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Other SAMS Using Neighbour-Joining Method (Fig. 2). Based On 1000 Replicates, The Phylogenetic Tree Was Divided Into Fig 2: Unrooted Phylogenic Tree Of Protein Sequences Of CcSAMS And Other SAMSs Constructed By The Neighbor-joining Method. Bootstrap Majority Consensus Values O Jan 7th, 2024

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3, Respectively. The PCR Conditions, With TaKaRa LA Taq Polymerase And GC Buffer I, Were Essentially The Same As Those Described Previ-ously (10). The Nucleotide Sequence Of The Amplified DNA Fragment (507 Bp From The 5-end Of Pld1) Was Apr 16th, 2024

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And Cloned Into The Same Sites Of PcDNA3.1/Hygro (Invitrogen, Carls-bad, CA), Resulting In PcDNA3.1-C4ST-1 (the Name Of C4ST-1 Was Given After The Determination Of Acceptor Specificity). The Second Gene Was Initially Identified In AA233362 And

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Gibson Cloning Procedure • Design Four PCR Primers With Overlap Between Insert/insert Or Insert/vector • Adjacent Segments Should Have Identical Sequences (A And B) • PCR Primers Should Contain 5' End That Is The Same As Adj Jan 6th, 2024

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And 1 Kb Plus DNA Ladder, Invitrogen (catalogue No. 10787-018) Was Used As Marker To Determine The Size Of DNA Fragment. DNA Recovery The Amplified DNA Fragment Verified With Gel Electrophoresis Was Extracted Using TM Purelink Quick Gel Extraction Kit From Invitrogen (catalogue No. K2100-12). Four Tubes Of PCR Reaction (25 Jan 7th, 2024)

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Bled Using Vector NTI Express Software (Life Technologies, Carlsbad, CA) Based On The Obtained Partial Fragment And The 3'-/5'-full RACE Products. Amino Acid ... (Table 1) Were Designed Using Primer Express 3.0 To Develop A Real-time PCR Assay For Detecting Duck MAPK1 Expression. The Target 213-bp Amplicon Was

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Gao Et Al. 3149 Table 1. Primers Used In This Study.

Primers Name Sequence(5' To 3') SMART IVTM

Oligonucleotide

AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG

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