Supplement to "Epidemics and control strategies for diseases of farmed salmonids: A parameter study," by Jonkers, Sharkey, Thrush, Turnbull, and Morgan

Outbreak Simulations

From November 2009 to January 2010 over three hundred thousand simulation jobs were executed on the University of Liverpool's *Condor* pool of circa 600 nodes, taking about 196,566 cpu hours to complete. The Condor project is a workload management system for compute-intensive jobs developed at the university of Wisconsin (http://www.cs.wisc.edu/condor/). Its main strength is its support of High Throughput Computing (HTC) on large collections of distributively-owned computing resources. Because epidemiological simulations do not rely on the outcomes of previous or adjacent calculations, they are ideal for an HTC environment. In actual simulations, a single randomly selected site was seeded (status set to "infected"; all other sites pathogen-free but susceptible), after which spreading and containment actions were simulated on the network, and all relevant data stored upon outbreak termination or timeout. For each chosen ensemble of parameter settings, this procedure was repeated 10,000 times to ensure that, on average, over 99% of the network sites would be seeded at least once. Upon completion, each simulation produced a history file of outbreak statistics plus a site-based tally of inward and outward transmissions per type (595 and 111 GB in total). Post-processing of these raw data produced another 300 thousand files, including about forty thousand images of detection delay-dependent outbreak distributions. The latter mainly served as input for a dedicated viewer interface that allowed each relevant parameter to be altered separately, to visualise ceteris paribus effects. For statistical analyses and other plots we also relied on commercial software (Minitab 15, version 1.30.0 (2007), see http://www.minitab.com) and open-source freeware (Generic Mapping Tools, version 4.1.4 (2006), see http://gmt.soest.hawaii.edu/).

Table S1 lists all model parameters incorporated in the simulations.

Table S1. Model parameters

Parameter description	**Values**	**References**
Local transmission likelihood per day	$p_{local} = \beta \exp\left[-\left(D^2\right)\lambda_L\right]$ $\beta = 0.05$, $\lambda_L = 10^{-6}$	See text (Network nodes and connections); Rodger & Mitchell 2007
Fomite transmission likelihood per day	$p_{fomite} = \gamma \exp\left[-\left(D^2\right)\lambda_F\right]$ $\gamma = 0.005$, $\lambda_F = 10^{-6}$	See text (Network nodes and connections); Chambers et al. 2008; Tobback et al. 2007
Transport transmission likelihood per day	$p_{trans} = T / 365.2524$	See text (Network nodes and connections); Green et al. 2009; Munro & Gregory 2009; Munro et al. 2010; Skall et al. 2005
Number of transports per year	Mean number of yearly transports: 1.647272; range: 1 – 50	Cefas Live Fish Movement database (see Thrush & Peeler 2006 for background)
River transmission likelihood per day	$p_{river} = \alpha \exp\left[-\theta\lambda_R\right]$ $\alpha = 0.005$, $\lambda_R = 1$	See text (Sites & transmissions; Supplement); Peeler et al. 2008; Skall et al. 2005; Taylor et al.

		2010; Toranzo & Hetrick (1982); Barja et al. (1983); Murray et al. (2005); Kocan et al. (2001)
Outbreak Severity	1, 2, 3, 4, 5, 10 (global transmission likelihood postfactor)	Tobback et al. 2007; Peeler et al. 2008; Algöet et al. 2009; Feist et al. 2002; Chambers et al. 2008 ; Sharkey et al. 2008
Latency delay	5, 10, 20, 50, 100, 200 days	Algöet et al. 2009; Munro et al. 2010; Ogut & Bishop 2007; Tobback et al. 2007
Detection delay	5, 10, 20, 50, 100, 200, 500, 1000 days	See text (Delay parameters); Munro et al. 2010; Stone et al. 2008; Algöet et al. 2009; Feist et al. 2002; Rodger & Mitchell 2007
Culling delay	1, 2, 5, 10, 20, 50 days	See text (Delay parameters); expert opinion
Restocking delay	5, 10, 20, 50, 100, 200, 500, 1000 days	See text (Delay parameters); expert opinion
Laboratory capacity	10, 20, 50, 100, 200, 500	See text (Control Strategies); Munro et al. 2010; Chambers et al. 2008
Public awareness campaign (AC)	Inactive, Active	See text (Control Strategies); McLaws et al. 2007
National Transport Ban (TB)	0, 30 days	Anonymous 2007; see text (Control Strategies); expert opinion
Reactive / Proactive Ratio (Hybrid)	10/1, 5/1, 5/2, 2/1, 1/1, 1/2, 2/5, 1/5, 1/10	See text (Control Strategies)

Note: transmission parameter ranges are explored in the Supplementary section Sensitivity analysis below

River stream flow

Table S2 lists the 37 locations at which the USGS measured river stream flow speed sufficiently long (between 100 days and three years) to be included in the sample. The total number of data was initially 26,200, but this included some negative and zero velocities, possibly due to tidal inflows. Their removal left 25,088 positive stream velocities which were converted into meters per second. This sample size is ample for distribution fitting purposes. Geographical sampling favours Florida and Texas, with smaller contributions from Rhode Island, Maryland, North Carolina, Georgia, and Oregon. All but six sites provided over one full year of continuous readings, limiting potential seasonal bias. The data were initially probability distribution-fitted using sixteen standard pdfs, but none passed the Anderson-Darling goodness-of-fit criterion at an acceptable significance level. Subsequently, data were binned (linear bins of width 0.1 m/s, offset 0.05, so centring on 0.1, 0.2, etc., bin range 0.1-4.4) to reveal a clear loglinear distribution (Figure 3 in main text). Log_{10}(frequencies) per bin were least-squares fitted to yield the following loglinear frequency distribution equation:

$$\log_{10}(frequency) = 3.521 - 0.575(bin)$$

which explains over 96% of observed variability; remaining residuals are approximately normally distributed (See Figure S1). Other bin widths and offsets yielded highly similar results. Overview of the relevant statistics:

```
Predictor       Coef  SE Coef       T      P
Constant    3.52106  0.04577   76.93  0.000
Slope      -0.57548  0.01772  -32.48  0.000
S = 0.149224   R-Sq = 96.2%   R-Sq(adj) = 96.1%

Analysis of Variance
Source          DF      SS      MS        F      P
Regression       1  23.497  23.497  1055.20  0.000
Residual Error  42   0.935   0.022
Total           43  24.432
```

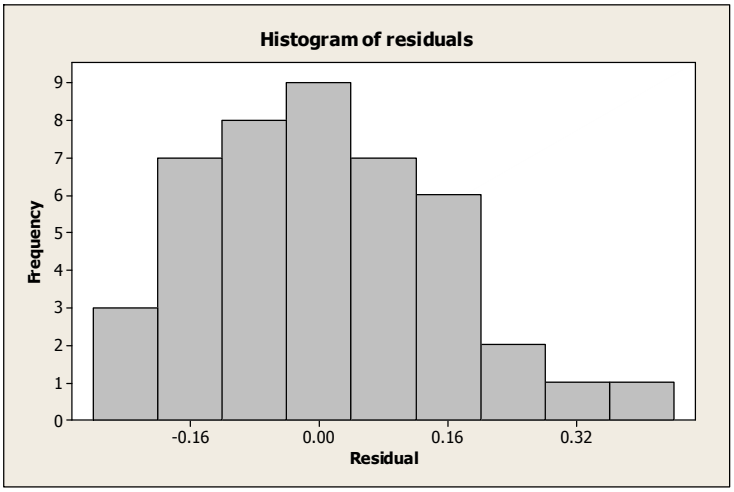

Figure S1. A histogram of flow speed residuals after linear regression shows an approximate Gaussian distribution with some minor skewness toward right.

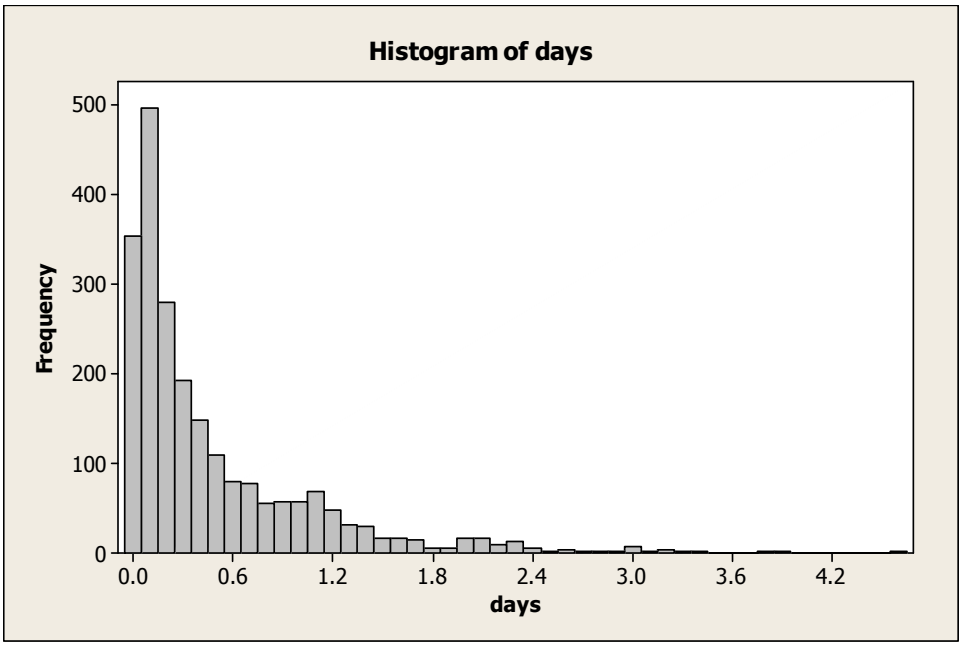

Figure S2. Histogram of the number of days a waterborne particle remains in river transit (based on the 2,232 river connections in the studied network). Most transits take less than two days.

Table S2. Sampled U.S. river sites providing >100 daily means of measured stream flow speed (sample size per site capped at three years of continuous readings)

USGS code	Data	Location	State
01115833	750	BIG RIVER HARKNEY HILL RD NR COVENTRY CTR	RI
01490140	327	LITTLE BLACKWATER RIVER AT SEWARD	MD
02098198	270	HAW R BELOW B. EVERETT JORDAN DAM NR MONCURE	NC
02272500	101	KISSIMMEE RIVER AT US 98 AT FORT BASINGER	FL
02272502	108	KISSIMMEE RIVER AT LOCKETT EST AT FORT BASINGER	FL
02297100	222	JOSHUA CREEK AT NOCATEE	FL
02299472	714	BIG SLOUGH AT WEST PRICE BLVD NEAR NORTH PORT	FL
02299482	712	COCOPLUM WATERWAY AT NORTH PORT	FL
02299692	838	BLACKBURN CANAL NEAR VENICE	FL
02300082	971	FROG CREEK NEAR RUBONIA	FL
02310747	1025	CRYSTAL RIVER AT BAGLEY COVE NEAR CRYSTAL RIVER	FL
02313700	718	WACCASASSA RIVER NR GULF HAMMOCK	FL
02319300	767	WITHLACOOCHEE RIVER NR MADISON,	FL
02319302	1047	MADISON BLUE SPRING NR BLUE SPRINGS	FL
02319394	760	WITHLACOOCHEE RIVER NR LEE	FL
02322800	348	SANTA FE RIVER NR HILDRETH	FL
02323500	743	SUWANNEE RIVER NEAR WILCOX	FL
02323502	1054	FANNING SPRINGS NR WILCOX	FL
02323566	681	MANATEE SPRING NR CHIEFLAND	FL
02323592	756	SUWANNEE RIVER AB GOPHER RIVER NR SUWANNEE	FL
02326550	746	AUCILLA RIVER NR MOUTH NEAR NUTALL RISE	FL
02327022	1062	WAKULLA RIVER NEAR CRAWFORDVILLE	FL
02338500	718	CHATTAHOOCHEE RIVER AT US 27, AT FRANKLIN	GA
02341505	1012	CHATTAHOOCHEE RIVER AT US 280, NEAR COLUMBUS	GA
02369600	1075	YELLOW RIVER NR MILTON	FL
02376033	751	ESCAMBIA RIVER NR MOLINO	FL
07346080	1037	BIG CYPRESS CK ABV SH 43 NR KARNACK	TX
08041749	702	PINE ISLAND BAYOU ABV BI PUMP PLANT, BEAUMONT	TX
08041780	526	NECHES RV SALTWATER BARRIER AT BEAUMONT	TX
08117300	965	BRAZOS RV AT GIWW FLOOD GATES NR FREEPORT	TX
08168913	690	COMAL RV (OC) NR LANDA LK, NEW BRAUNFELS	TX
08170990	878	JACOBS WELL SPG NR WIMBERLEY	TX
08211503	234	RINCON BAYOU CHANNEL NR CALALLEN	TX
14197900	1052	WILLAMETTE RIVER AT NEWBERG	OR
14211820	1041	COLUMBIA SLOUGH AT PORTLAND	OR
209303205	644	NEW RIVER BELOW HWY17 BRIDGE AT JACKSONVILLE	NC
21989773	155	SAVANNAH RIVER AT USACE DOCK, AT SAVANNAH	GA

Source: http://waterdata.usgs.gov/usa/nwis (surface water, daily data, parameter 55, in ft/sec)

Transmission histograms

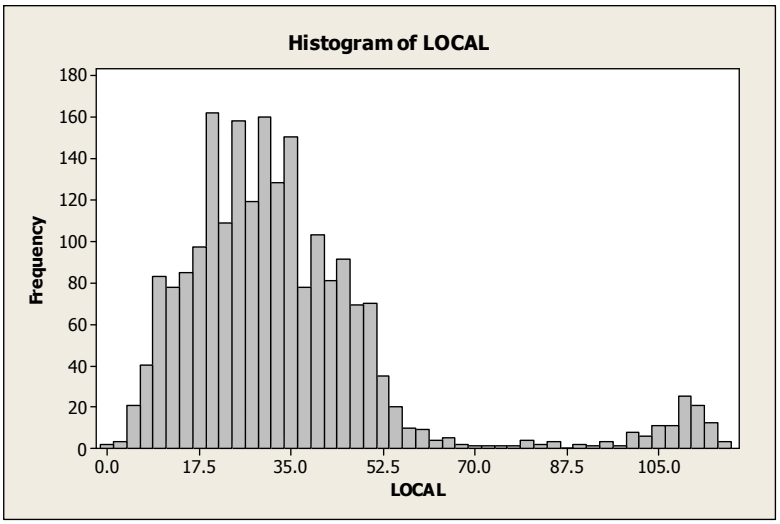

Figure S3a. Frequency histograms of outward connections per site, for local transmissions.

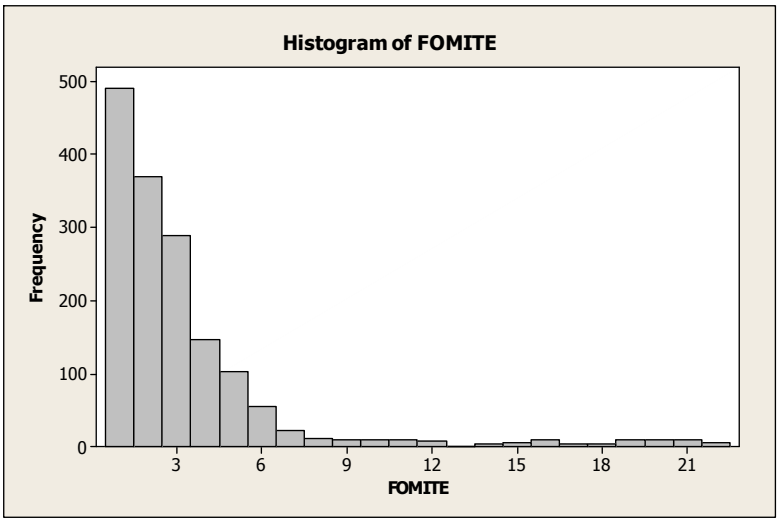

Figure S3b. Frequency histograms of outward connections per site, for fomite transmissions.

