Analysis of the *sericin*1 promoter and assisted detection of exogenous gene expression efficiency in the silkworm *Bombyx mori* L.

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Table S1. Statistical analysis of TFBSs on the three regions of the *Ser*1 promoter

Proximal region of the *Ser*1 promoter		**Middle region of the *Ser*1 promoter**		**Distal region of the *Ser*1 promoter**	
Potential TFBSs	Number (total=41)	Potential TFBSs	Number (total=87)	Potential TFBSs	Number (total=105)
BR-C Z	4	BR-C Z	2	BR-C Z	12
Croc	2	Croc	2	HSF	39
HSF	13	HSF	42	Dfd	18
Dfd	16	Dfd	16	Ttk	1
Bcd	1	Bcd	3	Hb	25
Ttk	1	Ttk	1	dl	3
Hb	4	Hb	10	CF2-II	5
		Ftz	3	GCM	2
		Abd-B	2		
		dl	1		
		STAT	2		
		CF2-II	2		
		Su(H)	1		

Table S2. Outcome of transgenesis

Transgenic strains	Microinjected eggs (G0)	Hatched eggs (Hatching rate, %)	G1 generation broods	*EGFP*-positive broods	Percentage of transgenic efficiency (%)
pBL1F	1751	89 (5.1)	47	8	17.0
pBL2F	2335	84 (3.6)	60	8	13.3
pBL4F	672	22 (3.3)	16	2	12.5
pBC2R	627	63 (10.0)	50	8	16.0
pBC3R	1320	154 (11.7)	21	5	23.8
pBC4R	950	96 (10.1)	40	6	15.0

Table S3. Integration sites of transgenic silkworms

Transgenic strains	Hit chromosome position	Hit scaffold position	Distribution of *piggyBac* insertions in genes	5'-flanking genomic DNA sequence	Vector	3'-flanking genomic DNA sequence
pBC2R1	Chr. 16	Bm_scaf 39	Exon	TTTAGATCTACCATTA**TTAA**	*piggyBac*	**TTAA**AAGAGGCTGGCGACA
pBC2R2	Chr. 21	Bm_scaf 7	Intergenic	TCTGTATTTGAGTTCA**TTAA**	*piggyBac*	**TTAA**GGGCTGGGCAAACGT
pBC2R3	Chr. 25	Bm_scaf 57	Intergenic	CGAAATTATATACCTCA**TTAA**	*piggyBac*	**TTAA**TAAGCTCTAAATTTTA
pBC2R4	Chr. 3	Bm_scaf 17	Intron	AATTAATACTTATTCA**TTAA**	*piggyBac*	**TTAA**TAAGTTTTACGAAGTT
pBC2R5	Chr. 21	Bm_scaf 7	Intergenic	ATAAGTATATCGTTGC**TTAA**	*piggyBac*	**TTAA**TATAATGTTAACAAAG
pBC2R6	Chr. 1	Bm_scaf 8	Intergenic	TTACTTGATTAATTCAC**TTAA**	*piggyBac*	**TTAA**CGGCGCTCATTACATA
pBC2R7	Chr. 10	Bm_scaf 253	Exon	ACTTTCTGAAGGGTCT**TTAA**	*piggyBac*	**TTAA**ACAATGATTTCAATAA

Table S4. Primers for study

Target genes	Forward primers (5'→3')	Reverse primers (5'→3')	Purpose
*Ser*1 promoter	GCACACACACTACATACCAT	GTTGGCGGTCTTTGGATCG	0.5 kb length *Ser*1 promoter cloning
*Ser*1 promoter	ATGCTCGTCTGTCAAGGGTCT	GTTGGCGGTCTTTGGATCG	2 kb length *Ser*1 promoter cloning
*Ser*1 promoter	CGGCTTCCAACGCCTTTGTTATT	GTTGGCGGTCTTTGGATCG	4 kb length *Ser*1 promoter cloning
FLuc	TAAAGACTTCAAGCGGTCAACTATG	TTATGTCCGGTTATGTAAACAATCC	qRT-PCR
RLuc	TTGGCACCTTCAACAATAGCAT	GCCTCGTGAAATCCCGTTAGT	qRT-PCR
EGFP	AGCAGAAGAACGGCATCAAGGTG	CGCTTCTCGTTGGGGTCTTTG	qRT-PCR
*Rp*49	TGCTCCCAAATGGATTCCGTAAG	CACGATCAGCTTCCGCTTCTTC	Reference gene for qRT-PCR
piggyBac left arm	CTTACCGCATTGACAAGCACGCC	GTTCTTTAGACGATGAGCATATCCT	Inverse PCR
piggyBac right arm	TATCTTTAACGTACGTCACAATATG	GGTCTGTATATCGAGGTTTATTTA	Inverse PCR