

Table S1. Sequence of primers used to construct plasmid. Yellow mark: enzyme loci;

Red mark: binding or mutation site.

Primers	Enzyme	Sequence (5'-3')
NKX3.2-CDS-F (pig)	EcoRI	ATTGAATTC TGGGCAGCGCAGGAGT
NKX3.2-CDS-R (pig)	BamHI	ATTGGATCC GGGCACAATCTGCATAGCC
NKX3.2-CDS-F (mouse)	EcoRI	ATTGAATTC CTGAGGTCGCCCAGAGCT
NKX3.2-CDS-R (mouse)	BamHI	ATTGGATCC CAAGTCCCAGCAGGATTTCA
NKX3.2-wt1-3'UTR-F	AsiSI	ATTGCGATCGC CCAGGATGCGCGCTCTGGCCTCGCC GTCTACCCAGAGGGGGGCGCCTTTCTCTAACTTGAG CAGTGGCATCTAGGGGCCCTGTTC
NKX3.2-wt1-3'UTR-R	PmeI	TAAGTTTAAAC CAAATCCAGCATTGTGGTGGTAATAA ATAACGTCCAAAGGCTTCCGGGAAGGTGAGGGGTGG GGGGAACAGGGCCCCTAGATGCC
NKX3.2-mut1-3'UTR-F	AsiSI	ATTGCGATCGC CCAGGATGCGCGCTCTGGCCTCGCCG TCTAGGGTCTCGGGGGCGCCTTTCTCTAACTTGAGCA GTGGCATCTAGGGGCCCTGTTC
NKX3.2-mut1-3'UTR-R	PmeI	TAAGTTTAAAC CAAATCCAGCATTGTGGTGGTAATAA ATAACGTCCAAAGGCTTCCGGGAAGGTGAGGGGTGG GGGGAACAGGGCCCCTAGATGCC
NKX3.2-wt2-3'UTR-F	AsiSI	ATTGCGATCGC ATTTGGATTGTGTCTGCCC GGTCGTTT CCCCAGAGCAGAGAGAACTCCTGGAGACCACAAAAG CCTGAATCCCAGAATTCAGGC
NKX3.2-wt2-3'UTR-R	PmeI	TAAGTTTAAAC TACACATAGATTGGTAGCATGGATACCA TGAAGTAGTGTGGCCTAGCGCACGAAGCTCCCGGCAGGC CTGAAATTCTGGGATTCA
NKX3.2-mut2-3'UTR-F	PmeI	ATTGCGATCGC ATTTGGATTGTGTCTGCCC GGTCGTTT GGGTCTCAGAGAGAACTCCTGGAGACCACAAAAGCC TGAATCCCAGAATTCAGGC
NKX3.2-mut2-3'UTR-R	AsiSI	TAAGTTTAAAC TACACATAGATTGGTAGCATGGATACCA TGAAGTAGTGTGGCCTAGCGCACGAAGCTCCCGGCAGGC CTGAAATTCTGGGATTCA

Table S2: The primer sequences for SqRT-PCR and qPCR.

