Supplementary materials

Figure S1. Statistics of the quantitative proteomics data of different samples.

(A) The distribution of peptide lengths in all samples. (B) The distribution of peptide coverage in all samples. (C) Numbers of proteins with different masses in all samples. (D) Principal coordinates analysis of four types of individuals. PC: principal coordinate.

Figure S2. GO and KEGG enrichment analysis of labeled proteins.

(A) GO enrichment analysis of labeled proteins. (B) KEGG enrichment analysis of labeled proteins.

Figure S3. GO and KEGG enrichment analysis and subcellular location of abundant proteins in two com-parison groups.

(A) GO enrichment analysis of differential proteins between male and pseudo-female. (B) The subcellular location of differential proteins between male and females. (C) GO enrichment analysis of differential proteins between female and pseudo-male. (D) The subcellular location of differential proteins between female and pseudo-male.

Figure S4. Cluster analysis on the differentially expressed proteins among four types of Chinese soft-shelled turtles.

Supplementary Table S1. The primers used in this study.

Supplementary Table S2. Top 30 differentially expressed proteins between male and pseudo-female.

Supplementary Table S3. Top 30 differentially expressed proteins between female and pseudo-male.
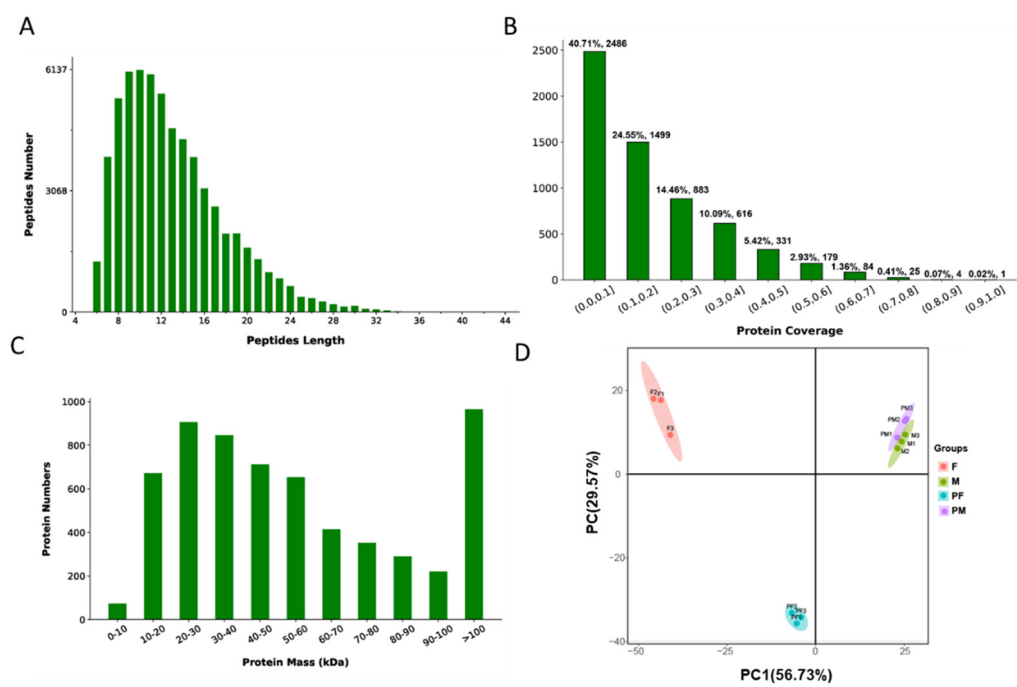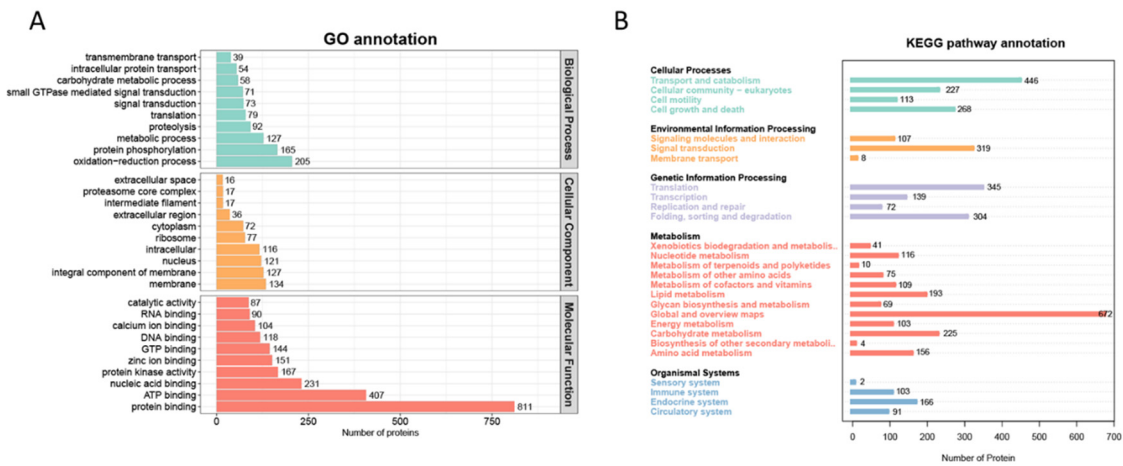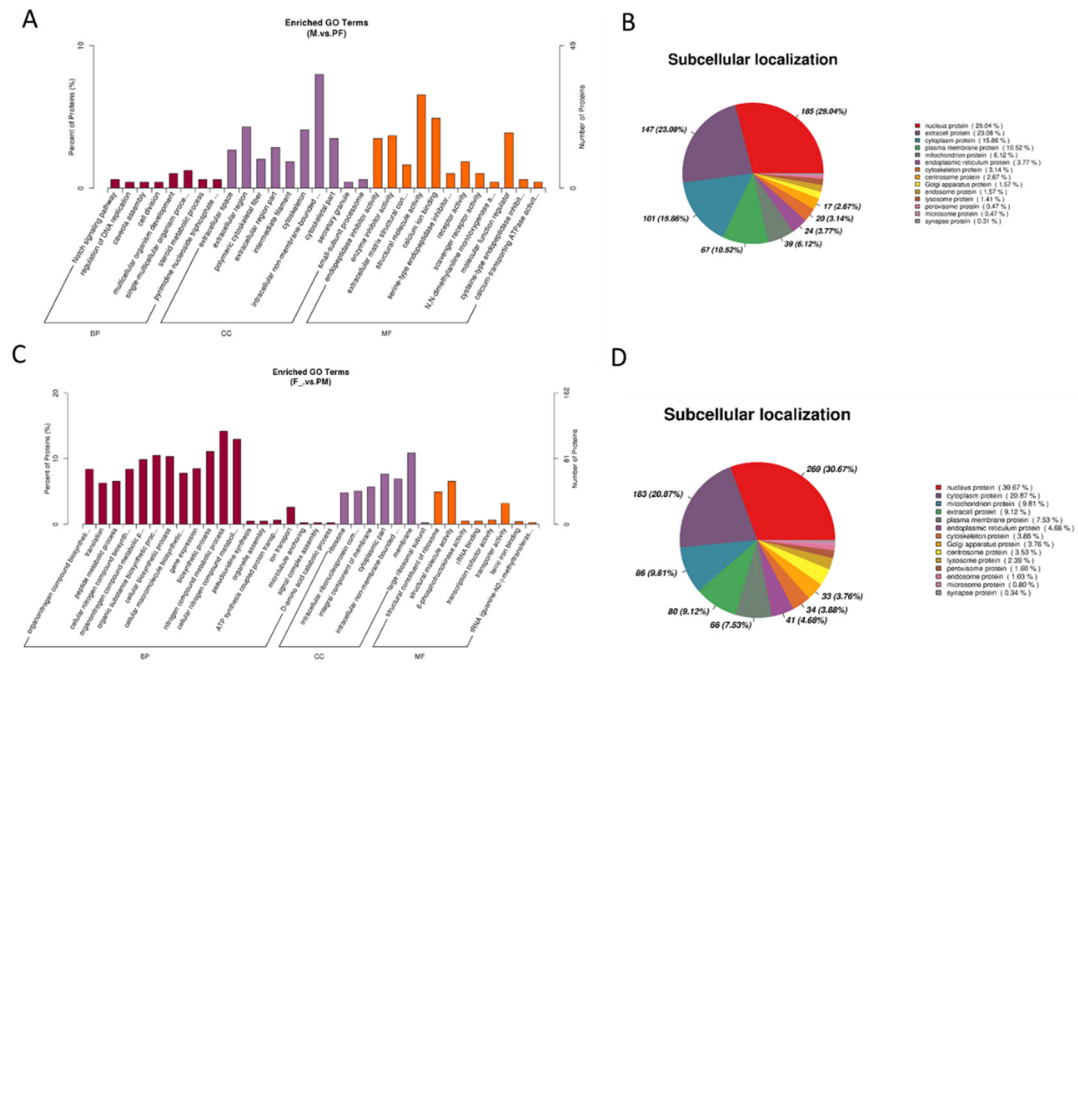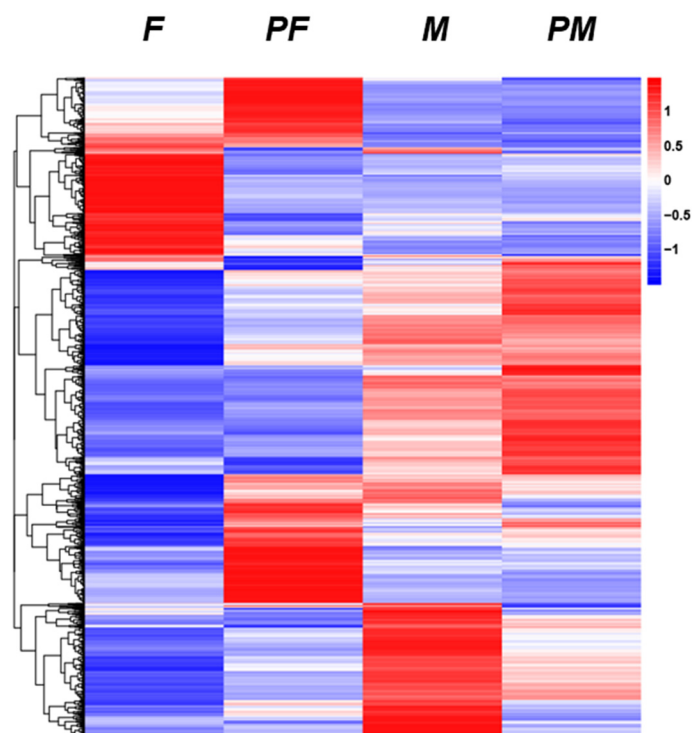
Figure S1

