**Manuscript Title**: A mother’s legacy: the strength of maternal effects in animal populations
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**File Name**: m2.main.csv

**Description**: Estimates of m2 and h2 used in the analyses described in the main text

**Rows**: 770. Each row corresponds to an estimate of m2 for a trait within a study

**Columns**: 14. *StudyCode*; *Species*; *Taxa*; *Class*; *Amniote*; *Livebearing*; *Trait.Type*; *Offspring.Sex*; *Maternal.Care*; *Life.Stage*; *m2*; *Total.Sample.Size*; *Maternal.Links; h2*

*StudyCode*: Number that corresponds to one of the individual studies listed in the Supporting Information.

*Species*: The species in which the trait was measured

*Taxa*: Whether the studied species is a vertebrate or invertebrate

*Class*: The taxonomic class (e.g. ave, mammalia, insecta) of the organism in which the trait was measured

*Amniote*: Whether the studied species is an amniote or anamniote

*Livebearing*: Whether the species is a livebearer or an egg-laying animal

*Trait.Type*: The type of trait for which the quantitative genetic estimates were generated (e.g. morphology, physiology, life history, behavior)

*Offspring.Sex*: The sex of the offspring (male, female) in which the trait was measured

*Maternal.Care*: Whether the species exhibits post-hatching or post-parturition care for its offspring

*Life.Stage*: The life stage of the trait for which quantitative genetic estimates were generated (i.e. embryonic, juvenile, adult)

*m2*: the proportion of phenotypic variance determined by maternal effects (m2)

*Total.Sample.Size*: the number of individuals for which the trait was measured

*Maternal.Links*: the number of known maternities in the pedigree used

*h2*: the proportion of phenotypic variance determined by additive genetic effects (h2; narrow-sense heritability)