Supplementary Table 5: Validation of isoforms through Multiple alignment of identified and validated 33 novel full-length transcripts isoforms with RefSeq (NCBI Reference Sequence Database.

Colours Assigned for Exons by Numbers

Exon Number	Colour Assigned
1	🟥
2	🟥
3	🟨
4	⬛
5	🟩
6	🟩
7	🟦
8	🟦
9	🟦
10	🟪

SCAMP3

Sequence	Header	AA Seq
Present	i1_HQ_samplec9816d|c20030/f5p0/1447	>VIRT31885
Absent	i1_HQ_samplec9816d|c29753/f2p0/1106	>VIRT38385
NCBI	NM_005698	NP_005689.2
	NM_052837	NP_443069.1

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>NM_005698.3 Homo sapiens secretory carrier membrane protein 3 (SCAMP3), transcript variant 1, mRNA
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PCSFVCWYRPMYKAFRSDSSFNFFVFFFIFFVQDVLFVLQAIGIPGWGFSGWISALVVPKGNTAVSVLML
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>NM_052837.2 Homo sapiens secretory carrier membrane protein 3 (SCAMP3), transcript variant 2, mRNA
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i1_HQ_samplec9816d|c29753/f2p0/1106      CCACCCTCAGCTCCCTCCTTGCAGCCCTCGAGAAAGCTCAGCCCCACAGAACCTAAGAAC 283
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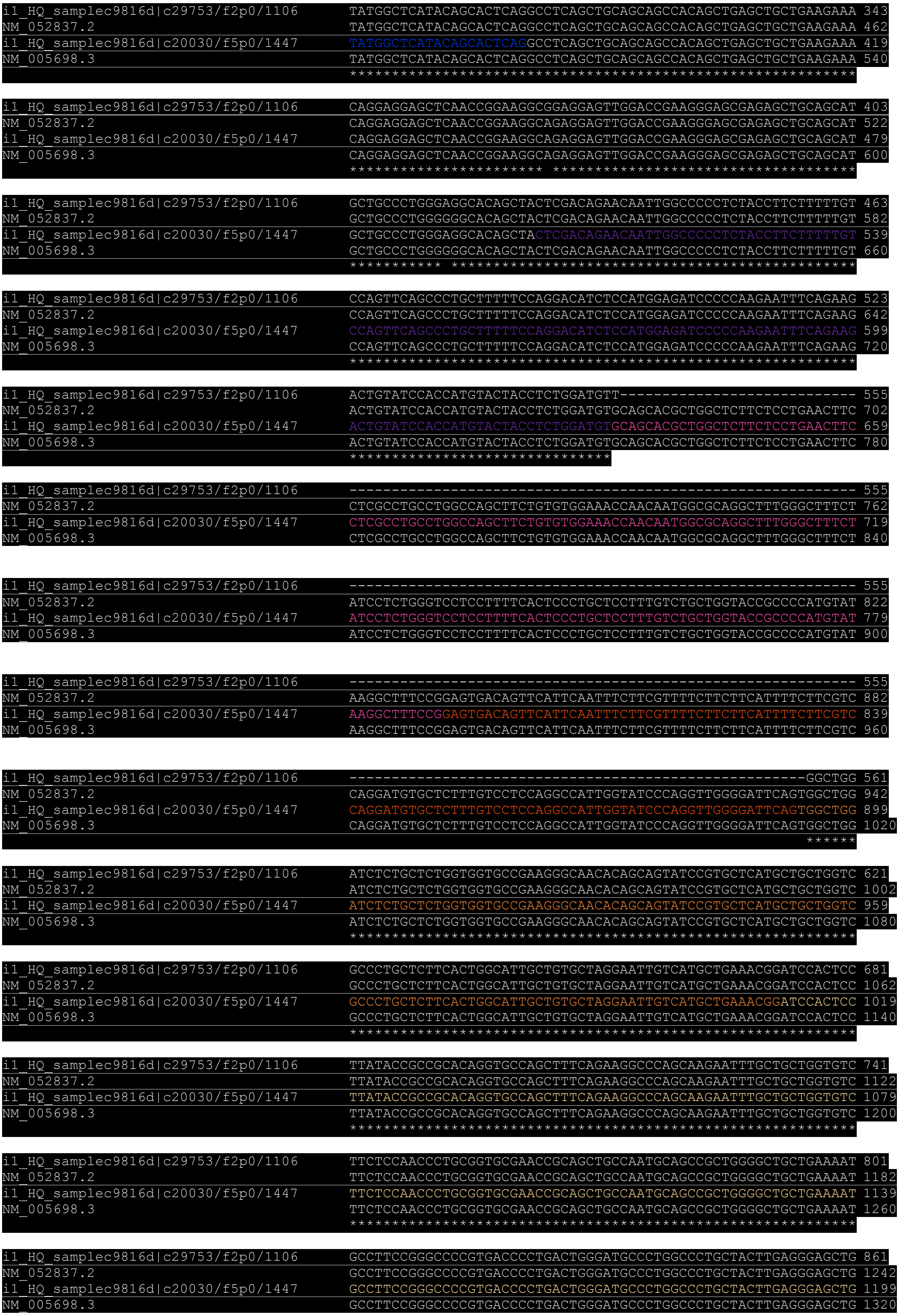

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i1_HQ_samplec9816d|c20030/f5p0/1447      TTCTCCAACCCTGCGGTGCGAACCGCAGCTGCCAATGCAGCCGCTGGGGCTGCTGAAAAT 1139
NM_005698.3                              TTCTCCAACCCTGCGGTGCGAACCGCAGCTGCCAATGCAGCCGCTGGGGCTGCTGAAAAT 1260
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VIRT38385        ------------------------------------------------------------     178
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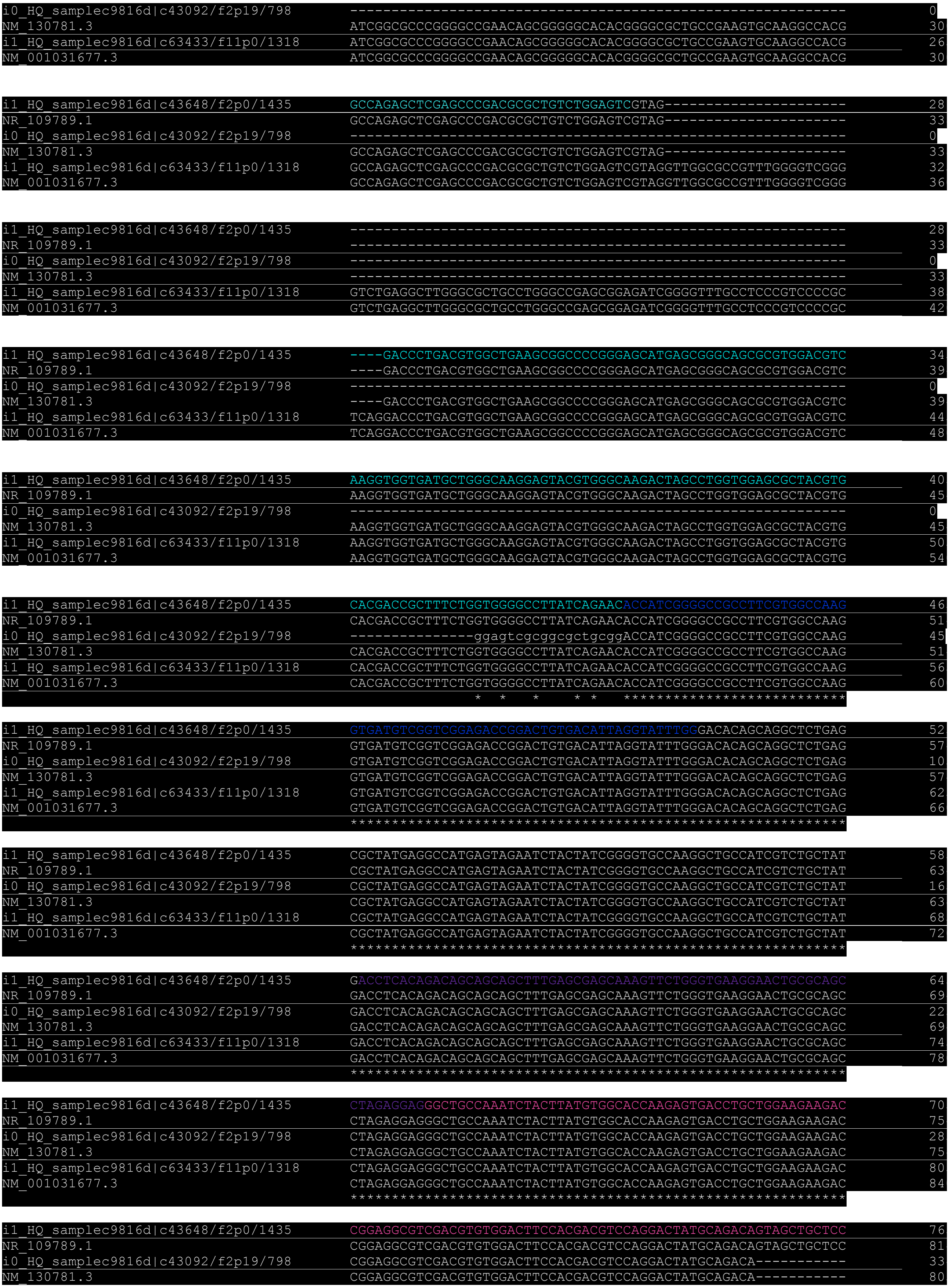

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i1_HQ_samplec9816d|c63433/f11p0/1318      ATCGGCGCCCGGGGCCGAACAGCGGGGGCACACGGGGCGCTGCCGAAGTGCAAGGCCACG          26
NM_001031677.3                            ATCGGCGCCCGGGGCCGAACAGCGGGGGCACACGGGGCGCTGCCGAAGTGCAAGGCCACG          30

i1_HQ_samplec9816d|c43648/f2p0/1435       GCCAGAGCTCGAGCCCGACGCGCTGTCTGGAGTCGTAG----------------------          28
NR_109789.1                               GCCAGAGCTCGAGCCCGACGCGCTGTCTGGAGTCGTAG----------------------          33
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          0
NM_130781.3                               GCCAGAGCTCGAGCCCGACGCGCTGTCTGGAGTCGTAG----------------------          33
i1_HQ_samplec9816d|c63433/f11p0/1318      GCCAGAGCTCGAGCCCGACGCGCTGTCTGGAGTCGTAGGTTGGCGCCGTTTGGGGTCGGG          32
NM_001031677.3                            GCCAGAGCTCGAGCCCGACGCGCTGTCTGGAGTCGTAGGTTGGCGCCGTTTGGGGTCGGG          36

i1_HQ_samplec9816d|c43648/f2p0/1435       ------------------------------------------------------------          28
NR_109789.1                               ------------------------------------------------------------          33
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          0
NM_130781.3                               ------------------------------------------------------------          33
i1_HQ_samplec9816d|c63433/f11p0/1318      GTCTGAGGCTTGGGCGCTGCCTGGGCCGAGCGGAGATCGGGGTTTGCCTCCCGTCCCCGC          38
NM_001031677.3                            GTCTGAGGCTTGGGCGCTGCCTGGGCCGAGCGGAGATCGGGGTTTGCCTCCCGTCCCCGC          42

i1_HQ_samplec9816d|c43648/f2p0/1435       ----GACCCTGACGTGGCTGAAGCGGCCCCGGGAGCATGAGCGGGCAGCGCGTGGACGTC          34
NR_109789.1                               ----GACCCTGACGTGGCTGAAGCGGCCCCGGGAGCATGAGCGGGCAGCGCGTGGACGTC          39
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          0
NM_130781.3                               ----GACCCTGACGTGGCTGAAGCGGCCCCGGGAGCATGAGCGGGCAGCGCGTGGACGTC          39
i1_HQ_samplec9816d|c63433/f11p0/1318      TCAGGACCCTGACGTGGCTGAAGCGGCCCCGGGAGCATGAGCGGGCAGCGCGTGGACGTC          44
NM_001031677.3                            TCAGGACCCTGACGTGGCTGAAGCGGCCCCGGGAGCATGAGCGGGCAGCGCGTGGACGTC          48

i1_HQ_samplec9816d|c43648/f2p0/1435       AAGGTGGTGATGCTGGGCAAGGAGTACGTGGGCAAGACTAGCCTGGTGGAGCGCTACGTG          40
NR_109789.1                               AAGGTGGTGATGCTGGGCAAGGAGTACGTGGGCAAGACTAGCCTGGTGGAGCGCTACGTG          45
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          0
NM_130781.3                               AAGGTGGTGATGCTGGGCAAGGAGTACGTGGGCAAGACTAGCCTGGTGGAGCGCTACGTG          45
i1_HQ_samplec9816d|c63433/f11p0/1318      AAGGTGGTGATGCTGGGCAAGGAGTACGTGGGCAAGACTAGCCTGGTGGAGCGCTACGTG          50
NM_001031677.3                            AAGGTGGTGATGCTGGGCAAGGAGTACGTGGGCAAGACTAGCCTGGTGGAGCGCTACGTG          54

i1_HQ_samplec9816d|c43648/f2p0/1435       CACGACCGCTTTCTGGTGGGGCCTTATCAGAACACCATCGGGGCCGCCTTCGTGGCCAAG          46
NR_109789.1                               CACGACCGCTTTCTGGTGGGGCCTTATCAGAACACCATCGGGGCCGCCTTCGTGGCCAAG          51
i0_HQ_samplec9816d|c43092/f2p19/798       ---------------ggagtcgcggcgctgcggACCATCGGGGCCGCCTTCGTGGCCAAG          45
NM_130781.3                               CACGACCGCTTTCTGGTGGGGCCTTATCAGAACACCATCGGGGCCGCCTTCGTGGCCAAG          51
i1_HQ_samplec9816d|c63433/f11p0/1318      CACGACCGCTTTCTGGTGGGGCCTTATCAGAACACCATCGGGGCCGCCTTCGTGGCCAAG          56
NM_001031677.3                            CACGACCGCTTTCTGGTGGGGCCTTATCAGAACACCATCGGGGCCGCCTTCGTGGCCAAG          60
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i1_HQ_samplec9816d|c43648/f2p0/1435       GTGATGTCGGTCGGAGACCGGACTGTGACATTAGGTATTTGGGACACAGCAGGCTCTGAG          52
NR_109789.1                               GTGATGTCGGTCGGAGACCGGACTGTGACATTAGGTATTTGGGACACAGCAGGCTCTGAG          57
i0_HQ_samplec9816d|c43092/f2p19/798       GTGATGTCGGTCGGAGACCGGACTGTGACATTAGGTATTTGGGACACAGCAGGCTCTGAG          10
NM_130781.3                               GTGATGTCGGTCGGAGACCGGACTGTGACATTAGGTATTTGGGACACAGCAGGCTCTGAG          57
i1_HQ_samplec9816d|c63433/f11p0/1318      GTGATGTCGGTCGGAGACCGGACTGTGACATTAGGTATTTGGGACACAGCAGGCTCTGAG          62
NM_001031677.3                            GTGATGTCGGTCGGAGACCGGACTGTGACATTAGGTATTTGGGACACAGCAGGCTCTGAG          66
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i1_HQ_samplec9816d|c43648/f2p0/1435       CGCTATGAGGCCATGAGTAGAATCTACTATCGGGGTGCCAAGGCTGCCATCGTCTGCTAT          58
NR_109789.1                               CGCTATGAGGCCATGAGTAGAATCTACTATCGGGGTGCCAAGGCTGCCATCGTCTGCTAT          63
i0_HQ_samplec9816d|c43092/f2p19/798       CGCTATGAGGCCATGAGTAGAATCTACTATCGGGGTGCCAAGGCTGCCATCGTCTGCTAT          16
NM_130781.3                               CGCTATGAGGCCATGAGTAGAATCTACTATCGGGGTGCCAAGGCTGCCATCGTCTGCTAT          63
i1_HQ_samplec9816d|c63433/f11p0/1318      CGCTATGAGGCCATGAGTAGAATCTACTATCGGGGTGCCAAGGCTGCCATCGTCTGCTAT          68
NM_001031677.3                            CGCTATGAGGCCATGAGTAGAATCTACTATCGGGGTGCCAAGGCTGCCATCGTCTGCTAT          72
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i1_HQ_samplec9816d|c43648/f2p0/1435       GACCTCACAGACAGCAGCAGCTTTGAGCGAGCAAAGTTCTGGGTGAAGGAACTGCGCAGC          64
NR_109789.1                               GACCTCACAGACAGCAGCAGCTTTGAGCGAGCAAAGTTCTGGGTGAAGGAACTGCGCAGC          69
i0_HQ_samplec9816d|c43092/f2p19/798       GACCTCACAGACAGCAGCAGCTTTGAGCGAGCAAAGTTCTGGGTGAAGGAACTGCGCAGC          22
NM_130781.3                               GACCTCACAGACAGCAGCAGCTTTGAGCGAGCAAAGTTCTGGGTGAAGGAACTGCGCAGC          69
i1_HQ_samplec9816d|c63433/f11p0/1318      GACCTCACAGACAGCAGCAGCTTTGAGCGAGCAAAGTTCTGGGTGAAGGAACTGCGCAGC          74
NM_001031677.3                            GACCTCACAGACAGCAGCAGCTTTGAGCGAGCAAAGTTCTGGGTGAAGGAACTGCGCAGC          78
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i1_HQ_samplec9816d|c43648/f2p0/1435       CTAGAGGAGGGCTGCCAAATCTACTTATGTGGCACCAAGAGTGACCTGCTGGAAGAAGAC          70
NR_109789.1                               CTAGAGGAGGGCTGCCAAATCTACTTATGTGGCACCAAGAGTGACCTGCTGGAAGAAGAC          75
i0_HQ_samplec9816d|c43092/f2p19/798       CTAGAGGAGGGCTGCCAAATCTACTTATGTGGCACCAAGAGTGACCTGCTGGAAGAAGAC          28
NM_130781.3                               CTAGAGGAGGGCTGCCAAATCTACTTATGTGGCACCAAGAGTGACCTGCTGGAAGAAGAC          75
i1_HQ_samplec9816d|c63433/f11p0/1318      CTAGAGGAGGGCTGCCAAATCTACTTATGTGGCACCAAGAGTGACCTGCTGGAAGAAGAC          80
NM_001031677.3                            CTAGAGGAGGGCTGCCAAATCTACTTATGTGGCACCAAGAGTGACCTGCTGGAAGAAGAC          84
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i1_HQ_samplec9816d|c43648/f2p0/1435       CGGAGGCGTCGACGTGTGGACTTCCACGACGTCCAGGACTATGCAGACAGTAGCTGCTCC          76
NR_109789.1                               CGGAGGCGTCGACGTGTGGACTTCCACGACGTCCAGGACTATGCAGACAGTAGCTGCTCC          81
i0_HQ_samplec9816d|c43092/f2p19/798       CGGAGGCGTCGACGTGTGGACTTCCACGACGTCCAGGACTATGCAGACA-----------          33
NM_130781.3                               CGGAGGCGTCGACGTGTGGACTTCCACGACGTCCAGGACTATGCAGACA-----------          80
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i1_HQ_samplec9816d|c63433/f11p0/1318      CGGAGGCGTCGACGTGTGGACTTCCACGACGTCCAGGACTATGCAGACA-----------      85
NM_001031677.3                            CGGAGGCGTCGACGTGTGGACTTCCACGACGTCCAGGACTATGCAGACA-----------      88
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i1_HQ_samplec9816d|c43648/f2p0/1435       TCAGCCCTTTGGGGGGTGGGGGTGTGTGGCTGTCTGGGTGGATCAAAGAAAATAGGGACT      82
NR_109789.1                               TCAGCCCTTTGGGGGGTGGGGGTGTGTGGCTGTCTGGGTGGATCAAAGAAAATAGGGACT      87
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------      33
NM_130781.3                               ------------------------------------------------------------      80
i1_HQ_samplec9816d|c63433/f11p0/1318      ------------------------------------------------------------      85
NM_001031677.3                            ------------------------------------------------------------      88


i1_HQ_samplec9816d|c43648/f2p0/1435       GCCTTGGCTGCCAGGGCAAGGTGCTCTAGGAGGTCTTCCTGGCCTCCTTGAACTGTGGGG      88
NR_109789.1                               GCCTTGGCTGCCAGGGCAAGGTGCTCTAGGAGGTCTTCCTGGCCTCCTTGAACTGTGGGG      93
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------      33
NM_130781.3                               ------------------------------------------------------------      80
i1_HQ_samplec9816d|c63433/f11p0/1318      ------------------------------------------------------------      85
NM_001031677.3                            ------------------------------------------------------------      88


i1_HQ_samplec9816d|c43648/f2p0/1435       TCCAGGAGACTCCCTGAACTGCTAGCCCTCCCTTTTGTCTGTTTATCTAATTCTCAGGTA      94
NR_109789.1                               TCCAGGAGACTCCCTGAACTGCTAGCCCTCCCTTTTGTCTGTTTATCTAATTCTCAGGTA      99
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------      33
NM_130781.3                               ------------------------------------------------------------      80
i1_HQ_samplec9816d|c63433/f11p0/1318      ------------------------------------------------------------      85
NM_001031677.3                            ------------------------------------------------------------      88


i1_HQ_samplec9816d|c43648/f2p0/1435       TGAGGCTTTAGTCACTTCTCTTTACAGATATCAAAGCTCAGCTCTTTGAAACATCCAGCA      10
NR_109789.1                               TGAGGCTTTAGTCACTTCTCTTTACAGATATCAAAGCTCAGCTCTTTGAAACATCCAGCA      10
i0_HQ_samplec9816d|c43092/f2p19/798       ---------------------------ATATCAAAGCTCAGCTCTTTGAAACATCCAGCA      36
NM_130781.3                               ---------------------------ATATCAAAGCTCAGCTCTTTGAAACATCCAGCA      83
i1_HQ_samplec9816d|c63433/f11p0/1318      ---------------------------ATATCAAAGCTCAGCTCTTTGAAACATCCAGCA      88
NM_001031677.3                            ---------------------------ATATCAAAGCTCAGCTCTTTGAAACATCCAGCA      92
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i1_HQ_samplec9816d|c43648/f2p0/1435       AGACAGGCCAGAGTGTGGACGAGCTCTTCCAGAAAGTGGCAGAGGATTACGTCAGTGTGG      10
NR_109789.1                               AGACAGGCCAGAGTGTGGACGAGCTCTTCCAGAAAGTGGCAGAGGATTACGTCAGTGTGG      11
i0_HQ_samplec9816d|c43092/f2p19/798       AGACAGGCCAGAGTGTGGACGAGCTCTTCCAGAAAGTGGCAGAGGATTACGTCAGTGTGG      42
NM_130781.3                               AGACAGGCCAGAGTGTGGACGAGCTCTTCCAGAAAGTGGCAGAGGATTACGTCAGTGTGG      89
i1_HQ_samplec9816d|c63433/f11p0/1318      AGACAGGCCAGAGTGTGGACGAGCTCTTCCAGAAAGTGGCAGAGGATTACGTCAGTGTGG      94
NM_001031677.3                            AGACAGGCCAGAGTGTGGACGAGCTCTTCCAGAAAGTGGCAGAGGATTACGTCAGTGTGG      98
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i1_HQ_samplec9816d|c43648/f2p0/1435       CTGCCTTCCAGGTGATGACAGAGGACAAGGGCGTGGATCTGGGCCAGAAGCCAAACCCCT      11
NR_109789.1                               CTGCCTTCCAGGTGATGACAGAGGACAAGGGCGTGGATCTGGGCCAGAAGCCAAACCCCT      11
i0_HQ_samplec9816d|c43092/f2p19/798       CTGCCTTCCAGGTGATGACAGAGGACAAGGGCGTGGATCTGGGCCAGAAGCCAAACCCCT      48
NM_130781.3                               CTGCCTTCCAGGTGATGACAGAGGACAAGGGCGTGGATCTGGGCCAGAAGCCAAACCCCT      95
i1_HQ_samplec9816d|c63433/f11p0/1318      CTGCCTTCCAGGTGATGACAGAGGACAAGGGCGTGGATCTGGGCCAGAAGCCAAACCCCT      10
NM_001031677.3                            CTGCCTTCCAGGTGATGACAGAGGACAAGGGCGTGGATCTGGGCCAGAAGCCAAACCCCT      10
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i1_HQ_samplec9816d|c43648/f2p0/1435       ACTTCTACAGCTGTTGTCATCACTGAGTCAGCACTCACCTGGCCTGGGGGAATTAAAGGA      11
NR_109789.1                               ACTTCTACAGCTGTTGTCATCACTGAGTCAGCACTCACCTGGCCTGGGGGAATTAAAGGA      12
i0_HQ_samplec9816d|c43092/f2p19/798       ACTTCTACAGCTGTTGTCATCACTGAGTCAGCACTCACCTGGCCTGGGGGAATTAAAGGA      54
NM_130781.3                               ACTTCTACAGCTGTTGTCATCACTGAGTCAGCACTCACCTGGCCTGGGGGAATTAAAGGA      10
i1_HQ_samplec9816d|c63433/f11p0/1318      ACTTCTACAGCTGTTGTCATCACTGAGTCAGCACTCACCTGGCCTGGGGGAATTAAAGGA      10
NM_001031677.3                            ACTTCTACAGCTGTTGTCATCACTGAGTCAGCACTCACCTGGCCTGGGGGAATTAAAGGA      11
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i1_HQ_samplec9816d|c43648/f2p0/1435       ATTCCCCGTAAGGGCTGGACCCAGCTCCTTTCTGGGCTTGGGTAGTCAAATGTCTGAGCT      12
NR_109789.1                               ATTCCCCGTAAGGGCTGGACCCAGCTCCTTTCTGGGCTTGGGTAGTCAAATGTCTGAGCT      12
i0_HQ_samplec9816d|c43092/f2p19/798       ATTCCCCGTAAGGGCTGGACCCAGCTCCTTTCTGGGCTTGGGTAGTCAAATGTCTGAGCT      60
NM_130781.3                               ATTCCCCGTAAGGGCTGGACCCAGCTCCTTTCTGGGCTTGGGTAGTCAAATGTCTGAGCT      10
i1_HQ_samplec9816d|c63433/f11p0/1318      ATTCCCCGTAAGGGCTGGACCCAGCTCCTTTCTGGGCTTGGGTAGTCAAATGTCTGAGCT      11
NM_001031677.3                            ATTCCCCGTAAGGGCTGGACCCAGCTCCTTTCTGGGCTTGGGTAGTCAAATGTCTGAGCT      11
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i1_HQ_samplec9816d|c43648/f2p0/1435       ACCCCAGGTCCTCATGTCAGCAGAGTGGCGCCTGCCTGTGCTGGCCCATGGAACGGAGAC      13
NR_109789.1                               ACCCCAGGTCCTCATGTCAGCAGAGTGGCGCCTGCCTGTGCTGGCCCATGGAACGGAGAC      13
i0_HQ_samplec9816d|c43092/f2p19/798       ACCCCAGGTCCTCATGTCAGCAGAGTGGCGCCTGCCTGTGCTGGCCCATGGAACGGAGAC      66
NM_130781.3                               ACCCCAGGTCCTCATGTCAGCAGAGTGGCGCCTGCCTGTGCTGGCCCATGGAACGGAGAC      11
i1_HQ_samplec9816d|c63433/f11p0/1318      ACCCCAGGTCCTCATGTCAGCAGAGTGGCGCCTGCCTGTGCTGGCCCATGGAACGGAGAC      11
NM_001031677.3                            ACCCCAGGTCCTCATGTCAGCAGAGTGGCGCCTGCCTGTGCTGGCCCATGGAACGGAGAC      12
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i1_HQ_samplec9816d|c43648/f2p0/1435       AGCATTGGGCTGACTGTGGGCATGAGGAGGGATAAGGCTGATTTGGACCCCAGGCTTCTG      13
NR_109789.1                               AGCATTGGGCTGACTGTGGGCATGAGGAGGGATAAGGCTGATTTGGACCCCAGGCTTCTG      14
i0_HQ_samplec9816d|c43092/f2p19/798       AGCATTGGGCTGACTGTGGGCATGAGGAGGGATAAGGCTGATTTGGACCCCAGGCTTCTG      72
NM_130781.3                               AGCATTGGGCTGACTGTGGGCATGAGGAGGGATAAGGCTGATTTGGACCCCAGGCTTCTG      11
i1_HQ_samplec9816d|c63433/f11p0/1318      AGCATTGGGCTGACTGTGGGCATGAGGAGGGATAAGGCTGATTTGGACCCCAGGCTTCTG      12
NM_001031677.3                            AGCATTGGGCTGACTGTGGGCATGAGGAGGGATAAGGCTGATTTGGACCCCAGGCTTCTG      12
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i1_HQ_samplec9816d|c43648/f2p0/1435       CCCTGGACAGCACTTGTGTCTGCAGATTATTTAAgtggcttttgatctgtaaataaaatc          14
NR_109789.1                               CCCTGGACAGCACTTGTGTCTGCAGATTATTTAAGTGGCTTTTGATCTGTAAATAAAATC          14
i0_HQ_samplec9816d|c43092/f2p19/798       CCCTGGACAGCACTTGTGTCTGCAGATTATTTAAGTGGCTTTTGATCTGTAAATAAAATC          78
NM_130781.3                               CCCTGGACAGCACTTGTGTCTGCAGATTATTTAAGTGGCTTTTGATCTGTAAATAAAATC          12
i1_HQ_samplec9816d|c63433/f11p0/1318      CCCTGGACAGCACTTGTGTCTGCAGATTATTTAAGTGGCTTTTGatctgtaaataaaatc          13
NM_001031677.3                            CCCTGGACAGCACTTGTGTCTGCAGATTATTTAAGTGGCTTTTGATCTGTAAATAAAATC          13
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i1_HQ_samplec9816d|c43648/f2p0/1435       agtgcactgt--------------------------------------------------          14
NR_109789.1                               AGTGCACTGTGCATCACACCCAGCCCCTTTCCCTGCTGTGTGGATTAGGTGTCAAGACAC          15
i0_HQ_samplec9816d|c43092/f2p19/798       AGTGCACTGTG-------------------------------------------------          79
NM_130781.3                               AGTGCACTGTGCATCACACCCAGCCCCTTTCCCTGCTGTGTGGATTAGGTGTCAAGACAC          13
i1_HQ_samplec9816d|c63433/f11p0/1318      agtgcactgtg-------------------------------------------------          13
NM_001031677.3                            AGTGCACTGTGCATCACACCCAGCCCCTTTCCCTGCTGTGTGGATTAGGTGTCAAGACAC          14
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i1_HQ_samplec9816d|c43648/f2p0/1435       ------------------------------------------------------------          14
NR_109789.1                               CTAGTTCTTCCTGGGGCCACCCGGCTGGCCTCACTGCTTATATTAAGGCTCCTCCCAACT          15
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          79
NM_130781.3                               CTAGTTCTTCCTGGGGCCACCCGGCTGGCCTCACTGCTTATATTAAGGCTCCTCCCAACT          13
i1_HQ_samplec9816d|c63433/f11p0/1318      ------------------------------------------------------------          13
NM_001031677.3                            CTAGTTCTTCCTGGGGCCACCCGGCTGGCCTCACTGCTTATATTAAGGCTCCTCCCAACT          14


i1_HQ_samplec9816d|c43648/f2p0/1435       ------------------------------------------------------------          14
NR_109789.1                               CTCATTTTCCTTTGGAAAACAAGACTTTTTTCCCCATGGTTACCGCTGAGATACTGGGGC          16
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          79
NM_130781.3                               CTCATTTTCCTTTGGAAAACAAGACTTTTTTCCCCATGGTTACCGCTGAGATACTGGGGC          14
i1_HQ_samplec9816d|c63433/f11p0/1318      ------------------------------------------------------------          13
NM_001031677.3                            CTCATTTTCCTTTGGAAAACAAGACTTTTTTCCCCATGGTTACCGCTGAGATACTGGGGC          15


i1_HQ_samplec9816d|c43648/f2p0/1435       ------------------------------------------------------------          14
NR_109789.1                               TGTAGTAGTATAAAAGCTCACAGTTCCTTCTGAGTGCTGAAAAGAGTGCATGAGTTGCTT          17
i0_HQ_samplec9816d|c43092/f2p19/798       ------------------------------------------------------------          79
NM_130781.3                               TGTAGTAGTATAAAAGCTCACAGTTCCTTCTGAGTGCTGAAAAGAGTGCATGAGTTGCTT          14
i1_HQ_samplec9816d|c63433/f11p0/1318      ------------------------------------------------------------          13
NM_001031677.3                            TGTAGTAGTATAAAAGCTCACAGTTCCTTCTGAGTGCTGAAAAGAGTGCATGAGTTGCTT          15


i1_HQ_samplec9816d|c43648/f2p0/1435       --------------------------------------------------          1435
NR_109789.1                               CGAAATAAAAGGGTCAAGCATTCCTACCTGAGACAGGTTAAAAAAAAAAA          1764
i0_HQ_samplec9816d|c43092/f2p19/798       --------------------------------------------------          798
NM_130781.3                               CGAAATAAAAGGGTCAAGCATTCCTACCTGAGACAGGTTAAAAAAAAAAA          1546
i1_HQ_samplec9816d|c63433/f11p0/1318      --------------------------------------------------          1318
NM_001031677.3                            CGAAATAAAAGGGTCAAGCATTCCTACCTGAGACAGGTTAAAAAAAAAAA          1632
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VIRT2751            MSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQNTIGAAFVAKVMSVGDRTVTLG 60
VIRT1094            MSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQNTIGAAFVAKVMSVGDRTVTLG 60
VIRT5954            -------------------------------------------------MSVGDRTVTLG 11
NP_001026847.1      MSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQNTIGAAFVAKVMSVGDRTVTLG 60
NP_570137.2         MSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQNTIGAAFVAKVMSVGDRTVTLG 60
                                                                     ***********

