ORIGINAL ARTICLE



Heme-Peroxidase 2 Modulated by POU2F1 and SOX5 is Involved in Pigmentation in Pacific Oyster (*Crassostrea gigas*)

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Abstract Q Q 9 9 2 2 9 9 9 Ø 29 Q, 929 9 e, 99 9 22 C 2 % **ς** 9 % 99049, 9 9 29 9 **9**2 . F **Q Q** 9 9 9 9-9 £ 299 9 299 (CgHPX2),9 CgHPX2 29 P a 9,00 **19 Q** 2 2 2 2 VE Crassostrea gigas. T 💯 🥰 9,00 √**2.00** 9 2 2CgHPX2 Q B-29 99 9.00 2 29 y**92** . I **9**2 . y⁰ Ø, 29 9 2 2 Q 2 202 Q Ø 99 0 CgHPX2 99 99 9 29 9 0 9 29 A Œ 29 2 $\sqrt[n]{g}$ %**@** 2 29 v**e** 99 9 29 9 0 e, 29 £9. I £99 8 9 900 99 Q98 8 29 2 9 92 9 VOD Q CgHPX2 2 2 29 y 9 2 2 e, T 9 9 CgHPX2 Q 29 29 É 2 e, 2 9,909 29 %I 2227 5 ff 9 9 9 9 CgHPX22 Q 98 9 9 9 9 2 2 9 29 2 F 29 9 8 99 49 9 2 2 9 2 2 POU £ 1 (*POU2F1*), **Q**22, **2 Q** SR8 2 2 2 5 (SOX5) 99 2 2 2 2 e, 2 CgHPX2 9 9 2 2 1229 9 9 . A **Q** CgPOU2F1 2√6 9 9 . T9 9 9 9 9 9 9 2 2 2 CgSOX5 RNA 12 99 9, 29 CgHPX2 999 99 QQ 2 92 2 929 39 CgSOX5 292 2 22 Q 2 2 299 9,00 99, 9 00 29 2 2 2 9 2 Q Qe, 922.

Keywords CgHPX2 T & 2 9 12 M = D, 9 2

Introduction

29 QD 9 Q q ę, 9-2 D/9 0 29 2 2 Q 2 £22 ff 9.9 2,29 2 y²2003). S 2992 (D.92.2019; P 90 999 9 2 29 Ø 29 2 9 2 20 2 NØ 2016; B **Q**(F.

L 92 . 2021; 9 2009). M **£**2 B 9 9 q 29 Q9 Q e, £2 § 292 29 ØØ 909H 99, 9 -2 8 9 9 2 29 9 22 9,9 Q . S.9 0 **Q**2 9229 98 9 9 12 T 99 **99 9** 9 99 9 29 9 199 Q9 Q Ø **29**2 % 92 q 9 Ø 2017). O 29 , 9 Q29 02 909 9 2 99 99 9 29, Ø 2 q 9 99. (A 9 9 9 9 2 . 2019). %29 9 0 09 0 9 M . 9 65 (B 5 62 5 5 2 . 2009; B. 92 . 2014). Of 9 % Q 9 9 8 2 29 q Ø 22229 **E** 2**9**29 **E** S 9 10 9 9 у⁶29 £, 29 9,29 2 29 29 22



Materials and Methods

Sample Collection

O9-\$7 - P \$90 999 999 y 24 **2**C 9 2 2999 9 92 y 2 (ISH). 9929 99 99 99 9 2, 92, , 929 19, 11,92-9 29, 929 280 27C 999 2 RNA & 2 . S 9 & 9 2 9 9 9 9 9 99 9 2299 **дς** Е % (2 99 **1**). 8 9899 29 92 ,2 9,9 %D-Q 9 9, 9 D-Q 9 **٩**, U 9, 9, 9 9, 92, 9, 2, 7, 9, 2, 9 Q 29 999 T9S1.L Q 9Q99 25 2 92 5 25 Q 5 Q 22 QQ 5 Q 5 5.