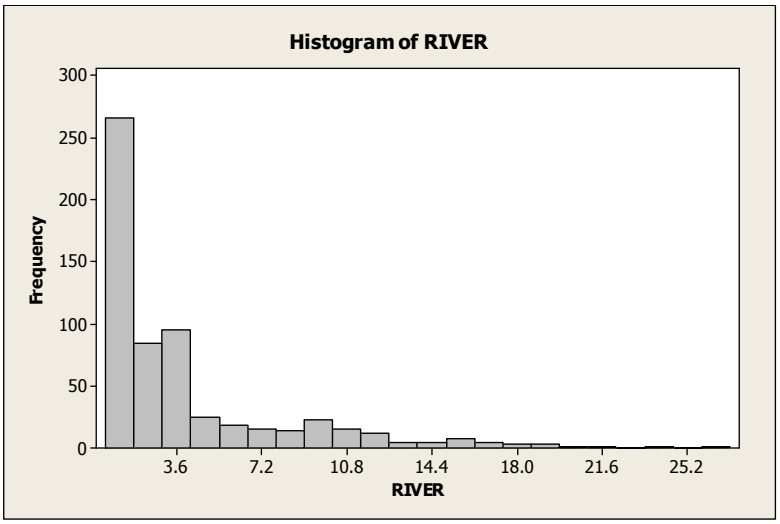

Figure S3c. Frequency histograms of outward connections per site, for river transmissions.

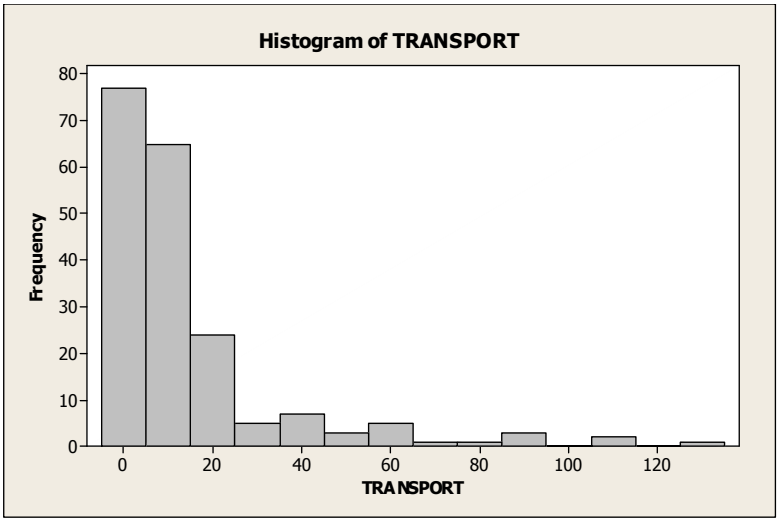

Figure S3d. Frequency histograms of outward connections per site, for transport transmissions.

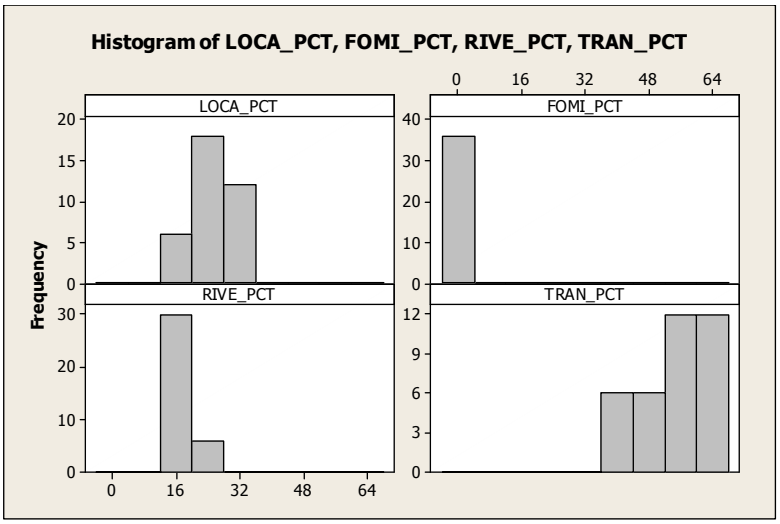

Figure S4a. Histograms of proportion (in %) of total transmissions, per type, for the baseline results (all severity settings combined)

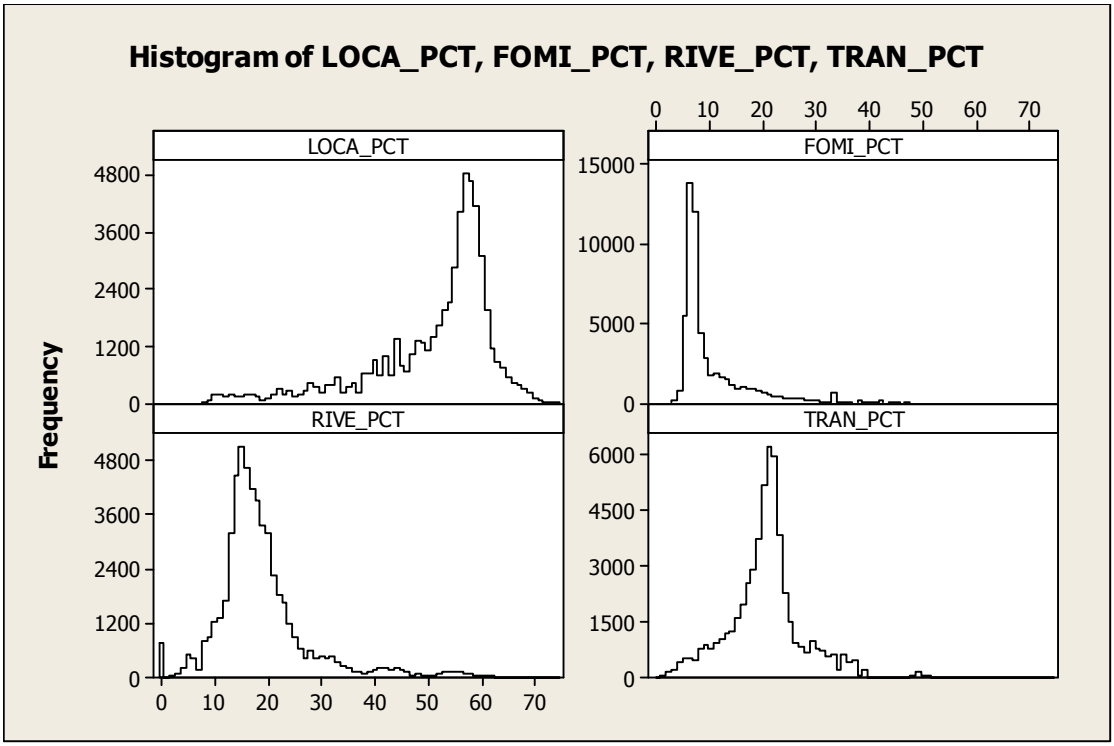

Figure S4b. Histograms of proportion (in %) of total transmissions, per type, for the reactive policy (all severity settings combined)

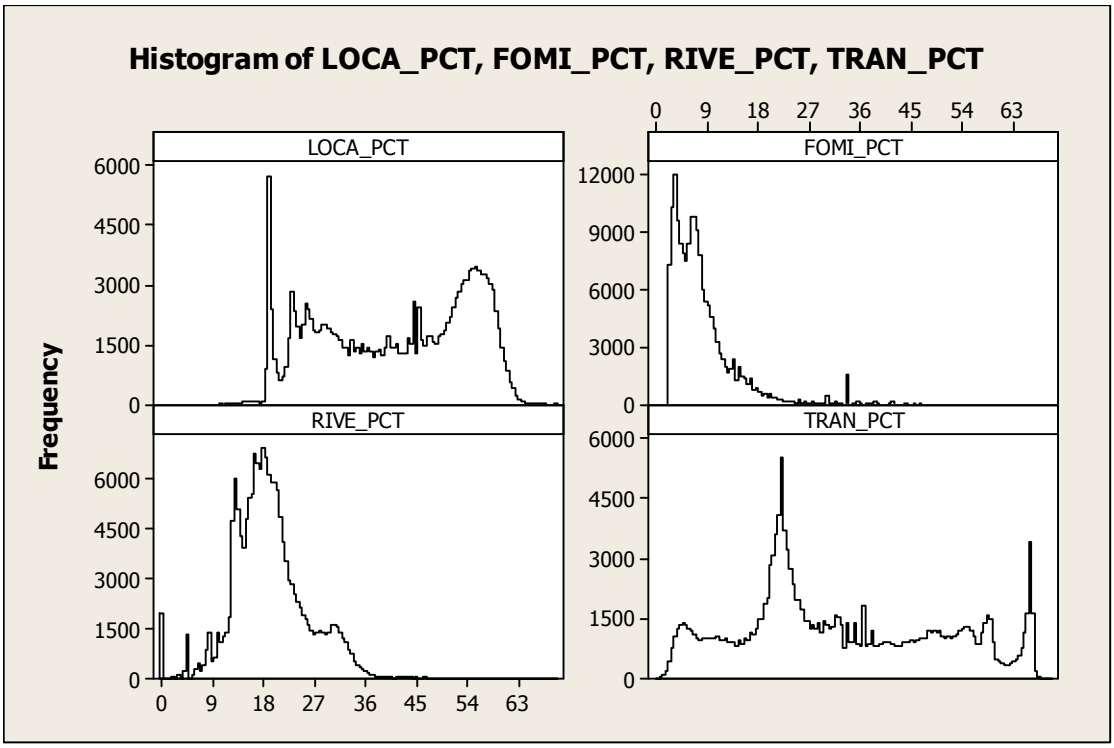

Figure S4c. Histograms of proportion (in %) of total transmissions, per type, for the proactive policy (all severity settings combined); the hybrid policy yields a similar image (see Figure S4f).

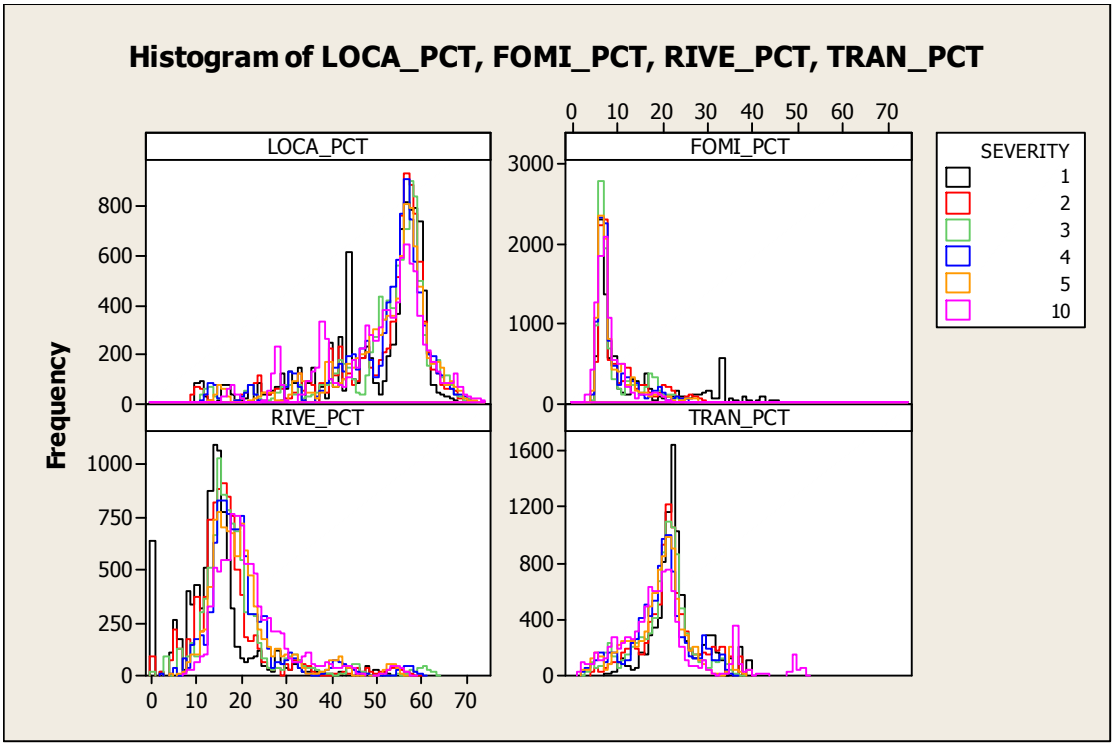

Figure S4d. Histograms of proportion (in %) of total transmissions, per type and severity, for the reactive policy

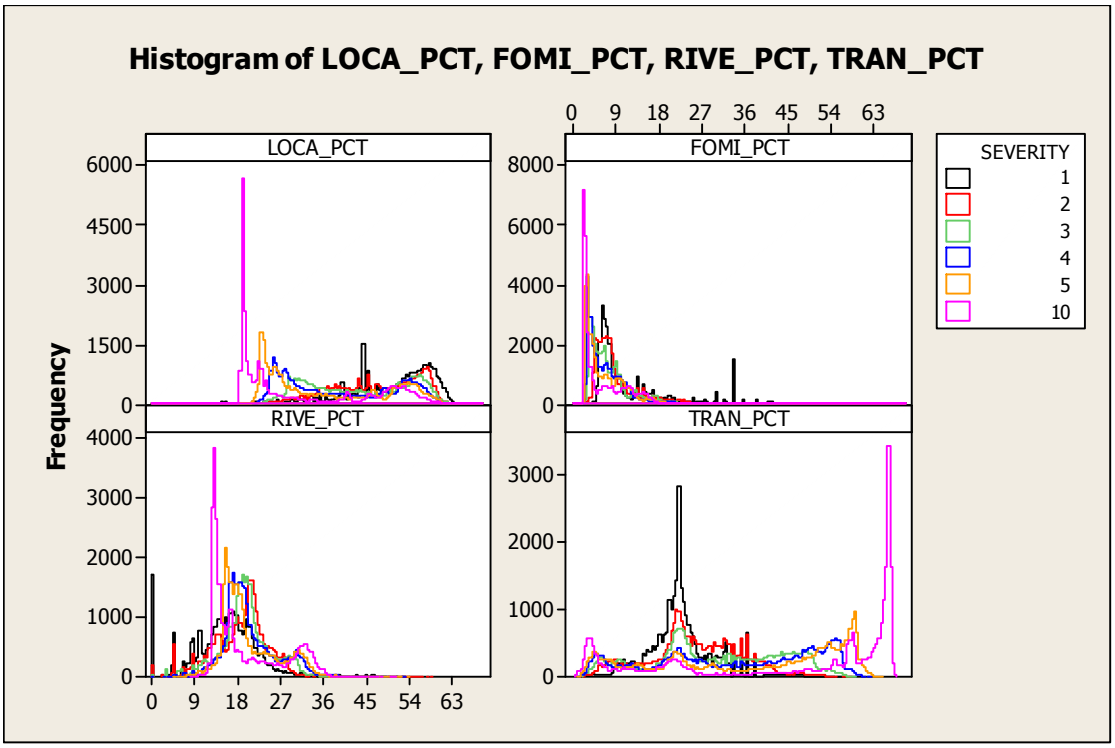

Figure S4e. Histograms of proportion (in %) of total transmissions, per type and severity, for the proactive policy