Species	Gene	Primers (5'-3')	Application
Pig	<i>NKX3.2</i> : NC_010450	F: GAACCGTCGCTACAAGACCAA R: CGGGAGGCAGTAATAAGGGT	qPCR
	<i>GREM1</i> : NC_010443	F: CATCATCAACCGCTTCTGCTAC R: TCTTCTTCTTGGTGGGTGGC	qPCR
	<i>WLS</i> : NC_010448	F: GCGGAATCACATAGCAGGGTA R: TGGACTGCTTCCCGCTGA	qPCR
	<i>FGFR3</i> : NC_010450	F: ATAGCCCGCACTACCTTTCA R: GCCATGAGAACAGAGCCCTA	qPCR
	<i>HHEX</i> : NC_010456	F: CCCAACTCCTCCTTCACCAG R: CAGGGCGTGCGTGTAGTCA	qPCR
	<i>WNT16</i> : NC_010460	F: ATCGCCTCCTTTGGGGTTC R: TCGGCAGCAGGTACGGTTT	qPCR
	<i>COL2A1</i> : NC_010447	F: CAGCCAGCGTTCCTCAAGA R: AGTGGTAGGTGATGTTCTGGGAG	qPCR
	<i>COL10A1</i> : NC_010443	F: CCCACCCGAAGGCTTTGTA R: TTTGGGTCATAGTGCTGTTGC	qPCR
	<i>NKX3.2</i> : NC_010443	F: TTCTGCTTTCCAGGATGCG R: AATTCTGGGATTCAGGCTTT	SqRT-PCR
	<i>β-actin</i> : NC_010445	F: AGAGCAAGAGAGGCATCCTG R: CACGCAGCTCGTTGTAGAAG	SqRT-PCR and qPCR
	ALDBSSCG0000004943	F: CGTTGGTTCCACGACTGCTA R: CGTCTGTTAGCCTCCCGTTC	qPCR
	XLOC_074900	F: TAGGGTTCATTCTGCCGTCT R: GCCTTCTCAAGCCAACTGC	qPCR
	XLOC_043998	F: TCGTGTCTCTGGCTGTTCA R: CTCAATGGTAGAGTCGGGTG	qPCR
	XLOC_007104	F: CAGAAGCACAGCAAGAAGGC R: AAGGTGGGGAGCGAGGATAG	qPCR
	ALDBSSCG0000006642	F: TTCAGAAAGGCTCAATCCCC R: CCCTTGCTCTTAGATGGTGCT	qPCR
	ALDBSSCG0000005264	F: GCGTGCCTCCTAACATAA R: CCTGGTGGGAAAACAGAAAT	qPCR
Mouse	<i>COL2A1</i> : NC_000081	F: GGAATTTGGTGTGGACATAGGG R: GGTCAGGTCAGCCATTCAGT	qPCR
	<i>COL10A1</i> : NC_000076	F: CCTGGTTCATGGGATGTT R: CCAGGAATGCCTTGTCT	qPCR
	<i>β-actin</i> : NC_000071	F: GATGTGGATCAGCAAGCAGGA R: AGGGTGTAACACGCAGCTCAG	qPCR

Figure S1. Histological analysis of differences in chondrocytes size in TIC obtained from Y1, Y4, W1 and W4. Red arrow indicates proliferating chondrocytes, Green arrow indicates hypertrophic chondrocytes.

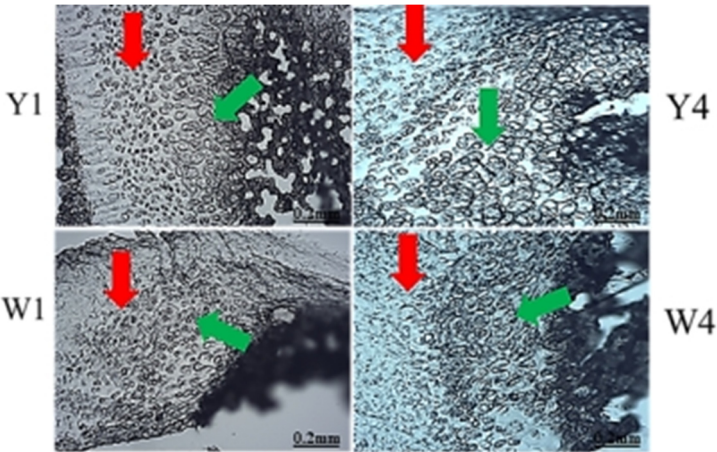


Figure S2. Pearson correlation coefficients of gene expression among the biological replicates from Y and W pigs.

