Taurus Energy AB

Attachment 5

THIS DOCUMENT CONTAINS CONFIDENTIAL BUSINESS INFORMATION

Promotor region from PGK1 with a copy of the XKS1 gene. DNA sequenced from a PCR reaction. Here is shown the 425nt of the PGK1 promotor segment underlined and starting **ATG** of XKS1 indicated that was amplified using the two primers PGKF-29 (at 29nt into the +500nt region of a PGK promotor segment) and XKS1RPGK (at aa 561 of XKS1) in a 30-cycle 50 µl PCR reaction with 10ng of genomic DNA and 0.05U/µl Phusion DNA polymerase (F-530, Thermo Scientific); Cycling parameters; 98°C 2min, then 30 cycles 98°C 12s, 58°C 30s, 72°C 30s; then final incubation at 72°C 10min, and cooling to 15°C. PGKF-29: 5'-ACCCAGACACGCTCGACTTCCT-3'; XKS1RPGK: 5'- CATGGGAAGTTGTCGTTCAAG-3'

ATTTCGTCACACAACAAGGTCCTAGCGACGGCTCACAGGTTTTGTAACAAGCAATCGAAGGTTCTGG
AATGGCGGGAAAGGGTTTAGTACCACATGCTATGATGCCCACTGTGATCTCCAGAGCAAAGTTCGTT
CGATCGTACTGTTACTCTCTCTCTTTCAAACAGAATTGTCCGAATCGTGTGACAACAACAGCCTGTT
CTCACACACTCTTTTCTTCTAACCAAGGGGGTGGTTTAGTTTAGTAGAACCTCGTGAAACTTACATT
TACATATATATAAACTTGCATAAATTGGTCAATGCAAGAAATACATATTTGGTCTTTTCTAATTCGT
AGTTTTTCAAGTTCTTAGATGCTTTCTTTTTCTCTTTTTTACAGATCATCAAGGAAGTAATTATCTA
CTTTTTACAACAAATATAAAACA

ATGTTGTGTTCTGTTATTCAAAGACAAACCAGAGAAGTTTCTAACACCATGTCTTTGGACTCTTACT
ACTTGGGTTTCGACTTGTCTACCCAACAATTGAAGTGTTTGGCTATTAACCAAGACTTGAAGATTGT
TCACTCTGAAACCGTTGAATTCGAAAAGGACTTGCCACACTACCACACCAAGAAGGGTGTTTACATT
CACGGTGACACCATTGAATGTCCAGTTGCTATGTGGTTGGAAGCTTTGGACTTGGTTTTGTCTAAGT
ACAGAGAAGCTAAGTTCCCATTGAACAAGGTTATGGCTGTTTCTGGTTCTTGTCAACAACACGGTTC
TGTTTACTGGTCTTCTCAAGCTGAATCTTTGTTGGAACAATTGAACAAGAAGCCAGAAAAGGACTTG
TTGCACTACGTTTCTTCTGTTGCTTTCGCTAGACAAACCGCTCCAAACTGGCAAGACCACTCTACCG
CTAAGCAATGTCAAGAATTCGAAGAATGTATTGGTGGTCCAGAAAAGATGGCTCAATTGACCGGTTC
TAGAGCTCACTTCAGATTCACCGGTCCACAAATTTTGAAGATTGCTCAATTGGAACCAGAAGCTTAC
GAAAAGACCAAGACCATTTCTTTGGTTTCTAACTTCTTGACCTCTATTTTGGTTGGTCACTTGGTTG
AATTGGAAGAAGCTGACGCTTGTGGTATGAACTTGTACGACATTAGAGAAAGAAAGTTCTCTGACGA
ATTGTTGCACTTGATTGACTCTTCTTCTAAGGACAAGACCATTAGACAAAAGTTGATGAGAGCTCCA
ATGAAGAACTTGATTGCTGGTACCATTTGTAAGTACTTCATTGAAAAGTACGGTTTCAACACCAACT
GTAAGGTTTCTCCAATGACCGGTGACAACTTGGCTACCATTTGTTCTTTGCCATTGAGAAAGAACGA
CGTTTTGGTTTCTTTGGGTACCTCTACCACCGTTTTGTTGGTTACCGACAAGTACCACCCATCTCCA
AACTACCACTTGTTCATTCACCCAACCTTGCCAAACCACTACATGGGTATGATTTGTTACTGTAACG
GTTCTTTGGCTAGAGAAAGAATTAGAGACGAATTGAACAAGGAAAGAGAAAACAACTACGAAAAGAC
CAACGACTGGACCTTGTTCAACCAAGCTGTTTTGGACGACTCTGAATCTTCTGAAAACGAATTGGGT
GTTTACTTCCCATTGGGTGAAATTGTTCCATCTGTTAAGGCTATTAACAAGAGAGTTATTTTCAACC
CAAAGACCGGTATGATTGAAAGAGAAGTTGCTAAGTTCAAGGACAAGAGACACGACGCTAAGAACAT
TGTTGAATCTCAAGCTTTGTCTTGTAGAGTTAGAATTTCTCCATTGTTGTCTGACTCTAACGCTTCT
TCTCAACAAAGATTGAACGAAGACACCATTGTTAAGTTCGACTACGACGAATCTCCATTGAGAGACT
ACTTGAACAAGAGACCAGAAAGAACCTTCTTCGTTGGTGGTGCTTCTAAGAACGACGCTATTGTTAA
GAAGTTCGCTCAAGTTATTGGTGCTACCAAGGGTAACTTCAGATTGGAAACCCCAAACTCTTGTGCT
TTGGGTGGTTGTTACAAGGCTATGTGGTCTTTGTTGTACGACTCTAACAA

