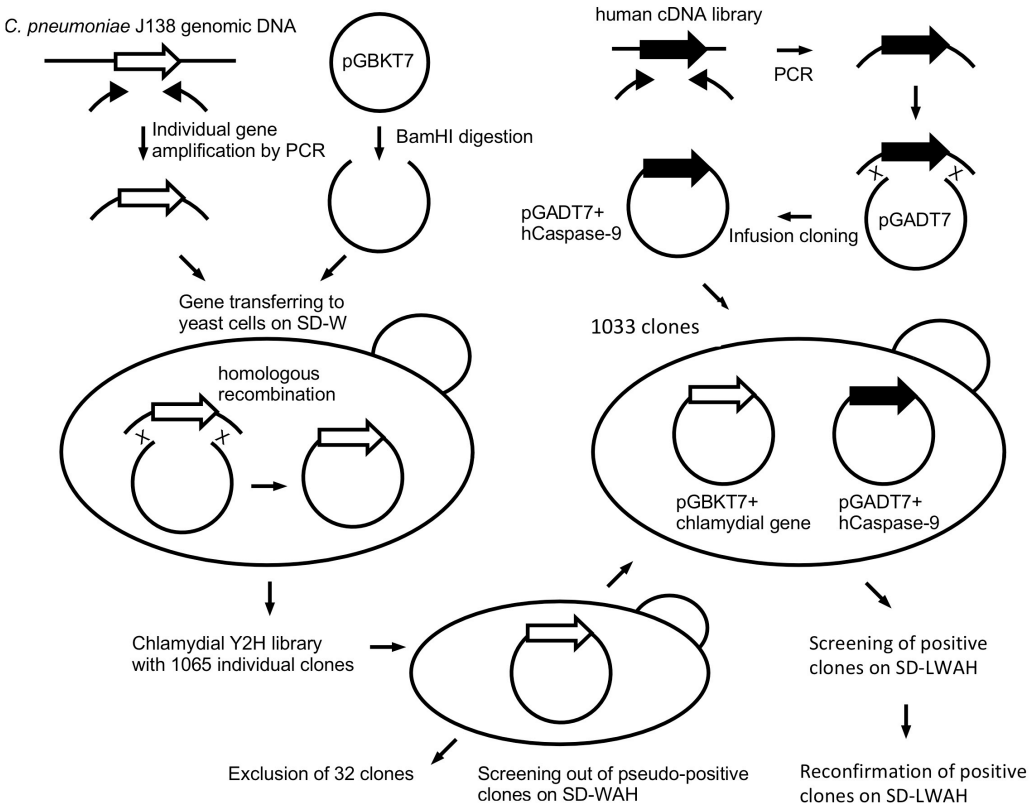

Fig. 10 Scheme of establishment of chlamydial genome library for Yeast two-hybrid (Y2H) and screening of chlamydial genes interacting with human caspase-9

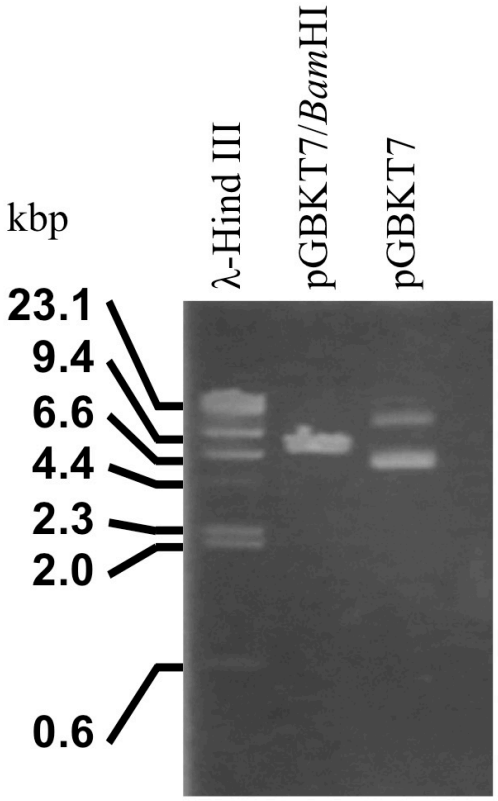

Fig. 11 Linearization of pGBKT7 by *Bam*HI for genomic library construction.

pGBKT7 vector isolated from *E. coli* DH5α (right lane). For chlamydial genomic library construction, isolated pGBKT7 vector was linearized by restriction digestion with *Bam*HI restriction enzyme purchased from Clontech TAKARA (middle lane). λ-phage genome DNA was digested by *Hind*III denoted as λ- *Hind*III used as size marker in kilo base pair (kbp) (left lane). Vector and size marker were resolved by 1% agarose-gel for 30 min at 100 V and stained with ethidium bromide for 15 min.

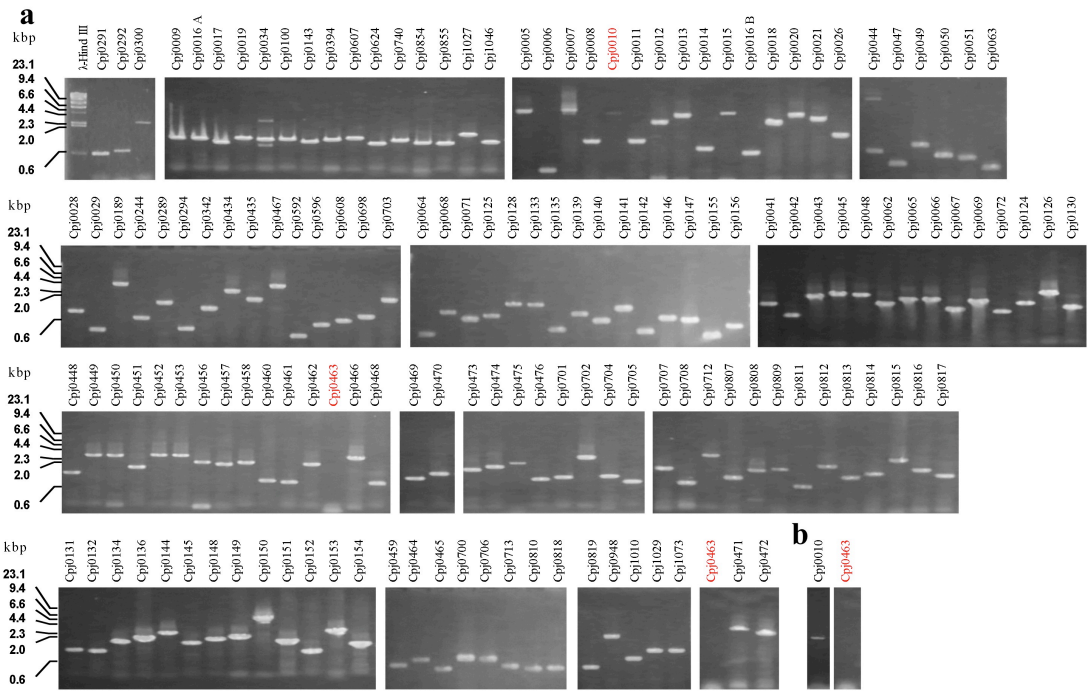

Fig. 12 PCR product of some randomely selected chlamydial genes

Chlamydial whole gene was amplified by PCR to construct genomic library into pGBKT7 by homologous recombination using primer with 20 base overhang sequence at both ends and *C. pneumoniae* J138 genomic DNA as a template.

a) After amplification 149 PCR product were selected randomly to check their expected size by agarose-gel electrophoresis.

b) Cpj0010 gene PCR product was recovered by second line PCR but Cpj0463 not.

