Supplemental Analyses

In examining associations between Disgust and infection variables, we first used simple models and then added random effects to account for non-independence. However, using random effects to adjust for covariance by household and community ignores the fact that this covariance is also of interest because it can reveal community and household patterns in infection and Disgust, which might result from shared environments or cultural transmission. Thus, our final models include explicit parameters for community and household effects, as described in the main text. We went through these steps so we could explicitly examine how accounting for clustering affected estimates.

Analyzed across all communities and households, with no adjustment for the non-independence of household and community members (**Figure S3**), strong negative associations were seen between both Disgust and Inflammation (Standardized β: -0.39, CI: -0.62, -0.16) and Disgust and Parasites (β: -0.20, CI: -0.43, 0.03).

Controlling for community and household with random effects terms (**Table S5**), the negative association between Disgust and Inflammation was largely unchanged (β: -0.34, CI: -0.60, -0.07), while the association between Disgust and Parasites was largely eliminated (β: -0.03, CI: -0.24, 0.18).

In building path models, we first examined the effects of household clustering before accounting for community (**Figure S3C-F**). In these models we found associations between an individual's infection levels and the disgust sensitivity of his or her household members. However, these effects were partially indirect and mediated through other pathways. For example, considered alone, the Disgust of an individual's other household members was associated with that individual's Inflammation (β: -0.41, CI: -0.74, -0.09), but when controlling for that individual's Disgust, this direct effect was reduced (β: -0.24, CI: -0.58, 0.10). However, household member Disgust was associated with individual Disgust (β: 0.54, CI: 0.15, 0.25), which was in turn associated with Inflammation (β: -0.32, CI: -0.56, -0.07).

A more dramatic example of this mediation is seen with Parasites. The association between Disgust and Parasites was greatly reduced when household and community level clustering of Parasites was considered (**Figure S3**).

We hypothesized that PDS would protect against infection, and our models were set up with this prediction in mind. However, it is worth cautioning that our models cannot conclusively establish causality or the direction of effects. As a final analysis step, we also constructed models with reversed causality, i.e. with infection predicting disgust. We ran models similar to **Figure 2**, but with PDS dependent on infection rather than vice-versa (**Figure S5**). Overall, these models yielded similar associations. Model fits (assessed with 10-fold cross validation) with reverse causality were not distinguishably better or worse than those in **Figure 2**.

Validation of Analysis Assumptions

The current analysis assumes that a cross-sectional sample of biomarkers can be used to assess whether disgust has protected someone against infection. Biomarkers are indirect measures in the sense that they measure a downstream consequence of infection, rather than infection itself. In our assays we measured two types of biomarker responses: markers of an inflammatory response (CRP and IL-6) typical of short-term infections [1-4], and a composite measure of parasite load/exposure, composed of fecal EPG and IgE. Apart from the biomarkers used to distinguish them, three primary features

differentiate these two measures. The first is the time course of infection: inflammatory responses are typical of short-term infections lasting a week or two [2-4], while parasitic infections may last months or years [1, 5-6]. The second is the way infections progress. Infections caused by viral, bacterial, or other single-celled organisms can become systemic as the pathogen replicates in the host. This causes a rapid increase in inflammatory biomarkers, followed by a relatively rapid drop after the infection resolves [3]. Infections caused by macroparasites, such as helminths, do not behave in this way. These parasites cannot replicate in the host, so parasite load is dependent on continued exposure to new infections. Helminth infections may last for months or years [7].

To examine whether the type of infection might affect our power to detect protective effects of disgust, we created a simple model which simulates each type of infection over time. Complete simulation code is available at https://github.com/adblackwell/shuardisgust. In the simulation each individual has a disgust value which modifies their daily probability of contracting a new infection. Disgust does not affect duration or intensity of infection once acquired. While infected, individuals experience elevated biomarkers. Biomarkers decline gradually after the infection ends. By varying the duration of infection and whether individuals are able to contract multiple infections we can simulate biomarker responses to either inflammatory or parasitic infections (**Figure S6**). Parameters for the models reflect the effect of disgust, the daily likelihood of infection, the distribution of infection durations, and the rate of decline of biomarkers when infection load ends or decreases.

We simulated biomarker responses for 750 individuals under a range of circumstances, varying the effect of disgust on infection risk (expressed as an odds-ratio per 1 standard deviation change in disgust) as well as the baseline infection risk at average disgust levels (**Figure S7**). From these simulated biomarker progressions, we sampled 75 individuals once each at random time points, to match the sample size used in the empirical study. We repeated this sampling 50 times, and each time tested whether we detected the association between disgust and infection that was used to generate the simulated infection progression.

The results suggest that for inflammatory infections that occur with 20% or higher probability per month, a sample size of 75 is sufficient to obtain reliable posterior estimates >80% of the time when a 1 standard deviation difference in disgust causes a reduction in infection risk of ~30%. Weaker effects of disgust should still be detected, but with less certainty. For effects on parasitic infections, the study should be even more sensitive (**Figure S7C-D**). This is because differences in disgust should result in long-term differences in biomarker levels, which are more readily measured by a sampling a random time point. This is illustrated by examining the interaction between infection duration and infection prevalence on power to detect an effect (**Figure S8**). Figure S8 shows that an infection must either be sufficiently prevalent or sufficiently long for an effect of disgust to be picked up in this kind of cross-sectional sampling.

Perhaps more relevant to evaluating our current results is the probability of detecting an effect when no effect is present. To this end, we ran a simulation in which Disgust had no effect on Inflammation and examined the proportion of trials in which we recovered a parameter estimate of -0.25 or lower. Out of 300 simulated trials, a false effect of this magnitude or stronger was detected in only 2% of trials.

Comparing the simulation results to our empirical data, 14% of our sample had elevated CRP or IL-6 in the cross-sectional sample. If we assume this is indicative of a recent or current infection and that an infection lasts 1-2 weeks, then this is likely equivalent to a monthly risk of about 30-50%. It is more

difficult to estimate monthly exposure to helminths, but in the sample roughly 60% were positive for helminth infections, and about 40% had high levels of infection, so likely this is relatively high as well.

The standardized parameter values obtained from the empirical results (**Figure 2**) are around -0.30 for inflammatory biomarkers, comparable to the results produced from an initial reduction in infection odds of about 30% (**Figure S9**). Given the cumulative nature of parasite infections, however, the biomarker is potentially more sensitive to disgust. The low parameter estimates we obtained (around -0.10 after correcting for clustering) are suggestive of a very small effect of disgust. Even larger values, as high as the -0.35 obtained for contagion disgust on parasites when with no cluster correction is applied (**Figure S3C**), would not be indicative of much more than a 10% reduction in infection risk.

Additional Methods Information

Style of Life Interviews and Variables. The selection of items used in the Shuar SOL scales was based on extensive ethnographic observations and pilot testing by one author (LSS). These SOL scales have been used in previous research among the Shuar [8-10]. Two scales were created from the MSL index: Traditional Style of Life (TSOL) and Market-Integrated Style of Life (MSOL). The final TSOL scale contained six items reflecting investment in a foraging lifestyle (fishing hook/line, hunting dogs, blowgun, firearm, fishing net, canoe), while the MSOL scale included 12 items reflecting investment in a market economy (radio, propane stove, mobile phone, television, chainsaw, bicycle, refrigerator, computer, outboard motor, motorcycle, car, truck). Individual scores on each of the MSOL and TSOL were calculated as the fraction of list items owned (range 0-1).

Seven household measures were also incorporated in the SOL questionnaire to capture household construction, access to water and electricity, market participation, and risk of pathogen exposure. These included, in order of increasing market integration, floor (0: dirt, 1: palmwood, 2: milled lumber, 3: concrete; 4: tile), wall (0: palmwood, 1: mixed, 2: milled lumber, 3: cinder block), latrine type (0: none, 1: pit toilet, 2: indoor toilet without water, 3: outdoor toilet with water, 4: indoor toilet with water), water source (0: river/stream/spring pond, 1: well or outdoor pipe, 2: indoor pipe), electricity (0: none, 1: lights only, 2: outlets), number of rooms in house (total number), and number of houses owned (total number). A Household Style of Life (HSOL) value for each household was computed based on a summation of the scores [8-9].

