

■ Table S1 Mapping Statistics

Statistics for sample mapping to the mouse genome, using Bowtie2.

| Statistics | WT | | | WT Stress | | | <i>Ccnc</i> ^{-/-} | | |
|---------------------------|--------|--------|--------|-----------|--------|--------|----------------------------|--------|--------|
| | 1 | 2 | 3 | 1 | 2 | 3 | 1 | 2 | 3 |
| Total Paired Reads Mapped | 2.18E7 | 2.29E7 | 2.31E7 | 2.41E7 | 2.62E7 | 1.89E7 | 2.35E7 | 2.44E7 | 2.37E7 |
| Alignment Rate (%) | 81.2 | 78.8 | 84.0 | 78.8 | 85.0 | 80.1 | 80.7 | 83.4 | 79.6 |