These datasets are from an experimental infection of mice with strains of *Borrelia burgdorferi*.

The use of mice and all procedures in this study were reviewed and approved by the Animal Research Ethics Board (AREB), which is part of the University Animal Care Committee (UACC) at the University of Saskatchewan. The AREB-assigned animal use protocol number for our study was 20190012. The UACC follows the animal experimentation guidelines of the Canadian Council on Animal Care (CCAC).

IMPORTANT! In the dataset: Ear punch qPCR testing master file, punch 4 is the same as R\_ear in the necropsy tissue dataset. If you are going to combine the datasets, remove punch 4, or R\_Ear

Both datasets contain “n/a” values. The structure of the datafile means many columns are not applicable to each sample row (i.e., there are no “Strain” values for uninfected control mice). Similarly, samples with no qPCR detection have no Cq value, and thus no values in the columns generated using Cq. Samples below the standards detection threshold of one *23S* copy/µL are likewise changed to “n/a” values to prevent the inclusion of false positive values in the analyses.

For questions or use of the data, contact Chris Zinck: [chris.zinck@usask.ca](mailto:chris.zinck@usask.ca)

Ear Punch legend

|  |  |
| --- | --- |
| Header | Details |
| Treatment | 2 levels: control, challenged. Denotes whether mice were infested with infected or uninfected nymphs |
| Status | 2 levels: Positive, Negative. The infection status of the mouse |
| Strain | The strain of Borrelia burgdorferi that the mice were challenged with (Having a strain value does not mean  The mouse is infected) |
| Punch | 5 levels: 0 - (pre-inf, left ear), 1 - (1st larval, right ear), 2 - (2nd larval, right ear),  3 - (3rd larval, right ear), 4 - (terminal sample, right ear) |
| Mouse | The mouse ID number |
| Cq | The quantification cycle for the 23s qPCR |
| spiro.extract | A value derived from the 23s standard regression.  Formula: ((((10^((G\_\_-40.351)/(-3.4055)))/2)\*[**55 OR 100]**)/3)  each ear punch extraction was in 55uL, with 3uL per qPCR. The terminal samples (punch 4) were in 100µL. |
| tissue.mg | The weight (mg) of the tissue sample used in the DNA extraction |
| spiro.tissue.mg | spiro.extrac/tissue.mg |
| log.spiro.tissue.mg | log10(spiro.tissue.mg) |
| DNA ng/ul | DNA concentration (ng/uL) of the sample, measured via Nanodrop |
| spiro.DNA.mg | spiro.extrac/(DNA.conc.ng.uL\*100)\*1000 |
| log.spiro.DNA.mg | log10(spiro.DNA.mg) |
| Beta.cq | The quantification cycle for the Beta actin qPCR |
| Beta.extrac | Like spiro.extrac, a value derived from the standard regression. Formula:  ((((10^((O\_-38.713)/(-3.4754)))/2)\*[**55 OR 100**])/1) each ear punch extraction was in 55uL,  with 1uL per qPCR. The terminal samples (punch 4) were in 100µL.  Beta actin has 2 copies per mouse cell |
| spiro.per.million.beta | (spiro.extrac/Beta.extrac)\*1000000 |
| log.spiro.per.million.beta | log10(spiro.per.million.beta) |
| tissue.inf.status | 2 levels: 1, 0. Binary variable representing infection status of the tissue |
| mouse.inf.status | 2 levels: 1, 0. Binary variable that is the same as Status |
| block | 5 levels: 1-5. Refers to sub-levels of temporal.block that were batch handled at slightly different  timepoints (i.e. morning versus evening) |
| temporal.block | 2 levels: 1 (first block), 2 (second block). The two batches of 60 mice processed at separate times.  Temporal.block contains block |
| sex | 2 levels: female, male. The sex of the mouse |
| n.total | n.total = 3: the total number of nymphs used to infest the mouse |
| n.engorged | the number of engorged nymphs recovered from n.total |
| n.eng.inf | the number of engorged nymphs that tested positive for B burgdorferi from n.engorged |
| Region | 2 levels: east, west. The geographic origins of the strains of Borrelia burgdorferi |

Necropsy Legend

|  |  |
| --- | --- |
| Column header | Details |
| Treatment | 2 levels: control, challenged. Denotes whether mice were infested with infected  or uninfected nymphs |
| Status | 2 levels: Positive, Negative. The infection status of the mouse |
| Strain | The strain of Borrelia burgdorferi that the mice were challenged with  (Having a strain value does not mean the mouse is infected) |
| Mouse | The mouse ID number |
| Tissue | 7 levels: Skin, L\_Ear, R\_Ear, Hrt, Blad, Kid, Joint. The specific tissue from each mouse |
| necrop.plate | An ID corresponding to the 96-well plates these samples were run on for 23s qPCR  (i.e., each sample with "1" was run at the same time, same plate) |
| Cq | The quantification cycle for the 23s qPCR |
| tissue.mg | The weight (mg) of the tissue sample used in the DNA extraction |
| spiro.extrac | A value derived from the 23s standard regression. Formula:  ((((10^((G\_\_-40.351)/(-3.4055)))/2)\*100)/3) each extraction was in 100uL,  with 3uL per qPCR. 23s has 2 copies per spirochete |
| spiro.tissue.mg | spiro.extrac/tissue.mg |
| log.spiro.tissue.mg | log10(spiro.tissue.mg) |
| DNA.conc.ng.ul | DNA concentration (ng/uL) of the sample, measured via Nanodrop |
| spiro.DNA.mg | spiro.extrac/(DNA.conc.ng.uL\*100)\*1000 |
| log.spiro.DNA.mg | log10(spiro.DNA.mg) |
| Beta.cq | The quantification cycle for the Beta actin qPCR |
| Beta.extrac | Like spiro.extrac, a value derived from the standard regression. Formula:  ((((10^((O\_-38.713)/(-3.4754)))/2)\*100)/1) each extraction was in 100uL, with 1uL  per qPCR. Beta actin has 2 copies per mouse cell |
| spiro.per.million.beta | (spiro.extrac/Beta.extrac)\*1000000 |
| log.spiro.per.million.beta | log10(spiro.per.million.beta) |
| log.spiroplusone.per.million.beta | log10(((spiro.extrac+1)/Beta.extrac)\*1000000) |
| log.spiroplusone.per.TENmillion.beta | log10(((spiro.extrac+1)/Beta.extrac)\*10000000) |
| beta.DNA.mg | Beta.extrac/(DNA.conc.ng.uL\*100)\*1000 |
| tissue.inf.status | 2 levels: 1, 0. Binary variable representing infection status of the tissue |
| mouse.inf.status | 2 levels: 1, 0. Binary variable that is the same as Status |
| block | 5 levels: 1-5. Refers to sub-levels of temporal.block that were batch handled  at slightly different timepoints (i.e. morning versus evening) |
| temporal.block | 2 levels: 1 (first block), 2 (second block). The two batches of 60 mice processed at  separate times. Temporal.block contains block |
| sex | 2 levels: female, male. The sex of the mouse |
| n.total | n.total = 3: the total number of nymphs used to infest the mouse |
| n.engorged | the number of engorged nymphs recovered from n.total |
| n.eng.inf | the number of engorged nymphs that tested positive for B burgdorferi from n.engorged |
| Region | 2 levels: east, west. The geographic origins of the strains of Borrelia burgdorferi |