VIRT2751            IWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSSFERAKFWVKELRSLEEGCQIYLCGT 120
VIRT1094            IWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSSFERAKFWVKELRSLEEGCQIYLCGT 120
VIRT5954            IWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSSFERAKFWVKELRSLEEGCQIYLCGT 71
NP_001026847.1      IWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSSFERAKFWVKELRSLEEGCQIYLCGT 120
NP_570137.2         IWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSSFERAKFWVKELRSLEEGCQIYLCGT 120
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VIRT2751            KSDLLEEDRRRRRVDFHDVQDYADSSCSSALWGVGVCGCLGGS--KKIGTALAARA---- 174
VIRT1094            KSDLLEEDRRRRRVDFHDVQDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQV 180
VIRT5954            KSDLLEEDRRRRRVDFHDVQDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQV 131
NP_001026847.1      KSDLLEEDRRRRRVDFHDVQDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQV 180
NP_570137.2         KSDLLEEDRRRRRVDFHDVQDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQV 180
                    ************************.  :. :   .  *   ..  :*:.   .: *

VIRT2751            ----RCSRRSSWP-P--------        184
VIRT1094            MTEDKGVDLGQKPNPYFYSCCHH        203
VIRT5954            MTEDKGVDLGQKPNPYFYSCCHH        154
NP_001026847.1      MTEDKGVDLGQKPNPYFYSCCHH        203
NP_570137.2         MTEDKGVDLGQKPNPYFYSCCHH        203
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ARPC1A

Sequence	Header	AA Seq	

Present	i1_HQ_samplec9816d|c18442/f2p0/1395	>VIRT50347 (3-5’)	VIRT61659 (5-3’)
Absent	i1_HQ_samplec9816d|c21346/f2p0/1056	VIRT64494 (3-5’)	VIRT65386 (5-3’)
NCBI	NM_001190996	NP_001177925.1	
	NM_006409	NP_006400.2	

>i1_HQ_samplec9816d|c18442/f2p0/1395
isoform=c18442;full_length_coverage=2;non_full_length_coverage=0;isoform_length=1395

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ACTCAAGGAGCACAACGGACACATCACAGGTATTGACTGGGCTCCCAAGAGCGACCGCATTGTCACTTGTGGGGCAGA
CCGCAATGCCTATGTCTGGAGTCAGAAAGATGGTGTTTGGAAGCCAACCCTGGTGATCCTGAGAATTAATCGCGCAGCT
ACTTTTGTGAAGTGGTCCCCCCTAGAGAACAAATTTGCTGTGGGAAGTGGAGCACGACTCATTTCTGTTTGTTACTTTGA
GTCTGAAAATGACTGGTGGGTGAGCAAGCACATTAAAAAGCCGATTCGCTCCACAGTCCTCAGCTTGGATTGGCATCCC
AACAACGTTTTGCTGGCAGCAGGATCATGTGACTTCAAATGCAGAGTGTTTTCTGCCTACATTAAAGAAGTGGATGAAA
AGCCAGCCAGCACGCCCTGGGGCAGCAAGATGCCTTTTGGGCAGCTGATGTCAGAGTTTGGTGGCAGTGGCACTGGTG
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>VIRT50347 (3-5’)
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variant 2, mRNA
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1, mRNA
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i1_HQ_samplec9816d|c21346/f2p0/1056      ATATGTAAATTgtccactagaaaattaaataaaagaactgaatgt--------------- 1056
NM_001190996.1                           ATATGTAAATTGTCCACTAGAAAATTAAATAAAAGAACTGAATGTGGAAAAAAAAAAAAA 1618
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i1_HQ_samplec9816d|c18442/f2p0/1395      -------------        1395
NM_006409.3                              AAA----------        1623
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NM_001190996.1                           AAAAAAAAAAAAA        1631
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VIRT50347                -------------------------MAEAHSAS------------HYPEALDGRLEGLEI  23
VIRT64494                -------------------------MAEAHSAS------------HYPEALDGRLEGLEI  23
NP_006400.2              MSLHQFLLEPITCHAWNRDRTQIALSPNNHEVHIYKKNGSQWVKAHELKEHNGHITGIDW  60
VIRT61659                ------------------------------------------------------------ 0
VIRT65386                ------------------------------------------------------------ 0
NP_001177925.1           --------------MPGTGIVLIALSPNNHEVHIYKKNGSQWVKAHELKEHNGHITGIDW  46


VIRT50347                P-------NCHGSIDA-----SSAKFATILLVHLINRDLSDAILVQRLQGRVAVLSCGSL  71
VIRT64494                P-------NCHGSIDA-----SSAKFATILLVHLINRDLSDAILVQRLQGRVAVLSCGSL  71
NP_006400.2              APKSDRIVTCGADRNAYVWSQKDGVWKPTLVILRINRAAT-FVKWSPLENKFAVGSGARL  119
VIRT61659                ------------------------------------------------------------ 0
VIRT65386                ------------------------------------------------------------ 0
NP_001177925.1           APKSDRIVTCGADRNAYVWSQKDGVWKPTLVILRINRAAT-FVKWSPLENKFAVGSGARL  105


VIRT50347                V-----------------------------------------------------------  72
VIRT64494                V-----------------------------------------------------------  72
NP_006400.2              ISVCYFESENDWWVSKHIKKPIRSTVLSLDWHPNNVLLAAGSCDFKCRVFSAYIKEVDEK  179
VIRT61659                ------------------------------------------------------------ 0
VIRT65386                ------------------------------------------------------------ 0
NP_001177925.1           ISVCYFESENDWWVSKHIKKPIRSTVLSLDWHPNNVLLAAGSCDFKCRVFSAYIKEVDEK  165


VIRT50347                -------------------------------------------------HVA--------  75
VIRT64494                -------------------------------------------------HVA--------  75
NP_006400.2              PASTPWGSKMPFGQLMSEFGGSGTGGWVHGVSFSASGSRLAWVSHDSTVSVADASKSVQV  239
VIRT61659                ---------MPFGQLMSEFGGSGTGGWVHGVSFSASGSRLAWVSHDSTVSVADASKSVQV  51
VIRT65386                ---------MPFGQLMSEFGGSGTGGWVHGVSFSASGSRLAWVSHDSTVSVADASKSVQV  51
NP_001177925.1           PASTPWGSKMPFGQLMSEFGGSGTGGWVHGVSFSASGSRLAWVSHDSTVSVADASKSVQV  225
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VIRT50347                ------------------------------------------------------------  75
VIRT64494                ------------------------------------------------------------  75
NP_006400.2              STLKTEFLPLLSVSFVSENSVVAAGHDCCPMLFNYDDRGCLTFVSKLDIPKQSIQRNMSA  299
VIRT61659                STLKTEFLPLLSVSFVSENSVVAAGHDCCPMLFNYDDRGCLTFVSKLDIPKQSIQRNMSA  111
VIRT65386                STLKTEFLPLLSVSFVSENSVVAAGHDCCPMLFNYDDRGCLTFVSKLDIPKQSIQRNMSA  111
NP_001177925.1           STLKTEFLPLLSVSFVSENSVVAAGHDCCPMLFNYDDRGCLTFVSKLDIPKQSIQRNMSA  285


VIRT50347                -----------------------------------------EAFHGRHVALDALFWNI--  92
VIRT64494                -----------------------------------------EAFHGRHVALDALFWNI--  92
NP_006400.2              MERFRNMDKRATTEDRNTALETLHQNSITQVSIYEVDKQDCRKFCTTGIDGAMTIWDFKT  359
VIRT61659                MERFRNMDKRATTEDRNTALETLHQNSITQVSIYEVDKQDCRKFCTTGIDGAMTIWDFKT  171
VIRT65386                MERFRNMDKRATTEDRNTALETLHQNSITQVSIYEVDKQDCRKFCTTGIDGAMTIWDFKT  171
NP_001177925.1           MERFRNMDKRATTEDRNTALETLHQNSITQVSIYEVDKQDCRKFCTTGIDGAMTIWDFKT  345
                                                                  . *    :     :*::

VIRT50347                -----------          92
VIRT64494                -----------          92
NP_006400.2              LESSIQGLRIM          370
VIRT61659                LESSIQGLRIM          182
VIRT65386                LESSIQGLRIM          182
NP_001177925.1           LESSIQGLRIM          356
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ARPC1B

Sequence	Header	AA Seq		
Present	i1_HQ_samplec9816d|c43701/f2p0/1471	VIRT91963 (3-5’)	VIRT95841 (3-5’)	VIRT89465 (5-3’)
Absent	i1_HQ_samplec9816d|c14866/f2p0/1185	>VIRT99058		
NCBI	NM_005720	>NP_005711.1		

>i1_HQ_samplec9816d|c43701/f2p0/1471
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>VIRT91963 (3-5’)

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>VIRT95841 (3-5’)

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SPKGILEPHGVGAGRSSTSLM

>VIRT89465 (5-3’)

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>VIRT99058

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>NM_005720.4 Homo sapiens actin related protein 2/3 complex subunit 1B (ARPC1B), mRNA
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VIRT95841        ------------------------------------------------------------    0
VIRT91963        ------------------------------------------------------------    0
VIRT89465        MAYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGAKWTKVHELKEHNGQVTGIDW    60
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VIRT95841        ------------------------------------------------MKVSASSGS---    9
VIRT91963        MP-------------------------PS---------------------------MPVV    8
VIRT89465        APESNRIVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNENKFAVGSGSRVI    120
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VIRT95841        -----------------------------------------V-SEARVATAIFLS-----    22
VIRT91963        -----------QNCEHLALPPLS----------------------TEIWLTLFLCSESRP    35
VIRT89465        SICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNNVLLAAGSCDFKCRIFSAYIKEVEERP    180
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VIRT99058        SICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNNVLLAAGSCDFKCRIFSAYIKEVEERP      180
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VIRT95841        -----------------------------ASARQTVLSWLTQATRLPLAEKQTP------      47
VIRT91963        APAA----VPPSELAFLSR---FWKRS----------RAVKPRCELCLGTSSRPP-----      73
VIRT89465        APTPWGSKMPFGELMFESSSSCGWVHGVCFSASGSRVAWVSHDSTVCLADADKKMAVATL      240
NP_005711.1      APTPWGSKMPFGELMFESSSSCGWVHGVCFSASGSRVAWVSHDSTVCLADADKKMAVATL      240
VIRT99058        APTPWGSKMPFGELMFESSSSCGWVHGVCFSASGSRVAWVSHDSTVCLADAD--------      232
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VIRT95841        ------------------------CTQPQLLLD---------SNISSP-----KGIL---      66
VIRT91963        -------------------------------------------KLSIPAAAS--------      82
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VIRT99058        ------------------------------------------------------------      232


VIRT95841        ----------EPHGVGAGRSSTSLM-----------------------------------      81
VIRT91963        ------------------------------------------------------------      82
VIRT89465        RFQNLDKKASSEGGTAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVK      360
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VIRT99058        --------------------------------------KAKCSQFCTTGMDGGMSIWDVK      254

VIRT95841        ------------  81
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VIRT99058        SLESALKDLKIK  266
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WDR4

Sequence	Header	AA Seq
Present		
Absent	i1_HQ_samplec9816d|c20457/f2p0/1218	VIRT138907
NCBI	NM_033661	NP_387510.1
	NM_001260476	NP_001247405.1

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>NM_033661.4 Homo sapiens WD repeat domain 4 (WDR4), transcript variant 2, mRNA
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VYRQQLAFQHQVWDVAFEETQGLWVLQDCQEAPLVLYRPVGDQWQSVPESTVLKKVSGVLRGNWAMLEGS
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>NM_001260476.1 Homo sapiens WD repeat domain 4 (WDR4), transcript variant 5, mRNA
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NM_001260476.1                           TGGCGTCACCGACCGGTGCGGACAGGAAGAGGCTCTGGGCTGGCACATGTGTATGGCGTG 79
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NM_033661.4                              AAAAA------------------------------------------------------- 1554

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NM_001260476.1                           TCTTCCTCTAGGAGCATCTGTGGGCTGACGTTTCTGGCATGGTGGATGTTTTCATGTTGT 1575
i1_HQ_samplec9816d|c20457/f2p0/1218      ------------------------------------------------------------ 1218
NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           TCCGCCGTCTCAGCATCCAGGTGACGTGCTGTCCCGCAGTAGCTGCTCGCCACACAGGCT 1635
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NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           GTTGAAACTCAGCACGAATGCTTGAGCCTGCCCCAGCCCCAGCCGTAGCCCTTGTGCTCA 1695
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NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           GGAGCTGCTCCTGGAGAGTGGCTCCCTTGTGGGAAGTGAGAAACACGTTTCGGAGTCGCA 1755
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NM_001260476.1                           GGGAGCTCTGTCTGGCATCGGTGGCACAGATGGTGAACTTGTTTCAGGAAGTGTGAGCAC 1815
i1_HQ_samplec9816d|c20457/f2p0/1218      ------------------------------------------------------------ 1218
NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           GGGCCTGGCTGGCACCCGGTTTACAGGGAGGTGATTGAGGACGTCGTTATGATTTGATTT 1875
i1_HQ_samplec9816d|c20457/f2p0/1218      ------------------------------------------------------------ 1218
NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           GACCTTGGCACACACTGCAGAGCCACAGGGATGTTGCTGAATTTCAATCACCGATCAGCA 1935
i1_HQ_samplec9816d|c20457/f2p0/1218      ------------------------------------------------------------ 1218
NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           AGGATGAACCTTCTCAACTTCCTAGGAATGTTTAGCAGCAACCTAATATACCAGGCAAAA 1995
i1_HQ_samplec9816d|c20457/f2p0/1218      ------------------------------------------------------------ 1218
NM_033661.4                              ------------------------------------------------------------ 1554

NM_001260476.1                           CTCAAAAAAAAAAAAAAAAAA         2016
i1_HQ_samplec9816d|c20457/f2p0/1218      ---------------------         1218
NM_033661.4                              ---------------------         1554
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NP_387510.1         ----------MAGSVGLALCGQTLVVRGGSRFLATSIASSDDDSLFIYDCSAAEKKSQEN  50
NP_001247405.1      ------------------------------------------------------------  0

VIRT138907          KGEDAPLDQGSGAILASTFSNSGSYFALTDDSKRLILFRTKPWQCLSVR-----------  109
NP_387510.1         KGEDAPLDQGSGAILASTFSKSGSYFALTDDSKRLILFRTKPWQCLSVRTVARRCTALTF  110
NP_001247405.1      ------------------------------------------------------------  0

VIRT138907          ------------------------------------------------------------  109
NP_387510.1         IASEEKVLVADKSGDVYSFSVLEPHGCGRLELGHLSMLLDVAVSPDDRFILTADRDEKIR  170
NP_001247405.1      ------------------------------------MLLDVAVSPDDRFILTADRDEKIR  24

VIRT138907          -------------------FVSRISVVPTQPGLLLSSSGDGTLRLWEYRSGRQLHCCHLA  150
NP_387510.1         VSWAAAPHSIESFCLGHTEFVSRISVVPTQPGLLLSSSGDGTLRLWEYRSGRQLHCCHLA  230
NP_001247405.1      VSWAAAPHSIESFCLGHTEFVSRISVVPTQPGLLLSSSGDGTLRLWEYRSGRQLHCCHLA  84
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VIRT138907          SLQELVDPQAPQKFAASSIAFWCQENCVALLCDGTSVVYIFQLDARRQQLVYRQQLAFQH  210
NP_387510.1         SLQELVDPQAPQKFAASRIAFWCQENCVALLCDGTPVVYIFQLDARRQQLVYRQQLAFQH  290
NP_001247405.1      SLQELVDPQAPQKFAASRIAFWCQENCVALLCDGTPVVYIFQLDARRQQLVYRQQLAFQH  144
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VIRT138907          QVWDVAFEETQGLWVLQDCQEAPLVLYRPVGDQWQSVPESTVLKKVSGVLRGNWAMLEGS  270
NP_387510.1         QVWDVAFEETQGLWVLQDCQEAPLVLYRPVGDQWQSVPESTVLKKVSGVLRGNWAMLEGS  350
NP_001247405.1      QVWDVAFEETQGLWVLQDCQEAPLVLYRPVGDQWQSVPESTVLKKVSGVLRGNWAMLEGS  204
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VIRT138907          AGADASFSSLYKATFDNVTSYLKKKRRDCSSS----------------------------  302
NP_387510.1         AGADASFSSLYKATFDNVTSYLKKKEERLQQQLEKKQRRRSPPPGPDGHAKKMRPGEATL  410
NP_001247405.1      AGADASFSSLYKATFDNVTSYLKKKEERLQQQLEKKQRRRSPPPGPDGHAKKMRPGEATL  264
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VIRT138907          --          302
NP_387510.1         SC          412
NP_001247405.1      SC          266
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SUMO3

Sequence	Header	AA Seq	
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Absent	i0_HQ_samplec9816d|c13953/f3p5/509	>VIRT175354	>VIRT176199
NCBI	NM_006936	NP_008867.2	
	NM_001286416		

>i0_HQ_samplec9816d|c13953/f3p5/509
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CCAATCAATGAAACTGACACTCCAGCACAGCTGGAGATGGAGGACGAGGACACCATCGACGTGTTCCAGCAGCAGACG
GGAGGTGTGCCGGAGAGCAGCCTGGCAGGGCACAGTTTCTAGAGGGCCCGTCCCCAGCCCGGGCCGTCCATCCTCGC
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>VIRT175354

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>VIRT176199

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>NM_006936.2 Homo sapiens small ubiquitin-like modifier 3 (SUMO3), transcript variant 1, mRNA
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CCCCGCGCCGCTCGCGCAGCCATGTCCGAGGAGAAGCCCAAGGAGGGTGTGAAGACAGAGAATGACCACA
TCAACCTGAAGGTGGCCGGGCAGGACGGCTCCGTGGTGCAGTTCAAGATCAAGAGGCACACGCCGCTGAG
CAAGCTGATGAAGGCCTACTGCGAGAGGCAGGGCTTGTCAATGAGGCAGATCAGATTCAGGTTCGACGGG
CAGCCAATCAATGAAACTGACACTCCAGCACAGCTGGAGATGGAGGACGAGGACACCATCGACGTGTTCC
AGCAGCAGACGGGAGGTGTGCCGGAGAGCAGCCTGGCAGGGCACAGTTTCTAGAGGGCCCGTCCCCAGCC
CGGGCCGTCCATCCTCGCATTGCTGTTGAATGGTGAGCACGTGACCATGCCGACCACAAAGGTGTCTGCG
GAAACTCGAGGACATTCACCACGATGATTTTCCTCTCTTTGATGTACTTCAAGTGCAACTCAAAACTATA
TCTGCAGGGATGAATCTGTAACTTAAATTGGCCAATCAGAATTGTTATCTTTGTTCAGGTAAAATGAGT
TGCAAGATATTGTGGGTACTTTTGTGTGCTCATTTGTGTTTTCCCCCCCTCCTACAACATTTTTTTAACC
CCAAAATTATAGCCTGAATGTTCGCTTTTAGTCTGGCCAGGGATCTGACTCCTGAGTTGGTTGCCTCTCC
CCTGCTCACTCCAGTCACATAGAGAATTGGTGTTTCCCGCAGTGGGGATGCAGCTGTTGGACAGGTATTG
GGGGCAAGGTTGGTAGGGAGGACAGACTGTCACTTGCTGTTACAGGCACAGGTGATTAAAATGCTAAATA
TTGCAAATTTAAGCTTTGTCAGTATATGGAAAAGTTGAAGGGAAAATACTGGAATGCTTCTTCAAAGGTT
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TCTGAGGCCCAGGACCCACCCCCCTGCCACCCCTCCCACCCCACTCCCTGCTCAGTACCTGGCGTTGGTA
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AGTGTGGTTACAAATGAACCCATGGAATGATGACTTCATGTTCTTCTCGTGGGTTTGTGCCGTGCTGCTT
TCCAAATAGGTATTGAATTTATGCATTAGTCTGGTGATTTCAGTTCTGTGAAATATTTTGGGATCTATAC
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CTGCCTTTTTACAGTCACCTGAACAATGACCCATCATCTCTTGCTTGCTTGAAATCTTGCTGAAATGTTC
TCATTTCCTGTTTGCTGTATGGGCTCGGGTGGATGTTTGTTGGCTCTGTTGTGTTTATTCACCAATTTG
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>NP_008867.2 small ubiquitin-related modifier 3 isoform 1 precursor [Homo sapiens]
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CCCCGCGCCGCTCGCGCAGCCATGTCCGAGGAGAAGCCCAAGGAGGGTGTGAAGACAGAGAATGACCACA
TCAACCTGAAGGTGGCCGGGCAGGACGGCTCCGTGGTGCAGTTCAAGATCAAGAGGCACACGCCGCTGAG
CAAGCTGATGAAGGCCTACTGCGAGAGGCAGGTGCGGCACCTTGCTCCCCCGCAGAGCCTCCCCGTGTGC
GCACTGGTCCTGTGCGTTCCAGGCATCCCCAGAGCACGAGCGTCTCGGGGCTGGACCCAGATGCAGCTGC
CCGAGGGCTTGTCAATGAGGCAGATCAGATTCAGGTTCGACGGGCAGCCAATCAATGAAACTGACACTCC
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ATTGGCCTTTTTCTCCCTCTTAATATTGAAGAAATTCCCACATTTCTCATTTGGTAATGGTGTTGTGGCC
TCAGATTTCTTCTAGTATTTGCTTCTGATGAATGATTATGGTCTATACATAAAAAAGTAAGACTAAGTAT
TGCTGAATTTGCAGTTATGTTGTCGTGTATAAGAGCTACTTCCAAGTGTGGTTACAAATGAACCCATGGA
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TATTGTCCTTCCCTGAGGCTCCATTGCTGCTTGGTGGCCATTCTCTGCCTTTTTACAGTCACCTGAACAA
TGACCCATCATCTCTTGCTTGCTTGAAATCTTGCTGAAATGTTCTCATTTCCTGTTTGCTGTATGGCTC
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GTAAACAGTAAATATAGTTTGGTATTCTGTCAAAAAAAAAAAAAAAAAAAAAAAA
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>NP_001273345.1 small ubiquitin-related modifier 3 isoform 2 [Homo sapiens]
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NM_001286416.1                          AGCCACGTGACCCCCGTGCCGGCCAACGGGTGCGCCGGGATTTGGGGGATAAAGCGCGGC  60


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NM_006936.2                             CCCGCGCACAGTTGCGGCGGGAGAGCGGCGGGGCCGAGAGCGTGACTCGCCCGCTCCGCG  120
NM_001286416.1                          CCCGCGCACAGTTGCGGCGGGAGAGCGGCGGGGCCGAGAGCGTGACTCGCCCGCTCCGCG  120


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NM_006936.2                             CTGCTTCCCCCGCGCCGCCTCCCCGCGCCGCTCGCGCAGCCATGTCCGAGGAGAAGCCCA  180
NM_001286416.1                          CTGCTTCCCCCGCGCCGCCTCCCCGCGCCGCTCGCGCAGCCATGTCCGAGGAGAAGCCCA  180


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NM_001286416.1                          AGGAGGGTGTGAAGACAGAGAATGACCACATCAACCTGAAGGTGGCCGGGCAGGACGGCT  240


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NM_001286416.1                          CCGTGGTGCAGTTCAAGATCAAGAGGCACACGCCGCTGAGCAAGCTGATGAAGGCCTACT  300
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NM_006936.2                             GCGAGAGGCA--------------------------------------------------  310
NM_001286416.1                          GCGAGAGGCAGGTGCGGCACCTTGCTCCCCCGCAGAGCCTCCCCGTGTGCGCACTGGTCC  360
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NM_001286416.1                          TGTGCGTTCCAGGCATCCCCAGAGCACGAGCGTCTCGGGGCTGGACCCAGATGCAGCTGC  420


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NM_001286416.1                          CCGAGGGCTTGTCAATGAGGCAGATCAGATTCAGGTTCGACGGGCAGCCAATCAATGAAA  480
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NM_001286416.1                          CTGACACTCCAGCACAGCTGGAGATGGAGGACGAGGACACCATCGACGTGTTCCAGCAGC  540
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NM_001286416.1                          AATGTTCGCTTTTAGTCTGGCCAGGGATCTGACTCCTGAGTTGGTTGCCTCTCCCCTGCT  960


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NM_001286416.1                          CACTCCAGTCACATAGAGAATTGGTGTTTCCCGCAGTGGGGATGCAGCTGTTGGACAGGT  1020


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NM_001286416.1                          CCACCCCTCCCACCCCACTCCCTGCTCAGTACCTGGCGTTGGTACACAGGCAAGGATTGG  1320


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NM_001286416.1                          CACAACCAAAATTGGCCTTTTTCTCCCTCTTAATATTGAAGAAATTCCCACATTTCTCAT  1380


i0_HQ_samplec9816d|c13953/f3p5/509      ------------------------------------------------------------  509
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NM_001286416.1                           AAGAGCTACTTCCAAGTGTGGTTACAAATGAACCCATGGAATGATGACTTCATGTTCTTC  1560

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NM_001286416.1                           TCGTGGGTTTGTGCCGTGCTGCTTTCCAAATAGGTATTGAATTTATGCATTAGTCTGGTG  1620

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NM_001286416.1                           ATTTCAGTTCTGTGAAATATTTTGGGATCTATACCAATTAAACATTTTCATAGTTCTGCC  1680

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NM_001286416.1                           TATTGTCCTTCCCTGAGGCTCCATTGCTGCTTGGTGGCCATTCTCTGCCTTTTTACAGTC  1740

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NM_006936.2                              ACCTGAACAATGACCCATCATCTCTTGCTTGCTTGAAATCTTGCTGAAATGTTCTCATTT  1686
NM_001286416.1                           ACCTGAACAATGACCCATCATCTCTTGCTTGCTTGAAATCTTGCTGAAATGTTCTCATTT  1800

i0_HQ_samplec9816d|c13953/f3p5/509       ------------------------------------------------------------  509
NM_006936.2                              CCTGTTTGCTGTATGGGCTCGGGTGGGATGTTTGTTGGCTCTGTTGTGTTTATTCACCAA  1746
NM_001286416.1                           CCTGTTTGCTGTATGGGCTCGGGTGGGATGTTTGTTGGCTCTGTTGTGTTTATTCACCAA  1860

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NM_006936.2                              TTTGTACATTATTTGTTGTCCTTTACTACTGTAAACAGTAAATATAGTTTGGTATTCTGT  1806
NM_001286416.1                           TTTGTACATTATTTGTTGTCCTTTACTACTGTAAACAGTAAATATAGTTTGGTATTCTGT  1920

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NM_006936.2                              CAAAAAAAAAAAAAAAAAAAAAAAA      1831
NM_001286416.1                           CAAAAAAAAAAAAAAAAAAAAAAAA      1945
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VIRT175354          ------------------------------------------------------------ 0
NP_008867.2         MSEEKPKEGVKTENDHINLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQ---------- 50
NP_001273345.1      MSEEKPKEGVKTENDHINLKVAGQDGSVVQFKIKRHTPLSKLMKAYCERQVRHLAPPQSL 60
VIRT176199          ------------------MKLTLQH--SWRWRTRTPSTCSSSRREVCRRAAWQGT----- 35

