effect\_id = unique identifier for each unique comparison/effect size

study\_id\_str = unique identifier for each study

outcome\_id\_str = unique identifier for each PPI testing protocol (experiment)

sex\_of\_animals = sex of animals in cohorts used to calculate effect size

disease\_cohort\_str = unique identifier for polyI:C group used to calculate effect size

control\_cohort\_str = unique identifier for control group used to calculate effect size

time = age of animals in days (PND) at time of PPI testing

d.mean = mean %PPI value for polyI:C cohort

d.sd = standard deviation of %PPI value for polyI:C cohort

d.n = number of animals in polyI:C cohort

c.mean = mean %PPI value for control cohort

c.sd = standard deviation of %PPI value for control cohort

c.n = number of animals in control cohort

title = title of study

authors = authors of study

breeder\_strain = details of the breeder animals were purchased from (this column was added to prevent

duplication of some data when joining datasets)

GD\_first\_administration = gestational day of first event of polyI:C administration to dams

cross.fost = details of whether authors reported cross-fostering of animals

poly\_I\_C\_daily\_dose\_mg\_kg = the dose of polyI:C administered to animals each day of induction protocol in mg/kg

intervention.no = column added to differentiate between cohorts that were otherwise identical but received different treatment interventions (I extracted baseline data for these animals)

year = year of publication

ro\_b\_assessment\_blinding\_of\_animal\_carers\_handlers = whether the authors reported blinding of animal handlers or not: low RoB = handlers were blinded, high RoB = handlers were not blinded, unclear RoB = blinding of animal handlers was not reported

ro\_b\_assessment\_blinding\_of\_outcome\_assessors = whether the authors reported blinding of outcome assessors or not: low RoB = assessors were blinded, high RoB = assessors were not blinded, unclear RoB = blinding of outcome assessors was not reported

ro\_b\_assessment\_random\_housing = whether the authors reported random housing of animals or not: low RoB = animals were housed randomly, high RoB = animals were not housed randomly, unclear RoB = random housing of animals was not reported

ro\_b\_assessment\_a\_priori\_power\_calculatinos = whether the authors performed a priori power calculations or not: low RoB = yes, and study was sufficiently powered, high RoB = yes, and study was underpowered, unclear RoB = a priori power calculations not reported

ro\_b\_assessment\_unit\_of\_analysis\_error = whether a unit of analysis error was present during calculations of results: low RoB = no, high RoB = yes, unclear RoB = the unit of analysis used during calculations was unclear

ro\_b\_assessment\_conflict\_of\_interest = whether the authors provided a COI statement or not: low RoB = yes, and no COI, high RoB = yes, and COI, unclear RoB = COI statement not provided

ro\_b\_assessment\_random\_outcome\_assessment = whether the authors reported random selection of animals for outcome assessment: low RoB = animals selected randomly from cohorts for PPI testing, high RoB = animals not selected randomly for PPI testing, unclear RoB = protocol for selection of animals for outcome assessment not reported

ro\_b\_assessment\_blinding\_of\_animal\_carers\_handlers = whether the authors reported blinding of animal handlers to whether animals were from polyI:C or control cohorts: low RoB = handlers were blinded, high RoB = handlers were not blinded, unclear RoB = blinding of animal handlers was not reported

ro\_b\_assessment\_baseline\_characteristics = whether the authors reported baseline characteristics of animals, and ensured equal distribution of animals based on differences (if present) to experimental cohorts: low RoB = characteristics reported and animals evenly distributed/uneven distribution accounted for, high RoB = characteristics reported but animals unevenly distributed/uneven distribution not accounted for, unclear RoB = baseline characteristics not reported

ro\_b\_assessment\_allocation\_concealment = whether the authors reported concealment of the sequence used to allocate animals to experimental cohorts to animal handlers/carers or not: low RoB = handlers blind to allocation sequence, high RoB = handlers not blind to allocation sequence, unclear RoB = not reported