RNA Extraction and Real-Time qPCR

9 **√2** € E PCR 9 2 2 9 Q(L 9 Q . 2021). $(ef1\alpha)$ Q \mathfrak{Q} 2 20 - **9**% **£** -9,9 \mathfrak{L} 1- $(efl\alpha)$, 2 1 (arf1), 99 9 9 9 9 9 9 9 9 (gaph) 99 **g g** 999 99 2 (H 92.2016). T.99 299 98 y⁶29 2 CT 92 . A 29 2 Q. Q G P P Q 8.0 \% 9 - \% ye, 9 9 9 9 9 ₽ - ÿ[®]ANOVA 9 9 9 29 Q QD 99 9Q 99 099 02202 2P < 0.05.

Identifying and Cloning the Coding Sequence of *CqHPX2*

yPCR **g** T.9 CgHPX2 9 9 9 Ø e, 2 %1 e, 9 9 9 29 N 2 C 2 B 2 (NCBI, 12 9// 9 **99** : LOC105324712). T.9 **99** -9 9 9 9 9 9 <u>99</u> 2 9 & P 2 M & 9 -T 9 S2. T.9 PCR &9 F \mathfrak{S} \mathfrak{D} NA \mathfrak{S} \mathfrak{S} $(V \mathfrak{S}, \mathfrak{S}, C)$ \mathfrak{L} \mathfrak{L} **2**2 9 9 9 9 9 √ 29 Q 2 PCR 1.5% g 999 2 900

Bioinformatics Analysis of CgHPX2

T9 899 2 2(I) 9 9 2(M) 9 9 9 9 9 9 9 9 9 9 I/M T 229 E PAQ 29 (12 :// 9 9 9 /). T.9 **9** 9 Q CgHPX2 99NCBI (₩ **½**// 9 8 29 CD-Si 2 . . . /S2 29/ / Q.). T9 Q 29 2 2 9 29 29 99 9 y⁶P. y⁶ 2 (. ₩ :// $. Q /_ . y = 9.$ ТĢ **9** 9 9 9 9 9 9 9 9 9 (Ly B & L & S S & CA) 29 C 92 y⁶ESP 23.0 (♣ 9 P 2 9 2014). T 9 √ 992 299 299 9 9 MEGA 7.0 (K 92.2016) & 29 9 (ML) 92 Q **2** 1000 1992 9 20

RNA Location Pattern Analysis of *CgHPX2* by in Situ Hybridization

T **99**5 **9 9**2 **9** 2 (TISH) 9 2 22 y RNA ỹ° 2 (ISH) 99 **§** 2 £**1** € 22929 0 99 299 92 9 Q9 2 9 V.T Q 29 Q 9 Q9 RNA 9009 DNA 9 9 9 9 9 9 9 Ø T 9 S2 2 9929 2 T7 9 9 9 (GAT CACTAATACGACTCACTATAGGG). T. 9 PCR 99 9 DNA 2 $\mathfrak{L}(T.9, USA)$.

2(R . 9, S 29). T. 9 TISH Q 9 9 9 Q A 2 2 e , y 15 % 2 , 29 🗗 2 2 NBT/BCIP & 2 (R 9, S 29) 9 9 29 24 2C 9 2 9 29 988,290.5%9 & & & 29.82 29.85 F y[%] **1**2 V & 99 6 8 ISH, 299 K (S 9-99 9 2 C.) £ 9 2 2 (H 9 9 2 . 2015). T. 9 9 2 9 9 9 Q 9 9 999 9 9 99 (L 9 2 . 2021; 8 9 9 2 . 2021). A 29 TISH ISH 9 6 9 9 9 9 9 9 (O y 9 2 DP80 **Q** J

