

Supplementary Information

Modeling of variables in cellular infection reveals CXCL10 levels are regulated by human genetic variation and the *Chlamydia*-encoded CPAF protease

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Supplementary Methods

R script used for modeling:

```
#####
```

```
master<-read.csv("PATH/TO/CXCL10_RANTES_Modeling.csv")
```

```
##RANTES Fold Change
```

```
glm.m1 = lm(master$log2.RANTES.Chlamydia...RANTES.Uninfected. ~
```

```
master$Population + master$X70hr.cell.death.Chlamydia +
```

```
master$Chlamydia.46hr..GFP.)
```

```
summary(glm.m1)
```

```
af <- anova(glm.m1)
```

```
afss <- af$"Sum Sq"
```

```
print(af)
```

```
print(afss)
```

```
print(cbind(af,PctExp=afss/sum(afss)*100))
```

```
##Remove the individual who is not genotyped at rs2869462 for modeling CXCL10
```

```
phenotypes
```

```
master<-master[-154,]
```

```
##CXCL10 Uninfected
```

```
glm.m1 = lm(master$log2.CXCL10.Uninfected. ~ master$rs2869462.Genotype +  
master$Population + master$X70hr.cell.death.Uninfected)
```

```
summary(glm.m1)
```

```
af <- anova(glm.m1)
```

```
afss <- af$"Sum Sq"
```

```
print(af)
```

```
print(afss)
```

```
print(cbind(af,PctExp=afss/sum(afss)*100))
```

```
##CXCL10 Chlamydia
```

```
glm.m1 = lm(master$log2.CXCL10.Chlamydia. ~ master$rs2869462.Genotype +  
master$Population + master$X70hr.cell.death.Chlamydia +  
master$Chlamydia.46hr..GFP.)
```

```
summary(glm.m1)
```

```
af <- anova(glm.m1)
```

```
afss <- af$"Sum Sq"
```

```
print(af)
```

```
print(afss)
```

```
print(cbind(af,PctExp=afss/sum(afss)*100))
```

```
##CXCL10 Fold Change
```

```
glm.m1 = lm(master$log2.CXCL10.Chlamydia...CXCL10.Uninfected. ~  
master$rs2869462.Genotype + master$Population +  
master$X70hr.cell.death.Chlamydia + master$Chlamydia.46hr..GFP.)
```

```
summary(glm.m1)
```

```
af <- anova(glm.m1)
```

```
afss <- af$"Sum Sq"
```

```
print(af)
```

```
print(afss)
```

```
print(cbind(af,PctExp=afss/sum(afss)*100))
```

```
#####
```

Supplementary Table

Phenotype data for levels of CXCL10 and RANTES is provided in:

TableS1_CXCL10_RANTES_Modeling

Full gels

Figure 4C