Biomarker Assays. Biomarkers were analyzed using commercially-available enzyme-linked immunosorbent assays (ELISAs) for IgE (E80-108; Bethyl Laboratories, Montgomery, TX) and IL-6 (HS600B; R&D Systems, Minneapolis, MN), and commercially-available antibodies for CRP (M86005M [coating], M86264M [detection]; Biodesign, Memphis, TN) based on previously established dried blood spot protocols [5-6, 11-13]. Immunoglobulin-E and CRP were run in duplicate and cases where CVs were over 12% were rerun. The average sample intra-assay CVs for IgE and CRP were 2.89% and 4.74%, respectively. Interleukin-6 was only run in single due the large amount of sample needed per assay and limited sample availability. Six samples yielded IL-6 levels below the limit of detection. These were set to the lower level of detection of the assay (0.006 pg/mL).

Statistical Analyses. For the 19 disgust questions, we used `principal` in the `psych` package [14] to first reduce the disgust scale to a single component. Scores were extracted via regression. In later analyses we extracted three rotated components, as suggested by parallel analysis and scrutiny of scree plots. An oblimin rotation was chosen to improve interpretability without assuming components to be

uncorrelated, since theoretically dimensions of disgust should covary. Overall, the three components were marginally correlated (r between 0.16 and 0.33).

Because the second component included three items related to consumption of raw animal products (**Table S1**), we repeated the factor analysis but replaced these three items with a single item representing the mean of these three questions. Components extracted with this single raw animal products score were nearly identical, suggesting the second factor was not purely dependent on the replication of these similar questions.

Infection variables (CRP, IL-6, *A. lumbricoides* and *T. trichiura* egg counts) were log transformed and standardized prior to analysis. Out of 75 cases, there were missing values for IgE, CRP, and IL-6 (n = 15, 11, and 19, respectively). Cases were missing due to insufficient blood spots available on DBS cards. To avoid excluding these cases and introducing bias, we used multivariate imputation by chained equations (`mice` [15]) to generate 10 imputed datasets, using random forest imputation. The 10 imputed datasets were merged, and a principal components analysis of infection variables was performed. Parallel analysis suggested two components (**Table S3**). These were clearly identifiable as Parasites and Inflammation and were labeled as such. Component scores were extracted for each individual in each of the ten imputed datasets via regression. Component scores were extracted for each individual in each of the ten imputed datasets. Mean correlations between component scores for each of the 10 imputed datasets were r=0.84±0.05 for Inflammation and r=0.95±0.02 for Parasites, reflecting the fact that only some of the variables contributing to overall scores were imputed.

For each individual, we calculated the mean disgust, infection, and market integration value for all household members excluding the target individual. We then calculated these values for all community members, excluding the household. In this way, each individual had a unique value for other household members excluding themselves, and for other community members excluding themselves and their household. This ensured that values for individual, household, and community were independent, since for each individual, the household was not a component of the value for other community members, and the individual is not a component of either the score of their neighbors or other household members. Modeling using these variables explicitly modeled the contribution of other household and community members to the variance in the dependent variable, an approach that differs from using random effects to control for covariance within hierarchical groupings. However, both approaches control for covariance by making it part of the model. Some models did include random effects to control for lack of independence in repeat measures, as appropriate.

Models were fit using `brm_multiple` in the `brms` package [16], which fits models based on multiple imputed datasets and then combines posterior estimates. All models used default non-informative priors except the models in Tables S4 and S5, which included regularizing priors for the effects of community-level inflammation. These were included since the posterior in a few (but not most) models suggested unlikely negative associations between inflammation at the community and at the household and individual levels. Components of multivariate path models were fit simultaneously in the same model. Inspection of individual model Rhats within the `brm_multiple` output was used to assess model convergence. Reported values are the mean posterior estimate and 95% credibility interval.

Code for all analyses is posted at http://doi.org/10.5281/zenodo.4487336.

Table S1. Disgust questionnaire principal components

	Single Factor	Three Factor		
		1: Contagion	2: Food	3: Various
Finding a worm in your food	0.590	0.855		-0.227
Stepping in feces with bare feet	0.746	0.772		
Drinking *chicha* made by someone who has no teeth	0.686	0.766		
Someone vomiting on your shoes	0.725	0.715	0.156	
Drinking *chicha* made by someone who is ill	0.753	0.713		0.199
Finding a cockroach in your food	0.524	0.635		-0.128
Someone coughing in your face	0.655	0.570		0.297
Knowing someone has not bathed in three days	0.495	0.549	-0.102	0.147
A dog licking your face	0.567	0.473		0.224
Drinking brown, dirty water	0.696	0.419	0.144	0.418
Eating raw fish	0.550	-0.111	0.928	
Eating raw chicken	0.576		0.923	
Eating raw beef	0.679	0.209	0.835	-0.108
Eating meat that has gone bad	0.512		0.716	
Picking up a dead animal with your hands	0.711	0.295	0.500	0.215
Not washing your hands before eating	0.514		0.351	0.522
Seeing a rat in your kitchen	0.627	0.150	0.316	0.513
Coming into contact with someone else's blood	0.442	0.236	-0.232	0.698
Finding a spider in your house	0.391	-0.106		0.860

Table S2. Infection data principal components

	1: Parasites	2: Inflammation
Ascaris EPG	0.847	
Trichuris EPG	0.472	-0.118
IgE	0.731	0.333
CRP	-0.534	0.583
IL-6	0.146	0.821

All variables were natural log transformed prior to analysis.

Table S3. Summary statistics by community

Community	1 (n=30)	2 (n=27)	3 (n=18)	$F_{2,72}$	p
Total Disgust	0.68 (0.63)	-0.35 (1.01)	-0.61 (0.77)	17.28	<0.01
C1: Contagion	0.60 (0.47)	-0.08 (1.06)	-0.89 (0.82)	18.58	<0.01
C2: Food	0.53 (0.49)	-0.53 (1.17)	-0.08 (0.88)	9.96	<0.01
C3: Various	0.27 (0.90)	-0.30 (0.94)	0.00 (1.10)	2.40	0.10
Parasites	-0.40 (0.67)	-0.19 (1.10)	0.95 (0.63)	10.59	<0.01
Inflammation	-0.29 (0.83)	0.21 (1.01)	0.18 (1.12)	1.27	0.29
MSOL	0.64 (1.06)	-0.16 (0.67)	-0.82 (0.45)	18.27	<0.01
HSOL	1.07 (0.55)	-0.56 (0.44)	-0.94 (0.28)	134.69	<0.01
TSOL	-0.23 (1.00)	-0.13 (0.69)	0.57 (1.15)	4.33	0.02
Age	20.2 (15.8)	19.7 (13.1)	19.3 (15.5)	0.02	0.98
Sex (% male)	33%	41%	56%	$X^2 = 2.30$	0.32

Values are means (standard deviations) except for sex. All values except sex and age are standardized and centered.

Table S4. Variance components estimated by random effects

Variable	Community	Household	Individual
Total Disgust	0.65	0.03	0.31
C1: Contagion	0.52	0.06	0.42
C2: Food	0.69	0.02	0.29
C3: Various	0.26	0.03	0.71
Parasites	0.69	0.15	0.16
Inflammation	0.27	0.11	0.62
MSOL	0.60	0.37	0.03
HSOL	0.91	0.09	0.00
TSOL	0.52	0.31	0.17

Table S5. Simplified models with household and community level random intercepts

Dependent	Independent	Estimate	l-95% CI	u-95% CI
Inflammation	Intercept	-0.20	-0.99	0.58
	Age	0.01	-0.00	0.03
	Sex	-0.16	-0.62	0.31
	Total Disgust	-0.34	-0.60	-0.07
	sd(Household)	0.29	0.01	0.71
	sd(Community)	0.41	0.01	1.87
Parasites	Intercept	0.04	-1.58	1.61
	Age	-0.00	-0.02	0.01
	Sex	0.23	-0.14	0.59
	Total Disgust	-0.03	-0.24	0.18
	sd(Household)	0.57	0.34	0.85
	sd(Community)	1.25	0.30	3.64

