Table S1. Primers used in quantitative RT-PCR (qRT-PCR) analysis.

Gene name	NCBI accession number	Primer sequences	Amplicon size (bp)
18S rRNA 5′		TACCACATCCAAAGAAGGCA [78,79]	245
18S rRNA 3′		TCGATCCCGAGATCCAACTA [78,79]	
ddit4 5′	XM_023413394.1	AAACTCCTGGAGCACATCGG	116
ddit4 3′		ATGCTCTCAAAGACAGCCCC	
Fosl1 5′	XM_023421640.1	AATGCCATCACATCCAGCCA	208
Fosl1 3′		CGTTTCTGCGCCTTGTTGAA	
Mmp13a 5′	XM_023417751.1	TGTCAACGGCATCCAGTCTC	121
Mmp13a 3′		GGTGACAGCATCCAAGACCA	
Nr4a3 5′	XM_023400814.1	GGGTTGAGGAGCTGCAGAAT	159
Nr4a3 3′		AGATTCGTTGAAGGCCCTGG	

Table S2. RNA-sequencing summary results of raw reads, clean reads, and values of Q20 and Q30.

Sample name	Raw reads	Clean reads	Clean reads (%)	Q20 (%)	Q30 (%)
C-N Skin	14666756	13893566	94.73	95.11	85.68
S-N Skin	15447566	14621780	94.65	95.10	85.64

C-N, fish fed with control diet; S-N, fish fed with silkrose-containing diet.

Table S3. RNA-sequencing summary results of mapping to reference genome.

Sample name	Clean reads	Number of unmapped reads to reference	Number of reads mapped to reference	Number of reads mapped to reference (multiple sites)
C-N Skin	13893566	5330340 (38.37%)	8098405 (58.29%)	464821 (3.35%)
S-N Skin	14621780	5684659 (38.88%)	8490849 (58.07%)	446272 (3.05)

C-N, fish fed with control diet; S-N, fish fed with silkrose-containing diet. Clean reads were mapped to reference genome of *Seriola lalandi dorsalis* (https://www.ncbi.nlm.nih.gov/assembly/GCF_002814215.1/) using hisat2 (v. 2.2.0) [42].

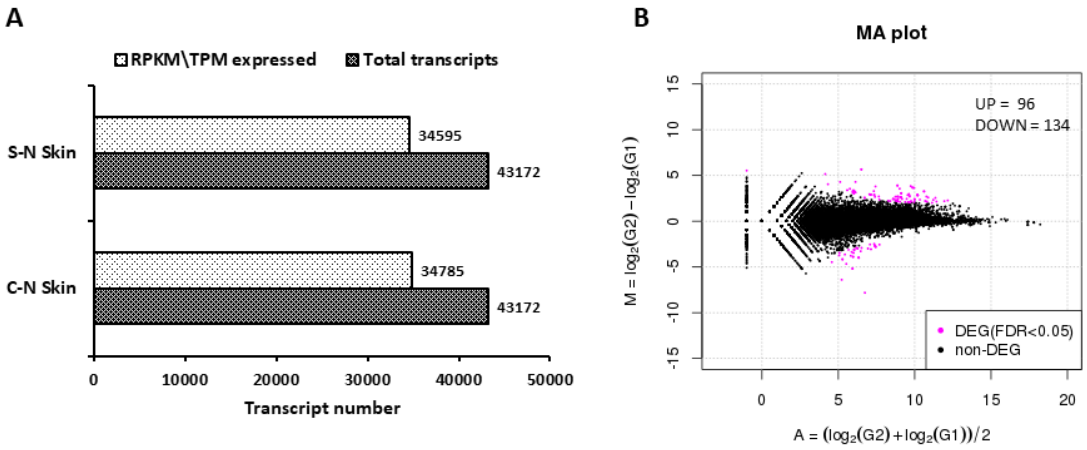

Figure S1. RNA-sequencing analysis of skin of yellowtail (*Seriola quinqueradiata*). C-N and S-N refer to fish fed with control diet and silkrose-containing diet, respectively. (A) Summary of expressed transcripts after normalization with RPKM and TPM. (B) Plot of differentially expressed genes (DEGs) in skin of yellowtail based on comparison between fish fed with control and silkrose-containing diets. Purple dots indicate DEGs, black dots indicate non-differentially expressed genes. In total, 134 genes were identified as DEGs, 96 upregulated and 38 downregulated genes. DEG analysis was calculated by the TCC (v. 1.26.0) package in R software.

