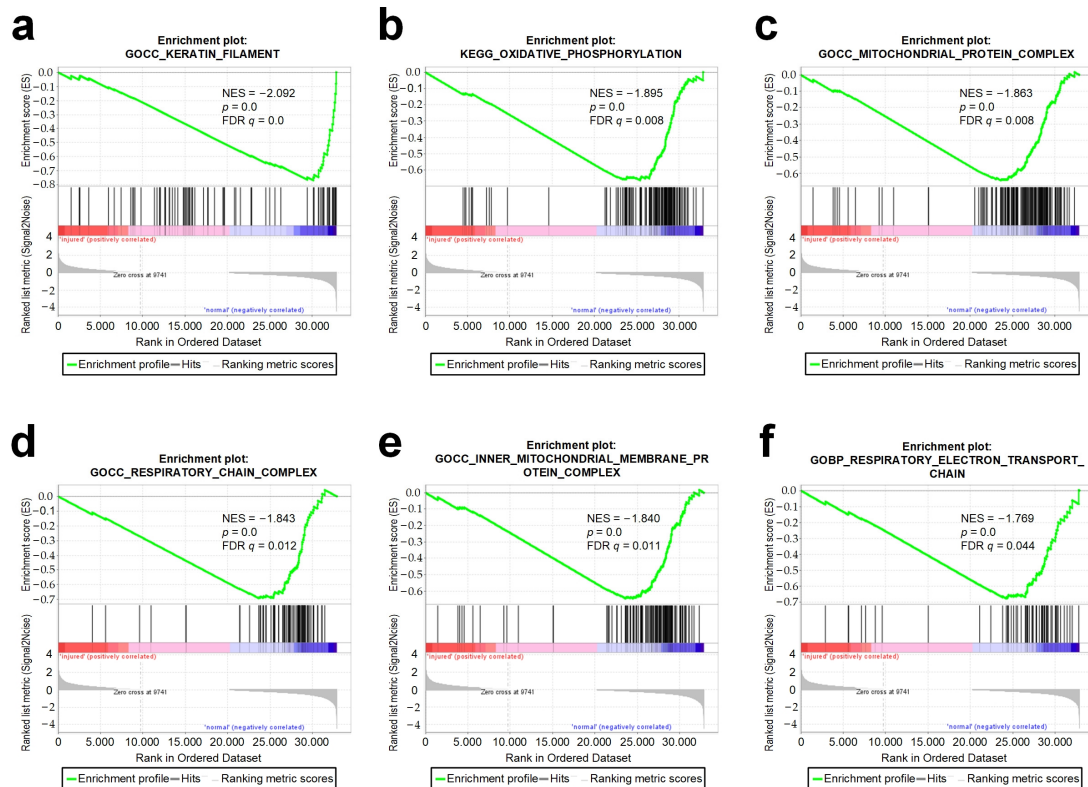
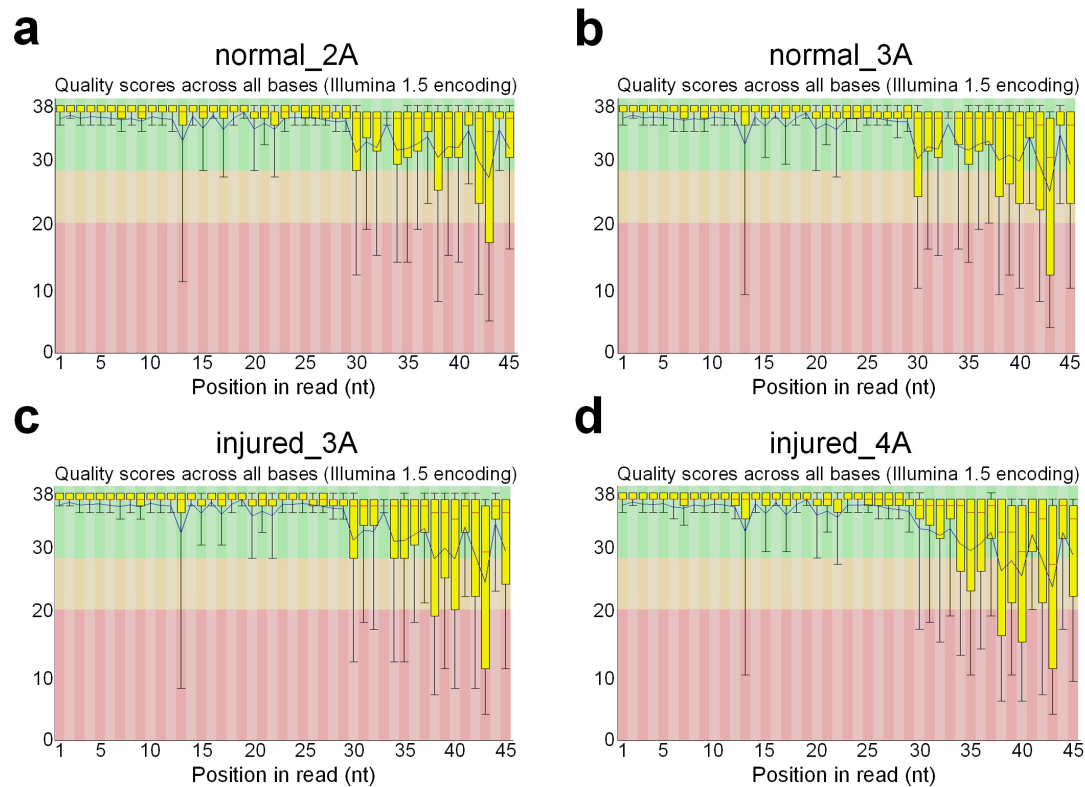


