File S2. A README file associated with raw datafiles for Everman et al. 2019. See "EvermanData.tar.gz" file.

Directory = DSPR_Data/

DSPR_1.txt
Tab-separated text file of raw DSPR starvation and desiccation resistance reported in hours for each fly per experimental vial. (Data are presented in Figure 1, Figure 3, Figure 6, Figure S2, Figure S5, Figure S7, Figure S11.)
Column headers:
 Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
 Trait = StarvationResistance or DesiccationResistance
 RIL.ID = Recombinant Inbred Line ID from the DSPR
 VialID = Unique number corresponding to each experimental vial
 Sex = (m) Male or (f) Female
 FlyID = Unique identifier for individual flies in each vial
 LifespanHrs = Lifespan in hours for each individual fly

DSPR_2.txt
Tab-separated text file of raw founder starvation resistance reported in hours for each fly per experimental vial. (Data are presented in Figure 1.)
Column headers:
 Trait = StarvationResistance
 DSPR.founder = DSPR founder line ID
 Sex = (m) Male or (f) Female
 RepVial = Vial replicate number
 FlyID = Unique identifier for individual flies in each vial
 LifespanHrs = Lifespan in hours for each individual fly

DSPR_3.txt
Tab-separated text file of raw female DSPR triglyceride levels reported per plate well. (Data are presented in Figure 5, Figure 6, Figure S3.)
Column headers:
 Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
 Trait = TriglycerideLevel
 RIL.ID = Recombinant Inbred Line ID from the DSPR
 NumericPlateID = Unique number corresponding to each plate
 WellID = ID corresponding to each well of the plate
 SampleID = Unique identifier for samples
 TrueSerumTriglyConc = Triglyceride level per sample based on five females per sample

DSPR_4.txt
Tab-separated text file of raw DSPR starvation resistance reported in hours using *Drosophila* Activity Monitors (DAM). (Data are presented in Figure S7.)
Column headers:
    Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
    Trait = StarvationResistance
    RIL.ID = Recombinant Inbred Line ID from the DSPR
    StarvationClass = Categorical variable (HighStarvClass or LowStarvClass)
        based on data from DSPR_1.txt
    Sex = (M) Male or (F) Female
    MonitorID = Unique identifier for DAM
    MonitorTubeID = Unique identifier for each tube in each DAM
    LifespanHrs = Lifespan in hours for each fly

DSPR_5.txt
Tab-separated text file of DSPR activity reported under non-stressful conditions using *Drosophila* Activity Monitors (DAM). (Data are presented in Figure 4.)
Column headers:
    Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
    RIL.ID = Recombinant Inbred Line ID from the DSPR
    Trait = Activity
    Sex = (m) Male or (f) Female
    StarvationClass = Categorical variable (HighStarvClass or LowStarvClass)
        based on data from DSPR_1.txt
    N = Number of flies tested
    ActLight.Mean = Mean activity levels under light conditions
    ActLight.SD = Standard deviation for activity levels under light conditions
    ActDark.Mean = Mean activity levels under dark conditions
    ActDark.SD = Standard deviation for activity levels under dark conditions

DSPR_6.txt
Tab-separated text file of DSPR activity reported under starvation conditions using *Drosophila* Activity Monitors (DAM). (Data are presented in Figure S13.)
Column headers:
    Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
    RIL.ID = Recombinant Inbred Line ID from the DSPR
    LightStatus = (L) light or (D) dark
    SamplingPeriod = Day of experiment
    FemaleMeanActivity = Mean activity of females
    MaleMeanActivity = Mean activity of males

DSPR_7.txt
Tab-separated text file of DSPR average starvation resistance reported in hours under different rearing density treatments. (Data are presented in Figure S1.)
Column headers:

      Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
      Trait = StarvationResistance
      RIL.ID = Recombinant Inbred Line ID from the DSPR
      Treatment = Density (60 eggs placed into rearing vials) or Population (females
            laid eggs for 1-2 days with visual assessment of density)
      TotalAdults = Total number of flies that emerged from each vial
      VialID = Unique identifier for each experimental vial
      N = Number of flies per experimental vial
      LifespanHrs = Average lifespan in hours for each experimental vial