Luciferase Vector Construction and Site-Directed Mutagenesis

T 9 2 5 29 9 99, 99 29 25 ff g 9 9 CgHPX2 99 Q 9 2 GL3-B & 9 2 (P 9 , USA) & C E 9 & II O 9 SQ C $K \mathfrak{L}(V \mathring{y}^{6}, C)$). S 5 9 9 2 $(P1: 2011_+ + 216, P2: 1726_+ + 216, P3: 1519_+ + 216,$ P4: 1221_ +216, P5: 453_ +216, P6: 351_ +216) CgHPX2 99 99 9 29 02 2 C. gigas 9 DNA & DNA **2** . I 2 , -QQ 9 9 299 9QQ 9 0 2 29 Q Q DNA3.1 9 2 (P 9 , USA) 9 9 Q 2 $\sqrt[4]{2}$ CDS $C_gPOU2F1$ C_gSOX5 2 2 -9 2 DNA3.1 9 2 . T. 9 29 - 9 2 29900 D 2 99 , 9 2 29 29 0 Q2 2 Q M 2E 9 Q M 2S F Q 2M 2 9 9 Q Q 2V2 (V y 9, C). A 29 & & 92 9 99 9 **%9** 9 **900** 29 9 9 9 9 9 Ø2 √ 9 T 9 S2.

Cell Culture, Transient Transfections, and Dual-Luciferase Reporter Assays

HEK-293T 9 Q 9 9 9 2 9 DMEM (S q g (Hy) q , USA)Q 9 9 9 2 10% 9 2 905, 2 % 2 2 9 2 2 1% 1 🕈 9 (H \mathring{y}^{0} 9, USA) 237 $\rat{2}$ C 2 5% CO₂. T. 9 9 $\rat{2}$ 9 9 9 9 2 9 2 24- 9 **Q**(CORNING, USA) ff 9 70 90% 9 & CG & 9 9 9 & & 9 29 9 9 0 9 2 9 3000 (I 2 9 , CA, USA) 2 29 29 & & 2 RT9 RL-TK & (P & , USA) & -2 & 6 Ø 9 2 2 9 2 9 2 9 **Q** 9 2 **Q** 2 , **Q** 500 **Q** 2 2 9 2 9 2 **2** 9 9 9 -2 **2** 10 RL-TK 2 24- 9 9 9 9 9 9 9 9 9 P



9 CgPOU2F1 *CgSOX5*, 250 2 DNA3.1 9 9,00 9 2,250 € GL3-B € 9 -99 8 **RL-TK** Q 9 % QQ Q 9 24- 9 9 9 9 9 **9** . L . A 🛭 9 e, , 9 0 48 Я **9**9 2 99 **Q**9 2 DPBS (S , C.) 9 g ygg 9 (P 9 , USA). 29 Ø F 9 ffv° R 9 8 2 25 2 9 9 9 9 ¥ 9 8 9 **9 99 9 99 99** (P **9** . USA) 29 9,09 9 99 229 2 2 (F 9 fty) 9 8 2 2/° R 9 8 y 9 - y ANOVA & G . P 2 2/9 ý°G P **Q** 8.0.

Subcellular Localization of POU2F1 and SOX5

T.9 9 9 9 CgPOU2F1 CgSOX5 Ø Q 2 299 9 2 9,00 EGFP-1 (g 9,00 GFP &) **9** . T. 9 HEK-293T 9 **₽** 8 2 29 2 C POU2F1- EGFP-1 (IS , USA) 992 99 9 C SO \$5- EGFP-1 9 29 9,00 9 2 2 48 , 29 9 9 9 9 9 2 2 -2- 9 % 9 (DAPI) (B) y 2 9, C. 4,6-**%**0 25 9 00 T.9 9 **Q**2 999 2 - -90 2 Q 9 19 TCS SP8 STED 3 🐔 ... 2 LS 2 S 9 10 2 9.P 9 0 0 Ø 2 **Q**2. 2 9 99 T 9 S2.

RNA Interference Experiment

RNA 9 9 9 99 99 **Q**RNA9 9,00 ${\bf g}_y^{\%}$ 2 **9**2 y **9**9 9 22 09 8 2 y (F) 92 . 2019). D. Я 29 **9** 99 9 ,9 22992 2 **9** (>200.) **9**2 U Qy9 **9** 2 29 9/ **BRNA**-Ð 2 9_ . T. 99 **Q**RNA-99 E. coli **Q**2 HT115 (DE3) 2 2 99 **Q Q**(CgPOU2F1-₽ & 9 **9**2. **9** ỹ⁄₀ -D-L4440, CgSOX5-L4440, EGFP-L4440) 2 **Q** 2 **Q** 9 (IPTG). T 9 *EGFP*-L4440 \mathbf{g} y o 29 2 y. A 9/ QD. 8 9 29 9 0 2 2 100 8 9 2 9 2 2 25, 000 **9 Q** Platymonas subcordiformis 98 98 99 99 9 2 90 9/9-2 2 299 . A 🖁 🥱 2 IPTG, Q Q 9 9 9 9 9 9009 9 P. subcordiformis 9 29 . L

