

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS GGGGCCAACTCCC CGCAATATGAAGCGCATGAATACAAGTTATTCATTGAAATGAAATTC
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS CGAATCAGCTTTGTCTACAAAAAGGAAGCTATAAGTAAGTAAGTACTAGGAATCTCATGGAGA
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS GTTCGATCCTGGCTCAGGATGAACGCTGGCGGCATGCTTAACACATGCAAGTCGGACGGG
GTTG.ATCCTG.GTCAGTATGAACGCTTGCTGCATGCTT.ACACATGCAAGTCGAACGGG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS AAGTGGTGTITTCAGTGGCGGACGGGTGAGTAACCGCTAAGAACCTGCCCTTGGGAGGGG
AAGTGGTGTITTCAGTGGCGGACGGGTGAGTAACCGCTAAGAACCTG.CCTTGGGAGGGG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS AACAAACAGCTGGAAACGGCTGCTAATACCCCGTAGGCTGAGGAGCAAAAAGGAGGAATCCG
AACAAACAGCTGGAAACGGCTGCTAATACCCG.TAAGCTGAGGAGCGAAAAGGAGGAATCCG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS CCCGAGGAGGGGCTCGCGTCTGATTAGCTAGTITGGTGAGG.CAATAGCTTACCAAGGCCGA
CCCAAG.GAGGGCTCGCGTCTGATTAGCTAGTITGGTGAGGGTACTAGCTTACAGG..CGG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS TGATCAGTAGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCCAGAC
TGATCAGTAGCTGGTCCGAGGG...ATGACACACACTGG.GATGAGACAAGGCCAGAC
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS TCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATG
TCCTACGGGAGGCAGCAGTGGGGAATTTTCCGCAATGG..GGAAGCCTGACG.AGCAATG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS CCGCGTGGAGGTAGAAGGCCTACGGGTCTGAACTTCTTTTCCCAGAGAAGAAGCAATGA
CCGCGTGGAGGTAAAAGGCCTACGGGTCTGAACTTCTTTTCTGGAG.AAAACCAATGA
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS CGGTATCTGGGGAATAAGCATCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGA
CGGTATCTGGGGAATAAGCATCGGCTAACACTGTGCCAGCAGCCGCGGTAAGACAGAGAT
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS TGCAAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGGTGGCTTTTTAAGTCCGC
G..CAGCGTTATCCGGAATGATTGGGCGTAAAGCGTCTGTAGG.GGCTTTTTAAGTTCCG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS CGTCAAATCCCAGGGCTCAACCCTGGACAGGCGGTGGAAACTACCAAGCTTG.AGTACGG
CG..CAATCCCAGG.CTCAACCTG.ACAGGTG.TGAAACTACTAAGCTAGGAATACGG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS TAGGGGCAGAGGGAATTTCCGGTGGAGCGGTGAAATGCGTAGAGATCGGAAAGAACACCA
TAGGGGCAGAGG.AATTTCCGGTGGAGCGATGAAATGCGTAGAGATCGGAAG..GAAACC
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS ACGGCGAAAGCACTCTGCTGGGCCGACACTGACACTGAGAGACGAAAGCTAGGGGAGCGA
ACGGCGAAAGCACCTG..CTGGCCGACACTGACACTGAGAGACGAAAGCTAGGGGAGCGA
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS ATGGGATTAGATACCCAGTAGTCTTAGCCGTAACGATGGATACTAGGCG.CTGTGCGT
ATGGGATTAGATACCCAGTAGTCTTAGCCG.AAACGATGGATAAAGGGCGGCTGTGCGT
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS ATCGACCCGTGCAATGCTGTAGCTAACGCGTTAAGTATCCCGCTGGGGAGTACGTTCCG
ATCGACCCGTGCAATGCTGTAGCTAACGCG.TAAGTATCCCGCTGGGGAGTAAGTTCCG
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS AAGAATGAAACTCAAAGGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTTAA
AAGAATGAAACTCAAAGGAATG.ACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTTAT
consensus>70

chr4_490072_490302
NONATHHT003850.1
f111.68878518.31_2627_CCS TTCGATGCAAAGCGAAGAACCTTACCAGGGCTTGACATGCCGCGAATCCTCTTGAAAGAG
TCGATGCATAAGCGAAGAACCTTACCAGGGCTGACCATGCCGCGAATCTACTTTGAAAGA
consensus>70

chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
AGGGGTGCCTTCGGGAACGCGGACACAGGTGGTGCATGGCTGTGCTCAG.CTCGTGCCGT
TAGGATTGCTGTGCGAACGCGGACACAGGTGGGGCATG.CTGTCGGCAAGCTCGTGCCGT
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
AAGGTGTTGGGTTAAGTCCCAGAACGAGCGCAACCCCTCGTGTTTAGTTGCCACCGTTGAG
GGTG...TTGGTTTAGTCCCGCAACGAGCGCAACCCCTCGGGTTTAGTTCCAAT..TTAG
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
TTTGGAAACCCTGAACAGACTGCCGGTGATAAGCCGGAGGAAGGTGAGGATGACGTCAAGT
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
CATCATGCCCTTATGCCCTGGGCGACA CACG.TGCTACAATGGACGGGACAAAGGATCG
CATCATGCCCTTATGCACTTGGCGACA CACG.TGCTACAATGGAA GGGACAAAGGATCG
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
CGA C C C G C G A G G T G A G C T A A C T T C A A A A C C C G T C C T C A G T T C G G A T T G T A G G C T G C A
CGA T C C C G C G A G G T G A G C T A A C T T C A A A A C C C G T C C T C A G T T C G G A T T G T A G G C T G C A
CGA C C C G A G G T G T G A G C T A A C T T C A A A A C C C G T C C T C A G T T C G G A T T G T A G G C T G C A
CGA . C C . G . G . G T G A G C T A A C T . C A A A A . C C . T C C T C A G T T C G . A T T G . A G G C . C A
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
ACTCGCCTA CATGAAGC GGA ATCGCTAG TAATCGCCGGTCAG C CATAACGGCGGTGAATT
ACTCGCCTG CATGAAGC GGA ATCGCTAG TAATCGCCGGTCAG C CATAACGGCGGTGAATT
ACTCGCCTA CATGAAGC GGA ATCGCTAG TAATCGCCGGTCAG C CATAACGGCGGTGAATT
ACTCGCCT . CATGAAGC . G . A TAATCGCCGGTCAG . CATAACGGCGGTGAATT
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
CGTTCC C G G C C T T G T A C A C A C C G C C C G T C A C A C T A T G G G A G C T G . G C C A T G C C C G A A G T
CGTTCC C G G C C T T G T A C A C A C C G C C C G T C A C A C T A T G G G A G C T G . G C C A T G C C C G A A G T
CGTTCC G G G . C C T T G T A C A C A C C G C C C G T C A C A C T A T G G G A G C T G C C C A T G C C C G A A G T
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
CGT TA C C T T A A C C G C A A G G A G
CGT TA C C T T A A C C G C A A G A G G G G G G T G . . C C G A A G G C A G G G C T A G T G A C T G G A G T G A A G
CGT A C C C T T A A C C G C A A G G A G G G G G G A T G A C C G A A G G C A G G G C T A T G . . A C T G A G T G A A G
CGT . . C C T T A A C C G C A A . G

chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
TCGTAACAAGGTAGCCGTACTGGAAGGTGCGGCTGGATCACCTCCTTT.....
TCGTAACAAG.TAGCCGTACTGGAAGGTGCGACTGGATCACATCCTTTTCAGGAACTATA
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
CTTTTCTGGGTTGTTTGGTTTACCTGCCTCACACCTCAATAAACTAAGAAGCGAAGAGCC
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
ATTAACAATCTAAAATTGTTGGATGACTTTTTCTTGTTTAAAAATAAAAATGGTGAATGA
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
CAAGTGGAACGGCACTCATAAGATTATTATCCTAGGTCGGAACAGTGATAGGAGCTCCCT
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
TTTTTTGTCCCATCTCGCCCGGGGCGACATGAGACAAAAAGGGGAAAGAGAGATGG
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
GGTTCTCTCGCTTTGACATAGTGGGCCCTACGGAGGCCACACAACGGGCTATTGTGACG
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
TGGTAGAGCGCGCCCTGATAATTGCGTCGTTGTGCCTGACTGTGGGGCTCTCAGCCAC
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
ATAGATAGTTCAATGTGCTCATCGGCGCTGACCTGAGATGTGTACTCCAAGGCACATTA
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
GCATGGCGTACTTCTCCTGTTTGAACCGGGGTTTGAACCAACTCTCCTCAGGAGGATAG
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chr4_490072_490302
NONATHHT003850.1
fl11.68878518.31_2627_CCS
consensus>70
ATGGGGCGATTTCGGTGAGATCCAATGTGATCAACTTCTATTACTCGTGGATCCGGGCGG
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chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS GTCCAGGGGGGACCATCTGGCTCCTCTCCTCTCGAGAATTCATATATCCTTATCAGTATA
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS TGAGCAGCTATCTCTCGAGCACGGTTTTAGTTTTGGCCTCAATAAAAAAATTGAAAACGAGC
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS ACCTAACAACTATCTTCACAGACCAAAAACTACGAGATCACCTCTTCATTTGGGGTGACG
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS GCGGGATCGTACCATTCTCTTGACTCGAAATGGGAGCAGGTAAGAAAAGATCTTAGAGTG
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS TCTCTACGCCTTCTTTTTTCTTCTCATCAGAGTTATTGTTATCCACAAATACTTATCATG
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS GTAAGGAAGAAGGGGAAACAGCACACTTGAGAGCGCAGTACATGGATAGTTGTATGCTGC
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS GTTCGGGAGGTGAATCGCTCCGAAAAGGAATTAATTGATTCTCTCCAATTGGATGGACC
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS GTAGGTGCGATGATTTACTTCACGGGCGAGGTCTCTGGTTCAAGTCCAGGATAGCCCGCT
consensus>70 .....

chr4_490072_490302 .....
NONATH003850.1 .....
f111.68878518.31_2627_CCS CTGCG
consensus>70 .....
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