

1 **Additional file 1:**

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3 **Krüppel-homolog 1 exerts anti-metamorphic and vitellogenic functions in insects**  
4 **via phosphorylation-mediated recruitment of specific cofactors**

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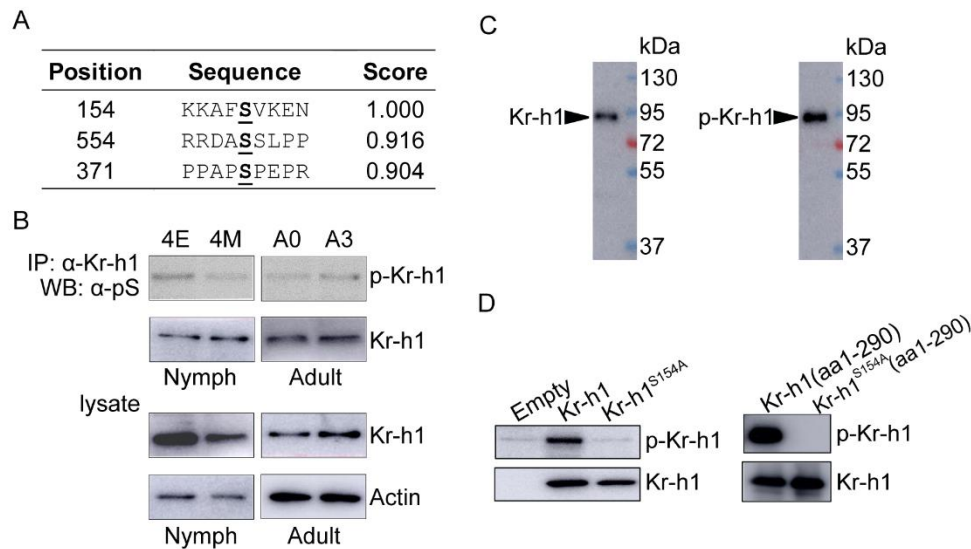
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22 **Additional file 1: Figure S1. Identification of Kr-h1 phosphorylation site.** (A) Top

23 three Kr-h1 phosphorylation sites predicted by the DISPHOS (V1.3) software. (B)

24 Immunoprecipitation (IP) and western blot (WB) showing the abundance of Kr-h1 and

25 phosphorylated Kr-h1 (p-Kr-h1) in the whole body of early (4E) and mid (4M)

26 penultimate 4<sup>th</sup> instar nymphs as well as the fat body of adult female locusts on day 0

27 (A0) and 3 (A3).  $\alpha$ -pS, phospho-(Ser) antibody;  $\alpha$ -Kr-h1, Kr-h1 antibody. (C) Western

28 blots with both anti-Kr-h1 and anti-p-Kr-h1 antibodies (arrows) shown in full extent

29 with molecular weight markers (color bands). (D) Verification of phospho-Kr-h1 (Ser<sup>154</sup>)