Table S6. Disgust and Inflammation or Parasites

		Model	
Dependent	**Independent**	**Inflammation**	**Parasites**
Infection	Intercept	-0.16 (-0.59, 0.28)	0.00 (-0.34,0.33)
Disgust	Intercept	0.11 (-0.27, 0.49)	0.11 (-0.27,0.49)
HHInfection	Intercept	-0.01 (-0.25, 0.23)	0.01 (-0.28,0.29)
HHDisgust	Intercept	-0.01 (-0.24, 0.23)	-0.01 (-0.23,0.22)
Infection	Age	0.01 (0.00, 0.03)	0.00 (-0.02,0.01)
Infection	Sex	-0.20 (-0.68, 0.28)	0.22 (-0.16,0.61)
Infection	Disgust	-0.31 (-0.56,-0.06)	-0.06 (-0.26,0.15)
Infection	HHDisgust	-0.21 (-0.58, 0.16)	0.10 (-0.18,0.38)
Infection	HHInfection	0.09 (-0.30, 0.45)	0.70 (0.46,0.93)
Infection	ViInfection	-0.06 (-0.35, 0.22)	0.28 (-0.09,0.66)
Disgust	Age	-0.01 (-0.02, 0.01)	-0.01 (-0.02,0.01)
Disgust	Sex	-0.04 (-0.46, 0.38)	-0.04 (-0.46,0.38)
Disgust	HHDisgust	0.26 (-0.06, 0.59)	0.26 (-0.06,0.59)
Disgust	ViDisgust	0.67 (0.23, 1.11)	0.68 (0.24,1.12)
HHInfection	HHDisgust	-0.34 (-0.73, 0.06)	-0.18 (-0.39,0.02)
HHInfection	ViInfection	-0.04 (-0.33, 0.24)	0.50 (0.00,0.99)
HHDisgust	ViDisgust	0.58 (0.19, 0.96)	0.61 (0.22,1.00)
HHInfection	sd(Household)	0.50 (0.25, 0.80)	0.73 (0.54,1.00)
HHDisgust	sd(Household)	0.53 (0.37, 0.75)	0.53 (0.36,0.76)
	cor(Household)	-0.34 (-0.82, 0.37)	0.03 (-0.42,0.47)

Model Formula:
Infection ~ Age + Sex + PDSTotal + HHPDSTotal + HHInfection + ViInfection
PDSTotal ~ Age + Sex + HHPDSTotal + ViPDSTotal
HHInfection ~ HHPDSTotal + ViInfection + (1 | p | Household)
HHPDSTotal ~ ViPDSTotal + (1 | p | Household)
Infection = Inflammation or Parasites, as indicated. Disgust = Total Disgust
HH = Household mean, excluding target individual. Vi = Village mean, excluding target household. Items below the grey bar are group level effects for Household

Table S7. Disgust and Inflammation or Parasites with Market Integration Variables

		Model	
Dependent	**Independent**	**Inflammation**	**Parasites**
Infection	Intercept	-0.17 (-1.19, 0.81)	0.04 (-1.02,1.06)
Disgust	Intercept	0.06 (-1.23, 1.44)	0.06 (-1.26,1.44)
HHInfection	Intercept	0.00 (-0.90, 0.90)	0.03 (-1.38,1.48)
HHDisgust	Intercept	-0.01 (-0.93, 0.82)	0.00 (-0.87,0.86)
Infection	Age	0.01 (-0.01, 0.03)	-0.01 (-0.02,0.01)
Infection	Sex	-0.19 (-0.66, 0.29)	0.20 (-0.19,0.58)
Infection	Disgust	-0.34 (-0.62,-0.06)	-0.02 (-0.23,0.20)
Infection	HHDisgust	-0.25 (-0.70, 0.21)	0.12 (-0.19,0.43)
Infection	HHInfection	0.03 (-0.36, 0.41)	0.66 (0.41,0.91)
Infection	MSOL	0.06 (-0.28, 0.39)	-0.15 (-0.39,0.10)
Infection	TSOL	-0.16 (-0.42, 0.11)	0.14 (-0.07,0.36)
Infection	HOUSE	0.04 (-0.37, 0.48)	0.04 (-0.29,0.40)
Disgust	Age	0.00 (-0.02, 0.01)	0.00 (-0.02,0.01)
Disgust	Sex	-0.04 (-0.46, 0.37)	-0.04 (-0.46,0.37)
Disgust	HHDisgust	0.06 (-0.30, 0.43)	0.07 (-0.30,0.43)
Disgust	MSOL	0.26 (-0.01, 0.53)	0.26 (-0.01,0.54)
Disgust	TSOL	-0.07 (-0.30, 0.15)	-0.07 (-0.29,0.15)
Disgust	HOUSE	0.05 (-0.41, 0.47)	0.05 (-0.40,0.47)
HHInfection	HHDisgust	-0.31 (-0.75, 0.14)	-0.13 (-0.34,0.07)
HHInfection	MSOL	0.03 (-0.25, 0.30)	0.13 (-0.12,0.37)
HHInfection	TSOL	-0.09 (-0.29, 0.11)	-0.11 (-0.26,0.05)
HHInfection	HOUSE	-0.08 (-0.51, 0.35)	-0.41 (-0.96,0.11)
HHDisgust	MSOL	0.15 (-0.09, 0.37)	0.15 (-0.08,0.37)
HHDisgust	TSOL	0.06 (-0.10, 0.20)	0.07 (-0.08,0.22)
HHDisgust	HOUSE	0.28 (-0.10, 0.61)	0.28 (-0.11,0.62)
HHInfection	sd(Household)	0.52 (0.25, 0.83)	0.75 (0.54,1.05)
HHDisgust	sd(Household)	0.46 (0.29, 0.67)	0.46 (0.29,0.68)
Infection	sd(Community)	0.59 (0.02, 2.47)	0.63 (0.02,2.58)
Disgust	sd(Community)	0.91 (0.03, 3.25)	0.91 (0.04,3.25)
HHInfection	sd(Community)	0.54 (0.01, 2.30)	1.06 (0.08,3.39)
HHDisgust	sd(Community)	0.54 (0.01, 2.33)	0.54 (0.01,2.32)

Model Formula:

Infection ~ Age + Sex + PDSTotal + HHPDSTotal + HHInfection + +(1 | q | Village) + MSOL + TSOL + HOUSE

PDSTotal ~ Age + Sex + HHPDSTotal + (1 | q | Village) + MSOL + TSOL + HOUSE

HHInfection ~ HHPDSTotal + (1 | q | Village) + (1 | p | Household) + MSOL + TSOL + HOUSE

HHPDSTotal ~ (1 | q | Village) + (1 | p | Household) + MSOL + TSOL + HOUSE

Infection = Inflammation or Parasites, as indicated. Disgust = Total Disgust

HH = Household mean, excluding target individual. Vi = Village mean, excluding target household

Items below the grey bar are group level effects for Household

Table S8. Three Disgust Components and Inflammation with Market Integration Variables