Results

Bioinformatics, Homology, and Phylogenetic Analysis of *CqHPX2*

 $A \mathcal{Q} = GC_gHPX2 + G$ 89 9 29 29 C. gigas Q e, 2 S. T.9 CgHPX2 **Q** 2 T 9 S3. T.9 9 DNA 8 9 9 *CgHPX2 Q*11,219 2 129 Ø 11 2 2 T.9 2 9 9099 **Q**2 GT-AG 9.T.9 9 2 DNA CgHPX2**@**3301 5 UTR, 566 £ 101 3 UTR, 2634 **ORF** QT9 9 9 877 8 e, CgHPX2 **Q**98.77 D Q99 2 2 **2**(I) y 92 29 9.49. T.9 229 Ø Ð Q Q 2 3% 92 92 **Q**(F . 1A). T.9 9 90 1 2 y 92 29 HP **♦**2 8 Q Q B 2 A, \mathfrak{L} 9 9 33% 9 \mathfrak{L} \mathfrak{L} 2 \mathfrak{L} Я (F . 1B). $\sqrt[8]{9}$ 9 2 99 CgHPX2 Т 9 9 \$ 9 90 29 99 90 B e, 29 9 9 9 9 2 54 9 9 9 9 9 q Oi -(Crassostrea virginica, P 022291683.1; Pecten maximus, P 033758659.1; Mizuhopecten yessoensis, ₱ 021358145.1; *Lingula anatina*, ₱ 013419078.1; *Octo*pus vulgaris, P 029656077.1; Amphibalanus amphitrite, KAF0313953.1; Bemisia tabaci, ♣P 018902871.1; Daphnia magna, ♣P 032798431.1; Rhopalosiphum maidis, ₱P 026811832.1). \$\frac{9}{9} \quad 9 9 2 CgHPX2 2 e, 29 29 922 9 Ø 9 9 99 9 9 9 9 99 99 Ø (F . S5). P % 9 9 2 VQQ Q9 9 9.00 9 29 2 yo q q Q 9 2 99 *CgHPX2* 29 9 2 2 T.9 99 9 90 9 0 9 T 9 S4. P 3 9 9 9 2 √**200** 9 2 2CgHPX2 9 9 **99** 9 **Q**(99% **Q** 29 Ø۶. 29 Q Q9 9Q 99 **92** 9 2 9 29 (F . 1C). T.9 9 9 Q -9 B 8 2 Ø y**99** HP **♦**2 9 ,2929 2 29 **Q**. c, 9 8 **Q**2 2 8 Q

