

Python-GDH plasmid

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ER-LBD gene

AAGAAGAATTCAGTGGCGTTGTCGCTTACGGCTGACCAAATGGTTTCTGCTCTGCTTGACGCCGAACCTC
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ATCTTATGGCGAAGGCAGGCTTAACACTTCAACAGCAACATCAGCGCCTTGCTCAGCTTCTGTTGATTTT
AAGCCATATCCGTCACATGTCAAACAAGGGTATGGAACACCTTTACAGTATGAAGTGTAAGAACGTCGT
TCCATTGTATGATTTGTTACTGGAAATGCTTGACGCTCACCGTCTGCATGCACCT

Oligo Primers	Sequence
GDH_oligoP_DI-1_FFrag1-59_56.8C	ATATAGATGCCGTCCCGTCT
GDH_oligoP_DI-1_RFrag1-59_56.2C	TCTTTCCTGTGCCACGT
GDH_oligoP_DI-2_FFrag60-116_59.1C	CCCTTTAATCAGATGCGTCGTC

GDH_oligoP_DI-2_RFrag60-116_56.9C	G TAGTAATAAGGGCGACCCG
GDH_oligoP_DI-3_FFrag117-174_58.1C	T TGGTCATGTGCTTTTCGTCTC
GDH_oligoP_DI-3_RFrag117-174_58.0C	G GTATCGGATACTCAGACGTCT
GDH_oligoP_DI-4_FFrag175-232_56.9C	T CCGACGGGGAGTATACG
GDH_oligoP_DI-4_RFrag175-232_56.9C	T AACTGCTTCAGGCCAACG
GDH_oligoP_DI-5_FFrag233-289_57.6C	C ATGTTTAGGAACGCTACCGT
GDH_oligoP_DI-5_RFrag233-289_55.9C	T AATCTCCGTTCCCTCCCC
GDH_oligoP_DI-6_FFrag290-346_57.8C	G TACATGAAACGATGGACCGTC
GDH_oligoP_DI-6_RFrag290-346_55.9C	G GTATAGTCTCCTCAGCGC
GDH_oligoP_DI-7_FFrag347-404_58.2C	G GCGAGAGGAGATATACGTCT
GDH_oligoP_DI-7_RFrag347-404_55.8C	A TCGAACAGCTGTGCACC
GDH_oligoP_DI-8_FFrag405-461_56.6C	T TATAATCATCCTCCCCGCG
GDH_oligoP_DI-8_RFrag405-461_58.1C	A AATAGGATGTGTGCTCGCG
Backbone Primers	Sequence
GDH_geneP_DI-1_RFrag1-5957.4C	A TACGTCTCGCATATGTATATCTCCTTCTTAAAGT TAAA
GDH_geneP_DI-1_FFrag1-5957.8C	A TACGTCTCCGTTAACCCGGAAAGCGG
GDH_geneP_DI-2_RFrag60-11659.5C	A TACGTCTCTAACGCGCAGAATTTTACCGG
GDH_geneP_DI-2_FFrag60-11658.4C	A TACGTCTCGCTGCCGAATCAGACCATCA
GDH_geneP_DI-3_RFrag117-17463.0C	A TACGTCTCGCAGCTCTTTGTCGGTACTTTTCG
GDH_geneP_DI-3_FFrag117-17457.1C	A TACGTCTCCCAACTGGCATACTGTTTCTG
GDH_geneP_DI-4_RFrag175-23256.7C	A TACGTCTCGTTGGTTACGGCCCTGATC

GDH_geneP_DI-4_FFrag175-23256.0C	ATACGTCTCGGGTCACCGTAATCCGC
GDH_geneP_DI-5_RFrag233-28957.0C	ATACGTCTCGACCCAGGGTATAGATATGGCT
GDH_geneP_DI-5_FFrag233-28960.0C	ATACGTCTCTAGCGCAGCGGCAAACAA
GDH_geneP_DI-6_RFrag290-34661.9C	ATACGTCTCCGCTATAATTCGCGTATGCATAGC
GDH_geneP_DI-6_FFrag290-34659.4C	ATACGTCTCCGAAATGACCTATATTTGCTGGCC
GDH_geneP_DI-7_RFrag347-40458.4C	ATACGTCTCTTTCGCCGCAGGTCGG
GDH_geneP_DI-7_FFrag347-40458.7C	ATACGTCTCCGTTCCGATGTTCAAAGCAA
GDH_geneP_DI-8_RFrag405-46159.3C	ATACGTCTCGAACGGCATCGTCGTAGGT
GDH_geneP_DI-8_FFrag405-46160.6C	ATACGTCTCATGACTCGAGTGAGATCCGGC

Oligo Pool	Sequence
GDH_DI_1-59_inse rtion7	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACAGCGGGAGACCGGGGTCTCTGAGCGACGTTCCGCTGACCCCGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGCACAGGAAAGA
GDH_DI_1-59_inse rtion8	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACAGCGGGAGACCGGGGTCTCTGAGCGTTCCGCTGACCCCGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGCACAGGAAAGA
GDH_DI_1-59_inse rtion9	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTAGCGGGAGACCGGGGTCTCTGAGCCCGCTGACCCCGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGCACAGGAAAGA
GDH_DI_1-59_inse rtion10	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGAGCGGGA GACCGGGGTCTCTGAGCCTGACCCCGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGCACAGGAAAGA
GDH_DI_1-	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGAGCGGGAGACCGGGGTCTCTGAGCACCCCGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCG

59_inse rtion11	ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion12	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCA GCGGGAGACCGGGGTCTCTGAGCCCGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion13	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCGGGAGACCGGGGTCTCTGAGCAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion14	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCAGCGGGAGACCGGGGTCTCTGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion15	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGAGCGGGAGACCGGGGTCTCTGAGCTTTGCGAAAGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion16	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTAGCGGGAGACCGGGGTCTCTGAGCGCGAAAGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion17	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAGCGGGAGACCGGGGTCTCTGAGCAAAGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion18	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAAGCGGGAGACCGGGGTCTCTGAGCGCGAAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion19	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAAGCGAGCGGGAGACCGGGGTCTCTGAGCAAAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA

GDH_DI _1- 59_inse rtion20	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGGGAGACCGGGGTCTCTGAGCAGCGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion21	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCAGCGGGAGACCGGGGTCTCTGAGCAGAGAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion22	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAGCGGGAGACCGGGGTCTCTGAGCAACTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion23	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACAGCGGGAGACCGGGGTCTCTGAGCTTCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion24	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCAGCGGGAGACCGGGGTCTCTGAGCG ACAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion25	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAGCGGGAGACCGGGGTCTCTGA GCAAAAAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion26	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAGCGGGAGACCGGGGTCTC TGAGCAAAGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion27	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGCGGGAGACCGGGG TCTCTGAGCGTCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion28	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCAGCGGGAGACCGG GGTCTCTGAGCATCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA