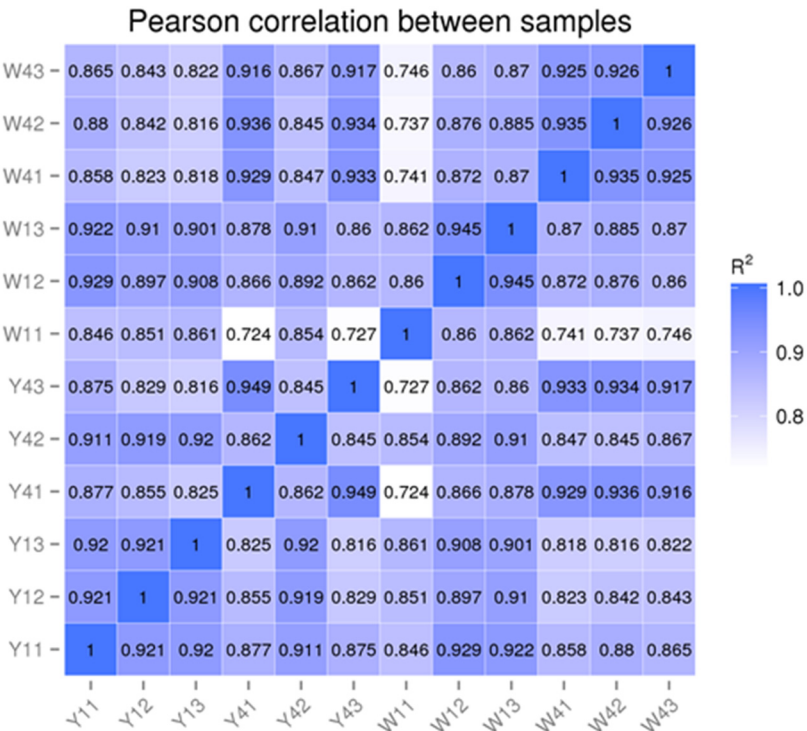
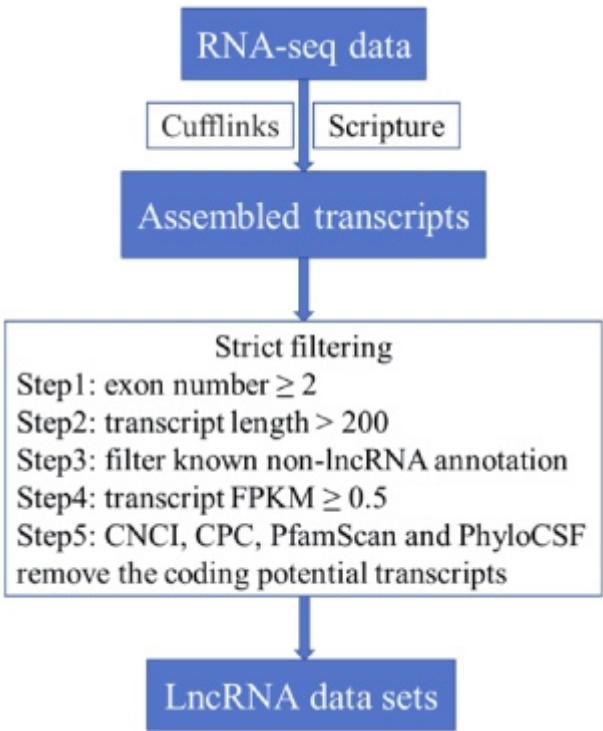


Figure S3. Identification lncRNAs in TIC transcriptome. (A) The workflow to select lncRNA. (B) Candidate lncRNAs were identified by using four applications: CNCI (coding-non-coding-index), CPC (coding potential calculator), PFAM-scan and PhyloCSF (phylogenetic codon substitution frequency) which detect and remove putative protein-coding transcripts.

A



B

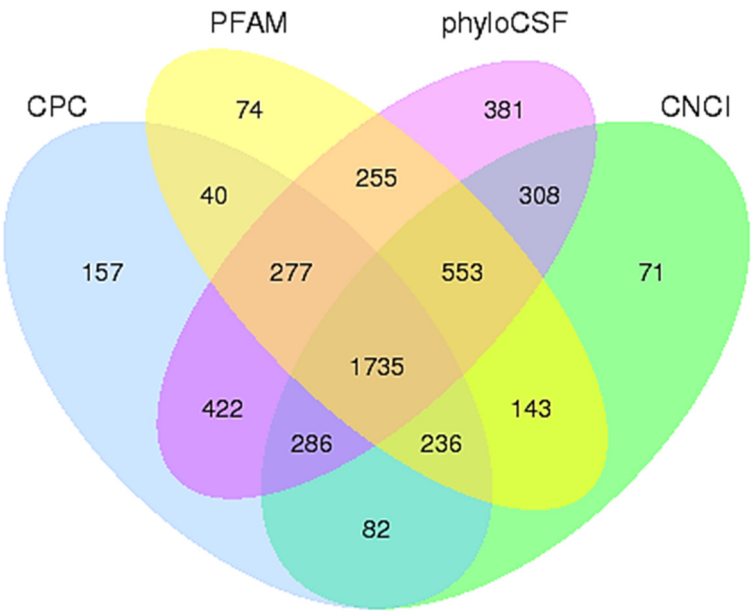
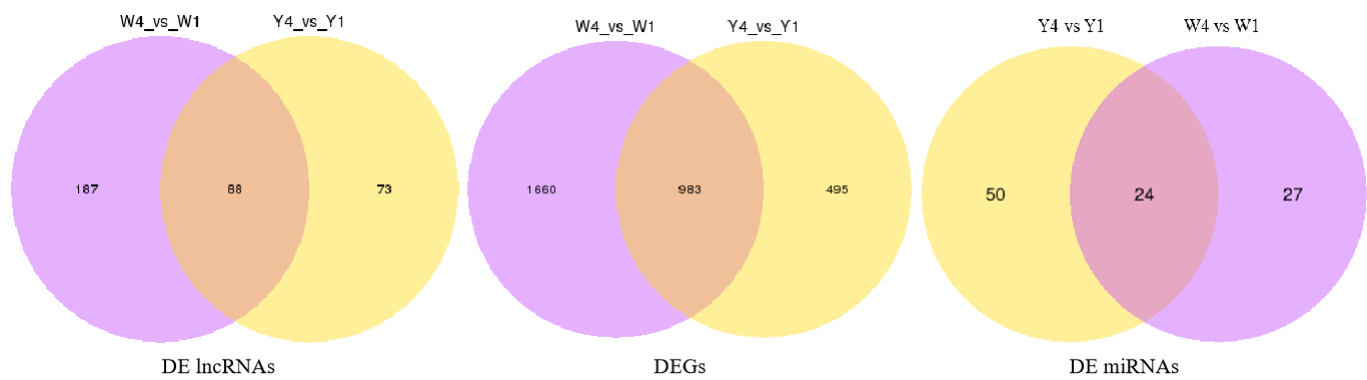