VIRT175354          ---------------------MSEEKPKGLSMRQIRFRFDGQPINETDTPAQLEMEDEDT 39
NP_008867.2         ----------------------------GLSMRQIRFRFDGQPINETDTPAQLEMEDEDT 82
NP_001273345.1      PVCALVLCVPGIPRARASRGWTQMQLPEGLSMRQIRFRFDGQPINETDTPAQLEMEDEDT 120
VIRT176199          -VSRGPVPSPGRPSSHCC------------------------------------------ 52

VIRT175354          IDVFQQQTGGVPESSLAGHSF                60
NP_008867.2         IDVFQQQTGGVPESSLAGHSF                103
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VIRT176199          ---------------------                52
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DGCR6L

Sequence	**Header**	**AA Seq**	
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Absent	i1_HQ_samplec9816d|c55690/f2p0/1026	VIRT195959	VIRT671
NCBI	NM_033257	NP_150282.2	

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GCAGCAGAAGTCTGGGCAGAGTTCATCTTCTTGACCTTTGGCCACTGCCTTCCCAGCTGCCCGCAGGGGGTTCCCCCTG
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CAGCCCCCATGCAGAAGAGGCTCCCAGGCCCAAGCTCTGTGTGACCCAGAGAaataaagatgcctcagtgtggcccacatgtggctt
gt

>VIRT194119

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GAAGGTGGCTGACCAGCAGAGCACACTGGAGAAGGCGGGGGTGGCTGGCTTCTACGTGACCACCAACCCACAGGAGC
TGATGCTGCAGATGAACCTGCTGGAACTCATCCGAAAGCTGCAGCAGAGGGGCTGCCGGGCAGGGAATGCAGCCCTG
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GCAGAAGTCTGGGCAGAGTTCATCTTCTTGACCTTTGGCCACTGCCTTCCCAGCTGCCCGCAGGGGGTTCCCCCTGCTG
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CACCGGGCACATCCCAACCTGCACTGGGGCCCACCCGAGCGCTTGTTCTGGTCTCAGCCGCTCCCTTGGCAGCTGCAGC
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>VIRT195959