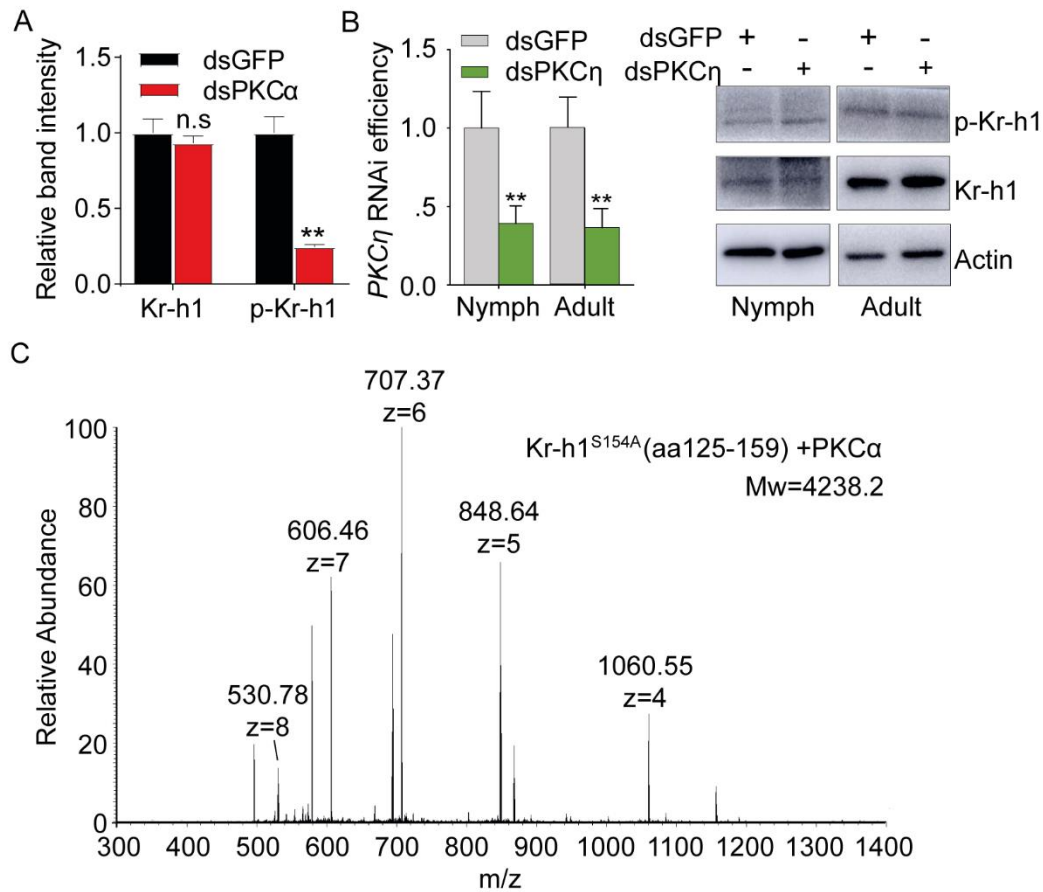
30 antibody specificity by western blots. Left panel: Flag-Kr-h1 and mutated Kr-h1<sup>S154A</sup>

31 expressed in *Drosophila* S2 cells treated with 10  $\mu$ M methoprene. Right panel: the

32 bacterially-expressed GST-tagged peptides of Kr-h1(aa1-290) and Kr-h1<sup>S154A</sup>(aa1-290)

33 preincubated with PKC $\alpha$ .

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36 **Additional file 1: Figure S2. Identification of kinase triggering Kr-h1**

37 **phosphorylation.** (A) Quantitative analysis of Kr-h1 and p-Kr-h1 band intensity in

38 western blots using protein extracts from the fat body of adult females injected with

39 dsPKC $\alpha$  vs. dsGFP controls (represented by Figure 1B right panel). \*\*,  $P < 0.01$ .  $n = 4$ .

40 (B) Effect of *PKC $\eta$*  knockdown on Kr-h1 phosphorylation. Left panel: *PKC $\eta$*

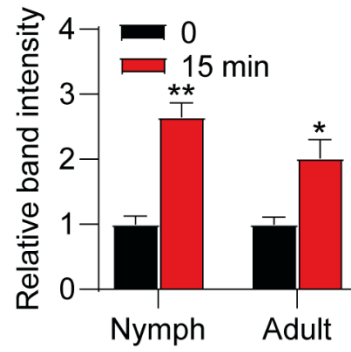
41 knockdown efficiency. Right panels: the levels of Kr-h1 and p-Kr-h1. Nymph, the

42 whole body of mid penultimate 4<sup>th</sup> instar nymphs. Adult, the fat body of 3-day-old adult

43 females. \*\*,  $P < 0.01$ .  $n = 8$ . (C) LC-MS/MS analysis of mutated Kr-h1<sup>S154A</sup>(aa125-159)

44 peptide preincubated with PKC $\alpha$ .  $m/z$  indicates the mass to charge ratio.

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47 **Additional file 1: Figure S3. Effect of 15-min exposure of methoprene on Kr-h1**

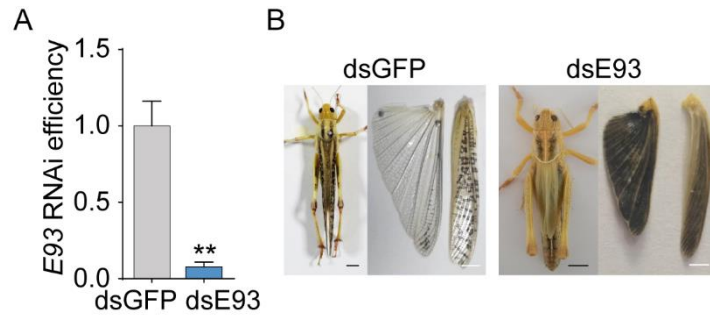
48 **phosphorylation.** Quantitative analysis of p-Kr-h1 band intensity in western blots

49 using the whole body of mid 5<sup>th</sup> instar nymphs and the fat body from newly-emerged

50 adult females treated with 100 µg methoprene for 15 min (represented by Figure 2B

51 and 2E, respectively). \*,  $P < 0.01$ ; \*\*,  $P < 0.01$ ;  $n = 3$ .

