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