59_inse rtion28	ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion29	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCAGCGGGAGAC CGGGGTCTCTGAGCCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion30	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCGGGA GACCGGGGTCTCTGAGCAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion31	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC AGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAGCG AGACCGGGGTCTCTGAGCAACCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA CAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC AGGAAAGA
GDH_DI _1- 59_inse rtion32	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACA GCGGGAGACCGGGGTCTCTGAGCCTGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion33	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAGCGGGAGACCGGGGTCTCTGAGCAATAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion34	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAGCGGGAGACCGGGGTCTCTGAGCAAACCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion35	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAAAGCGGGAGACCGGGGTCTCTGAGCCCGCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion36	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGAGCGGGAGACCGGGGTCTCTGAGCCACGCTCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA

GDH_DI _1- 59_inse rtion37	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCCCG AGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACCTGA ATAAACCGCACAGCGGGAGACCGGGGTCTCTGAGCGCTCTGCTGTGGGGTCCGGATAATC AGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGCACA GGAAAGA
GDH_DI _1- 59_inse rtion38	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTAGCGGGAGACCGGGGTCTCTGAGCCTGCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion39	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGAGCGGGAGACCGGGGTCTCTGAGCCTGTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion40	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGAGCGGGAGACCGGGGTCTCTGAGCTGGGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion41	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGAGCGGGAGACCGGGGTCTCTGAGCGGTCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion42	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTAGCGGGAGACCGGGGTCTCTGAGCCCGGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion43	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGAGCGGGAGACCGGGGTCTCTGAGCGATA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion44	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAGCGGGAGACCGGGGTCTCTGAGCA ATCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion45	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGC GAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATAGCGGGAGACCGGGGTCTCTGA

59_inse rtion45	GCCAGATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion46	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGAGCGGGAGACCGGGGTCTC TGAGCATTTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion47	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTAGCGGGAGACCGGGGT CTCTGAGCTGGCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion48	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGAGCGGGAGACCGG GGTCTCTGAGCCTGACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion49	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGAGCGGGAGAC CGGGGTCTCTGAGCACCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion50	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCAGCGGGA GACCGGGGTCTCTGAGCGAACGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion51	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAAAGCG GGAGACCGGGGTCTCTGAGCCGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion52	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCA GCGGGAGACCGGGGTCTCTGAGCGCAACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion53	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAAGCGGGAGACCGGGGTCTCTGAGCACCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA

GDH_DI _1- 59_inse rtion54	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAACCGGCGGGAGACCGGGGTCTCTGAGCGGTAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion55	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAACCGGTAGCGGGAGACCGGGGTCTCTGAGCAAAATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion56	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAACCGGTAAAAGCGGGAGACCGGGGTCTCTGAGCATTCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion57	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAACCGGTAAAATTAGCGGGAGACCGGGGTCTCTGAGCCTGCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion58	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAACCGGTAAAATTCTGAGCGGGAGACCGGGGTCTCTGAGCCGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _1- 59_inse rtion59	ATATAGATGCCGTCCCGTCTCCTATGCACCACCACCACCACCACGACGTTCCGCTGACCC CGAGCCAGTTTGCGAAAGCGAAAAGCGAGAACTTCGACAAAAAAGTCATCCTGAGCAACC TGAATAAACCGCACGCTCTGCTGTGGGGTCCGGATAATCAGATTTGGCTGACCGAACGCG CAACCGGTAAAATTCTGCGCAGCGGGAGACCGGGGTCTCTGAGCGTTAGGAGACGTGGGC ACAGGAAAGA
GDH_DI _60- 116_ins ertion6 0	CCCTTTAATCAGATGCGTCGTCTCCCGTTAGCGGGAGACCGGGGTCTCTGAGCAACCCGG AAAGCGGCAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 1	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACAGCGGGAGACCGGGGTCTCTGAGCCCGG AAAGCGGCAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAGCGGGAGACCGGGGTCTCTGAGCG AAAGCGGCAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA

ertion6 2	TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 3	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGGAGACCGGGGTCTCTGA GCAGCGGCAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 4	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCAGCGGGAGACCGGGGTCTC TGAGCGGCAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 5	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGGGAGACCGGGGT CTCTGAGCAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 6	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCAGCGGGAGACCGG GGTCTCTGAGCGTTAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 7	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAGCGGGAGAC CGGGGTCTCTGAGCAAAACCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion6 8	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAAGCGGGAG ACCGGGGTCTCTGAGCACCCTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAA AACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAG CGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCCTTATT ACTAC
GDH_DI _60- 116_ins ertion6 9	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCAGCG GGAGACCGGGGTCTCTGAGCGTCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 0	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCA GCGGGAGACCGGGGTCTCTGAGCTTTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC

GDH_DI _60- 116_ins ertion7 1	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGCGGGAGACCGGGGTCTCTGAGCCAGGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 2	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGAGCGGGAGACCGGGGTCTCTGAGCGTTCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 3	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTAGCGGGAGACCGGGGTCTCTGAGCCCGGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 4	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGAGCGGGAGACCGGGGTCTCTGAGCGAAATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 5	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAAGCGGGAGACCGGGGTCTCTGAGCATCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 6	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCAGCGGGAGACCGGGGTCTCTGAGCGTTAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 7	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAGCGGGAGACCGGGGTCTCTGAGCAACGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion7 8	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACAGCGGGAGACCGGGGTCTCTGAGCGACGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACAGCGGGAGACCGGGGTCTCTGAGCGCAGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA

ertion7 9	TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 0	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAAGCGGGAGACCGGGGTCTCTGAGCGACGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 1	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACAGCGGGAGACCGGGGTCTCTGAGCGGTC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 2	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTAGCGGGAGACCGGGGTCTCTGAGCC AAAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 3	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAGCGGGAGACCGGGGTCTCTGA GCAACGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 4	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAACAGCGGGAGACCGGGGTCTC TGAGCGGTCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 5	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAACGGTAGCGGGAGACCGGGGT CTCTGAGCCTGCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 6	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAACGGTCTGAGCGGGAGACCGG GGTCTCTGAGCCTGGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 7	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAACGGTCTGCTGAGCGGGAGAC CGGGGTCTCTGAGCGGTTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTCGCCC TTATTACTAC

GDH_DI _60- 116_ins ertion8 8	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTAGCGGGA GACCGGGGTCTCTGAGCTTTGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion8 9	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTAGCG GGAGACCGGGGTCTCTGAGCGCGTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 0	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGA GCGGGAGACCGGGGTCTCTGAGCTTTTCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 1	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTAGCGGGAGACCGGGGTCTCTGAGCCATCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 2	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATAGCGGGAGACCGGGGTCTCTGAGCCCGGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 3	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGAGCGGGAGACCGGGGTCTCTGAGCGACTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 4	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACAGCGGGAGACCGGGGTCTCTGAGCTTCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 5	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAGCGGGAGACCGGGGTCTCTGAGCAAAAACAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAGCGGGAGACCGGGGTCTCTGAGCAACAACCCGTACATCTACA

ertion9 6	TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 7	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAGCGGGAGACCGGGGTCTCTGAGCAACCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 8	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACAGCGGGAGACCGGGGTCTCTGAGCCCGTACATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion9 9	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCTTT CAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGTTTC ATCCGGACTTCAAAAACAACCCGAGCGGGAGACCGGGGTCTCTGAGCTACATCTACATCAG CGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCCATT ACTAC
GDH_DI _60- 116_ins ertion1 00	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACAGCGGGAGACCGGGGTCTCTGAGCATCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 01	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCAGCGGGAGACCGGGGTCTCTGAGCTACA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 02	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACAGCGGGAGACCGGGGTCTCTGAGCA TCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 03	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGGAGACCGGGGTCTCTGA GCAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 04	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCAGCGGGAGACCGGGGTCTC TGAGCGGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC