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54 **Additional file 1: Figure S4. Effect of *E93* knockdown on locust metamorphosis.**

55 (A) *E93* RNAi efficiency in the final instar nymphs. \*\*,  $P < 0.01$ .  $n = 8$ . (B)

56 Representative phenotypes of delayed adult eclosion (super nymphs) after *E93*

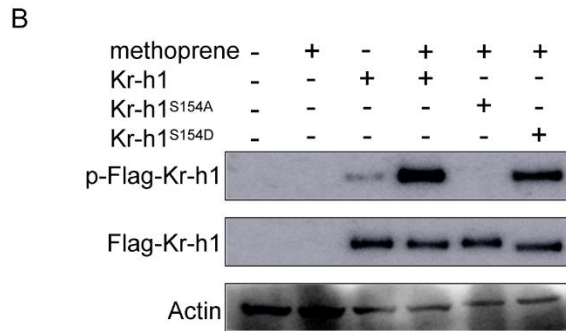
57 knockdown. Scale bar: black, 5 mm; white, 0.5 mm.

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A

<i>BmBroad</i>	-4464	TATCCG	TGACCT	ACGCTA	-4447
<i>BmE93</i>	-2844	CAACAC	TGACCT	TTCTCA	-2827
<i>BmSpo</i>	-1950	TAAAAC	CGACCT	TTAATT	-1933
<i>DmSpok</i>	-85	TGCGTT	TGACCT	ATGAAA	-68
<i>LmE93</i>	-623	CTCTTA	TGACCT	TTCCGG	-606
<i>LmRL36</i>	-1647	AGGAAC	TGACCT	TCCACC	-1632

KBS



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60 **Additional file 1: Figure S5. Responsiveness of Kr-h1 phosphorylation to JH. (A)**

61 Alignment of DNA sequences containing the core KBS motif in the upstream of *Br-C*,

62 *E93* and *Spo* from the silkworm *Bombyx mori* (*Bm*), *Spok* from *Drosophila*

63 *melanogaster* (*Dm*) (references 13, 17 and 18), as well as *E93* (GenBank: MT081312)

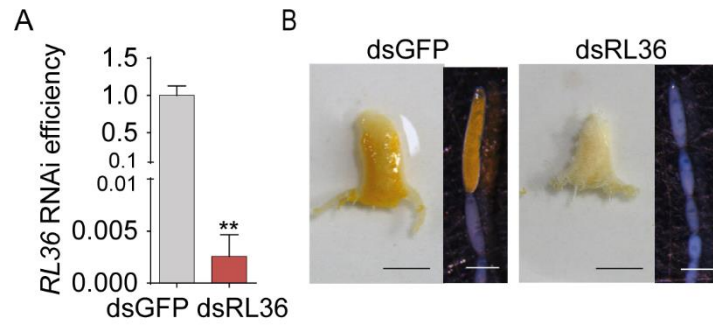
64 and *RL36* (GenBank: MT081313) from *Locusta migratoria* (*Lm*). (B) Western blot

65 showing the expression of recombinant Flag-Kr-h1, Flag-Kr-h1<sup>S154A</sup> and Flag-Kr-

66 h1<sup>S154D</sup> in *Drosophila* S2 cells with or without 10  $\mu$ M methoprene treatment. p-Kr-h1,

67 phospho-Kr-h1 (Ser<sup>154</sup>) antibody. Flag-Kr-h1, Kr-h1 antibody.