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MLCSVIQRQTREVSNTMSLDSYYLGFDLSTQQLKCLAINQDLKIVHSETVEFEKDLPHYHTKKGV
YIHGDTIECPVAMWLEALDLVLSKYREAKFPLNKVMAVSGSCQQHGSVYWSSQAESLLEQLNKKP
EKDLLHYVSSVAFARQTAPNWQDHSTAKQCQEFEECIGGPEKMAQLTGSRAHFRFTGPQILKIAQ
LEPEAYEKTKTISLVSNFLTSILVGHLVELEEADACGMNLYDIRERKFSDELLHLIDSSSKDKTI
RQKLMRAPMKNLIAGTICKYFIEKYGFNTNCKVSPMTGDNLATICSLPLRKNDVLVSLGTSTTVL
LVTDKYHPSPNYHLFIHPTLPNHYMGMICYCNGSLARERIRDELNKERENNYEKTNDWTLFNQAV
LDDSESSENELGVYFPLGEIVPSVKAINKRVIFNPKTGMIEREVAKFKDKRHDAKNIVESQALSC
RVRISPLLSDSNASSQQRLNEDTIVKFDYDESPLRDYLNKRPERTFFVGGASKNDAIVKKFAQVI
GATKGNFRLETPNSCALGGCYKAMWSLLYDSN

CLUSTAL 2.1 multiple sequence alignment of XKS1PGK in T13-T17 with XKS1 in S. cerevisiae

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XKS1            MLCSVIQRQTREVSNTMSLDSYYLGFDLSTQQLKCLAINQDLKIVHSETVEFEKDLPHYH 60
XKS1PGK         MLCSVIQRQTREVSNTMSLDSYYLGFDLSTQQLKCLAINQDLKIVHSETVEFEKDLPHYH 60
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XKS1            TKKGVYIHGDTIECPVAMWLEALDLVLSKYREAKFPLNKVMAVSGSCQQHGSVYWSSQAE 120
XKS1PGK         TKKGVYIHGDTIECPVAMWLEALDLVLSKYREAKFPLNKVMAVSGSCQQHGSVYWSSQAE 120
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XKS1            SLLEQLNKKPEKDLLHYVSSVAFARQTAPNWQDHSTAKQCQEFEECIGGPEKMAQLTGSR 180
XKS1PGK         SLLEQLNKKPEKDLLHYVSSVAFARQTAPNWQDHSTAKQCQEFEECIGGPEKMAQLTGSR 180
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XKS1            AHFRFTGPQILKIAQLEPEAYEKTKTISLVSNFLTSILVGHLVELEEADACGMNLYDIRE 240
XKS1PGK         AHFRFTGPQILKIAQLEPEAYEKTKTISLVSNFLTSILVGHLVELEEADACGMNLYDIRE 240
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XKS1            RKFSDELLHLIDSSSKDKTIRQKLMRAPMKNLIAGTICKYFIEKYGFNTNCKVSPMTGDN 300
XKS1PGK         RKFSDELLHLIDSSSKDKTIRQKLMRAPMKNLIAGTICKYFIEKYGFNTNCKVSPMTGDN 300
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XKS1            LATICSLPLRKNDVLVSLGTSTTVLLVTDKYHPSPNYHLFIHPTLPNHYMGMICYCNGSL 360
XKS1PGK         LATICSLPLRKNDVLVSLGTSTTVLLVTDKYHPSPNYHLFIHPTLPNHYMGMICYCNGSL 360
                ************************************************************

XKS1            ARERIRDELNKERENNYEKTNDWTLFNQAVLDDSESSENELGVYFPLGEIVPSVKAINKR 420
XKS1PGK         ARERIRDELNKERENNYEKTNDWTLFNQAVLDDSESSENELGVYFPLGEIVPSVKAINKR 420
                ************************************************************

XKS1            VIFNPKTGMIEREVAKFKDKRHDAKNIVESQALSCRVRISPLLSDSNASSQQRLNEDTIV 480
XKS1PGK         VIFNPKTGMIEREVAKFKDKRHDAKNIVESQALSCRVRISPLLSDSNASSQQRLNEDTIV 480
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XKS1            KFDYDESPLRDYLNKRPERTFFVGGASKNDAIVKKFAQVIGATKGNFRLETPNSCALGGC 540
XKS1PGK         KFDYDESPLRDYLNKRPERTFFVGGASKNDAIVKKFAQVIGATKGNFRLETPNSCALGGC 540
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XKS1            YKAMWSLLYDSNKIAVPFDKFLNDNFPWHVMESISDVDNENWDRYNSKIVPLSELEKTLI 600
XKS1PGK         YKAMWSLLYDSN---------------------------------------------- 552
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