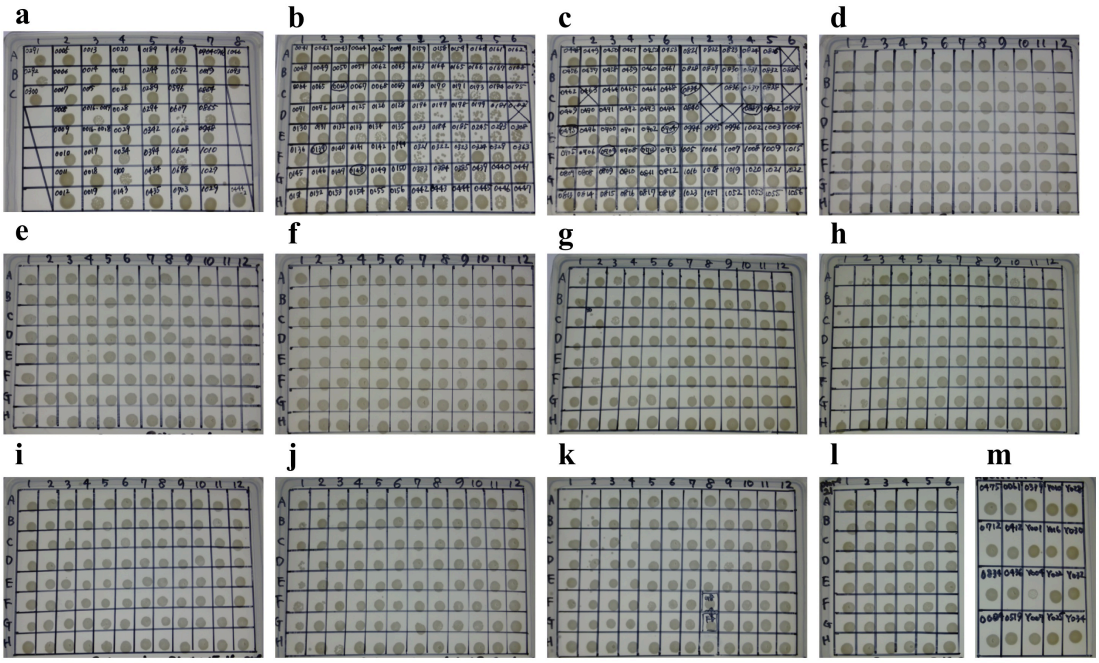

Fig. 13 Chlamydial whole genomic library

a-m) To construct chlamydial genomic library, amplified chlamydial genes by PCR were individually transfer along with linearized pGBKT7 vector into *Saccharomyces cerevisiae* (AH109) and positive clones were selected on SD-W plate. Single crossed (/) in panel (a) was unassigned any genes and 7 cross(x)-marked locations for Cpj0182, Cpj0463, Cpj0827, Cpj0835, Cpj0839, Cpj0841, and Cpj0849 genes. These 7 genes were not cloned.

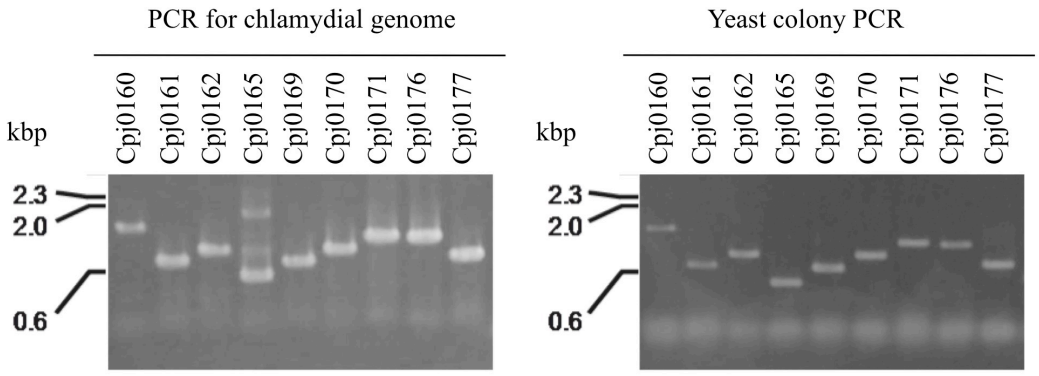

Fig. 14 Preparation of the chlamydial genome library for Y2H

Right: PCR products from randomly selected 9 samples are shown as representative findings from the experiment. DNA size markers (kbp) are shown on the left.

Left: PCR products of colony PCR confirmed the insertion of DNA in the pGBKT7 vector in the yeast strains containing the same genes used in the right panel.

