Supplementary Information

Table S1. Conservation of dynein complex genes * between *Chlamydomonas reinhardtii*and *Mus musculus*.

| Chlamydomonas Gene | Mouse (HUMAN) Gene | MGI /HGNC Number ** | KO Mouse | | | |
|-------------------------------|---------------------|---------------------|---|--|--|--|
| Outer arm dynein (OAD) | | | | | | |
| <i>IC69</i> | Dnaic2 (DNAI2) | 2685574/18744 | No | | | |
| <i>IC</i> 78 | Dnaic1 (DNAI1) | 1916172/2954 | Yes (ciliary dyskinesia) | | | |
| LC1 | Dnall (DNAL1) | 1921462/23247 | No | | | |
| | Tctex1d1 (TCTEX1D1) | 1914594/26882 | No | | | |
| 1.02 | Tctex1d2 (TCTEX1D2) | 1913311/28482 | No | | | |
| LC2 | Tctex1d4 (TCTEX1D4) | 3045358/32315 | No | | | |
| | Tcte3 (TCTE3) | 98642/11695 | Yes (infertile; impaired spermatogenesis) | | | |
| 1.02/1.05 | Nme8 (NME8) | 1920662/16473 | Yes (fertile) | | | |
| <i>LC3/LC3</i> | Nme9 (NME9) | 4359686/21343 | No | | | |
| LC4 | No determined (ND) | - | - | | | |
| | Dnal4 (DNAL4) | 1859217/2955 | No | | | |
| LC6/LC8/LC10 | Dynll1 (DYNLL1) | 1861457/15476 | Yes (pre-weaning lethality) | | | |
| | Dynll2 (DYNLL2) | 1915347/24596 | No | | | |
| 1.07 | Dynlrb1 (DYNLRB1) | 1914318/15468 | No | | | |
| LC7 | Dynlrb2 (DYNLRB2) | 1922715/15467 | No | | | |
| DC1 | ND | - | - | | | |
| DCI | Ccdc114 (CCDC114) | 2446120/26560 | No | | | |
| DC2 | Ccdc63 (CCDC63) | 3607777/26669 | No | | | |
| DC3 | ND | - | - | | | |
| Inner arm dynein (IAD) (f/l1) | | | | | | |
| IC138 | Wdr78 (WDR78) | 2385328/ 26252 | No | | | |
| IC140 | Wdr63 (WDR63) | 3045269/30711 | No | | | |
| <i>IC</i> 97 | Casc1 (CASC1) | 2444480/29599 | Yes (higher incidence of lung tumour) | | | |
| FAP120 | Ank2 (ANK2) | 88025/493 | Yes (embryonically lethal) | | | |
| | Dynlt1a (DYNLT1) | 3807506/11697 | No | | | |
| TCTEXI | Dynlt1b (DYNLT1) | 98643/11697 | No | | | |
| | Dynlt1c (DYNLT1) | 3807476/11697 | No | | | |
| | Dynlt1f (DYNLT1) | 3780996/11697 | No | | | |
| | Tctex1d1 (TCTEX1D1) | 1914594/26882 | No | | | |
| TOTEVID | Tctex1d2 (TCTEX1D2) | 1913311/28482 | No | | | |
| ICIEX2B | Tctex1d4 (TCTEX1D4) | 3045358/32315 | No | | | |
| | Tcte3 (TCTE3) | 98642/11695 | Yes (infertile; impaired spermatogenesis) | | | |

* Note; only intermediate, light chains and docking complexes are listed. ** MGI URL: http://www.informatics.jax.org/; HGNC URL: http://www.genenames.org/.