GDH_DI _60- 116_ins ertion1 05	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCAGCGGGAGACCGGGGT CTCTGAGCACCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 06	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCGAGCGGGAGACCGG GGTCTCTGAGCTTCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 07	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAGCGGGAGAC CGGGGTCTCTGAGCAAAAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 08	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAGCGGGA GACCGGGGTCTCTGAGCAACCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 09	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACAGCG GGAGACCGGGGTCTCTGAGCCCCGAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 10	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA GCGGGAGACCGGGGTCTCTGAGCAAAAAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 11	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA AAAGCGGGAGACCGGGGTCTCTGAGCAGTACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 12	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA AAAGTAGCGGGAGACCGGGGTCTCTGAGCACCGACAAAGAGCTGCGGAGACGGGTGCGCC TTATTACTAC
GDH_DI _60- 116_ins	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA

ertion1 13	AAAGTACCAGCGGGAGACCGGGGTCTCTGAGCGACAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 14	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA AAAGTACCGACAGCGGGAGACCGGGGTCTCTGAGCAAAGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 15	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA AAAGTACCGACAAAAGCGGGAGACCGGGGTCTCTGAGCGAGCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _60- 116_ins ertion1 16	CCCTTTAATCAGATGCGTCGTCTCCCGTTAACCCGGAAGCGGCAGCGTTAAAACCGTCT TTCAGGTTCCGGAAATCGTTAACGACGCAGACGGTCAAAACGGTCTGCTGGGTTTTGCGT TTCATCCGGACTTCAAAAACAACCCGTACATCTACATCAGCGGCACCTTCAAAAACCCGA AAAGTACCGACAAAAGAGAGCGGGAGACCGGGGTCTCTGAGCCTGCGGAGACGGGTGCCCC TTATTACTAC
GDH_DI _117- 174_ins ertion1 17	TTGGTCATGTGCTTTTCGTCTCCGCTGAGCGGGAGACCGGGGTCTCTGAGCCCGAATCAG ACCATCATCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 18	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAGCGGGAGACCGGGGTCTCTGAGCAATCAG ACCATCATCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 19	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATAGCGGGAGACCGGGGTCTCTGAGCCAG ACCATCATCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 20	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGAGCGGGAGACCGGGGTCTCTGAGC ACCATCATCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 21	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCAGCGGGAGACCGGGGTCTCTG AGCATCATCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC

GDH_DI _117- 174_ins ertion1 22	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCAGCGGGAGACCGGGGTCT CTGAGCATCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 23	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCAGCGGGAGACCGGGG TCTCTGAGCCGTCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 24	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTAGCGGGAGACCG GGGTCTCTGAGCCGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 25	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTGCGAGCGGGAGA CCGGGGTCTCTGAGCTATACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 26	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTGCTATAGCGGG AGACCGGGGTCTCTGAGCACCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 27	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTGCTATACCAGC GGGAGACCGGGGTCTCTGAGCTACAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 28	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTGCTATACCTAC AGCGGGAGACCGGGGTCTCTGAGCAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 29	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTGCTATACCTAC AACAGCGGGAGACCGGGGTCTCTGAGCAACAAAAGCACCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTGCTATACCTACAAC AAAAGCGGGAGACCGGGGTCTCTGAGCAGCACCGACACCCTGGAAAAACCGGTTGATCTG CTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCGACC

ertion1 30	AGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGTATCCG ATACC
GDH_DI _117- 174_ins ertion1 31	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCAGCGGGAGACCGGGGTCTCTGAGCACCACACCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 32	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGCGGGAGACCGGGGTCTCTGAGCGACACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 33	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGCAGCGGGAGACCGGGGTCTCTGAGCACCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 34	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGACACCAGCGGGAGACCGGGGTCTCTGAGCCTGGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 35	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGACACCCTGAGCGGGAGACCGGGGTCTCTGAGCGAAAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 36	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGACACCCTGGAAAGCGGGAGACCGGGGTCTCTGAGCAAACCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 37	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGACACCCTGGAAAAAAGCGGGAGACCGGGGTCTCTGAGCCCGGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 38	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCAGACACCCTGGAAAAACCGAGCGGGAGACCGGGGTCTCTGAGCGTTGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC

GDH_DI _117- 174_ins ertion1 39	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTAGCGGGAGACCGGGGTCTCTGAGCGAT CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 40	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATAGCGGGAGACCGGGGTCTCTGAGC CTGCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 41	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGAGCGGGAGACCGGGGTCTCTG AGCCTGGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 42	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGAGCGGGAGACCGGGGTCT CTGAGCGCAGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 43	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAAGCGGGAGACCGGGG TCTCTGAGCGGTCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 44	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTAGCGGGAGACCG GGGTCTCTGAGCCTGCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 45	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGAGCGGGAGA CCGGGGTCTCTGAGCCCGAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 46	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGCGGG AGACCGGGGTCTCTGAGCAGTAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGC GGGAGACCGGGGTCTCTGAGCAGTAAAGATCATCAGAGCGGTCTGTCTGGTAATTGGTCCG

ertion1 47	GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 48	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AGCGGGAGACCGGGGTCTCTGAGCAAAGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 49	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAAGCGGGAGACCGGGGTCTCTGAGCGATCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 50	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATAGCGGGAGACCGGGGTCTCTGAGCCATCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 51	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATAGCGGGAGACCGGGGTCTCTGAGCCAGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 52	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGGAGACCGGGGTCTCTGAGCAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 53	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCAGCGGGAGACCGGGGTCTCTGAGCGGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 54	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTAGCGGGAGACCGGGGTCTCTGAGCCGTCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 55	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCTAGCGGGAGACCGGGGTCTCTGAGCCTGCTGGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC

GDH_DI _117- 174_ins ertion1 56	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGAGCGGGAGACCGGGGTCTCTGAGCGTAATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 57	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAAGCGGGAGACCGGGGTCTCTGAGCATTGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 58	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTAGCGGGAGACCGGGGTCTCTGAGCGGTCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 59	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTAGCGGGAGACCGGGGTCTCTGAGCCCCG GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 60	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGAGCGGGAGACCGGGGTCTCTGAGC GACCAGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 61	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTACAAC AAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGTAAAG ATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACAGCGGGAGACCGGGGTCTCTGAGCC AGAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGTATCCG ATACC
GDH_DI _117- 174_ins ertion1 62	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAGCGGGAGACCGGGGTCT CTGAGCAAAAATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 63	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAAGCGGGAGACCGGGG TCTCTGAGCATCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCAGCGGGAGACCG

ertion1 64	GGGTCTCTGAGCTACTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 65	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACAGCGGGAGA CCGGGGTCTCTGAGCTATACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 66	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATAGCGGG AGACCGGGTCTCTGAGCACCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 67	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATACCAGC GGGAGACCGGGTCTCTGAGCATTGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 68	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATACCATT AGCGGGAGACCGGGTCTCTGAGCGGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 69	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATACCATT GGCAGCGGGAGACCGGGTCTCTGAGCGATCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 70	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATACCATT GGCGATAGCGGGAGACCGGGTCTCTGAGCCAGGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 71	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATACCATT GGCGATCAGAGCGGGAGACCGGGTCTCTGAGCGGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 72	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCGTCTGGTAATTGGTCCGGACCAGAAAATCTACTATACCATT GGCGATCAGGGCAGCGGGAGACCGGGTCTCTGAGCCGTAACCAACGGAGACGTCTGAGT ATCCGATACC

GDH_DI _117- 174_ins ertion1 73	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCTGTGTAATTGGTCCGGACCAGAAAATCTACTATACCATT GGCGATCAGGGCCGTAGCGGGAGACCGGGGTCTCTGAGCAACCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _117- 174_ins ertion1 74	TTGGTCATGTGCTTTTCGTCTCCGCTGCCGAATCAGACCATCATCCGTCGCTATACCTAC AACAAAAGCACCGACACCCTGGAAAAACCGGTTGATCTGCTGGCAGGTCTGCCGAGTAGT AAAGATCATCAGAGCGGTCTGTGTAATTGGTCCGGACCAGAAAATCTACTATACCATT GGCGATCAGGGCCGTAAACAGCGGGAGACCGGGGTCTCTGAGCCAACGGAGACGTCTGAGT ATCCGATACC
GDH_DI _175- 232_ins ertion1 75	TCCGACGGGGAGTATACGTCTCCCCAAAGCGGGAGACCGGGGTCTCTGAGCCTGGCATACTGTTTCTGCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCTGAAGCAGTTA
GDH_DI _175- 232_ins ertion1 76	TCCGACGGGGAGTATACGTCTCCCCAACTGAGCGGGAGACCGGGGTCTCTGAGCGCATACTGTTTCTGCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCTGAAGCAGTTA
GDH_DI _175- 232_ins ertion1 77	TCCGACGGGGAGTATACGTCTCCCCAACTGGCAAGCGGGAGACCGGGGTCTCTGAGCTACTGTTTCTGCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCTGAAGCAGTTA
GDH_DI _175- 232_ins ertion1 78	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGAGCGGGAGACCGGGGTCTCTGAGCTGTTTCTGCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCTGAAGCAGTTA
GDH_DI _175- 232_ins ertion1 79	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGAGCGGGAGACCGGGGTCTCTGAGCTTTCTGCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCTGAAGCAGTTA
GDH_DI _175- 232_ins ertion1 80	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGAGCGGGAGACCGGGGTCTCTGAGCCTGCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCTGAAGCAGTTA
GDH_DI _175- 232_ins	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGAGCGGGAGACCGGGGTCTCTGAGCCCCGAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC

ertion1 81	AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 82	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAGCGGGAGACCG GGGTCTCTGAGCAACCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 83	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACAGCGGGAGA CCGGGGTCTCTGAGCCAAGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 84	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAAGCGGG AGACCGGGGTCTCTGAGCGCACAAACATACCCCGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 85	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAAGCAAGC GGGAGACCGGGGTCTCTGAGCCAACATACCCCGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 86	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAAGCACAA AGCGGGAGACCGGGGTCTCTGAGCCATACCCCGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 87	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAAGCACAA CATAGCGGGAGACCGGGGTCTCTGAGCACC CGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 88	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAAGCACAA CATACCAGCGGGAGACCGGGGTCTCTGAGCCCCGACCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 89	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAAGCACAA CATACCCCGAGCGGGAGACCGGGGTCTCTGAGCACC CAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA

GDH_DI _175- 232_ins ertion1 90	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAGCGGGAGACCGGGGTCTCTGAGCCAACAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 91	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAAAGCGGGAGACCGGGGTCTCTGAGCCAAGAACTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 92	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA TACCCCGACCCAACAAGCGGGAGACCGGGGTCTCTGAGCGAACTGAACGGCAAAGACTA CCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAAC CCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCTGAAG CAGTTA
GDH_DI _175- 232_ins ertion1 93	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAAAGCGGGAGACCGGGGTCTCTGAGCCTGAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 94	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAGCGGGAGACCGGGGTCTCTGAGCAACGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 95	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACAGCGGGAGACCGGGGTCTCTGAGCGGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 96	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAGCGGGAGACCGGGGTCTCTGAGCAAAGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 97	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAAGCGGGAGACCGGGGTCTCTGAGCGAC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACAGCGGGAGACCGGGGTCTCTGAGC TACCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC

ertion1 98	AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion1 99	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACAGCGGGAGACCGGGGTCTCTG AGCCACACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 00	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACAGCGGGAGACCGGGGTCT CTGAGCACCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 01	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCAGCGGGAGACCGGGG TCTCTGAGCTACATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 02	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACAGCGGGAGACCG GGGTCTCTGAGCATGGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 03	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGAGCGGGAGA CCGGGGTCTCTGAGCGGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 04	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAGCGGG AGACCGGGGTCTCTGAGCAAAGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 05	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAAGC GGGAGACCGGGGTCTCTGAGCGTTCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 06	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT AGCGGGAGACCGGGGTCTCTGAGCCTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA

GDH_DI _175- 232_ins ertion2 07	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGAGCGGGAGACCGGGGTCTCTGAGCCGTCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 08	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTAGCGGGAGACCGGGGTCTCTGAGCCTGAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 09	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAGCGGGAGACCGGGGTCTCTGAGCAATCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 10	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATAGCGGGAGACCGGGGTCTCTGAGCCTGGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 11	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGAGCGGGAGACCGGGGTCTCTGAGCGACGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 12	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACAGCGGGAGACCGGGGTCTCTGAGCGGTAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 13	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCGGGAGACCGGGGTCTCTGAGCAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 14	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCAGCGGGAGACCGGGGTCTCTGAGCATTCCGAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTAGCGGGAGACCGGGGTCTCTGAGCCCGAAAGAC

ertion2 15	AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 16	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAGCGGGAGACCGGGGTCTCTGAGCAAAGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 17	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAAGCGGGAGACCGGGGTCTCTGAGCGAC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 18	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAGCGGGAGACCGGGGTCTCTGAGC AACCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 19	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACAGCGGGAGACCGGGGTCTCTG AGCCCGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 20	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCGGGAGACCGGGGTCT CTGAGCAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 21	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCAGCGGGAGACCGGGG TCTCTGAGCTTCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 22	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAGCGGGAGACCG GGGTCTCTGAGCAACGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 23	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA TACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTTCTG CGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACAGCGGGAGACCGG GGTCTCTGAGCGGCGTTGTTAGCCATATCTATACCCTGGGTTCGGAGACGTTGGCCTGAAGC AGTTA