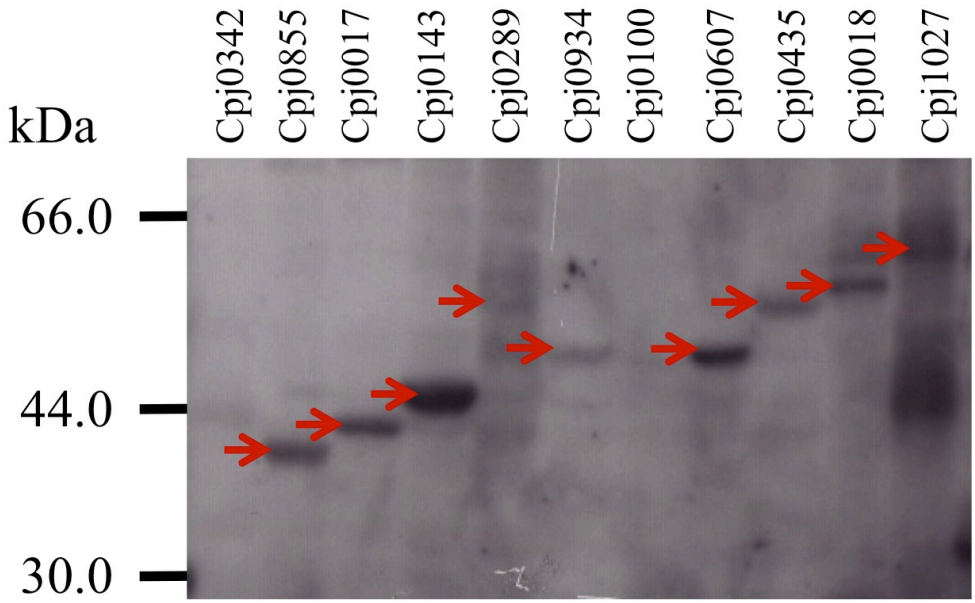

Fig. 15 Chlamydial protein accumulation in yeast transformants

Yeast strains were randomly selected and protein accumulation in yeast was analyzed by western blotting. Results from only 9 samples are shown as representative findings from the experiment. Protein size markers (kDa) are shown on the left.

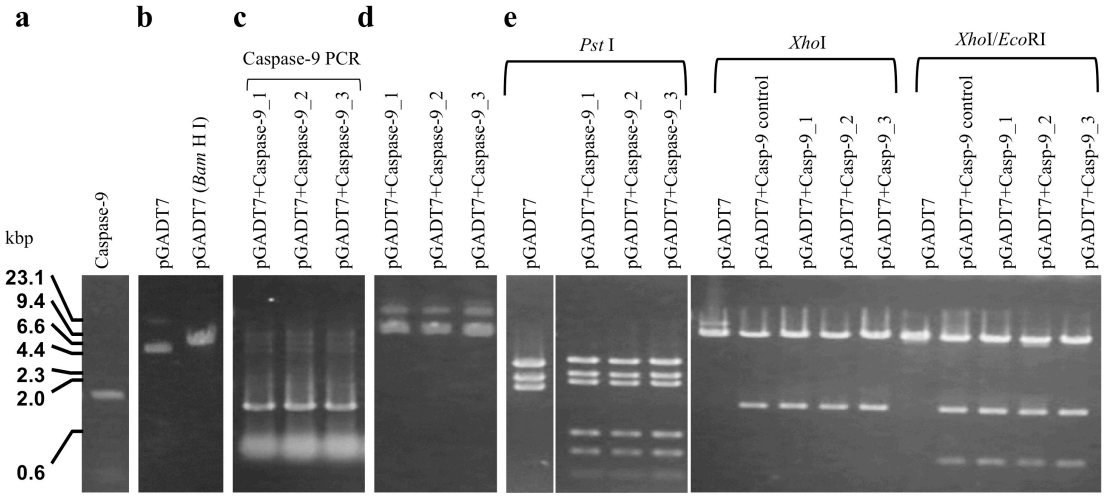

Fig. 16 Cloning of caspase-9 into pGADT7

a) Caspase-9 was amplified using human aorta cDNA library for infusion cloning into pGADT7 using infusion cloning primer (Table: 4).

b) For cloning by homologous recombination technique pGADT7 was linearized by *Bam*HI restriction enzyme. Linearized vector and caspase-9 PCR product were cloned by infusion cloning kit purchased from Clontech TAKARA and transformed into *E. coli* DH5α.

c) Colony PCR was carried out to check insertion of caspase-9 using *E. coli* DH5α 3 colony after infusion cloning and transformation using same primers for cloning. Comparing its size with the amplified caspase-9 DNA fragment, all 3 colonies showed that these vectors included appropriate caspase-9 gene.

d) pGADT7+caspase-9 plasmid vector was then isolated from those 3 colonies.

e) pGADT7 vector and isolated pGADT7+caspase-9 vectors (from 3 colony) were digested with restriction enzyme (*Pst*I, *Xho*I and *Xho*I/*Eco*RI), to check the correct size of DNA fragment and insert.

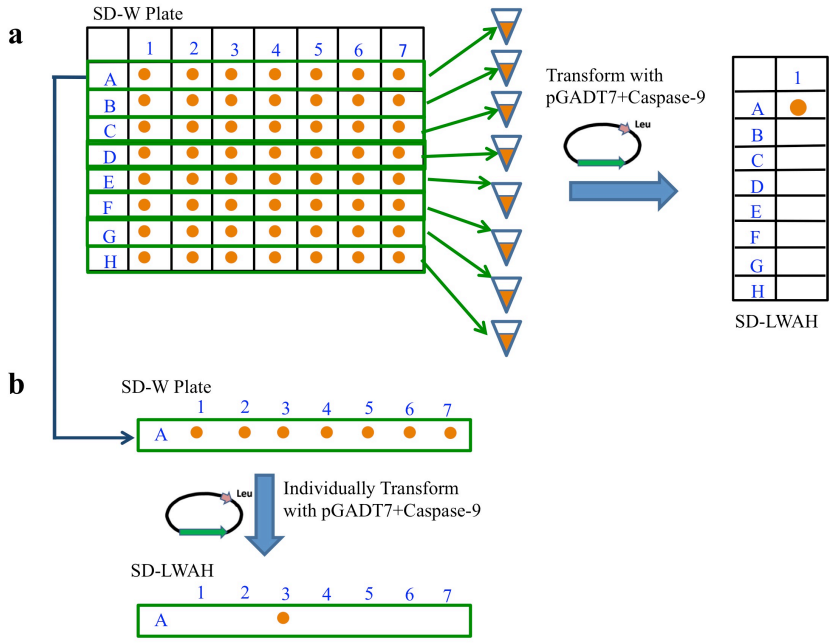

Fig. 17 Schematic flow sheet for screening interaction of caspase-9 with chlamydial genomic library.

a) Mix colonies from each row (indicated in figure) of yeast containing *C. pneumoniae* gene in one tube (30 μL from each colony), and centrifuge. Mixed cells were transformed with pGADT7+caspase-9 and positive clones were selected on SD-LWAH.

b) Those mixed cells showed positive interaction were individually transformed with pGADT7+caspase-9 and finally positive clones were selected on SD-LWAH.

