a

MNDVSLRKVTEPDETQQRVRSGVTLKVMEYTYDEDLEELCPVCGDKVSGYHYGLLTCESCKGFFKRTVQNNKRYTCAENQECKIDKTQRKRCPFCRFQKCLNVGMRLEAVRADRMRGGRNKFGPMYKRDRALKQQKKALIRSNGFKLESTAPPPASPLQADYGFTGTLHTLPTISKSLLPSTPSSITPTDYEANLYGPPSLGMAMQSHVPLTTQYQYTAFPGRAIKAECPDYTSSPETLTGYPYPDMYPSASPQPPSLPPLVLELLRCDPDELVVQNKIVTHLQQEQNGRGRLEKPSTFSLMCRMADQTLFSIVEWARSCIFFKELRVGDQMKLLHNCWSELLVLDHIFRQVQHAKEDSILLVTGQEVELSSILSQAEGTLSSLVQRGQELAARLRVLQVDRREIACLKFLLLFNPNVKLLENQAFVEGVQEQVNAALLEYTLSAYPQFQEKFSQLLVRLPELRSLSTQAEDYLCYMHVSGEVPCNNLLIEMLHAKRACV

b

MLGDKAHGVTLKVMEYTYDEDLEELCPVCGDKVSGYHYGLLTCESCKGFFKRTVQNNKRYTCAENQECKIDKTQRKRCPFCRFQKCLNVGMRLEAVRADRMRGGRNKFGPMYKRDRALKQQKKALIRSNGFKLESTAPPPASPLQADYGFTGTLHTLPTISKSLLPSTPSSITPTDYEANLYGPPSLGMAMQSHVPLTTQYQYTAFPGRAIKAECPDYTSSPETLTGYPYPDMYPSASPQPPSLPPLVLELLRCDPDELVVQNKIVTHLQQEQNGRGRLEKPSTFSLMCRMADQTLFSIVEWARSCIFFKELRVGDQMKLLHNCWSELLVLDHIFRQVQHAKEDSILLVTGQEVELSSILSQAEGTLSSLVQRGQELAARLRVLQVDRREIACLKFLLLFNPNVKLLENQAFVEGVQEQVNAALLEYTLSAYPQFQEKFSQLLVRLPELRSLSTQAEDYLCYMHVSGEVPCNNLLIEMLHAKRACV

**C**

**Figs. 1 sf1 protein sequence information and marker map of Nile tilapia *Oreochromis niloticus*. a, b** 尼The protein sequence information of Nile tilapia sf1 (a: NM\_001279560.2) and sf1 transcript variant X1 (b: XM\_025911872.1). The red font and box marked the difference protein sequence between sf1 and sf1 transcript variant X1. The purple font and box are marked with the protein sequence information used in the western blot experiment in this work. **c** sf1 protein (55-65 kDa) was detected in Nile tilapia gonadal tissue sample.

a

b

Figs. 2. GO enrichment analyses of DE gene--DA protein pairs. **a** The GO enrichment of DE genes-DA proteins pairs in gonad tissues of male fish after sf1 transcription knockout. **b** The GO enrichment of DE genes-DA proteins pairs in gonad tissues of female fish after sf1 transcription knockout. GO term analyses of DE gene--DA protein pairs that was catalogued as biological process, cellular component, and molecular function. The abscissa represents quantity.



**Figs. 3.** **Network interaction of DE genes based on related DE gene--DE protein pairs.** **a** Network interaction of DE genes in male. Each node represents a gene. **b** Network interaction of DE genes in female.

a



b



**Figs. 4.** **The correlation analysis between gene transcription level and protein level in the top 10 KEGG enrichment pathways. a** Thecorrelation analysis between male fish gene transcription level and protein level. A, B, C, D, E, F, G, H, I, and J represent the top 10 pathways in the KEGG analysis, respectively. The calculation formula is: Log2FC (sf1 transcription knockout/ control). The abscissa is gene transcription levels of sf1 transcription knockout group and control group based on transcriptome sequencing; the ordinate is protein levels of sf1 transcription knockout group and control group based on proteome sequencing. **a** The correlation analysis between female fish gene transcription level and protein level. A, B, C, D, E, F, G, H, I, and J represent the top 10 pathways in the KEGG analysis, respectively.