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>VIRT671
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GGAGGAGGTGGCGGACGGTGCCCGGCAGCAGGAGCGACACTACCAGTTGCTGTCGGCGCTACAGAGCCTG
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```

```
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CDQKGSPVPP
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i1_HQ_samplec9816d|c55690/f2p0/1026      ----------------------------------------------Cgccgcgctcggga 14
i1_HQ_samplec9816d|c64363/f2p0/1107      ------------------------------------------------------------ 0
NM_033257.3                              GGGCGGAGCGCGCCGCGCGTGGGACAATCGTAAAAGGGGCGGGACGCGCCGCGCTCGGGA 60


i1_HQ_samplec9816d|c55690/f2p0/1026      tgtcgtagctggg-------gagctgtcgccgcgccgcggctagcgggcgtcgcgCCATG 67
i1_HQ_samplec9816d|c64363/f2p0/1107      ----------------------GtcgccgccgccggcggctagcgggcgtccgCGCCATG 38
NM_033257.3                              TGTCGTGAAGCTGGGGGAGCTCGTCGCCGCCGCCGGCGGCTAGCGGGCGTCCGCGCCATG 120
                                                               *  * ******     *      **    *********

i1_HQ_samplec9816d|c55690/f2p0/1026      GAGCGCTACGCGGCCGCCTTGGAGGAGGTGGCGGACGGTGCCCGGCAGCAGGAGCGACAC 127
i1_HQ_samplec9816d|c64363/f2p0/1107      GAGCGCTACGCGGCCGCCTTGGAGGAGGTGGCGGACGGTGCCCGGCAGCAGGAGCGACAC 98
NM_033257.3                              GAGCGCTACGCGGCCGCCTTGGAGGAGGTGGCGGACGGTGCCCGGCAGCAGGAGCGACAC 180
                                         ************************************************************

i1_HQ_samplec9816d|c55690/f2p0/1026      TACCAGTTGCTGTCGGCGCTACAGAGCCTGGTGAAGGAGTTGCCCAGCTCTTTCCAGCAG 187
i1_HQ_samplec9816d|c64363/f2p0/1107      TACCAGTTGCTGTCGGCGCTACAGAGCCTGGTGAAGGAGTTGCCCAGCTCTTTCCAGCAG 158
NM_033257.3                              TACCAGTTGCTGTCGGCGCTACAGAGCCTGGTGAAGGAGTTGCCCAGCTCTTTCCAGCAG 240
                                         ************************************************************

i1_HQ_samplec9816d|c55690/f2p0/1026      CGCCTGTCCTACACCACGCTCAGCGACCTGGCCCTGGCGCTTCTCGACGGCACCGTGTTC 247
i1_HQ_samplec9816d|c64363/f2p0/1107      CGCCTGTCCTACACCACGCTCAGCGACCTGGCCCTGGCGCTTCTCGACGGCACCGTGTTC 218
NM_033257.3                              CGCCTGTCCTACACCACGCTCAGCGACCTGGCCCTGGCGCTTCTCGACGGCACCGTGTTC 300
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i1_HQ_samplec9816d|c55690/f2p0/1026      GAAATCGTGCAGGGGCTACTGGAGATCCAGCACCTCACCGAAAAGAGCCTGTACAACCAG 307
i1_HQ_samplec9816d|c64363/f2p0/1107      GAAATCGTGCAGGGGCTACTGGAGATCCAGCACCTCACCGAAAAGAGCCTGTACAACCAG 278
NM_033257.3                              GAAATCGTGCAGGGGCTACTGGAGATCCAGCACCTCACCGAAAAGAGCCTGTACAACCAG 360
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i1_HQ_samplec9816d|c55690/f2p0/1026      CGCCTGCGCCTACAGAACGAGCACCGA--------------------------------- 334
i1_HQ_samplec9816d|c64363/f2p0/1107      CGCCTGCGCCTACAGAACGAGCACCGAGTGCTCAGGCAGGCGCTGCGGCAGAAGCACCAG 338
NM_033257.3                              CGCCTGCGCCTACAGAACGAGCACCGAGTGCTCAGGCAGGCGCTGCGGCAGAAGCACCAG 420
                                         ***************************

i1_HQ_samplec9816d|c55690/f2p0/1026      ------------------------------------------------------------ 334
i1_HQ_samplec9816d|c64363/f2p0/1107      GAAGCCCAGCAGGCCTGCCGGCCCCACAACCTGCCTGTGGTTCAGGCGGCTCAGCAGCGA 398
NM_033257.3                              GAAGCCCAGCAGGCCTGCCGGCCCCACAACCTGCCTGTGGTTCAGGCGGCTCAGCAGCGA 480


i1_HQ_samplec9816d|c55690/f2p0/1026      --------GGCCGTGGAACACCGGATCCGTGAGGAGCAGCGGGCGATGGACCAGAAGATC 386
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i1_HQ_samplec9816d|c64363/f2p0/1107      GAACTAGAGGCCGTGGAACACCGGATCCGTGAGGAGCAGCGGGCGATGGACCAGAAGATC 458
NM_033257.3                              GAACTAGAGGCCGTGGAACACCGGATCCGTGAGGAGCAGCGGGCGATGGACCAGAAGATC 540
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i1_HQ_samplec9816d|c55690/f2p0/1026      ATCCTGGAGCTGGACCGGAAGGTGGCTGACCAGCAGAGCACACTGGAGAAGGCGGGGGTG 446
i1_HQ_samplec9816d|c64363/f2p0/1107      ATCCTGGAGCTGGACCGGAAGGTGGCTGACCAGCAGAGCACACTGGAGAAGGCGGGGGTG 518
NM_033257.3                              ATCCTGGAGCTGGACCGGAAGGTGGCTGACCAGCAGAGCACACTGGAGAAGGCGGGGGTG 600
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i1_HQ_samplec9816d|c55690/f2p0/1026      GCTGGCTTCTACGTGACCACCAACCCACAGGAGCTGATGCTGCAGATGAACCTGCTGGAA 506
i1_HQ_samplec9816d|c64363/f2p0/1107      GCTGGCTTCTACGTGACCACCAACCCACAGGAGCTGATGCTGCAGATGAACCTGCTGGAA 578
NM_033257.3                              GCTGGCTTCTACGTGACCACCAACCCACAGGAGCTGATGCTGCAGATGAACCTGCTGGAA 660
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i1_HQ_samplec9816d|c55690/f2p0/1026      CTCATCCGAAAGCTGCAGCAGAGGGGCTGCCGGGCAGGGAATGCAGCCCTGGGACTGGGA 566
i1_HQ_samplec9816d|c64363/f2p0/1107      CTCATCCGAAAGCTGCAGCAGAGGGGCTGCCGGGCAGGGAATGCAGCCCTGGGACTGGGA 638
NM_033257.3                              CTCATCCGAAAGCTGCAGCAGAGGGGCTGCCGGGCAGGGAATGCAGCCCTGGGACTGGGA 720
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i1_HQ_samplec9816d|c55690/f2p0/1026      GGTCCCTGGCAGTCGCCTGCTGCCCAGTGTGACCAGAAAGGCAGCCCTGTCCCACCATAG 626
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NM_033257.3                              GGTCCCTGGCAGTCGCCTGCTGCCCAGTGTGACCAGAAAGGCAGCCCTGTCCCACCATAG 780
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i1_HQ_samplec9816d|c55690/f2p0/1026      CCACAGGCAGCAGAAGTCTGGGCAGAGTTCATCTTCTTGACCTTTGGCCACTGCCTTCCC 686
i1_HQ_samplec9816d|c64363/f2p0/1107      CCACAGGCAGCAGAAGTCTGGGCAGAGTTCATCTTCTTGACCTTTGGCCACTGCCTTCCC 758
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i1_HQ_samplec9816d|c55690/f2p0/1026      AGCTGCCCGCAGGGGGTTCCCCCTGCTGAGGAGAGACCAGGTGGACCCCAGCTGCCTGTC 746
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i1_HQ_samplec9816d|c55690/f2p0/1026      ACCCTTCATCTGGGACTTGCTGTCAAACCCTAGGATAGTCTCATAAAGGGGAGGCTGGGC 806
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NM_033257.3                              ACCCTTCATCTGGGACTTGCTGTCAAACCCTAGGATAGTCTCATAAAGGGGAGGCTGGGC 960
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i1_HQ_samplec9816d|c55690/f2p0/1026      CAGCCTGCTGCTGTCTGCTTCAGGACCAGGCAGAGAGTGAGGCTGGGGGTTCTCACACCT 866
i1_HQ_samplec9816d|c64363/f2p0/1107      CAGCCTGCTGCTGTCTGCTTCAGGACCAGGCAGAGAGTGAGGCTGGGGGTTCTCACACCT 938
NM_033257.3                              CAGCCTGCTGCTGTCTGCTTCAGGACCAGGCAGAGAGTGAGGCTGGGGGTTCTCACACCT 1020
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i1_HQ_samplec9816d|c55690/f2p0/1026      TACTCCACCGGGCACATCCCAACCTGCACTGGGGCCCACCCGAGCGCTTGTTCTGGTCTC 926
i1_HQ_samplec9816d|c64363/f2p0/1107      TACTCCACCGGGCACATCCCAACCTGCACTGGGGCCCACCCGAGCGCTTGTTCTGGTCTC 998
NM_033257.3                              TACTCCACCGGGCACATCCCAACCTGCACTGGGGCCCACCCGAGCGCTTGTTCTGGTCTC 1080
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i1_HQ_samplec9816d|c55690/f2p0/1026      AGCCGCTCCCTTGGCAGCTGCAGCCCCCATGCAGAAGAGGCTCC-AGGCCCAAGCTCTGT 985
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NM_033257.3                              AGCCGCTCCCTTGGCAGCTGCAGCCCCCATGCAGAAGAGGCTCCCAGGCCCAAGCTCTGT 1140
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i1_HQ_samplec9816d|c64363/f2p0/1107      GTGACCCAGAGAaataaagatgcctcagtgtggcccacatgtggcttgt----------- 1107
NM_033257.3                              GTGACCCAGAGAAATAAAGATGCCTCAGTGTGGCCCAAATGTGGCTTGTGTGATAGCTGC 1200
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i1_HQ_samplec9816d|c55690/f2p0/1026      -----------------   1026
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VIRT671          ------------------------------------------------------------     0
NP_150282.2      MERYAAALEEVADGARQQERHYQLLSALQSLVKELPSSFQQRLSYTTLSDLALALLDGTV     60


VIRT195959       FEIVQGLLEIQHLTEKSLYNQRLRLQNEHRGRGTPDP-----------------------     97
VIRT194119       FEIVQGLLEIQHLTEKSLYNQRLRLQNEHRVLRQALRQKHQEAQQACRPHNLPVVQAAQQ     120
VIRT671          ------------------------------------------------------------     0
NP_150282.2      FEIVQGLLEIQHLTEKSLYNQRLRLQNEHRVLRQALRQKHQEAQQACRPHNLPVVQAAQQ     120


VIRT195959       ------------------------------------------------------------     97
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VIRT194119        RELEAVEHRIREEQRAMDQKIILELDRKVADQQSTLEKAGVAGFYVTTNPQELMLQMNLL     180
VIRT671           ----------------MDQKIILELDRKVADQQSTLEKAGVAGFYVTTNPQELMLQMNLL     44
NP_150282.2       RELEAVEHRIREEQRAMDQKIILELDRKVADQQSTLEKAGVAGFYVTTNPQELMLQMNLL     180
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VIRT195959        ----------------------------------------    97
VIRT194119        ELIRKLQQRGCRAGNAALGLGGPWQSPAAQCDQKGSPVPP    220
VIRT671           ELIRKLQQRGCRAGNAALGLGGPWQSPAAQCDQKGSPVPP    84
NP_150282.2       ELIRKLQQRGCRAGNAALGLGGPWQSPAAQCDQKGSPVPP    220
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PDCD10

Sequence	Header	AA Seq
Present		
Absent	i0_HQ_samplec9816d|c43184/f2p1/954	>VIRT111671
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	NM_145860	NP_665859.1
	NM_007217	NP_009148.2

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DGKAINVFVSANRLIHQTNLILQTSKLWPESCIC
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>NM_145859.1 Homo sapiens programmed cell death 10 (PDCD10), transcript variant 2, mRNA
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GCTGAGACCACATCCATGGTTTCTATGCCCCTCTATGCAGTCATGTATCCTGTGTTTAATGAGCTAGAAC
GAGTAAATCTGTCTGCAGCCCAGACACTGAGAGCCGCTTTCATCAAGGCTGAAAAAGAAAATCCAGGTCT
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CGTATGGCAGCTGATGATGTAGAAGAGTATATGATTGAACGACCAGAGCCAGAATTCCAAGACCTAAACG
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>NP_665858.1 programmed cell death protein 10 [Homo sapiens]
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LLDTVNNVFKKYQYQNRRALEHQKKEFVKYSKSFSDTLKTYFKDGKAINVFVSANRLIHQTNLILQTFKT
VA


>NM_145860.1 Homo sapiens programmed cell death 10 (PDCD10), transcript variant 3, mRNA
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CACTGAGAGCCGCTTTCATCAAGGCTGAAAAAGAAAATCCAGGTCTCACACAAGACATCATTATGAAAAT
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TGCAATAAAAGAACTTCTTGATACAGTGAATAATGTCTTCAAGAAATATCAATACCAGAACCGCAGGGCA
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VA


>NM_007217.3 Homo sapiens programmed cell death 10 (PDCD10), transcript variant 1, mRNA
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>NP_009148.2 programmed cell death protein 10 [Homo sapiens]
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VA


NM_007217.3                             GGTAAGGTGTAGCTGTTCTGTCCCAGTCCCCGTAGCTCTGCACCGAGCAGAAGAGGTCTA  60
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NM_145859.1                             ------------------------------------------------------------  0
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NM_145860.1                             ------------------------------------------------------------  0

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NM_145860.1                             ------------------------------------------------------------  0

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NM_145860.1                             ------------------------------------------------------------  0

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NM_145859.1                             -AAGTGACTAACAGCATTTTGGCATGAGAAAGCCCTAAAAAGATCAGTGTGTTTTTTGTG  149
NM_145860.1                             -----TGCAAGGTGGGAAGTGAAGTCAGTGCCTCAGTTGCTGATCAGTGTGTTTTTTGTG  55

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NM_145860.1                             TGAAGAATGAAGCTGAGACCACATCCATGGTTTCTATGCCCCTCTATGCAGTCATGTATC  235

NM_007217.3                             CTGTGTTTAATGAGCTAGAACGAGTAAATCTGTCTGC---AGCCCAGACACTGAGAGCCG  537
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NM_145859.1                             CTGTGTTTAATGAGCTAGAACGAGTAAATCTGTCTGC---AGCCCAGACACTGAGAGCCG  386
NM_145860.1                             CTGTGTTTAATGAGCTAGAACGAGTAAATCTGTCTGC---AGCCCAGACACTGAGAGCCG  292
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NM_145860.1                             CTTTCATCAAGGCTGAAAAAGAAAATCCAGGTCTCACACAAGACATCATTATGAAAATTT  352
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NM_145860.1                             TAGAGAAAAAAAGCGTGGAAGTTAACTTCACGGAGTCCCTTCTTCGTATGGCAGCTGATG  412
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NM_145860.1                             ATGTAGAAGAGTATATGATTGAACGACCAGAGCCAGAATTCCAAGACCTAAACGAAAAGG  472
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NM_145859.1                             TTCTGCAGACAATCAAGGATATAGCTAGTGCAATAAAAGAACTTCTTGATACAGTGAATA  686
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NP_665859.1      DIIMKILEKKSVEVNFTESLLRMAADDVEEYMIERPEPEFQDLNEKARALKQILSKIPDE    120
NP_009148.2      DIIMKILEKKSVEVNFTESLLRMAADDVEEYMIERPEPEFQDLNEKARALKQILSKIPDE    120
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                                          * ***  *    ** **  *     ** **      * **   **        *****

i0_HQ_samplec9816d|c2034/f4p1/662       GCTGGAGGGAAGAGGAGAAGGAAGAAGAGAAGGTTCCATCTGG---TAGCCAGGATGGTG  250
i0_HQ_samplec9816d|c1580/f7p10/768      GCAA-ACAGAAGTAAGG---ATGGACTGGATATTACCATCATCCACCATCCTGGCTACCA  349
NM_173080.2                             GCAA-ACAGAAGTAAGG---ATGGACTGGATATTACCATCATCCACCATCCTGGCTACCA  344
                                        **   *  ****    *      **   **   * *****       * ** ** *

i0_HQ_samplec9816d|c2034/f4p1/662       GATGATGGCCAGACCTCCCCCACTTCCTCTTCCCAAGCCTAGCAACACTAAGAATGTAAT  310
i0_HQ_samplec9816d|c1580/f7p10/768      GATGGAACCTTCTCTTCTTCCTTCTCCTCTTCCCTCC-----AGCTCTTGAGCCTACCCT  404
NM_173080.2                             GATGGAACCTTCTCTTCTTCCTTCTCCTCTTCCCTCC-----AGCTCTTGAGCCTACCCT  399
                                        ****    *    * **  **   **********              * **  *    *

i0_HQ_samplec9816d|c2034/f4p1/662       ATTCTGGGTTCCAGATTCTGGTTCTGCATTCCACCTC-----CAAGAAGAACACCATCTC  365
i0_HQ_samplec9816d|c1580/f7p10/768      C-------CTCTCACATCTCCTCCTGCCCAAGATGTAAGGAAGCATTGTAAGGATTTCTT  457
NM_173080.2                             C-------CTCTCACATCTCCTCCTGCCCAAGATGTAAGGAAGCATTGTAAGGATTTCTT  452
                                                 **     ***  * ****     *  *        *    **     ***

i0_HQ_samplec9816d|c2034/f4p1/662       CACCTGCAGCCCTCACTTCCACATACCCCCAGTCCTCTGTGCTCTTGCTGATATGAACTC  425
i0_HQ_samplec9816d|c1580/f7p10/768      CCCATCGTACCCTTCCCCACACATACCACCTTGGCTT-CTTCTATATCCCACCCCGATGC  516
NM_173080.2                             CCCATCGTACCCTTCCCCACACATACCACCTTGGCTT-CTTCTATATCCCACCCCGATGC  511
                                        * * *    ****  *   ******** **    **   * ** *  *  *     *  *

i0_HQ_samplec9816d|c2034/f4p1/662       TCCACAAGGAAACTACGCAGCAAGACAGA-------------TTTGCATGGACATAGACC  472
i0_HQ_samplec9816d|c1580/f7p10/768      TCTCCCAGGTGGGTGTGAGAGAGACCTCATTCTCTGCAGGCTCCAGCGTGGCCACAGCTA  576
NM_173080.2                             TCTCCCAGGTGGGTGTGAGAGAGACCTCATTCTCTGCAGGCTCCAGCGTGGCCACAGCTA  571
                                        **  * ***    *  *    *   *  *                ** *** ** **

i0_HQ_samplec9816d|c2034/f4p1/662       AAGGCTTTTCATATACCTGGTGCCTTGAAGGCACTG------GTATGTGTGTATTGCCTG  526
i0_HQ_samplec9816d|c1580/f7p10/768      AGGCCCATCCATTTCCCAAAGTGAGGAAAGTGTCTGGGCTTCTTCTGGGGTTCCACCCTG  636
NM_173080.2                             AGGCCCATCCATTTCCCAAAGTGAGGAAAGTGTCTGGGCTTCTTCTGGGGTTCCACCCTG  631
                                        * * *  * *** * **          ***   ***       * ** *  *    ****

i0_HQ_samplec9816d|c2034/f4p1/662       T-------GAACAGATGGGCAGCTCCATCCCTCATGTCCCAGTCACCCA-TGTGGGTTTA  578
i0_HQ_samplec9816d|c1580/f7p10/768      ACAAGTAGGGTCACAGAGGCTGGTGCACAGTTTCTGCCTCATTCCTCTCCATGATGCCCC  696
NM_173080.2                             ACAAGTAGGGTCACAGAGGCTGGTGCACAGTTTCTGCCTCATTCCTCTCCATGATGCCCC  691
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i0_HQ_samplec9816d|c2034/f4p1/662       CTGCAATGAATTTTACTCCTATTTTTCCCAATTTCATCATTGCCCTTTTAtttattaata  638
i0_HQ_samplec9816d|c1580/f7p10/768      CTGCTCTGGGCTTCTCTCCTGTTTTCCCCAATAAATATGTGCCTCATGTAATAAA-----  751
NM_173080.2                             CTGCTCTGGGCTTCTCTCCTGTTTTCCCCAATAAATATGTGCCTCATGTAATAAA-----  746
                                        ****  **   **  ***** **** ******       *  * * * ** * *

i0_HQ_samplec9816d|c2034/f4p1/662       aaggactcctgcttagttttgaag        662
i0_HQ_samplec9816d|c1580/f7p10/768      ---TGTGTCTGCTTCCTGGG----        768
NM_173080.2                             ---AAAAAAA--------------        753
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VIRT55277        ---------------------------MLPYILGRRRCERRVGSRAGGKRRRKKRRFHLV     33
VIRT53999        ------------------------MMARPPPLPLPKPSNTK----------------NVI     20
NP_775103.1      MSSQQQQRQQQQCPPQRAQQQQVKQPCQPPPVKCQETCAPKTKDPCA---------PQVK     51
                                              * :   . .  :                ::

VIRT55277        ARMVDDGNIQ---------------SILTSVCSWRLAGLRDTSAGLE      65
VIRT53999        FWVPDSGSAFHLQEEHHLHLQPSLPHTPSPLCSC-------------      54
NP_775103.1      KQCPPKGTIIPAQQKCPSAQQASKSKQK-------------------      79
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JAGN1

Sequence	Header	AA Seq
Present	i1_HQ_samplec9816d|c7012/f2p0/1248	
Absent	i1_HQ_samplec9816d|c64100/f41p0/1184	
NCBI	NM_032492	

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GGTACCTGGTGCAGACCAGGCCAAAGTTCTGGAAAGCTCCTTTTGCCATCTGCTGAGGTGGCAAAACTATAATTTATTC
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>VIRT87749

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>VIRT88771
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GCCGGCACCGACGGCAGCGACTTTCAGCACCGGGAGCGCGTCGCCATGCACTACCAGATGAGTGTGACTC
TCAAGTATGAAATCAAGAAGCTGATCTACGTACATCTGGTCATATGGCTGCTGCTGGTTGCTAAGATGAG
CGTGGGACACCTGAGGCTCTTGTCACATGATCAGGTGGCCATGCCCTATCAGTGGGAATACCCGTATTTG
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CTGGTGTTGGTGTTGGCAGTGCAAGTGCATGCCTGGCAGTTGTACTACAGCAAGAAGCTCCTAGACTCTT
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>NP_115881.3 protein jagunal homolog 1 isoform a [Homo sapiens]
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PYQWEYPYLLSILPSLLGLLSFPRNNISYLVLSMISMGLFSIAPLIYGSMEMFPAAQQLYRHGKAYRFLF
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i1_HQ_samplec9816d|c64100/f41p0/1184       ggggccggaagtTCTCTTTCAACGGAGCCGCGCGGCTGCGGGGGGCGCAAATAGGGTCAC           60
NM_032492.4                                ---------------CTCTTCACGGAGCCGCGCG-GCTGCGGGGGCGCAAATAGGGTCAG           44
                                                          ** *  **********             ***     *

i1_HQ_samplec9816d|c7012/f2p0/1248         agtgggcgcttggGGTGTCGTTGCGGTACCAGGTCCGCGTGAGGGGTTCGGGGGTTCTGG           96
i1_HQ_samplec9816d|c64100/f41p0/1184       TGGGCCGCTTGGCGGTGTCGTTGCGGTACCAGGTCCGCGTGAGGGGTTCGGGGGTTCTGG           12
NM_032492.4                                TGGGCCGCTTGGCGGTGTCGTTGCGGTACCAGGTCCGCGTGAGGGGTTCGGGGGTTCTGG           10
                                            * *     * * ***********************************************

i1_HQ_samplec9816d|c7012/f2p0/1248         GCAGGCACAATGGCGTCTCGAGCAGGCCCGCGAGCGGCCGGCACCGACGGCAGCGACTTT           15
i1_HQ_samplec9816d|c64100/f41p0/1184       GCAGGCACAATGGCGTCTCGAGCAGGCCCGCGAGCGGCCGGCACCGACGGCAGCGACTTT           18
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NM_032492.4                               GCAGGCACAATGGCGTCTCGAGCAGGCCCGCGAGCGGCCGGCACCGACGGCAGCGACTTT          16
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i1_HQ_samplec9816d|c7012/f2p0/1248        CAGCACCGGGAGCGCGTCGCCATGCACTACCAGATGAGGCCCCGGCTGAAAGGGCCCTCA          21
i1_HQ_samplec9816d|c64100/f41p0/1184      CAGCACCGGGAGCGCGTCGC----------------------------------------          20
NM_032492.4                               CAGCACCGGGAGCGCGTCGC----------------------------------------          18
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i1_HQ_samplec9816d|c7012/f2p0/1248        CAACTTAAGCAGGTGTTTTCATGCCAGCCCAGAGTAGAAACATCGCCTTTAGGGATATGA          27
i1_HQ_samplec9816d|c64100/f41p0/1184      ------------------------------------------------------------          20
NM_032492.4                               ------------------------------------------------------------          18

i1_HQ_samplec9816d|c7012/f2p0/1248        GGAGGATACGTTTGGGACGTGAGAGAATTAGAAGAATAAGATAATGTGACTCTCAAGTAT          33
i1_HQ_samplec9816d|c64100/f41p0/1184      --------------------------CATGCACTACCAGATGAGTGTGACCCTCAAGTAT          23
NM_032492.4                               --------------------------CATGCACTACCAGATGAGTGTGACTCTCAAGTAT          21
                                                                    *  *  *  *    * ****** *********

i1_HQ_samplec9816d|c7012/f2p0/1248        GAAATCAAGAAGCTGATCTACGTACATCTGGTCATATGGCTGCTGCTGGTTGCTAAGATG          39
i1_HQ_samplec9816d|c64100/f41p0/1184      GAAATCAAGAAGCTGATCTACGTACATCTGGTCATATGGCTGCTGCTGGTTGCTAAGATG          29
NM_032492.4                               GAAATCAAGAAGCTGATCTACGTACATCTGGTCATATGGCTGCTGCTGGTTGCTAAGATG          27
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i1_HQ_samplec9816d|c7012/f2p0/1248        AGCGTGGGACACCTGAGGCTCTTGTCACATGATCAGGTGGCCATGCCCTATCAGTGGGAA          45
i1_HQ_samplec9816d|c64100/f41p0/1184      AGCGTGGGACACCTGAGGCTCTTGTCACATGATCAGGTGGCCATGCCCTATCAGTGGGAA          35
NM_032492.4                               AGCGTGGGACACCTGAGGCTCTTGTCACATGATCAGGTGGCCATGCCCTATCAGTGGGAA          33
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i1_HQ_samplec9816d|c7012/f2p0/1248        TACCCGTATTTGCTGAGCATTTTGCCCTCTCTCTTGGGCCTTCTCTCCTTTCCCCGCAAC          51
i1_HQ_samplec9816d|c64100/f41p0/1184      TACCCGTATTTGCTGAGCATTTTGCCCTCTCTCTTGGGCCTTCTCTCCTTTCCCCGCAAC          41
NM_032492.4                               TACCCGTATTTGCTGAGCATTTTGCCCTCTCTCTTGGGCCTTCTCTCCTTTCCCCGCAAC          39
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i1_HQ_samplec9816d|c7012/f2p0/1248        AACATTAGCTACCTGGTGCTCTCCATGATCAGCATGGGACTCTTTTCCATCGCTCCACTC          57
i1_HQ_samplec9816d|c64100/f41p0/1184      AACATTAGCTACCTGGTGCTCTCCATGATCAGCATGGGACTCTTTTCCATCGCTCCACTC          47
NM_032492.4                               AACATTAGCTACCTGGTGCTCTCCATGATCAGCATGGGACTCTTTTCCATCGCTCCACTC          45
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i1_HQ_samplec9816d|c7012/f2p0/1248        ATTTATGGCAGCATGGAGATGTTCCCTGCTGCACAGCAGCTCTACCGCCATGGCAAGGCC          63
i1_HQ_samplec9816d|c64100/f41p0/1184      ATTTATGGCAGCATGGAGATGTTCCCTGCTGCACAGCAGCTCTACCGCCATGGCAAGGCC          53
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i1_HQ_samplec9816d|c7012/f2p0/1248        TACCGTTTCCTCTTTGGTTTTTCTGCCGTTTCCATCATGTACCTGGTGTTGGTGTTGGCA          69
i1_HQ_samplec9816d|c64100/f41p0/1184      TACCGTTTCCTCTTTGGTTTTTCTGCCGTTTCCATCATGTACCTGGTGTTGGTGTTGGCA          59
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i1_HQ_samplec9816d|c7012/f2p0/1248        GTGCAAGTGCATGCCTGGCAGTTGTACTACAGCAAGAAGCTCCTAGACTCTTGGTTCACC          75
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i1_HQ_samplec9816d|c7012/f2p0/1248        ATGTTGGTACCTGGTGCAGACCAGGCCAAAGTTCTGGAAAGCTCCTTTTGCCATCTGCTG          93
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i1_HQ_samplec9816d|c7012/f2p0/1248        AGGTGGCAAAACTATAATTTATTCCTGGTTGGCTAGAACTGGGTGACCAACAGCTATGAA          99
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NM_032492.4                               AGGAAATAGGGAATAAATCAAATTACTTCATCTCTAGGTCACGGGTCAGGAAACATTTGG      10
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i1_HQ_samplec9816d|c7012/f2p0/1248        GCAGCTGCTCCCTTGGCAGGCTGTGGTCTCCTCTgcaagcattttaattaaaaactcaat      12
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NM_032492.4                               GCAGCTGCTCCCTTGGCAGGCTGTGGTCTCCTCTGCAAAGCATTTTAATTAAAAACCTCA      11
                                          ****************** *******************    *** * * ****  *

i1_HQ_samplec9816d|c7012/f2p0/1248        aaa--gatgcctgc----------------------------------------------      12
i1_HQ_samplec9816d|c64100/f41p0/1184      ATAAAGATGGCCCTGCCCACActgtgccttgtgtttggggcttgatagagt---------      11
NM_032492.4                               ATAAAGATGGCCCTGCCCACACTGTGCCTTGTGTTTGGGGCTTGATAGAGTGTGAAAGGT      11
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i1_HQ_samplec9816d|c7012/f2p0/1248        ------------------------------------------------------------      12
i1_HQ_samplec9816d|c64100/f41p0/1184      ------------------------------------------------------------      11
NM_032492.4                               GTGTTGCTTGAAAGGTGTGGCCTTAGACACTAGGAGATGATGGGTAGAAGCTCCTTGAGA      12

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VIRT87749        HLHCQHQHQVHDGNGRKTKE--ETVGLAMAVELLCSREH------LHAAINEWSDGKESH      53
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VIRT87749        ADHGEHQVANVVAGKGEKAQERGQNAQQIRVFPLIGHGHLIM           95
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EMC3

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i1_HQ_samplec9816d|c26333/f2p57/1162      tcggctcacagtcgcaggagagttctggggtacACGGGCAAAGGGGCTTGAGAAGGCCCG    77
i1_HQ_samplec9816d|c26920/f2p0/1048       tcggctcacagtcgcaggagagttctggggtacacgggcaaagggccttgaGAA-GCCCG    76
NM_018447.3                               TCGGCTCACAGTCGCAGGAGAGTTCTGGGGTACACGGGCAAAGGGGCTTGAGAAGGCCCG    385
                                          ** **          *****  *         *    ***  *   *  * * * ** *

NR_103821.1                               TCCATTGTATTAAAATGTTTTTGCCTGTGTCCACCGCCGAAAAGGAGGAATAAGATGACC    1074
i1_HQ_samplec9816d|c26333/f2p57/1162      G-AGGCGAAGCCGAAGA--GAAGCAACTGTGCCCCGGAGAAGAGAAGCT---CGCCCATT    131
i1_HQ_samplec9816d|c26920/f2p0/1048       G-AGGCGAAGCCGAAGA--GAAGCAACTGTGCCCCGGAGAAGAGAAGCT---CGCCCATT    130
NM_018447.3                               G-AGGCGAAGCCGAAGA--GAAGCAACTGTGCCCCGGAGAAGAGAAGCT---CGCCCATT    439
                                                * *    **       **   *** * ***  *** ** **      *   *

NR_103821.1                               CCAACATAGTTGCACGGCTGAAGACAAAAATCAAGTTGGTGGGGTCAATATTGTTACCAT    1134
i1_HQ_samplec9816d|c26333/f2p57/1162      CCAGAC-------TGGGAACCAGCTTTCAGTGAAGATGGCAGGGCCAGAACTGTTGCTCG    184
i1_HQ_samplec9816d|c26920/f2p0/1048       CCAGAC-------TGGGAACCAGCTTTCAGTGAAGATGGCAGGGCCAGAACTGTTGCTCG    183
NM_018447.3                               CCAGAC-------TGGGAACCAGCTTTCAGTGAAGATGGCAGGGCCAGAACTGTTGCTCG    492
                                          ***            **    **     * * *** ***  *** **  * **** *

NR_103821.1                               AGTCACTAC----ACTTAGAGTAGTTT------------TA----TAGTCAGTGTAGACA    1174
i1_HQ_samplec9816d|c26333/f2p57/1162      ACTCCAACATCCGCCTCTGGGTGGTCCTACCCATCGTTATCATCACTTTCTTCGTAGGCA    244
i1_HQ_samplec9816d|c26920/f2p0/1048       ACTCCAACATCCGCCTCTGGGTGGTCCTACCCATCGTTATCATCACTTTCTTCGTAGGCA    243
NM_018447.3                               ACTCCAACATCCGCCTCTGGGTGGTCCTACCCATCGTTATCATCACTTTCTTCGTAGGCA    552
                                          * **          **  * ** **              *        **   **** **

NR_103821.1                               GGTGGCACCATGCAGCAGGGATCAGCCTCCACC------------ACACCTGACCAGGAG    1222
i1_HQ_samplec9816d|c26333/f2p57/1162      TGATCCGCCACTACGTGTCCATCCTGCTGCAGAGCGACAAGAAGCTCACCCAGGAACAAG    304
i1_HQ_samplec9816d|c26920/f2p0/1048       TGATCCGCCACTACGTGTCCATCCTGCTGCAGAGCGACAAGAAGCTCACCCAGGAACAAG    303
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NM_018447.3                               TGATCCGCCACTACGTGTCCATCCTGCTGCAGAGCGACAAGAAGCTCACCCAGGAACAAG    612
                                           *   * ***    *     ***   ** **               ****     *  **

NR_103821.1                               CTCCAGAACTGTAAAATCCTGGACACCATTGGCCGTGGCACGTTCAGTGAGGTCCAGGAT    1282
i1_HQ_samplec9816d|c26333/f2p57/1162      TATCTGACAGAAAATATCTTTCAGGCCTGGTGCAATGGCTCACACCTATAATCCCAGCAC    364
i1_HQ_samplec9816d|c26920/f2p0/1048       TATCTGACA---------------------------------------------------    312
NM_018447.3                               TATCTGACA---------------------------------------------------    621
                                             * **

NR_103821.1                               C--------ACATGCTGATTGGGACCCAAATGGCCATCAAAATCATCCCCAAGGCTGGCT    1334
i1_HQ_samplec9816d|c26333/f2p57/1162      TTTGGGGGGCTGAGATGGGAGGATCCCTTGAGCCCAGGAATTT-GAGACCAACCTTGGCA    423
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    312
NM_018447.3                               ------------------------------------------------------------    621


NR_103821.1                               ----CCCTTGGCATCACTCTCCAGAGAGTGATAAGT--ATTTTAAAGTTACTCTGTCACT    1388
i1_HQ_samplec9816d|c26333/f2p57/1162      GCATGTCAAGTCCTAATTCGAAGCAGAGTCCTCAGGGAAAATGGAAAATACATTCCCAAA    483
i1_HQ_samplec9816d|c26920/f2p0/1048       ----GTCAAGTCCTAATTCGAAGCAGAGTCCTCAGGGAAAATGGAAAATACATTCCCAAA    368
NM_018447.3                               ----GTCAAGTCCTAATTCGAAGCAGAGTCCTCAGGGAAAATGGAAAATACATTCCCAAA    677
                                                *  * * * * **     *****  * **   *  *  **  ***  *  **

NR_103821.1                               TCAATATTGTACGGTTGTATCAAGTGATTGACACCCCCAACACCAGTTATTTATTTAGTA    1448
i1_HQ_samplec9816d|c26333/f2p57/1162      -CAGTCTTTCTTGACACGAAAATATTATTTCAACAACCCAGAGGATGGATTTTTCAAAAA    542
i1_HQ_samplec9816d|c26920/f2p0/1048       -CAGTCTTTCTTGACACGAAAATATTATTTCAACAACCCAGAGGATGGATTTTTCAAAAA    427
NM_018447.3                               -CAGTCTTTCTTGACACGAAAATATTATTTCAACAACCCAGAGGATGGATTTTTCAAAAA    736
                                           ** * **    *     *  *  * ***   **  ** * *  *   **** *  *  *

NR_103821.1                               ACGGAGTATGCAAGAGGAGGACACCCACGCAACCAATACACCACCATGGCCTCATGAGGG    1508
i1_HQ_samplec9816d|c26333/f2p57/1162      AACTA-AACGGAAGGTAGTGCCACCTT---CTCCTATGACTGATCCTACT----------    588
i1_HQ_samplec9816d|c26920/f2p0/1048       AACTA-AACGGAAGGTAGTGCCACCTT---CTCCTATGACTGATCCTACT----------    473
NM_018447.3                               AACTA-AACGGAAGGTAGTGCCACCTT---CTCCTATGACTGATCCTACT----------    782
                                          *   *  * * ***     * ****       ** **     * * *

NR_103821.1                               AGGAGAAGGCCTAGACCATGTTCAGGCAGATTCTGTCGGCCATGCAGTAGTGCCATAGCA    1568
i1_HQ_samplec9816d|c26333/f2p57/1162      -----------------ATGTTGAC------------AGACATGATGAAAGGG-------    612
i1_HQ_samplec9816d|c26920/f2p0/1048       -----------------ATGTTGAC------------AGACATGATGAAAGGG-------    497
NM_018447.3                               -----------------ATGTTGAC------------AGACATGATGAAAGGG-------    806
                                                           ***** *              * ****  * *  *

NR_103821.1                               AATTGCGCAGAGACCTGAACCCAGAAAACATCATCCTTGATGAGGACGGTAACGTTAAGA    1628
i1_HQ_samplec9816d|c26333/f2p57/1162      -----------AATGTAACAAATGTCCTCCCTATGATTCTTATTGGTGGATGGATCAACA    661
i1_HQ_samplec9816d|c26920/f2p0/1048       -----------AATGTAACAAATGTCCTCCCTATGATTCTTATTGGTGGATGGATCAACA    546
NM_018447.3                               -----------AATGTAACAAATGTCCTCCCTATGATTCTTATTGGTGGATGGATCAACA    855
                                                      *  * *     *    *   **  **  *   *  **     * ** *

NR_103821.1                               TCGCAGACTTCGGCTTTGGTACCACATTCCATGATGGGCAGAAGCTGACAGCCCTTTGTA    1688
i1_HQ_samplec9816d|c26333/f2p57/1162      TGACATTCTCAGGCTTTGTCACAACCAAG---GTCCCATTTCCACTGACCCTCCGTTTTA    718
i1_HQ_samplec9816d|c26920/f2p0/1048       TGACATTCTCAGGCTTTGTCACAACCAAG---GTCCCATTTCCACTGACCCTCCGTTTTA    603
NM_018447.3                               TGACATTCTCAGGCTTTGTCACAACCAAG---GTCCCATTTCCACTGACCCTCCGTTTTA    912
                                          *  **  **  *******  ** **       *           *****   ** ** **

NR_103821.1                               GCACTTAACCCCTACATGGCCCTGGAACGTTTCCTAGGCCAGGGCTACCAATGTGCCACC    1748
i1_HQ_samplec9816d|c26333/f2p57/1162      -------------------------AGCCTATGTTACAGCAAGGAATCGAGCTACTCACA    753
i1_HQ_samplec9816d|c26920/f2p0/1048       -------------------------AGCCTATGTTACAGCAAGGAATCGAGCTACTCACA    638
NM_018447.3                               -------------------------AGCCTATGTTACAGCAAGGAATCGAGCTACTCACA    947
                                                                   * * * *  **   ** **   * *      ***

NR_103821.1                               A-----------TGGATATTCAGAGCCTCAGAGTAATTTTATACCACATGGTGGCTGGGG    1797
i1_HQ_samplec9816d|c26333/f2p57/1162      TTAGATGCATCCTGGGTGAGTTCTGCATCCTGGTACTT-----CCTCAATGTATTTGGGC    808
i1_HQ_samplec9816d|c26920/f2p0/1048       TTAGATGCATCCTGGGTGAGTTCTGCATCCTGGTACTT-----CCTCAATGTATTTGGGC    693
NM_018447.3                               TTAGATGCATCCTGGGTGAGTTCTGCATCCTGGTACTT-----CCTCAATGTATTTGGGC    1002
                                                      *** *       ** **   *** **     ** **  **   ****

NR_103821.1                               TTCTGCCCTTCTGCTCATGCAGCATTAGGGTCCTCTCAGCAAAAATTTAAAGTGGAAGCT    1857
i1_HQ_samplec9816d|c26333/f2p57/1162      TTCGGAGCATTTACTCTCTGAT--------------------------------------    830
i1_HQ_samplec9816d|c26920/f2p0/1048       TTCGGAGCATTTACTCTCTGAT--------------------------------------    715
NM_018447.3                               TTCGGAGCATTTACTCTCTGAT--------------------------------------    1024
                                          *** *  * * * ***    *

NR_103821.1                               ATTTTTCCCCAGTCTACTTTTCCTGAGGTCTTAAAAGCCTCATTAAAAAACTATTAACAG    1917
i1_HQ_samplec9816d|c26333/f2p57/1162      --TCTGGGCCAAGATAATGCCGCTGACCA--ATCACGAATGATGCAGGAGCAGATGACGG    886
i1_HQ_samplec9816d|c26920/f2p0/1048       --TCTGGGCCAAGATAATGCCGCTGACCA--ATCACGAATGATGCAGGAGCAGATGACGG    771
NM_018447.3                               --TCTGGGCCAAGATAATGCCGCTGACCA--ATCACGAATGATGCAGGAGCAGATGACGG    1080
                                            * *   ***   ** *    ****        * *  * **  *  * *   * ** *

NR_103821.1                               TAGACCCCAGGGAGCAGACCACAC---TAGAAGAAGTTATGA---------GGGACCCGT    1965
i1_HQ_samplec9816d|c26333/f2p57/1162      GAGCAGCCATGGCCATGCCCGCAGACACAAACAAAGCTTTCAAGACAGAGTGGGAAGCTT    946
i1_HQ_samplec9816d|c26920/f2p0/1048       GAGCAGCCATGGCCATGCCCGCAGACACAAACAAAGCTTTCAAGACAGAGTGGGAAGCTT    831
NM_018447.3                               GAGCAGCCATGGCCATGCCCGCAGACACAAACAAAGCTTTCAAGACAGAGTGGGAAGCTT    1140
                                           **   *** **    * ** **     * *  *** * * *         ****  * *

NR_103821.1                               GGGTGAACAGTGGTCAGGAGTTGCCTCTG--ACAACATGAAGAACAAATCCTGGACCACC    2023
i1_HQ_samplec9816d|c26333/f2p57/1162      TGGAGCTGACGGATCACCAGTGGGCACTAGATGATGTCGAAGAAGAGCTCATGGCCAAAG    1006
i1_HQ_samplec9816d|c26920/f2p0/1048       TGGAGCTGACGGATCACCAGTGGGCACTAGATGATGTCA-AGAAGAGCTCATGGCCAAAG    890
NM_018447.3                               TGGAGCTGACGGATCACCAGTGGGCACTAGATGATGTCGAAGAAGAGCTCATGGCCAAAG    1200
                                           ** *   *  * ***  *** * * **     *      **** *  ** *** * *

NR_103821.1                               TGAATCCCAAAACAACCCAGCTTTTGGTGGCCATGGGATTCCAGGCTGAGA---------    2074
i1_HQ_samplec9816d|c26333/f2p57/1162      AC-CTCCACTTCGAAGGC-----ATGTTCAAAAAGGAATTACAGACCTCTATTTTTTGAA    1060
i1_HQ_samplec9816d|c26920/f2p0/1048       AC-CTCCACTTCGAAGGC-----ATGTTCAAAAAGGAATTACAGACCTCTATTTTTTGAA    944
NM_018447.3                               AC-CTCCACTTCGAAGGC-----ATGTTCAAAAAGGAATTACAGACCTCTATTTTTTGAA    1254
                                              ***      **  *      ** *    * ** *** *** *    *

NR_103821.1                               -ACCTATCTGTGGCAATCAAAGAAAAATTATTCAGTTATCCCATGGCCACCTACCTTGTT    2133
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i1_HQ_samplec9816d|c26333/f2p57/1162      GACCGAGCAGGGATTAGCTGTGTCAGGAACTTGGAGTTGCACTTAACCTTGTAACTTTGT    1120
i1_HQ_samplec9816d|c26920/f2p0/1048       GACCGAGCAGGGATTAGCTGTGTCAGGAACTTGGAGTTGCACTTAACCTTGTAACTTTGT    1004
NM_018447.3                               GACCGAGCAGGGATTAGCTGTGTCAGGAACTTGGAGTTGCACTTAACCTTGTAACTTTGT    1314
                                           *** * * * *   * *   *  *     **    *  * * *  **   ** ***  *

NR_103821.1                               TTGGAACAAACAAAACAGAA-------GAAGCGGTCCACTATCAGACCACAGACCCTTCC    2186
i1_HQ_samplec9816d|c26333/f2p57/1162      TTGGAgctggcacctcttgaaataaaaaggaggatgcacgag------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       TTGGAGCTggcacctcttgaaataaaaaggaggatgcacgagcg----------------    1048
NM_018447.3                               TTGGAGCTGGCACCTCTTGAAATAAAAAGGAGGATGCACGAGCTGGCAG-----GCATGC    1369
                                          ***** *   **   *   *            * * *** *

NR_103821.1                               TCCTGGGGATCCCACTTGTCCTCTCTACATTGAAGTTTCCACCTTCCCTCTTTCACTGAA    2246
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               AGCA-AGGCTTGTTCTTGTCTGGGCTGGG-------TTCCCCTTTATGTTTGAAAC-TAG    1420

NR_103821.1                               GCGGGCTCATAGCATTCAGCAGAAGACTGTGGGTGCCAAGTCTGGGCAGGGCCTTTGCCC    2306
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               AGGAAATAGGAGTATGCTGGGCAACTTGTTATTTTTAAAATGTTGTAAA-----------    1469

NR_103821.1                               TTGGGAGTCCTGTTTTAGACCCAGCTCCACCACGTGGCCCTGGCCTCTTCTCTGCCCTGT    2366
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               ---------------------------------------------------------TGT    1472

NR_103821.1                               CTGTGCTTGCAGCCATGGTGCCCAGTCTGGCCCCACCAGGAGACACCAGAACGACTGTCC    2426
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               TCCTTCTGGTGACTCTAGTAATGAAAGTCAGAGAAAGGGGGAAACCTCAGGCTACTGATA    1532

NR_103821.1                               ATGTGTCTACTCCTTGGCACC--------------------TTCCCCGCATGGTGGGTAG    2466
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               ATATATAAAATCTTGGCCAGGCGCAGTGGCTCACGCCTGTAATCCCAGGATTTTGGGAGG    1592

NR_103821.1                               ATGGGCAGGGAGGGGT---------GGG------AATCTGTGTAACCGTGGAAGGGAACG    2511
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               CTGAGGCGGGTGGGTCACGAGATCAGGAGTTCAAGATCAGCCTGGCCAAGATGGTGAAAC    1652

NR_103821.1                               GCCCTCAGACCCA--------GAGGGTTTGGAGCCTGGGGT----ATTGTCACCGACAGT    2559
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               CCCATCTCTACTAAAAATACAAAAAAAAATTAGCCGGGCGTGGTGGTGGGCACCTGTAAT    1712

NR_103821.1                               GGCCTTAGCCTAGCTAGCACAGTTAGTGCTGTGCATCACAGCATAGCTTTTAGAGGCAGG    2619
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               C--------CCAGCTACTTGGGAGGCTGAGGCAGAGAACTGCTTAAACCTAGGAGGCGGA    1764

NR_103821.1                               ATTTGTAGTCAGTATAG---------TTGGGAGGCACCATGGAGCAG-GGATCACCCTCC    2669