Expression Profiles of CqHPX2

T 992 929 9 9 29 C_gHPX2 9 9 29 C_gHPX2 9 92 C_gHPX2



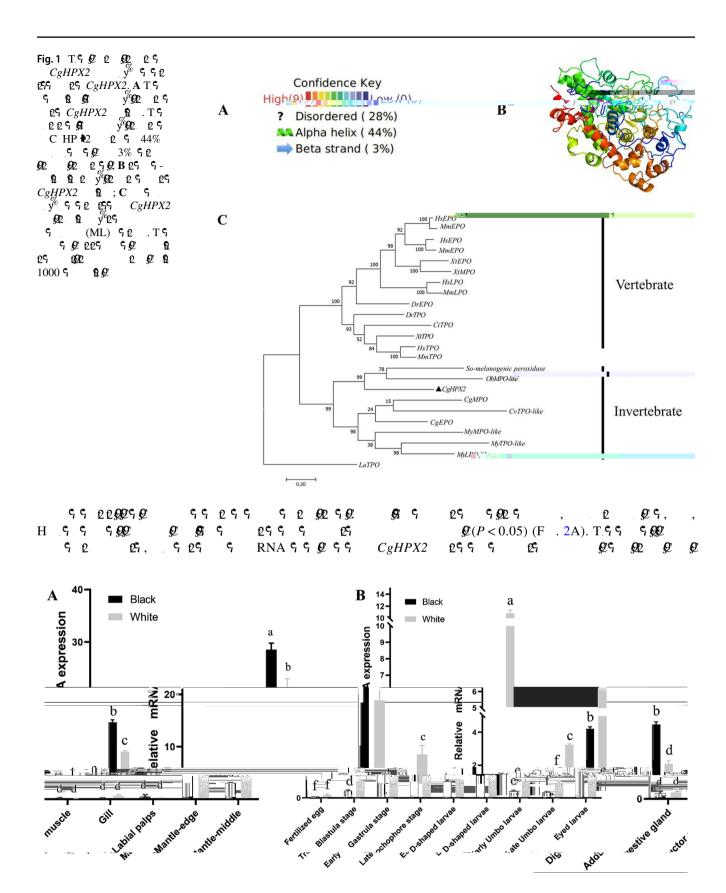


Fig. 2 T.9 RNA9 9 0 9 CgHPX2. A

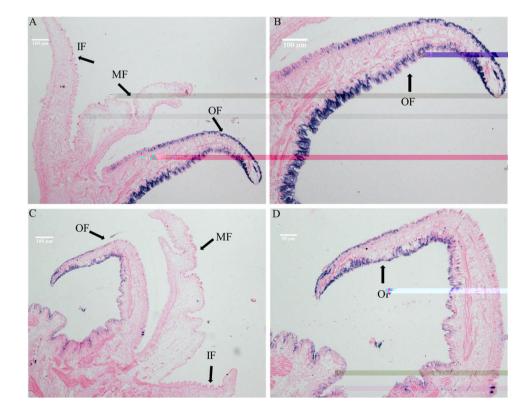
2 % Q 9 2 2 29 22 2 M 9 9, **Q**9 **Q** 99 289 2 25 29 **9**) **9** (F . 3). I 29 9 29, 29, 29 . . I Ø 9 8 8 29 9 29 **9 9 6**% 9 9 2 1/92 9 2 29 99 2 **9 9**9 . ₩₋ 99 299 9 2, CgHPX2 \mathbf{D} RNA9 999 90990 **9**) (F . 2B). T 99 98 Q9 **Q**2 **Q**(9 **g g** $\sqrt[9]{}$ Q CgHPX2Q2 9. e, 9 92 9, 299 22 9,00 2 %. CgHPX2 9 09 99 QQ 9 (P < 0.05). A **9 2 Q**2 9 92 9, 299 CgHPX22 9,00 29 9,29 & 2 B & CgHPX2 RNA9 9& y ISH 99 yg 9299 9 (F . 4). T.9 Q29 Q 2 9. I 2 09 Q9 9,29 Q29 Q Q98 8 29 2 **92** (F . 4-I-E). I D-**9** 9 ۹, 9 92 9 99 e, 9.29.09 **Q**2 Q29 Q 999 988 ν 29 299 9 29 £ (F . 4-I). C e, 2 9 (F . 4-II), 29 **9**2 2 25 5 ÿ92 9,9 9 2 2 900 29 9 92 9. 99 2 2 29 9 -2 9 PCR 9 9 29