DSPR_8.txt
Tab-separated text file of DSPR % survival on starvation media under different rearing density treatments. (Data are presented in Figure S1.)
Column headers:

      Mapping.Panel = DSPR, Drosophila Synthetic Population Resource
      Trait = StarvationResistance
      RIL.ID = Recombinant Inbred Line ID from the DSPR
      Treatment = Density (60 eggs placed into rearing vials) or Population (females
            laid eggs for 1-2 days with visual assessment of density)
      TotalAdults = Total number of flies that emerged from each vial
      VialID = Unique identifier for each experimental vial
      ScreenpointHrs = Hour intervals at which flies in each vial were counted
      Survival% = Percent of flies in each vial that were alive at each screenpoint

DSPR_9.txt
Tab-separated text file of DSPR LOD score from QTL mapping analysis. (Data are presented in Figure S14 and Figure S15.)
Column headers:

      DSPR.Panel = pA or pB mapping panel from the DSPR
      Trait = StarvationResistance or TriglycerideLevels
      sex = (m) Male or (f) Female
      chr = Chromosome (X, 2L, 2R, 3L, 3R)
      Ppos = Position on chromosome based on assembly 5.0
      Gpos = Genetic position
      LOD = LOD score from QTL mapping analysis

DSPR_10.txt
Tab-separated text file of observed and estimated starvation resistance in DSPR founders. (Data are presented in Figure 7.)
Column headers:

      DSPR.founder = pA or pB mapping panel from the DSPR
      ObservedStarvationResistance = Mean observed starvation resistance of each
            founder line
      EstimatedStarvationResistance = Weighted estimated mean starvation resistance
            of each founder line determined from QTL analysis

DSPR_11.txt
Tab-separated text file of DSPR starvation resistance and triglyceride level after accounting for variation due to haplotype at overlapping peaks. (Data are presented in Figure S16.)
Column headers:
      FounderHaplotype = Predicted haplotype at overlapping QTL
      StarvationResistance = Mean starvation resistance
      TriglycerideLevel = Mean triglyceride level
      N_Starv = Number of RILs with the corresponding predicted founder
          haplotype for Starvation QTL
      N_Tri = Number of RILs with the corresponding predicted founder
          haplotype for Triglyceride QTL

Directory = DGRP _Data/

DGRP_1.txt

Tab-separated text file of raw DGRP starvation resistance reported in hours for each fly per experimental vial. Average response per sex and line was used in GWA. (Data are presented in Figure 2, Figure S4, Figure S5, Figure S8, Figure S12, used to generate Figure 17, Figure S18, Figure S19.)
Column headers:
      Mapping.Panel = DGRP, Drosophila Genetic Reference Panel
      Trait = StarvationResistance
      RAL.ID = Line ID based on RAL identifier
      Bloomington.ID = Bloomington stock ID
      Sex = (M) Male or (F) Female
      VialID = Unique identifier for each experimental vial
      FlyID = Unique identifier for individual flies in each vial
      LifespanHrs = Lifespan in hours for each individual fly

DGRP_2.txt
Tab-separated text file of DGRP average starvation resistance reported in hours in different environments and on different starvation media types. (Data are presented in Figure S9.)
Column headers:
      Mapping.Panel = DGRP, Drosophila Genetic Reference Panel
      Trait = StarvationResistance
      RAL.ID = Line ID based on RAL identifier
      Environment = Flies were maintained at 25°C with a 12:12hr L:D cycle
          (25°C_12hr) or 23°C with constant light (23°C_24hr)
      Media = Preservatives or NoPreservatives in the starvation media
      VialID = Unique identifier for each experimental vial
      N = Number of flies per experimental vial
      LifespanHrs = Average lifespan in hours for each experimental vial