Figure S2

Figure S3

Figure S4

Supplement Table S1

Primers		Sequence (5′-3′)
K7FKG1	Forward	GAACAACTTCCCTGTCCTGCCTAC
	Reverse	GCCCATCTTGATGACGCTGATA
K7GIQ2	Forward	GTCCCAGAAGGCCTCCAGTGG
	Reverse	CCTCCCGTCCCAGGAACTCAC
COL4A6	Forward	CCAGCATCCAGGTGCAGATCT
	Reverse	GTGCCTTTGTAAACAGCCGAGT
K7F2U2	Forward	CTACAAATACACCCAGGAGCACC
	Reverse	AGCAGAGCCCACAGAACAGGA
K7FF80	Forward	TCATCCCGCTCCTCCTCTTTC
	Reverse	GCTCCTGTTTGCAGGCAACGT
RPL28	Forward	CGACGGCAAGGGCATTGTGGT
	Reverse	ACGCAGGCTGTTGAGGGTGGC
SRSF3	Forward	GAACAACTTCCCTGTCCTGCCTAC
	Reverse	GCCCATCTTGATGACGCTGATA
SNRNP40	Forward	GTCCTGCCTACCAACGGCTTCA
	Reverse	GCATTGCCTGTTCTTACAGACCC
HNRNPK	Forward	GGGAAAGCCCGACGGAAAGAG
	Reverse	GGTGCAGCAAAGCTATGATGACAC
4085	Forward	GTTTGAAGTGCTGCTGGGAAG
	Reverse	TTCCCCGTATAAAGCCAGGG
COI	Forward	CAACCAACCACAAAGACATTGGCAC
	Reverse	ACCTCAGGGTGTCCGAARAATCARAA