The Sequence Analysis of the 5 -Upstream Regulatory Region of *CgHPX2* Gene

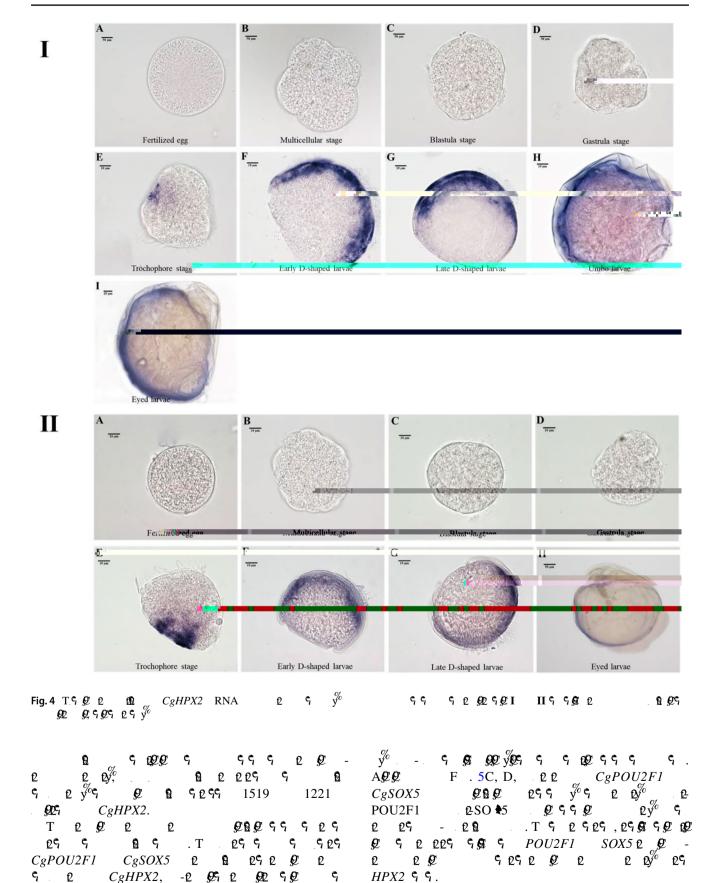
T.9 2227 5 **f**f 29 C. gigas 9 9 2 S. P 9 9 9 9 Q 9 2 229 2 Q 2 2Q 2Q Q Q 2 216 29 92 2 ATG, 29 9 9 92TATA **Q Q** 2 730 . P **Q** 2 2 **Q** 2 9 *POU2F1*, *SOX5*, . 2 - 99 QQQ 2 (MITF), AMP 9 & 9999 9 -2 **Q** (CREB), GATA-3, **Q** (F . 5A). T. 9 **Q** Q 2 99 9 99 29 2 2 2 CgHPX2 9 9. 9 2

Identification of the Core Region of the *CgHPX2* Promoter and Key Transcription Factor

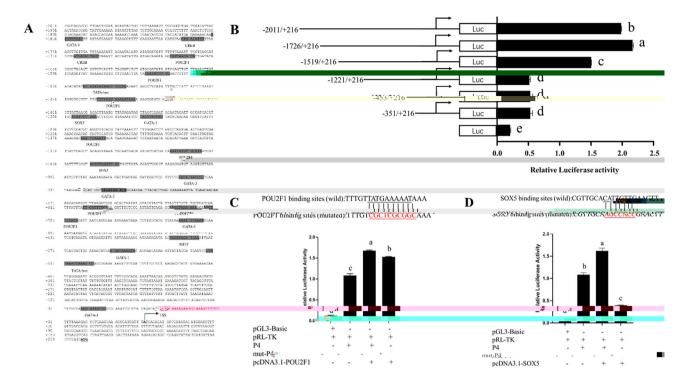
9**9** 229 2 **9** 2 2 29 2 9 129 5 ff . 2 2 99 29 99 9 9 2 GL3- Q 9 -29 2 8 2 2 2 8 2 ₽ HEK-293 T 9 ₽ 2 2 0% **QQ** 2y 9 9 **9** 2 2 2 29 992 CgHPX2 5 ff **9** 9 (F . 5B). 2 y \mathfrak{L} \mathfrak{D}^{0} $\mathfrak{C}_{g}HPX2$ $\mathfrak{Q}\mathfrak{Q}$ T.9 2 & Đ. 9 9 \$ \$65.69% \$ 992 1519_ 1221 9 2 C 9 2 P4 (1221/+214), 29 29 992







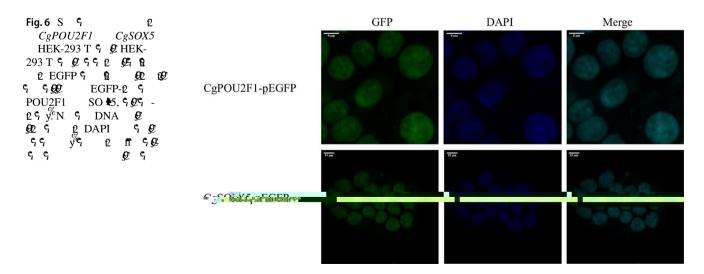




9 9 2P4 9 9 8 19 ; P4 9 9 9 9 9 ₽ ₽ ₽ 22 2 POU2F1 SO 🕏 **QQ** DNA3.1-SO \$5 9 9 8 229 DNA3.1-POU2F1 2 1 9 2 Q + 2 2 2 29 Ø Q2 Q 9 **2** 29 HEK-293 T 2D 99 29 12 9 2 0 2 99 9 P<0.05