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               GGATGCAGTGAGCTGACATCGTGCCACTGCGCTCCAGCCTGGGCGACAGAGCAAAACTCC    1824

NR_103821.1                               ACCTCACTTGACAAGGAGATACAAAACTATCAGTTCATAGACACCATCTGATAGGGAACT    2729
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               AT-----CTGAAAAAAAAAAAAAAATATATATATATAT----------ATATATATATCT    1869

NR_103821.1                               GGCTCAGCATAGGCCAACTGGG------ACCCAGG------TTGCCATCTTGAAGACTTT    2777
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               ATCTTAGCAGAAGCCCAGTCTTCGAAGGAAGCATTGTTAATTATAGCTAATGATTATGTG    1929

NR_103821.1                               CCATCACCCAAATATCATTCAGCTCTTCCAGGTGGTGAGGGAGTAAACCAGAGGAGGAGA    2837
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               CAGTCAGCCTGACATCTAGCCACAGTAAACTCCTGTTTTCTTGGGATCCAAACACCCTGT    1989

NR_103821.1                               GTTGCACCACCAGATATACCACTATGGCCACATCGAGGAGGAAGAGGAGGCCCG------    2891
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               GTTTTACCATTAGTTTTGTTAGTATTGTTAACTTTCTTTACACAAGTAAACCATTTCCAC    2049

NR_103821.1                               ---------------GACCATGTTCAGGCAGATTCTGTCAGCCCTGCAGTACTGCCACTT    2936
i1_HQ_samplec9816d|c26333/f2p57/1162      ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048       ------------------------------------------------------------    1048
NM_018447.3                               TACCAAAGGTTTAGAAACTATGGATGAACAAAATGAATCTCCCTGTTCATTTTGAGCCTA    2109
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NR_103821.1                                 AAAAAAAAAAAAAAAAATCACACATCCAGACCTAAAGCCACAAAACATCCTATTCAAAGAA    2996
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 CATAGACATAGAGACCAAATATGTCAAAACCTTATTCAAATAAACTC--TCTTCAGA---    2164

NR_103821.1                                 TGAGGCAACATACATTGTGGACTTTGGCTTCAGTACAACATTCAGAGAGGGGCAGATGCT    3056
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 --------------------------------GTGAATACCCAGGGTCAGGACAGACTCA    2192

NR_103821.1                                 GACAGCTTTTTGTGGCA-------------TGTACCCCTACGTGGCCCCAGAACGCTCCC    3103
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 GCAAACCTTCTATATCACTTAATTCTGCCCAGTGAAAATCAGTGACCCTGAGGCACTGCC    2252

NR_103821.1                                 TGGGCCAGGCATGCCAGTGACCCGCCAGGGACATACAAAGCCTCAGTGTCATACTGTATT    3163
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 AGATTCTAAAGT-----------------GCCTTTGGGATCATCAGAGA----CTGTCTA    2291

NR_103821.1                                 TCAGGAATACAGTAGGTAGAAGGGCCAGGACTTTGCCCTTTTACTCAGGGAAGCCTCCAA    3223
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 TAAATAATGCAAAATCTTGATCTGGATGTCAGTGTATCAAATCTTATCAAATCCATTGAC    2351

NR_103821.1                                 ACTTCAAGA-AAAAATTCTC--ACAG----GAAGATACCATGCCCCACCACTTCTTGCCC    3276
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 AAATCAGTGGTGCTATACTGGAAATGGCTACTCCTTTGGATGAAGGACCTCATTTCCCAG    2411

NR_103821.1                                 TTCAACTTGACTCATTAAAAAATTACTAATGCTGAACGCCAGGAAGTGTCCTTCACTGTA    3336
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 TTGCTTGGAACAAAAGAGAATTTACATATTGCTGTAAGAA-GGGAGAGACGGCAGTTGTT    2470

NR_103821.1                                 ACTGATGAAAAATCCATGGGTGAAAAGTAGCCAGAAGATGCCACTGATACCATACGAAGA    3396
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 GGTAGACACACAGATAAGGGTGCCC--------AAGAATAATTCTGTCTGGATTAAAGGT    2522

NR_103821.1                                 GCCACTCCTGGACCACCCCAAACAATCCAGCTCATGGTGGCCATGGGATTTCAGGCCAAG    3456
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 CCCAGGGAAGTGACGGTGCCATTTCTGTACCAAGAGGTGA--ATATAATTTG-------C    2573

NR_103821.1                                 AACATCTCTGTGGCAATCATAGAAAGAAAATTCAACTATCCCATGGCCACCTACCTCATT    3516
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 ATGTTGAGTGCAGTAATTAAGAACAAACGACTCGACTCCACAAATTAAACCGTCCTGTTT    2633

NR_103821.1                                 TTAGAGCACACAAAACAAGAGAGGAAGTGCTCCACCATCAGAGAACTGTCCCTTCCTCCC    3576
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 TCTCTTCTTAAAAAAAAAAAAAAAAAA---------------------------------    2660

NR_103821.1                                 GGGGTTCCCACCTCTCCTTCCCCATCCACTGAACTTTCCACCTTCCCTCTCTCACTGATG    3636
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 ------------------------------------------------------------    2660

NR_103821.1                                 CGGGCTCATAGGGAGCCAGCTTTTAACGTTCAGCCTCCCGAAGAAAGCCAGATGTCAGGG    3696
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 ------------------------------------------------------------    2660

NR_103821.1                                 CAGAAGACCGCCATTCTTGCCAGTACACCTGCCAGCCTACAGAGGAAGCCAGATCGGGGA    3756
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 ------------------------------------------------------------    2660

NR_103821.1                                 AGCCAGGAAGTTTTAGTGAAGCCCCCAGCATGACCCTATTGTCTCCCCTTTCACCCAGAG    3816
i1_HQ_samplec9816d|c26333/f2p57/1162        ------------------------------------------------------------    1162
i1_HQ_samplec9816d|c26920/f2p0/1048         ------------------------------------------------------------    1048
NM_018447.3                                 ------------------------------------------------------------    2660

NR_103821.1                                 CACCAGCAACTGGTGAAGTCTTAGAAACGTCCCTGATACACCAAAAACCATCCCAGGAAG    3876
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VIRT151947       MAGPELLLDSNIRLWVVLPIVIITFFVGMIRHYVSILLQSDKKLTQEQVSDRKYLSGLVQ     60
NP_060917.1      MAGPELLLDSNIRLWVVLPIVIITFFVGMIRHYVSILLQSDKKLTQEQVSD---------     51
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VIRT153469       -----------------------------SQVLIRSRVLRENGKYIPKQSFLTRKYYFNN     82
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VIRT151947       PEDGFFKKTKRKVVPPSPMTDPTMLTDMMKGNVTNVLPMILIGGWINMTFSGFVTTKVPF    180
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VIRT153469       PLTLRFKPMLQQGIELLTLDASWVSSASWYFLNVFGLRSIYSLILGQDNAADQSRMMQEQ    202
VIRT151947       PLTLRFKPMLQQGIELLTLDASWVSSASWYFLNVFGLRSIYSLILGQDNAADQSRMMQEQ    240
NP_060917.1      PLTLRFKPMLQQGIELLTLDASWVSSASWYFLNVFGLRSIYSLILGQDNAADQSRMMQEQ    202
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VIRT153469       MTGAAMAMPADTNKAFKTEWEALELTDHQWALDDVKKSSWPKTSTSKACSKRNYRPLFFE    262
VIRT151947       MTGAAMAMPADTNKAFKTEWEALELTDHQWALDDVEEELMAKDLHFEGMFKKELQTSIF-    299
NP_060917.1      MTGAAMAMPADTNKAFKTEWEALELTDHQWALDDVEEELMAKDLHFEGMFKKELQTSIF-    261
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VIRT153469       DRAGISCVRNLELHLTL    279
VIRT151947       -----------------    299
NP_060917.1      -----------------    261
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MCM3

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NM_001270472.1                          GAAGAAGAAGAAGCTTTTGATTGGACAGTCGCTAGTCCGACCTCAGAGAACTCAGCCAAT     60

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             CATAATGCTTATATGCTCCCAAGGTCCCCGCCTCTTCCTCGAGGTAACCTTTGGTGGCGG     120
NM_001270472.1                          CATAATGCTTATATGCTCCCAAGGTCCCCGCCTCTTCCTCGAGGTAACCTTTGGTGGCGG     120

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             GAAGAGTTCGGAAGTTTTCGCGCCGGGGTGGAGTCATCCTGGGAACCTCCACGCGACTTT     180
NM_001270472.1                          GAAGAGTTCGGAAGTTTTCGCGCCGGGGTGGAGTCATCCTGGGAACCTCCACGCGACTTT     180

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             GGTGGAGGTAGTTCTTTGGCAGCGGGCATGGCGGGTACCGTGGTGCTGGACGATGTGGAG     240
NM_001270472.1                          GGTGGAGGTAGTTCTTTGGCAGCGGGCATGGCGGGTACCGTGGTGCTGGACGATGTGGAG     240

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             CTGCGGGAGGCTCAGAGAGATTACCTGGACTTCCTGGACGACGAGGAAGACCAGGGAATT     300
NM_001270472.1                          CTGCGGGAGGCTCAGAGAGATTACCTGGACTTCCTGGACGACG-----------------     283

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             TATCAGAGCAAAGTTCGGGAGCTGATCAGTGACAACCAATACCGGCTGATTGTCAATGTG     360
NM_001270472.1                          ------------------------------------------------------------     283

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             AATGACCTGCGCAGGAAAAACGAGAAGAGGGCTAACCGGCTTCTGAACAATGCCTTTGAG     420
NM_001270472.1                          ------------------------------------AGGCTTCTGAACAATGCCTTTGAG     307

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             GAGCTGGTTGCCTTCCAGCGGGCCTTAAAGGATTTTGTGGCCTCCATTGATGCTACCTAT     480
NM_001270472.1                          GAGCTGGTTGCCTTCCAGCGGGCCTTAAAGGATTTTGTGGCCTCCATTGATGCTACCTAT     367

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             GCCAAGCAGTATGAGGAGTTCTACGTAGGACTGGAAGGCAGCTTTGGCTCCAAGCACGTC     540
NM_001270472.1                          GCCAAGCAGTATGAGGAGTTCTACGTAGGACTGGAAGGCAGCTTTGGCTCCAAGCACGTC     427

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             TCCCCGCGGACTCTTACCTCCTGCTTCCTCAGCTGTGTGGTCTGTGTGGAGGGCATTGTC     600
NM_001270472.1                          TCCCCGCGGACTCTTACCTCCTGCTTCCTCAGCTGTGTGGTCTGTGTGGAGGGCATTGTC     487

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             ACTAAATGTTCTCTAGTTCGTCCCAAAGTCGTCCGCAGTGTCCACTACTGTCCTGCTACT     660
NM_001270472.1                          ACTAAATGTTCTCTAGTTCGTCCCAAAGTCGTCCGCAGTGTCCACTACTGTCCTGCTACT     547

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             AAGAAGACCATAGAGCGACGTTATTCTGATCTCACCACCCTGGTGGCCTTTCCCTCCAGC     720
NM_001270472.1                          AAGAAGACCATAGAGCGACGTTATTCTGATCTCACCACCCTGGTGGCCTTTCCCTCCAGC     607

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             TCTGTCTATCCTACCAAGGATGAGGAGAACAATCCCCTTGAGACAGAATATGGCCTTTCT     780
NM_001270472.1                          TCTGTCTATCCTACCAAGGATGAGGAGAACAATCCCCTTGAGACAGAATATGGCCTTTCT     667

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166     ------------------------------------------------------------     0
NM_002388.4                             GTCTACAAGGATCACCAGACCATCACCATCCAGGAGATGCCGGAGAAGGCCCCAGCCGGC     840
NM_001270472.1                          GTCTACAAGGATCACCAGACCATCACCATCCAGGAGATGCCGGAGAAGGCCCCAGCCGGC     727

i1_HQ_samplec9816d|c23601/f2p0/1036     ------------------------------------------------------------     0
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i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              CAGCTCCCCCGCTCTGTGGACGTCATTCTGGATGATGACTTGGTGGATAAAGCGAAGCCT     900
NM_001270472.1                           CAGCTCCCCCGCTCTGTGGACGTCATTCTGGATGATGACTTGGTGGATAAAGCGAAGCCT     787

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GGTGACCGGGTTCAGGTGGTGGGAACCTACCGTTGCCTTCCTGGAAAGAAGGGAGGCTAC     960
NM_001270472.1                           GGTGACCGGGTTCAGGTGGTGGGAACCTACCGTTGCCTTCCTGGAAAGAAGGGAGGCTAC     847

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              ACCTCTGGGACCTTCAGGACTGTCCTGATTGCCTGTAATGTTAAGCAGATGAGCAAGGAT     1020
NM_001270472.1                           ACCTCTGGGACCTTCAGGACTGTCCTGATTGCCTGTAATGTTAAGCAGATGAGCAAGGAT     907

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GCTCAGCCCTCTTTCTCTGCTGAGGATATAGCCAAGATCAAGAAGTTCAGTAAAACCCGA     1080
NM_001270472.1                           GCTCAGCCCTCTTTCTCTGCTGAGGATATAGCCAAGATCAAGAAGTTCAGTAAAACCCGA     967

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              TCCAAGGATATCTTTGACCAGCTGGCCAAGTCATTGGCCCCAAGTATCCATGGGCATGAC     1140
NM_001270472.1                           TCCAAGGATATCTTTGACCAGCTGGCCAAGTCATTGGCCCCAAGTATCCATGGGCATGAC     1027

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              TATGTCAAGAAAGCAATCCTCTGCTTGCTCTTGGGAGGGGTGGAACGAGACCTAGAAAAT     1200
NM_001270472.1                           TATGTCAAGAAAGCAATCCTCTGCTTGCTCTTGGGAGGGGTGGAACGAGACCTAGAAAAT     1087

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GGCAGCCACATCCGTGGGGACATCAATATTCTTCTAATAGGAGACCCATCCGTTGCCAAG     1260
NM_001270472.1                           GGCAGCCACATCCGTGGGGACATCAATATTCTTCTAATAGGAGACCCATCCGTTGCCAAG     1147

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              TCTCAGCTTCTGCGGTATGTGCTTTGCACTGCACCCCGAGCTATCCCCACCACTGGCCGG     1320
NM_001270472.1                           TCTCAGCTTCTGCGGTATGTGCTTTGCACTGCACCCCGAGCTATCCCCACCACTGGCCGG     1207

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GGCTCCTCTGGAGTGGGTCTGACGGCTGCTGTCACCACAGACCAGGAAACAGGAGAGCGC     1380
NM_001270472.1                           GGCTCCTCTGGAGTGGGTCTGACGGCTGCTGTCACCACAGACCAGGAAACAGGAGAGCGC     1267

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              CGTCTGGAAGCAGGGGCCATGGTCCTGGCTGACCGAGGCGTGGTTTGCATTGATGAATTT     1440
NM_001270472.1                           CGTCTGGAAGCAGGGGCCATGGTCCTGGCTGACCGAGGCGTGGTTTGCATTGATGAATTT     1327

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GACAAAATGTCTGACATGGATCGCACAGCCATCCATGAAGTGATGGAGCAGGGTCGAGTG     1500
NM_001270472.1                           GACAAAATGTCTGACATGGATCGCACAGCCATCCATGAAGTGATGGAGCAGGGTCGAGTG     1387

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              ACCATTGCCAAGGCTGGCATCCATGCTCGGCTGAATGCCCGCTGCAGTGTTTTGGCAGCT     1560
NM_001270472.1                           ACCATTGCCAAGGCTGGCATCCATGCTCGGCTGAATGCCCGCTGCAGTGTTTTGGCAGCT     1447

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GCCAACCCTGTCTACGGCAGGTATGACCAGTATAAGACTCCAATGGAGAACATTGGGCTA     1620
NM_001270472.1                           GCCAACCCTGTCTACGGCAGGTATGACCAGTATAAGACTCCAATGGAGAACATTGGGCTA     1507

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              CAGGACTCACTGCTGTCACGATTTGACTTGCTCTTCATCATGCTGGATCAGATGGATCCT     1680
NM_001270472.1                           CAGGACTCACTGCTGTCACGATTTGACTTGCTCTTCATCATGCTGGATCAGATGGATCCT     1567

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GAGCAGGATCGGGAGATCTCAGACCATGTCCTTCGGATGCACCGTTACAGAGCACCTGGG     1740
NM_001270472.1                           GAGCAGGATCGGGAGATCTCAGACCATGTCCTTCGGATGCACCGTTACAGAGCACCTGGG     1627

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              GAGCAGGATGGCGATGCTATGCCCTTGGGTAGTGCTGTGGATATCCTGGCCACAGATGAT     1800
NM_001270472.1                           GAGCAGGATGGCGATGCTATGCCCTTGGGTAGTGCTGTGGATATCCTGGCCACAGATGAT     1687
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i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              CCCAACTTTAGCCAGGAAGATCAGCAGGACACCCAGATTTATGAGAAGCATGACAACCTT     1860
NM_001270472.1                           CCCAACTTTAGCCAGGAAGATCAGCAGGACACCCAGATTTATGAGAAGCATGACAACCTT     1747

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              CTACATGGGACCAAGAAGAAAAAGGAGAAGATGGTGAGTGCAGCATTCATGAAGAAGTAC     1920
NM_001270472.1                           CTACATGGGACCAAGAAGAAAAAGGAGAAGATGGTGAGTGCAGCATTCATGAAGAAGTAC     1807

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ------------------------------------------------------------     0
NM_002388.4                              ATCCATGTGGCCAAAATCATCAAGCCTGTCCTGACACAGGAGTCGGCCACCTACATTGCA     1980
NM_001270472.1                           ATCCATGTGGCCAAAATCATCAAGCCTGTCCTGACACAGGAGTCGGCCACCTACATTGCA     1867

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ---------------------------------------------------aggacatct     9
NM_002388.4                              GAAGAGTATTCACGCCTGCGCAGCCAGGATAGCATGAGCTCAGACACCGCCAGGACATCT     2040
NM_001270472.1                           GAAGAGTATTCACGCCTGCGCAGCCAGGATAGCATGAGCTCAGACACCGCCAGGACATCT     1927

i1_HQ_samplec9816d|c23601/f2p0/1036      ------------------------------------------------------------     0
i1_HQ_samplec9816d|c22727/f2p0/1166      ccagttacagcccgaacactggaaactctgattcgactggccacagcccatgcgaaggcC     69
NM_002388.4                              CCAGTTACAGCCCGAACACTGGAAACTCTGATTCGACTGGCCACAGCCCATGCGAAGGCC     2100
NM_001270472.1                           CCAGTTACAGCCCGAACACTGGAAACTCTGATTCGACTGGCCACAGCCCATGCGAAGGCC     1987

i1_HQ_samplec9816d|c23601/f2p0/1036      --------------------------ggattca---------------tACGACCCCTAT     19
i1_HQ_samplec9816d|c22727/f2p0/1166      CGCATGAGCAAGACTGTGGACCTGCAGGATGCAGAGGAAGCTGTGGAGTTGGTCCAGTAT     129
NM_002388.4                              CGCATGAGCAAGACTGTGGACCTGCAGGATGCAGAGGAAGCTGTGGAGTTGGTCCAGTAT     2160
NM_001270472.1                           CGCATGAGCAAGACTGTGGACCTGCAGGATGCAGAGGAAGCTGTGGAGTTGGTCCAGTAT     2047
                                                                   **** **               *  * **  ***

i1_HQ_samplec9816d|c23601/f2p0/1036      GACTTCAGTGACACA---------GAGGAGGAAATGCCTCAAGTAC---------ACACT     61
i1_HQ_samplec9816d|c22727/f2p0/1166      GCTTACTTTAAGAAGGTTCTGGAGAAGGAGAAGAAACGTAAGAAGCGAAGTGAGGATGAA     189
NM_002388.4                              GCTTACTTTAAGAAGGTTCTGGAGAAGGAGAAGAAACGTAAGAAGCGAAGTGAGGATGAA     2220
NM_001270472.1                           GCTTACTTTAAGAAGGTTCTGGAGAAGGAGAAGAAACGTAAGAAGCGAAGTGAGGATGAA     2107
                                         *  * *  * * *            ***** * *  * * *    *         *

i1_HQ_samplec9816d|c23601/f2p0/1036      CCAAAGACGGCAGACTCACAGGAGACCAAGGAATCCCAGAAAGTGGAGTTGAGTGAATCC     121
i1_HQ_samplec9816d|c22727/f2p0/1166      TCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGGAGCAGAAGAGGAAGAGA     249
NM_002388.4                              TCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGGAGCAGAAGAGGAAGAGA     2280
NM_001270472.1                           TCAGAGACAGAAGATGAAGAGGAGAAAAGCCAAGAGGACCAGGAGCAGAAGAGGAAGAGA     2167
                                          ** **** * ***   * ******  *   **    *  * * * **  ***  *

i1_HQ_samplec9816d|c23601/f2p0/1036      AGAGACGGGATCTCACCATGTTGCCCAGGCTGGTCTTGGACTCCTGGCCTCAAGCAGTCC     181
i1_HQ_samplec9816d|c22727/f2p0/1166      -AGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTCATACGACCCCTAT-GACTTCA     307
NM_002388.4                              -AGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTCATACGACCCCTAT-GACTTCA     2338
NM_001270472.1                           -AGGAAGACTCGCCAGCCAGATGCCAAAGATGGGGATTCATACGACCCCTAT-GACTTCA     2225
                                            ** *      ** *  * **** * * ***   *  *  *    ***   *   **

i1_HQ_samplec9816d|c23601/f2p0/1036      TTCTACCTGAGCCTCCCA----AAAGGCTGGGATTACAGGCATAAGCCACTGTGCTTGTT     237
i1_HQ_samplec9816d|c22727/f2p0/1166      GTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGGCAGACTCACAGGAGA     367
NM_002388.4                              GTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGGCAGACTCACAGGAGA     2398
NM_001270472.1                           GTGACACAGAGGAGGAAATGCCTCAAGTACACACTCCAAAGACGGCAGACTCACAGGAGA     2285
                                          *    * ***      *      * *     * * **   *      ***

i1_HQ_samplec9816d|c23601/f2p0/1036      TGATCTCATTCTTTTTAATGACTGCAGGGTTTCCATGGTTGAAGGCATTCAAGGT-GGCC     296
i1_HQ_samplec9816d|c22727/f2p0/1166      CCAAGGAATCCCAGAAAGTGGAGTTGAGTGAATCCAGGTTGAAGGCATTCAAGGTGGCCC     427
NM_002388.4                              CCAAGGAATCCCAGAAAGTGGAGTTGAGTGAATCCAGGTTGAAGGCATTCAAGGTGGCCC     2458
NM_001270472.1                           CCAAGGAATCCCAGAAAGTGGAGTTGAGTGAATCCAGGTTGAAGGCATTCAAGGTGGCCC     2345
                                           *    ** *     * **       *     *  ******************* * **

i1_HQ_samplec9816d|c23601/f2p0/1036      CTCTTGGTGTGTTCCGGGAAGCTCATGCGCAGTCAATCGGCATGAATCGCCTCACAGAAT     356
i1_HQ_samplec9816d|c22727/f2p0/1166      TCTTGGATGTGTTCCGGGAAGCTCATGCGCAGTCAATCGGCATGAATCGCCTCACAGAAT     487
NM_002388.4                              TCTTGGATGTGTTCCGGGAAGCTCATGCGCAGTCAATCGGCATGAATCGCCTCACAGAAT     2518
NM_001270472.1                           TCTTGGATGTGTTCCGGGAAGCTCATGCGCAGTCAATCGGCATGAATCGCCTCACAGAAT     2405
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i1_HQ_samplec9816d|c23601/f2p0/1036      CCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCCAGGCTGCTCTGAGCA     416
i1_HQ_samplec9816d|c22727/f2p0/1166      CCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCCAGGCTGCTCTGAGCA     547
NM_002388.4                              CCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCCAGGCTGCTCTGAGCA     2578
NM_001270472.1                           CCATCAACCGGGACAGCGAAGAGCCCTTCTCTTCAGTTGAGATCCAGGCTGCTCTGAGCA     2465
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i1_HQ_samplec9816d|c23601/f2p0/1036      AGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCCTCATCTGAGGAG     476
i1_HQ_samplec9816d|c22727/f2p0/1166      AGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCCTCATCTGAGGAG     607
NM_002388.4                              AGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCCTCATCTGAGGAG     2638
NM_001270472.1                           AGATGCAGGATGACAATCAGGTCATGGTGTCTGAGGGCATCATCTTCCTCATCTGAGGAG     2525
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i1_HQ_samplec9816d|c23601/f2p0/1036      GCCTCGTCTCTGAACTTGGGTTGTGCCGAGAGAGTTTGTTCTGTGTTTCCCACCCTCTCC     536
i1_HQ_samplec9816d|c22727/f2p0/1166      GCCTCGTCTCTGAACTTGGGTTGTGCCGAGAGAGTTTGTTCTGTGTTTCCCACCCTCTCC     667
NM_002388.4                              GCCTCGTCTCTGAACTTGGGTTGTGCCGAGAGAGTTTGTTCTGTGTTTCCCACCCTCTCC     2698
NM_001270472.1                           GCCTCGTCTCTGAACTTGGGTTGTGCCGAGAGAGTTTGTTCTGTGTTTCCCACCCTCTCC     2585
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i1_HQ_samplec9816d|c23601/f2p0/1036      CTGACCCAAGTCTTTGCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGGCGAGGAA     596
i1_HQ_samplec9816d|c22727/f2p0/1166      CTGACCCAAGTCTTTGCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGGCGAGGAA     727
NM_002388.4                              CTGACCCAAGTCTTTGCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGGCGAGGAA     2758
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NM_001270472.1                         CTGACCCAAGTCTTTGCCTCTACTCCCTTAACAGTGTTGAATTCAACTGAAGGCGAGGAA    2645
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i1_HQ_samplec9816d|c23601/f2p0/1036    TGTTGGTGATGAAGCTGAGTTCAGGACTCGGTGGACCCTTTGGGAATGGGTCATGAAAGC    656
i1_HQ_samplec9816d|c22727/f2p0/1166    TGTTGGTGATGAAGCTGAGTTCAGGACTCGGTGGACCCTTTGGGAATGGGTCATGAAAGC    787
NM_002388.4                            TGTTGGTGATGAAGCTGAGTTCAGGACTCGGTGGACCCTTTGGGAATGGGTCATGAAAGC    2818
NM_001270472.1                         TGTTGGTGATGAAGCTGAGTTCAGGACTCGGTGGACCCTTTGGGAATGGGTCATGAAAGC    2705
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i1_HQ_samplec9816d|c23601/f2p0/1036    TGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGACTATTGCATCTTCATT    716
i1_HQ_samplec9816d|c22727/f2p0/1166    TGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGACTATTGCATCTTCATT    847
NM_002388.4                            TGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGACTATTGCATCTTCATT    2878
NM_001270472.1                         TGCCATGGGGTGAGGAAAGAGGAGACAGTGGGAGAGGACAATGACTATTGCATCTTCATT    2765
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i1_HQ_samplec9816d|c23601/f2p0/1036    GCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCCAATTGTAAATAAC    776
i1_HQ_samplec9816d|c22727/f2p0/1166    GCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCCAATTGTAAATAAC    907
NM_002388.4                            GCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCCAATTGTAAATAAC    2938
NM_001270472.1                         GCAAAAGCACTGGCTCATCCGCCCTACTTCCCATCCCACACAAACCCAATTGTAAATAAC    2825
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i1_HQ_samplec9816d|c23601/f2p0/1036    ATATGACTTCTGAGTACTTTTGGGGGCACAACTGTTTTCTGTTTGCTGTTTTTTTGTTTT    836
i1_HQ_samplec9816d|c22727/f2p0/1166    ATATGACTTCTGAGTACTTTTGGGGGCACAACTGTTTTCTGTTTGCTGTTTTTTTGTTTT    967
NM_002388.4                            ATATGACTTCTGAGTACTTTTGGGGGCACAACTGTTTTCTGTTTGCTGTTTTTTTGTTTT    2998
NM_001270472.1                         ATATGACTTCTGAGTACTTTTGGGGGCACAACTGTTTTCTGTTTGCTGTTTTTTTGTTTT    2885
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i1_HQ_samplec9816d|c23601/f2p0/1036    GTTTTTTTTCTCCAGAGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGA    896
i1_HQ_samplec9816d|c22727/f2p0/1166    GTTTTTTTTCTCCAGAGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGA    1027
NM_002388.4                            GTTTTTTTTCTCCAGAGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGA    3058
NM_001270472.1                         GTTTTTTTTCTCCAGAGCACTTTGGTCTAGACTAGGCTTTGGGTGGTTCCAATTGGTGGA    2945
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i1_HQ_samplec9816d|c23601/f2p0/1036    GAGAAGCTCTGAGGCACGTCATGCAGGTCAAGAAAGCTTTCTTTGCAGTAGCACCAGTTA    956
i1_HQ_samplec9816d|c22727/f2p0/1166    GAGAAGCTCTGAGGCACGTCATGCAGGTCAAGAAAGCTTTCTTTGCAGTAGCACCAGTTA    1087
NM_002388.4                            GAGAAGCTCTGAGGCACGTCATGCAGGTCAAGAAAGCTTTCTTTGCAGTAGCACCAGTTA    3118
NM_001270472.1                         GAGAAGCTCTGAGGCACGTCATGCAGGTCAAGAAAGCTTTCTTTGCAGTAGCACCAGTTA    3005
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VIRT162782            ------------------------------------------------------------   0
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VIRT162782            ----------------------MSKTVDLQDAEEAVELVQYAYFKKVLEKEKKRKKRSED   38
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VIRT162782            -----AFKVALLDVFREAHAQSIGMNRLTESINRDSEEPFSSVEIQAALSKMQDDNQVMV   168
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VIRT69015        MLPALQLSCPTPGVAIPVRCPPPCTWHYPDCQSPGWPHLHHVPGPALALTAAKHHAGGHS     60
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NP_004139.2      --EEYELNGGLPPGTP--------------------------------------------     19
VIRT68216        CLSAAVPRRQLPPGTWGLATIAQRVRTGQLQRPVPREGSRPTQGHTAGPWMGWMSDQGQP    120
VIRT69015        CLSAAVPRRQLPPGTWGLATIAQRVRTGQLQRPVPREGSRPTQGHTAGPWMGWMSDQGQP    120
                   .    .  *****

NP_004139.2      -------------------------------------------------GSPDASPARWG     30
VIRT68216        LSQDIPEGQGDVSPSPKAPASLPPVGPVRVALVTPASVHFLTQGPCTARTAFGPTDGHWL    180
VIRT69015        LSQDIPEGQGDVSPSPKAPASLPPVGPVRVALVTPASVHFLTQGPCTARTAFGPTDGHWL    180
                                                                   : . : .:*

NP_004139.2      WRHGPINVNHYASKKSAAESMLDIALLMANASQLKAVVEQGPSFAFYVPLVVLISISLVL     90
VIRT68216        WSKVPGLGGHQEGASQACEGRRPCIY------PAPAVTGQSPTPSTGVPA----------    224
VIRT69015        WSKVPGLGGHQEGASQACEGRRPCIY------PAPAVTGQSPTPSTGVPA----------    224
                 * : *   .*  . ..*.*.               **. *.*: :  **

NP_004139.2      QIGVGVLLIFLVKYDLNNPAKHAKLDFLNNLATGLVFIIVVVNIFITAFGVQKPLMDMAP    150
VIRT68216        ----PTFLIMNEQYKAHALCQ---------------------------------------    241
VIRT69015        ----PTFLIMNEQ-----------------------------------------------    233
                      .:**:  :

NP_004139.2      QQ    152
VIRT68216        --    241
VIRT69015        --    233
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SMIM7

Sequence	**Header**	**AA Seq**
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Absent	i0_HQ_samplec9816d|c421/f18p17/953	
NCBI	NM_024104	
	NM_001300925	

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>VIRT77545

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>VIRT83564

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GAATCTTCATCGCCCTGTGGAACATCTTCATGATGTTCTGCATGATTGTGCTGTTCGGCTCTTGAATCCC
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>NP_077009.2 small integral membrane protein 7 isoform 2 precursor [Homo sapiens]
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>NP_001287854.1 small integral membrane protein 7 isoform 1 precursor [Homo sapiens]
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i0_HQ_samplec9816d|c421/f18p17/953       ------------------------------------------------------------     0
NM_024104.3                              ------------------------------------------------------------     0

NM_001300925.1                           -----------------------------------------CCCTGGGGCTTCCGCTTCC     19
i1_HQ_samplec9816d|c15024/f2p0/1053      aatGCCGGGCGGTGCTGAACTTTAAGCTGAAAAAGAAGGACACGCAGGGCTTTGGGGAGG     120
i0_HQ_samplec9816d|c421/f18p17/953       -----------------------------------------------ggcttccgcttcc     13
NM_024104.3                              -----------------------------------------CCCTGGGGCTTCCGCTTCC     19
                                                                                *****  *

NM_001300925.1                           GGTTCTGAC-GGACGCTTCGGCCGTAACGATGATCGGAGACATCCT-GCTGTTCGGGACG     77
i1_HQ_samplec9816d|c15024/f2p0/1053      AGTCCAGGGAGCCCAGCACAGGGCTTGAGAGGGAGAGTGATTGACTGGAAACCCTGGAAG     180
i0_HQ_samplec9816d|c421/f18p17/953       ggttctGAC-GGACGCTTCGGCCGTAACGATGATCGGAGACATCCT-GCTGTTCGGGACG     71
NM_024104.3                              GGTTCTGAC-GGACGCTTCGGCCGTAACGATGATCGGAGACATCCT-GCTGTTCGGGACG     77
                                          ** * *   *  *    * *   *   ** *    * **    ** *     * *** *

NM_001300925.1                           TTGCTGATGAATGCCGGGGCGGTGCTGAA-CTTTAAGCTGAAAAAGAAGGACACGCAGGG     136
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i0_HQ_samplec9816d|c421/f18p17/953       TTGCTGATGAATGCCGGGGCGGTGCTGAA-CTTTAAGCTGAAAAAGAAGGACACGCAGGG     130
NM_024104.3                              TTGCTGATGAATGCCGGGGCGGTGCTGAA-CTTTAAGCTGAAAAAGAAGGACACGCAGGG     136
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NM_001300925.1                           CTTTGGGGAGGAGTCCAGGGAGCCCAGCACAGGTGACAACATCCGGGAATTCTTGCTGAG     196
i1_HQ_samplec9816d|c15024/f2p0/1053      GTTTCTGTTCCTTGGCATTCAAGGGGACCAGAGTGACAACATCCGGGAATTCTTGCTGAG     300
i0_HQ_samplec9816d|c421/f18p17/953       CTTTGGGGAGGAGTCCAGGGAGCCCAGCACAGGTGACAACATCCGGGAATTCTTGCTGAG     190
NM_024104.3                              CTTTGGGGAGGAGTCCAGGGAGCCCAGCACAGGTGACAACATCCGGGAATTCTTGCTGAG     196
                                          ***  *        **   *      *    ****************************

NM_001300925.1                           CCTCAGATACTTTCGAATCTTCATCGCCCTGTGGAACATCTTCATGATGTTCTGCATGAT     256
i1_HQ_samplec9816d|c15024/f2p0/1053      CCTCAGATACTTTCGAATCTTCATCGCCCTGTGGAACATCTTCATGATGTTCTGCATGAT     360
i0_HQ_samplec9816d|c421/f18p17/953       CCTCAGATACTTTCGAATCTTCATCGCCCTGTGGAACATCTTCATGATGTTCTGCATGAT     250
NM_024104.3                              CCTCAGATACTTTCGAATCTTCATCGCCCTGTGGAACATCTTCATGATGTTCTGCATGAT     256
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NM_001300925.1                           TGTGCTGAGAAAACTCAAGCAGATTGCCTTTCCATCTAGCACTGGGGCCATAACT---CT     313
i1_HQ_samplec9816d|c15024/f2p0/1053      TGTGCTGTTCGGCTCTTGAATCCCAGCGATGAAACCAGGAACTCACTTTCCCGGGATGCC     420
i0_HQ_samplec9816d|c421/f18p17/953       TGTGCTGTTCGGCTCTTGAATCCCAGCGATGAAACCAGGAACTCACTTTCCCGGGATGCC     310
NM_024104.3                              TGTGCTGTTCGGCTCTTGAATCCCAGCGATGAAACCAGGAACTCACTTTCCCGGGATGCC     316
                                         *******                  **  *   * *  * ***               *

NM_001300925.1                           GATACTACTGTTAACGAATTGTGAGATTTGCTGTAAATGGATTTAGGAAAAGACACGAC-     372
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i0_HQ_samplec9816d|c421/f18p17/953       GAGTCTCCATTCCTCCATTCCTGATGACTTCAAGAA-TGTTTTTGACCAGAAAACCGACA     369
NM_024104.3                              GAGTCTCCATTCCTCCATTCCTGATGACTTCAAGAA-TGTTTTTGACCAGAAAACCGACA     375
                                         **  ** *  *   * * *  ***    * *   ** **  ***    * * *  ****

NM_001300925.1                           ------------GGGAGAATCTGGTGTTCTT--GGCCTCTGTGGGTCCATCCCTGTATGC     418
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i0_HQ_samplec9816d|c421/f18p17/953       ACCTTCCCAGAAAGTCCAAGCTCGTGGTGGGTGGAAAAGTGTTCGCCGAGGTGTGCATGG     429
NM_024104.3                              ACCTTCCCAGAAAGTCCAAGCTCGTGGTGGGTGGAAAAGTGTTCGCCGAGGTGTGCATGG     435
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NM_001300925.1                           TTCCCCCAGAAAGAGAGAGGACAAAAAGTTGTCTGTCCTGAGTGATTGAGACTCCGAATG     478
i1_HQ_samplec9816d|c15024/f2p0/1053      TTTCCCAGCCACGTCCCTGTTTTCAAAGATAGTTTCACT-------TTGGTCTCTGAAT-     591
i0_HQ_samplec9816d|c421/f18p17/953       TTTCCCAGCCACGTCCCTGTTTTCAAAGATAGTTTCACT-------TTGGTCTCTGAAT-     481
NM_024104.3                              TTTCCCAGCCACGTCCCTGTTTTCAAAGATAGTTTCACT-------TTGGTCTCTGAAT-     487
                                         ** ***    * *     *     **** *   *   **       *  * *** ****

NM_001300925.1                           TGGGGTTGCTGTCCAGTCTGCG--TGCCACCCCAGTGGCTGTTTGCGAAGATGCTTCCAG     536
i1_HQ_samplec9816d|c15024/f2p0/1053      -TGAAATGCTGTCTACTGAAAGGGTTTCAGGAGCGTTTATGTAAGGGGCTGTGATGAAAT     650
i0_HQ_samplec9816d|c421/f18p17/953       -TGAAATGCTGTCTACTGAAAGGGTTTCAGGAGCGTTTATGTAAGGGGCTGTGATGAAAT     540
NM_024104.3                              -TGAAATGCTGTCTACTGAAAGGGTTTCAGGAGCGTTTATGTAAGGGGCTGTGATGAAAT     546
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NM_001300925.1                           GACATA--------------------------------GGAGATCTGG---GGAGGATGG     561
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i0_HQ_samplec9816d|c421/f18p17/953       TGCATTCCCCATAGATAAAAGAAAAATCATTTCTATCCAGAGATCTGAGCAGAAGGATTG     600
NM_024104.3                              TGCATTCCCCATAGATAAAAGAAAAATCATTTCTATCCAGAGATCTGAGCAGAAGGATTG     606
                                           ***                                  ********    * ***** *

NM_001300925.1                           CATTTCACCCTCATCACAAGGACCGTGATGTATTCCCAGGAAGACTGTTGCCAAGGTATC     621
i1_HQ_samplec9816d|c15024/f2p0/1053      GCTTGTTAGTTTAACACAGCCGTATTTTTGGACATTCAGTGT--TACTTGCTGAGTCTGA     768
i0_HQ_samplec9816d|c421/f18p17/953       GCTTGTTAGTTTAACACAGCCGTATTTTTGGACATTCAGTGT--TACTTGCTGAGTCTGA     658
NM_024104.3                              GCTTGTTAGTTTAACACAGCCGTATTTTTGGACATTCAGTGT--TACTTGCTGAGTCTGA     664
                                           **      * * ****       *  ** *    ***        ****  **

NM_001300925.1                           CTACCTGGCAGAGAGGATCTGAGAGCATGTATGAGACTTGCCTAGGAACAAAG--AAGGC     679
i1_HQ_samplec9816d|c15024/f2p0/1053      CAGCCTCTGGGCCCGGCCAGGGGCCCTGTTAACAAACTGCTTTCACATCCCAACAGGGTC     828
i0_HQ_samplec9816d|c421/f18p17/953       CAGCCTCTGGGCCCGGCCAGGGGCCCTGTTAACAAACTGCTTTCACATCCCAACAGGGTC     718
NM_024104.3                              CAGCCTCTGGGCCCGGCCAGGGGCCCTGTTAACAAACTGCTTTCACATCCCAACAGGGTC     724
                                         *  ***    *   **    * *  *   **  * ***    *   * *  *     * *

NM_001300925.1                           TTGTGAGGAGATCAAGGAACTTACATGAAA----------TTGTAGGAACGG-CC---AG     725
i1_HQ_samplec9816d|c15024/f2p0/1053      TGCTTGGCCACTCAGTGCAGCTGCGATTAACCCTAAAGGCTTTAAGGAACGGGCCACCTG     888
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NM_024104.3                              TGCTTGGCCACTCAGTGCAGCTGCGATTAACCCTAAAGGCTTTAAGGAACGGGCCACCTG     784
                                         *  *  *    ***  * *  * *    **          **  ******** **    *

NM_001300925.1                           GGGCAGTGG----CTCAGGCCTGTAATCCCAGTACTTTGGGAGGCCAA--GGTGGGAGA-     778
i1_HQ_samplec9816d|c15024/f2p0/1053      TAACAGAGACACCAGCCTTCCTGTATAGACACTAAATTGTTAGCAAGAGTGTTGAGCTAG     948
i0_HQ_samplec9816d|c421/f18p17/953       TAACAGAGACACCAGCCTTCCTGTATAGACACTAAATTGTTAGCAAGAGTGTTGAGCTAG     838
NM_024104.3                              TAACAGAGACACCAGCCTTCCTGTATAGACACTAAATTGTTAGCAAGAGTGTTGAGCTAG     844
                                            *** *       *   ******    ** **  ***  **    *  * ** *  *

NM_001300925.1                           ----------ATTGCTTGAGCCCAGGAGTTCAAGACCAGCCTGGGCAGCATGGT-GAAAC     827
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i0_HQ_samplec9816d|c421/f18p17/953       TTCCTGGTGAAGTGTTTCCACAGAAGACATGTGGAGCAGTTGTGGGGATATTAAGGGAAA     898
NM_024104.3                              TTCCTGGTGAAGTGTTTCCACAGAAGACATGTGGAGCAGTTGTGGGGATATTAAGGGAAA     904
                                                   * ** **   *  * **  *   ** ***    **    **    * **

NM_001300925.1                           CCTG-----------------TCTTTACCAAAAATAAAAAAATTAGCCGAGTGTAAAAAA     870
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i0_HQ_samplec9816d|c421/f18p17/953       CTTTCCTCTGCCTTGACCCCTTTGTTAAATAAAATGACTTTGGGAGCCAttcatt-----     953
NM_024104.3                              CTTTCCTCTGCCTTGACCCCTTTGTTAAATAAAATGACTTTGGGAGCCATTCATTGTACA     964
                                         * *                  *  * *   ***** *       **

NM_001300925.1                           AAAAAAAAAA--------------------------------------------------     880
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NM_001300925.1                          ------------------------------------------------------------     880
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NM_001300925.1                          ------------------------------------------------------------     880
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NM_001300925.1                          ------------------------------------------------------------     880
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NM_001300925.1                          ------------------------------------------------------------     880
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NM_024104.3                             GCTTTTAGGACTGAGTAGCCTTGAAAATAAACCTCATTTCTAAAAAGGAAAAAAAAAAAA     1384

NM_001300925.1                          ------            880
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NM_024104.3                             AAAAAA            1390
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NP_077009.2         MIGDILLFGTLLMNAGAVLNFKLKKKDTQGFGEESREPSTGDNIREFLLSLRYFRIFIAL   60
NP_001287854.1      MIGDILLFGTLLMNAGAVLNFKLKKKDTQGFGEESREPSTGDNIREFLLSLRYFRIFIAL   60
VIRT77545           ------------------------------------------------------------   0
VIRT83180           ------------------------------------------------------------   0

VIRT83564           WNIFMMFCMIVLFGS---------------------------------------------   75
NP_077009.2         WNIFMMFCMIVLFGS---------------------------------------------   75
NP_001287854.1      WNIFMMFCMIVLRKLKQIAFPSSTGAITL--ILLLTNCEICCKWI---------------   103
VIRT77545           ----MTSRMF--LTRKPTTFPESPSSWWVE------KCSPRCAWFPSH------VPVFKD   42
VIRT83180           -------------MKPGTHFPGMPSLHSSIPDDFKNVFDQKTDNLPRKSKLVVGGKVFAE   47

VIRT83564           ------------------------   75
NP_077009.2         ------------------------   75
NP_001287854.1      ------------------------   103
VIRT77545           SFTLVSELKCCLLKGFQERLCKGL   66
VIRT83180           -VCMVSQPRPCFQR----------   60
```

