|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Study** | **Technique** | **Animal** | **Tissue** | **Method** |
| Al Mudares *et al.,* | RNA seq | Mouse | Whole lung | Hyperoxia |
| Bao *et al.,* | Microarray | Mouse | Whole lung | Hyperoxia |
| Bhaskaran *et al.,* | Microarray | Rat | Whole lung | Hyperoxia |
| Bhattacharya *et al.,* | RNA seq | Mouse | Whole lung | Hyperoxia |
| Chao *et al.,* | Microarray | Mouse\* | Whole lung | Hyperoxia |
| Chen *et al.,* | DNA Methylation | Rat | Whole lung | Hyperoxia |
| Cheng *et al.,* | RNA seq | Rat | Right lung lobe | Hyperoxia |
| Coarfa *et al.,* | RNA seq | Mouse | Whole lung | Hyperoxia |
| Dénervaud *et al.,* | RNA microarray | Rat | Whole lung | Hyperoxia |
| Na Dong *et al.,* | RNA seq | Rat | Whole lung | Hyperoxia |
| Dravet Gounot *et al.,* | RNA seq | Rat | Whole lung | Induced IUGR |
| El Saie *et al.,* | Mass Spec | Mouse | Whole lung | Hyperoxia |
| Hurskainen *et al.,* | scRNAseq | Mouse | Whole lung | Hyperoxia |
| Natarajan *et al.,* | Microarray | Mouse\* | Whole lung | Hyperoxia |
| Nichols *et al.,* | QTL analysis | Mouse | Whole lung | NA |
| Nitkin *et al.,* | RNA seq | Mouse | Whole lung | LPS treated |
| Rao *et al.,* | RNA seq | Mouse\* | Whole lung | Hyperoxia |
| Revhaug *et al.,* | Microarray | Mouse | Whole lung | Hyperoxia |
| Scaffa *et al.,* | scRNAseq | Mouse | Whole lung | Hyperoxia |
| Shrestha *et al.,* | Microarray | Rat | Whole lung | Hyperoxia |

**Table 2: Characteristics of studies included in Rodent BPD MAIC analysis**. Techniques are outlined in supplementary table X. Mouse\* = Mouse line with specific mutation. NA = No treatment. IUGR = Intrauterine growth restrictin. LPS = Lipopolysaccharide.