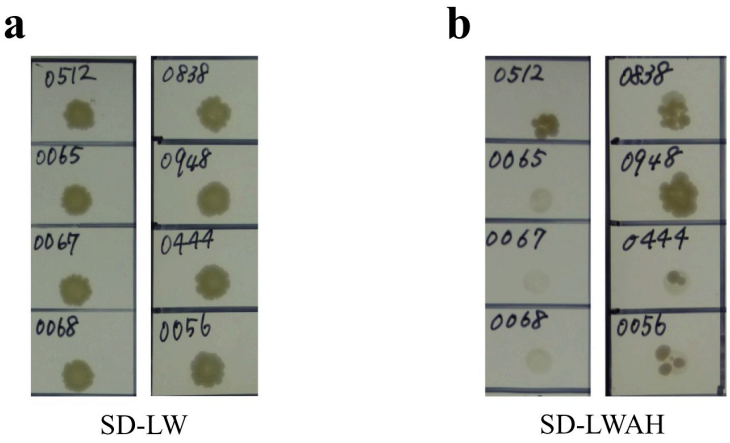

Fig. 18 Positive results from chlamydial genomic library screening with human caspase-9

Growth of 1033 strains carrying pGADT7-hcaspase-9 and pGBKT7-chlamydial genes was evaluated on a) SD medium without Leu and Trp (SD-LW), and b) SD medium without Leu, Trp, Ade, and His (SD-LWAH).

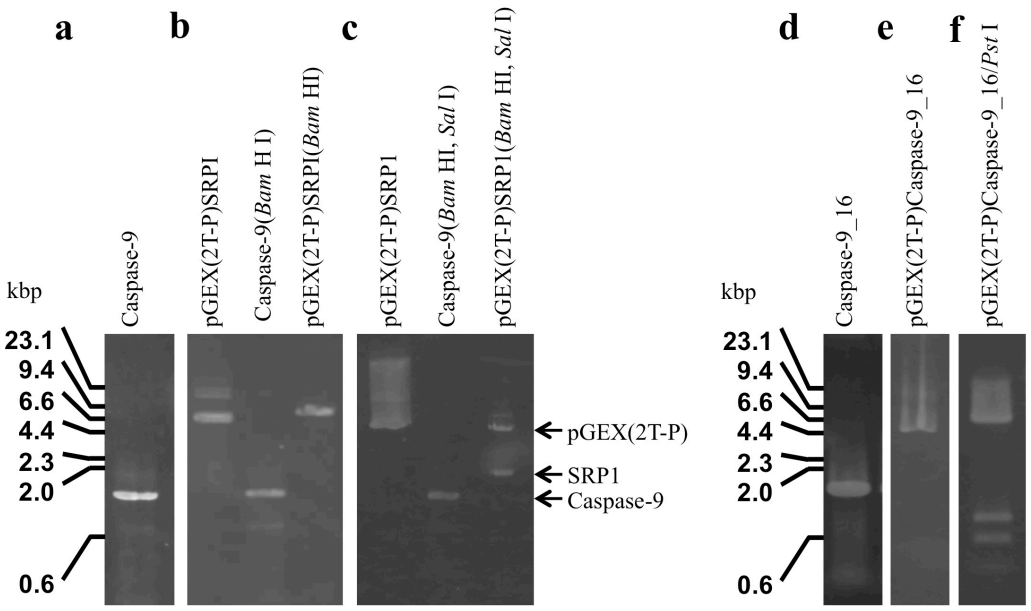

Fig. 19 Caspase-9 cloning into pGEX(2T-P) vector

a) Caspase-9 was amplified from human aorta cDNA library for cloning into pGEX(2T-P) vector by restriction digestion and ligation method using primers shown in Table: 4.

b) For cloning, amplified caspase-9 DNA fragment and pGEX(2T-P) SRP1 was digested by restriction enzyme *Bam*HI.

c) *Bam*HI digested caspase-9 DNA fragment and pGEX(2T-P) SRP1 was again digested by restriction enzyme *Sal*I for cloning by removing SRP1 fragment from pGEX(2T-P) SRP1 vector. After ligation cloned vector was transformed into *E. coli* DH5α.

d) Colony PCR was carried out to check the insertion of caspase-9 using the same primers for cloning. Comparing size with amplified caspase-9 DNA fragment using *E.coli* pGEX(2T-P)Caspase-9_16 colony showed the vector included caspase-9 gene.

e) pGEX(2T-P) caspase-9 plasmid vector was then isolated from *E.coli* pGEX(2T-P)Caspase-9_16 colony.

f) Isolated vector was then digested by restriction enzyme *Pst*I to check the correct sizes of caspase-9 DNA fragment and insert.

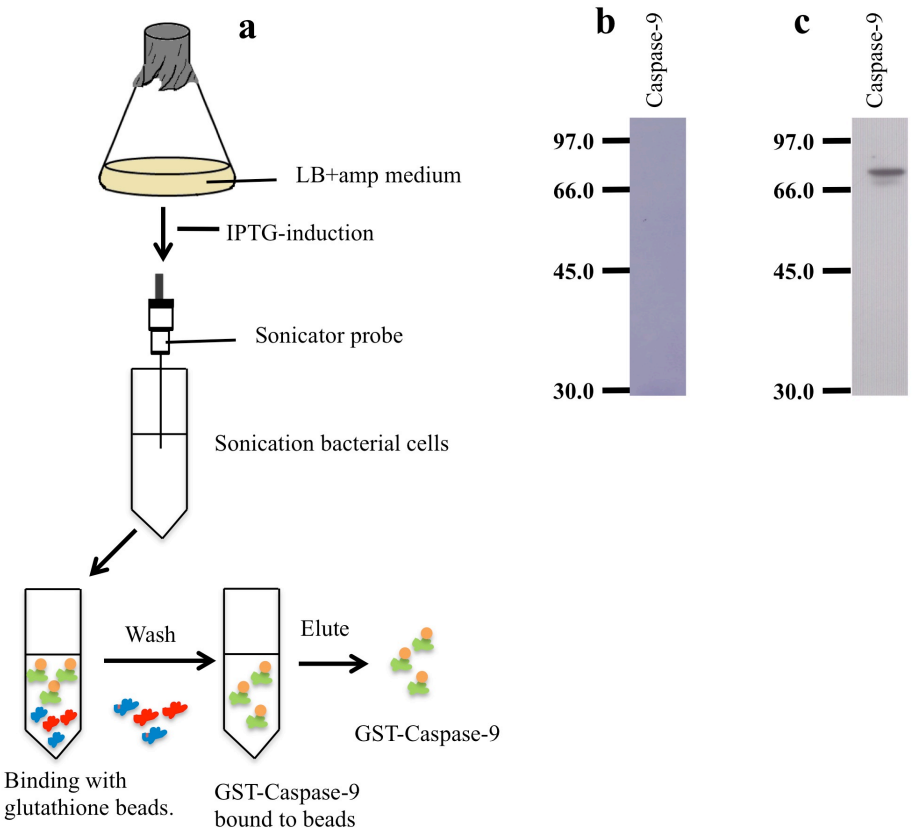

Fig. 20 Expression and partial purification of GST-Caspase-9 protein

a) For purification of GST-Caspase-9 IPTG induced bacterial cells were harvested and lysed by ultrasonication with lysis buffer.