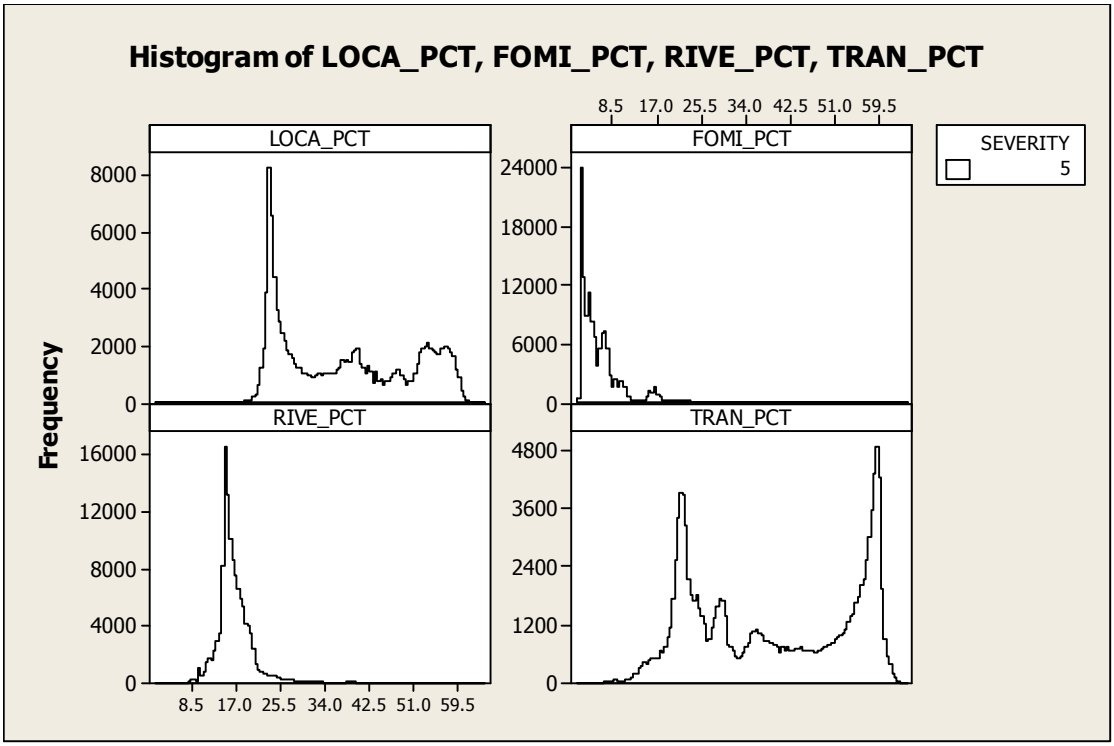

Figure S4f. Histograms of proportion (in %) of total transmissions, per type, for the hybrid policy (severity=5)

Contact structure histograms

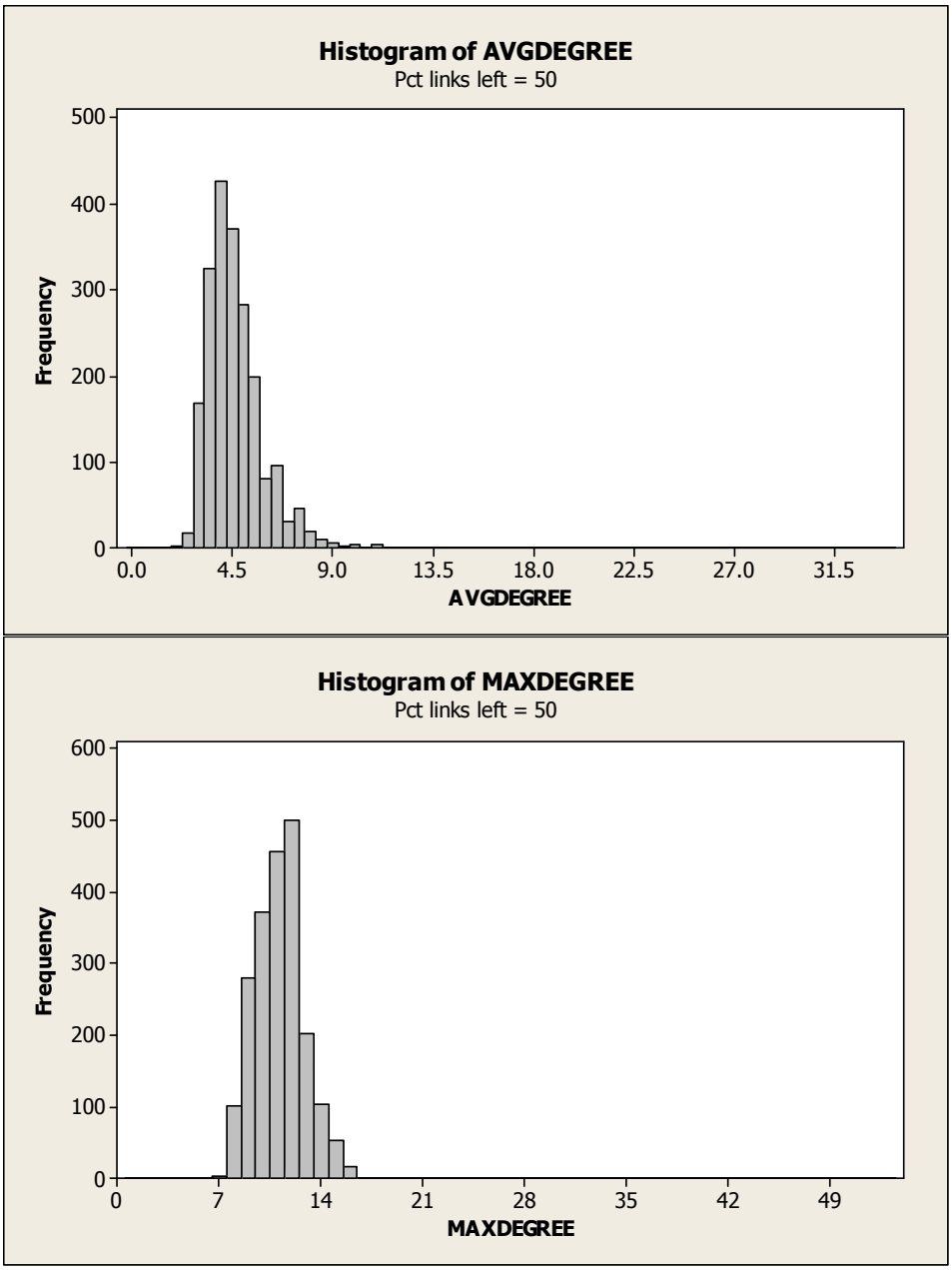

Figure S5a. Degree distribution per site, for average (top panel) and maximum degree (bottom panel), when 50% of links selected at random have been removed. The Giant Strongly Connected Component (GSCC, comprising Giant Component plus its sink sites) is still completely intact.

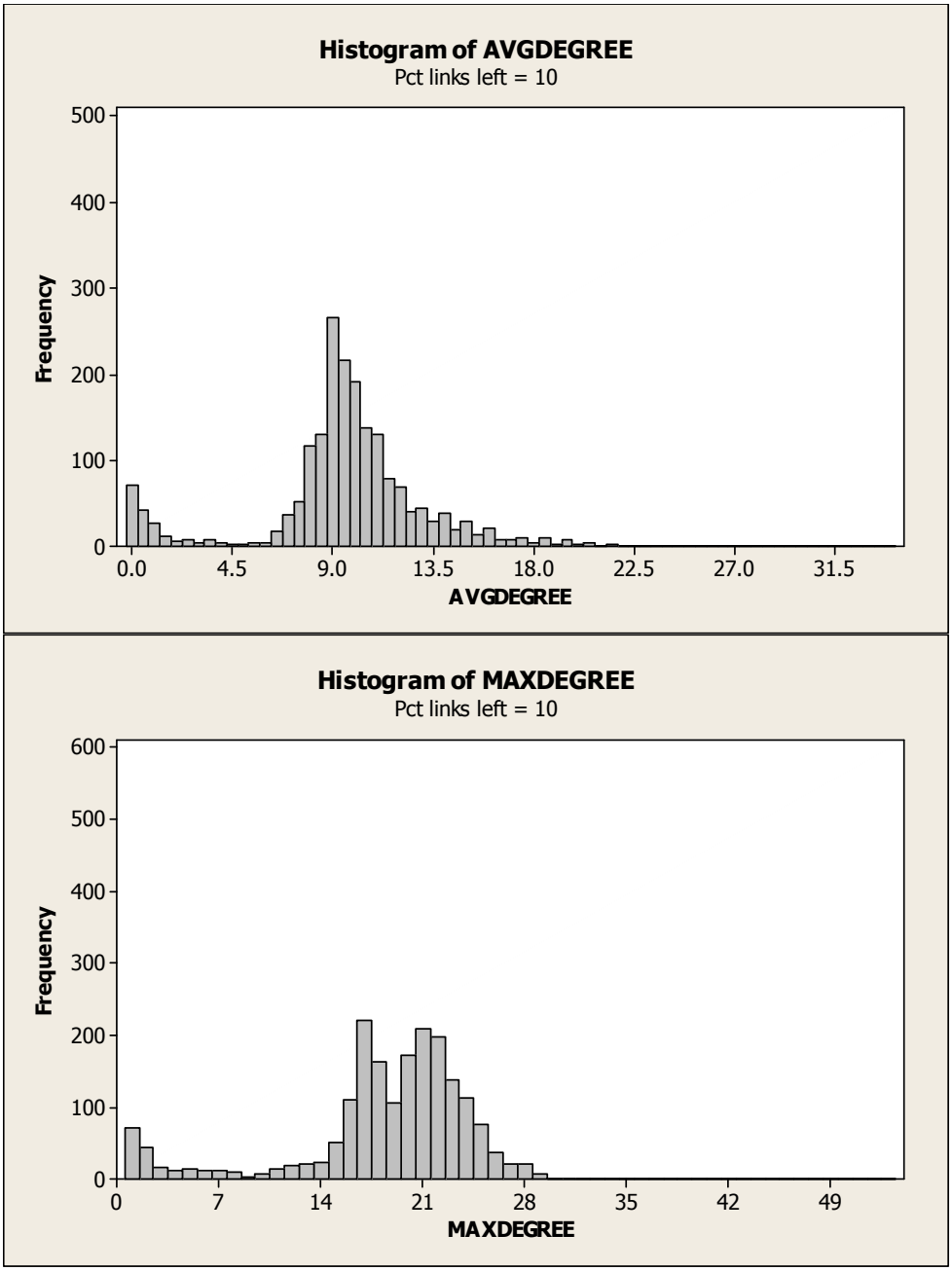

Figure S5b. Degree distribution per site when 90% of links selected at random have been removed. Part of the GSCC has become fragmented into small clusters, giving rise to a second distribution on the extreme left, whereas path lengths within the GSCC have become much longer.

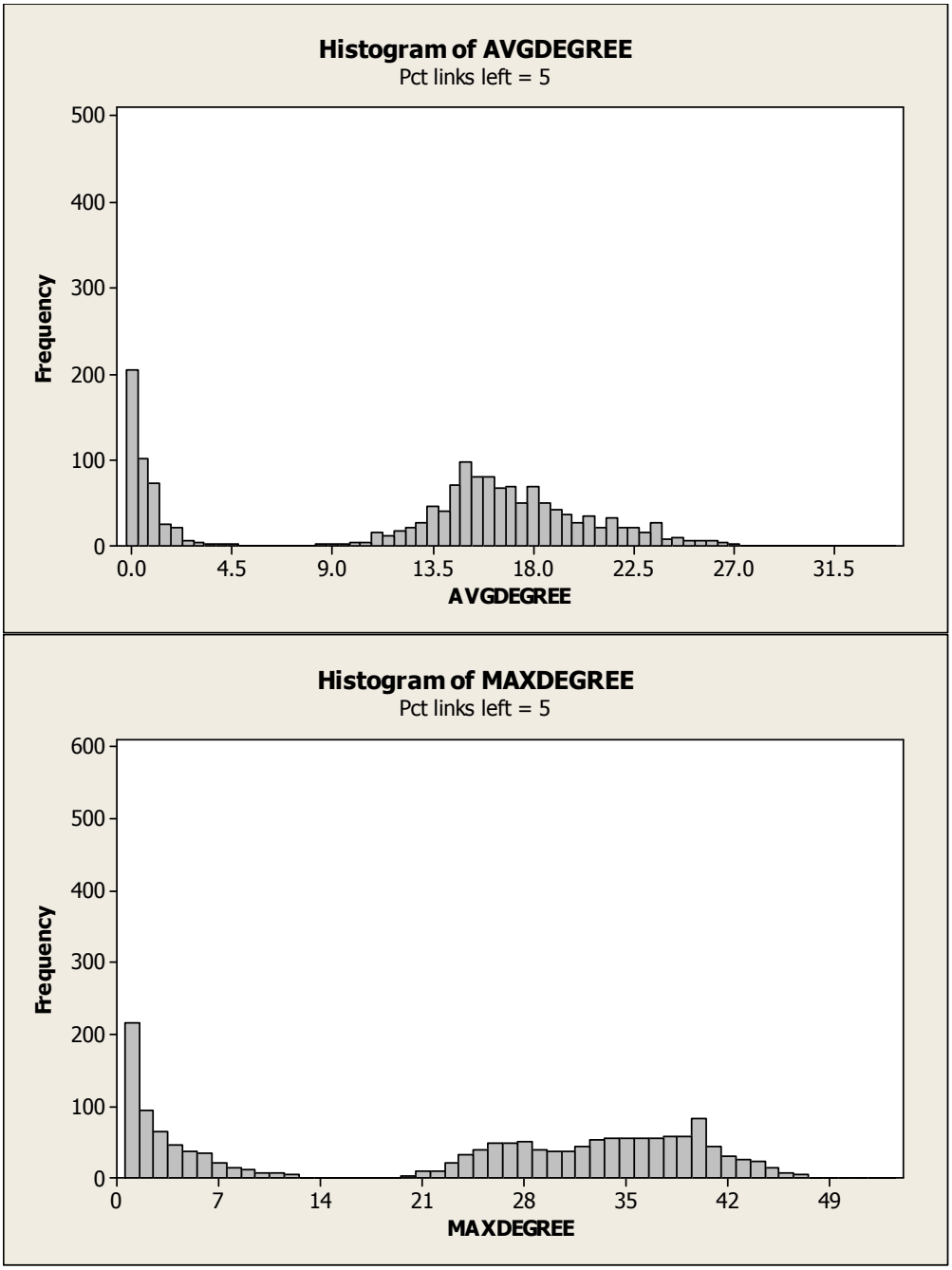

Figure S5c. Degree distribution per site when 95% of links selected at random have been removed. The GSCC has become smaller yet its path lengths have become even longer. The degree distribution of small clusters no longer overlaps at all with that of the GSCC to right of it, and a third entity of single sites (zero degree peak) has become dominant.