		Model		
Dependent	**Independent**	**C1:Contagion**	**C2:Food**	**C3:Other**
Inflam	Intercept	-0.29 (-2.28, 1.68)	-0.31 (-2.65,1.94)	-0.24 (-1.54,1.12)
Disgust	Intercept	-0.06 (-3.07, 2.83)	-0.10 (-3.32,3.10)	0.39 (-0.72,1.52)
HHInflam	Intercept	0.00 (-1.63, 1.72)	0.05 (-1.58,1.89)	0.01 (-1.14,1.16)
HHDisgust	Intercept	-0.08 (-2.50, 2.38)	0.04 (-1.92,1.83)	0.01 (-1.06,1.07)
Inflam	Age	0.02 (0.00, 0.03)	0.02 (0.00,0.04)	0.02 (0.00,0.03)
Inflam	Sex	-0.16 (-0.64, 0.32)	-0.13 (-0.62,0.35)	-0.08 (-0.55,0.40)
Inflam	Disgust	-0.39 (-0.66,-0.12)	-0.29 (-0.57,0.01)	0.11 (-0.14,0.36)
Inflam	HHDisgust	-0.21 (-0.66, 0.23)	-0.13 (-0.55,0.27)	-0.19 (-0.60,0.23)
Inflam	HHInflam	0.00 (-0.42, 0.41)	0.05 (-0.40,0.49)	0.20 (-0.20,0.56)
Inflam	MSOL	0.00 (-0.29, 0.29)	0.05 (-0.29,0.39)	-0.09 (-0.40,0.21)
Inflam	TSOL	-0.17 (-0.43, 0.11)	-0.10 (-0.37,0.18)	-0.10 (-0.38,0.18)
Inflam	HOUSE	0.11 (-0.33, 0.61)	0.05 (-0.41,0.58)	0.06 (-0.40,0.63)
Disgust	Age	0.00 (-0.02, 0.01)	0.00 (-0.01,0.02)	-0.01 (-0.03,0.00)
Disgust	Sex	0.12 (-0.30, 0.54)	0.01 (-0.42,0.43)	-0.35 (-0.83,0.12)
Disgust	HHDisgust	0.17 (-0.20, 0.55)	-0.16 (-0.51,0.20)	-0.17 (-0.57,0.23)
Disgust	MSOL	0.16 (-0.11, 0.44)	0.44 (0.14,0.73)	-0.05 (-0.35,0.26)
Disgust	TSOL	-0.09 (-0.32, 0.13)	-0.02 (-0.26,0.22)	0.05 (-0.22,0.31)
Disgust	HOUSE	-0.04 (-0.50, 0.39)	-0.12 (-0.57,0.32)	0.27 (-0.18,0.69)
HHInflam	HHDisgust	-0.40 (-0.86, 0.04)	-0.26 (-0.60,0.06)	0.26 (-0.05,0.57)
HHInflam	MSOL	-0.01 (-0.28, 0.26)	0.01 (-0.28,0.30)	-0.01 (-0.32,0.33)
HHInflam	TSOL	-0.12 (-0.31, 0.07)	-0.08 (-0.27,0.12)	-0.12 (-0.33,0.08)
HHInflam	HOUSE	-0.01 (-0.45, 0.43)	-0.07 (-0.50,0.40)	-0.16 (-0.62,0.37)
HHDisgust	MSOL	0.09 (-0.15, 0.32)	0.23 (-0.01,0.45)	-0.02 (-0.25,0.22)
HHDisgust	TSOL	0.00 (-0.15, 0.15)	0.12 (-0.04,0.28)	0.08 (-0.09,0.24)
HHDisgust	HOUSE	0.20 (-0.21, 0.60)	0.08 (-0.30,0.42)	0.27 (-0.09,0.64)
HHInflam	sd(Household)	0.49 (0.20, 0.82)	0.53 (0.24,0.86)	0.65 (0.39,0.98)
HHDisgust	sd(Household)	0.51 (0.33, 0.74)	0.36 (0.19,0.57)	0.42 (0.21,0.67)
Inflam	sd(Community)	1.12 (0.02, 5.84)	1.30 (0.03,6.63)	0.83 (0.02,3.17)
Disgust	sd(Community)	1.83 (0.07, 8.16)	2.07 (0.28,8.56)	0.70 (0.03,2.70)
HHInflam	sd(Community)	0.94 (0.02, 5.18)	0.97 (0.02,5.31)	0.72 (0.02,2.89)
HHDisgust	sd(Community)	1.48 (0.07, 6.80)	1.09 (0.03,5.59)	0.69 (0.03,2.68)

Model Formula:

Inflam ~ Age + Sex + Disgust + HHDisgust + HHInflam + (1 | q | Village) + MSOL + TSOL + HOUSE

Disgust ~ Age + Sex + Disgust + (1 | q | Village) + MSOL + TSOL + HOUSE

HHInflam ~ HHDisgust + (1 | q | Village) + (1 | p | Household) + MSOL + TSOL + HOUSE

HHDisgust ~ (1 | q | Village) + (1 | p | Household) + MSOL + TSOL + HOUSE

Disgust = The component indicated for each model (C1-C3)

HH = Household mean, excluding target individual. Vi = Village mean, excluding target household

Items below the grey bar are group level effects for Household

Table S9. Three Disgust Components and Parasites with Market Integration Variables

		Model		
Dependent	**Independent**	**C1:Contagion**	**C2:Food**	**C3:Other**
Parasites	Intercept	0.04 (-1.92,1.99)	0.03 (-2.11,2.07)	0.05 (-0.94,1.05)
Disgust	Intercept	-0.06 (-3.12,2.92)	-0.11 (-3.34,3.05)	0.39 (-0.70,1.54)
HHParasites	Intercept	0.04 (-2.76,2.87)	0.05 (-3.03,3.10)	0.04 (-1.36,1.45)
HHDisgust	Intercept	-0.06 (-2.27,2.14)	0.04 (-2.04,2.06)	-0.01 (-1.01,1.00)
Parasites	Age	0.00 (-0.02,0.01)	0.00 (-0.02,0.01)	-0.01 (-0.02,0.01)
Parasites	Sex	0.14 (-0.24,0.52)	0.13 (-0.24,0.51)	0.17 (-0.21,0.56)
Parasites	Disgust	-0.07 (-0.28,0.16)	-0.02 (-0.23,0.20)	0.06 (-0.14,0.26)
Parasites	HHDisgust	0.07 (-0.26,0.40)	0.23 (-0.06,0.53)	-0.05 (-0.35,0.26)
Parasites	HHParasites	0.66 (0.39,0.93)	0.64 (0.36,0.90)	0.68 (0.43,0.92)
Parasites	MSOL	-0.12 (-0.36,0.13)	-0.18 (-0.44,0.08)	-0.13 (-0.37,0.10)
Parasites	TSOL	0.13 (-0.08,0.34)	0.10 (-0.10,0.31)	0.15 (-0.06,0.36)
Parasites	HOUSE	0.08 (-0.26,0.44)	0.08 (-0.26,0.46)	0.08 (-0.25,0.45)
Disgust	Age	0.00 (-0.02,0.01)	0.00 (-0.01,0.02)	-0.01 (-0.03,0.00)
Disgust	Sex	0.12 (-0.30,0.54)	0.01 (-0.41,0.43)	-0.35 (-0.82,0.12)
Disgust	HHDisgust	0.17 (-0.20,0.54)	-0.16 (-0.51,0.20)	-0.17 (-0.57,0.22)
Disgust	MSOL	0.16 (-0.11,0.43)	0.44 (0.14,0.74)	-0.04 (-0.34,0.27)
Disgust	TSOL	-0.09 (-0.31,0.13)	-0.02 (-0.25,0.22)	0.04 (-0.21,0.30)
Disgust	HOUSE	-0.04 (-0.49,0.38)	-0.12 (-0.58,0.31)	0.26 (-0.16,0.68)
HHParasites	HHDisgust	-0.11 (-0.33,0.11)	-0.15 (-0.31,0.01)	0.01 (-0.16,0.17)
HHParasites	MSOL	0.15 (-0.09,0.39)	0.13 (-0.12,0.37)	0.13 (-0.11,0.37)
HHParasites	TSOL	-0.11 (-0.25,0.03)	-0.10 (-0.23,0.04)	-0.11 (-0.24,0.03)
HHParasites	HOUSE	-0.39 (-0.92,0.12)	-0.39 (-0.94,0.13)	-0.43 (-0.93,0.06)
HHDisgust	MSOL	0.09 (-0.15,0.32)	0.24 (0.01,0.46)	0.02 (-0.21,0.25)
HHDisgust	TSOL	0.00 (-0.15,0.15)	0.12 (-0.04,0.29)	0.08 (-0.09,0.25)
HHDisgust	HOUSE	0.26 (-0.17,0.67)	0.02 (-0.37,0.38)	0.19 (-0.18,0.55)
HHParasites	sd(Household)	0.73 (0.51,1.04)	0.75 (0.54,1.06)	0.76 (0.55,1.07)
HHDisgust	sd(Household)	0.52 (0.34,0.76)	0.35 (0.18,0.56)	0.43 (0.19,0.67)
Parasites	sd(Community)	1.08 (0.02,5.95)	1.16 (0.02,6.07)	0.61 (0.02,2.51)
Disgust	sd(Community)	1.87 (0.08,8.28)	2.04 (0.27,8.29)	0.70 (0.03,2.68)
HHParasites	sd(Community)	1.66 (0.08,7.29)	1.88 (0.13,8.02)	1.03 (0.08,3.35)
HHDisgust	sd(Community)	1.34 (0.05,6.34)	1.21 (0.04,6.12)	0.63 (0.02,2.60)

Model Formula:

Parasites ~ Age + Sex + Disgust + HHDisgust + HHParasites + +(1 | q | Village) + MSOL + TSOL + HOUSE

Disgust ~ Age + Sex + HHDisgust + (1 | q | Village) + MSOL + TSOL + HOUSE

HHParasites ~ HHDisgust + (1 | q | Village) + (1 | p | Household) + MSOL + TSOL + HOUSE