b) GST-caspase-9 protein was transferred onto 0.45 μm PVDF blotting membrane and stained with CBB.

c) CBB stained PVDF membrane was then stained with antibody anti-pro-caspase-9 mouse monoclonal antibody

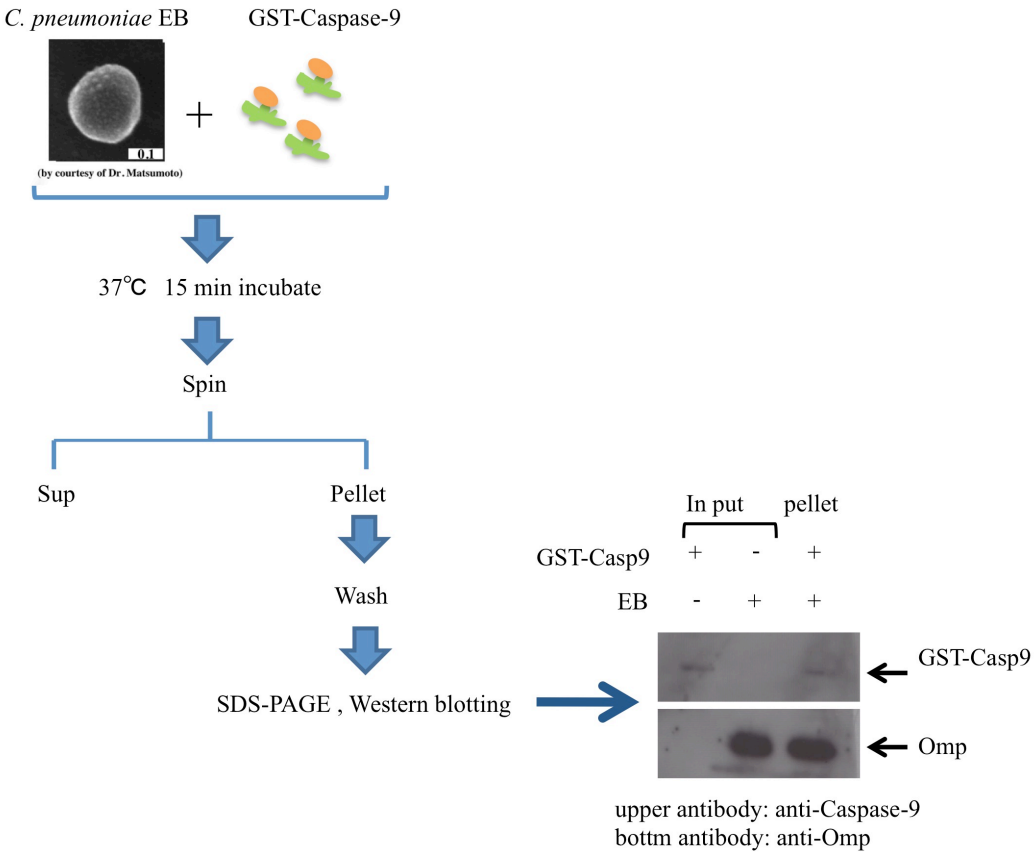

Fig. 21 Direct interaction between human apoptotic factor caspase-9 and *C. pneumoniae* EB

After mixing with GST-Casp9, EBs were retrieved and analyzed the binding proteins by western blotting, shown as “pellet”. Input samples of GST-Casp9 and EBs washed control were separately analyzed, shown as “input”.

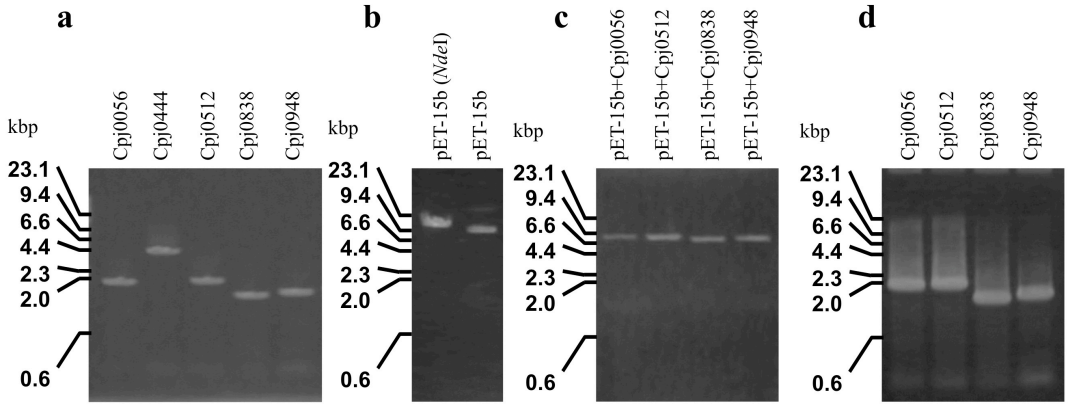

Fig. 22 Cloning of chlamydial five genes into pET-15b

a) *Chlamydia pneumoniae* five genes interacting with caspase-9 was amplified by PCR for cloning into pET-15b from chlamydial genomic DNA using primers listed in Table: 4.

b) For cloning by Infusion cloning method pET-15b vector was linearized.

c) Example of plasmid vectors cloned with the chlamydial genes note; one gene Cpj0444 did not cloned.

d) Isolated 4 vectors were re-transformed into *E. coli* BL21(DE3) and checked by colony PCR using infusion primers for each gene.