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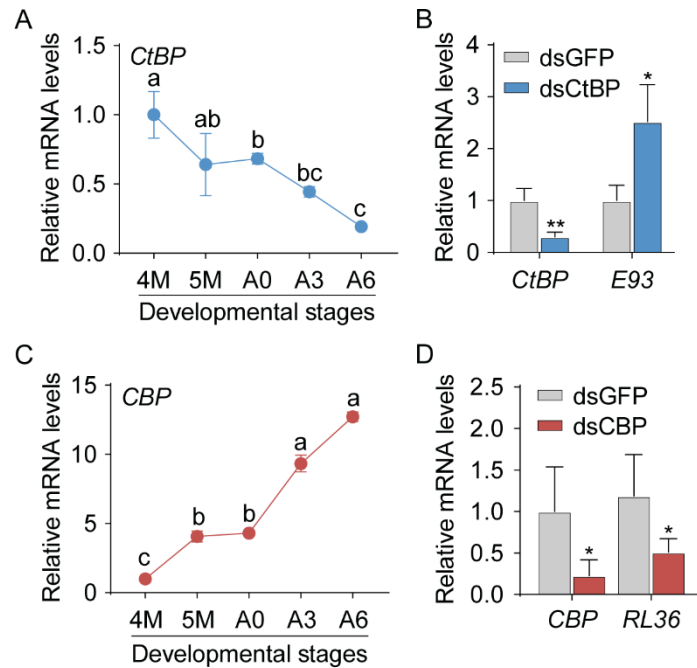
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70 **Additional file 1: Figure S6. Effect of *RL36* knockdown on locust reproduction. (A)**

71 *RL36* RNAi efficiency in the fat body of 6-day-old adult females. \*\*,  $P < 0.01$ . n=8. (B)

72 Representative phenotypes of ovaries and primary oocytes after *RL36* knockdown.

73 Scale bar: black, 1 cm; white, 1 mm.



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75 **Additional file 1: Figure S7. Effect of CtBP or CBP knockdown on E93 or RL36**

76 **expression.** (A) Developmental profiles of CtBP in the whole body of mid 4<sup>th</sup> (4M) and

77 5<sup>th</sup> (5M) instar nymphs as well as adult females on day 0 (A0), 3 (A3) and 6 (A6).

78 Means labeled with different letters indicate significant difference at  $P < 0.05$ .  $n = 8$ . (B)

79 Effect of CtBP knockdown on the expression of E93 in mid 4<sup>th</sup> instar nymphs. \*,  $P < 0.05$

80 and \*\*,  $P < 0.01$ .  $n = 8$ . (C) Developmental dynamics of CBP in the fat body of 4M and

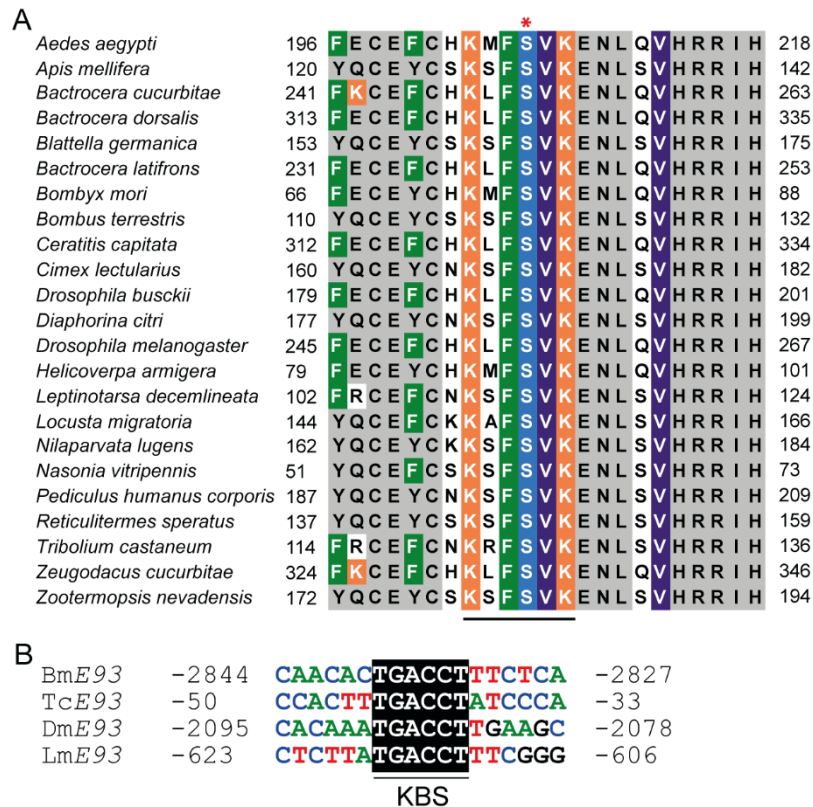
81 5M instar nymphs as well as A0, A3 and A6 adult females. Means labeled with different

82 letters indicate significant difference at  $P < 0.05$ .  $n = 8$ . (D) Effect of CBP knockdown on

83 the expression of RL36 in the fat body of 3-day-old adult females. \*,  $P < 0.05$ .  $n = 8$ .