HHDisgust ~ (1 | q | Village) + (1 | p | Household) + MSOL + TSOL + HOUSE

Disgust = The component indicated for each model (C1-C3)

HH = Household mean, excluding target individual. Vi = Village mean, excluding target household

Items below the grey bar are group level effects for Household

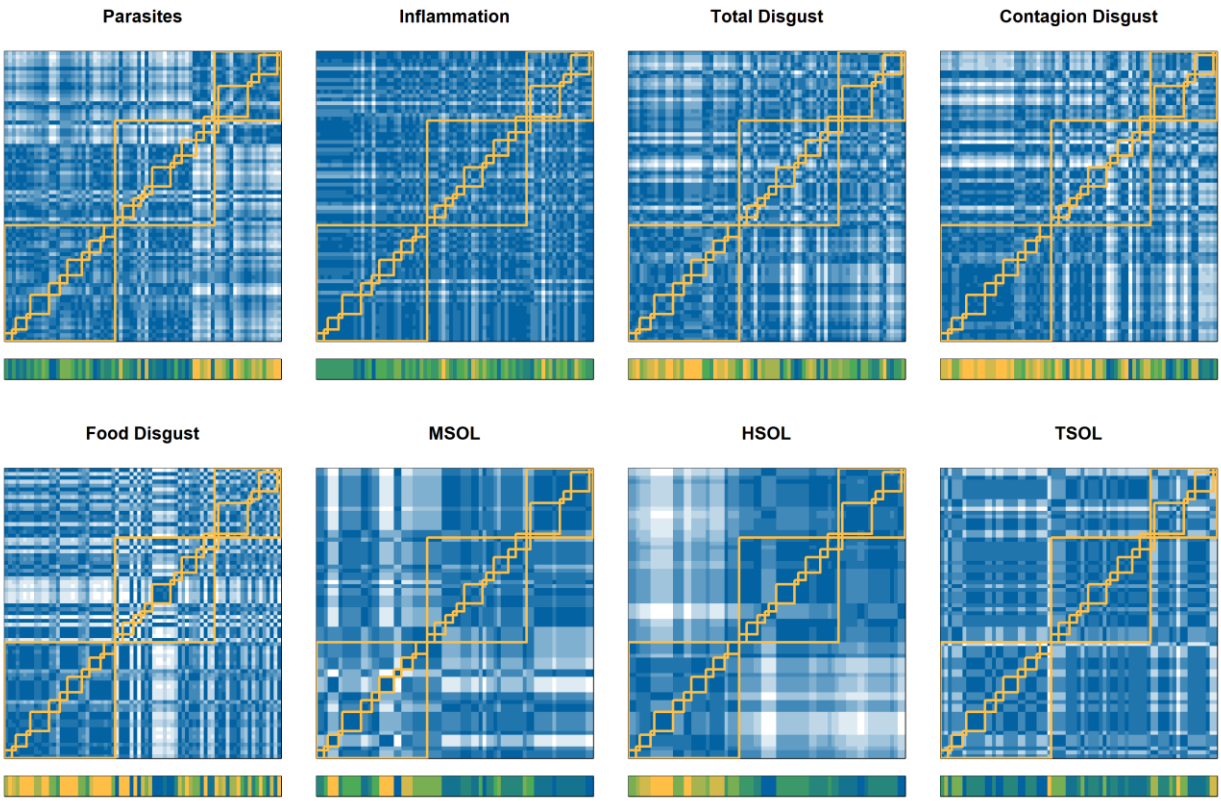

Figure S1. Similarity matrix plots for all individuals in the dataset showing household and community clustering. Each x or y line indicates an individual. Each cell represents the similarity between two individuals, with darker blue cells indicating more similarity and yellow indicating more divergence. Individuals are ordered by household and community, and households and communities are outlined in yellow. Squares of blue indicate clusters of similarity, while disordered patterns indicate independence. Wider bands in SOL measures indicate that these measures were largely collected at the household level. The colored bars below the plots show the relative absolute value of the measure for the individual in that column (yellow=high, green=intermediate, blue=low).

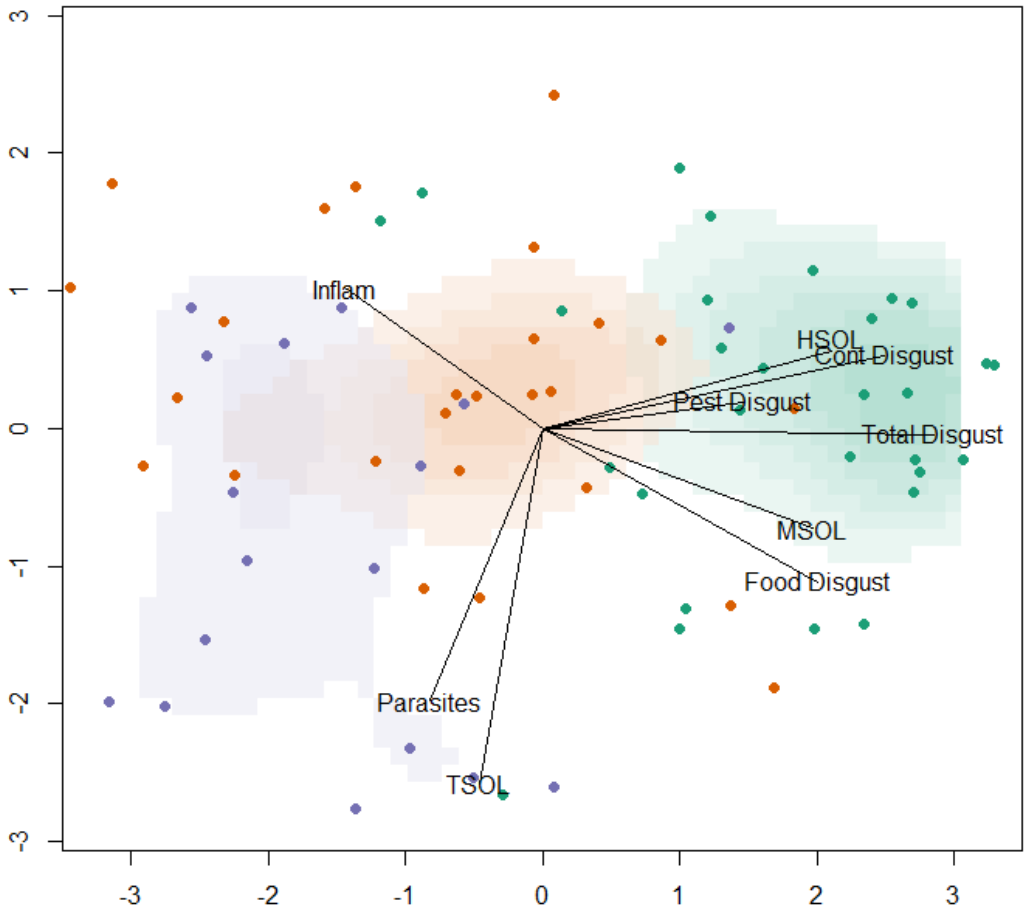

Figure S2. Multidimensional scaling based on variables of interest. Points are individual participants. Colors indicate the three communities, with shading indicating the density function for that community (green=community 1, orange=community 2, purple=community 3). Note, figure does not control for age, sex, or household clustering.