Sensitivity Analysis

The sensitivity of results to changes in relative likelihood of specific transmission types was investigated by running a series of 1,176 baseline simulations (10,000 seedings each; fixed latency delay of 50 days; no biosecurity controls in place; each outbreak allowed to spread for thirty years without any intervention). For convenience, we recall the four transmission likelihoods, given recorded transports per year T, stochastically reconstructed river transit times in days θ, and Euclidean distance D in meters between sites, based on their Ordnance Survey grid coordinates, and other parameters as follows:

$$p_{trans} = T / 365.2524$$

$$p_{river} = \alpha \exp[-\theta\lambda_R],\ \alpha = 0.005,\ \lambda_R = 1$$

$$p_{local} = \beta \exp[-(D^2)\lambda_L],\ \beta = 0.05,\ \lambda_L = 10^{-6}$$

$$p_{fomite} = \gamma \exp[-(D^2)\lambda_F],\ \gamma = 0.005,\ \lambda_F = 10^{-6}.$$

For each pairing of two out of these four transmission types (i.e., six permutations: local-river, local-transport, local-fomite, river-transport, river-fomite, and transport-fomite), we first explored a two-dimensional parameter space, by independently varying T, α, β, or γ respectively, in a multiplier range from 0.1 to 10 in seven steps (0.1, 0.2, 0.5, 1, 2, 5, 10), yielding 49 points per pairing. We ran simulations for severity factors 1, 2, and 5, and plotted the results per severity value in a half-matrix of all pair combinations (Figure S6a-c), using a fixed linear colour scale for the average outbreak size (range: 0-300), and log-log axes for the respective probability post-factors. Each panel thus represents a two-dimensional section through a four-dimensional space; the central point in each plane corresponds with the actual operative settings of the simulator in normal runs.

The same general pattern is recovered for each of the three global severity factors tested, albeit with higher absolute outbreak sizes. Results are most sensitive to changes in the transport likelihood, and least affected by fomite transmissions. Between these two extremes, changes in the river transmission likelihood are more influential than those in local transmissibility (seen most clearly in the top left panel of Figure S6c). Thus outbreak size is most sensitive to changes in likelihood of the two types of directed links, which are empirically best constrained. These links are also associated with the fewest source sites, suggesting that targeted biosecurity should be highly effective in this network.

Secondly, we investigated the sensitivity of results to the two λ scalars for the two undirected transmission types incorporated in our simulations. Again we separately investigated severity factors 1, 2, and 5, using the same plotting scheme as previously. Note, however, that the effect of these scalars is reversed with respect to the previous case, i.e., scalars larger than unity result in smaller transmission likelihoods and vice versa. Figure S6d shows that the sensitivity of results is almost completely dominated by the local λ_L for values smaller than 0.5, but for larger ones, the fomite λ_F becomes increasingly important. When λ_L reaches a factor 10, results become predominantly sensitive to changes in λ_F when the latter exceeds unity. As in the previous case, raising the outbreak severity causes a shift in absolute outbreak sizes, but the spatial pattern remains largely unchanged.

Thirdly, we separately studied the relative effect of changes in the two river scalars, i.e., plotting average outbreak size for the two-dimensional section of the average transmission rate α versus the river transit time scalar λ_R (Figure S6e). As

before, each variable was altered within a range of two orders of magnitude around the value used in actual simulations, testing each of 49 combinations per panel with 10,000 seedings each, without any controls in place, for severity factors 1,2, and 5. Note that outbreak size tends to increase with larger α and smaller λ_R respectively. Apart from larger absolute values, the relative distribution of outbreak sizes is again largely insensitive to choices of severity; it furthermore shows that results are mostly affected by changes in α, whereas only the smallest values of λ_R make an appreciable contribution to larger outbreak sizes.

Finally, the relative contributions to outbreak size of each of the eight factors considered (four premultipliers, three distance-related scalars, plus outbreak severity) were quantified statistically using a General Linear Model, which is an appropriate procedure for unbalanced fixed factors, as is the case here (a fully balanced design as applied elsewhere proved computationally too expensive to pursue). All fixed factors explore seven values (0.1, 0.2, 0.5, 1, 2, 5, and 10) except severity (settings: 1, 2, and 5). From the output reproduced below, one can glean that over 83% of all variability in the investigated continuous response variable (average outbreak size) is explained by the eight factors considered, and that no superfluous factors have been included (as R-sq(adj) is almost as large as the original R-sq). The two most important columns are the adjusted sum of squares (Adj. SS) and the p-value (rightmost column). The latter indicates that effects of the two fomite factors (γ and λ_F) and λ_R (waterborne pathogen decay rate) are not statistically significant for any reasonable confidence level chosen. Of the remaining factors (aside from severity), changes in transport transmission likelihood affect the outbreak size most, followed by the local area scalar λ_L and the river transmission rate α; the contribution of the local transmission rate β is much smaller. For an explanation of the various column headings, see the section on balanced ANOVA below.

Analysis of Variance for OUTAV1, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
BETA	6	121793	116277	19379	14.00	0.000
ALPHA	6	379372	331510	55252	39.92	0.000
T	6	2986979	2999833	499972	361.21	0.000
GAMMA	6	15333	5138	856	0.62	**0.716***
LAMBDA_L	6	496689	442541	73757	53.29	0.000
LAMBDA_F	6	11259	10899	1817	1.31	**0.248***
LAMBDA_R	6	12363	12363	2061	1.49	**0.179***
SEVERITY	2	4004873	4004873	2002436	1446.69	0.000
Error	1131	1565477	1565477	1384		
Total	1175	9594137				

S = 37.2042 R-Sq = 83.68% R-Sq(adj) = 83.05%

***** = not significant

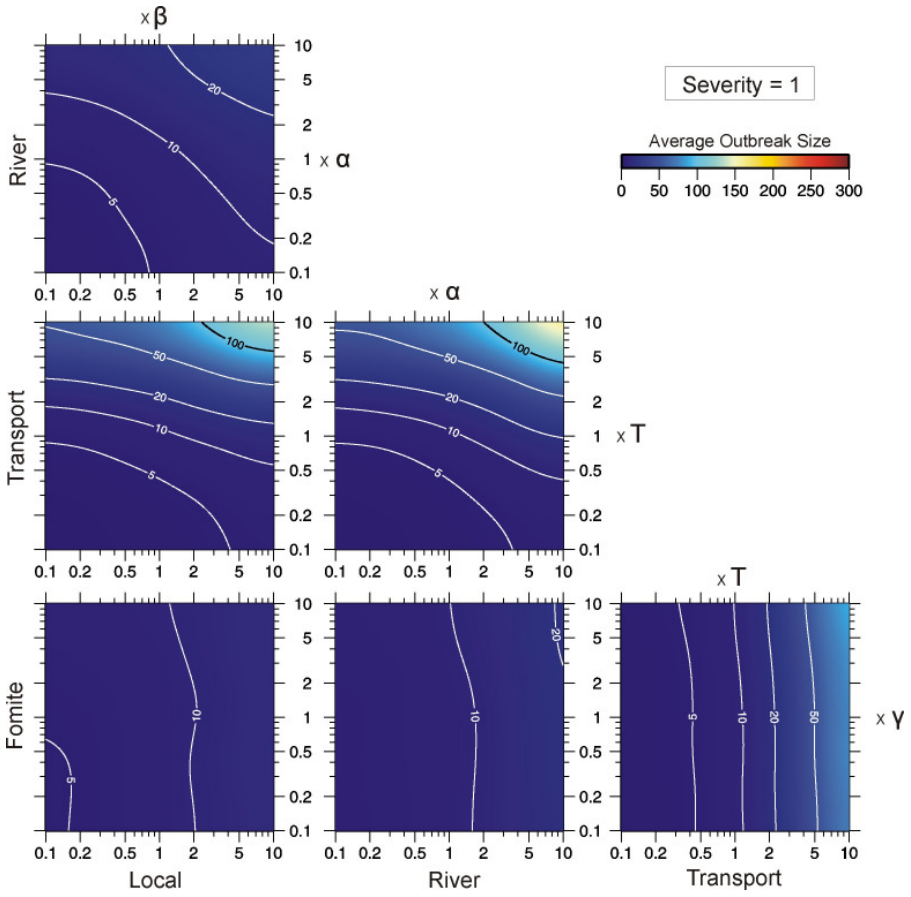

Figure S6a. Sensitivity analysis for baseline results (no control measures, 30-year timespan, latency delay: 50 days) for severity factor 1. Average outbreak size (colour scale with contour lines) for six panels of transmission likelihood pairs (log-log scale), independently varied by two orders of magnitude each (49 grid points per panel, 10,000 seedings per point).

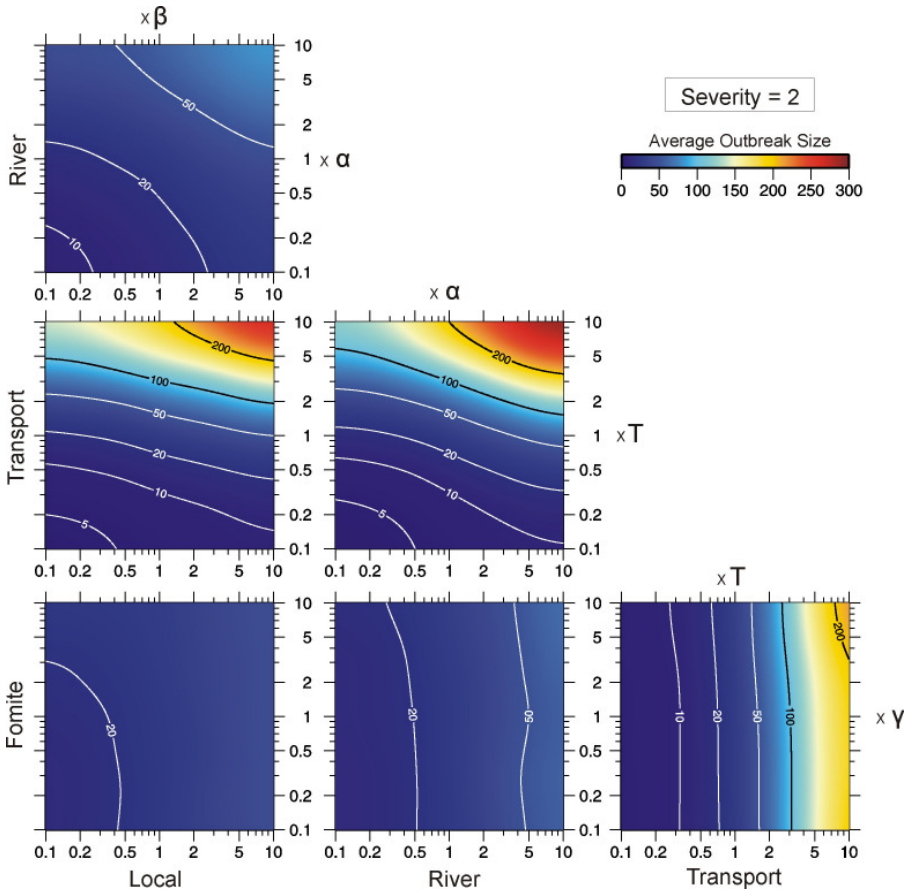

Figure S6b. Sensitivity analysis for baseline results for severity factor 2.

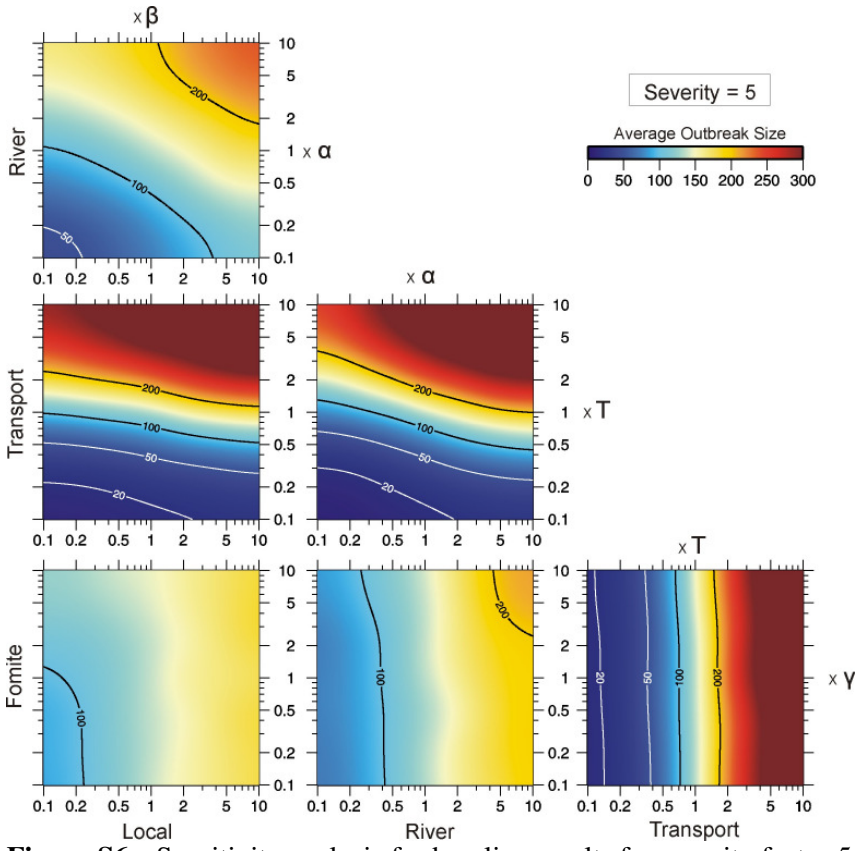

Figure S6c. Sensitivity analysis for baseline results for severity factor 5.

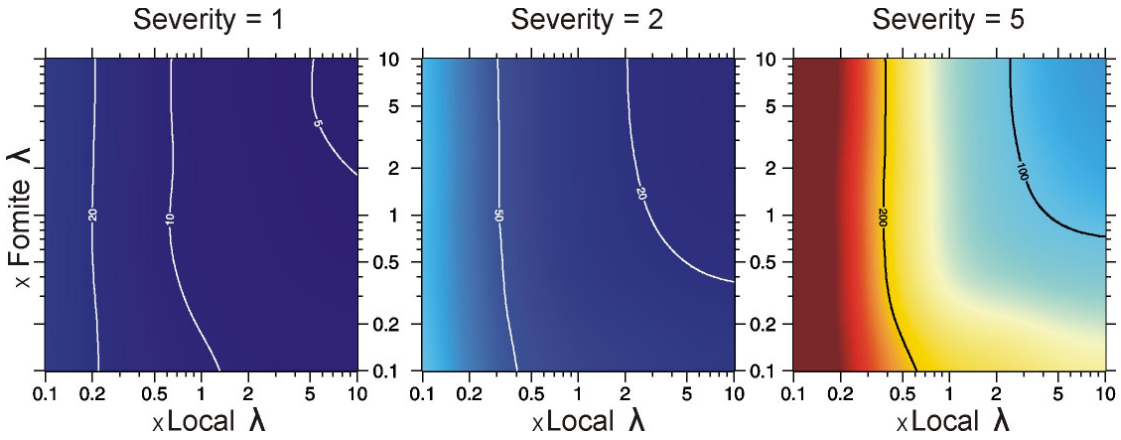

Figure S6d. Sensitivity of average outbreak size of baseline results for severity factors 1,2, and 5 (left to right), given changes in local and fomite distance scalars. Same colour scale and resolution as in previous figure (49 grid points per panel, 10,000 seedings per point).

