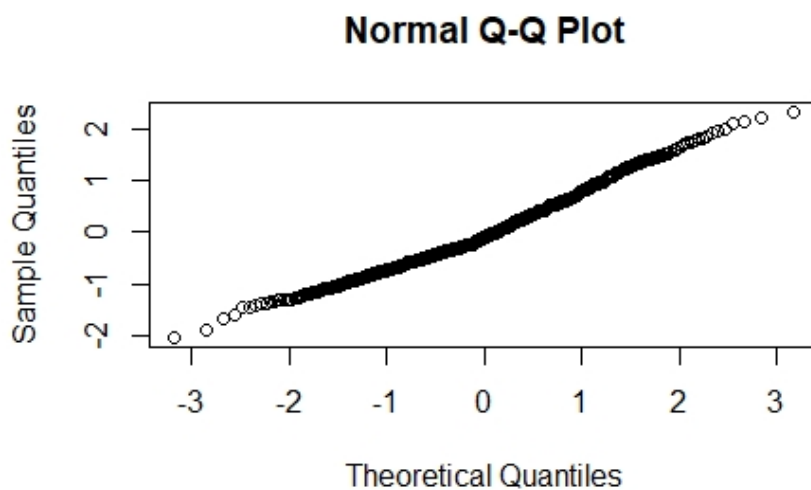
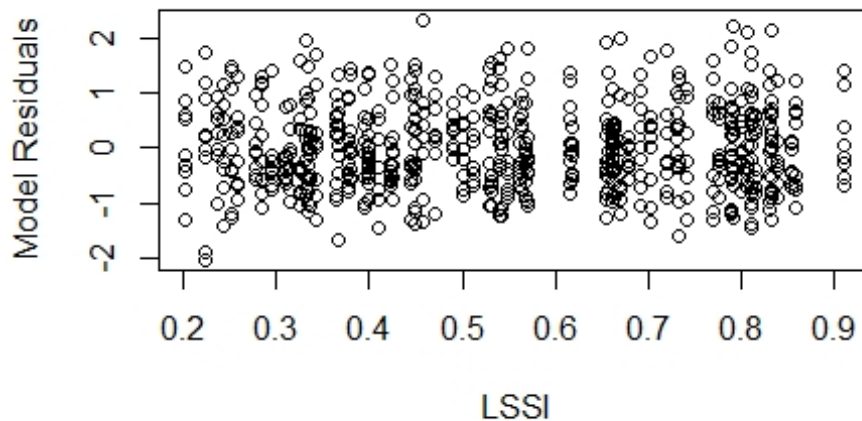


S3 Fig. LSSI Model Diagnostics.

Plotting model residuals (of \log_{10} E. coli per gram dry soil) vs. LSSI shows that the linearity assumption in regression is true and the QQ plot shows the residuals are normally distributed. We performed Levene's test on our model, rejected the null hypothesis ($p=0.79$), and assumed homoscedasticity.



Lmer model output

```
Linear mixed model fit by REML ['lmerMod']
Formula: ecoli_log50 ~ Sun + Local + cssi_10 + Chicken + Duck + poverty_q +
  (1 | compound/household)
Data: soildata
```

REML criterion at convergence: 1792.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.49	-0.65	-0.12	0.64	2.85

Random effects:

Groups	Name	Variance	Std.Dev.
household:compound	(Intercept)	0.05	0.21
compound	(Intercept)	0.16	0.40
Residual		0.66	0.81

Number of obs: 675, groups: household:compound, 600; compound, 75

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	2.61	0.24	10.76
Sun_partial	0.13	0.12	1.09
Sun_shade	0.39	0.12	3.26
Localfood	0.19	0.14	1.37
Localentrance	0.29	0.14	2.09
LocalHH	0.14	0.14	1.04
LocalHH2	0.14	0.14	0.98
LocalLatrine	0.45	0.14	3.23
Localgarbage	0.74	0.14	5.29
Localdishes	0.82	0.14	5.88
Localclothes	0.75	0.14	5.41
lssi_10	-0.05	0.03	-1.77
ChickenYes	0.65	0.17	3.79
DuckYes	0.42	0.25	1.69
poverty_q	-0.09	0.05	-1.81

	2.5 %	97.5 %
.sig01	0.00	0.47
.sig02	0.30	0.49
.sigma	0.70	0.88
(Intercept)	2.14	3.07
Sun_partial	-0.10	0.35
Sun_shade	0.16	0.62
Localfood	-0.08	0.47
Localentrance	0.02	0.56
LocalHH	-0.13	0.42
LocalHH2	-0.13	0.41
LocalLatrine	0.18	0.73
Localgarbage	0.47	1.01
Localdishes	0.55	1.10
Localclothes	0.48	1.02
cssi_10	-0.11	0.00
ChickenYes	0.33	0.99
DuckYes	-0.06	0.90
poverty_q	-0.19	0.01

anova(Levene.Model) #displays the results
Analysis of Variance Table

Response: Model.Res2	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cssi_10	1	0.04	0.04	0.07	0.79
Residuals	673	391.70	0.58		