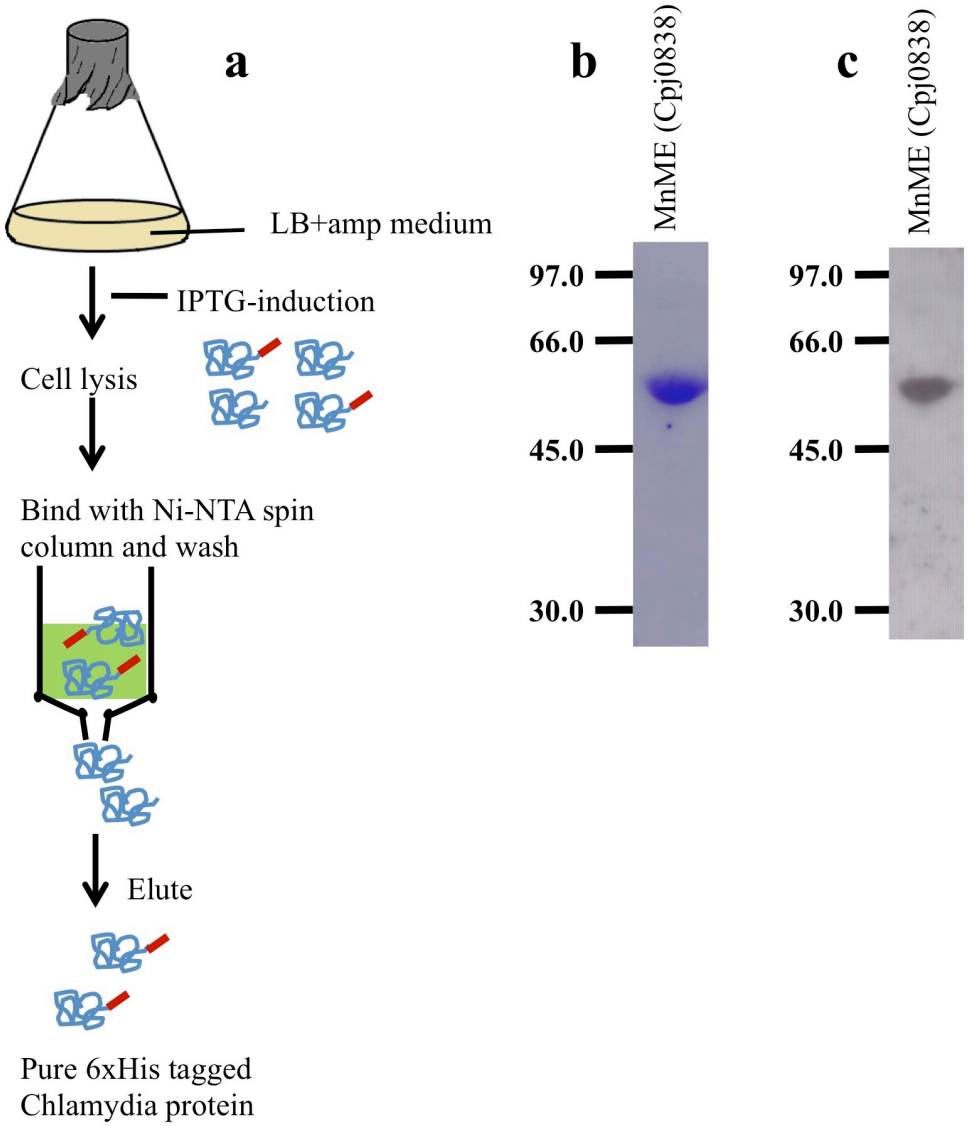

Fig. 23 Expression and purification of *Chlamydia* protein Cpj0838

a) For purification of 6x His tagged chlamydial Cpj0838 protein, IPTG induced bacterial cells were harvested and lyses with lysis buffer and purified by Ni-NTA spin column

b) Protein was transferred onto 0.45 µm PVDF blotting membrane and stained with CBB.

c) CBB stained PVDF membrane was stained with anti-6X His tag antibody monoclonal antibody (mAb).

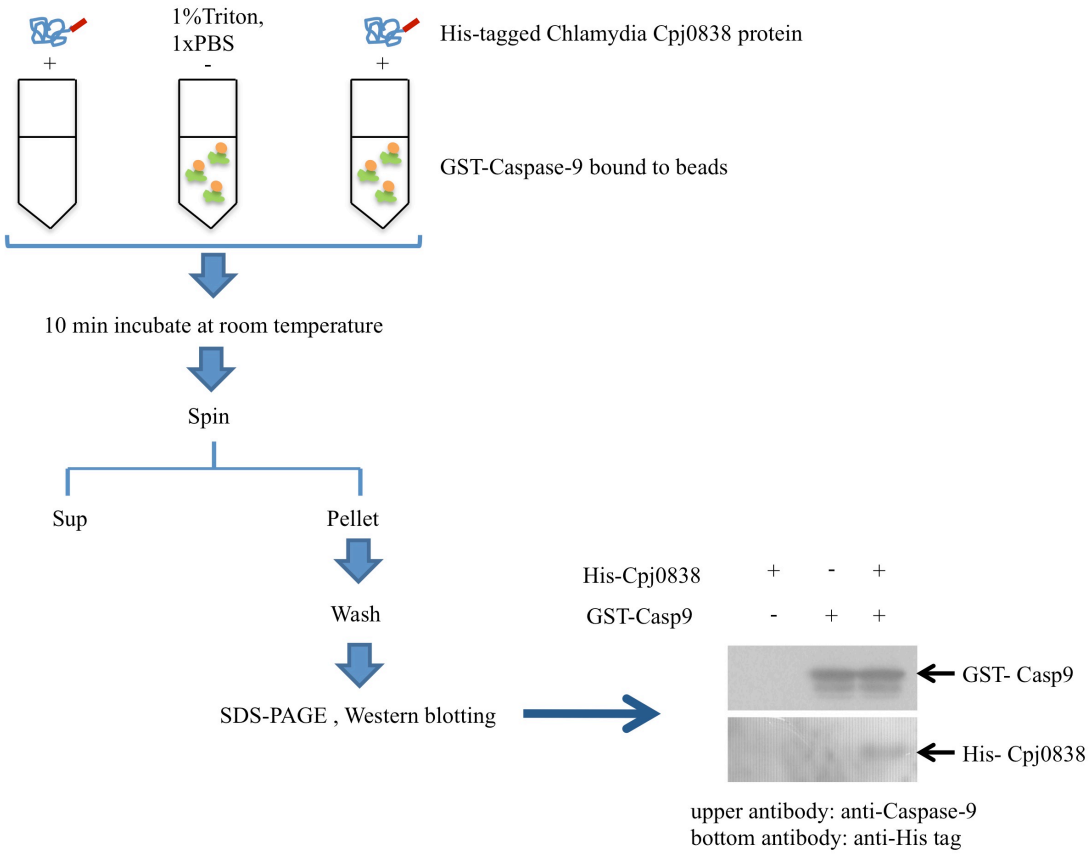

Fig. 24. Direct interaction between human apoptotic factor caspase-9 and *C. pneumoniae* Cpj0838 protein

GST-Casp9 and His-Cpj0838 were mix together and pulled down with glutathione beads. GST-Casp9 and His-Cpj0838 were detected separately.