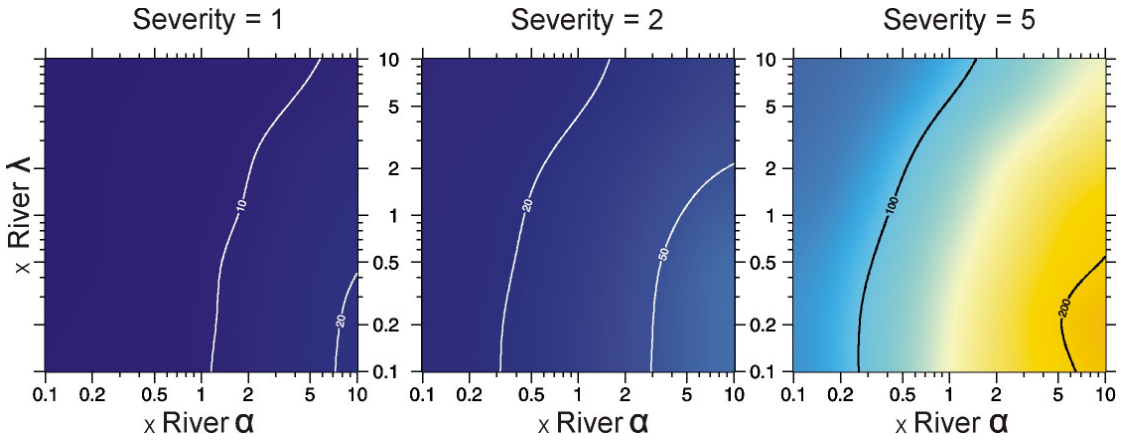

Figure S6e. Sensitivity of average outbreak size of baseline results for severity factors 1,2, and 5 (left to right), given changes in the two river transmission scalars. Same colour scale and resolution as in previous figures (49 grid points per panel, 10,000 seedings per point).

Kruskal-Wallis analysis of transmission totals

The Kruskal-Wallis test is a nonparametric alternative to one-way ANOVA (which assumes a Gaussian parent distribution). It is used to assess whether the medians from two independently sampled populations (or two population subsets) are equal (H_0 hypothesis) or significantly different (H_1). The only additional assumption made is that both sampled populations have continuous distributions with similar shape. Given some response variable, results quantify the response's median for each subset, the average rank of the subset, their Z-score relative to the overall averaged rank, and the *P*-value or likelihood that any observed differences are due to chance. If *P* is less than or equal to the predetermined alpha level (here we use 5%, i.e., the 95% confidence interval), the subset distinction expresses significant differences in medians.

We applied Kruskal-Wallis to the number of inward and outward links per site (per transmission type and combined) for the subset of fish farms versus that of fisheries, to determine whether their respective network architecture is significantly different (Table S3). We also ran simulations for each of the three main containment strategies (100,000 seedings each, no additional containment controls, severity = 5, laboratory capacity = 50 tests per year, hybrid ratio 1/1), to compare with one another, and with the network architecture result. With the exception of two inward transport

transmission totals (for proactive and hybrid policy), all remaining 38 tests confirmed that fish farms and fisheries should be considered different entities, both in network architecture and recorded transmissions. In terms of links, outward transport is most distinctive (see Z-scores in Table S3), followed by inward transport and inward river transmissions. Outward links represent most of the overall differences. In comparison with reactive controls, the two contact-tracing policies exacerbate measured differences in outward transmissions, but lessen those in inward transmissions. Based on these findings, fish farms can be seen from a biosecurity perspective as high-risk senders, both to other fish farms (via transport and river contacts) and to fisheries (transport), whereas fishery sites are primarily at risk as receivers. Table S4 of link statistics per site type moreover shows that fish farms tend on average to reside in areas with higher site density, increasing the number of local and fomite infection routes. Furthermore, all transport links originate at fish farms.

Table S3. Kruskal-Wallis tests of links and transmission totals per policy: medians per subset, mean ranks per subset, Z-score and p-value, for 1855 fisheries (left) and 235 fish farms (right)

		Links	Reactive	Proactive	Hybrid
Local	In	30; 33 1031; 1160 3.10; 0.002	0; 0 1024; 1213 4;51; 0.000	1; 9 1026; 1204 4.26; 0.000	0; 2 1026; 1203 4.25; 0.000
	Out	30; 33 1031; 1160 3.10; 0.000	0; 0 1022; 1232 5.02; 0.000	0; 10 1019; 1252 5.56; 0.000	0; 2 1021; 1238 5.19; 0.000
Fomite	In	2; 2 1021; 1240 5.24; 0.000	0; 0 1034; 1134 2.39; 0.000	0; 1 1030; 1167 3.28; 0.001	0; 0 1029; 1179 3.60; 0.000
	Out	2; 2 1021;1240 5;24; 0.000	0; 0 1028; 1185 3.75; 0.017	0; 1 1022; 1232 5.02; 0.000	0; 0 1025; 1206 4.32; 0.000
River	In	0; 1 1010; 1327 7.59; 0.000	0; 0 1012; 1314 7.23; 0.000	0; 3 1014; 1297 6.79; 0.000	0; 1 1014; 1298 6.82; 0.000
	Out	0; 0 1020; 1248 5.46; 0.000	0; 0 1012; 1314 4.76; 0.000	0; 0 1018; 1266 5.95; 0.000	0; 0 1019; 1257 5.69; 0.000
Transport	In	1; 2 1007; 1352 8.27; 0.000	1; 3 1006; 1359 8.46; 0.000	112; 115 1042; 1072 0.70; 0.482*	14; 16 1037; 1109 1.72; 0.086*
	Out	0; 4 949; 1811 20.65; 0.000	0; 5 958; 1740 18.73; 0.000	0; 147 951; 1791 20.11; 0.000	0; 21 951; 1791 20.11; 0.000
Total	In	33; 39 1023; 1225 4.85; 0.000	2; 11 997; 1428 10.32; 0.000	182; 296 1018; 1260 5.80; 0.000	23; 45 1012; 1307 7.05; 0.000
	Out	32; 48 1003;1385 9.14; 0.000	0; 16 974; 1605 15.07; 0.000	2; 317 968; 1654 16.41; 0.000	0; 47 971; 1635 15.89; 0.000

Note: severity=5 for all policies; overall mean rank: 1045.5; * = H_1 rejected

Table S4. Number of links per site type (mean, Q1/Q2/Q3)

Transmission type		Fisheries (1855)	Fish farms (235)	All sites (2090)
Local	In	33.098 20/30/41	39.40 22/33/47	33.806 21/30/41
	Out	33.098 20/30/41	39.40 22/33/47	33.806 21/30/41
Fomite	In	2.3456 0/2/3	3.630 1/2/4	2.49 1/2/3
	Out	2.3456 0/2/3	3.630 1/2/4	2/49 1/2/3
River	In	0.9391 0/0/1	2.085 0/1/3	1.0679 0/0/1
	Out	0.9876 0/0/1	1.702 0/0/2	1.0679 0/0/1
Transport	In	1.1822 1/1/1	2.370 1/2/3	1.316 1/1/1
	Out	0 0/0/0	11.70 1/4/13	1.316 0/0/0
Total	In	37.564 23/33/45	47.48 25/39/56	38.679 23/34/46
	Out	36.431 22/32/44	56.43 25/39/56	38.679 23/34/46

Note: Q1, Q3 = 1st, 3rd quartile, Q2 = median

Geographic Risk Maps per policy

Long simulations of 100,000 seedings each were run for each of the three main control policies, with the following fixed parameter settings: severity factor 5; latency delay 5 days; detection delay 100 days, culling delay 10 days, restocking delay 100 days. For proactive and hybrid policies, the laboratory capacity was limited to 50 conclusive site tests per year; for the hybrid policy a reactive / proactive ratio of 1/1 was chosen. Inward and outward transmissions were stored separately per site, averaged per river catchment, and the latter transformed by computing their natural log. The largest overall value of ln(4440.4) then provided the maximum for a range of 15 equal-width bins, with negative log-values moved into the first bin, and empty bins being allocated to an additional zero bin. Figures S7a-c display geographic risk per catchment, per policy. A clear discrepancy between outward (more concentrated) and inward transmissions pervades all plots. Risk in the proactive policy is most severe and most widespread. However, in contrast to the average and maximum outbreak statistics computed over entire ensembles of delay parameters, this particular realisation (with medium-high severity) shows the hybrid strategy to result in higher risk than the reactive policy. Some specific (relative) high-risk catchments can be identified in all three plots.

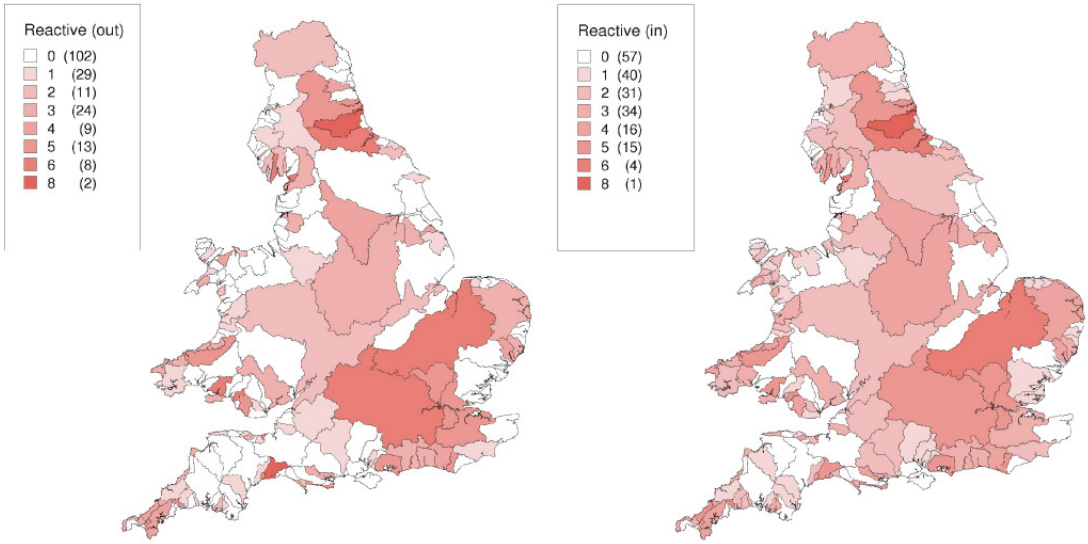

Figure S7a. Geographic risk distribution per catchment, for the reactive policy. Fixed colour scale, levels 0-15. *Left*: outward transmissions. *Right*: inward transmissions.

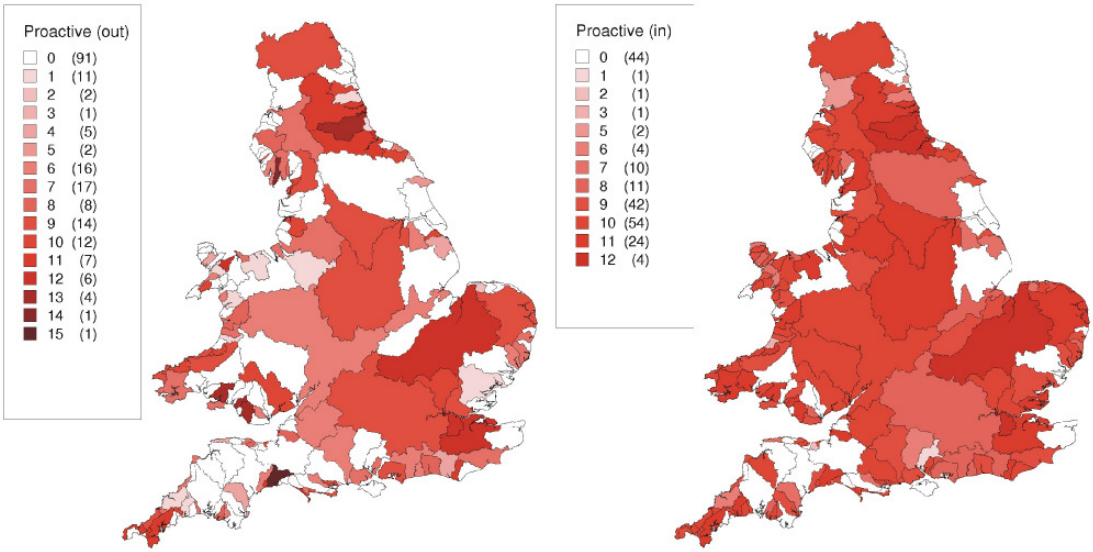

Figure S7b. Geographic risk distribution per catchment, for the proactive policy. Fixed colour scale, levels 0-15. *Left*: outward transmissions. *Right*: inward transmissions.

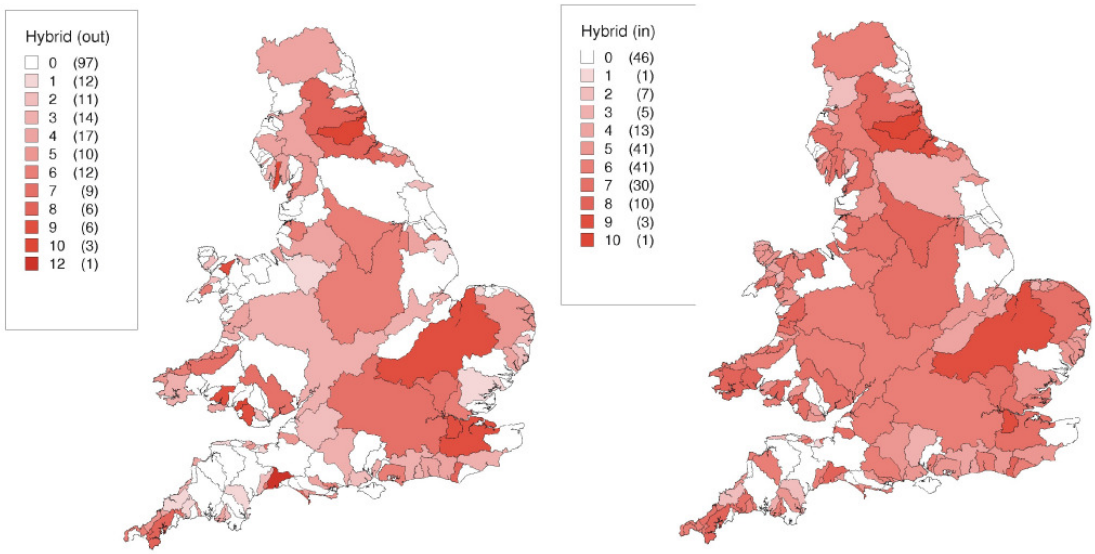

Figure S7c. Geographic risk distribution per catchment, for the hybrid policy. Fixed colour scale, levels 0-15. *Left*: outward transmissions. *Right*: inward transmissions.

Balanced ANOVA results

Given the balanced design of parameter (or "factor") combinations explored in the simulations (i.e., the number of observations for each combination of the various factor levels is the same), balanced ANOVA is an appropriate statistical technique to examine the effects of multiple factors on several continuous response variables such as average and maximum outbreak size, duration, and the number of endemic outbreaks. Note that the maximum outbreak size is the largest outbreak recorded per 10,000 seedings; this is not necessarily an endemic outbreak (stopped by timeout after thirty years of simulated time); if no endemic outbreaks were recorded in a sample, the maximum represents the largest number of sites ever infected after a single seeding.