ro\_b\_assessment\_incomplete\_outcome\_data = whether the authors omitted outcome data or not: low RoB = no, n of animals for each cohort in methods matched n of animals in each cohort for results OR n of animals for each cohort in methods did not match n of animals in each cohort for results but a valid reason (e.g. death of animal) was provided, high RoB = yes, n of animals for each cohort in methods did not match n of animals in each cohort for results and a reason was not provided, unclear RoB = whether the n of animals for each cohort in methods matched n of animals in each cohort for results was unclear

species\_of\_animal = species of animals in cohorts

strain = strain of animals in cohorts

outcome\_label = SyRF label (description of PPI testing protocol (experiment) for which effect size is calculated for)

prepulse\_intensity\_d\_b = intensity of prepulse used in dB

pulse\_intensity\_d\_b = intensity of startle pulse used in dB

prepulse\_duration\_ms = duration of prepulse noise in ms

interstimulus\_interval\_ms = interstimulus interval duration in ms (duration between prepulse and pulse)

is\_this\_ppi\_for\_a\_specific\_pre\_pulse\_intensity\_or\_averaged = whether the mean %PPI reported for each group corresponds to a value for a single prepulse intensity, or whether it corresponds to a value averaged across multiple prepulse intensities (i.e. across multiple individual experiments)

is\_this\_ppi\_for\_a\_specific\_pulse\_intensity\_or\_averaged = whether the mean %PPI reported for each group corresponds to a value for a single pulse intensity, or whether it corresponds to a value averaged across multiple pulse intensities (i.e. across multiple individual experiments)

disease\_model = SyRF label (description of MIA induction protocol i.e. details of polyI:C administration)

acute\_or\_chronic = whether the MIA induction protocol was acute (single injection of polyI:C) or chronic (polyI:C injected more than once)

duration\_days\_if\_chronic = the duration of the time period in days across which polyI:C was administered to animals if disease induction protocol was chronic

administration\_route = route of polyI:C and vehicle administration to animals

frequency\_of\_administration\_if\_chronic = frequency of polyI:C administration if polyI:C injected more than once

sham\_equivalent = details of the sham procedure given to control cohort

vehicle = the vehicle used in both the polyI:C and vehicle only injections

author = authors of study (need to remove this! - duplicate column)

background\_db = level of background/white noise during PPI testing procedure in dB

pre\_pulse\_level\_above\_back = difference in intensity between prepulse and background noise in dB (post-hoc)

d.mean.adj = adjusted mean %PPI for use when calculating lnCVR (adjusted so that PPI values lie on ratio scale: calculated as ‘100 - d.mean’. A value of 100 would indicate complete inhibition of PPI, a value of 0 indicates no inhibition of PPI, values >100 indicate that animals showed increased startle response to pulse when not given a prepulse (post-hoc)

c.mean.adj = adjusted mean %PPI for use when calculating lnCVR (adjusted so that PPI values lie on ratio scale: calculated as ‘100 - c.mean’. A value of 100 would indicate complete inhibition of PPI, a value of 0 indicates no inhibition of PPI, values >100 indicate that animals showed increased startle response to pulse when not given a prepulse (post-hoc)

developmental\_stage\_PPI = category of developmental stage of animals at time of PPI testing based on applying the stages of mouse and rat development defined by zsanett bahor to the time variable (post-hoc)

polyIC.dose.cat = variable for whether PPI dose was low, moderate or high: categories adapted from <https://www.sciencedirect.com/science/article/pii/S0149763405000813> (post-hoc)

SMD = standardised mean difference (hedges g)

SMDV = standard error estimate for SMD

same\_cohort\_diff\_PPI\_param = variable used to match effect sizes within studies that were derived from the same cohorts but where a different protocol was used to measure PPI

same\_coh\_same\_PPI\_param\_diff\_time = variable used to match effect sizes within studies and within PPI protocol clusters that were derived from the same disease and control cohorts but testing performed on different postnatal days