TABLE SI Primers used in quantitative RT-PCR.

Gene ID	Name	Primer sequence
CPj0148	-	5’-AGTCCTCAAGGTCCTGCTCA-3’
		5’-CAGCCCCAGGATTATTACGA-3’
CPj0238	*zwf*	5’-ACCCGCTCTATATCACCTCAC-3’
		5’-GGAGAAAATTGTATGACAGCTTG-3’
CPj0331	-	5’-TCCGATAGTGGTGAGGGAAC-3’
		5’-CCCATACCCGAAGCATCTAA-3’
CPj0332	-	5’-GATCCCTCTAGCTCGACAGC-3’
		5’-AAAAACGCAAGGTGAAACAC-3’
CPj0333	*ltuB*	5’-GAACGGATAGGGCTTTGGCTC-3’
		5’-GAGCACGGTGTTTAAGAGTTTTC-3’
CPj0384	*hctB*	5’-ATGATTGGAGCGCAAAAAAAGC-3’
		5’-TTATCGAGACATCATTTTGA-3’
CPj0416	*himD*	5’-GTAAACTTTACAGCGCGTCTAG-3’
		5’-TTTGGTGTGTTGCAAGTAGTAG-3’
CPj0453	*pmp14*	5’-GTCTACTTGCCTGTTTATGTAGTG-3’
		5’-CTCGCCCCCAAGAAGTTTGAAC-3’
CPj0466	*pmp15*	5’-AGACCTATATTACATTAAGTCCTG-3’
		5’-GATAGTACTTATAGTCCAAGATG-3’
CPj0558	*omcA*	5’-CAATGTTTTGTGGAGTAGTTAGC-3’
		5’-CAAGCATTACCGCCGCAAGATC-3’
CPj0559	-	5’-GTAACATTATTTCCTGACATCTC-3’
		5’-AATTCTAAGGAATGCGCTTTATTG-3’
CPj0577	-	5’-GCCCAGAACCGAAATTGTAA-3’
		5’-TGGTCATTTGGAACATGTCG-3’
CPj0678	-	5’-CCTACCAGCTCCCTCGGTAG-3’
		5’-ATCGGGAGCTCCAAGAGGTAG-3’
CPj0695	*ompA*	5’-TTGCCTGTAGGGAACCCTTCTG-3’
		5’-CCAGTAGGCTTGGCTCCCATAG-3’
CPj0708	-	5’-GAATGTTTCCCCAACCTTGATG-3’
		5’-GAGCAGCATAAGATCCCAAAGC-3’
CPj0709	-	5’-GATTTGGAAGTATTTCAAGCAGAC-3’
		5’-GATTAGGGTTTAGAATATGGAGAG-3’
CPj0710	-	5’-AATAAGATGCTAGACGGCGTATG-3’
		5’-TGCATACGGAATTGCAAATTAAAC-3’
CPj0728	-	5’-GATCTGCAGACGTGGACTCA-3’
		5’-CCAAAGCAGCCTGTATGTCA-3’
CPj0769	*topA*	5’-ATGCAAGATCCCAAAACGAC-3’
		5’-AGTGACGGGCTTTCTCTTCA-3’
CPj0854	*ompB*	5’-TCTTGCAGGAAGCCTCAAAT-3’
		5’-AGAGGTAATGGTTGGCGTTG-3’
CPj0886	*hctA*	5’ATGGCGCTAAAAGATACGGCAA-3’
		5’TTATTTTCTAAATCCGCGTG-3’
CPj0933	-	5’-TGATCAATGGCATCATGCTT-3’
		5’-ACTGGTGGCGAATGTACTCC-3’
CPj0934	*rnpA*	5’-CCAAGACGATGTAACCCCTCTG-3’
		5’-TTGTTTTCCCCAAGGGACATAAAC-3’
CPj0935	*rl34*	5’-GACTAGGGAATGCCTACCGTG-3’
		5’-GTGAAACGGACTTATCAACCTAG-3’
CPj0970	*yccA2*	5’-TCTCGAGTGCAGGGAACTTT-3’
		5’-ACCACACCCACCAAAAAGAA-3’
CPj0971	*ftsY*	5’-GGATACCTTTCGAGCTGCTG-3’
		5’-TGCAGATTGAATCCCATCAA-3’
-	*16S rRNA*	5’-GGTAAAGAAGCACCGGCTAAC-3’
		5’-ACTTTCCTTTCCGCCTACACGC-3’

Fig. S1 Chlamydial gene expression profile on the genome map.
Chlamydial gene expression profile on the genome map. The data of the DNA microarray were represented as colored bars on the genome map. The innermost circle represents locations of spots with lower intensity than threshold (undetectable) when any cDNA was hybridized. The next 5 circles represent the DNA microarray data at 24, 36, 48, 60 and 72 hpi from inner to outer, respectively. Color of the line represents relative intensity of each spot. The outermost circle indicates the location of all DNA fragments included on the DNA microarray. A blue arrow head indicates an undetected cluster of genes encoding *C. pneumoniae*-specific hypothetical proteins (CPj0456-CPj465).