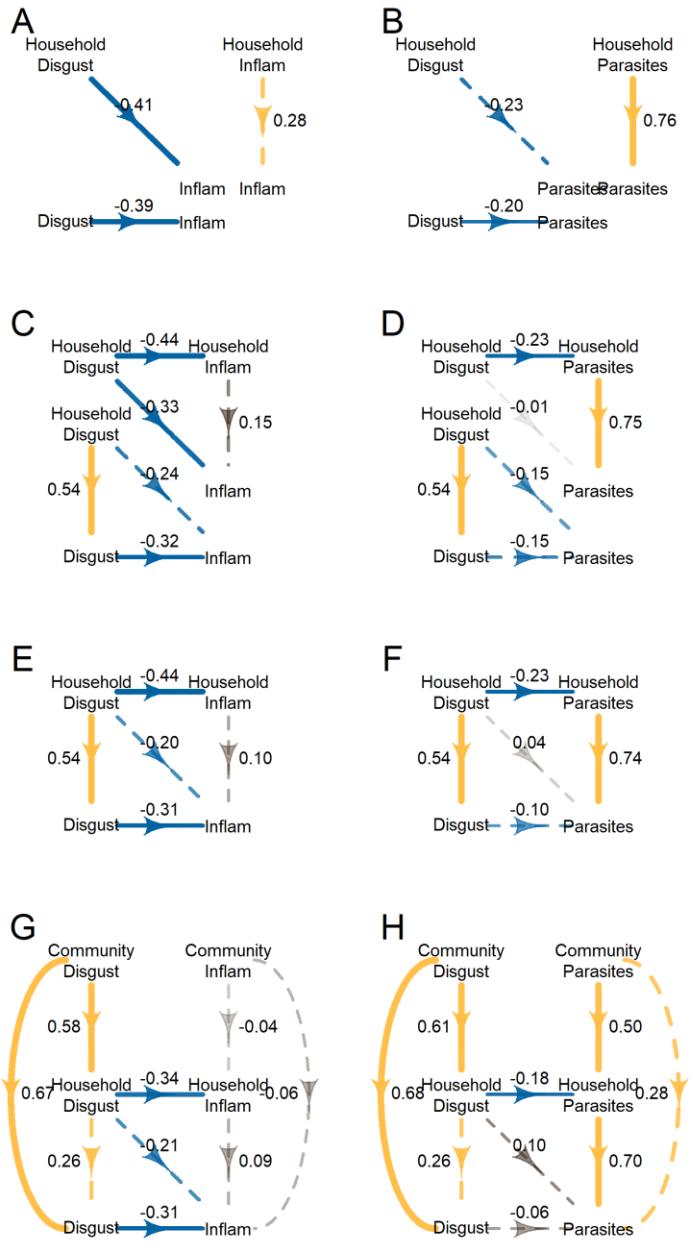

Figure S3. Associations between infection and disgust variables, A-D) Simple associations. E-H) Tests of whether family infection level or individual disgust mediate associations between family disgust and infection. I-L) Combined models showing associations between family level and individual level variables. M-P) Complete models with community level variables. Line type indicates the posterior certainty: solid line, more than 95% of the posterior is on one side of zero; long dashes, <95% of the posterior is on one side of zero. Color indicates the direction of the effect: blue=negative, yellow=positive. Effects with less than 80% of the posterior on one side of zero are shaded grey-white, proportional to the credibility intervals.

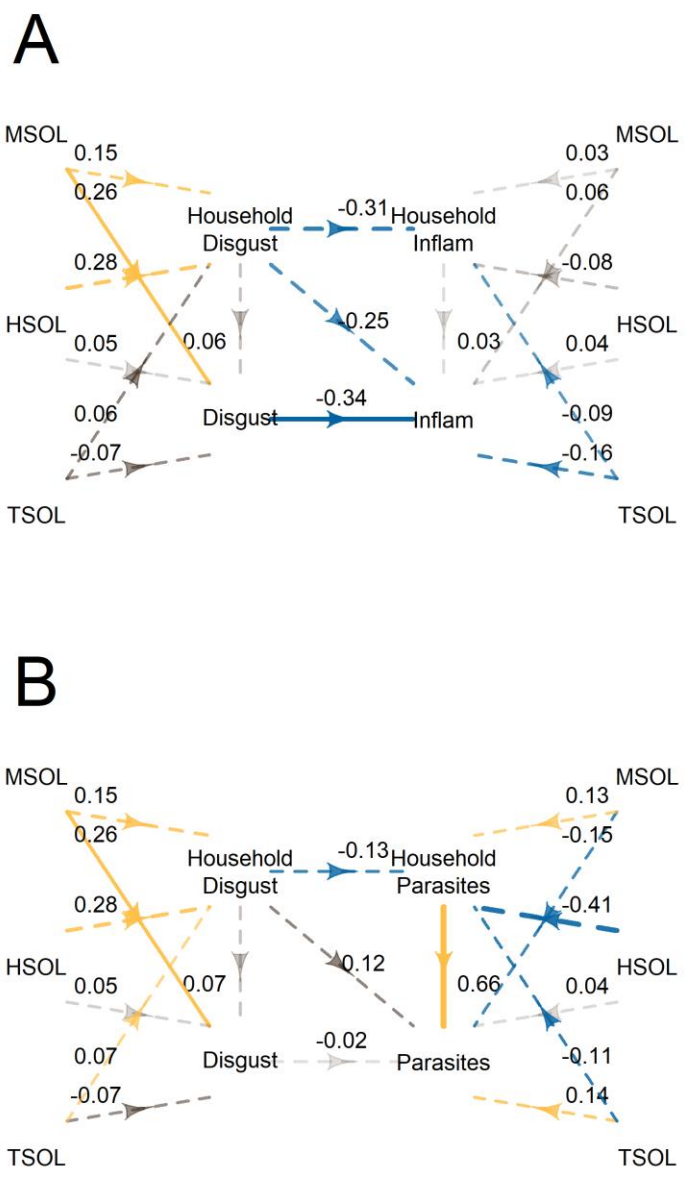

Figure S4. Associations between style of life variables, infection, and disgust. Note, style of life variables are shown twice to improve graph organization. Models control for Community with a random effect term. Multivariate models were specified as: Infection ~ Age + Sex + Disgust + HHDisgust + HHInfection + MSOL + TSOL + HOUSE + (1|q|Community); Disgust ~ Age + Sex + HHDisgust + MSOL + TSOL + HOUSE +(1|q|Community); HH Infection ~ HH Disgust + MSOL + TSOL + HOUSE) + (1|p|Family) + (1|q|Community); HH Disgust ~ MSOL + TSOL + HOUSE + (1|q|Community) + (1|p|Family). Line type indicates the posterior certainty: solid line, more than 95% of the posterior is on one side of zero; long dashes, <95% of the posterior is on one side of zero. Color indicates the direction of the effect: blue=negative, yellow=positive. Effects with less than 80% of the posterior on one side of zero are shaded grey-white, proportional to the credibility intervals.

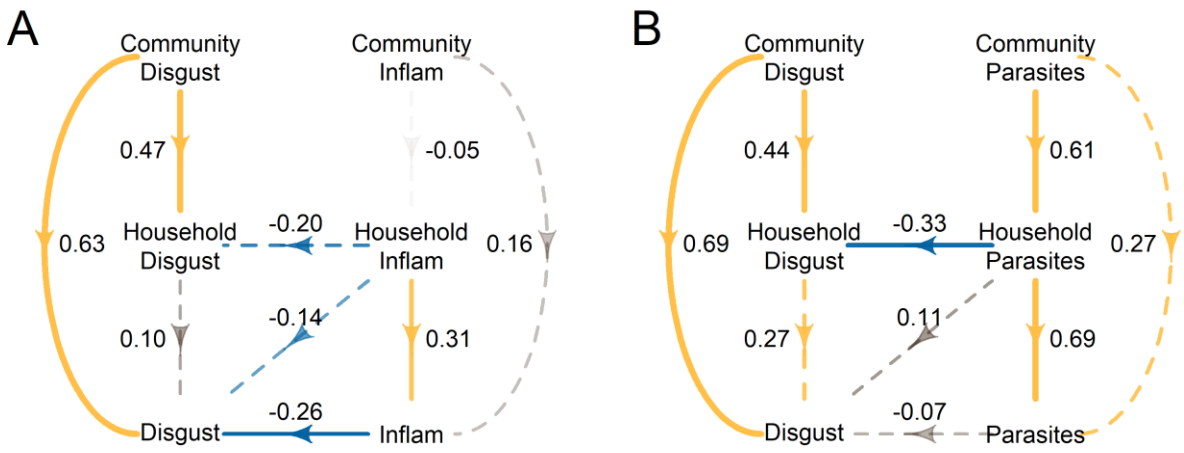

Figure S5. Models comparable to Figure 2, but with a reversed relationship between infection and disgust. Line thickness is proportional to the mean posterior effect size. Line type indicates the posterior certainty: solid line, more than 95% of the posterior is on one side of zero; long dashes, <95% of the posterior is on one side of zero. Color indicates the direction of the effect: blue=negative, yellow=positive. Effects with less than 80% of the posterior on one side of zero are shaded grey-white, proportional to the credibility intervals.

