**Table S4:** PCR array validation by quantitative PCR.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene** | **Status** | **Experiment** | **Fold change** | **p-value** |
| **Tnfrsf13c** | **Infection** | **PCR Array** | **-1,8483** | 0,013 (two-way ANOVA) |
| 0,004 (test) |
| **Quantitative PCR** | **-2,349** | 0,036 (t-test) |
| **Genotype** | **PCR Array** | **-2,786** | 0,00015 (two-way ANOVA) |
| 0,014 (t-test) |
| **Quantitative PCR** | **-2,266** | 0,046 (t-test) |
| **S100a8** | **Genotype** | **PCR Array** | **2,614** | 0,003 (two-way ANOVA) |
| 0,014 (t-test) |
| **Quantitative PCR** | **3,418** | 0,018 (t-test) |

Quantitative real-time PCR was performed to validate the Array data. Comparison of qPCR and array data for **(A)** genotype

and **(B)** infection status.