Balanced ANOVA differs from General Linear Models (Munro et al. 2010), which allows for unbalanced data, and from fully-nested ANOVA, which requires a hierarchical design and assumes that all factors are randomly drawn. By contrast, in this study all factors (parameters) are considered fixed, i.e., they are discrete variables that are altered systematically. ANOVA then examines whether the factor level means are significantly different from each other, and quantifies respective factor contributions to the studied response.

ANOVA procedures assume, and we tested to confirm, that errors are independent and approximately normally distributed with zero mean, and that error variance is itself invariant for different factor terms. We did find that response variables tended to depart somewhat from normality in producing heavier distribution tails (i.e., more large values than predicted by a Gaussian pdf). To correct for this, we applied the Box-Cox transformation to all response variables to stabilise their variance prior to ANOVA. These results are the ones presented below. However, when we compared these outputs to those based on the original responses we found no appreciable differences in the conclusions drawn. We also tested for, but did not find, marked interaction effects between different factor pairs. All of the above, in combination with the large sample sizes acquired, suggest that the performed analyses are robust.

The relevance of specific factors is quantified as follows. For each continuous response variable evaluated, balanced ANOVA yields a list of all factors considered. Per factor it computes the degrees of freedom (DF), the sum of squares (SS), the mean squares (MS), the F statistic, and the probability (P). The DF expresses how much independent information is available to calculate each SS; the SS quantifies the total amount of variation in the response explained by the factor; the MS does the same per factor level (MS = SS / DF); the F statistic is used to determine the p-value. The latter represents the probability of obtaining results as extreme (or greater) in the absence of a real effect. Thus given some alpha-level of desired significance (here we use 0.05, i.e., a 95% one-sided confidence limit), any p-value above it implies that the effect is not significant, and is rejected. In the results tabulated below (and elsewhere), a p-value of zero indicates a true value below 0.0005.

The complete analysis per response variable is quantified in terms of *S*, R^2, and adjusted R^2. The first term (*S*) is the square root of the mean-squared-residual-error, quantifying remaining data variance after the relationship between the response and the predictors has been taken into account. The coefficient of determination *R-Sq*(uared) expresses the percentage of variation in the response explained by the predictors. Table S5 presents this measure for the listed balanced ANOVA results, showing that all ensembles explain more than half of all observed variation in up to seven different response variables. Remaining variability may be due to the identity of the seeding site, as well as dynamic interactions between the changing outbreak configuration, selected contingency measures, and delay parameters. We note that *R-Sq* can be artificially high if unnecessary factors are included. To test for this, the adjusted *R-Sq* modifies the overall *R-Sq* for the included number of factors. A large decrease in adjusted *R-Sq* with respect to the original *R-Sq* would imply that unnecessary factors are present. However, results clearly show that all considered factors are relevant. In the following tables, the factor "awareness" designates the public awareness campaign (halving all detection delays after the first one); TB indicates the national transport ban (in force for 30 days, plus possible extension whenever new infected sites are discovered within that period). The raw output tables are followed by a brief summary.

Table S5. Percentage of variance explained per response measure

	Baseline	**Reactive**	**Proactive**	**Hybrid**
Average outbreak size (all seedings)	99.58%	91.14%	80.01%	82.00%
Average outbreak size (subset)	99.56%	92.31%	75.25%	67.61%
Maximum outbreak size	99.88%	95.58%	69.70%	57.36%
Number of endemic outbreaks	n/a	69.67%	82.09%	70.43%
Average outbreak duration	n/a	93.46%	92.07%	77.17%
Average lab queue length	n/a	n/a	72.64%	69.38%
Wasted laboratory capacity	n/a	n/a	54.23%	61.82%

n/a = not applicable

Balanced ANOVA results for: Baseline tests

```
Analysis of Variance for: Average outbreak size (all seedings)
Source   DF      SS     MS        F      P
LATENCY   5    2112    422     8.51  0.000
SEVERITY  5  291229  58246  1173.74  0.000
Error    25    1241     50
Total    35  294581
S = 7.04445   R-Sq = 99.58%   R-Sq(adj) = 99.41%

Analysis of Variance for: Average outbreak size (excluding outbreaks
of one single site)
Source   DF      SS      MS        F      P
LATENCY   5    7912    1582     9.30  0.000
SEVERITY  5  964171  192834  1133.68  0.000
Error    25    4252     170
Total    35  976335
S = 13.0421   R-Sq = 99.56%   R-Sq(adj) = 99.39%

Analysis of Variance for: Maximum outbreak size
Source   DF       SS       MS        F      P
LATENCY   5    19499     3900     8.98  0.000
SEVERITY  5  9106796  1821359  4194.32  0.000
Error    25    10856      434
Total    35  9137151
S = 20.8385   R-Sq = 99.88%   R-Sq(adj) = 99.83%
```

Balanced ANOVA results for: Reactive policy

```
Analysis of Variance for: Average outbreak size (all seedings)
Source         DF       SS      MS         F      P
DETECTION       7  5189.47  741.35  71639.15  0.000
LATENCY         5     0.07    0.01      1.43  0.210* not significant
CULLING         5     2.33    0.47     45.11  0.000
RESTOCKING      7     3.87    0.55     53.49  0.000
SEVERITY        5   675.41  135.08  13053.44  0.000
TB              1     2.31    2.31    223.31  0.000
AWARENESS       1     8.98    8.98    867.87  0.000
Error       55264   571.90    0.01
Total       55295  6454.36
S = 0.101727   R-Sq = 91.14%   R-Sq(adj) = 91.13%

Analysis of Variance for: Average outbreak size (excluding outbreaks
of one single site)
Source         DF       SS      MS         F      P
DETECTION       7  689.955  98.565  83779.80  0.000
LATENCY         5    0.012   0.002      2.03  0.071* not significant
CULLING         5    0.206   0.041     35.10  0.000
RESTOCKING      7    0.819   0.117     99.40  0.000
SEVERITY        5   86.526  17.305  14709.35  0.000
TB              1    0.673   0.673    571.94  0.000
AWARENESS       1    2.193   2.193   1864.43  0.000
Error       55264   65.017   0.001
Total       55295  845.402
S = 0.0342998   R-Sq = 92.31%   R-Sq(adj) = 92.31%

Analysis of Variance for: Maximum outbreak size
Source         DF        SS       MS          F      P
DETECTION       7  1605.654  229.379  147029.75  0.000
LATENCY         5     0.052    0.010       6.71  0.000
CULLING         5     0.806    0.161     103.32  0.000
RESTOCKING      7     1.763    0.252     161.45  0.000
SEVERITY        5   242.285   48.457   31060.46  0.000
TB              1     1.636    1.636    1048.36  0.000
AWARENESS       1    10.008   10.008    6414.98  0.000
```

```
Error       55264    86.217    0.002
Total       55295  1948.420
S = 0.0394979   R-Sq = 95.58%   R-Sq(adj) = 95.57%

Analysis of Variance for: Number of endemic outbreaks
Source         DF       SS      MS         F      P
DETECTION       7  4999.82  714.26  16163.12  0.000
LATENCY         5    34.56    6.91    156.43  0.000
CULLING         5     0.06    0.01      0.28  0.925* not significant
RESTOCKING      7   106.53   15.22    344.38  0.000
SEVERITY        5   321.26   64.25   1453.99  0.000
TB              1     0.76    0.76     17.22  0.000
AWARENESS       1   146.97  146.97   3325.77  0.000
Error       55264  2442.15    0.04
Total       55295  8052.12
S = 0.210216   R-Sq = 69.67%   R-Sq(adj) = 69.65%

Analysis of Variance for: Average outbreak duration (excluding
outbreaks of one single site and endemic outbreaks)
Source         DF        SS       MS         F      P
DETECTION       7   78.0408  11.1487  91514.90  0.000
LATENCY         5   16.9639   3.3928  27849.93  0.000
CULLING         5    0.8064   0.1613   1323.95  0.000
RESTOCKING      7    0.0314   0.0045     36.85  0.000
SEVERITY           5    0.2028   0.0406    332.95  0.000
TB              1    0.0006   0.0006      5.13  0.024
AWARENESS       1    0.1094   0.1094    897.79  0.000
Error       55264    6.7325   0.0001
Total       55295  102.8878
S = 0.0110374   R-Sq = 93.46%   R-Sq(adj) = 93.45%
```

Balanced ANOVA results for: Proactive policy

```
Analysis of Variance for: Average outbreak size (all seedings)
Source          DF        SS       MS         F      P
DETECTION        7   7167.45  1023.92  43263.53  0.000
LATENCY          5     57.32    11.46    484.36  0.000
CULLING          5    658.73   131.75   5566.64  0.000
RESTOCKING       7    157.46    22.49    950.47  0.000
SEVERITY         5   5919.49  1183.90  50023.06  0.000
LAB              5   1286.25   257.25  10869.53  0.000
TB               1    465.53   465.53  19669.80  0.000
Error       165852   3925.23     0.02
Total       165887  19637.46
S = 0.153841   R-Sq = 80.01%   R-Sq(adj) = 80.01%

Analysis of Variance for: Average outbreak size (excluding outbreaks
of one single site)
Source          DF       SS      MS         F      P
DETECTION        7   756.83  108.12   9428.08  0.000
LATENCY          5    56.91   11.38    992.58  0.000
CULLING          5   518.84  103.77   9048.68  0.000
RESTOCKING       7   131.24   18.75   1634.96  0.000
SEVERITY         5  2600.04  520.01  45345.53  0.000
LAB              5  1347.40  269.48  23499.16  0.000
TB               1   372.15  372.15  32452.03  0.000
Error       165852  1901.94    0.01
Total       165887  7685.34
S = 0.107087   R-Sq = 75.25%   R-Sq(adj) = 75.25%


Analysis of Variance for: Maximum outbreak size
Source          DF        SS      MS         F      P
DETECTION        7   11220.9  1603.0   7772.87  0.000
LATENCY          5     890.3   178.1    863.45  0.000
CULLING          5    8939.3  1787.9   8669.31  0.000
```

RESTOCKING	7	2570.4	367.2	1780.58	0.000
SEVERITY	5	36419.9	7284.0	35319.87	0.000
LAB	5	10699.2	2139.8	10376.07	0.000
TB	1	7936.4	7936.4	38483.48	0.000
Error	165852	34203.5	0.2		
Total	165887	112880.1			

S = 0.454124 R-Sq = 69.70% R-Sq(adj) = 69.69%

Analysis of Variance for: Number of endemic outbreaks

Source	DF	SS	MS	F	P
DETECTION	7	2185.65	312.24	47019.15	0.000
LATENCY	5	24.98	5.00	752.22	0.000
CULLING	5	330.87	66.17	9964.94	0.000
RESTOCKING	7	18.51	2.64	398.12	0.000
SEVERITY	5	1266.03	253.21	38130.00	0.000
LAB	5	1210.66	242.13	36462.18	0.000
TB	1	12.81	12.81	1929.73	0.000
Error	165852	1101.36	0.01		
Total	165887	6150.87			

S = 0.0814900 R-Sq = 82.09% R-Sq(adj) = 82.09%

Analysis of Variance for: Average outbreak duration (excluding outbreaks of one single site and endemic outbreaks)

Source	DF	SS	MS	F	P
DETECTION	7	41294.9	5899.3	112055.05	0.000
LATENCY	5	1955.1	391.0	7427.23	0.000
CULLING	5	1992.0	398.4	7567.46	0.000
RESTOCKING	7	6.1	0.9	16.47	0.000
SEVERITY	5	405.6	81.1	1540.86	0.000
LAB	5	55710.3	11142.1	211640.24	0.000
TB	1	7.4	7.4	140.11	0.000
Error	165852	8731.5	0.1		
Total	165887	110102.8			

S = 0.229448 R-Sq = 92.07% R-Sq(adj) = 92.07%

Analysis of Variance for: Average length of the site-testing queue

Source	DF	SS	MS	F	P
DETECTION	7	28.9408	4.1344	17207.56	0.000
LATENCY	5	0.0041	0.0008	3.40	0.005
CULLING	5	31.7197	6.3439	26403.80	0.000
RESTOCKING	7	0.0027	0.0004	1.61	0.128* not significant
SEVERITY	5	6.7407	1.3481	5611.04	0.000
LAB	5	38.3694	7.6739	31939.04	0.000
TB	1	0.0030	0.0030	12.31	0.000
Error	165852	39.8486	0.0002		
Total	165887	145.6289			

S = 0.0155005 R-Sq = 72.64% R-Sq(adj) = 72.63%

Analysis of Variance for: wasted laboratory capacity (negative tests)

Source	DF	SS	MS	F	P
DETECTION	7	43.477	6.211	2910.66	0.000
LATENCY	5	3.131	0.626	293.42	0.000
CULLING	5	204.556	40.911	19172.20	0.000
RESTOCKING	7	4.159	0.594	278.42	0.000
SEVERITY	5	51.190	10.238	4797.87	0.000
LAB	5	107.045	21.409	10032.93	0.000
TB	1	5.845	5.845	2739.02	0.000
Error	165852	353.908	0.002		
Total	165887	773.311			

S = 0.0461939 R-Sq = 54.23% R-Sq(adj) = 54.23%

Balanced ANOVA results for: Hybrid policy

Analysis of Variance for: Average outbreak size (all seedings)

Source	DF	SS	MS	F	P
DETECTION	7	6984.04	997.72	51618.73	0.000
LATENCY	5	558.78	111.76	5781.86	0.000
CULLING	5	539.52	107.90	5582.63	0.000
RESTOCKING	7	2.67	0.38	19.75	0.000
LAB	5	2498.92	499.78	25857.16	0.000
RATIO	8	367.77	45.97	2378.43	0.000
Error	124378	2404.06	0.02		
Total	124415	13355.76			

S = 0.139027 R-Sq = 82.00% R-Sq(adj) = 81.99%

Analysis of Variance for: Average outbreak size (excluding outbreaks of one single site)

Source	DF	SS	MS	F	P
DETECTION	7	779.53	111.36	7488.34	0.000
LATENCY	5	505.22	101.04	6794.51	0.000
CULLING	5	458.75	91.75	6169.64	0.000
RESTOCKING	7	1.68	0.24	16.16	0.000
LAB	5	1829.35	365.87	24602.44	0.000
RATIO	8	285.62	35.70	2400.73	0.000
Error	124378	1849.66	0.01		
Total	124415	5709.80			

S = 0.121948 R-Sq = 67.61% R-Sq(adj) = 67.60%

Analysis of Variance for: Maximum outbreak size

Source	DF	SS	MS	F	P
DETECTION	7	89273.0	12753.3	6979.76	0.000
LATENCY	5	43262.0	8652.4	4735.39	0.000
CULLING	5	73834.5	14766.9	8081.79	0.000
RESTOCKING	7	77.4	11.1	6.05	0.000
LAB	5	87369.1	17473.8	9563.27	0.000
RATIO	8	11949.4	1493.7	817.47	0.000
Error	124378	227261.1	1.8		
Total	124415	533026.5			