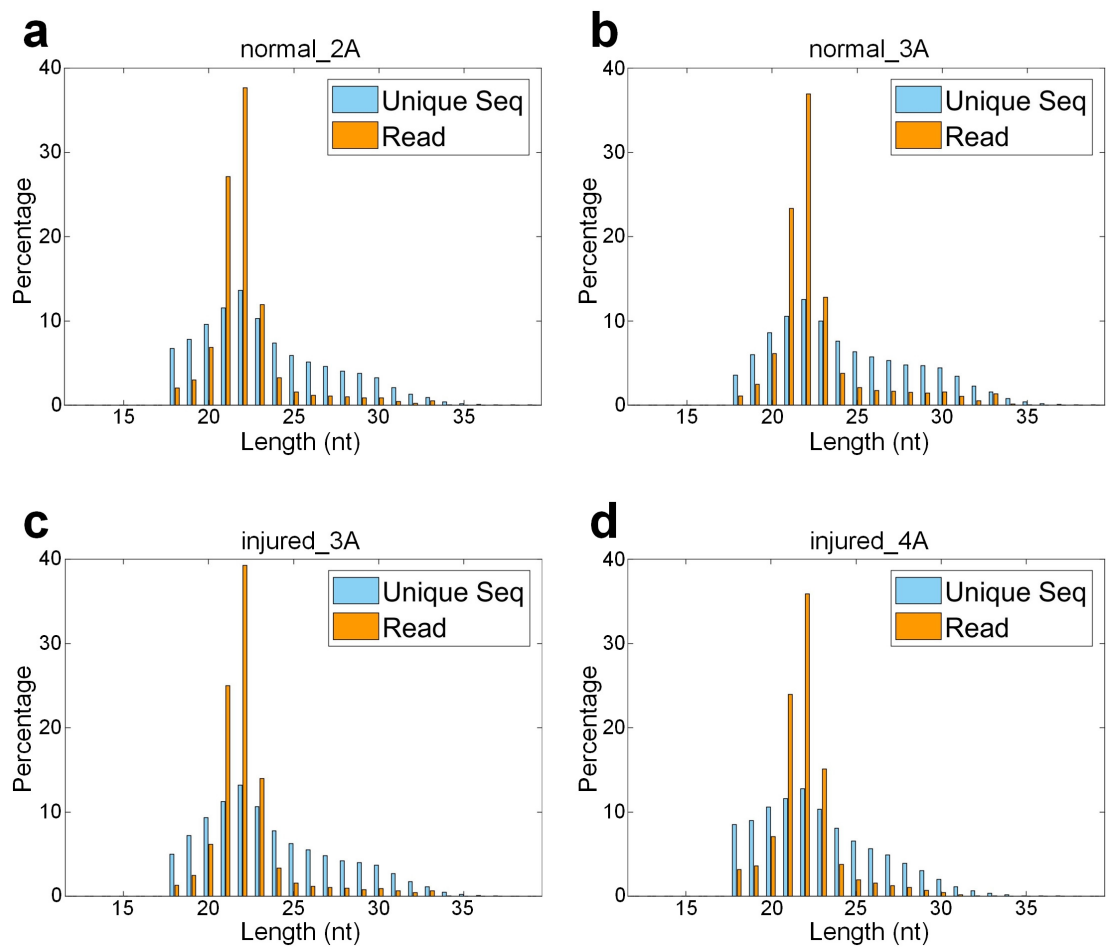
**Figure S1.** Per base sequence quality of 4 RNA-seq sequencing profiles (**a–h**). The y-axis is quality scores.



**Figure S2.** GSEA analysis of 6 representative significantly enriched gene sets in phenotype normal. Enrichment plots comparing normal toward injured phenotype were depicted with following sets of genes: (a) GOCC keratin filament, (b) KEGG oxidative phosphorylation, (c) GOCC mitochondrial protein complex, (d) GOCC respiratory chain complex, (e) GOCC inner mitochondrial membrane protein complex and (f) GOBP respiratory electron transport chain. Comparison of samples, NES, nominal  $p$ -value, and FDR  $q$ -value were determined by the GSEA software, and were indicated within each enrichment plot.



**Figure S3.** Per base sequence quality of 4 small RNA sequencing profiles (**a–d**). The y-axis is quality scores.



**Figure S4.** The length distributions of reads and unique sequences of 4 sRNA-seq profiles of rat urethra tissues (**a–d**).