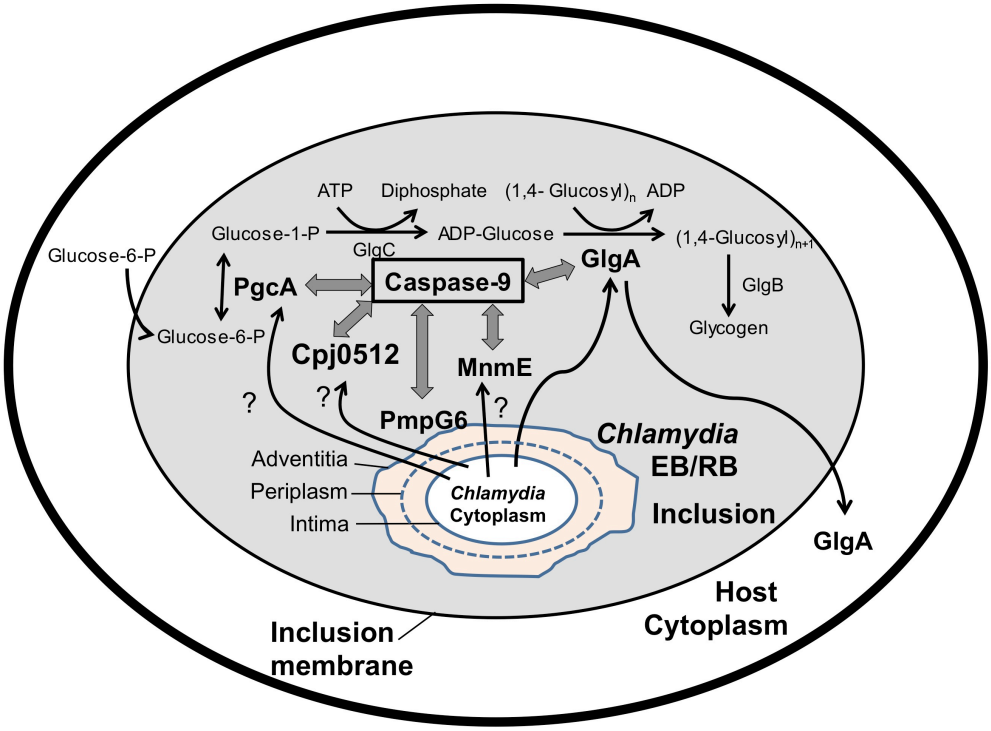

Fig. 25 Summary of interactions between human caspase-9 and *C. pneumoniae* proteins.

Five proteins, PmpG6, MnmE, PgcA, GlgC and GlgB, are encoded by genes, Cpj0444, Cpj0838, Cpj0056, CPj0607 and CPj0475, respectively.

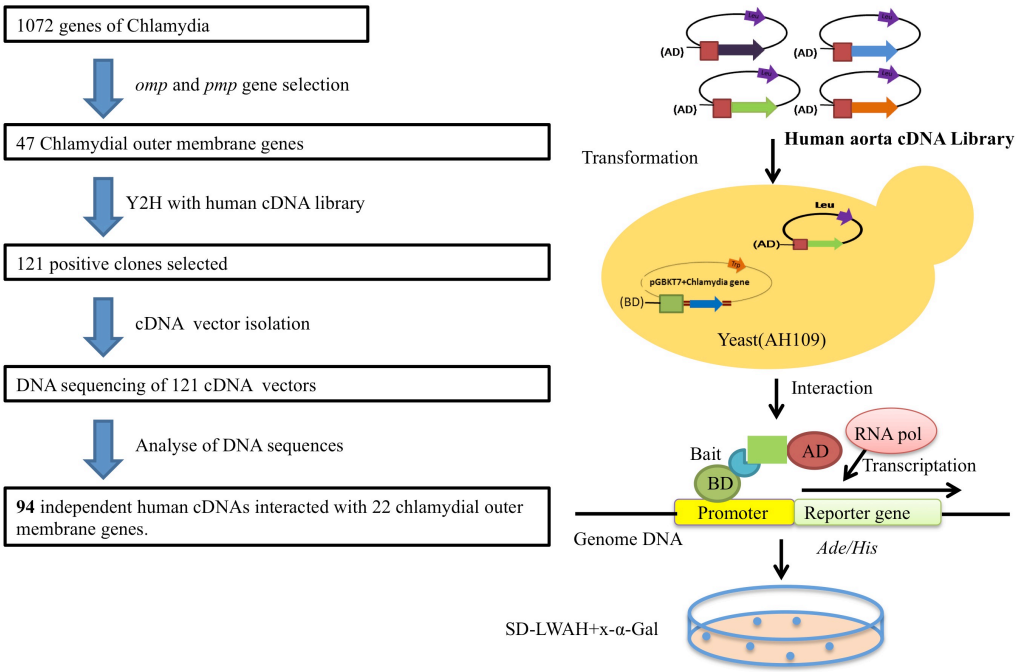

Fig. 26 Screening of the human genes interacting with chlamydial outer membrane protein genes

Human aorta cDNA library purchased from Contech TAKARA were individually transformed into the yeast containing each chlamydial 47 outer membrane gene and positive clones were selected on SD-LWAH+x-α-Gal plate. RNA pol denotes for RNA polymerase II, AD for activation domain and BD for DNA binding domain.

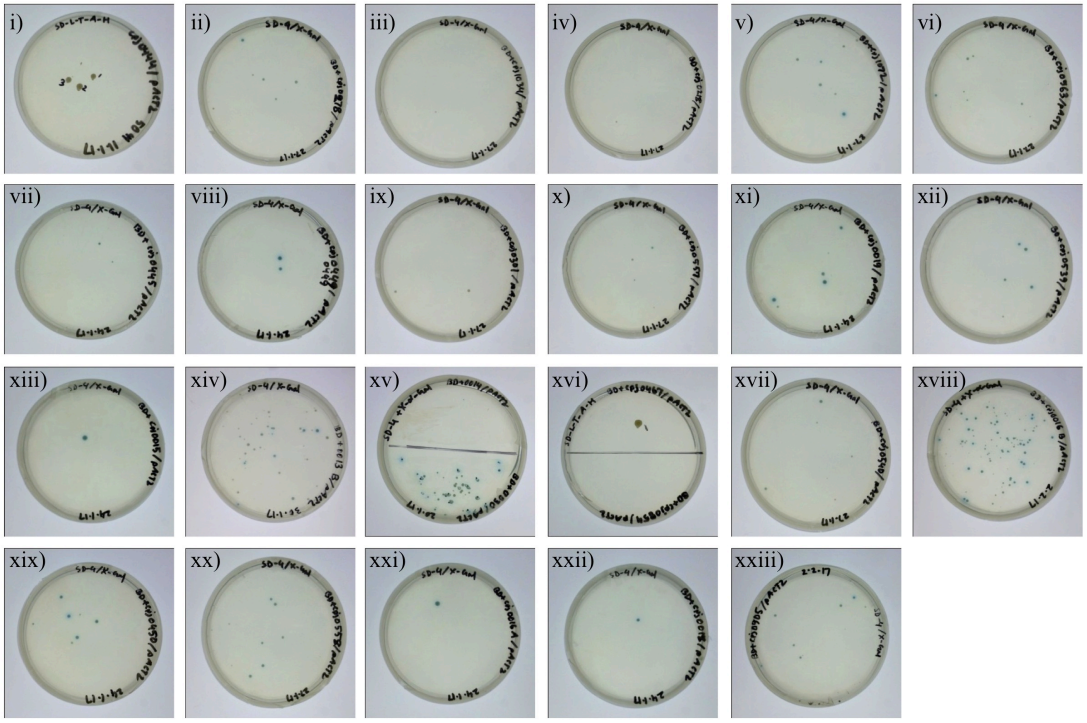

Fig. 27 Interaction of chlamydial 47 outer membrane protein with human aorta cDNA library