GDH_DI _175- 232_ins ertion2 24	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCAGCGGG AGACCGGGGTCTCTGAGCGTTGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 25	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTAGC GGGAGACCGGGGTCTCTGAGCGTTAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 26	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT AGCGGGAGACCGGGGTCTCTGAGCAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 27	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT AGCAGCGGGAGACCGGGGTCTCTGAGCCATATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 28	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT AGCCATAGCGGGAGACCGGGGTCTCTGAGCATCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 29	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT AGCCATATCAGCGGGAGACCGGGGTCTCTGAGCTATACCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 30	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT AGCCATATCTATAGCGGGAGACCGGGGTCTCTGAGCACCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins ertion2 31	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT AGCCATATCTATACCAGCGGGAGACCGGGGTCTCTGAGCCTGGGTCTGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _175- 232_ins	TCCGACGGGGAGTATACGTCTCCCCAACTGGCATACTGTTTCTGCCGAACCAAGCACAA CATACCCCGACCCAACAAGAACTGAACGGCAAAGACTACCACACCTACATGGGCAAAGTT CTGCGTCTGAATCTGGACGGTAGCATTCCGAAAGACAACCCGAGCTTCAACGGCGTTGTT

ertion2 32	AGCCATATCTATACCCTGAGCGGGAGACCGGGGTCTCTGAGCGGTCGGAGACGTTGGCCT GAAGCAGTTA
GDH_DI _233- 289_ins ertion2 33	CATGTTTAGGAACGCTACCGTCTCCGGGTAGCGGGAGACCGGGGTCTCTGAGCCACCGTA ATCCGCAAGGTCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 34	CATGTTTAGGAACGCTACCGTCTCCGGGTCACAGCGGGAGACCGGGGTCTCTGAGCCGTA ATCCGCAAGGTCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 35	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAGCGGGAGACCGGGGTCTCTGAGCA ATCCGCAAGGTCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 36	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATAGCGGGAGACCGGGGTCTCTGA GCCCCAAGGTCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 37	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGAGCGGGAGACCGGGGTCTC TGAGCCAAGGTCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 38	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAAGCGGGAGACCGGGGT CTCTGAGCGGTCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 39	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTAGCGGGAGACCGG GGTCTCTGAGCCTGGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 40	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGAGCGGGAGAC CGGGGTCTCTGAGCGCATTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA

GDH_DI _233- 289_ins ertion2 41	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCAAGCGGGA GACCGGGGTCTCTGAGCTTTACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 42	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTAGCG GGAGACCGGGGTCTCTGAGCACCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 43	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCA GCGGGAGACCGGGGTCTCTGAGCCCGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 44	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAGCGGGAGACCGGGGTCTCTGAGCAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 45	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACAGCGGGAGACCGGGGTCTCTGAGCGGTAAACTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 46	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAGCGGGAGACCGGGGTCTCTGAGCAAAGTCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 47	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAAAGCGGGAGACCGGGGTCTCTGAGCCTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 48	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGAGCGGGAGACCGGGGTCTCTGAGCCTGCTGCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGAGCGGGAGACCGGGGTCTCTGAGCCAGTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG

ertion2 49	CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 50	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGAGCGGGAGACCGGGGTCTCTGAGCTCTGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 51	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTAGCGGGAGACCGGGGTCTCTGAGCGAACAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 52	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAAAGCGGGAGACCGGGGTCTCTGAGCCAGGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 53	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGAGCGGGAGACCGGGGTCTCTGAGCGGTCCGA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 54	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCCCG AACGGTAAACTGCTGCAGTCTGAACAGGGTAGCGGGAGACCGGGGTCTCTGAGCCCGAAT TCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAG GCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGAACG GAGATTA
GDH_DI _233- 289_ins ertion2 55	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAGCGGGAGACCGGGGTCTCTGAGCA ATTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 56	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATAGCGGGAGACCGGGGTCTCTGA GCTCTGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 57	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTAGCGGGAGACCGGGGTCTC TGAGCGACGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA

GDH_DI _233- 289_ins ertion2 58	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACAGCGGGAGACCGGGGT CTCTGAGCGACGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 59	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACAGCGGGAGACCGG GGTCTCTGAGCGAAATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 60	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAAGCGGGAGAC CGGGGTCTCTGAGCATCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 61	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAGCGGGA GACCGGGGTCTCTGAGCAACCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 62	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACAGCG GGAGACCGGGGTCTCTGAGCCTGATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 63	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA GCGGGAGACCGGGGTCTCTGAGCATCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 64	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCAGCGGGAGACCGGGGTCTCTGAGCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 65	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAGCGGGAGACCGGGGTCTCTGAGCAAAGGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGCGGGAGACCGGGGTCTCTGAGCGGCGGCAATTACGGTTGGCCGAACGTTG

ertion2 66	CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 67	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCGGGAGACCGGGGTCTCTGAGCGGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 68	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCGGGAGACCGGGGTCTCTGAGCAATTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 69	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCAATTAGCGGGAGACCGGGGTCTCTGAGCTACGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 70	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCAATTACAGCGGGAGACCGGGGTCTCTGAGCGGTTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 71	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCAATTACGGTAGCGGGAGACCGGGGTCTCTGAGCTGGCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 72	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCAATTACGGTTGGAGCGGGAGACCGGGGTCTCTGAGCCCGAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 73	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCAATTACGGTTGGCCGAGCGGGAGACCGGGGTCTCTGAGCAACGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 74	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCAGCAATTACGGTTGGCCGAACAGCGGGAGACCGGGGTCTCTGAGCGTTG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGGA ACGGAGATTA

GDH_DI _233- 289_ins ertion2 75	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTAGCGGGAGACCGGGGTCTCTGAGCG CAGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 76	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAAGCGGGAGACCGGGGTCTCTGA GCGGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 77	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCAGCGGGAGACCGGGGTCTC TGAGCTATAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 78	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAGCGGGAGACCGGGGT CTCTGAGCAAAGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 79	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGCGGGAGACCGG GGTCTCTGAGCGACGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 80	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACAGCGGGAGAC CGGGGTCTCTGAGCGATAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGGA ACGGAGATTA
GDH_DI _233- 289_ins ertion2 81	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGGA GACCGGGGTCTCTGAGCAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins ertion2 82	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCAGCG GGAGACCGGGGTCTCTGAGCGGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCA

ertion2 83	GCGGGAGACCGGGGTCTCTGAGCTATGCATACGCGAATTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins ertion2 84	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCT ATAGCGGGAGACCGGGGTCTCTGAGCGCATACGCGAATTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins ertion2 85	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCCCG AACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGATCG TTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCTATGC AAGCGGGAGACCGGGGTCTCTGAGCTACGCGAATTATAGCGGGAGACGGGGAGGGAACG GAGATTA
GDH_DI _233- 289_ins ertion2 86	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCT ATGCATACAGCGGGAGACCGGGGTCTCTGAGCGCGAATTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins ertion2 87	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCT ATGCATACGCGAGCGGGAGACCGGGGTCTCTGAGCAATTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins ertion2 88	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCT ATGCATACGCGAATAGCGGGAGACCGGGGTCTCTGAGCTATAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _233- 289_ins ertion2 89	CATGTTTAGGAACGCTACCGTCTCCGGGTCACCGTAATCCGCAAGGTCTGGCATTACCC CGAACGGTAAACTGCTGCAGTCTGAACAGGGTCCGAATTCTGACGACGAAATCAACCTGA TCGTTAAAGGCGGCAATTACGGTTGGCCGAACGTTGCAGGCTATAAAGACGATAGCGGCT ATGCATACGCGAATTATAGCGGGAGACCGGGGTCTCTGAGCAGCGGGAGACGGGGAGGG AACGGAGATTA
GDH_DI _290- 346_ins ertion2 90	GTACATGAAACGATGGACCGTCTCCTAGCAGCGGGAGACCGGGGTCTCTGAGCGCAGCGG CAAACAAAAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 91	GTACATGAAACGATGGACCGTCTCCTAGCGCAAGCGGGAGACCGGGGTCTCTGAGCGCGG CAAACAAAAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC

GDH_DI _290- 346_ins ertion2 92	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGAGCGGGAGACCGGGGTCTCTGAGCG CAAACAAAAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 93	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAGCGGGAGACCGGGGTCTCTGA GCAACAAAAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 94	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAGCGGGAGACCGGGGTCTC TGAGCAAAAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 95	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAAAAGCGGGAGACCGGGGT CTCTGAGCAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 96	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAAAAGCAGCGGGAGACCGG GGTCTCTGAGCATCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 97	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAAAAGCATCAGCGGGAGAC CGGGGTCTCTGAGCAAAGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 98	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAAAAGCATCAAAGACGGGA GACCGGGGTCTCTGAGCGACCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion2 99	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAAAAGCATCAAAGACAGCG GGAGACCGGGGTCTCTGAGCCTGGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAACAAAAGCATCAAAGACCTGA GCGGGAGACCGGGGTCTCTGAGCGCCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA

ertion3 00	CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 01	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCAGCGGGAGACCGGGGTCTCTGAGCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 02	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAGCGGGAGACCGGGGTCTCTGAGCAACGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 03	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACAGCGGGAGACCGGGGTCTCTGAGCGGTGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 04	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTAGCGGGAGACCGGGGTCTCTGAGCGTTAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 05	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAGCGGGAGACCGGGGTCTCTGAGCAAAGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 06	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAAGCGGGAGACCGGGGTCTCTGAGCGTTGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 07	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTAGCGGGAGACCGGGGTCTCTGAGCGCAGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 08	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAAGCGGGAGACCGGGGTCTCTGAGCGCAGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC

GDH_DI _290- 346_ins ertion3 09	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAAGCGGGAGACCGGGGTCTCTGAGCGGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 10	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCAGCGGGAGACCGGGGTCTCTGAGCGTTCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 11	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTAGCGGGAGACCGGGGTCTCTGAGCCCGG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 12	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGAGCGGGAGACCGGGGTCTCTGAGCG TTACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 13	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGTTAGCGGGAGACCGGGGTCTCTGA GCACCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 14	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGTTACGAGCGGGAGACCGGGGTCTC TGAGCAAAGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 15	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGTTACCAAAGCGGGAGACCGGGGT CTCTGAGCGAAAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 16	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGGC CCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGTTACCAAAGAAAGCGGGAGACCGGG GTCTCTGAGCAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACC GTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGGAG ACTATACC
GDH_DI _290- 346_ins	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGTTACCAAAGAAAGCAGCGGGAGAC CGGGGTCTCTGAGCGAGTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA

ertion3 17	CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 18	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGAGCGGGA GACCGGGGTCTCTGAGCTGGACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 19	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGAGCG GGAGACCGGGGTCTCTGAGCACCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 20	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCA GCGGGAGACCGGGGTCTCTGAGCGGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 21	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAGCGGGAGACCGGGGTCTCTGAGCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 22	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAGCGGGAGACCGGGGTCTCTGAGCAACTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 23	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACAGCGGGAGACCGGGGTCTCTGAGCTTTGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 24	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTAGCGGGAGACCGGGGTCTCTGAGCGTTCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 25	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTAGCGGGAGACCGGGGTCTCTGAGCCCCGCCGCTGAAAACCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC

GDH_DI _290- 346_ins ertion3 26	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGAGCGGGAGACCGGGGTCTCTGAGCCCGCTGAAAACCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 27	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGAGCGGGAGACCGGGGTCTCTGAGCCTGAAAACCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 28	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAGCGGGAGACCGGGGTCTCTGAGCAAACCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 29	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAAGCGGGAGACCGGGGTCTCTGAGCACCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 30	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCAGCGGGAGACCGGGGTCTCTGAGCCTGTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 31	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGAGCGGGAGACCGGGGTCTCTGAGCTATA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 32	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATAGCGGGAGACCGGGGTCTCTGAGCA CCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 33	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCAGCGGGAGACCGGGGTCTCTGA GCGTCCAGGACACCTACAACCTATAACGATCCGACCTGCGGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCAGCGGGAGACCGGGGTCTC

ertion3 34	TGAGCCAGGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 35	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGAGCGGGAGACCGGGGT CTCTGAGCGACACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 36	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACAGCGGGAGACCGG GGTCTCTGAGCACCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 37	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCAGCGGGAGAC CGGGGTCTCTGAGCTACAACCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 38	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAGCGGGA GACCGGGGTCTCTGAGCAACTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 39	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACAGCG GGAGACCGGGGTCTCTGAGCTATAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAGG AGACTATACC
GDH_DI _290- 346_ins ertion3 40	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA GCGGGAGACCGGGGTCTCTGAGCAACGATCCGACCTGCGGCGAAAGGAGACGCGCTGAG GAGACTATACC
GDH_DI _290- 346_ins ertion3 41	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA ACAGCGGGAGACCGGGGTCTCTGAGCGATCCGACCTGCGGCGAAAGGAGACGCGCTGAG GAGACTATACC
GDH_DI _290- 346_ins ertion3 42	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA ACGATAGCGGGAGACCGGGGTCTCTGAGCCCGACCTGCGGCGAAAGGAGACGCGCTGAG GAGACTATACC

