## Appendix for: Effect of habitat quality and phenotypic variation on abundance- and trait-based early warning signals of population collapses

## Appendix 1:

Table S1: Latitude, longitude and elevation details of the freshwater ponds and lakes in Switzerland from where the four populations were collected.

| Population | Latitude | Longitude | Elevation |
| :--- | :--- | :--- | :--- |
| Pond1 | 46.79059 | 9.4981 | 2100 m |
| Pond2 | 46.03314 | 8.89623 | 1000 m |
| Lake 3 | 47.300 | 8.577 | 405 m |
| Lake 4 | 46.7658 | 9.530 | $\sim 1500$ |

Table S2 : Mineral concentrations in filtered Volvic water used for growing A. volvox populations.

| Mineral name | Concentration $\boldsymbol{m g} / \mathbf{L}$ |
| :--- | :--- |
| Calcium | 11.5 |
| Chloride | 13.5 |
| Bicarbonate | 71 |
| Nitrate | 6.3 |
| Potassium | 6.2 |
| Silica | 31.7 |
| Sodium | 11.6 |

Table S3: Variable estimates, confidence intervals of the best model for Kendall's tau value AR1

## Kendall tau

| Predictors | Estimates | $C I$ | $p$ | $d f$ |
| :--- | :---: | :---: | :---: | :---: |
| (Intercept) | -0.05 | $-0.16-0.06$ | 0.359 | 119.00 |
| Poor | -0.09 | $-0.23-0.06$ | 0.231 | 112.00 |

## Random Effects

| $\sigma^{2}$ | 0.19 |
| :--- | :--- |
| $\tau_{00 \text { Diversity:X }}$ | 0.01 |
| $\tau_{00 \mathrm{X}}$ | 0.00 |
| ICC $_{\text {Diversity:X }}$ | 0.07 |
| ICC $_{X}$ | 0.00 |
| Observations | 153 |

Table S4: Variable estimates, confidence intervals of the best model for Kendall's tau value $S D$

|  | Kendall tau |  |  |  |
| :--- | :---: | :---: | :---: | :---: |
| Predictors | Estimates | $C I$ | $p$ | $d f$ |
| (Intercept) | -0.62 | $-0.77--0.47$ | $<0.001$ | 147.00 |
| Fast | 0.17 | $-0.04-0.37$ | 0.117 | 147.00 |
| Slow | 0.57 | $0.35-0.78$ | $<0.001$ | 90.00 |
| Poor | 0.08 | $-0.13-0.28$ | 0.467 | 147.00 |
| TreatmentFast:HabitatPoor | -0.09 | $-0.37-0.19$ | 0.536 | 131.00 |
| TreatmentSlow:HabitatPoor | -0.61 | $-0.90--0.32$ | $<0.001$ | 110.00 |
|  |  |  |  |  |
| Random Effects | 0.14 |  |  |  |
| $\sigma^{2}$ | 0.00 |  |  |  |
| $\tau_{00}$ Diversity:X | 0.00 |  |  |  |
| $\tau_{00}$ | 0.00 |  |  |  |
| ICCDiversity:X 0.00   <br> ICC    <br> Observations 153   |  |  |  |  |

Table. S5: Variable estimates, confidence intervals of the best model for Kendall's tau value mean.size

## Kendall tau

| Predictors | Estimates | $C I$ | $p$ | $d f$ |
| :--- | :---: | :---: | :---: | :---: |
| (Intercept) | -0.91 | $-1.09--0.74$ | $<0.001$ | 146.00 |
| Poor | 0.56 | $0.31-0.80$ | $<0.001$ | 146.00 |
| Fast | 1.01 | $0.76-1.26$ | $<0.001$ | 147.00 |
| Slow | 1.49 | $1.24-1.75$ | $<0.001$ | 87.00 |
| HabitatPoor:TreatmentFast | -0.12 | $-0.46-0.21$ | 0.472 | 130.00 |
| HabitatPoor:TreatmentSlow | -0.98 | $-1.33--0.64$ | $<0.001$ | 110.00 |

Random Effects

| $\sigma^{2}$ | 0.16 |
| :--- | :--- |
| $\tau_{00 \text { Diversity:X }}$ | 0.03 |
| $\tau_{00 \mathrm{X}}$ | 0.00 |
| ICC $_{\text {Diversity:X }}$ | 0.17 |
| ICC $_{\mathrm{X}}$ | 0.02 |
| Observations | 153 |
| Marginal R2 / Conditional R2 | $0.573 / 0.652$ |

Table S6: Variable estimates, confidence intervals of the best model for Kendall's tau value SDsize

|  | Kendall tau |  |  |  |
| :--- | :---: | :---: | :---: | :---: |
| Predictors | Estimates | $C I$ | $p$ | $d f$ |
| (Intercept) | -0.88 | $-1.05--0.71$ | $<0.001$ | 147.00 |
| Poor | 0.00 | $-0.22-0.23$ | 0.971 | 147.00 |
| Fast | 1.07 | $0.83-1.30$ | $<0.001$ | 147.00 |
| Slow | 0.98 | $0.73-1.22$ | $<0.001$ | 104.00 |
| HabitatPoor:TreatmentFast | -0.13 | $-0.45-0.19$ | 0.437 | 129.00 |
| HabitatPoor:TreatmentSlow | 0.40 | $0.07-0.73$ | $\mathbf{0 . 0 2 0}$ | 112.00 |
| Random Effects |  |  |  |  |
| $\sigma^{2}$ | 0.17 |  |  |  |
| $\tau_{00 \text { Diversity:X }}^{\tau_{00}}$ | 0.00 |  |  |  |
| ICC |  |  |  |  |
| ICC |  |  |  |  |
| Observations | 0.00 |  |  |  |