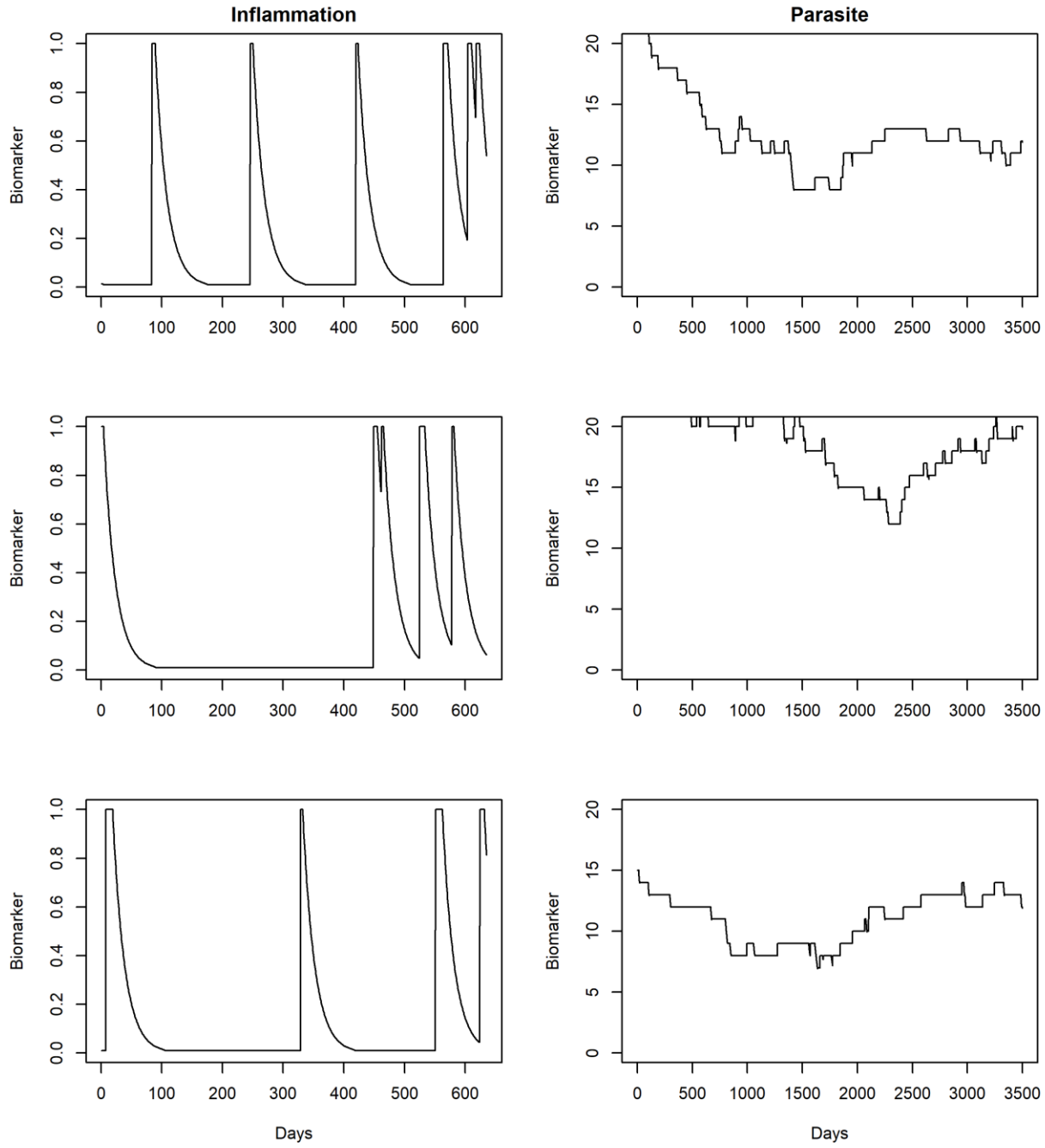

Figure S6. Example simulated biomarker responses to short-term inflammatory infections (left) and long-term microparasite infections (right). Units on the y-axis are arbitrary. Note that the long-term infection is simulated for a longer period of time, and that the simulation was run for 365 days (short-term) or 3500 days (long term) before recording values (not shown of the graph), in order to equilibrate baseline biomarker levels.

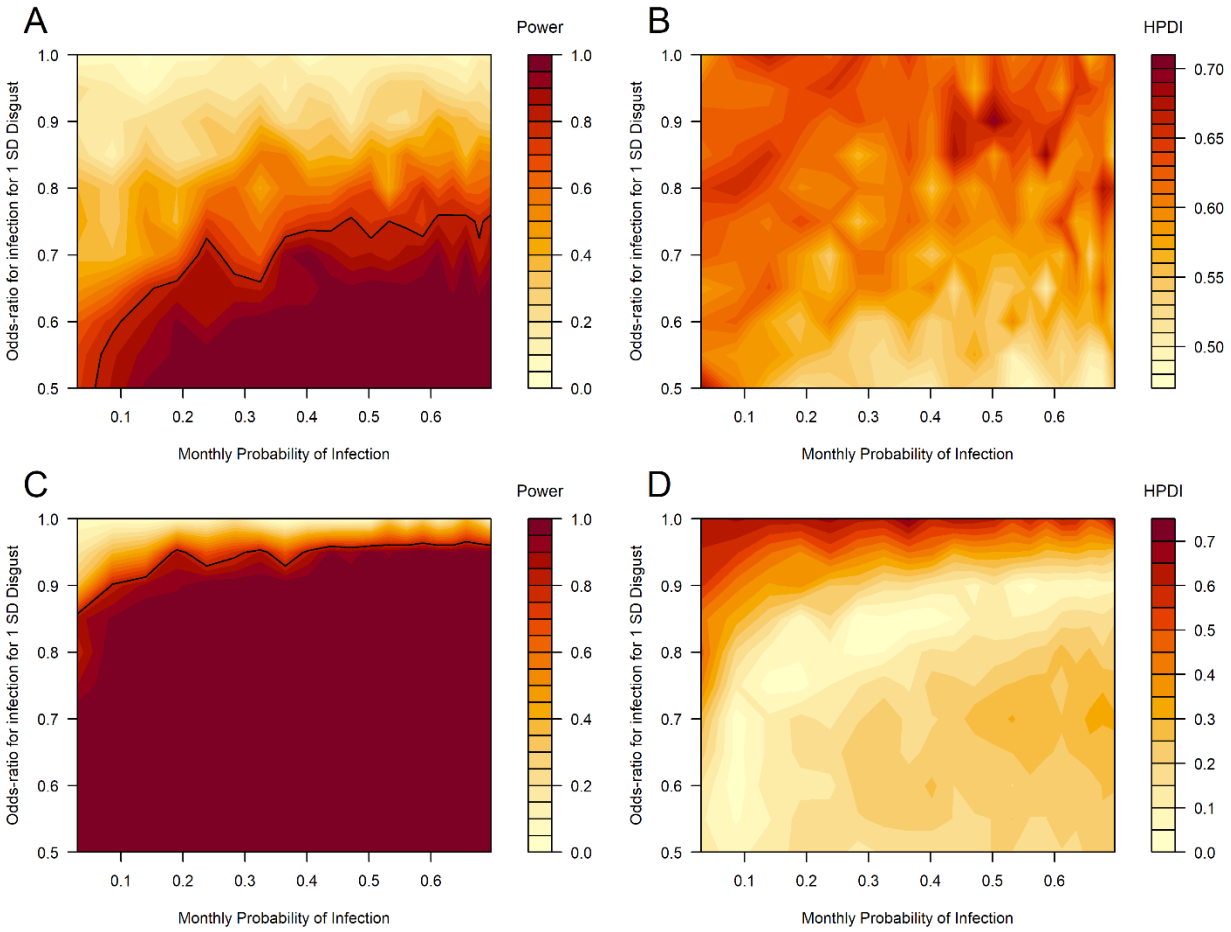

Figure S7. Power to credibly detect an effect given different probabilities of infection and different effect sizes for disgust. In the simulation, 75 individuals were sampled from a pool of 750, with sampling repeated 50 times. A and C show the proportion of simulated samples that produced a posterior estimate in which ≥90% of the posterior distribution showed a protective effect of disgust. B and D show the average range of the 95% highest posterior density interval, with lower values indicating more certainty in the posterior. A and B show an "inflammatory" infection with an average duration of 7 days, as in the left of Figure SX. C and D show a "parasitic" infection with an average duration of 2000 days, stacking infections (i.e. additional exposure increases parasitic load) and a slow return of the biomarker to baseline (right of Figure SX).

