Supplementary Table S5.*Positive samples in qPCR for E. canis based on dsb with their respective quantification values, reaction parameters, and positive samplesin qPCR for Ehrlichia spp. based on groEL gene and in cPCRassays for Ehrlichia spp. based on 16SrRNA gene*.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Host | N° of copies/μL | Efficiency (%) | R2 | Slope | Y-int | qPCR *groEL* | cPCR 16SrRNA |
| *Canis familiaris* | 1.652x104 | 95.6 | 0.996 | -3.431 | 42.6 | 2.478x103 | **-** |
| *Canis familiaris* | 2.395x103 | 95.6 | 0.996 | -3.431 | 42.6 | 3.596x102 | **+** |
| *Canis familiaris* | 1.958x103 | 95.6 | 0.996 | -3.431 | 42.6 | 2.141x102 | **+** |
| *Canis familiaris* | 1.043x103 | 90.3 | 0.998 | -3.579 | 44.5 | 1.990x101 | **+** |
| *Canis familiaris* | 4.920x102 | 95.6 | 0.996 | -3.431 | 42.6 | **-** | **+** |
| *Canis familiaris* | 2.778x102 | 90.3 | 0.998 | -3.579 | 44.5 | **-** | **+** |
| *Canis familiaris* | 1.136x102 | 90.3 | 0.998 | -3.579 | 44.5 | **-** | **+** |
| *Canis familiaris* | 9.722x101 | 90.3 | 0.998 | -3.579 | 44.5 | **-** | **+** |
| *Canis familiaris* | 5.171x101 | 90.3 | 0.998 | -3.579 | 44.5 | **-** | **-** |
| *Polygenis (P.) bohlsi bohlsi* | 4.00x101 | 101.4 | 0.989 | -3.288 | 42.4 | **-** | **+** |

N° of copies - Number of copies/μL, R2 - Correlation coefficient, Y-int - intercepton the axis Y