# Supplementary

**Table S1 : Tabula Muris permuted datasets.**

| Tissue | Technology | Cells (filtered) | Closest cell-types | Permuted Genes |
|---|---|---|---|---|
| Heart | Smartseq2 | 4098 | Smooth muscle cell<br>Endothelial cell | 2912 |
| Kidney | Smartseq2 | 517 | Fenestrated cell<br>Endothelial cell | 5728 |
| Pancreas | Smartseq2 | 1204 | Pancreatic PP cell<br>Pancreatic A cell | 7300 |
| Trachea | Smartseq2 | 813 | Leukocyte<br>Epithelial cell | 4156 |
| Lung | Smartseq2 | 1198 | Stromal cell<br>Endothelial cell | 1862 |
| Bladder | Smartseq2 | 1287 | Bladder cell<br>Basal cell of urothelium | 5460 |
| Muscle | Smartseq2 | 1831 | Skeletal muscle stem cell<br>Skeletal muscle cell | 2665 |
| Tongue | Smartseq2 | 1394 | Keratinocyte<br>Basal cell of epidermis | 3600 |
| Liver | Smartseq2 | 646 | Kupffer cell<br>Endothelial cell hepatic sinusoid | 5288 |
| Mammary | Smartseq2 | 2255 | Basal cell<br>Luminal epithelial cell | 2335 |
| Marrow | Smartseq2 | 4442 | Neutrophil<br>Granulocyte | 1359 |
| Skin | Smartseq2 | 2218 | Epidermal cell<br>Basal cell of epidermis | 4417 |
| Mammary | 10X | 4295 | T cell<br>B cell | 4295 |
| Bladder | 10X | 2375 | Bladder cell<br>Basal cell of urothelium | 6239 |

| | | | | |
|---|---|---|---|---|
| Muscle | 10X | 4224 | T cell<br>B cell | 3260 |
| Marrow | 10X | 3285 | Hematopoietic stem cell<br>B cell | 2243 |
| Kidney | 10X | 2447 | Macrophage<br>Fenestrated cell | 3630 |
| Lung | 10X | 4247 | Stromal cell<br>Endothelial cell | 1936 |

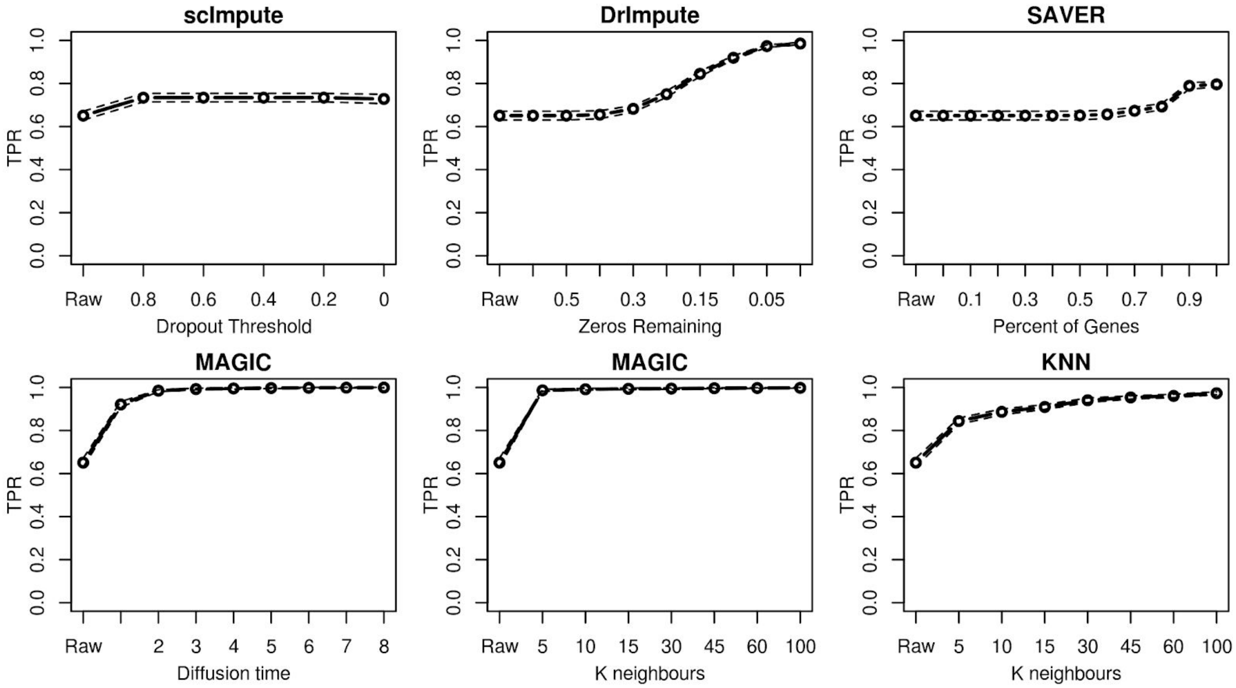

**Figure S1: Sensitivity single-cell imputation methods.** (B) True positive rate, aka sensitivity, to gene-gene correlations as imputation parameters are changed. Dashed lines are 95% CIs based on 10 replicates.