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86 **Additional file 1: Figure S8. Alignment of the 3<sup>rd</sup> zinc-finger domain of Kr-h1 and**

87 **the partial promoter sequences of *E93* with KBS motifs.** (A) Alignment of the 3<sup>rd</sup>

88 zinc-finger domain of Kr-h1 from 23 insect species with available cDNA sequences in

89 NCBI database. Numbers donate starting and ending positions. Asterisk indicates the

90 conserved serine residues homology to Ser<sup>154</sup> of locust Kr-h1. Underlined amino acids

91 indicate the conserved motif recognized by PKC. (B) Alignment of DNA sequences

92 containing the core KBS motif in the promoters of *E93* from *Bombyx mori* (Bm),

93 *Tribolium castaneum* (Tc) (GenBank: XM\_015983777), *Drosophila melanogaster* (Dm)

94 (FlyBase: FBgn0264490) and *Locusta migratoria* (Lm) (GenBank: MT081312).

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**Additional file 1: Table S1. Primers used for cloning and gene expression**

<b>Gene</b>	<b>Forward primer (5' to 3')</b>	<b>Reverse primer (5' to 3')</b>
<i>Kr-h1</i>	ATGGTGGGCTACTTCAACGG	TTACGAGGCGCCCGCGTAGT
<i>Kr-h1</i> (aa1-290)	ATGGTGGGCTACTTCAACGG	GCTGCAGATGGTGCACCTGT
<i>Kr-h1</i> (aa89-312)	TCCTTCTGCCAGAAGACGTT	GGGGTGCTGCTGCTCCGAGT
<i>Kr-h1</i> (aa291-591)	GAGACGTTTCGCCTCCAAGAA	TTACGAGGCGCCCGCGTAGT
<i>CtBP</i>	ATGGACAAGCGCAAGATGCT	TTAATGTACTTCTGATGGCTC
<i>CBP</i>	GATGGAGTGGATGTATGCTT	TTAACCAGGAGGATTCCTTTC
<i>BmKr-h1</i>	ATGGAATCATTACCTATTTT	CTATGATTCTGTAGCTGGCG
<i>DmKr-h1</i>	ATGGTTTACTATTCCGCCA	CTAGGAGGCCTTGCGGAA
<i>TcKr-h1</i>	ATGCCGAAATGGTCGGT	ACGACGCTCCTGCATATTG

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98 **Additional file 1: Table S2. Primers used for site-directed mutagenesis**

