Objective:
To establish the added value of chromosomal microarray analysis (CMA) above conventional karyotyping to assess the genetic causes of stillbirth

Methods:
A systematic search was performed to identify relevant studies published in English and Spanish with no time restrictions.

Inclusion criteria:
- Observational studies of fetal losses >20 weeks undergoing CMA
- All subjects were normal karyotyping
- The incremental yield using log transformed proportion by random-effects model (weighting by inverse of variance) was used.

Conclusions:
- There is a 4% increment of genetic causes of stillbirth regarding pathogenic copy number of variants (pCNVs) and 8% in case of variants of unknown significance (VOUS).
- CMA, used in stillbirth work-up, improves the detection of genetic anomalies over conventional karyotyping