

Supplementary data for "A high-quality Genome and Comparison of Short versus Long Read Transcriptome of the Palearctic duck *Aythya fuligula* (Tufted Duck)"

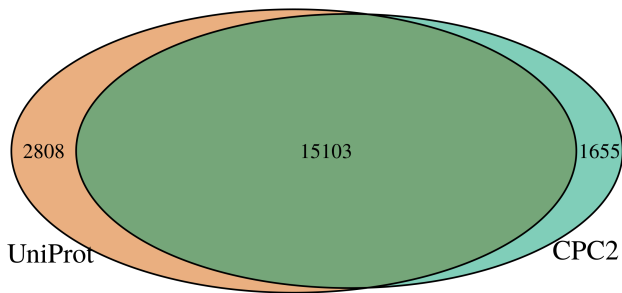


Fig. S1. Protein-coding potential calculated by CPC2 intersected with hits against the UniRef50 database (merged transcripts of all tissues and pipelines).

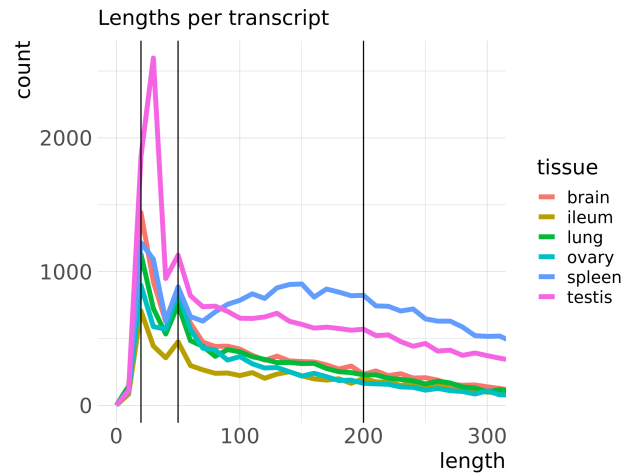


Fig. S2. Length distribution of small RNA transcripts follow decaying function with peaks at 20 bp (30 bp in testis) and 50 bp. Vertical bars at 20 bp, 50 bp and 200 bp were added.

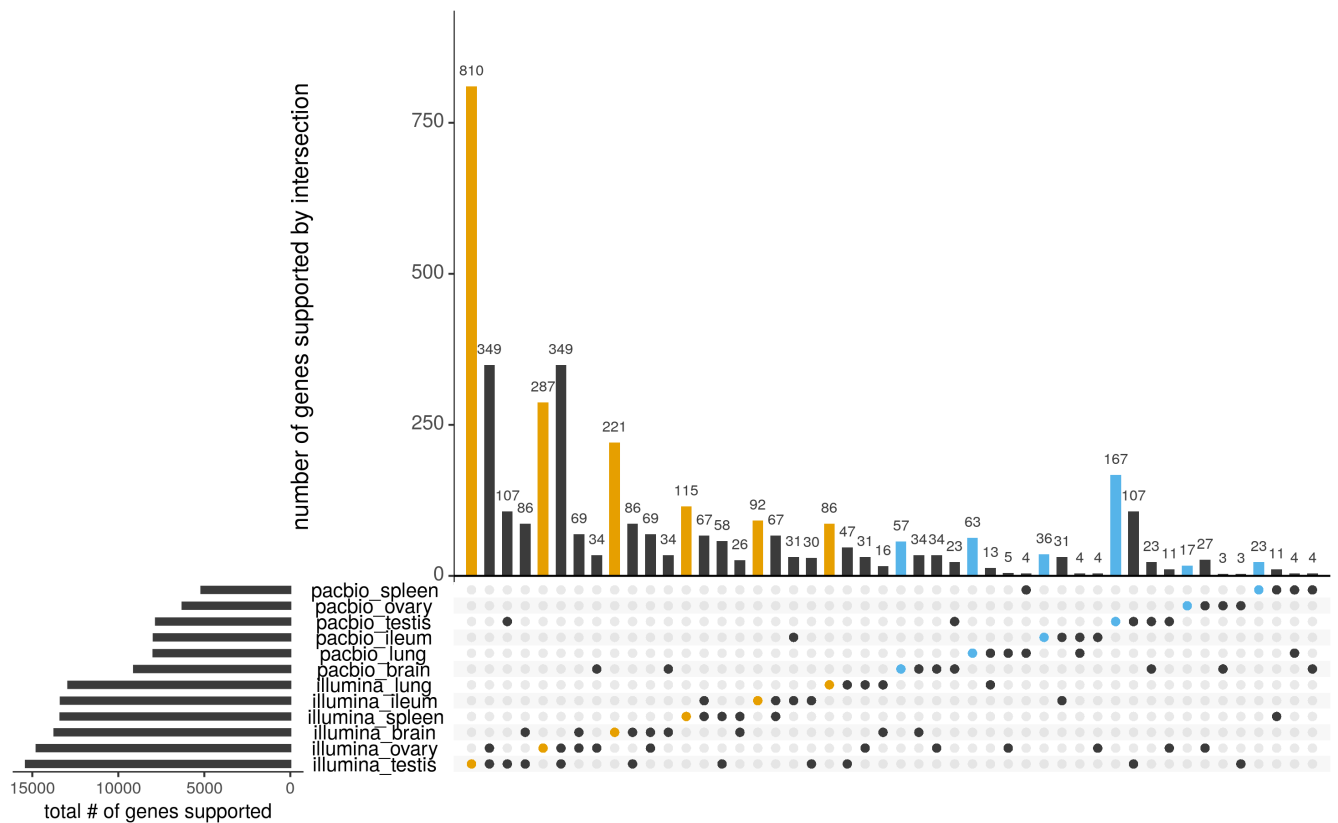


Fig. S3. Pipeline-tissue-specific expression of genes found in UniProt: Tissue-exclusive Illumina genes marked yellow, tissue-exclusive PacBio genes marked blue. Bottom left panel: total number of identified genes by pipeline and tissue ordered by the number of identified genes. Main panel: 12 grouped sets (pipeline-tissue) with exclusive genes plus top three intersections with other pipeline or tissue. The number of annotated genes was generally higher with Illumina transcriptome reconstruction than with that of PacBio. In both pipelines, testis expressed the highest number of genes exclusively, with 810 in Illumina data and 167 from PacBio.

Tab. S1. RNA extraction

Sample	Weight [mg]	Concentration [ng/ μ L]	RIN
TD_brain_52037	123	202.7	9.2
TD_ileum_52037	42	958.2	10.0
TD_lung_52037	37	221.6	9.5
TD_ovary_52037	55	1037.4	9.5
TD_spleen_52037	53	2109.8	9.4
TD_testis_54068	63	989.3	9.7

Tab. S2. small RNA extraction

Sample	Weight [mg]	Concentration [ng/ μ L]	RIN
TD_brain_F52037	29	852.87	9.3
TD_ileum_F52037	16	727.93	10.0
TD_lung_F50325	15	402.63	9.7
TD_ovary_F50325	12	368.79	9.4
TD_spleen_F50325	5	823.70	9.5
TD_testis_M54068	19	722.62	9.4

Tab. S3. cDNA libraries for Iso-Seq

Sample	Concentration [ng/ μ L]
TD_brain_52037	46.2
TD_ileum_52037	43.2
TD_lung_52037	33.2
TD_ovary_52037	41.0
TD_spleen_52037	66.8
TD_testis_54068	45.2