Fig. S2 Quantitative RT-PCR of chlamydial gene.
Expression of some chlamydial genes was analyzed with quantitative RT-PCR during chlamydial development. Data normalized with 16S rRNA were represented. The maximum point of each gene is used as a reference. A. Genes induced drastically at 48 h or more after infection. Their relative expression is very low at 24 and 36 hpi, less than 0.2, followed by a rapid increase, reaching a peak at 72 hpi. Transcript of *hctA* and *hctB* genes was under detection limit at 24 hpi and increased drastically at 48 hpi and later. B. Genes up-regulated at 48 h and later after infection. Their relative expression is between 0.2 and 0.5 at 24 and/or 36 hpi, followed by a gradual increase, reaching a peak at 72 hpi, except for CPj0416 (*himD*) and CPj0466 (*pmp_15*), the expression of which culminates at 60 hpi. C. Constitutively expressed genes during the infection. Their expression is between 0.5 and 1 at all points examined.

Fig. S1

Miura et al. Fig. S1. Top side

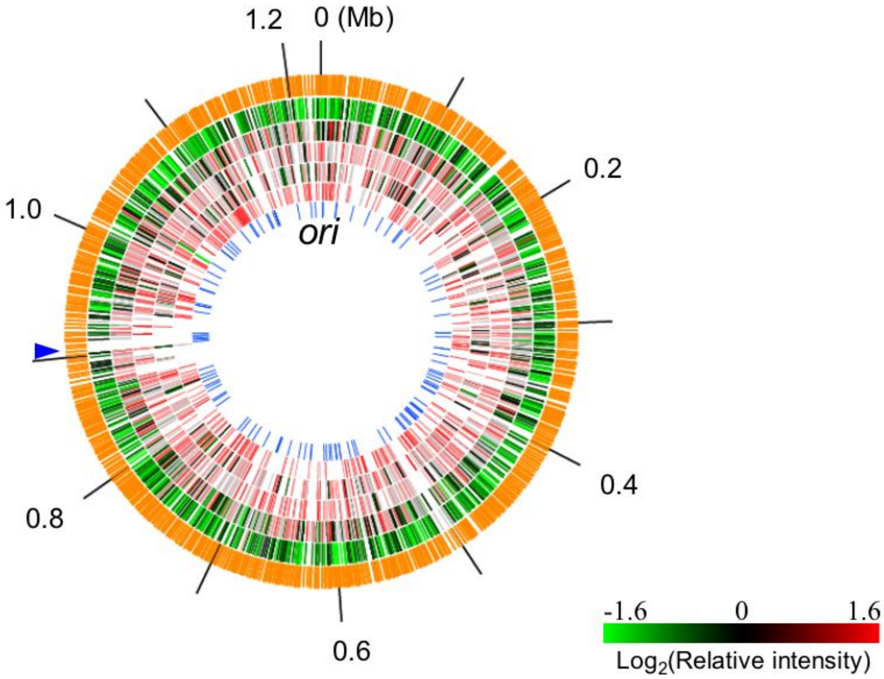
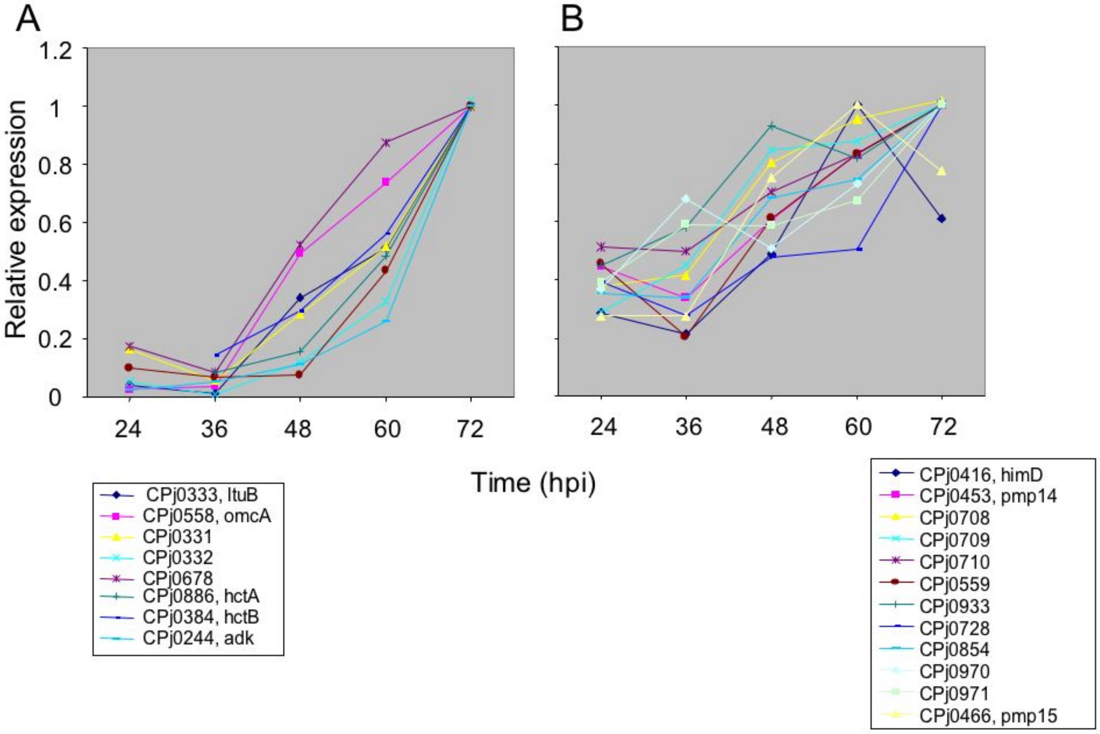


Fig. S2

Miura et al. Fig. S2A, S2B. Top side



Miura et al. Fig. S2C. Top side