DGRP_3.txt
Tab-separated text file of DGRP % survival in different environments and on different starvation media types. (Data are presented in Figure S9.)
Column headers:
- Mapping.Panel = DGRP, Drosophila Genetic Reference Panel
- Trait = StarvationResistance
- RAL.ID = Line ID based on RAL identifier
- Media = Preservatives or NoPreservatives in the starvation media
- Environment = Flies were maintained at 25°C with a 12:12hr L:D cycle (25°C_12hr) or 23°C with constant light (23°C_24hr)
- VialID = Unique identifier for each experimental vial
- ScreenpointHrs = Hour intervals at which flies in each vial were counted
- Survival% = Percent of flies in each vial that were alive at each screenpoint

DGRP_4.txt
Tab-separated text file of DGRP starvation resistance for lines shared between this study, Mackay et al. 2012, and Everman and Morgan 2018. (Data are presented in Figure S8, Figure S10.)
Column headers:
- RAL.ID = Line ID based on RAL identifier
- Sex = (M) Male or (F) Female
- LifespanHrs_EvermanetAl.2019 = Mean starvation resistance reported in this study
- LifespanHrs_MackayEtAl.2012 = Mean starvation resistance reported in Mackay et al. 2012
- LifespanHrs_Everman&Morgan.2018 = Mean starvation resistance reported in Everman and Morgan 2018

DGRP_5.txt
Tab-separated text file of bootstrap results of the sign of SNPs across DGRP data collected in this study, Mackay et al. 2012 and Everman and Morgan 2018. These data are compiled from original bootstrap files. The code presented in File S1 (see file "File_S1.txt") is formatted to read each file by DataID. (Data are presented in Figure 8.)
Column headers:
- %SNPs_SameSign = Percent of SNPs that have the same sign between studies following boostrap analysis of random samples of SNPs.
- Density = Density calculated from original bootstrap files
- Sex = Female or Male
- DataID = Dataset ID for plotting in File S1
- Comparison = Direction of comparison of SNPs (ThisStudy_vs_MackayEtAl2012, ThisStudy_vs_Everman&Morgan2018, Everman&Morgan2018_vs_ThisStudy, Everman&Morgan2018_vs_MackayEtAl2012, MackayEtAl2012_vs_ThisStudy, or MackayEtAl2012_vs_Everman&Morgan2018)

DGRP_6.txt
Tab-separated text file of adjusted mean starvation resistance DGRP data collected in this study, Mackay et al. 2012 and Everman and Morgan 2018. These data are compiled from original GWA-generated files; code presented in File S1 (see file "File_S1.txt") is formatted to read each file by Study. Data are used in bootstrap analysis.
Column headers:
      RAL.ID = Line ID based on RAL identifier
      AdjustedMeanStarvationResistance = Adjusted mean phenotype from GWA of
          each study
      Study = Study in which the original starvation resistance data was collected
          (ThisStudy, MackayEtAl2012, or Everman&Morgan2018)
      Sex = (f) female or (m) male

DGRP_7.csv
Comma-separated text file of SNP frequencies for bootstrap analysis, used in File S1 (see file "File_S1.txt"), generated from dgrp.t.txt in code file. Data are used in bootstrap analysis.
Column headers:
      rAF = Reference allele frequency
      aAf = Alternate allele frequqncy
      SNP = SNP ID

DGRP_8.txt
Large space-separated matrix of SNP calls for bootstrap analysis, used in File S1 S1 (see file "File_S1.txt"), called as dgrp.t.txt in code file. Data originally available from dgrp2.gnets.ncsu.edu. Data are used in bootstrap analysis.
Column headers:
      id = Line ID based on RAL identifier, formatted "line_XXX"
      *Remaining Columns: SNP id

Sub-directory = DGRP _Data/GWAS_AVG_Starvation/

Contains DGRP analysis output files (produced by dgrp2.gnets.ncsu.edu) for the average starvation resistance measure calculated for overlapping DGRP lines between this study, Mackay et al. 2012 and Everman and Morgan 2018.

Sub-directory = DGRP _Data/GWAS_SJM_Starvation/

Contains DGRP analysis output files (produced by dgrp2.gnets.ncsu.edu) for the average starvation resistance from this study.