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**Abstract**

**Background**

Describe the context and purpose of the study.

**Results**

Write the main findings.

**Conclusions**

Present a brief summary and potential implications.

**Keywords**

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**Fig. 1**



Comparison of single-cell and single-nucleus libraries. **a** Cell type composition for kidneys from Balb/c female mice. Average percentages for scRNA-seq libraries are shown in blue and for snRNA-seq libraries in gray. BSEQ-sc estimates are shown for bulk RNA-seq of intact and dissociated kidneys. Error bars are standard error of mean. **b** Abundance of renal epithelial cell types in Clark et al. study [[34](https://genomebiology.biomedcentral.com/articles/10.1186/s13059-020-02048-6#ref-CR34)] in comparison to our data from Balb/c female mice.

**Table 1 Table title (max 15 words). Legend (max 300 words) should be included underneath the table**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Characteristics** | **Group A** | **Group B** | **Group A+B** | **Group C** |
| **Age (years)** | 3.0 (0.9–7.5) | 1.0 (1.0–4.5) | 1.0 (1.0–4.5) | 1.0 (1.0–4.5) |
| > 2.5 | 22/43 (51%) | 21/43 (49%) | 21/43 (49%) | 21/43 (49%) |
| ≤ 2.5 | 21/43 (49%) | 4/7 (57%) | 4/7 (57%) | 4/7 (57%) |
| **Sex** |
| male | 23/43 (53%) | 5/7 (71%) | 5/7 (71%) | 5/7 (71%) |
| female | 20/43 (47%) | 2/7 (29%) | 2/7 (29%) | 2/7 (29%) |
| **Clinical status** |
| Asymptomatica | 0/43 (0%) | 2/7 (29%) | 2/50 (4%) | 0/26 (0%) |
| Very mild | 0/43 (0%) | 5/7 (71%) | 5/50 (10%) | 0/26 (0%) |
| Mild | 41/43 (95%) | 0/7 (0%) | 41/50 (82%) | 26/26 (100%) |
| Severe | 0/43 (0%) | 0/7 (0%) | 0/50 (0%) | 0/26 (0%) |
| Critically ill | 2/43 (5%) | 0/7 (0%) | 2/50 (4%) | 0/26 (0%) |
| **Symptoms** |
| Fever | 29/43 (67%) | 3/7 (43%) | 32/50 (64%) | 21/26 (81%) |
| Cough | 21/43 (49%) | 1/7 (14%) | 22/50 (44%) | 19/26 (73%) |
| Myalgia/fatigue | 2/43 (5%) | 0/7 (0%) | 2/50 (4%) | 0/26 (0%) |
| Sore throat  | 1/43 (2%) | 0/7 (0%) | 1/50 (2%) | 0/26 (0%) |
| Diarrhea | 3/43 (7%) | 0/7 (0%) | 3/50 (6%) | 0/26 (0%) |

aNo clinical symptoms and no abnormal CT findings

Results that would otherwise be indicated as "data not shown" should be included as additional files. BioMed Central requires that supporting data are included as additional files or deposited in a recognized repository. The maximum file size for additional files is recommended as 20 MB each. Each additional file should be cited in sequence within the main body of text. For more information on additional files, visit: [here](https://genomebiology.biomedcentral.com/submission-guidelines/preparing-your-manuscript?utm_source=other_website&utm_medium=display&utm_content=mpu&utm_campaign=BSCN_3_CZ01_CN_GB_Template#preparing+additional+files).

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**Conclusions**

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* the type of statistical analysis used, including a power calculation if appropriate.

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