PSME2 (Exon 3 extended as well as two extra exons are present between 2&3**)**

Sequence	**Header**	**AA Seq**
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i0_HQ_samplec9816d|c91455/f11p9/956      GTGGAGGTCTTCAGGCAGAATCTTTTCCAGGAGGTCTTCAGTTTCCTCATTTGCAAGTCT 180
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i0_HQ_samplec9816d|c91455/f11p9/956      TGGACCCAGTGATTTCCAAAGGCCCTTCCAGTTCCATTTGTCAGACATCTCATTGAGCAT 240
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VIRT19198        -----------------METDKQEKKEVPKCGFLPGNEKVLSLLALVKPEVWTLKEKCIL    43
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VIRT19198        VITWIQHLIPKIEDGNDFGVAIQEKVLERVNAVKTKVEA-----FQTTISKYFSERGDAV     98
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IL37

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>VIRT93267

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CTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTTGGGGTGA
CAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCC
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AACACCAAACCTGCTCACTAAAAAAAAAAAAAAAAAA
>NP_775297.1 interleukin-37 isoform 5 [Homo sapiens]
MSGCDRRETETKGKNSFKKRLRGPKVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS
SLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNM
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NM_173205.1                             ------------------------------------------------------------      0
NM_173204.1                             ------------------------------------------------------------      0
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NM_173202.1                             ------------------------------------------------------------      0

NM_173205.1                             ------------------------------------------------------------      0
NM_173204.1                             ---------------------------------CTTCATTCCATTTTCTGTTGAGTAATA      27
i0_HQ_samplec9816d|c22741/f2p0/859      cagACCACGAGGATCCCTGGCCCAGGTCTTGGACTTCATTCCATTTTCTGTTGAGTAATA      120
NM_173202.1                             ---------------------------------CTTCATTCCATTTTCTGTTGAGTAATA      27

NM_173205.1                             ------------------------------------------------------------      0
NM_173204.1                             AACTCAACGTTGAAAATGTCCTTTGTGGGGGAGAACTCAGGAGTGAAAATGGGCTCTGAG      87
i0_HQ_samplec9816d|c22741/f2p0/859      AACTCAACGTTGAAAATGTCCTTTGTGGGGGAGAACTCAGGAGTGAAAATGGGCTCTGAG      180
NM_173202.1                             AACTCAACGTTGAAAATGTCCTTTGTGGGGGAGAACTCAGGAGTGAAAATGGGCTCTGAG      87

NM_173205.1                             -----------------------------------ATGTCAGGCTGTGATAGGAGGGAAA      25
NM_173204.1                             GACTGGGAAAAAGATGAACCCCAGTGCTGCTTAGAAGACCCGGCTGGAAGCC--CCCTGG      145
i0_HQ_samplec9816d|c22741/f2p0/859      GACTGGGAAAAAGATGAACCCCAGTGCTGCTTAGAAGACCCGGCTGTAAGCC--CCCTGG      238
NM_173202.1                             GACTGGGAAAAAGATGAACCCCAGTGCTGCTTAGAAGG----------------------      125
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NM_173205.1                             CAGAAACCAAAGGAAAGAACAGCTTTAAGAAGCGCTTAAGAGGTCCAAAGGTGAAGAACT      85
NM_173204.1                             AACCAGGCCCAAGCCTCCCCACCATGAATTTTGTTC------------------------      181
i0_HQ_samplec9816d|c22741/f2p0/859      AACCAGGCCCAAGCCTCCCCGCCATGAATTTTGTTCACACAAGTCCAAAGGTGAAGAACT      298
NM_173202.1                             -------------------------------------------TCCAAAGGTGAAGAACT      142

NM_173205.1                             TAAACCCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTG      145
NM_173204.1                             ------------------------------------------------------------      181
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NM_173202.1                             TAAACCCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTG      202

NM_173205.1                             GGAATCTCATAGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAG      205
NM_173204.1                             ------------------------------------ACACAAAGATCTTCTTTGCATTAG      205
i0_HQ_samplec9816d|c22741/f2p0/859      GGAATCTCATAGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAG      418
NM_173202.1                             GGAATCTCATAGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAG      262
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NM_173205.1                             CCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTA      265
NM_173204.1                             CCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTA      265
i0_HQ_samplec9816d|c22741/f2p0/859      CCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTA      478
NM_173202.1                             CCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTA      322
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NM_173205.1                             AAGGGGAGTTTTGTCTCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGC      325
NM_173204.1                             AAGGGGAGTTTTGTCTCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGC      325
i0_HQ_samplec9816d|c22741/f2p0/859      AAGGGGAGTTTTGTCTCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGC      538
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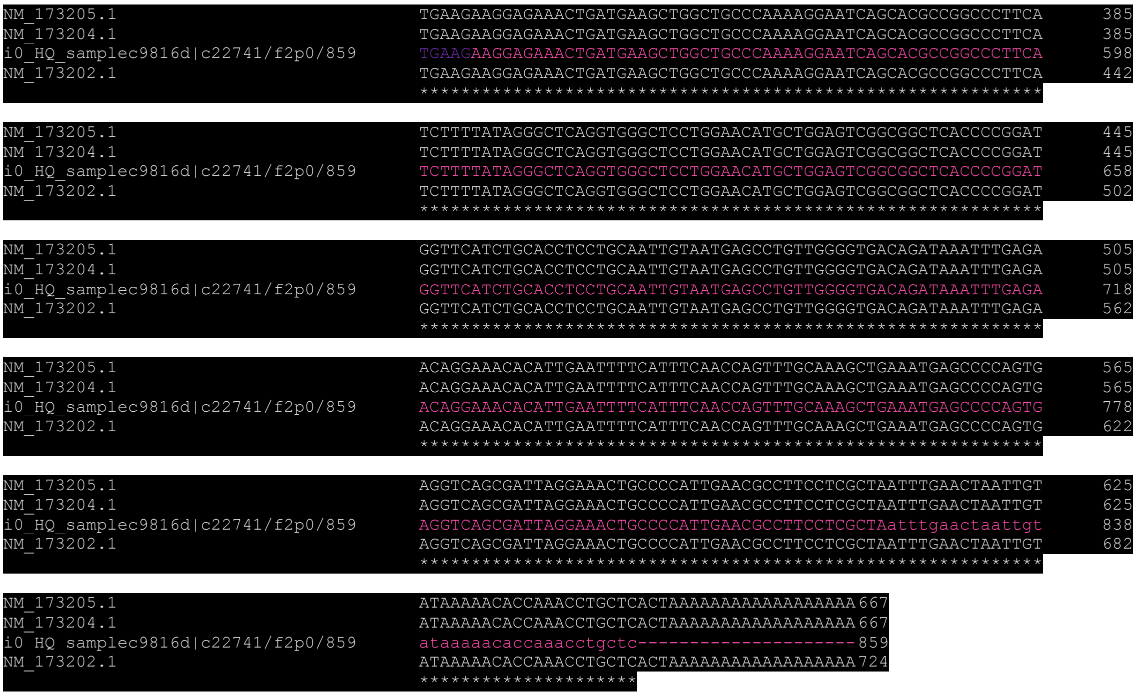

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NM_173205.1                               TGAAGAAGGAGAAACTGATGAAGCTGGCTGCCCAAAAGGAATCAGCACGCCGGCCCTTCA    385
NM_173204.1                               TGAAGAAGGAGAAACTGATGAAGCTGGCTGCCCAAAAGGAATCAGCACGCCGGCCCTTCA    385
i0_HQ_samplec9816d|c22741/f2p0/859        TGAAGAAGGAGAAACTGATGAAGCTGGCTGCCCAAAAGGAATCAGCACGCCGGCCCTTCA    598
NM_173202.1                               TGAAGAAGGAGAAACTGATGAAGCTGGCTGCCCAAAAGGAATCAGCACGCCGGCCCTTCA    442
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NM_173205.1                               TCTTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGAT    445
NM_173204.1                               TCTTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGAT    445
i0_HQ_samplec9816d|c22741/f2p0/859        TCTTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGAT    658
NM_173202.1                               TCTTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGAT    502
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NM_173205.1                               GGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTTGGGGTGACAGATAAATTTGAGA    505
NM_173204.1                               GGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTTGGGGTGACAGATAAATTTGAGA    505
i0_HQ_samplec9816d|c22741/f2p0/859        GGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTTGGGGTGACAGATAAATTTGAGA    718
NM_173202.1                               GGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTTGGGGTGACAGATAAATTTGAGA    562
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NM_173205.1                               ACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCCCAGTG    565
NM_173204.1                               ACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCCCAGTG    565
i0_HQ_samplec9816d|c22741/f2p0/859        ACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCCCAGTG    778
NM_173202.1                               ACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAAAGCTGAAATGAGCCCCAGTG    622
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NM_173205.1                               AGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTAATTTGAACTAATTGT    625
NM_173204.1                               AGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTAATTTGAACTAATTGT    625
i0_HQ_samplec9816d|c22741/f2p0/859        AGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTAatttgaactaattgt    838
NM_173202.1                               AGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTAATTTGAACTAATTGT    682
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NM_173205.1                               ATAAAAACACCAAACCTGCTCACTAAAAAAAAAAAAAAAAAA 667
NM_173204.1                               ATAAAAACACCAAACCTGCTCACTAAAAAAAAAAAAAAAAAA 667
i0_HQ_samplec9816d|c22741/f2p0/859        ataaaaacaccaaacctgctc--------------------- 859
NM_173202.1                               ATAAAAACACCAAACCTGCTCACTAAAAAAAAAAAAAAAAAA 724
                                          *********************
```

```
VIRT93267          -----------------------------MAGRLGP------------------------      7
NP_775296.1        MSFVGENSGVKMGSEDWEKDEPQCCLEDPAGSPLEPGP-------------------SLP      41
NP_775294.1        MSFVGENSGVKMGSEDWEKDEPQCCLEGPKVKNLNPKKFSIHDQDHKVLVLDSGNLIAVP      60
NP_775297.1        MSGCD-----RRETETKGKNSFKKRLRGPKVKNLNPKKFSIHDQDHKVLVLDSGNLIAVP      55
                                                    * *

VIRT93267          ------------------------------------------------------------      7
NP_775296.1        TMNFVHTKIFFALASSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLM      101
NP_775294.1        DKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLM      120
NP_775297.1        DKNYIRPEIFFALASSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLM      115

VIRT93267          --------------------GSRGLTAGSSKQHWGSSFS--------------------Q      27
NP_775296.1        KLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEF      161
NP_775294.1        KLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEF      180
NP_775297.1        KLAAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEF      175
                                       ** .:  .:::  *  . *

VIRT93267          SSEPIFTPEFSPTKDIFNVEFITQQKME  55
NP_775296.1        SFQPVCKAEMSPSEVSD-----------  178
NP_775294.1        SFQPVCKAEMSPSEVSD-----------  197
NP_775297.1        SFQPVCKAEMSPSEVSD-----------  192
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CGB8

Sequence	Header	AA Seq
Present	i0_HQ_samplec9816d|c13287/f2p2/890	
Absent		
NCBI	NM_033183	

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CTCACCCTTGGCGCTGGACCAGTGAGAGGAGAGGGCTGGGGCGCTCCGCTGAGCCACTCCTGCGCCCCCCTGGCCTTG
TCTACCTCTTGCCCCCCGAAGGGTTAGTGTCGAGCTCACTCCAGCATCCTACAACCTCCTGGTGGCCTTGCCGCCCCCAC
AACCCCGAGGTTTAAAGCCAGGTACACGAGGCAGGGGACACACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTT
GCTGCTGCTGAGCATGGGCGGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGCCACCCT
GGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACC
CGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGG
CTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCGCC
GCAGCACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCCTC
AAAGGCCCCTCCCCCCAGCCTTCCAAGTCCATCCCGACTCCCGGGGCCCTCGGacaccccgatcctcccacaataaaggcttctcaat
cc

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>VIRT171498
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MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT
MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC
GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ
```

```
>NM_033183.2 Homo sapiens chorionic gonadotropin subunit beta 8 (CGB8), mRNA
GCTTCAGTCCAGCACCTTTCTCGGGTCACGGCCTCCTCCTGGCTCCCAGGACCCCACCATAGGCAGAGGC
AGGCCTTCCTACACCCTACTCCCTGTGCCTCCAGGCTCGACTAGTCCCTAGCACTCGACGACTGAGTCTC
TGAGGTCACTTCACCGTGGTCTCCGCCTCACCCTTGGCGCTGGACCAGTGAGAGGAGAGGGCTGGGGCGC
TCCGCTGAGCCACTCCTGCGCCCCCCTGGCCTTGTCTACCTCTTGCCCCCCGAAGGGTTAGTGTCGAGCT
CACTCCAGCATCCTACAACCTCCTGGTGGCCTTGCCGCCCCCACAACCCCGAGGTTTAAAGCCAGGTACA
CGAGGCAGGGGACACACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGA
AGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCG
CGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCC
ATCCGGCTCCCTGGCTGCCCGCGCGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAAT
GTGCACTCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCC
CCGCTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCCAGCCTTCCAAGTCCATCCCGACTCCCGGGG
CCCTCGGACACCCCGATCCTCCCACAATAAAGGCTTCTCAATCCGCAAAAAAAAAAAAAAAAAA
>NP_149439.1 chorionic gonadotropin, beta polypeptide 8 precursor [Homo sapiens]
MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLP
ALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSS
SKAPPPSLPSPSRLPGPSDTPILPQ
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i0_HQ_samplec9816d|c13287/f2p2/890      acttgggtgtgctcgaggtggaggtgttgggcgaggtgcctgcagctggcggcagt-tcC  59
NM_033183.2                             GCTTCAGTC-----CAGC-AC-CTTTCTCGGGTCACGGCCTCCTCCTGGCTCCCAGGACC  53
                                         ***  **       **       *  * **      **** *  *****  *     **

i0_HQ_samplec9816d|c13287/f2p2/890      CTCTGCCAGCACTTCTTTGTCACCGCTTCGAGGCCGATAACTCTGAGGAAGGCTCGACTA  119
NM_033183.2                             CCACCATAGGCAGAGGCAGGCCTTCCTACACCCTACTCCCTGTGCCTCCAGGCTCGACTA  113
                                        *      **         * *    ** *                    ***********

i0_HQ_samplec9816d|c13287/f2p2/890      GTCCCTAGCACTCGACGACTGAGTCTCTGAGGTCACTTCACCGTGGTCTCCGCCTCACCC  179
NM_033183.2                             GTCCCTAGCACTCGACGACTGAGTCTCTGAGGTCACTTCACCGTGGTCTCCGCCTCACCC  173
                                        ************************************************************

i0_HQ_samplec9816d|c13287/f2p2/890      TTGGCGCTGGACCAGTGAGAGGAGAGGGCTGGGGCGCTCCGCTGAGCCACTCCTGCGCCC  239
NM_033183.2                             TTGGCGCTGGACCAGTGAGAGGAGAGGGCTGGGGCGCTCCGCTGAGCCACTCCTGCGCCC  233
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i0_HQ_samplec9816d|c13287/f2p2/890      CCCTGGCCTTGTCTACCTCTTGCCCCCCGAAGGGTTAGTGTCGAGCTCACTCCAGCATCC  299
NM_033183.2                             CCCTGGCCTTGTCTACCTCTTGCCCCCCGAAGGGTTAGTGTCGAGCTCACTCCAGCATCC  293
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i0_HQ_samplec9816d|c13287/f2p2/890      TACAACCTCCTGGTGGCCTTGCCGCCCCCACAACCCCGAGGTTTAAAGCCAGGTACACGA  359
NM_033183.2                             TACAACCTCCTGGTGGCCTTGCCGCCCCCACAACCCCGAGGTTTAAAGCCAGGTACACGA  353
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i0_HQ_samplec9816d|c13287/f2p2/890      GGCAGGGGACACACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAG  419
NM_033183.2                             GGCAGGGGACACACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAG  413
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i0_HQ_samplec9816d|c13287/f2p2/890      CATGGGCGGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGC  479
NM_033183.2                             CATGGGCGGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGC  473
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i0_HQ_samplec9816d|c13287/f2p2/890      CACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTG  539
NM_033183.2                             CACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTG  533
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i0_HQ_samplec9816d|c13287/f2p2/890      TGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCA  599
NM_033183.2                             TGCCGGCTACTGCCCCACCATGACCCGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCA  593
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i0_HQ_samplec9816d|c13287/f2p2/890      GGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCG  659
NM_033183.2                             GGTGGTGTGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCG  653
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i0_HQ_samplec9816d|c13287/f2p2/890      CGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCG  719
NM_033183.2                             CGGCGTGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCG  713
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i0_HQ_samplec9816d|c13287/f2p2/890      CCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCG  779
NM_033183.2                             CCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCG  773
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i0_HQ_samplec9816d|c13287/f2p2/890      CTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCCAGCCTTCCAAGTCCATCCCGACT  839
NM_033183.2                             CTTCCAGGACTCCTCTTCCTCAAAGGCCCCTCCCCCCAGCCTTCCAAGTCCATCCCGACT  833
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i0_HQ_samplec9816d|c13287/f2p2/890      CCCGGGGCCCTCGGacaccccgatcctcccacaataaaggcttctcaatcc---------  890
NM_033183.2                             CCCGGGGCCCTCGGACACCCCGATCCTCCCACAATAAAGGCTTCTCAATCCGCAAAAAAA  893
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i0_HQ_samplec9816d|c13287/f2p2/890      -----------          890
NM_033183.2                             AAAAAAAAAAA          904
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VIRT171498        MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT      60
NP_149439.1       MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT      60
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VIRT171498        MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC      120
NP_149439.1       MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC      120
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VIRT171498        GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ           165
NP_149439.1       GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ           165
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RPS5

Sequence	**Header**	**AA Seq**
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Absent	i0_HQ_samplec9816d|c18100/f19p0/740	
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TGGCCGCGGCGAGGAGTCAGAGGGAACTGAACTGGCTACTCCCGCGGCAGGTGGGATTTAAGGATGACCGGTGGGA
GACAGCAGCACCAGCGGTGGCAGAGACCCCAGACATCAAGCTCTTTGGGAAGTGGAGCACCGATGATGTGCAGATCA
ATGACATTTCCCTGCAGGATTACATTGCAGTGAAGGAGAAGTATGCCAAGTACCTGCCTCACAGTGCAGGGCGGTATG
CCGCCAAACGCTTCCGCAAAGCTCAGTGTCCCATTGTGGAGCGCCTCACTAACTCCATGATGATGCACGGCCGCAACAA
CGGCAAGAAGCTCATGACTGTGCGCATCGTCAAGCATGCCTTCGAGATCATACACCTGCTCACAGGCGAGAACCCTCTG
CAGGTCCTGGTGAACGCCATCATCAACAGTGGTCCCCGGGAGGACTCCACACGCATTGGGCGCGCCGGGACTGTGAGA
CGACAGGCTGTGGATGTGTCCCCCCTGCGCCGTGTGAACCAGGCCATCTGGCTGCTGTGCACAGGCGCTCGTGAGGCT
GCCTTCCGGAACATTAAGACCATTGCTGAGTGCCTGGCAGATGAGCTCATCAATGCTGCCAAGGGCTCCTCGAACTCCT

ATGCCATTAAGAAGAAGGACGAGCTGGAGCGTGTGGCCAAGTCCAACCGCTGATTTTCCCAGCTGCTGCCcaataaacctg
tctgccctttggggcagcccc

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>VIRT30957
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MSSSARHSAMVLMFRKAASRAPVHSSQMAWFTRRRGDTSTACRLTVPARPMRVESSRGPL
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isoform=c18100;full_length_coverage=19;non_full_length_coverage=0;isoform_length=740

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GAGACAGCAGCACCAGCGGTGGCAGAGACCCCAGACATCAAGCTCTTTGGGAAGTGGAGCACCGATGATGTGCAGAT
CAATGACATTTCCCTGCAGGATTACATTGCAGTGAAGGAGAAGTATGCCAAGTACCTGCCTCACAGTGCAGGGCGGTAT
GCCGCCAAACGCTTCCGCAAAGCTCAGTGTCCCATTGTGGAGCGCCTCACTAACTCCATGATGATGCACGGCCGCAACA
ACGGCAAGAAGCTCATGACTGTGCGCATCGTCAAGCATGCCTTCGAGATCATACACCTGCTCACAGGCGAGAACCCTCT
GCAGGTCCTGGTGAACGCCATCATCAACAGTGGTCCCCGGGAGGACTCCACACGCATTGGGCGCGCCGGGACTGTGAG
ACGACAGGCTGTGGATGTGTCCCCCCTGCGCCGTGTGAACCAGGCCATCTGGCTGCTGTGCACAGGCGCTCGTGAGGC
TGCCTTCCGGAACATTAAGACCATTGCTGAGTGCCTGGCAGATGAGCTCATCAATGCTGCCAAGGGCTCCTCGAACTCC
TATGCCATTAAGAAGAAGGACGAGCTGGAGCGTGTGGCCAAGTCCAACCGCTGATTTTCCCAGCTGCTGCCCAATAAAC
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>VIRT31560
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```
>NM_001009.3 Homo sapiens ribosomal protein S5 (RPS5), mRNA
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GGATGACCGAGTGGGAGACAGCAGCACCAGCGGTGGCAGAGACCCCAGACATCAAGCTCTTTGGGAAGTG
GAGCACCGATGATGTGCAGATCAATGACATTTCCCTGCAGGATTACATTGCAGTGAAGGAGAAGTATGCC
AAGTACCTGCCTCACAGTGCAGGGCGGTATGCCGCCAAACGCTTCCGCAAAGCTCAGTGTCCCATTGTGG
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CAAGCATGCCTTCGAGATCATACACCTGCTCACAGGCGAGAACCCTCTGCAGGTCCTGGTGAACGCCATC
ATCAACAGTGGTCCCCGGGAGGACTCCACACGCATTGGGCGCGCCGGGACTGTGAGACGACAGGCTGTGG
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CCGGAACATTAAGACCATTGCTGAGTGCCTGGCAGATGAGCTCATCAATGCTGCCAAGGGCTCCTCGAAC
TCCTATGCCATTAAGAAGAAGGACGAGCTGGAGCGTGTGGCCAAGTCCAACCGCTGATTTTCCCAGCTGC
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RLTNSMMMHGRNNGKKLMTVRIVKHAFEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVD
VSPLRRVNQAIWLLCTGAREAAFRNIKTIAECLADELINAAKGSSNSYAIKKKDELERVAKSNR
i0_HQ_samplec9816d|c29292/f2p0/819       acggcaacctggacctgcggagggcggcggtgaccactgggcctcactccgctaacccag     60
i0_HQ_samplec9816d|c18100/f19p0/740      ------------------------------------------------------------     0
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i0_HQ_samplec9816d|c18100/f19p0/740      ---ctcttcctgtctgtac---------------cagggcggcgcGTGGTCTACG-----     37
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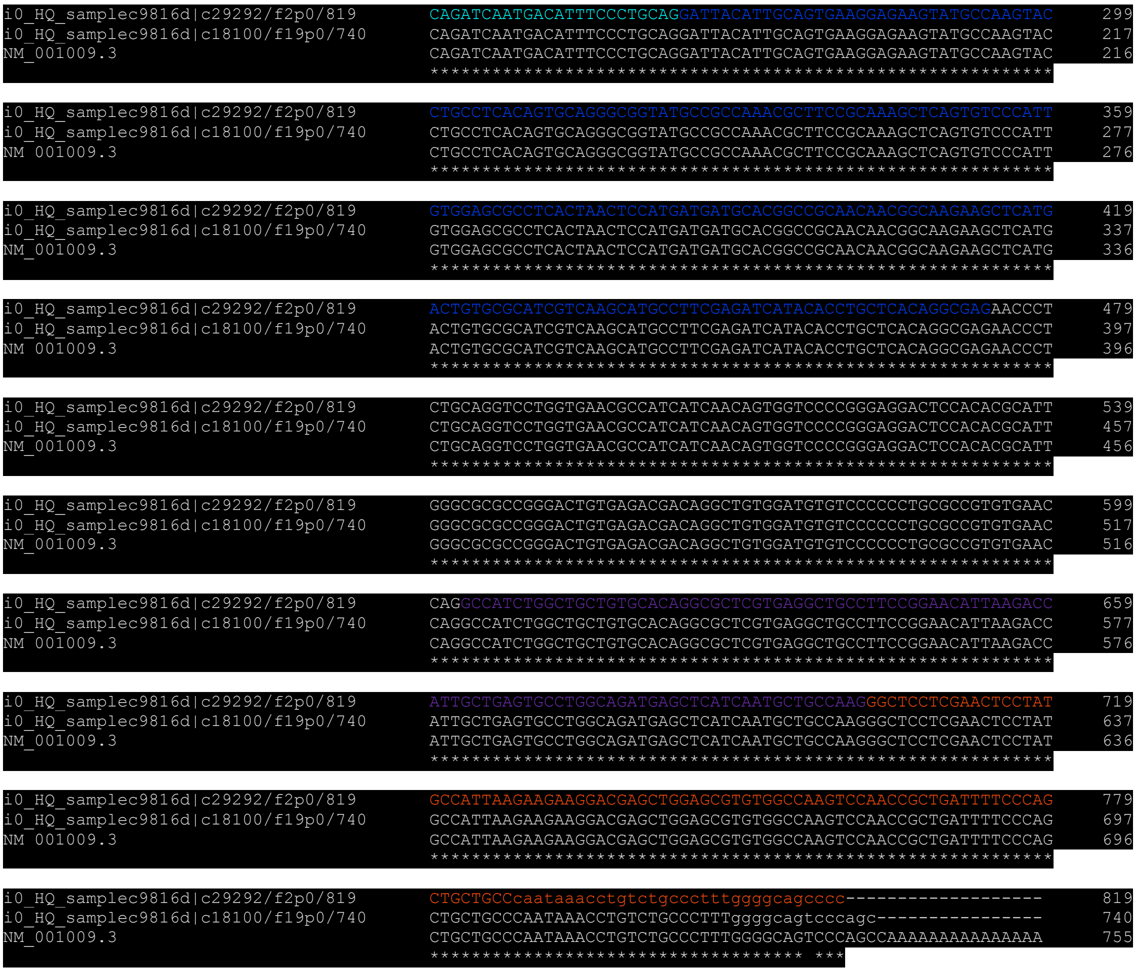