Figure S4. Venn diagrams of DE lncRNAs, DEGs and DE miRNAs showing Y4 vs. Y1 compared to W4 vs. W1 as well as Y4 vs. W4 compared to Y1 vs. W1. (A) Number of DE lncRNAs, DEGs and DE miRNAs for two comparisons of Y4 vs Y1 and W4 vs W1. (B) Number of DE lncRNAs, DEGs and DE miRNAs for two comparisons of Y4 vs W4 and Y1 vs W1.

A



B

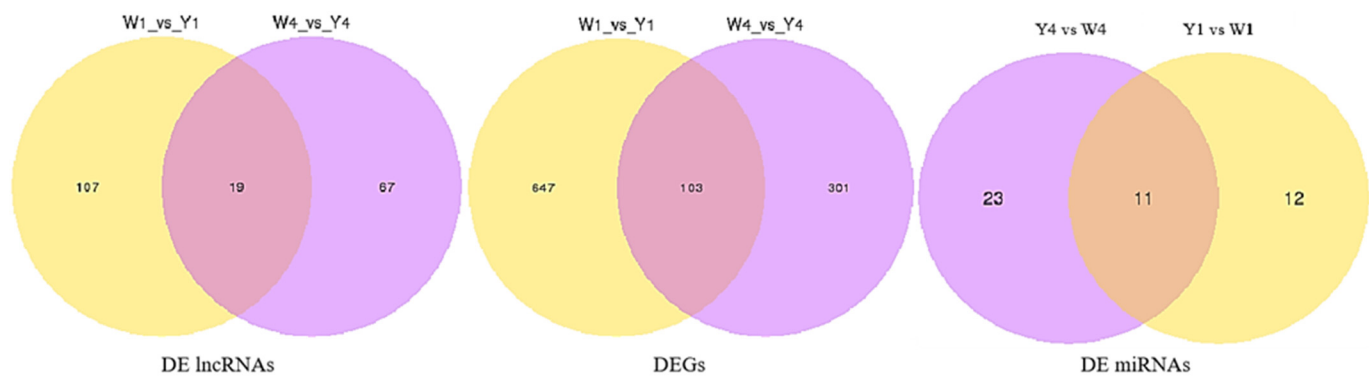
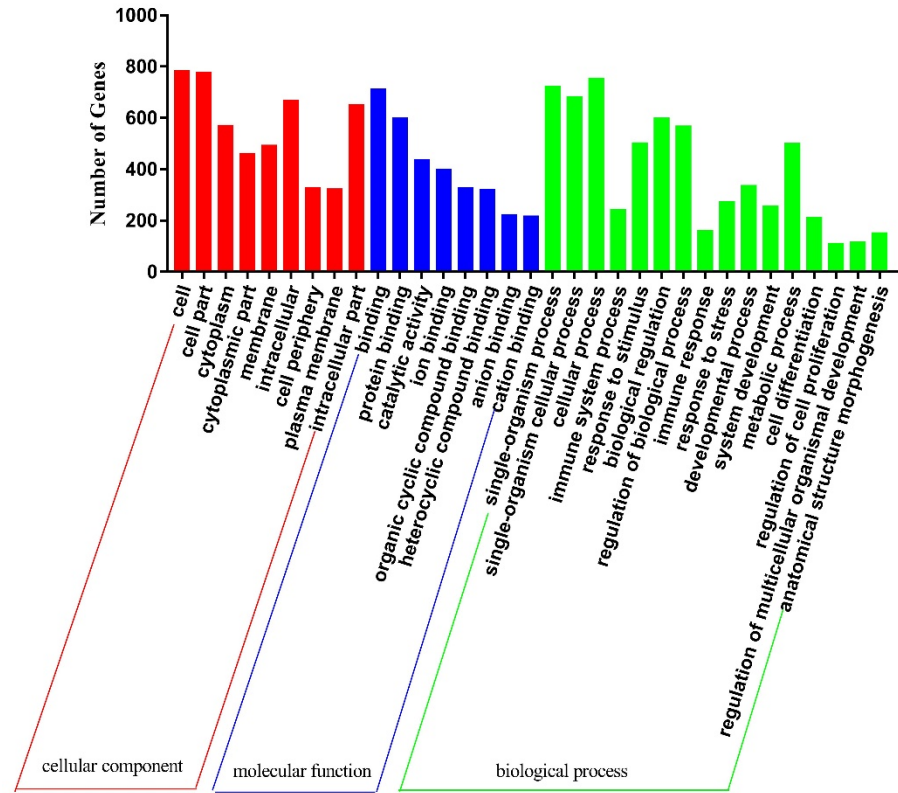
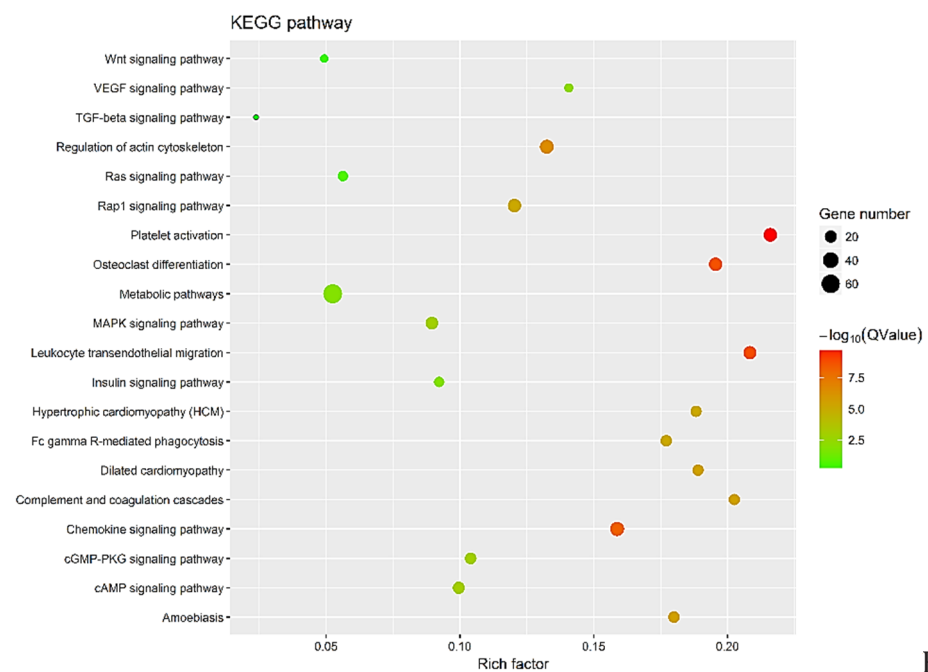