Figure S1. A) Temperature performance curves for A.volvox populations. Absolute maximum growth rate $\left(r_{\max }\right)$ plotted against a gradient of temperatures from $15^{0} \mathrm{C}$ to $28^{0} \mathrm{C}$ for the three clonal populations $\mathrm{C} 1, \mathrm{C} 2, \mathrm{C} 3$. Note that temperature performance curves were calculated to evaluate if there were any differences between the clonal populations. B) Preliminary experimental data on optimal food quantity. Three levels of food quantity (Cryptomonas) given to $A$. volvox over a period of 14 days to evaluate the dynamics and carrying capacity of $A$. volvox. A.volvox populations were provided with 0.5 ml of three food treatments (density of $\sim 12000$ individual of Cryptomonas per ml; ~35000 individuals of Cryptomonas per ml; and ~72000 individuals of Cryptomonas per ml ) (with 3 replicates each) every 3 days. For the population collapse experiment in the main-text (experiment 2 ) we decided on feeding 0.5 ml of $35000 \mathrm{ml}^{-1}$ Cryptomonas every 3 days to create the good quality habitat and 0.5 $m l$ of $12000 \mathrm{ml}^{-1}$ Cryptomonas every 3 days to create the poor quality habitat.


Figure S2: Density (Individuals per $m l$ ), mean body size (in $\mu \mathrm{m}$ ) and standard deviation of body size over time till population collapse for all the four replicates for the single level of phenotypic diversity treatment (one clones) across two qualities of habitat (Good and Poor) and across two rates of warming - A) Slow warming B) Fast warming. The thick blue lines are loess smoothing across replicates and dashed vertical black line indicates estimated bifurcation point across replicates.


Figure S3: Density (Individuals per $m l$ ), mean body size (in $\mu \mathrm{m}$ ) and standard deviation of body size over time till population collapse for all the four replicates for two levels of phenotypic diversity treatment (two clones together) across two qualities of habitat (Good and Poor) and across two rates of warming - A) Slow warming B) Fast warming. The thick blue lines are loess smoothing across replicates; vertical black dashed line indicates estimated bifurcation point across replicates.


Figure S4: Density (Individuals per $m l$ ), mean body size (in $\mu \mathrm{m}$ ) and standard deviation of body size over time for the control treatment (no warming) for two different levels of habitat quality (Good and Poor) and split across three different levels of phenotypic diversity ( A : one ; $\mathrm{B}=$ two and C : Three). The thick blue lines are loess smoothing across replicates.


Figure S5: Density (Individuals per $m l$ ), mean body size (in $\mu \mathrm{m}$ ) and standard deviation of body size plotted against temperature for all the four replicates for one level of phenotypic diversity treatment (two clones together) across two qualities of habitat (Good and Poor) and across two rates of warming - A) Slow warming B) Fast warming. The thick blue lines are loess smoothing across replicates; vertical black dashed line indicates estimated bifurcation time point across replicates.


Figure S6: Density (Individuals per $m l$ ), mean body size (in $\mu \mathrm{m}$ ) and standard deviation of body size plotted against temperature for all the four replicates for two levels of phenotypic diversity treatment (two clones together) across two qualities of habitat (Good and Poor) and across two rates of warming - A) Slow warming B) Fast warming. The thick blue lines are loess smoothing across replicates; vertical black dashed line indicates estimated bifurcation point across replicates.

Slow warming


Fast warming


Figure S7: Density (Individuals per $m l$ ), mean body size (in $\mu \mathrm{m}$ ) and standard deviation of body size plotted against temperature for all the four replicates for three levels of phenotypic diversity treatment (two clones together) across two qualities of habitat (Good and Poor) and across two rates of warming - A) Slow warming B) Fast warming. The thick blue lines are loess smoothing across replicates; vertical black dashed line indicates estimated bifurcation point across replicates.


Figure. S8: Snapshots and ImageJ masks of example videos taken. On the left: is the snapshot of a video where the red circles indicate the various A.volvox individuals. On the right: ImageJ masks with threshold values : minimum is 55 and maximum is 255 . Note BEMOVI uses a black background to calculate the masks.


Figure. S9: Snapshots and ImageJ masks of example videos taken. On the left: is the snapshot of a video where the red circles indicate the various A.volvox individuals. On the right: ImageJ masks with threshold values : minimum is 55 and maximum is 255 . Note BEMOVI uses a black background to calculate the masks.


Figure. S10: Snapshots and ImageJ masks of example videos taken. On the left: is the snapshot of a video where the red circles indicate the various A.volvox individuals. On the right: ImageJ masks with threshold values : minimum is 55 and maximum is 255 . Note BEMOVI uses a black background to calculate the masks.


Figure. S11: Snapshots and ImageJ masks of example videos taken. On the left: is the snapshot of a video where the red circles indicate the various A.volvox individuals. On the right: ImageJ masks with threshold values : minimum is 55 and maximum is 255 . Note BEMOVI uses a black background to calculate the masks.


Figure S12. Mean extinction time points for slow and fast warming treatments for two levels of habitat quality (Good and Poor) and three levels of phenotypic diversity (one,
two three). The error bars represent $95 \%$ confidence intervals.