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VIRT30957        ----TRRRGDTSTACRLTVPARPMRVESSRGPLLMMAFTRTCRGFSPVSRCMISKACLTM      87
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VIRT30957        RTVMSFLPLLRPCIIMELVRRSTMGH-------------------     113
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>VIRT54307

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i0_HQ_samplec9816d|c69792/f39p31/881      -gga-agcggcggcggCGGCG------------------AAGGCGGCGGCT---------    31
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NM_006002.4                               GTCAGAGCTGGAGGGCCGGGCACCGCGGCCATGGAGGGTCAACGCTGGCTGCCGCTGGAG    101
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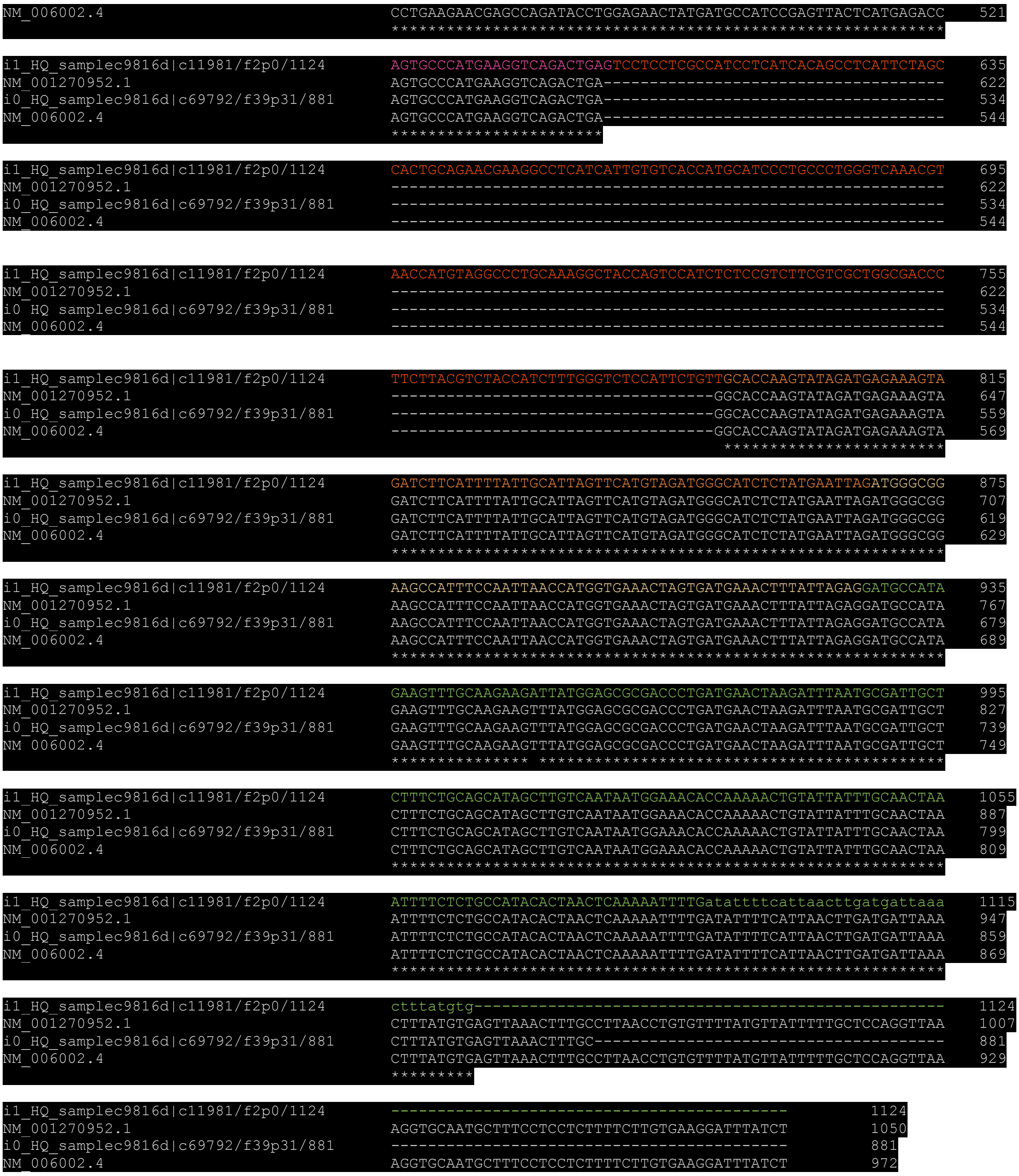

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i1_HQ_samplec9816d|c11981/f2p0/1124      GAAGTTTGCAAGAAGATTATGGAGCGCGACCCTGATGAACTAAGATTTAATGCGATTGCT    995
NM_001270952.1                           GAAGTTTGCAAGAAGTTTATGGAGCGCGACCCTGATGAACTAAGATTTAATGCGATTGCT    827
i0_HQ_samplec9816d|c69792/f39p31/881     GAAGTTTGCAAGAAGTTTATGGAGCGCGACCCTGATGAACTAAGATTTAATGCGATTGCT    739
NM_006002.4                              GAAGTTTGCAAGAAGTTTATGGAGCGCGACCCTGATGAACTAAGATTTAATGCGATTGCT    749
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i1_HQ_samplec9816d|c11981/f2p0/1124      CTTTCTGCAGCATAGCTTGTCAATAATGGAAACACCAAAAACTGTATTATTTGCAACTAA    1055
NM_001270952.1                           CTTTCTGCAGCATAGCTTGTCAATAATGGAAACACCAAAAACTGTATTATTTGCAACTAA    887
i0_HQ_samplec9816d|c69792/f39p31/881     CTTTCTGCAGCATAGCTTGTCAATAATGGAAACACCAAAAACTGTATTATTTGCAACTAA    799
NM_006002.4                              CTTTCTGCAGCATAGCTTGTCAATAATGGAAACACCAAAAACTGTATTATTTGCAACTAA    809
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i1_HQ_samplec9816d|c11981/f2p0/1124      ATTTCTCTGCCATACACTAACTCAAAAATTTTGatattttcattaacttgatgattaaa    1115
NM_001270952.1                           ATTTCTCTGCCATACACTAACTCAAAAATTTTGATATTTTCATTAACTTGATGATTAAA    947
i0_HQ_samplec9816d|c69792/f39p31/881     ATTTCTCTGCCATACACTAACTCAAAAATTTTGATATTTTCATTAACTTGATGATTAAA    859
NM_006002.4                              ATTTCTCTGCCATACACTAACTCAAAAATTTTGATATTTTCATTAACTTGATGATTAAA    869
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i1_HQ_samplec9816d|c11981/f2p0/1124      ctttatgtg---------------------------------------------------    1124
NM_001270952.1                           CTTTATGTGAGTTAAACTTTGCCTTAACCTGTGTTTTATGTTATTTTTGCTCCAGGTTAA    1007
i0_HQ_samplec9816d|c69792/f39p31/881     CTTTATGTGAGTTAAACTTTGC--------------------------------------    881
NM_006002.4                              CTTTATGTGAGTTAAACTTTGCCTTAACCTGTGTTTTATGTTATTTTTGCTCCAGGTTAA    929
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NM_001270952.1                           AGGTGCAATGCTTTCCTCCTCTTTTCTTGTGAAGGATTTATCT         1050
i0_HQ_samplec9816d|c69792/f39p31/881     -------------------------------------------         881
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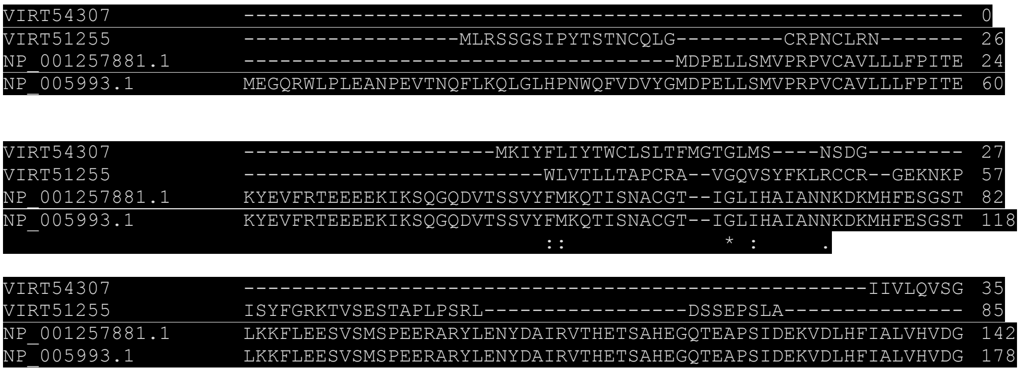

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VIRT51255              ------------------MLRSSGSIPYTSTNCQLG---------CRPNCLRN------- 26
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NP_005993.1            MEGQRWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGMDPELLSMVPRPVCAVLLLFPITE 60


VIRT54307              ---------------------MKIYFLIYTWCLSLTFMGTGLMS----NSDG-------- 27
VIRT51255              -------------------------WLVTLLTAPCRA--VGQVSYFKLRCCR--GEKNKP 57
NP_001257881.1         KYEVFRTEEEEKIKSQGQDVTSSVYFMKQTISNACGT--IGLIHAIANNKDKMHFESGST 82
NP_005993.1            KYEVFRTEEEEKIKSQGQDVTSSVYFMKQTISNACGT--IGLIHAIANNKDKMHFESGST 118
                                                ::             * :     .

VIRT54307              ----------------------------------------------------IIVLQVSG 35
VIRT51255              ISYFGRKTVSESTAPLPSRL-----------------DSSEPSLA--------------- 85
NP_001257881.1         LKKFLEESVSMSPEERARYLENYDAIRVTHETSAHEGQTEAPSIDEKVDLHFIALVHVDG 142
NP_005993.1            LKKFLEESVSMSPEERARYLENYDAIRVTHETSAHEGQTEAPSIDEKVDLHFIALVHVDG 178
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VIRT54307           SFFRAH----------------------------------------------        41
VIRT51255           ----------------------------------------------------        85
NP_001257881.1      HLYELDGRKPFPINHGETSDETLLEDAIEVCKKFMERDPDELRFNAIALSAA        194
NP_005993.1         HLYELDGRKPFPINHGETSDETLLEDAIEVCKKFMERDPDELRFNAIALSAA        230
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PAXX

Sequence	**Header**	**AA Seq**	
Present	i1_HQ_samplec9816d|c19870/f5p21/1131	>VIRT110879	>VIRT112892
Absent			
NCBI	NM_183241	NP_899064.1	
	NR_138076		

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GAGCTTTGGAGCACCTGCTTCACGCCGGACAGCCTGGCGGCCCTCGTGGGTAACTGGGCGGGTCTGGGAGCCGCCACA
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CGGTGTCCAGGAGAGTCGCTCATCAACCCCGGGTTCAAGAGTAAGAAACCAGCTGGTGGCGTGGACTTCGATGAGACC
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>VIRT112892

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>NM_183241.2 Homo sapiens PAXX, non-homologous end joining factor (PAXX), transcript variant 2, mRNA
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CTCTACGTGACCGACGCCGCGGAGCTTTGGAGCACCTGCTTCACGCCGGACAGCCTGGCGGCCCTCAAAG
CCCGTTTTGGCCTGAGTGCGGCTGAGGACATCACCCCCCGGTTCAGGGCAGCCTGTGAGCAGCAAGCTGT
GGCTCTGACTCTGCAGGAGGACAGAGCATCCCTGACGCTTTCAGGGGGGCCCTCGGCACTGGCCTTTGAC
CTCTCCAAGGTACCAGGCCCAGAGGCAGCCCCCAGGCTGCGGGCGCTGACACTGGGCCTGGCAAAACGCG
TGTGGAGCCTGGAGCGGCGACTGGCAGCTGCAGAAGAGACAGCTGTCAGCCCGAGGAAGAGCCCCCGGCC
TGCAGGGCCTCAGCTCTTCTTACCAGACCCAGATCCCCAGAGAGGTGGCCCTGGACCTGGAGTCAGGAGG
CGGTGTCCAGGAGAGTCGCTCATCAACCCCGGGTTCAAGAGTAAGAAACCAGCTGGTGGCGTGGACTTCG
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GAGGCCCCCATCAGAGACCCCCCGCCACCACCTCCACCTGCCTGTCCTGGGCCAGGACTAACACGGCTCC
TCAAATTCCTTCCCTGTCAAATAAACAGCTCCCTTGGTTGGAGGCTCTGGTGGGAAAAA
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>NP_899064.1 protein PAXX isoform 2 [Homo sapiens]
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AAEETAVSPRKSPRPAGPQLFLPDPDPQRGGPGPGVRRRCPGESLINPGFKSKKPAGGVDFDET
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>NR_138076.1 Homo sapiens PAXX, non-homologous end joining factor (PAXX), transcript variant 6, non-
coding RNA
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CTCTACGTGACCGACGCCGCGGAGCTTTGGAGCACCTGCTTCACGCCGGACAGCCTGGCGGCCCTCGTGG
GGCAGCCTGTGAGCAGCAAGCTGTGGCTCTGACTCTGCAGGAGGACAGAGCATCCCTGACGCTTTCAGGG
GGGCCCTCGGCACTGGCCTTTGACCTCTCCAAGGTACCAGGCCCAGAGGCAGCCCCCAGGCTGCGGGCGC
TGACACTGGGCCTGGCAAAACGCGTGTGGAGCCTGGAGCGGCGACTGGCAGCTGCAGAAGAGACAGCTGT
CAGCCCGAGGAAGAGCCCCCGGCCTGCAGGGCCTCAGCTCTTCTTACCAGACCCAGATCCCCAGAGAGGT
GGCCCTGGACCTGGAGTCAGGAGGCGGTGTCCAGGAGAGTCGCTCATCAACCCCGGGTTCAAGAGTAAGA
AACCAGCTGGTGGCGTGGACTTCGATGAGACCTGAAGGTGCAGCACAAGCGTGGCCCCGCGGGGAGTCCG
CCTATGAGGGGAGAGGCAGTCTTTGAGGCCCCCATCAGAGACCCCCCGCCACCACCTCCACCTGCCTGTC
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CTGGTGGG
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i1_HQ_samplec9816d|c19870/f5p21/1131      cccaagccccgcccgccggttcccgctcgcggcgccatggatccgctgtcgccGGCTCTG
NM_183241.2                               ------------------------------------------------------------          0
NR_138076.1                               ------------------------------------------------------------          0


i1_HQ_samplec9816d|c19870/f5p21/1131      ACGCTGCCGCCGGGCCCCGAGCCGCCCCGCTTCGTGTGCTACTGCGAAGGGGAGGAAAGC          12
NM_183241.2                               ------------------------------------------------------------          0
NR_138076.1                               ------------------------------------------------------------          0


i1_HQ_samplec9816d|c19870/f5p21/1131      GGGGAGGGGGACCGCGGCGGCTTCAACCTCTACGTGACCGACGCCGCGGAGCTTTGGAGC          18
NM_183241.2                               ------------------------------------------------------------          0
NR_138076.1                               ------------------------------------------------------------          0


i1_HQ_samplec9816d|c19870/f5p21/1131      ACCTGCTTCACGCCGGACAGCCTGGCGGCCCTCGTGGGTAACTGGGCGGGTCTGGGAGCC          24
NM_183241.2                               ------------------------------------------------------------          0
NR_138076.1                               ------------------------------------------------------------          0


i1_HQ_samplec9816d|c19870/f5p21/1131      GCCACACCCCTCCTTGCAGTGCAGATCGTCTATGGGGCGACAGACATCTGGGATTCCCCA          30
NM_183241.2                               ----------------------------------------CGCCGGGTTCCCGCTCGCCC          20
NR_138076.1                               ----------------------------------------CGCCGGGTTCCCGCTCGCCC          20
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i1_HQ_samplec9816d|c19870/f5p21/1131      GAAGGCTCTGACACCCTCTGCCCGCCCTGTAGCTGTAGTCCTCCCATTGGCTAGGGCTCT          36
NM_183241.2                               GGCGCCATGGATCCG-----------CTGTCGCCGCCGCTCTGCACGCTGCCGCCGGGCC          69
NR_138076.1                               GGCGCCATGGATCCG-----------CTGTCGCCGCCGCTCTGCACGCTGCCGCCGGGCC          69
                                          *  * *   **  *            **** ** *  *  ** *     **    *  *

i1_HQ_samplec9816d|c19870/f5p21/1131      GGGGTCGGGCAGGTTTCGGGTGCCCCCAGTGGGCCTCGGGTTCCAGGCAGCTCGTGACAA          42
NM_183241.2                               CCGAGCCGCCCCGCTTCGTGTGCTACTGCGAAGGGGAGGAAAGCGGGGAGGGGGACCGCG          12
NR_138076.1                               CCGAGCCGCCCCGCTTCGTGTGCTACTGCGAAGGGGAGGAAAGCGGGGAGGGGGACCGCG          12
                                            *  * * *  * **** ****  *      *    **    * ** **   *

i1_HQ_samplec9816d|c19870/f5p21/1131      GCCCCTGTGCTCTCTAGAAAGCCCGTTTTGGCCTGAGTGCGGCTGAGGACATCACCCCCC          48
NM_183241.2                               GCGGCTTCAACCTCTACGT-------GACCGAC-----GCCGCGGAGCTTTGGAGCACCT          17
NR_138076.1                               GCGGCTTCAACCTCTACGT-------GACCGAC-----GCCGCGGAGCTTTGGAGCACCT          17
                                          **  **     *****              * *     ** ** ***      * * **

i1_HQ_samplec9816d|c19870/f5p21/1131      GGTTCAGGTGAGA--CCCAAGCAGGGAGGAAGGACGGGTGGGGAGGAGGAGGGTCTGCCA          53
NM_183241.2                               GCTTCACGCCGGACAGCCTGGCGGCCCTCAAAGCCCGTTT--------TGGCCTGAGTGC          22
NR_138076.1                               GCTTCACGCCGGACAGCCTGGCGGCCCTCG------------------------------          20
                                          * **** *   **   **  ** *

i1_HQ_samplec9816d|c19870/f5p21/1131      CAGCTCTCCGCACCTCTCCTCTCCCAGGGCAGCCTGTGAGCAGCAAGCTGTGGCTCTGAC          59
NM_183241.2                               GGCTGAGGACATCACCCCCCGGTTCAGGGCAGCCTGTGAGCAGCAAGCTGTGGCTCTGAC          28
NR_138076.1                               ------------------------TGGGGCAGCCTGTGAGCAGCAAGCTGTGGCTCTGAC          24
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i1_HQ_samplec9816d|c19870/f5p21/1131      TCTGCAGGAGGACAGAGCATCCCTGACGCTTTCAGGGGGGCCCTCGGCACTGGCCTTTGA          65
NM_183241.2                               TCTGCAGGAGGACAGAGCATCCCTGACGCTTTCAGGGGGGCCCTCGGCACTGGCCTTTGA          34
NR_138076.1                               TCTGCAGGAGGACAGAGCATCCCTGACGCTTTCAGGGGGGCCCTCGGCACTGGCCTTTGA          30
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NM_183241.2                                   CCTCTCCAAGGTACCAGGCCCAGAGGCAGCCCCCAGGCTGCGGGCGCTGACACTGGGCCT       40
NR_138076.1                                   CCTCTCCAAGGTACCAGGCCCAGAGGCAGCCCCCAGGCTGCGGGCGCTGACACTGGGCCT       36
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i1_HQ_samplec9816d|c19870/f5p21/1131          GGCAAAACGCGTGTGGAGCCTGGAGCGGCGACTGGCAGCTGCAGAAGAGACAGCTGTCAG       77
NM_183241.2                                   GGCAAAACGCGTGTGGAGCCTGGAGCGGCGACTGGCAGCTGCAGAAGAGACAGCTGTCAG       46
NR_138076.1                                   GGCAAAACGCGTGTGGAGCCTGGAGCGGCGACTGGCAGCTGCAGAAGAGACAGCTGTCAG       42
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i1_HQ_samplec9816d|c19870/f5p21/1131          CCCGAGGAAGAGCCCCCGGCCTGCAGGGCCTCAGCTCTTCTTACCAGACCCAGATCCCCA       83
NM_183241.2                                   CCCGAGGAAGAGCCCCCGGCCTGCAGGGCCTCAGCTCTTCTTACCAGACCCAGATCCCCA       52
NR_138076.1                                   CCCGAGGAAGAGCCCCCGGCCTGCAGGGCCTCAGCTCTTCTTACCAGACCCAGATCCCCA       48
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i1_HQ_samplec9816d|c19870/f5p21/1131          GAGAGGTGGCCCTGGACCTGGAGTCAGGAGGCGGTGTCCAGGAGAGTCGCTCATCAACCC       89
NM_183241.2                                   GAGAGGTGGCCCTGGACCTGGAGTCAGGAGGCGGTGTCCAGGAGAGTCGCTCATCAACCC       58
NR_138076.1                                   GAGAGGTGGCCCTGGACCTGGAGTCAGGAGGCGGTGTCCAGGAGAGTCGCTCATCAACCC       54
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i1_HQ_samplec9816d|c19870/f5p21/1131          CGGGTTCAAGAGTAAGAAACCAGCTGGTGGCGTGGACTTCGATGAGACCTGAAGGTGCAG       95
NM_183241.2                                   CGGGTTCAAGAGTAAGAAACCAGCTGGTGGCGTGGACTTCGATGAGACCTGAAGGTGCAG       64
NR_138076.1                                   CGGGTTCAAGAGTAAGAAACCAGCTGGTGGCGTGGACTTCGATGAGACCTGAAGGTGCAG       60
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i1_HQ_samplec9816d|c19870/f5p21/1131          CACAAGCGTGGCCCCGCGGGGAGTCCGCCTATGAGGGGAGAGGCAGTCTTTGAGGCCCCC       10
NM_183241.2                                   CACAAGCGTGGCCCCGCGGGGAGTCCGCCTATGAGGGGAGAGGCAGTCTTTGAGGCCCCC       70
NR_138076.1                                   CACAAGCGTGGCCCCGCGGGGAGTCCGCCTATGAGGGGAGAGGCAGTCTTTGAGGCCCCC       66
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i1_HQ_samplec9816d|c19870/f5p21/1131          ATCAGAGACCCCCCGCCACCACCTCCACCTGCCTGTCCTGGGCCAGGACTAACACGGCTC       10
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i1_HQ_samplec9816d|c19870/f5p21/1131          CTCAAATTCCTTCCCTGTCAAAtaaacagctcccttggttggaggctctggtg-------       11
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NR_138076.1                                   CTCAAATTCCTTCCCTGTCAAATAAACAGCTCCCTTGGTTGGAGGCTCTGGTGGG-----       77
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VIRT110879        MGASKTASPLIGGLPAG---PRLCCTFRSHRSPRHQLVS---YS----------------      38
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VIRT110879        ------------------------------------------------------------      38
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VIRT110879        ------------------------------------------------------------      38
VIRT112892        EPQLAAH-----RLPWERRGA-----ESCGRPSS---------------------SPPVL      37
NP_899064.1       APRLRALTLGLAKRVWSLERRLAAAEETAVSPRKSPRPAGPQLFLPDPDPQRGGPGPGVR      177

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Sequence	Header	AA Seq	
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NCBI	NM_003641	>NP_003632.3	

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>VIRT177472
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GCCGCCCATAGCCTGCAACCTTTGCACTCCACTGTGCAATGCTGGCCCTGCACGCTGGGGCTGTTGCCCC
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>NP_003632.3 interferon-induced transmembrane protein 1 [Homo sapiens]
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i1_HQ_samplec9816d|c2133/f4p0/1237      gagaaactgaaacgacaggggaaaggaggtctcactgagcaccgtcccagcatcCGGACA 60
i0_HQ_samplec9816d|c33361/f2p4/957      ------------------------------------------------------------ 0
i0_HQ_samplec9816d|c49271/f4p37/679     ------------------------------------------------------------ 0
NM_003641.3                             ------------------------------------------------------------ 0

i1_HQ_samplec9816d|c2133/f4p0/1237      CCACAGCGGCCCTTCGCTCCACGCAGAAAACCACACTTCTCAAACCTTCACTCAACACTT 120
i0_HQ_samplec9816d|c33361/f2p4/957      ------------------------------------------------------------ 0
i0_HQ_samplec9816d|c49271/f4p37/679     ------------------------------------------------------------ 0
NM_003641.3                             ------------------------------------------------------------ 0

i1_HQ_samplec9816d|c2133/f4p0/1237      CCTTCCCCAAAGCCAGAAGATGCACAAGGAGGAACATGAGGTGGCTGTGCTGGGGGCACC 180
i0_HQ_samplec9816d|c33361/f2p4/957      ------------------------------------------------------------ 0
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NM_003641.3                             ------------------------------------------------------------ 0