(i-xxiii) Human aorta cDNA library purchased from Clontech TAKARA were individually transformed into the yeast containing each chlamydial 47 outer membrane gene and positive clones were selected on SD-LWAH or SD-LWAH+x-α-Gal plate. Gene no. of each photo was shown in Table :7.

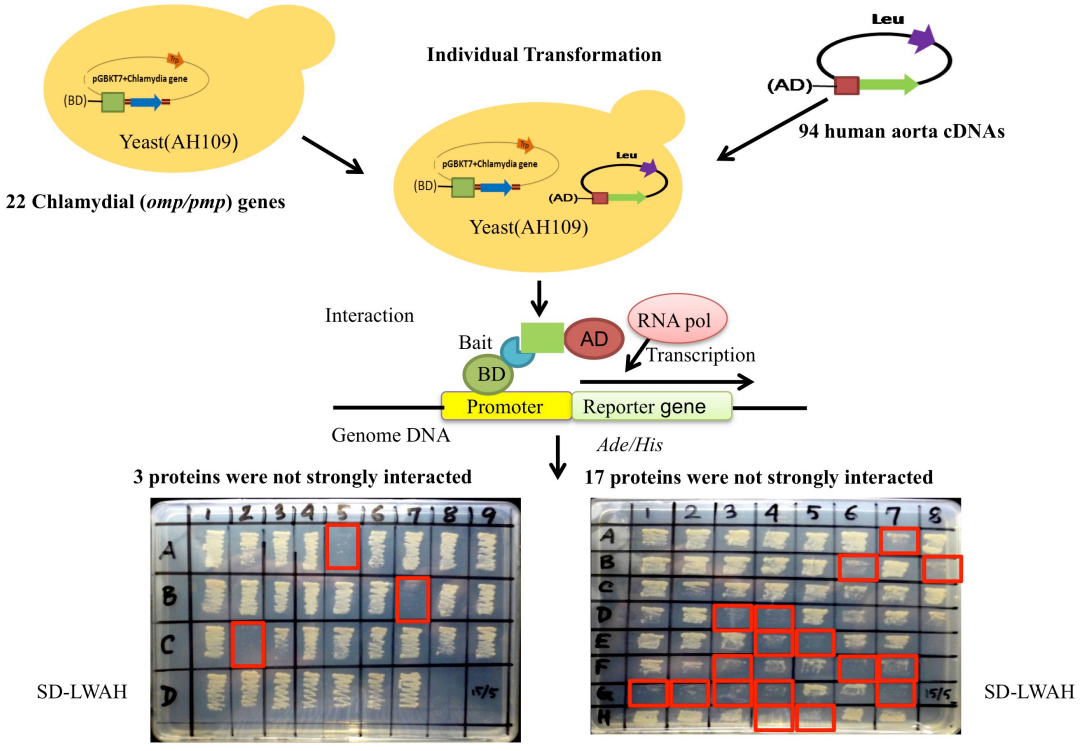

Fig. 28 Confirmation of the interaction between chlamydial 22 outer membrane protein and 94 human protein

From human aorta cDNA library and chlamydial 47 outer membrane gene screening, 22 outer membrane protein were found to interact 94 human protein after DNA sequencing analysis. These 22 outer membrane gene containing yeast were individually screened with isolated human 94 cDNA vector.

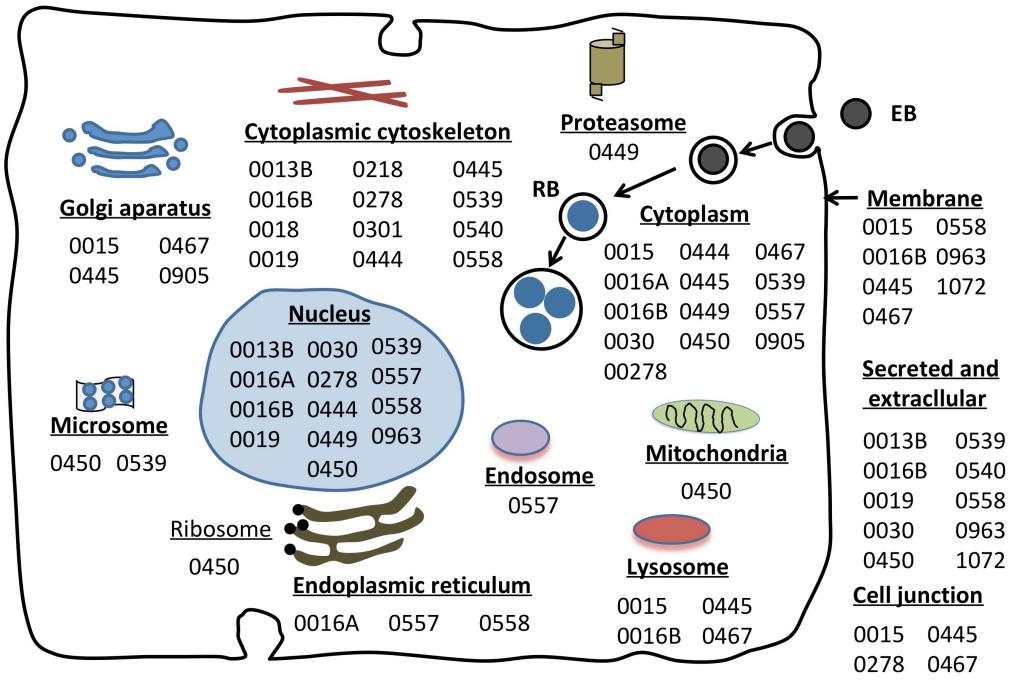

Fig. 29 Sub-cellular location of proteins interacting with chlamydial outer membrane proteins

Number in different sub-cellular location indicate the *C. pneumoniae* gene that interact with human protein located in respective cellular location.