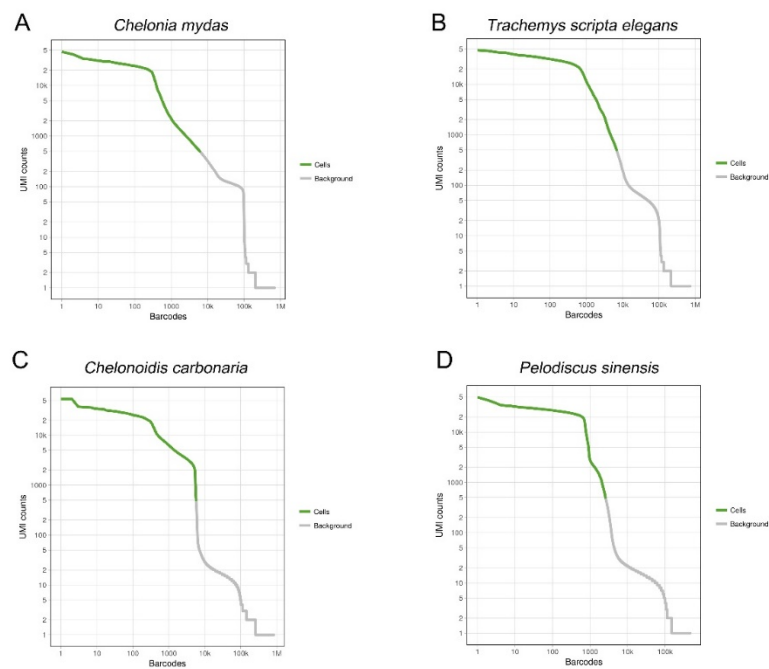**Supplementary Figure S1.**

Figure S1. Map of valid cell identification
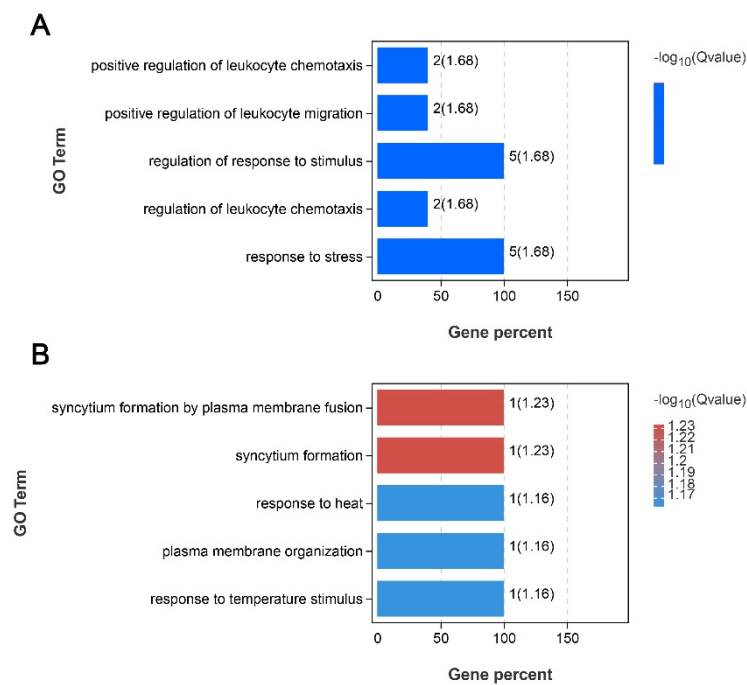
Supplementary Figure S2.

Figure S2. GO enrichment analysis. (A): LGALS1, LY86, PLBD1, MYOF, BPI, and CSF1R genes; (B): MYOF.

Supplementary Table S1. Morphological characteristics of testudines

Species	Carapace length (cm)	Carapace width (cm)	Body weight (kg)
Chelonia mydas	74.2±5.2	65.7±6.0	43.1±5.8
Trachemys scripta elegans	24.5±1.6	17.8±1.2	2.2±0.3
Chelonoidis carbonaria	19.9±0.7	12.9±0.2	1.5±0.1
Pelodiscus sinensis	22.8±0.7	19.2±1.0	1.6±0.2

Supplementary Table S2. Number of cells in each sample before and after filtration

Species	Retained	Excluded
Chelonia mydas	2976	2912
Trachemys scripta elegans	5739	965
Chelonoidis carbonaria	5507	110
Pelodiscus sinensis	2356	178

Supplementary Table S3. The results of quality control

Species	Number of reads	Valid barcodes	Sequencing saturation	Q30 bases in barcode	Q30 bases in RNA read	Q30 bases in UMI
Chelonia mydas	368,610,050	97.0%	84.7%	95.3%	92.2%	94.4%
Trachemys scripta elegans	431,034,089	98.2%	81.8%	95.5%	91.5%	94.6%
Chelonoidis carbonaria	392,723,491	97.8%	81.9%	95.6%	92.3%	94.8%
Pelodiscus sinensis	443,802,858	98.2%	90.0%	95.5%	92.0%	94.6%