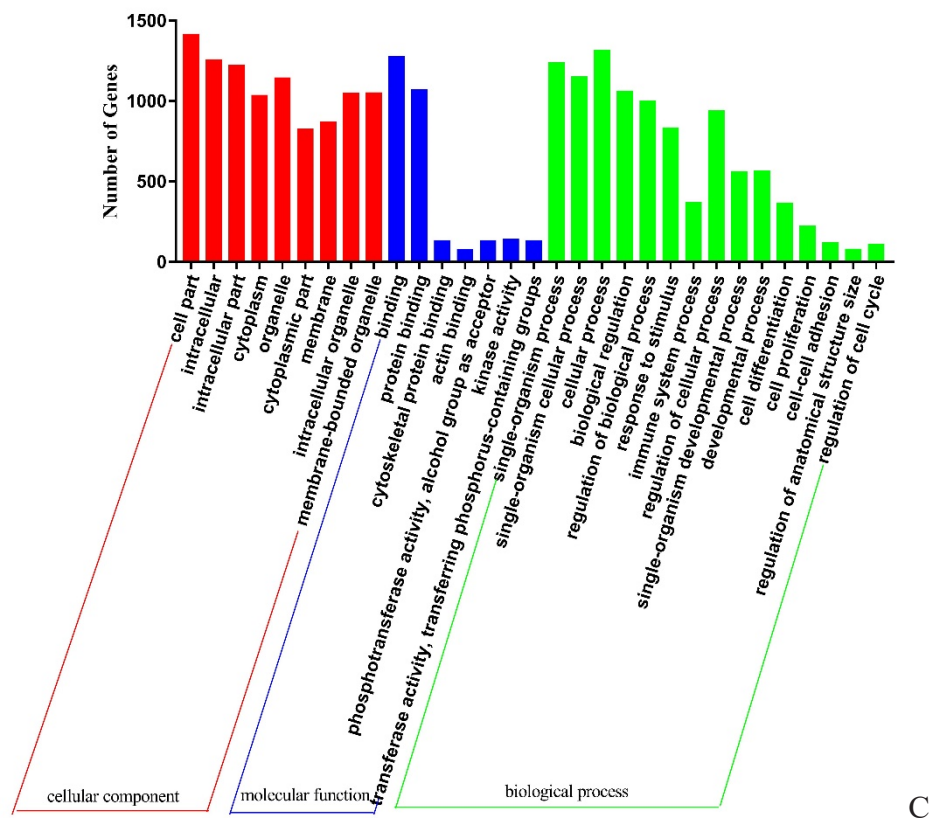
Figure S5. Crucial pathways were clustered from differentially expressed genes and noncoding RNAs target genes. GO terms analysis (A, C, E) and KEGG pathways (B, D, F) clustered by DEGs, DE lncRNAs and DE miRNAs, respectively.