Supplement Table S2

Protein	M1	M2	M3	PF1	PF2	PF3	Up	Down
K7FE08	11.4	9.9	11.8	120.5	114	102.5	*	--
K7F5N5	93	68.3	52.4	525.5	523.5	569.8	*	--
K7FDA4	85.9	122.5	59.5	670.3	640.4	680.3	*	--
K7FJB7	89.4	83.9	94.3	673.3	607.7	624.4	*	--
TSPAN1	21.4	22.8	16	139.7	140.3	136.9	*	--
K7FTP9	96.8	113.4	79.1	630.7	648.7	643.9	*	--
ZP1	377.8	382.7	340.7	2336.1	2526.1	2393	*	--
PATL2	927.7	940.3	786.5	5466.7	5773.5	5737.2	*	--
MYL9	86.7	134.3	86.8	631.2	649	639.4	*	--
K7EW41	606.2	664.5	533.2	3640.7	3320.7	3823	*	--
RBP7	688.5	685.4	580.9	3802.3	4073.2	3558.3	*	--
LSM14B	323	287	265.9	1607.3	1765.6	1613.5	*	--
HPCAL4	763.1	729.6	658.5	3691	4075.3	4161.2	*	--
COL4A4	138.4	132.6	105.2	672.9	692.9	658.9	*	--
ACSL5	4038.8	4049.7	3492.8	18486.3	19827.2	20903.3	*	--
K7FSY5	840.5	835.3	801.3	126.1	153.5	155.5	--	*
DYNLL1	924.6	604.5	800	121.2	139.5	151.1	--	*
YBX1	1462.1	909.7	1116.7	175.5	221.6	222.5	--	*
AK6	621.1	572	663.2	107.8	137.2	133.9	--	*
K7FZ96	1308.6	1312.2	1399.2	285.9	298.2	290.4	--	*
K7G186	123.7	117.1	121	22	29.1	28.6	--	*
SARNP	648.1	490.9	706.5	121.2	146	154.2	--	*
SYF2	553.3	420.7	443.2	91.2	98.8	136.1	--	*
TCF4	188.4	173.9	146.9	38.1	40.6	40	--	*
K7EXC8	45.4	28.5	33.7	3	13.2	9	--	*
K7GE94	380.3	430.3	391.7	81	101.6	115.9	--	*
DCK	821.1	745.4	836.6	182.3	212	203	--	*
K7FRC0	880.7	720.9	911.2	209.1	216.6	214.8	--	*
ACBD7	4991.7	4541.7	6223	1333.6	1398	1433	--	*
GJC2	18.1	15.8	14.4	4.4	5.2	3.2	--	*

Supplement Table S3

Protein	F1	F2	F3	PM1	PM2	PM3	Up	Down
DYNLL1	90.5	59.1	78.1	590	1002.3	892.9	*	--
K7FX63	86.2	59.6	68.2	665.3	728.1	793	*	--
K7EXP1	42.3	46.8	55.7	365	510.2	554	*	--
K7FHJ3	98.2	59.6	82.7	665.6	763.8	845.5	*	--
K7G5Y2	38.4	36.5	50.7	322.7	353.7	461.8	*	--
PFKP	44	24.7	38.2	268.6	245.5	301.2	*	--
RBM45	89.2	83.2	77.7	570.7	607.9	589.3	*	--
LDHA	316.7	243	262.7	1751.4	1980.5	1787.9	*	--
K7EZ03	409.8	328.8	340.8	2333.3	2484.1	2409.9	*	--
RNLS	59.8	59.1	76.1	418.7	438.3	426.6	*	--
ATP6	29	21.6	40.3	197.7	186.4	201	*	--
RBX1	223.7	185.5	253.5	1234.9	1466.9	1413.5	*	--
PIH1D1	26	19.5	36.2	158.8	172.9	172.9	*	--
K7G186	18.8	14.9	27.8	115.6	123.4	133	*	--
CAMLG	42.7	25.2	48.2	214.6	234.2	248.7	*	--
DENND4A	11927.4	14986.1	12737.7	119.1	116.5	99.1	--	*
EIF6	5740	5401.6	6056.9	204.3	177.8	200.8	--	*
BRPF3	1190.5	1165.8	1287.6	44.4	41.3	44.4	--	*
ARHGAP5	766.2	876.5	701.2	33.5	26.3	31.5	--	*
POLR2H	2315.7	2168.3	1702.4	99.6	90.1	93	--	*
HDGFL2	7703.2	7421.9	6167.5	369.1	339.4	333.7	--	*
K7FDG6	566.9	688	778.5	37.9	32.5	32.8	--	*
K7GG70	967516.7	1019208	1004697	58918.2	54339.6	55180.5	--	*
K7GGJ3	134159.5	145429.5	169903.3	10049.1	9405	9237	--	*
K7GID9	10766.8	13260.2	8832.9	729	724.7	748.2	--	*
K7F1A5	922.4	800.5	416	56.4	46.6	46.5	--	*
K7GEE1	885.3	949	615.5	57.8	60.6	56.8	--	*
CEP20	1721.1	1878	1652.5	126.3	129.7	123.3	--	*
ARL5A	814.9	974.2	606	66.3	56.7	59.7	--	*
PM20D2	17025.8	16955	14568.5	1226.7	1288.2	1331	--	*