

**Supplementary Table S2 Summary of sperm transcriptomes**

<b>Sample</b>	<b>Raw Reads</b>	<b>Raw Bases</b>	<b>Clean Reads</b>	<b>Clean Bases</b>	<b>Valid Bases</b>	<b>Q30</b>
M1	45.97M	6.90G	45.20M	6.68G	96.95%	94.62%
M2	44.80M	6.72G	44.02M	6.52G	96.99%	94.50%
M3	43.63M	6.54G	42.87M	6.34G	96.83%	92.42%
M4	46.39M	6.96G	45.64M	6.76G	97.09%	94.71%
PM1	44.62M	6.69G	43.77M	6.46G	96.58%	94.02%
PM2	45.88M	6.88G	45.02M	6.65G	96.60%	94.22%
PM3	45.82M	6.87G	45.04M	6.65G	96.75%	94.07%
PM4	42.83M	6.43G	41.92M	6.19G	96.32%	93.80%