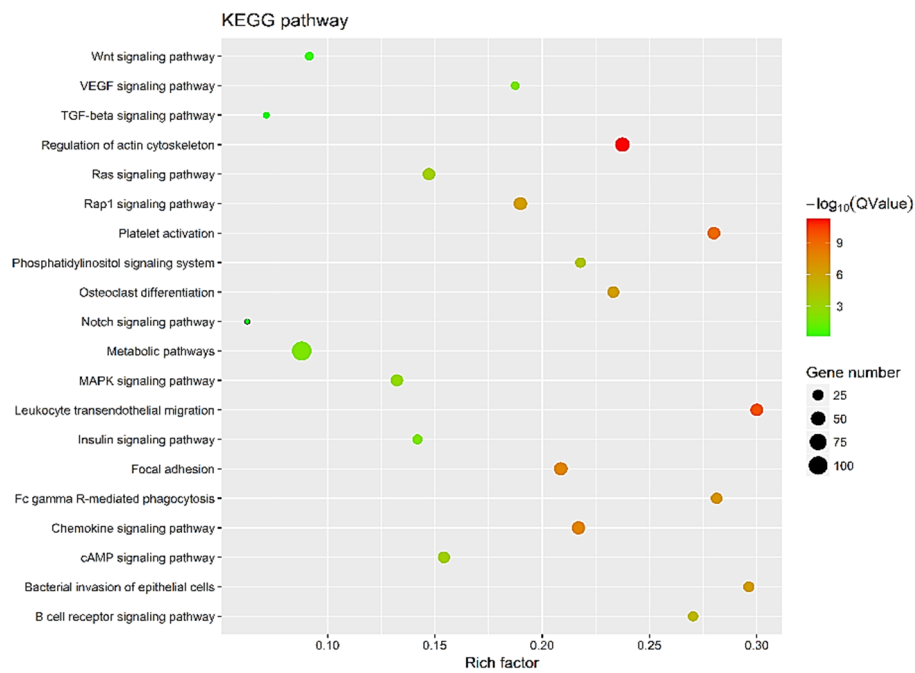
A

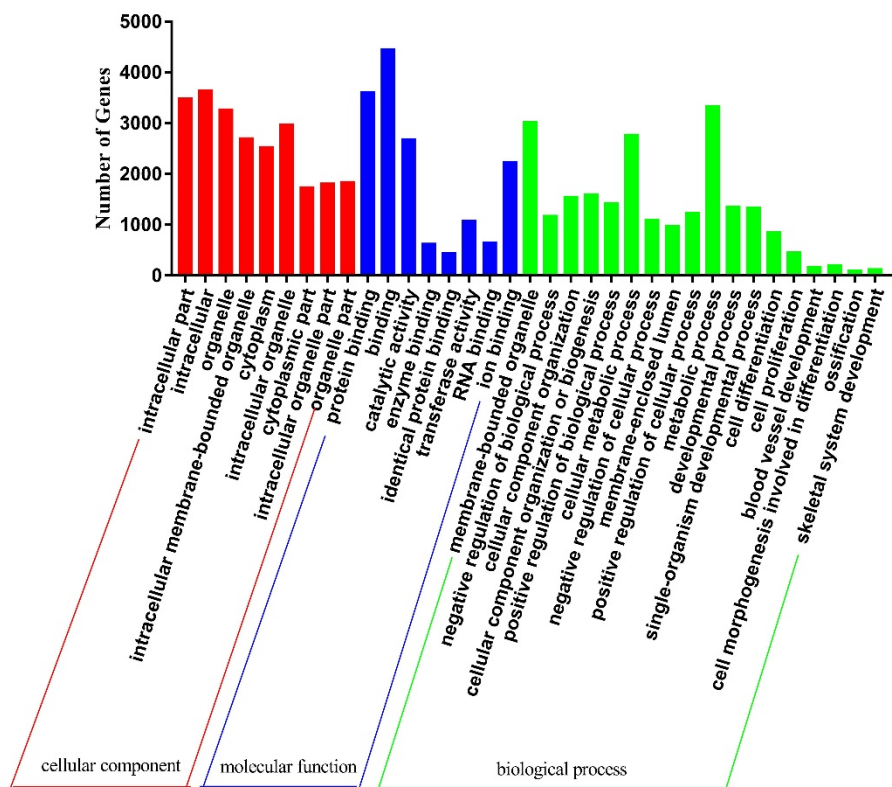


B

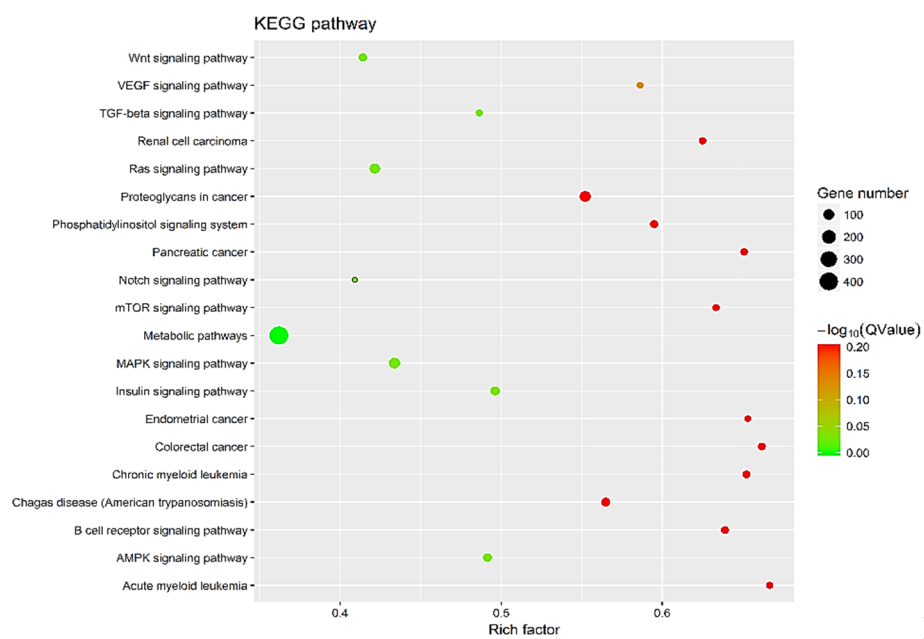


D





E



F