CgPOU2F1 and CgSOX5 are Located in the Nucleus in HEK-293 T Cells

HEK-293 T \$ \$\mathref{Q}\$ I C POU2F1- EGFP- C SO \$5-EGFP-\mathref{Q}\$ \mathref{Q}\$ \mathref{Q}\$





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CgPOU2F1 and CgSOX5 Knockdown Led to a Decrease in CgHPX2 Expression

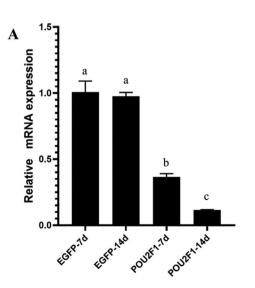
%29 2 29 CgPOU2F1 29 CgSOX5 29 9 2 CgHPX2, CgPOU2F1Ø CgSOX5 gena ge 9 PRNAP P 5 E. coli D P T99 999 9 9 2 0.4 M IPTG 237 **2**C 4... B & PRNA 9 & ₽ POU2F1 SOX5 99**9** 9 9 9 2 9 2 T7 2 2 9 9 9 9 29 IPTG- 9 E. coli (F . S6), 2 29 90 9 90 **₽**RNA *E. coli*. T 98 22 92999 99, PCR 98 8 Q 9 2 2299 990 99 9 9 9 9 9 2 % **QQ** CgPOU2F1 CgSOX5 **G**RNA e, %14, Ø 9 2 29 2 999 29 %(F . S7). C 9 2 29 9 2 EGFP **G**RNA-9 9,000 9 ,299 9,000 9,9 **Q**25 (F . 7). I POU2F1 **GRNA** 9 **99 9** -**2**⁵ **9** QQ, 299 990 99 CgHPX2 2v [%]69% 2 29 9 29 88%9 %14, 9, 99 29 % I SOX5 2 9RNA9 999 \mathfrak{Q} - \mathfrak{L} \mathfrak{Q} , CgHPX2 RNA √°14. 9 900 99 9 £ 57%

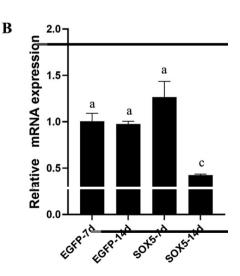
Discussion

HG 9-9 29 9 \$ 2 \$ 9 9 999 9 9 √° **99 99** 9 9 Ø $\sqrt[\infty]{2}$ T9 9292 9 9 Q 9 29 2 2 1/2 9 9 9 I \$, . . & 9,89 2 9 2 29 **9 Q**(S 9 2 . 2017). Hr 9 9

£ % 5 £ 2 9 9 e, 90 9 22 9 % 90 9 9 2 . 2008). CgHPX2 9 Q2 29 (L , . **Q Q** 2 2 90 ç, **⑤** (MPO), ℓ ⁶ 9 **©** (LPO), 9 **©** 2 y **©** (EPO), **②** (TPO) (L 92 . 2008). P y 9 9 9 2 y**©©** CgHPX2 **G Q** 29 29 9 29 9 9 2 2 CgHPX2 Q 999 9 9 9 **Q b**/9, 9 2 229 2 9 **80 8** √Q 9 Q 2 . I Sepia officinalis, 9 -9 **9** 929 **9**29 ³9 9 9 9 -**9**% 29 **99** (C. 9<u>22014</u>). T. <u>Q</u> C_{gHPX2} QQ $\sqrt{6}$ QQ QQ QQ29 QQ 2 QQQ 2 2 29 9 QRNA 9 9 -9 2(F) 92 . 2019). \$ 99Q 9 2 Ø% 29 Ø Ø 9 9,000,00 9 2 2 (C. 9 2014; D 9 9 1968). I 2 9 92 y, 8 y 92 9 9 9 9 2 2 CgHPX2 9 92 . 2017; T 9 9,00 292 929 9 Q9 **Q**2 **Q**2 **9**2 **9**2 **y**7 **Q Q CgHPX2** 99 2 98 . 9 ς, . F **9**2 √, 2 ς **Q**9 9 29 9 22 Ø 哟, 2 9 9 Ø B % 99 9gg 2 Ð 29 9 9 **9**2 9 2 Q 299 2 **2**% 9 20 2 2 2 . I 9 gg , g q B Ø **Q**2 9 2 2 2 ₿, 9 2 92 29 2 9 9 9 9 . 59 **9** 2 29 2 9 92 9 92 **9**2 9

