Supplementary material

Sup Figure 1. Survival (solid line) of oysters injected with either OsHV-1 suspension (pathogen donors) or sterile seawater (controls) as a function of time (hours post infection; hpi). Log-rank: Chi-square: 5117, p-value <0.001. The dots indicate the quantification of OsHV-1 DNA in the water, expressed as copies per litre. Data were log (x+1) transformed.

Sup Table 4: Permutational analysis of variance of oyster microbial community composition, with Infection, Family, Collection date, and their interaction terms as factors. Significant p values are highlighted in bold.

| Term                | R2  | p value |
|---------------------|-----|---------|
| Infection           | 0.097 | 0.001  |
| Family              | 0.113 | 0.001  |
| Collection date     | 0.036 | 0.001  |
| Family * Infection  | 0.063 | 0.913  |
| Collection date * Family | 0.061 | 0.951  |
| Residuals           | 0.629 |         |
**Sup Figure 2:** Venn diagram of shared bacterial genera between oyster family types (Highly resistant, Resistant, Vulnerable).

**Supplementary Table 5.** Genera unique to each family type

| Vulnerable families | Highly resistant families |
|---------------------|--------------------------|
| Aerococcus          | Arhodomonas              |
| Alishewanella       | Caminicella              |
| Amaricoccus         | Corallomonas             |
| Arenibacter         | MD3-55                   |
| Bosea               | Nocardioides             |
| Burkholderia-Caballeronia-Paraburkholderia | Paracoccus |
| Candidatus Amoebophilus | Pectobacterium   |
| Clostridium sensu stricto 13 | Pseudoceanicola |
| Delfia              | Rhodococcus              |
| Desulforosporinus   | Simiduia                 |
| Lactococcus         | Sulfurimonas             |
| Methylphaga         | Sunxiuqinia              |
| Nordella            | Tistlia                  |
| Oceanisphaera       | Waddlia                  |
| Pleurocapsa PCC-7319|                         |
| Psychrobacter       |                         |
| Saccharosporillum   |                         |
| Temperatibacter     |                         |
| Terrabacter         |                         |
| Treponema           |                         |

**Sup Figure 3.** Microbiome relative abundance (A) and prevalence (B) between vulnerable and highly resistant families at genus level. Only genera with a prevalence above 30% and among the 30 most abundant are displayed.
**Supplementary Table 6:** Mean live weight (± SE), in grams, of ten families (F1 to F10) of recipient oysters from the control treatment, collected at the start (T0h) and the end of the experimental challenge (T336h).

| Family | T0h     | T 336h  |
|--------|---------|---------|
| F1     | 1.24±0.4| 1.79±0.5|
| F2     | 1.03±0.3| 1.2±0.2 |
| F3     | 1.52±0.2| 1.65±0.3|
| F4     | 1.06±0.3| 1.36±0.5|
| F5     | 0.65±0.2| 0.77±0.2|
| F6     | 1.11±0.3| 1.69±0.9|
| F7     | 1.75±0.4| 1.99±0.6|
| F8     | 1.34±0.4| 1.6±0.9 |
| F9     | 1.53±0.4| 1.74±0.7|
| F10    | 1.41±0.3| 1.60±0.6|