S = 1.35173 R-Sq = 57.36% R-Sq(adj) = 57.35%

Analysis of Variance for: Number of endemic outbreaks

Source	DF	SS	MS	F	P
DETECTION	7	2048.51	292.64	12350.18	0.000
LATENCY	5	638.52	127.70	5389.41	0.000
CULLING	5	1257.65	251.53	10615.10	0.000
RESTOCKING	7	1.80	0.26	10.84	0.000
LAB	5	2647.18	529.44	22343.23	0.000
RATIO	8	425.04	53.13	2242.17	0.000
Error	124378	2947.21	0.02		
Total	124415	9965.90			

S = 0.153934 R-Sq = 70.43% R-Sq(adj) = 70.42%

Analysis of Variance for: Average outbreak duration (excluding outbreaks of one single site and endemic outbreaks)

Source	DF	SS	MS	F	P
DETECTION	7	12070.74	1724.39	32010.34	0.000
LATENCY	5	312.17	62.43	1158.96	0.000
CULLING	5	826.42	165.28	3068.20	0.000
RESTOCKING	7	0.36	0.05	0.95	0.466* not significant
LAB	5	8285.10	1657.02	30759.70	0.000
RATIO	8	1153.20	144.15	2675.90	0.000
Error	124378	6700.22	0.05		
Total	124415	29348.20			

S = 0.232099 R-Sq = 77.17% R-Sq(adj) = 77.16%

Analysis of Variance for: Average length of the site-testing queue

Source	DF	SS	MS	F	P
DETECTION	7	315.865	45.124	10113.81	0.000

```
LATENCY          5    31.737    6.347   1422.66  0.000
CULLING          5   565.687  113.137  25358.12  0.000
RESTOCKING       7     0.001    0.000      0.03  1.000* not significant
LAB              5   287.060   57.412  12868.09  0.000
RATIO            8    57.110    7.139   1600.06  0.000
Error       124378   554.923    0.004
Total       124415  1812.382
S = 0.0667951   R-Sq = 69.38%   R-Sq(adj) = 69.37%

Analysis of Variance for: wasted laboratory capacity (negative tests)
Source          DF        SS       MS         F      P
DETECTION        7   261.780   37.397   3570.34  0.000
LATENCY          5   168.035   33.607   3208.50  0.000
CULLING          5   943.306  188.661  18011.67  0.000
RESTOCKING       7     0.624    0.089      8.50  0.000
LAB              5   433.971   86.794   8286.33  0.000
RATIO            8   301.971   37.746   3603.69  0.000
Error       124378  1302.783    0.010
Total       124415  3412.470
S = 0.102344   R-Sq = 61.82%   R-Sq(adj) = 61.81%
```

Summarising the reactive case, the detection delay is by far the most important factor affecting average and maximum outbreak size, outweighing even outbreak severity. A distant third is the public awareness campaign (AC), followed by minor contributions from the restocking delay, the national transport ban (TB), and the culling delay; latency delay appears to have little effect here. For endemic outbreaks, the top two remain unchanged, but restocking is here almost as influential as the AC, followed by latency. Outbreak durations (for non-endemic outbreaks larger than a single site) are almost exclusively determined by detection and latency (in that order), with a tiny contribution from the culling delay. Thus a higher global transmission likelihood (the severity parameter) has hardly any effect on how long an outbreak lasts, although it does occasion a general shift towards more endemic outbreaks. Comparing the two additional measures, the AC consistently exceeds the TB in efficacy.

The proactive strategy offers a more complex picture. Starting with mean outbreak size, the severity factor is almost par with detection (most influential) when the average is computed over all seedings, and it achieves first ranking when excluding single-site outbreaks. In the latter case, lab capacity is the second most important factor (otherwise third). Of the other delay parameters, culling ends highest, and even more so when assessing maximum outbreak size. The TB has a minor effect, followed by restocking and latency. The number of endemic outbreaks relies as previously on the detection delay. The outbreak severity multiplier and lab capacity have about equal effect on this response, followed by culling. Furthermore, outbreak duration is foremost a function of lab capacity, followed by detection and minor contributions from latency and culling. The average length of the site-testing queue is affected most by the lab capacity, but the culling delay is close behind, followed by detection. The response measure of the number of negative laboratory tests (i.e., wasted capacity) yields a similar profile, but with outbreak severity as an added influence. Remaining parameters have little effect.

Finally, the hybrid policy (tested at severity factor five only) is to first order determined by detection delay and lab capacity. Detection is most influential for average outbreak size (all seedings) and duration; available testing resources are most relevant for large and endemic outbreaks; for maximum outbreak size their effects are roughly equal. Next in line, latency and culling delay yield similar contributions to the two outbreak size averages, but culling has the advantage in all other response

variables. Overall, the hybrid-specific ratio of reactive versus proactive detections represents a minor contribution, whereas the restocking delay has virtually no effect.

We separately tested for the presence of parameter interaction, i.e., when the response at a factor level strongly depends on the levels of other factors. For this we plotted the means for each level of a factor while a second factor was kept constant. Parallel lines (but not necessarily horizontal or overlapping) indicate no interaction. Three examples are shown. In the reactive example of average outbreak size (all seedings) we find some weak interaction for the highest detection delay only (1,000 days), with the highest culling delay (one point) and low restocking delays respectively. All other level combinations of all parameters do not appear to interact at all. Similar states are found in the proactive case (number of endemic outbreaks) and the hybrid example (average outbreak duration); very mild interactions affect the largest detection delay for largest culling delay and smallest restocking delay.

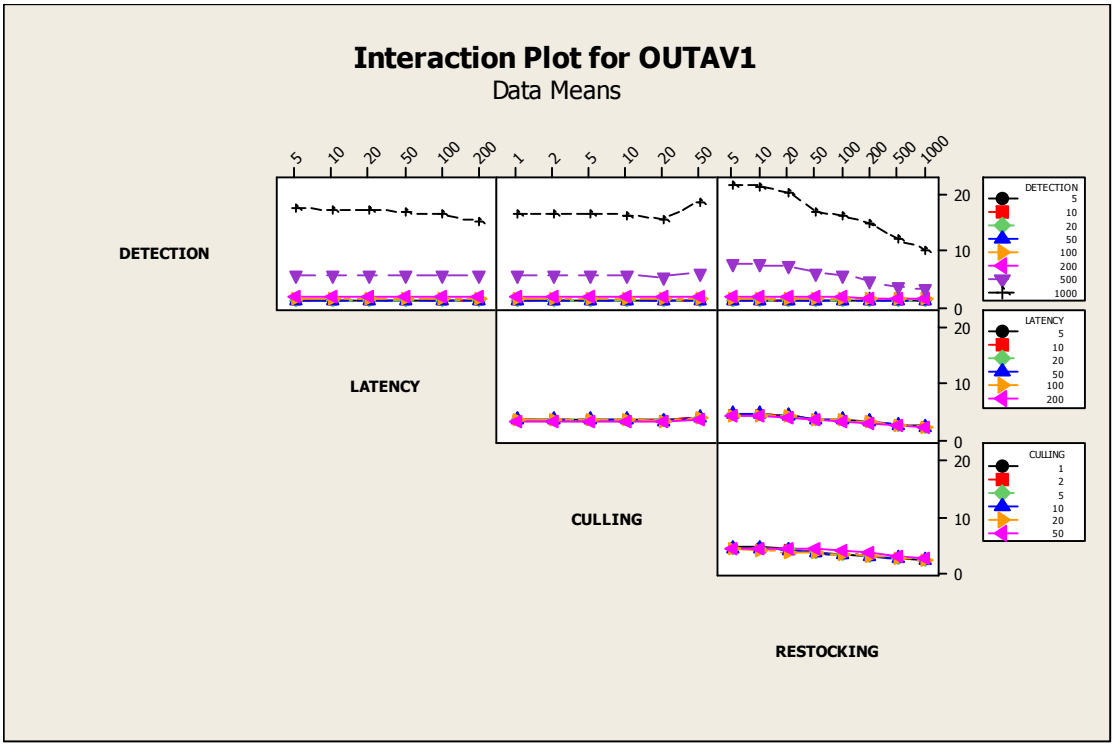

Figure S8a. Interaction plot for average outbreak size (all seedings) in the reactive policy

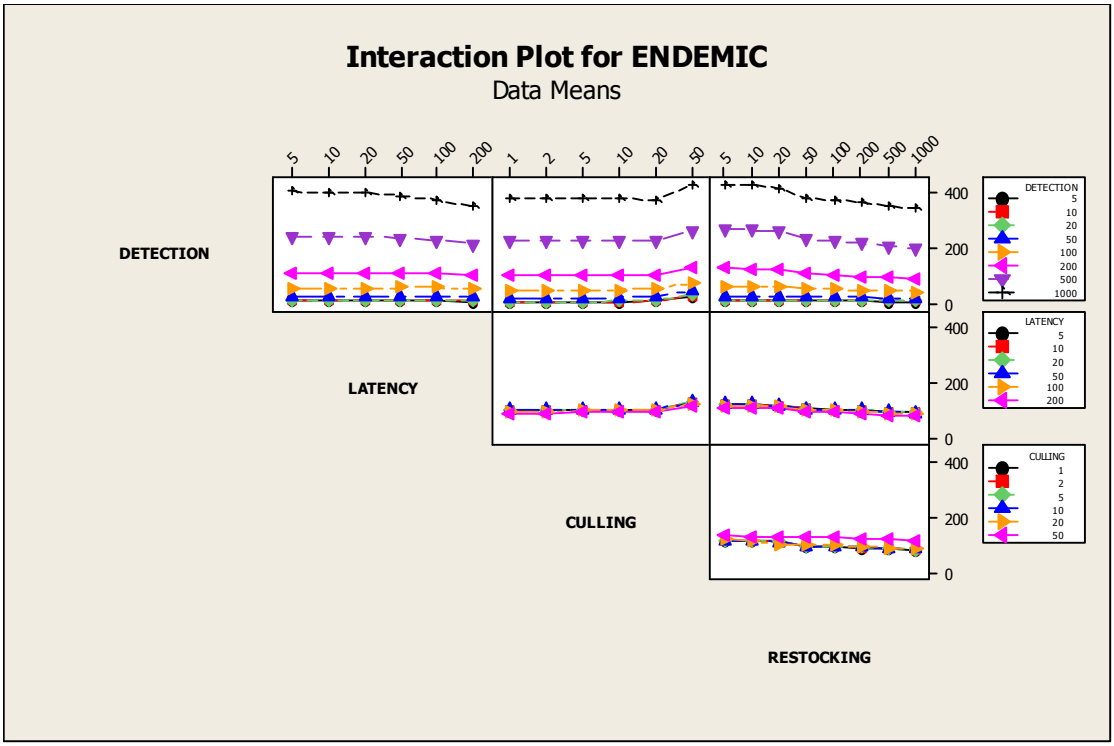

Figure S8b. Interaction plot for the number of endemic outbreaks in the proactive policy

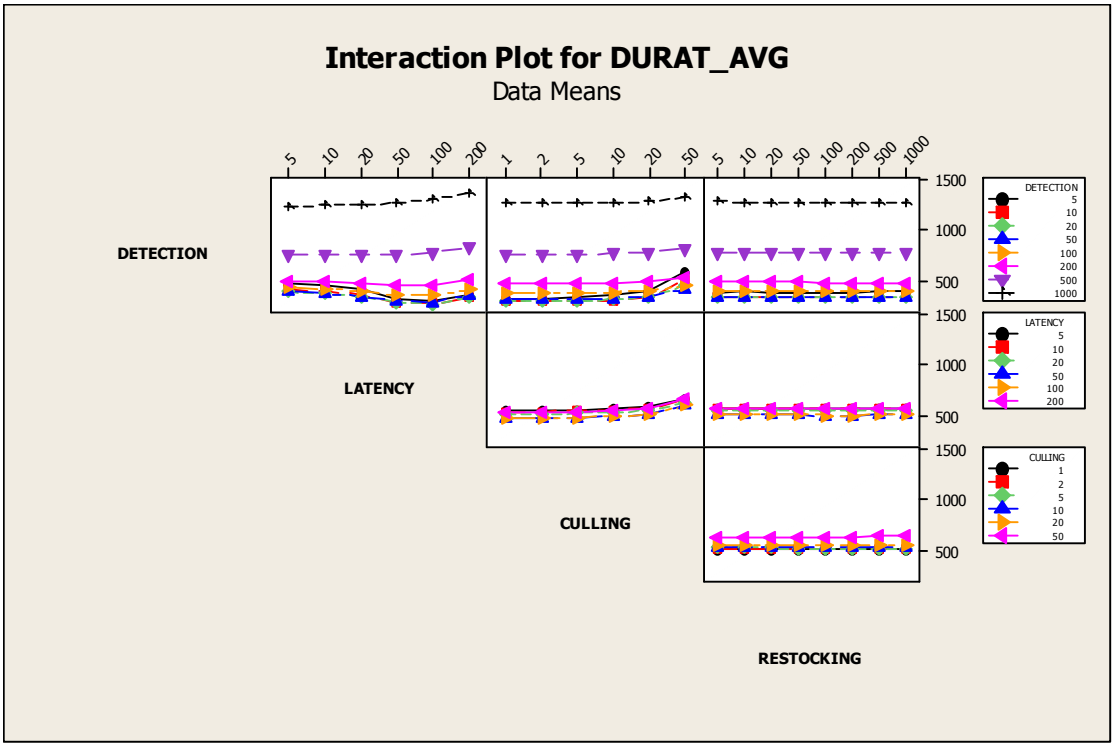

Figure S8c. Interaction plot for average outbreak duration (single-site and endemic outbreaks excluded) in the hybrid policy

Main Effects

Within the context of ANOVA, a "main effect" occurs when the mean response changes significantly across the levels of a considered factor. It is commonly evaluated in a plot of the line-connected response mean for each factor level, relative to a horizontal reference of the overall response mean. If all plotted points coincide with this horizontal, a main effect is absent for this factor. The greater the slope of a plotted line segment, the larger the effect across the two factor levels that define that segment. Comparing slopes of different factors indicates their relative strength in affecting the response. Thus main effects plots help to quickly identify which factors (and which factor levels) influence a chosen response the most. However, whether a perceived pattern is statistically significant has to be evaluated separately (see Balanced ANOVA results). Here we present five examples (Figures S9a-e) for outbreak size and duration, followed by summary tables of all results.