| Mouse Genotype | Incubation Time (min) | Motility (%) | Progressive Motility (%) | Average Path Velocity (VAP) | Linear Velocity (VSL) | Curvilinear Velocity (VCL) |
|---------------------------------|--------------------------|-----------------|-----------------------------|--------------------------------|--------------------------|-------------------------------|
| | | | | (µm/s) | (µm/s) | (µm/s) |
| Ctrl | 10 | 87.0 ± 7.9 | 67.7 ± 5.0 | 119.7 ± 6.7 | 90.1 ± 7.6 | 234.4 ± 5.4 |
| | 120 | 89.3 ± 4.0 | 57.0 ± 3.5 | 114.4 ± 9.4 | 75.5 ± 6.1 | 244.8 ± 34.7 |
| Dnaic1 ^{em1Osb/em1Osb} | 10 | 91.0 ± 6.1 | 73.3 ± 5.1 | 125.6 ± 7.3 | 96.2 ± 2.2 | 217.6 ± 29.5 |
| | 120 | 78.7 ± 17.0 | 54.0 ± 6.9 | 120.9 ± 4.7 | 73.3 ± 4.0 | 255.0 ± 8.8 |

Table S2. Mean computer assisted sperm analysis (CASA) values for *Dnaic1*^{em1Osb/em1Osb} mice *vs.* control mice.





Figure S1. (A) RT-PCR for *Wdr63* in control and sKO testes; (B) RT-PCR for *Wdr78* in various tissues and (C) testes samples at different ages; (D) Semi-quantitative RT-PCR of *Wdr78* in control and sKO testes; *Actb* (β -*actin*) as control.

Table S3. Mean computer assisted sperm analysis (CASA) values for $Wdr63^{-472/-472}$ mice *vs.* control mice.

| Mouse Genotype | Incubation Time (min) | Motility (%) | Progressive Motility (%) | Average Path Velocity (VAP) (μm/s) | Linear Velocity (VSL) (µm/s) | Curvilinear Velocity (VCL) (µm/s) |
|----------------------------|--------------------------|-----------------|-----------------------------|---------------------------------------|---------------------------------|---|
| Ctrl | 10 | 93.3 ± 4.7 | 75.0 ± 3.6 | 115.5 ± 4.6 | 87.4 ± 4.9 | 221.0 ± 21.6 |
| | 120 | 85.7 ± 13.6 | 54.3 ± 7.8 | 112.8 ± 14.2 | 71.1 ± 6.5 | 242.8 ± 37.4 |
| Wdr63 ^{-472/-472} | 10 | 93.3 ± 4.2 | 80.0 ± 7.5 | 117.3 ± 6.3 | 95.7 ± 6.2 | 188.0 ± 12.8 |
| | 120 | 91.0 ± 6.9 | 57.0 ± 5.0 | 103.3 ± 2.4 | 64.1 ± 4.4 | 188.7 ± 15.0 |

Data are expressed as means \pm SD (n = 3).



Figure S2. (A) Example of sequencing for a founder mosaic mouse. Black arrow indicates double wave (2 alleles) and red arrow indicates triple wave (3 alleles) (B) RT-PCR of *Ccdc63* in control and sKO testes. *Actb* (β -*actin*) as control.

| Table S4. Off-target (OT) analysis of Ccdc63 F0 mic | e. |
|--|----|
|--|----|

| Target | sgRNA Sequence + PAM* | Location | Mutation |
|--------|--|---------------------------|--------------|
| Ccdc63 | CCTTCTCG <u>GAAAGTTCCGAA<mark>AGG</mark></u> | Chr5: 122129838-122129860 | Yes (mosaic) |
| OT-1 | AAAATGAT <u>GAAAGTTCCGAA<mark>GGG</mark></u> | Chr1: 132472528-132472550 | No |
| OT-2 | CCT <u>TTCGGAACTTTC</u> TAAATTGA | Chr4: 101217425-101217447 | No |
| OT-3 | CAGACTCT <u>GAAAGTTCCGAA</u> GGG | Chr19: 18320482-18320504 | No |

* PAM—protospacer adjacent motif; shown in red; 12 nucleotides homologous to *Ccdc63* target sgRNA underlined in black.



Figure S3. Morphological analysis of testes from control and $Ccdc63^{+1/+1}$ mice. (A) Hematoxylin/Eosin stained seminiferous tubules; (B) PAS/Hematoxylin staining of seminiferous tubules (stage III–IV), red arrows indicate developing acrosomes.



Figure S4. (A) RT-PCR for *Ccdc114* in various tissues and (B) testes samples at different ages. (C) Semi-quantitative RT-PCR of *Ccdc114* in control and sKO testes; *Actb* (β -*actin*) as control.