GDH_DI _290- 346_ins ertion3 43	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA ACGATCCGAGCGGGAGACCGGGGTCTCTGAGCACCTGCGGCGAAAGGAGACGCGCTGAG GAGACTATACC
GDH_DI _290- 346_ins ertion3 44	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA ACGATCCGACCAGCGGGAGACCGGGGTCTCTGAGCTGCGGCGAAAGGAGACGCGCTGAG GAGACTATACC
GDH_DI _290- 346_ins ertion3 45	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA ACGATCCGACCTGCAGCGGGAGACCGGGGTCTCTGAGCGGCGAAAGGAGACGCGCTGAG GAGACTATACC
GDH_DI _290- 346_ins ertion3 46	GTACATGAAACGATGGACCGTCTCCTAGCGCAGCGGGCAAACAAAAGCATCAAAGACCTGG CCCAGAACGGTGTTAAAGTTGCAGCAGGCGTTCCGGTTACCAAAGAAAGCGAGTGGACCG GCAAAAACCTTTGTTCCGCCGCTGAAAACCCTGTATACCGTCCAGGACACCTACAACCTATA ACGATCCGACCTGCGGCAGCGGGAGACCGGGGTCTCTGAGCGAAAGGAGACGCGCTGAG GAGACTATACC
GDH_DI _347- 404_ins ertion3 47	GGCGAGAGGAGATATACGTCTCCCGAAAGCGGGAGACCGGGGTCTCTGAGCATGACCTAT ATTTGCTGGCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGA TCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATC AAACTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACAGCTG TTCGAT
GDH_DI _347- 404_ins ertion3 48	GGCGAGAGGAGATATACGTCTCCCGAAATGAGCGGGAGACCGGGGTCTCTGAGCACCTAT ATTTGCTGGCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 49	GGCGAGAGGAGATATACGTCTCCCGAAATGACCAGCGGGAGACCGGGGTCTCTGAGCTAT ATTTGCTGGCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 50	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATAGCGGGAGACCGGGGTCTCTGAGC ATTTGCTGGCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTAGCGGGAGACCGGGGTCTCTG AGCTGCTGGCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC

ertion3 51	ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 52	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCAGCGGGAGACCGGGGTCT CTGAGCTGGCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 53	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGAGCGGGAGACCGGGG TCTCTGAGCCCGACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 54	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGAGCGGGAGACCG GGGTCTCTGAGCACCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 55	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCAGCGGGGAGA CCGGGGTCTCTGAGCGTTGCACCGAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 56	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTAGCGGG AGACCGGGGTCTCTGAGCGCACCGAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 57	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCAAGC GGGAGACCGGGGTCTCTGAGCCCGAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 58	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGCGGGAGACCGGGGTCTCTGAGCAGTTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 59	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTAGCGGGAGACCGGGGTCTCTGAGCTCTGCATACGTTTACAAAGGCGGCCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT

GDH_DI _347- 404_ins ertion3 60	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTAGCGGGAGACCGGGGTCTCTGAGCGCATACGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 61	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCAAGCGGGAGACCGGGGTCTCTGAGCTACGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 62	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACAGCGGGAGACCGGGGTCTCTGAGCGTTTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 63	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTAGCGGGAGACCGGGGTCTCTGAGCTACAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 64	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAGCGGGAGACCGGGGTCTCTGAGCAAAGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 65	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAAGCGGGAGACCGGGGTCTCTGAGCGGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 66	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCAGCGGGAGACCGGGGTCTCTGAGCGGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 67	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAGCGGGAGACCGGGGTCTCTGAGCAAAAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAGCGGGAGACCGGGGTCTCTGAGCAAAGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC

ertion3 68	ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 69	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGGGAGACCGGGGTCTCTGAGCGCG ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 70	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGAGCGGGAGACCGGGGTCTCTGAGC ATCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 71	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCAGCGGGAGACCGGGGTCTCTG AGCACCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 72	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCAGCGGGAGACCGGGGTCT CTGAGCGGTTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 73	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCAGTAGCGGGAGACCGGGG TCTCTGAGCTGGGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 74	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCAGTTGGAGCGGGAGACCG GGGTCTCTGAGCGAAAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 75	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCAGTTGGGAAAGCGGGAGA CCGGGGTCTCTGAGCAATACCCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 76	GCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCAGTTGGGAAAATAGCGGG AGACCGGGGTCTCTGAGCACCTGCTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTCCGAGACGGTGCACA GCTGTTCGAT

GDH_DI _347- 404_ins ertion3 77	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCAGC GGGAGACCGGGGTCTCTGAGCCTGCTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 78	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCGA GTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTGAG CGGGAGACCGGGGTCTCTGAGCCTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCATC AAACTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACAGCTG TTCGAT
GDH_DI _347- 404_ins ertion3 79	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGAGCGGGAGACCGGGGTCTCTGAGCGTTCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 80	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTAGCGGGAGACCGGGGTCTCTGAGCCCGAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 81	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGCGGGAGACCGGGGTCTCTGAGCAGTCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 82	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTAGCGGGAGACCGGGGTCTCTGAGCCTGAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 83	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAGCGGGAGACCGGGGTCTCTGAGCAAACGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 84	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAAAGCGGGAGACCGGGGTCTCTGAGCCGCGGCGTTATCTTCCGC ATCAAACCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCAGCGGGAGACCGGGGTCTCTGAGCGGCGTTATCTTCCGC

ertion3 85	ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 86	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCAGCGGGAGACCGGGGTCTCTGAGCGTTATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 87	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTAGCGGGAGACCGGGGTCTCTGAGCATCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 88	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCAGCGGGAGACCGGGGTCTCTGAGCTTCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 89	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCAGCGGGAGACCGGGGTCTCTGAGCCGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 90	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCAGCGGGAGACCGGGGTCTCTGAGC ATCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 91	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAGCGGGAGACCGGGGTCTCTG AGCAAAGTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 92	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAAGCGGGAGACCGGGGTCT CTGAGCCTGGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 93	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAAGTGAAGCGGGAGACCGGGG TCTCTGAGCGATCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT

GDH_DI _347- 404_ins ertion3 94	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATAGCGGGAGACCG GGGTCTCTGAGCCCGACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 95	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGAGCGGGAGA CCGGGGTCTCTGAGCACCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 96	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCAGCGGG AGACCGGGGTCTCTGAGCTATAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 97	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCTATAGC GGGAGACCGGGGTCTCTGAGCAGTACCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 98	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCTATAGT AGCGGGAGACCGGGGTCTCTGAGCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion3 99	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCTATAGT ACCAGCGGGAGACCGGGGTCTCTGAGCACCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion4 00	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCTATAGT ACCACCAGCGGGAGACCGGGGTCTCTGAGCTACGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins ertion4 01	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCTATAGT ACCACCTACAGCGGGAGACCGGGGTCTCTGAGCGACGATGCCGTTTCGGAGACGGTGCACA GCTGTTCGAT
GDH_DI _347- 404_ins	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAACCTGGATCCGACCTATAGT