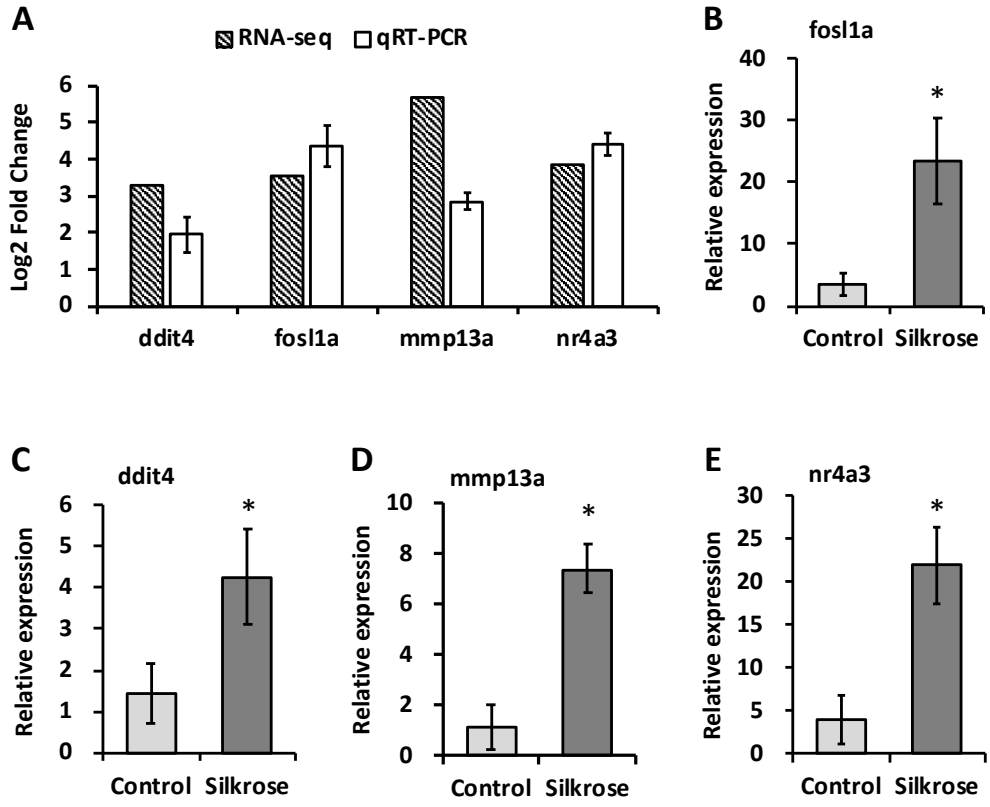

Figure S2. Confirmation of RNA-seq results by quantitative RT-PCR (qRT-PCR). (A) Comparison of relative fold changes of four selected genes between RNA-seq and qRT-PCR results in yellowtail skin. Relative mRNA expression of (A) DNA damage inducible transcript 4 (ddit4) gene by qRT-PCR; (C) FOS like 1, AP-1 transcription factor subunit (fosl1a) gene by qRT-PCR; (D) matrix metallopeptidase 13a/collagenase 3-like (mmp13a) gene by qRT-PCR; and (E) nuclear receptor subfamily 4 group A member 3 (nr4a3) gene by qRT-PCR. qRT-PCR values were normalized to 18S ribosomal RNA as endogenous reference using $2^{-\Delta\Delta Ct}$ method. Results are expressed as means ± SEM. Vertical bars indicate SEM of four samples ($n = 4$). * $p < 0.05$ versus control group.