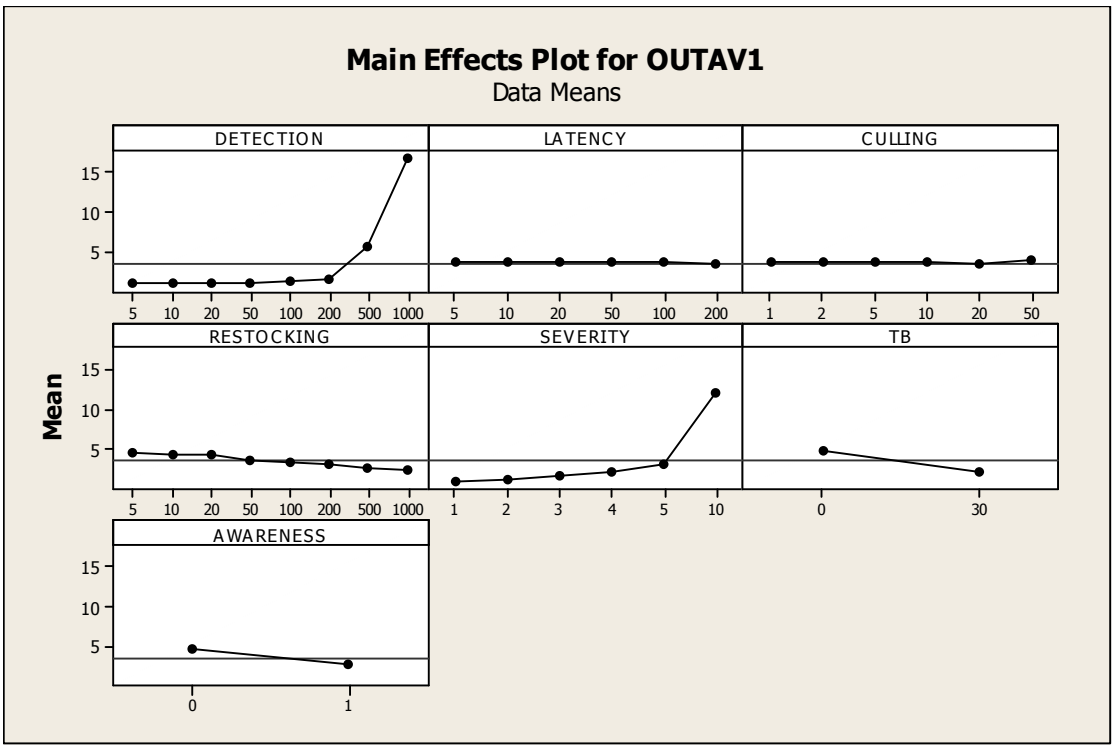

Figure S9a. Main effects plot for average outbreak size (all seedings) in the reactive policy; detection delay and severity are most influential, especially the highest terms; minor effects are due to restocking delay, national transport ban, and awareness campaign; changes in latency and culling delay have hardly any effect.

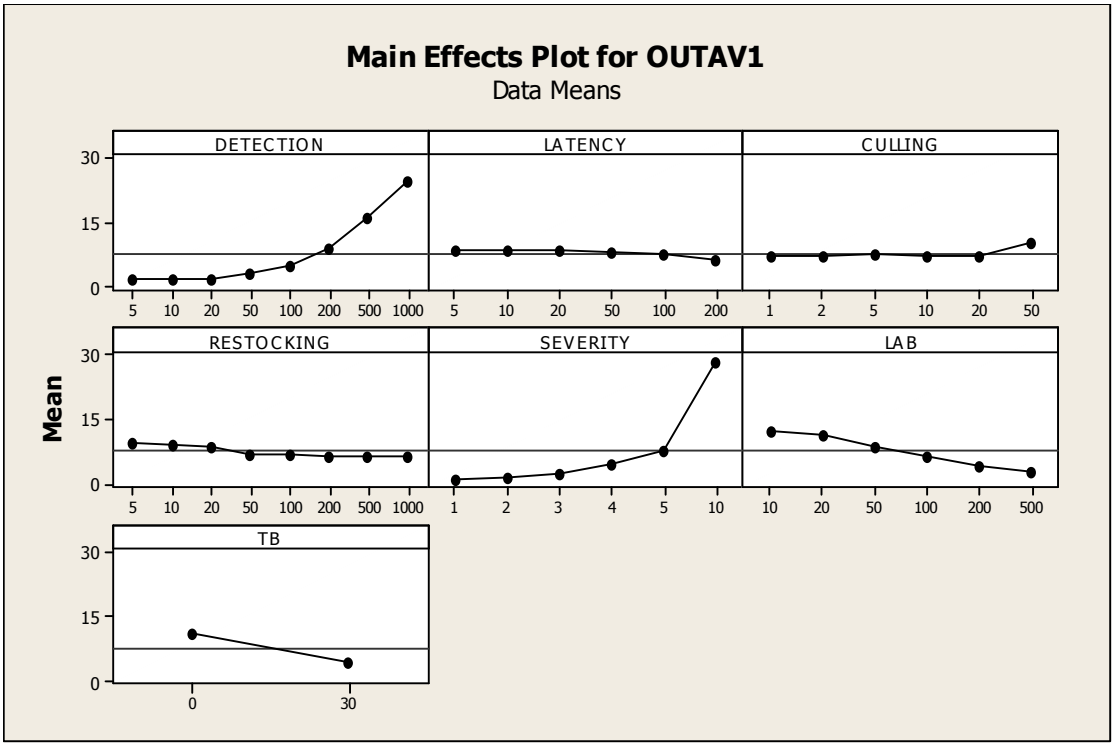

Figure S9b. Main effects plot for average outbreak size (all seedings) in the proactive policy; detection delay and severity are most influential, but especially the former parameter across a larger range; laboratory capacity also has a substantial effect, as does the national transport ban and the largest delay in latency and culling.

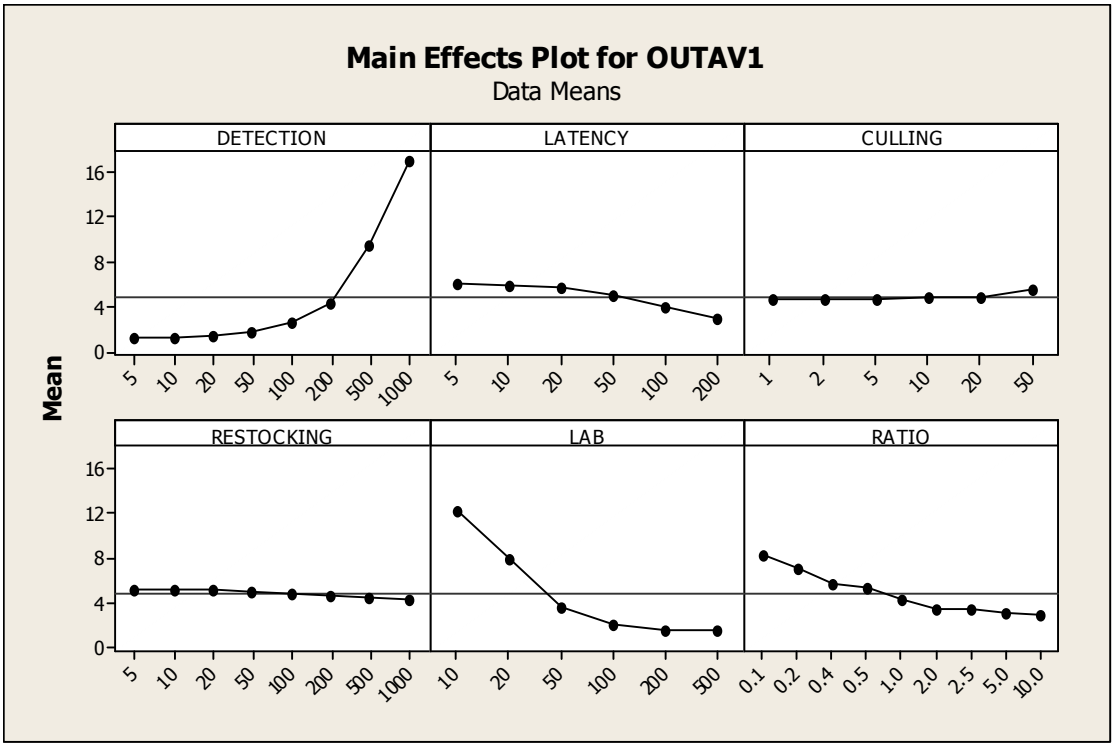

Figure S9c. Main effects plot for average outbreak size (all seedings) in the hybrid policy (fixed severity) is similar to the proactive case; the optimum rota ratio favours reactive detections.

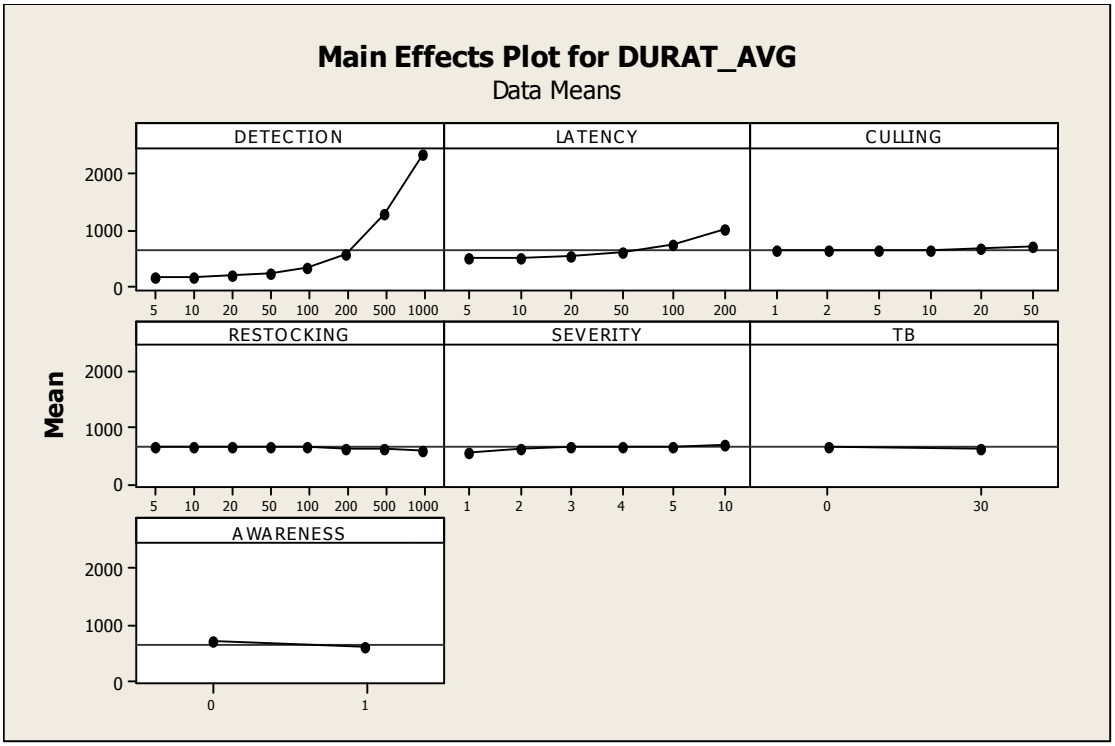

Figure S9d. Main effects plot for average outbreak duration (excluding single-site and endemic outbreaks) in the reactive policy; the response variable is mostly sensitive to changes in detection and latency delay; none of the other factors has much effect.

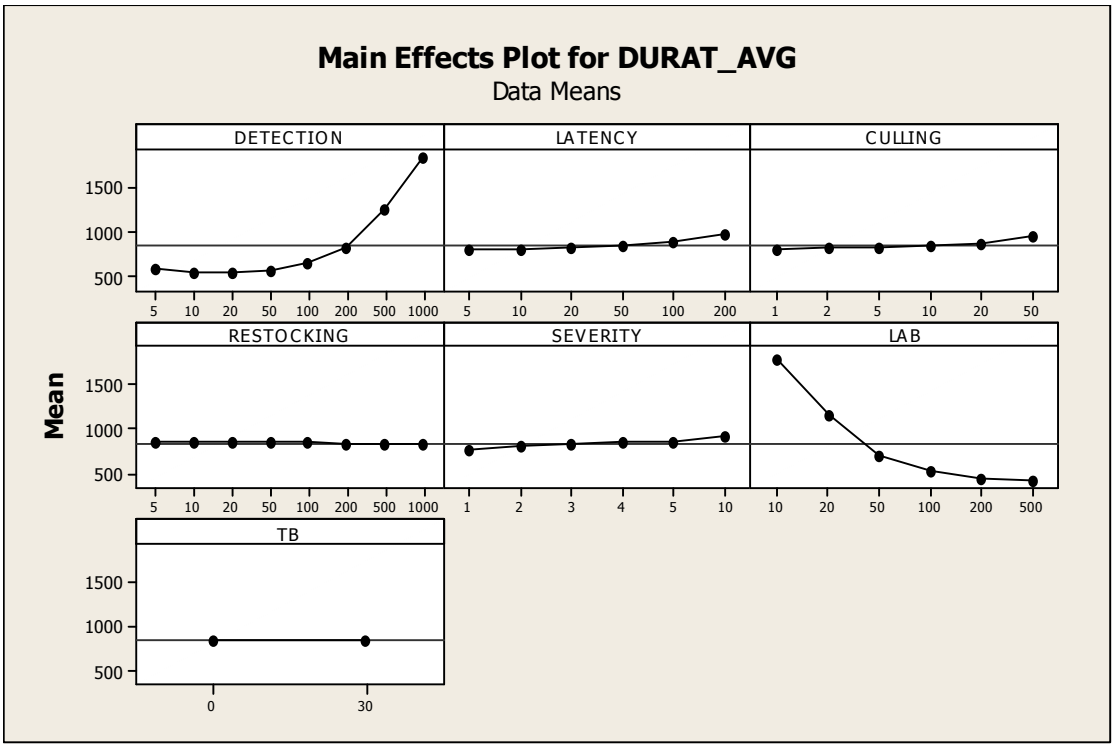

Figure S9e. Main effects plot for average outbreak duration (excluding single-site and endemic outbreaks) in the proactive case. Detection delay and laboratory capacity are the two main factors.

In the following five tables (Table S6a-e) we list for the five main response measures and each of the three control policies (columns) lower c.q. upper bounds in factor levels for detection, culling, and restocking delays in days, and laboratory site-testing capacity per year. These bounds are derived from the main effects plots and represent parameter choices beyond which the response variable will on average exceed its overall mean. This criterion is itself arbitrary; perhaps even the average response is deemed unacceptably high, or practical considerations may make a suggested value unfeasible to achieve. Nevertheless, these bounds provide quantified suggestions of specific control policy aims for the studied English and Welsh fish farms and fisheries network. In addition, horizontal comparisons between columns and vertical comparisons of the same cell between tables both attest to the robustness of the results. Note that the proactive policy (silent spreading) often requires more conservative bounds than the other policies which assume that clinical expression of the hunted pathogen will drive (at least part of) the response. These tables form the basis for the general advice given in the main text's Discussion section.

Table S6a. Average outbreak size (all seedings)

	Reactive	**Proactive**	**Hybrid**
Detection	<= 200	<= 100	<= 200
Culling	<= 20	<= 20	<= 20
Restocking	>100	>= 50	> 200
Lab Capacity	n/a	>= 100	>= 50

n/a = not applicable

Table S6b. Average outbreak size (excluding outbreaks of one single site)

	Reactive	**Proactive**	**Hybrid**
Detection	<= 200	<= 100	<= 200
Culling	<= 20	< 20	< 10
Restocking	>= 200	>= 50	>= 500
Lab Capacity	n/a	>= 100	>=50

Table S6c. Maximum outbreak size

	Reactive	**Proactive**	**Hybrid**
Detection	<= 200	<= 50	<= 50
Culling	<= 20	<= 20	<= 10
Restocking	>= 100	>= 50	>= 500
Lab Capacity	n/a	>= 100	>= 100

Table S6d. Number of endemic outbreaks

	Reactive	**Proactive**	**Hybrid**
Detection	<= 200	< 200	< 200
Culling	Flat	<= 20	<= 10
Restocking	>= 200	> 100	>= 200
Lab Capacity	n/a	>= 100	>= 50

Table S6e. Average outbreak duration (excluding outbreaks of one single site and endemic outbreaks)

	Reactive	**Proactive**	**Hybrid**
Detection	<= 200	< 200	<= 200
Culling	<= 10	<= 10	<= 10
Restocking	Flat	Flat	Flat*
Lab Capacity	n/a	>= 50	>= 50

* = not significant in balanced ANOVA