<b>Mutation</b>	<b>Primer sequence (5' to 3')</b>
Kr-h1 <sup>S154A</sup> -F	AAGGCCTTC <u>GCC</u> GTCAAGGAGAACCTGAGCGTGCACCGGCG
Kr-h1 <sup>S154A</sup> -R	TCTCCTTGAC <u>GCG</u> GAAGGCCTTCTTGCAGAACTCGCACTGG
Kr-h1 <sup>S371A</sup> -F	GCCGGCGCC <u>GCG</u> CCCGGAGCCCCGCCTCGAACCCCGCCTCG
Kr-h1 <sup>S371A</sup> -R	GGGCTCCGG <u>GCG</u> CCCGGCGCCGGCGGGAGGTAGGTGCTGTT
Kr-h1 <sup>S554A</sup> -F	CGCGACGCC <u>GCC</u> TCGCTGCCGCCCCGCAAGCGCTGCAAGG
Kr-h1 <sup>S554A</sup> -R	GGCAGCGAG <u>GCG</u> CGGCGTCGCGGCGGTTCGGGCGACGCGGGGG
Kr-h1 <sup>S154D</sup> -F	AAGGCCTTC <u>GAC</u> GTCAAGGAGAACCTGAGCGTGCACCGGC
Kr-h1 <sup>S154D</sup> -R	TCTCCTTGAC <u>GTC</u> GAAGGCCTTCTTGCAGAACTCGCACTGGT
BmKr-h1 <sup>S76A</sup> -F	AAATGTTT <u>GCT</u> GTGAAAGAAAATTTGCAAGTACACCGTC
BmKr-h1 <sup>S76A</sup> -R	TCTTTCAC <u>AGC</u> AAACATTTTATGGCAATATTCACATTCA
BmKr-h1 <sup>S76D</sup> -F	AAATGTTT <u>GAT</u> GTGAAAGAAAATTTGCAAGTACACCGTC
BmKr-h1 <sup>S76D</sup> -R	TCTTTCAC <u>ATC</u> AAACATTTTATGGCAATATTCACATTCA
DmKr-h1 <sup>S255A</sup> -F	CACAAGCTGTT <u>GCC</u> GTGAAGGAGAACCTCCAGGTGCAC
DmKr-h1 <sup>S255A</sup> -R	CTTCAC <u>GCG</u> GAACAGCTTGTGGCAGAACTCGCACTCGAA
DmKr-h1 <sup>S255D</sup> -F	CACAAGCTGTT <u>GAC</u> GTGAAGGAGAACCTCCAGGTGCAC
DmKr-h1 <sup>S255D</sup> -R	CTTCAC <u>GTC</u> GAACAGCTTGTGGCAGAACTCGCACTCGAA
TcKr-h1 <sup>S124A</sup> -F	AGCGATT <u>GCC</u> GTTAAAGAAAACCTTGAGCGTTCATCGAAGA
TcKr-h1 <sup>S124A</sup> -R	TCTTTAAC <u>GCG</u> GAATCGCTTATTGCAAATTCGCAACGGAA
TcKr-h1 <sup>S124D</sup> -F	AGCGATT <u>GAC</u> GTTAAAGAAAACCTTGAGCGTTCATCGAAGA
TcKr-h1 <sup>S124D</sup> -R	TCTTTAAC <u>GTC</u> GAATCGCTTATTGCAAATTCGCAACGGAA

**Additional file 1: Table S3. Primers used for qRT-PCR, RNAi and ChIP**

	<b>Gene</b>	<b>Forward primer (5' to 3')</b>	<b>Reverse primer (5' to 3')</b>
<b>qRT-PCR</b>	<i>Kr-h1</i>	AGTGCCAGGTGTGCTCCAAGA	CGAACGACTTGCCGCAGATGT
	<i>E93</i>	CAGGCTGGCGATGACAACA	AGTCCGATGGCGTGCTACT
	<i>RL36</i>	ACGAATGTGTGTGCCAAGC	CGTCCGTCAAGACTAAAGGG
	<i>PKC<math>\alpha</math></i>	AAGGCTCGGTTGTGGAACA	AGGAGGTTGGACTTCACGAT
	<i>PKC<math>\eta</math></i>	AGCAACCAGCAACAAGAGGA	TCGTTCTGCCAGCATCACTT
	<i>CtBP</i>	GCGGTTGGTGCCCTAATGTG	TGAGGCAAAGGGTGGTGTCT
	<i>CBP</i>	TGCGTGTCAATGCCGTGATG	CTGCTGAACCTGCTCCACCA
	<i>Rp49</i>	CGTAAACCGAAGGGAATTGA	GAAGAAACTGCATGGGCAAT
<b>RNAi</b>	<i>Kr-h1</i>	GTCAAGGAGAACCTGAGCGTGC	TGCTGCTGCTCCGAGTGGCT
	<i>PKC<math>\alpha</math></i>	CGTTCCTCCCTTAACCCTGT	AACCTTTCCAAAGCTGCCTT
	<i>PKC<math>\eta</math></i>	GCAGGCGTGTCCATCAAGTA	GGAGGTGTGAGCTTGTCTGT
	<i>E93</i>	AGGCTGGCGATGACAACACT	GCTGCACGGCGAGTTCCTAA
	<i>RL36</i>	GAAGGGACACCGGACGACAA	GTGTGTGCCAAGCCTCCTCT
	<i>CtBP</i>	TGGTGAACACAGCACGAGGT	ACGGAGTGTGGCACTTGGTC
	<i>CBP</i>	TGCGTGTCAATGCCGTGATG	CTGCTGAACCTGCTCCACCA
	<i>GFP</i>	CACAAGTTCAGCGTGTCCG	GTTACCTTGATGCCGTTC
<b>ChIP</b>	<i>E93</i>	CCGTGGCAAGCTCGTTTT	GCACTTGGGGCAAACCTGT
	<i>RL36</i>	GGAGAGTCAGTAGTAACTG	CAGCAGCCAAACTCTCTT

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