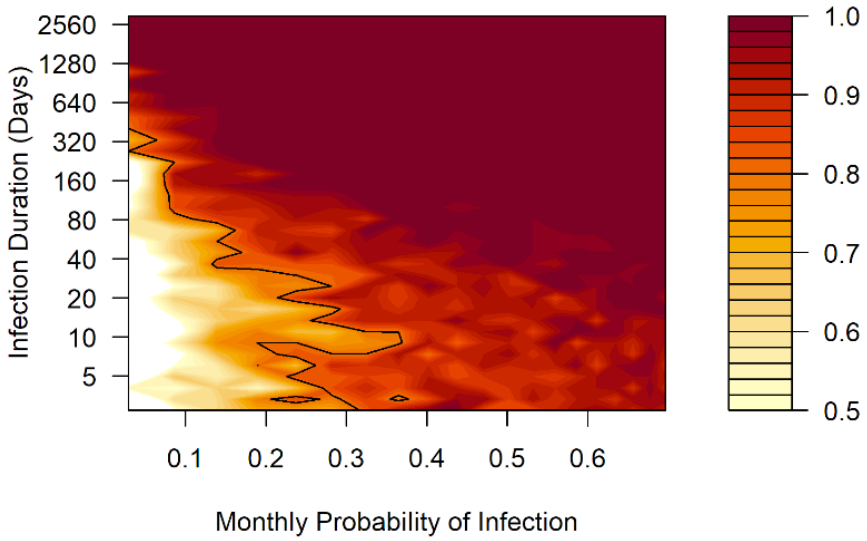

Figure S8. Simulated effect of infection duration and risk of infection on the power to detect a credible effect with a disgust odds-ratio of infection of 0.7 / SD Disgust. Black line shows 80% of trials resulted in posterior estimates with ≥90% of the posterior distribution showing a protective effect of disgust.

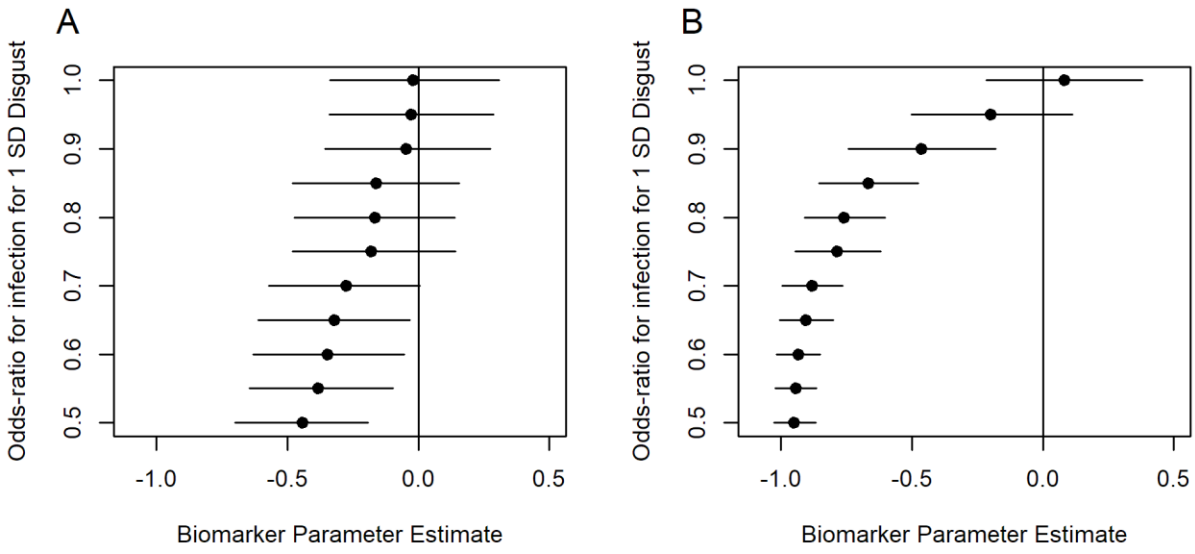

Figure S9. Simulated relationship between the initial effect of disgust on infection and the posterior parameter estimate for the effect of disgust on biomarker level. A) Parameter for a short-term "inflammatory" infection. B) Parameter for a long-term "parasite" infection. Lines show the 95% highest posterior density interval. Simulated biomarkers were logged and standardized before model fitting. and shown for daily infection risk = 0.015 (36% infection probability per month).

SI References

1. Urlacher SS, Ellison PT, Sugiyama LS, Pontzer H, Eick G, Liebert MA, Cepon-Robins TJ, Gildner TE, Snodgrass JJ (2018) Tradeoffs between immune function and childhood growth among Amazonian forager-horticulturalists. *PNAS* 115: E3914-E3921.
2. Perez L (2019) Acute phase protein response to viral infection and vaccination. *Arch Biochem* 671: 196-202.
3. Slaats J, ten Oever J, van d Veerdonk FL, Netea MG (2016) IL-1B/IL-6/CRP and IL-18/ferritin: Distinct Inflammatory Programs in Infections. *PLoS Pathogens* 12: e1005973.
4. Rose-John S, Winthrop K, Calabrese L (2017) The role of IL-6 in host defense against infections: immunobiology and clinical implications. *Nat Rev Rheumatol* 13: 399-409.
5. Iancovici Kidon M, et al. (2005) Serum immunoglobulin E levels in Israeli-Ethiopian children: Environment and genetics. *Isr Med Assoc J* 7: 799-802
6. Blackwell AD, Gurven M, Sugiyama LS, Madimenos FC, Liebert MA, Martin MA, Kaplan HS, Snodgrass JJ (2011) Evidence for a Peak Shift in a Humoral Response to Helminths: Age Profiles of IgE in the Shuar of Ecuador, the Tsimane of Bolivia, and the U.S. NHANES. *PLoS Negl Trop Dis* 5:e1218.
7. Bethony J, Brooker S, Albonico M, Geiger SM, Loukas A, Diemert D, Hotez PJ (2006) Soil-transmitted helminth infections: ascariasis, trichuriasis, and hookworm. *Lancet* 367: 1521-1532.
8. Liebert MA, Snodgrass JJ, Madimenos FC, Cepon TJ, Blackwell AD, Sugiyama LS (2013) Implications of market integration for cardiovascular and metabolic health among an Indigenous Amazonian Ecuadorian population. *Ann Hum Biol* 40: 228-242.
9. Urlacher SS, Liebert MA, Snodgrass JJ, Blackwell AD, Cepon-Robins TJ, Gildner TE, Madimenos FC, Amir D, Bribiescas RG, Sugiyama LS (2016) Heterogeneous effects of market integration on sub-adult body size and nutritional status among the Shuar of Amazonian Ecuador. *Ann Hum Biol* 43(4): 316-329.
10. Gildner TE, Cepon-Robins TJ, Liebert MA, Urlacher SS, Schrock JM, Harrington CJ, Madimenos FC, Snodgrass JJ, Sugiyama LS. 2020. Market integration and soil-transmitted helminth infection among the Shuar of Amazonian Ecuador. *PLoS ONE* 15: e0236924.
11. Blackwell AD, Snodgrass JJ, Madimenos FC, Sugiyama LS (2010) Life history, immune function, and intestinal helminths: trade-offs among immunoglobulin E, C-reactive protein, and growth in an Amazonian population. *Am J Hum Biol* 22: 836-848.
12. McDade, T. W., Burhop, J., Dohnal, J. (2004). High-sensitivity enzyme immunoassay for C-reactive protein in dried blood spots. *Clin Chem,* 50, 652-654.
13. Tanner S, McDade T. 2007. Enzyme immunoassay for total immunoglobulin E in dried blood spots. *Am J Hum Biol* 19: 440-442.
14. Revelle WR (2020) psych: Procedures for Personality and Psychological Research. Available from: http://cran.r-project.org/package=psych
15. Van Buuren S, Groothuis-Oudshoorn K, Buuren S, Groothuis-Oudshoorn K (2011) MICE: Multivariate imputation by chained equations in R. J Stat Softw VV:1–67.
16. Bürkner P-C (2017) brms: An R package for Bayesian multilevel models using Stan. J Stat Softw 80