ertion4 02	ACCACCTACGACAGCGGGAGACCGGGGTCTCTGAGCGATGCCGTTCCGGAGACGGTGCACA GCTGTTTCGAT
GDH_DI _347- 404_ins ertion4 03	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAAGTGGATCCGACCTATAGT ACCACCTACGACGATAGCGGGAGACCGGGGTCTCTGAGCGCCGTTCCGGAGACGGTGCACA GCTGTTTCGAT
GDH_DI _347- 404_ins ertion4 04	GGCGAGAGGAGATATACGTCTCCCGAAATGACCTATATTTGCTGGCCGACCGTTGCACCG AGTTCTGCATACGTTTACAAAGGCGGCAAAAAAGCGATCACCGGTTGGGAAAATACCCTG CTGGTTCGAGTCTGAAACGCGGCGTTATCTTCCGCATCAAAGTGGATCCGACCTATAGT ACCACCTACGACGATGCCAGCGGGAGACCGGGGTCTCTGAGCGTTCGGAGACGGTGCACA GCTGTTTCGAT
GDH_DI _405- 461_ins ertion4 05	TTATAATCATCCTCCCCGCGTCTCCCGTTAGCGGGAGACCGGGGTCTCTGAGCCCGATGT TCAAAAGCAACAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTTCAAGAACGACGCGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 06	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGAGCGGGAGACCGGGGTCTCTGAGCATGT TCAAAAGCAACAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTTCAAGAACGACGCGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 07	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGAGCGGGAGACCGGGGTCTCTGAGCT TCAAAAGCAACAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTTCAAGAACGACGCGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 08	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTTCAAGCGGGAGACCGGGGTCTCTGA GCAAAAGCAACAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTTCAAGAACGACGCGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 09	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTTCAAAAGCGGGAGACCGGGGTCTCTG AGCAGCAACAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCT GACCGATACCGCAGGTAACGTTTCAAGAACGACGCGGTAGCGTTACCAATACCCTGGAAAAT CCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACACATCCT ATTT
GDH_DI _405- 461_ins ertion4 10	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTTCAAAAGCAGCGGGAGACCGGGGT CTCTGAGCAACAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTTCAAGAACGACGCGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT

GDH_DI _405- 461_ins ertion4 11	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAGCGGGAGACCGG GGTCTCTGAGCAACCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 12	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACAGCGGGAGAC CGGGGTCTCTGAGCCGTTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 13	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTAGCGGGA GACCGGGGTCTCTGAGCTATCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 14	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATAGCG GGAGACCGGGGTCTCTGAGCCGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 15	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCA GCGGGAGACCGGGGTCTCTGAGCGACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 16	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACAGCGGGAGACCGGGGTCTCTGAGCGTTATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 17	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTAGCGGGAGACCGGGGTCTCTGAGCATTGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 18	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTAGCGGGAGACCGGGGTCTCTGAGCGCAAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGCGGGAGACCGGGGTCTCTGAGCAGTCCGGACGGTAACGTTCTGTACG TTCTGACCGGATACCGCAGGTAACGTTAGAAAGACGACGGTAGCGTTACCAATACCCTGG

ertion4 19	AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 20	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTAGCGGGAGACCGGGGTCTCTGAGCCCGGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 21	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGAGCGGGAGACCGGGGTCTCTGAGCGACGGTAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 22	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACAGCGGGAGACCGGGGTCTCTGAGCGGTAAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 23	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAGCGGGAGACCGGGGTCTCTGAGCAACGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 24	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACAGCGGGAGACCGGGGTCTCTGAGCGTTCTGTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 25	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTAGCGGGAGACCGGGGTCTCTGAGCCTGTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 26	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGAGCGGGAGACCGGGGTCTCTGAGCTACG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 27	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACAGCGGGAGACCGGGGTCTCTGAGCG TTCTGACCGATACCGCAGGTAACGTTCAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT

GDH_DI _405- 461_ins ertion4 28	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTAGCGGGAGACCGGGGTCTCTGA GCCTGACCGATACCGCAGGTAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 29	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGAGCGGGAGACCGGGGTCTC TGAGCACCGATACCGCAGGTAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 30	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCAGCGGGAGACCGGGGT CTCTGAGCGATACCGCAGGTAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 31	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATAGCGGGAGACCGG GGTCTCTGAGCACCGCAGGTAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 32	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCAGCGGGAGAC CGGGGTCTCTGAGCGCAGGTAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 33	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAAGCGGGA GACCGGGGTCTCTGAGCGGTAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 34	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAGCG GGAGACCGGGGTCTCTGAGCAACGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 35	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACA GCGGGAGACCGGGGTCTCTGAGCGTTTCAAGAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTAGCGGGAGACCGGGGTCTCTGAGCCAGAAAGACGACGGTAGCGTTACCAATACCCTGG

ertion4 36	AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 37	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAGCGGGAGACCGGGGTCTCTGAGCAAAGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 38	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAAGCGGGAGACCGGGGTCTCTGAGCGACGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 39	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACAGCGGGAGACCGGGGTCTCTGAGCGACGGTAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 40	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCGACG TTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACGTTTACG AAAGACGACAGCGGGAGACCGGGGTCTCTGAGCGGTAGCGTTACCAATACCCTGGAAAAT CCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACACATCCT ATTT
GDH_DI _405- 461_ins ertion4 41	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGGGAGACCGGGGTCTCTGAGCAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 42	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCAGCGGGAGACCGGGGTCTCTGAGCGTTACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 43	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTAGCGGGAGACCGGGGTCTCTGAGCACCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 44	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAGCGGGAGACCGGGGTCTCTGAGCAATACCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT

GDH_DI _405- 461_ins ertion4 45	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATAGCGGGAGACCGGGGTCTCTGAGCACCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 46	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCAGCGGGAGACCGGGGTCTCTGAGCCTGG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 47	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGAGCGGGAGACCGGGGTCTCTGAGCG AAAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 48	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAGCGGGAGACCGGGGTCTCTGA GCAATCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 49	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATAGCGGGAGACCGGGGTCTC TGAGCCCGGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 50	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGAGCGGGAGACCGGGGT CTCTGAGCGGTAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 51	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCGGGAGACCGG GGTCTCTGAGCAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 52	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCAGCGGGAGAC CGGGGTCTCTGAGCCTGATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGAGCGGGA

ertion4 53	GACCGGGGTCTCTGAGCATCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 54	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAGCG GGAGACCGGGGTCTCTGAGCAAATTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 55	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAA GCGGGAGACCGGGGTCTCTGAGCTTCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 56	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAT TCAGCGGGAGACCGGGGTCTCTGAGCACCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 57	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAT TCACCAGCGGGAGACCGGGGTCTCTGAGCTACAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 58	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAT TCACCTACAGCGGGAGACCGGGGTCTCTGAGCAAAGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 59	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAT TCACCTACAAAAGCGGGAGACCGGGGTCTCTGAGCGCGAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 60	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAT TCACCTACAAAGCGAGCGGGAGACCGGGGTCTCTGAGCAAATGACGGAGACGCGAGCACA CATCCTATTT
GDH_DI _405- 461_ins ertion4 61	TTATAATCATCCTCCCCGCGTCTCCCGTTCCGATGTTCAAAAGCAACAACCGTTATCGCG ACGTTATTGCAAGTCCGGACGGTAACGTTCTGTACGTTCTGACCGATACCGCAGGTAACG TTCAGAAAGACGACGGTAGCGTTACCAATACCCTGGAAAATCCGGGTAGCCTGATCAAAT TCACCTACAAAGCGAAAAGCGGGAGACCGGGGTCTCTGAGCTGACGGAGACGCGAGCACA CATCCTATTT