This file contains all of the data from the experimental components of the paper, with each experiment in a different tab:

**Plasticity Screen** contains the results of the screen of the 192 aphid genotypes for percent winged offspring produced in response to crowded conditions. The columns give the aphid genotype number, number of unwinged offspring in replicate 1, number of winged offspring in replicate 1, number of unwinged offspring in replicate 2, number of winged offspring in replicate 2, and the average winged offspring, with each genotype represented on a different row.

**Panel solitary+crowding** gives the phenotype data from a second screen of the percent winged offspring produced by the panel of 10 highly and 10 weakly-inducible genotypes, this time in response to both solitary and crowded conditions. The columns give aphid genotype number, treatment (solitary vs crowded), phenotype (weakly vs. highly inducible) and the percentage of winged offspring produced.

**Fecundity** gives the data from the fecundity screen of the 10 highly and weakly-inducible genotypes in response to solitary and crowded conditions. The columns show aphid genotype number, phenotype, treatment, biological replicate, and the fecundity (number of aphid babies produced) on day 2 of the experiment.

**Apns-1 qPCR** gives gene expression data for *Apns-1* (ACYPI085607) as measured by quantitative PCR. Columns show aphid genotype number, phenotype (highly vs. weakly inducible), treatment (solitary vs crowded conditions), and the negative delta\_Ct value (qPCR output) for each biological replicate.

**Apns-2 qPCR** is the same but for *Apns-2* (ACYPI36509).

**Head qPCR** gives the qPCR data for the measures of gene expression of *Apns-1* and *Apns-2* in heads vs. heads+body samples. Columns show tissue type (head vs. head+body), and negative delta\_Ct values for *Apns-1* and *Apns-2*.

**RNAi qPCR** gives the qPCR output from the RNAi experiment. Columns show treatment, biological replicate number, and negative delta\_Ct values for *Apns-1* and *Apns-2.*

**RNAi p\_winged** gives the phenotype data from the RNAi screen. Columns show aphid genotype name, treatment (lacZ control or *Apns* dsRNA injected, method (injection vs. crowding first), the number of unwinged offspring produced, the number of winged offspring produced, and the percentage winged offspring produced by each biological replicate.

**Highly-inducible gene list:** Results of the RNAseq analysis on pooled highly-inducible aphid genotypes. The aphid gene ID numbers (ACYPI) are listed in Col. A, each representing a gene in the aphid genome for which gene expression differences in response to crowding were measured. The log of the Fold Change (between solitary and crowded aphids) is given in Col. B for each gene, and log of the number of read counts (per million) mapped to each gene in shown in Col. C. Col. D gives the output of the likelihood ratio test (adjusted GLM for significance of differential expression), with the p-value and adjusted p-value (FDR: False Discovery Rate) in Col. E and Col. F, respectively.

Weakly-inducible gene list: Results of the RNAseq analysis on pooled weakly-inducible aphid genotypes. The aphid gene ID numbers (ACYPI) are listed in Col. A, each representing a gene in the aphid genome for which gene expression differences in response to crowding were measured. The log of the Fold Change (between solitary and crowded aphids) is given in Col. B for each gene, and log of the number of read counts (per million) mapped to each gene is shown in Col. C. Col. D gives the output of the likelihood ratio test (adjusted GLM for significance of differential expression), with the p-value and adjusted p-value (FDR: False Discovery Rate) in Col. E and Col. F, respectively.