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9 % **909** (C. 9 £ . 2009). CREB & G G G G & D , . . . **Q** 9 2 Hyriopsis cumingii (92.2021). \mathcal{Q} , \mathcal{Q} \mathcal{Q} 9 @MITF (M 9 2 . 2019; 9 2 . 2018), 9 9 9 3 (PAX3) (8 9 2 . 2018), 2 9 9 (TYR), \mathfrak{G}^{N} \mathfrak{Q} \mathfrak{G} - \mathfrak{G} \mathfrak{Q} \mathfrak{G} 1 2 (TYRP1 TYRP2) (9 2 . 2021). I 29 9 8 292 5, 2 2 9 2 2 2 9 CgPOU2F1 CgSOX5, 99 9 29 . POU2F1, & QO 21 OTF-1 (B) Q . B) 2014), 9 Q 2013). R 9 2 9 9 9 9 2 2 POU2F1 9 29 3 9 29 2 2 2 9 9 9 9 9 11 2 999 2 9999 Q (D, 9 S 9 2014; N 92 . 2018, 2014). M 9 9 , 29 9 9 9 9 9 2 2 R-21 -5 9 - 2 9 9 9 MITF \$ 2 9 SOX5 (92 . 2016). I 2 992 y, 99 1999 9 2 2CgPOU2F1 CgSOX5 $\mathfrak{L}^{\mathfrak{q}}$ \mathfrak{L} $\mathfrak{L}^{\mathfrak{q}}$ CgHPX2, \mathfrak{L} 2 2%, 2 2 2 2 2 2 2 2 2 2 2 2 3 4 -**Q** CgHPX2. QQ 9 9 Q9 CgPOU2F1 CgSOX5 Q 9 2 29 9 Q T 9 9 9 **a** 2 2*CgPOU2F1 CgSOX5* % **a** 25 2 -2 9 2 9 9 2 9 9 2 1 2 , -CgPOU2F1 CgSOX5 \mathfrak{L} \mathfrak{L} 29 y 9 12 CgHPX29 9 9 . A 9 9 8 CgHPX2 29 9 09

Conclusions

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Funding T. Q QQ & ½ ½ 25 EQ N Q N Q N Q N Q S 5 5 F Q C (31972789), E 5 F Q C (2020L GC016), C A Q 5 F Q S S Q P 5 Q S P 5 Q (2018NS01), I QQ D5 5 5 Q P 5 Q Q C Q (20 3-4 16-Q).

Declarations

References

F 2 16:47 A JA, M JEAR, 9 A, L 9 & SGBC (2015) M & 99 Nodipecten nodosus (M & : B Q Q 2 29 99 92 29 9Q **②** BMC D B 15:22 S A 106:6837 6842 B A, M D C, G\$\forall F, E, F\text{ BM (2014) C 2 \ 9\forall F \ 2 \ \gamma \text{ M D (2014) C 2 \ 9\forall F \ 2 \ \gamma \text{ 11:62 \ C \ \forall D (2014) C \ \text{ I : P 2 , C.\forall \ \text{ GZ y, F 2 \ 9\text{ QZ y, A 2 & M D &12:2700 2730 D B 332:408 417 2 2 9 9 D Q BMC 9 29 D B 17:1 2 . S R 7:45754



Fig. D, L Q, $\sqrt[8]{}$ H (2019) RNA I **1** 9 9 9 9 $\sqrt[6]{}$ 9 9 9 9 9 PRNA-



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