

**Table S4.** Composition of TEA-defined pathogen-associated genes within Tn-seq gene sets.

<b>Gene Set</b> (total genes)	<b>observed</b> (% of gene set)	<b>theoretical</b>	<b>p value</b>
F11 genome (5,148)	1,166 (22.65)	-	-
Hypo-tolerant (609)	120 (19.70)	127.84	0.803
Hyper-tolerant (431)	81 (18.79)	91.06	0.899
■ <i>in piscis</i> (970)	246 (25.36)	218.11	0.009
Multi-niche (76)	15 (19.74)	17.31	0.786
■ PC (122)	39 (31.97)	27.52	0.008
■ Blood (772)	192 (24.87)	173.54	0.0485
■ Advantageous (227)	69 (30.39)	50.46	0.004

Significant enrichment of pathogen-associated genes within Tn-seq gene sets was detected using 1,000 Monte Carlo simulations. For the 'Blood' gene set, 10,000 simulations were performed to generate a more discernable *p* value. Significant enrichments ( $p < 0.05$ ) are marked with a blue box.