i1_HQ_samplec9816d|c2133/f4p0/1237      CCCCAGCACCATCCTTCCAAGGTCCACCGTGATCAACATCCACAGCGAGACCTCCGTGCC 240
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NM_003641.3                             ------------------------------------------------------------ 0
```

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i0_HQ_samplec9816d|c49271/f4p37/679      ------------------------------------------------------------ 0
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i1_HQ_samplec9816d|c2133/f4p0/1237       TCATAGCATTCGCCTACTCCGTGAAGGTGCGTATGGCCCTGGCGGAAATCCAGGGGGTGC 359
i0_HQ_samplec9816d|c33361/f2p4/957       CCCCAGAGTCCCCGTT---------------CCTGGGCCTGGAGGGCTGCTTTGG--GGC 116
i0_HQ_samplec9816d|c49271/f4p37/679      ------------------------------------------------------------ 0
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i1_HQ_samplec9816d|c2133/f4p0/1237       CGGTGAGCCTGGGGCTCCACCTGCCCACATGCTGCCTGG---GGTGGGGACTTGTGTGTC 416
i0_HQ_samplec9816d|c33361/f2p4/957       AGGAAACTTTGGCCACCAGGCCTCTGACCTGCACCAGGAGACACTGGGAGGTTTAGTCCC 176
i0_HQ_samplec9816d|c49271/f4p37/679      ------------------------------------------------------------ 0
NM_003641.3                              ------------------------------------------------------------ 0

i1_HQ_samplec9816d|c2133/f4p0/1237       CCTGTGACTGTGAGTTTGTGTGCACCTCTGCCCCGTGTG-------TGCTCACGTCAGTA 469
i0_HQ_samplec9816d|c33361/f2p4/957       CAA---AC----CCGCACAGAGCAGGACTGCAGCCTGAGGAAAGAGCAAGGATTTCAGGA 229
i0_HQ_samplec9816d|c49271/f4p37/679      ------------------------------------------------------------ 0
NM_003641.3                              ------------------------------------------------------------ 0

i1_HQ_samplec9816d|c2133/f4p0/1237       GCTTTGTCTGTGTGATCTGTGTGT--GTGTGTGGCTTTGGGGAATCTGCCCAGTGCAGGT 527
i0_HQ_samplec9816d|c33361/f2p4/957       GAGAGGCCTGCGACAAGTGAGCAGGAAATAGAAACTTAAGA-GAAATACACACTTCTGAG 288
i0_HQ_samplec9816d|c49271/f4p37/679      ---------------------------------------------------tcttctgag 9
NM_003641.3                              ---------------AAACAGCAGGAAATAGAAACTTAAGA-GAAATACACACTTCTGAG 44
                                                                                      * * *

i1_HQ_samplec9816d|c2133/f4p0/1237       CTAGGAGGAGGCTCCAGGAGGCTGGCTGGCTGGCTCAGAGTCTGTCCCTGGCTATCCATT 587
i0_HQ_samplec9816d|c33361/f2p4/957       AAAC--TGAAACGACAGGGGAAAGGAGGTCTCACTGAGCAC-CGTCCCAGCATCCGG--- 342
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NM_003641.3                              AAAC--TGAAACGACAGGGGAAAGGAGGTCTCACTGAGCAC-CGTCCCAGCATCCGG--- 98
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i1_HQ_samplec9816d|c2133/f4p0/1237       AGCCCAGAGCAATTCTCCCTATAGCCCAGTAAGAAATTACACCCTCACCTTCCAGACTGG 647
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i1_HQ_samplec9816d|c2133/f4p0/1237       CACCCAGGC---TCTCCCAGAAAGTGAGAAGGGAACTCACAGGTGACTTCACCCCATGGT 704
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                                          *     **   * * *  **    * * **  *  *     **    **    *

i1_HQ_samplec9816d|c2133/f4p0/1237       TCCCCCAGTCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCT 942
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i0_HQ_samplec9816d|c49271/f4p37/679      ATGCTGGCCCTGCACGCTGGGGCTGTTGCCCCTGCCCCCTTGGTCCTGCCCCTAGATACA 623
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i1_HQ_samplec9816d|c2133/f4p0/1237       GCAGTTTATACCCACACACCTGTCTACAGTGTCATTcaataaagtgcacgtgctt----- 1237
i0_HQ_samplec9816d|c33361/f2p4/957       GCAGTTTATACCCACACACCTGTCTACAGTGTCATTCAATAAAGTGCACGTGCTT----- 957
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VIRT168080       ---------MVGHGGLAVDVDHGGPWKDG------AGGCPQHSHLMFLLVHLLALG-KEV    44
VIRT177472       ---------MVGHGGLAVDVDHGGPWKDG------AGGCPQHSHLMFLLVHLLALG-KEV    44
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                          ::*                .          *        *   *

VIRT175835       LCAGLGTKPPSVSWCRSEAWWPKFPAPKQPSRPRNGDS-GEN------------------    90
VIRT168080       LSEGLRS----VVFCV----------E-RRAAVVSGCWDGAQ------------------    71
VIRT177472       LSEGLRS----VVFCV----------E-RRAAVVSGCWDGAQ------------------    71
NP_003632.3      CCLGFIA----FAYSV----------K-SRDRKMVGDVTGAQAYASTAKCLNIWALILGI    94
                  . *: :    . :.                    *   * :

VIRT175835       -------------------------------   90
VIRT168080       -------------------------------   71
VIRT177472       -------------------------------   71
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IFITM3

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Absent	i0_HQ_samplec9816d|c108452/f2p0/628		
NCBI	NM_021034	NP_066362.2	
	NR_049759	>VIRT13170	

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>VIRT11976

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>VIRT13170
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>NM_021034.2 Homo sapiens interferon induced transmembrane protein 3 (IFITM3), transcript variant 1, mRNA
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ACCCGACCGCCGCTGGTCTTCGCTGGACACCATGAATCACACTGTCCAAACCTTCTTCTCTCCTGTCAAC
AGTGGCCAGCCCCCCAACTATGAGATGCTCAAGGAGGAGCACGAGGTGGCTGTGCTGGGGGCGCCCCACA
ACCCTGCTCCCCCGACGTCCACCGTGATCCACATCCGCAGCGAGACCTCCGTGCCCGACCATGTCGTCTG
GTCCCTGTTCAACACCCTCTTCATGAACCCCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAG
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>NP_066362.2 interferon-induced transmembrane protein 3 [Homo sapiens]
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>NR_049759.1 Homo sapiens interferon induced transmembrane protein 3 (IFITM3), transcript variant 2, non-coding RNA
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i0_HQ_samplec9816d|c108452/f2p0/628      CCTTCTTCTCTCCTGTCAACAGCGGCCAGCCCCCCAACTATGAGATGCTCAAGGAGGAGC 144
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i0_HQ_samplec9816d|c108452/f2p0/628      ACGAGGTGGCTGTGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCC 204
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i1_HQ_samplec9816d|c8447/f5p0/1206       ACATCCGCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCT 269
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NM_021034.2                              ------------------------------------------------------------ 340


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NM_021034.2                              ------------------------------------------------------------ 340


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i1_HQ_samplec9816d|c8447/f5p0/1206       GGCTATCCACTAGCCCAGAGCAGTTCTCCCTATAGCCCAGTAAGAAATTACACCTTCACC 629
NR_049759.1                              ------------------------------------------------------------ 340
i0_HQ_samplec9816d|c108452/f2p0/628      ------------------------------------------------------------ 304
NM_021034.2                              ------------------------------------------------------------ 340


i1_HQ_samplec9816d|c8447/f5p0/1206       TTCCAGACTGGCACCCACGCTCTCCCAGAAAGTGAGAAGGGAACTCACAGGTGACTTCAC 689
NR_049759.1                              ------------------------------------------------------------ 340
i0_HQ_samplec9816d|c108452/f2p0/628      ------------------------------------------------------------ 304
NM_021034.2                              ------------------------------------------------------------ 340


i1_HQ_samplec9816d|c8447/f5p0/1206       CCCATGGTGGGGAGAACAGCCTGTGCTGGGGTCAAGGCAGAAGGAGGATGAGCCCCGAGG 749
NR_049759.1                              ------------------------------------------------------------ 340
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i0_HQ_samplec9816d|c108452/f2p0/628      ------------------------------------------------------------ 304
NM_021034.2                              ------------------------------------------------------------ 340

i1_HQ_samplec9816d|c8447/f5p0/1206       CTCCTGGAGAGTCTGAGCCTGGGTGAGGAAGGGGAGGAGGTGGTCCCTGATCTCAGGGCG 809
NR_049759.1                              ------------------------------------------------------------ 340
i0_HQ_samplec9816d|c108452/f2p0/628      ------------------------------------------------------------ 304
NM_021034.2                              ------------------------------------------------------------ 340

i1_HQ_samplec9816d|c8447/f5p0/1206       GGGAGAGCCAATGAGGAGACGGAGCCATAGCACGCGGCTCTCAGCTGGGGGATCCTGGTC 869
NR_049759.1                              ------------------------------------------------------------ 340
i0_HQ_samplec9816d|c108452/f2p0/628      ------------------------------------------------------------ 304
NM_021034.2                              ------------------------------------------------------------ 340

i1_HQ_samplec9816d|c8447/f5p0/1206       CCCTCACCATCTCCTCTCCCCCAGTCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGG 929
NR_049759.1                              --------------CTCCGTGAA-----GGGACAGGAAGATGGTTGGCGACGTGACCGGG 381
i0_HQ_samplec9816d|c108452/f2p0/628      --------------CTCCGTGAAGTCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGG 350
NM_021034.2                              --------------CTCCGTGAAGTCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGG 386
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i1_HQ_samplec9816d|c8447/f5p0/1206       GCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCTGGGCCCTGATTCTGGGCATC 989
NR_049759.1                              GCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCTGGGCCCTGATTCTGGGCATC 441
i0_HQ_samplec9816d|c108452/f2p0/628      GCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCTGGGCCCTGATTCTGGGCATC 410
NM_021034.2                              GCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCTGGGCCCTGATTCTGGGCATC 446
                                         ************************************************************

i1_HQ_samplec9816d|c8447/f5p0/1206       CTCATGACCATTCTGCTCATCGTCATCCCAGTGCTGATCTTCCAGGCCTATGGATAGATC 1049
NR_049759.1                              CTCATGACCATTCTGCTCATCGTCATCCCAGTGCTGATCTTCCAGGCCTATGGATAGATC 501
i0_HQ_samplec9816d|c108452/f2p0/628      CTCATGACCATTCTGCTCATCGTCATCCCAGTGCTGATCTTCCAGGCCTATGGATAGATC 470
NM_021034.2                              CTCATGACCATTCTGCTCATCGTCATCCCAGTGCTGATCTTCCAGGCCTATGGATAGATC 506
                                         ************************************************************

i1_HQ_samplec9816d|c8447/f5p0/1206       AGGAGGCATCACTGAGGCCAGGAGCTCTGCCCATGACCTGTATCCCACGTACTCCAACTT 1109
NR_049759.1                              AGGAGGCATCACTGAGGCCAGGAGCTCTGCCCATGACCTGTATCCCACGTACTCCAACTT 561
i0_HQ_samplec9816d|c108452/f2p0/628      AGGAGGCATCACTGAGGCCAGGAGCTCTGCCCATGACCTGTATCCCACGTACTCCAACTT 530
NM_021034.2                              AGGAGGCATCACTGAGGCCAGGAGCTCTGCCCATGACCTGTATCCCACGTACTCCAACTT 566
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i1_HQ_samplec9816d|c8447/f5p0/1206       CCATTCCTCGCCCTGCCCCCGGAGCCGAGTCCTGTATCAGCCCTTTATCCTCACACGCTT 1169
NR_049759.1                              CCATTCCTCGCCCTGCCCCCGGAGCCGAGTCCTGTATCAGCCCTTTATCCTCACACGCTT 621
i0_HQ_samplec9816d|c108452/f2p0/628      CCATTCCTCGCCCTGCCCCCGGAGCCGAGTCCTGTATCAGCCCTTTATCCTCACACGCTT 590
NM_021034.2                              CCATTCCTCGCCCTGCCCCCGGAGCCGAGTCCTGTATCAGCCCTTTATCCTCACACGCTT 626
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i1_HQ_samplec9816d|c8447/f5p0/1206       TTctacaatggcattcaataaagtgcacgtgtttctg---------------         1206
NR_049759.1                              TTCTACAATGGCATTCAATAAAGTGCACGTGTTTCTGGTGCTAAAAAAAAAA         673
i0_HQ_samplec9816d|c108452/f2p0/628      TTCTACAATGGCATTCAataaagtgcacgtgtttctgg--------------         628
NM_021034.2                              TTCTACAATGGCATTCAATAAAGTGCACGTGTTTCTGGTGCTAAAAAAAAAA         678
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VIRT11976        MNQTVQTFFSPVNSGQPPNYEMLKEEHEVAVLGAPHNPAPPTSTVIHIRSETSVPDHVVW    60
VIRT13170        MNQTVQTFFSPVNSGQPPNYEMLKEEHEVAVLGAPHNPAPPTSTVIHIRSETSVPDHVVW    60
NP_066362.2      MNHTVQTFFSPVNSGQPPNYEMLKEEHEVAVLGAPHNPAPPTSTVIHIRSETSVPDHVVW    60
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VIRT11976        SLFNTLFMNPCCLGFIAFAYSVKVRMAPGNAQRVPLSLELHLPTCCLGWGLVCPCDCEFV    120
VIRT13170        SLFNTLFMNPCCLGFIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGILMTIL    120
NP_066362.2      SLFNTLFMNPCCLGFIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGILMTIL    120
                 *********************** *     .: .  .      .*   *.*:      ::

VIRT11976        CTSVPCVPTSVALSV          135
VIRT13170        LIVIPVLIFQA-YG-          133
NP_066362.2      LIVIPVLIFQA-YG-          133
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GSTP1

Sequence	Header	AA Seq
Present	i1_HQ_samplec9816d|c1892/f2p5/1103	VIRT85086
Absent	i0_HQ_samplec9816d|c3248/f3p6/738	VIRT85693
NCBI	NM_000852	NP_000843.1

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GCTGGCAGATCAGGGCCAGAGCTGGAAGGAGGAGGTGGTGACCGTGGAGACGTGGCAGGAGGGCTCACTCAAAGCC
TCCTGCCTATACGGGCAGCTCCCCAAGTTCCAGGACGGAGACCTCACCCTGTACCAGTCCAATACCATCCTGCGTCACCT
GGGCCGCACCCTTGGTGAGTCTTGAACCTCCAAGTCCAGGGCAGGCATGGGCAAGCCTCTGCCCCCGGAGCCCTTTTGT
TTAAATCAGCTGCCCCGCAGCCCTCTGGAGTGGAGGAAACTGAGACCCACTGAGGTTACGTAGTTTGCCCAAGGTCAA
GCCTGGGTGCCTGCAATCCTTGCCCTGTGCCAGGCTGCCTCCCAGGTGTCAGGTGAGCTCTGAGCACCTGCTGTGTGGC
AGTCTCTCATCCTTCCACGCACATCCTCTTCCCCTCCTCCCAGGCTGGGGCTCACAGACAGCCCCCTGGTTGGCCCATCCC
CAGTGACTGTGTGTTGATCAGGCGCCCAGTCACGCGGCCTGCTCCCCTCCACCCAACCCCAGGGCTCTATGGGAAGGAC
CAGCAGGAGGCAGCCCTGGTGGACATGGTGAATGACGGCGTGGAGGACCTCCGCTGCAAATACATCTCCCTCATCTAC
ACCAACTATGAGGCGGGCAAGGATGACTATGTGAAGGCACTGCCCGGGCAACTGAAGCCTTTTGAGACCCTGCTGTCC
CAGAACCAGGGAGGCAAGACCTTCATTGTGGGAGACCAGATCTCCTTCGCTGACTACAACCTGCTGGACTTGCTGCTGA
TCCATGAGGTCCTAGCCCCTGGCTGCCTGGATGCGTTCCCCCTGCTCTCAGCATATGTGGGGCGCCTCAGTGCCCGGCC
CAAGCTCAAGGCCTTCCTGGCCTCCCCTGAGTACGTGAACCTCCCCATCAATGGCAACGGGAAACAGTGAGGGTTGGG
GGGACTCTGAGCGGGAGGCAGAGTTTGCCTTCctttctccaggaccaataaaatttctaagagag
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>VIRT85086
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MDQQQVQQVVVSEGDLVSHNEGLASLVLGQQGLKRLQLPGQCLHIVILARLIVGVDEGDV
FAAEVLHAVIHHVHQGCLLLVLPIEPWGWVEGSRPRDWAPDQHTVTGDGPTRGLSVSPSL
GGGEEDVRGRMRDCHTAGAQSSPDTWEAAWHRARIAGTQA
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>i0_HQ_samplec9816d|c3248/f3p6/738
isoform=c3248;full_length_coverage=3;non_full_length_coverage=6;isoform_length=738
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GCTCACTCAAAGCCTCCTGCCTATACGGGCAGCTCCCCAAGTTCCAGGACGGAGACCTCACCCTGTACCAGTCCAATACC
ATCCTGCGTCACCTGGGCCGCACCCTTGGGCTCTATGGGAAGGACCAGCAGGAGGCAGCCCTGGTGGACATGGTGAAT
GACGGCGTGGAGGACCTCCGCTGCAAATACGTCTCCCTCATCTACACCAACTATGAGGCGGGCAAGGATGACTATGTG
AAGGCACTGCCCGGGCAACTGAAGCCTTTTGAGACCCTGCTGTCCCAGAACCAGGGAGGCAAGACCTTCATTGTGGGA
GACCAGATCTCCTTCGCTGACTACAACCTGCTGGACTTGCTGCTGATCCATGAGGTCCTAGCCCCTGGCTGCCTGGATGC
GTTCCCCCTGCTCTCAGCATATGTGGGGCGCCTCAGTGCCCGGCCCAAGCTCAAGGCCTTCCTGGCCTCCCCTGAGTAC
GTGAACCTCCCCATCAATGGCAACGGGAAACAGTGAGGGTTGGGGGGACTCTGAGCGGGAGGCAGAGTTTGCCTTCC
TTTCTCCAGGACCAATAAAATTTCTAAGAGAG
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```
>VIRT85693
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MDQQQVQQVVVSEGDLVSHNEGLASLVLGQQGLKRLQLPGQCLHIVILARLIVGVDEGDV
FAAEVLHAVIHHVHQGCLLLVLPIEPKGAAQVTQDGIGLVQGEVSVLELGELPV
```

```
>NM_000852.3 Homo sapiens glutathione S-transferase pi 1 (GSTP1), mRNA
TGGGAAAGAGGGAAAGGCTTCCCCGGCCAGCTGCGCGGCGACTCCGGGGACTCCAGGGCGCCCCTCTGCG
GCCGACGCCCGGGGTGCAGCGGCCGCCGGGGCTGGGGCCGGCGGGAGTCCGCGGGACCCTCCAGAAGAGC
GGCCGGCGCCGTGACTCAGCACTGGGGCGGAGCGGGGCGGGACCACCCTTATAAGGCTCGGAGGCCGCGA
GGCCTTCGCTGGAGTTTCGCCGCCGCAGTCTTCGCCACCATGCCGCCCTACACCGTGGTCTATTTCCCAG
TTCGAGGCCGCTGCGCGGCCCTGCGCATGCTGCTGGCAGATCAGGGCCAGAGCTGGAAGGAGGAGGTGGT
```

```
GACCGTGGAGACGTGGCAGGAGGGCTCACTCAAAGCCTCCTGCCTATACGGGCAGCTCCCCAAGTTCCAG
GACGGAGACCTCACCCTGTACCAGTCCAATACCATCCTGCGTCACCTGGGCCGCACCCTTGGGCTCTATG
GGAAGGACCAGCAGGAGGCAGCCCTGGTGGACATGGTGAATGACGGCGTGGAGGACCTCCGCTGCAAATA
CATCTCCCTCATCTACACCAACTATGAGGCGGGCAAGGATGACTATGTGAAGGCACTGCCCGGGCAACTG
AAGCCTTTTGAGACCCTGCTGTCCCAGAACCAGGGAGGCAAGACCTTCATTGTGGGAGACCAGATCTCCT
TCGCTGACTACAACCTGCTGGACTTGCTGCTGATCCATGAGGTCCTAGCCCCTGGCTGCCTGGATGCGTT
CCCCCTGCTCTCAGCATATGTGGGGCGCCTCAGTGCCCGGCCCAAGCTCAAGGCCTTCCTGGCCTCCCCT
GAGTACGTGAACCTCCCCATCAATGGCAACGGGAAACAGTGAGGGTTGGGGGGACTCTGAGCGGGAGGCA
GAGTTTGCCTTCCTTTCTCCAGGACCAATAAAATTTCTAAGAGAGCTAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA
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>NP_000843.1 glutathione S-transferase P [Homo sapiens]
MPPYTVVYFPVRGRCAALRMLLADQGQSWKEEVVTVETWQEGSLKASCLYGQLPKFQDGDLTLYQSNTIL
RHLGRTLGLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGG
KTFIVGDQISFADYNLLDLLLIHEVLAPGCLDAFPLLSAYVGRLSARPKLKAFLASPEYVNLPINGNGKQ
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i1_HQ_samplec9816d|c1892/f2p5/1103      gctggagtttcgccgccgcagtcttcgccaccatgccgccctaacccgtggtctatttcc  60
i0_HQ_samplec9816d|c3248/f3p6/738       ------------------------------------------------------------  0
NM_000852.3                             ------------------------------------------------------------  0

i1_HQ_samplec9816d|c1892/f2p5/1103      caGTTCGAGGCCGCTGCGCGGCCCTGCGCATGCTGCTGGCAGATCAGGGCCAGAGCTGGA  120
i0_HQ_samplec9816d|c3248/f3p6/738       ------------------------------------------------------------  0
NM_000852.3                             -------------------------------------------------------TGGGA  5

i1_HQ_samplec9816d|c1892/f2p5/1103      AGGAGGAGGTGGTGACCGTGGAGACGTGGCAG----GAGGGCTCACTCAAAGCCTCCTGC  176
i0_HQ_samplec9816d|c3248/f3p6/738       ------------------------------------------------------------  0
NM_000852.3                             AAGAGGGAAAGGCTTCCCCGGCCAGCTGCGCGGCGACTCCGGGGACTCCAGGGCGC--CC  63

i1_HQ_samplec9816d|c1892/f2p5/1103      CTATACGGGCAGCTCCCCAAGTTCCAGGACGGA---GACCTCACCCTGTACCAGTCCAAT  233
i0_HQ_samplec9816d|c3248/f3p6/738       ------------------------------------------------------------  0
NM_000852.3                             CTCTGCGGCCGACGCCCGGGGTGCAGCGGCCGCCGGGGCTGGGGCCGGCGGGAGTCCGCG  123

i1_HQ_samplec9816d|c1892/f2p5/1103      ACCATCCTGCGTCACC-TGGGCCGCACCCTTGGTGAGTCTTGAACCTCCAAGTCCAGGGC  292
i0_HQ_samplec9816d|c3248/f3p6/738       ------------------------------------------------------------  0
NM_000852.3                             G-GACCCTCCAGAAGAGCGGCCGGCGCCGTGACTCAGCACTGGGGCGGAGCGGGGCGGGA  182

i1_HQ_samplec9816d|c1892/f2p5/1103      AGGCATGGGCAAGCCTCTGCCC-CCGGAGCCCTTTTGTTTAAATCAGCTGCCCCGCAGCC  351
i0_HQ_samplec9816d|c3248/f3p6/738       -----------------------------------gctGGAGTTTC-----GCCGCCGCA  20
NM_000852.3                             CCACCCTTATAAGGCTCGGAGGCCGCGAGGCCTTCGCTGGAGTTTC-----GCCGCCGCA  237
                                                                             *  *  *        **** **

i1_HQ_samplec9816d|c1892/f2p5/1103      CTCTGGAGTGGAGGAAACTGAGACCCACTGAGGTTACGTAGTTTGCCCAAGGTCAAGCCT  411
i0_HQ_samplec9816d|c3248/f3p6/738       GTCT-------TCGCCACCATGCCGCCCTACACCGTGGTCTATTTCC-CAGTTCGAGGCC  72
NM_000852.3                             GTCT-------TCGCCACCATGCCGCCCTACACCGTGGTCTATTTCC-CAGTTCGAGGCC  289
                                         ***         *  **   * * * **        **   ** **  ** ** ** *

i1_HQ_samplec9816d|c1892/f2p5/1103      GGGTGCCTGCAATCCTTGCCCTGTGCCAGGCTGC--CTCCCAGGTGTCAGGTGAGCTCTG  469
i0_HQ_samplec9816d|c3248/f3p6/738       GCTGCGCGGCCCTGCGCATGCTGCTGGCAGATCAGGGCCAGAGCTGGAAGGAGGAGGTGG  132
NM_000852.3                             GCTGCGCGGCCCTGCGCATGCTGCTGGCAGATCAGGGCCAGAGCTGGAAGGAGGAGGTGG  349
                                        *     * **  * *     ***      * *      *  ** **  *** *      *

i1_HQ_samplec9816d|c1892/f2p5/1103      AGCACCTGCTGTGTGGCAGTCTCTCATCCTTCCACGCACATCCTCTTCCCCTCCTCCCAG  529
i0_HQ_samplec9816d|c3248/f3p6/738       TGAC-----CGTGGAGACGTGGCAGGAGGGCTCA--------CTCAAAGCCTCCTGCCTA  179
NM_000852.3                             TGAC-----CGTGGAGACGTGGCAGGAGGGCTCA--------CTCAAAGCCTCCTGCCTA  396
                                         *        ***  *  **  *         **        ***    ****** **

i1_HQ_samplec9816d|c1892/f2p5/1103      GCTGGGGCTCACAGACAGCCCCCTGGTTGGCCCATCCCCAGTGACTGTGTGTTGATCAGG  589
i0_HQ_samplec9816d|c3248/f3p6/738       TACGGGCAGCTCCCCAAGTTCCAG---------------GACGGAGACCTCACCCTGTAC  224
NM_000852.3                             TACGGGCAGCTCCCCAAGTTCCAG---------------GACGGAGACCTCACCCTGTAC  441
                                           ***   * *    **  **                    *      *     *

i1_HQ_samplec9816d|c1892/f2p5/1103      CGCCCAGTCACGCGGCCTGCTCCCCTCCACCCAACCCCAGGGCTCTATGGAAGGACCAG  649
i0_HQ_samplec9816d|c3248/f3p6/738       CAGTCCAATACCATCCTGCGTCACCTGGGCCGCACCCTTGGGCTCTATGGAAGGACCAG  284
NM_000852.3                             CAGTCCAATACCATCCTGCGTCACCTGGGCCGCACCCTTGGGCTCTATGGAAGGACCAG  501
                                        *   *    **    *    ** ***   **  ****  *********************

i1_HQ_samplec9816d|c1892/f2p5/1103      CAGGAGGCAGCCCTGGTGGACATGGTGAATGACGGCGTGGAGGACCTCCGCTGCAAATAC  709
i0_HQ_samplec9816d|c3248/f3p6/738       CAGGAGGCAGCCCTGGTGGACATGGTGAATGACGGCGTGGAGGACCTCCGCTGCAAATAC  344
NM_000852.3                             CAGGAGGCAGCCCTGGTGGACATGGTGAATGACGGCGTGGAGGACCTCCGCTGCAAATAC  561
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i1_HQ_samplec9816d|c1892/f2p5/1103      ATCTCCCTCATCTACACCAACTATGAGGCGGGCAAGGATGACTATGTGAAGGCACTGCCC  769
i0_HQ_samplec9816d|c3248/f3p6/738       GTCTCCCTCATCTACACCAACTATGAGGCGGGCAAGGATGACTATGTGAAGGCACTGCCC  404
NM_000852.3                             ATCTCCCTCATCTACACCAACTATGAGGCGGGCAAGGATGACTATGTGAAGGCACTGCCC  621
                                         ***********************************************************

i1_HQ_samplec9816d|c1892/f2p5/1103      GGGCAACTGAAGCCTTTTGAGACCCTGCTGTCCCAGAACCAGGGAGGCAAGACCTTCATT  829
i0_HQ_samplec9816d|c3248/f3p6/738       GGGCAACTGAAGCCTTTTGAGACCCTGCTGTCCCAGAACCAGGGAGGCAAGACCTTCATT  464
NM_000852.3                             GGGCAACTGAAGCCTTTTGAGACCCTGCTGTCCCAGAACCAGGGAGGCAAGACCTTCATT  681
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i1_HQ_samplec9816d|c1892/f2p5/1103      GTGGGAGACCAGATCTCCTTCGCTGACTACAACCTGCTGGACTTGCTGCTGATCCATGAG  889
i0_HQ_samplec9816d|c3248/f3p6/738       GTGGGAGACCAGATCTCCTTCGCTGACTACAACCTGCTGGACTTGCTGCTGATCCATGAG  524
NM_000852.3                             GTGGGAGACCAGATCTCCTTCGCTGACTACAACCTGCTGGACTTGCTGCTGATCCATGAG  741
                                        ************************************************************

i1_HQ_samplec9816d|c1892/f2p5/1103      GTCCTAGCCCCTGGCTGCCTGGATGCGTTCCCCCTGCTCTCAGCATATGTGGGGCGCCTC  949
i0_HQ_samplec9816d|c3248/f3p6/738       GTCCTAGCCCCTGGCTGCCTGGATGCGTTCCCCCTGCTCTCAGCATATGTGGGGCGCCTC  584
NM_000852.3                             GTCCTAGCCCCTGGCTGCCTGGATGCGTTCCCCCTGCTCTCAGCATATGTGGGGCGCCTC  801
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i1_HQ_samplec9816d|c1892/f2p5/1103      AGTGCCCGGCCCAAGCTCAAGGCCTTCCTGGCCTCCCCTGAGTACGTGAACCTCCCCATC  1009
i0_HQ_samplec9816d|c3248/f3p6/738       AGTGCCCGGCCCAAGCTCAAGGCCTTCCTGGCCTCCCCTGAGTACGTGAACCTCCCCATC  644
NM_000852.3                             AGTGCCCGGCCCAAGCTCAAGGCCTTCCTGGCCTCCCCTGAGTACGTGAACCTCCCCATC  861
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i1_HQ_samplec9816d|c1892/f2p5/1103      AATGGCAACGGGAAACAGTGAGGGTTGGGGGGACTCTGAGCGGGAGGCAGAGTTTGCCTT  1069
i0_HQ_samplec9816d|c3248/f3p6/738       AATGGCAACGGGAAACAGTGAGGGTTGGGGGGACTCTGAGCGGGAGGCAGAGTTTGCCTT  704
NM_000852.3                             AATGGCAACGGGAAACAGTGAGGGTTGGGGGGACTCTGAGCGGGAGGCAGAGTTTGCCTT  921
                                        ************************************************************

i1_HQ_samplec9816d|c1892/f2p5/1103      Cctttctccaggaccaataaaatttctaagagag--------------------------  1103
i0_HQ_samplec9816d|c3248/f3p6/738       CCTTTCTCCAGGACCAATAAAATTTCTAAGAGAG--------------------------  738
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i1_HQ_samplec9816d|c1892/f2p5/1103      -----      1103
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VIRT85693        ------------------------------------------------------------    0


NP_000843.1      LTLYQSNTILRHLGRTLGLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYV    120
VIRT85086        ---------------------MDQQQVQQV------------------------------    9
VIRT85693        ---------------------MDQQQVQQV------------------------------    9
                                       ***:.  *

NP_000843.1      KALPGQLKPFETLLSQNQGGKTFIVGDQIS---------------------FADYNLLDL    159
VIRT85086        ------VVSEGDLVSHNEGLASLVLGQQGLKRLQLPGQCLHIVILARLIVGVDEGDVFAA    63
VIRT85693        ------VVSEGDLVSHNEGLASLVLGQQGLKRLQLPGQCLHIVILARLIVGVDEGDVFAA    63
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NP_000843.1      LLIH---EVLAPGCLDAFPLLSAYVGRLSARPKLKAFLAS----------PEYVNLPING    206
VIRT85086        EVLHAVIHHVHQGCLLLVLPIEPWGWVEGSRPR--DWAPDQHTVTGDGPTRGLSVSPSLG    121
VIRT85693        EVLHAVIHHVHQGCLLLVLPIEPKGAAQVTQD-------------GIGLVQGEVSVLEL-    109
                  ::*   . :  ***  .  :.       ::

NP_000843.1      NGKQ-----------------------------------     210
VIRT85086        GGEEDVRGRMRDCHTAGAQSSPDTWEAAWHRARIAGTQA     160
VIRT85693        -GELPV---------------------------------     114
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KRT14

Sequence	Header	AA Seq
Present	i1_HQ_samplec9816d|c41519/f7p0/1143	VIRT5673
	i0_HQ_samplec9816d|c8457/f2p5/954	VIRT6606
Absent	i1_HQ_samplec9816d|c11199/f3p18/1241	VIRT7678
NCBI	NM_000526	NP_000517.2

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>VIRT5673

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>i0_HQ_samplec9816d|c8457/f2p5/954
isoform=c8457;full_length_coverage=2;non_full_length_coverage=5;isoform_length=954

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CTTTTCTATTTTCACAGCCTCTCCTCCTCCCAGTTCTCCTCTGGATCGCAGTCATCCAGAGATGGTAAGACCCTCCTCCTCT
GCAGGCCTGGGCTCCAGGCCACCCTCTGTACCCCAAGCAGGTCTAGGCATTGGCTAGGGGCTCCGTGAGGGGCTGAGC
TCTAGTGCTGTCACCCAGTTTCCCTTGTGAACCTCCTTGGGTGGAAGAAGCTATTTTCTAAACCCTCCTTAGGGCTAGGA
GAGGCAGCCCCCACCTCTTGCTTCTACGTGGTGTCTGTGGCAGATCCTATTGCTGTTGTGGTCAGCACCATGAACAGGG
CCCTACAGGGCTCTTCCCACTGAGACCACTCCATTGGGTGAATATGGATGGAACCAGCCAGGTGTGAGCTCTTAGGAAG
CTCTAATCTGAGGGCAAAGACTCTGTCTCTGACCTTTGGGAGCCCTCGTCTGAAAGAAATGTGTTGATGGTATCAGTGC
TTGGGCAACAGCAGGGAGTGAAGCAGTAATCAGGGGAGAGGGCAATGGGGAGCCAGTTTGAGTTTCCTCACCTTCTT
GGCCTCCTTACTCCTGATTAGTCCATTGTCTGTCCACCTCTGGTAACGTCCTCTTCCCACCTCTTCCCCAGTGACCTCCTCC
AGCCGCCAAATCCGCACCAAGGTCATGGATGTGCACGATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCACC
AAGAACTGAGGCTGCCCAGCCCCGCTCAGGCCTAGGAGGCCCCCGTGTGGACACAGATCCCACTGGAAGATCCCCTCT
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>VIRT6606

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>i1_HQ_samplec9816d|c11199/f3p18/1241
isoform=c11199;full_length_coverage=3;non_full_length_coverage=18;isoform_length=1241
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CTTCTGGTGGGCAGTGAGAAGGTGACCATGCAGAACCTCAACGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGCT
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CTGCAGATTGACAATGCCCGTCTGGCCGCGGATGACTTCCGCACCAAGTATGAGACAGAGTTGAACCTGCGCATGAGT
GTGGAAGCCGACATCAATGGCCTGCGCAGGGTGCTGGACGAACTGACCCTGGCCAGAGCTGACCTGGAGATGCAGAT
TGAGAGCCTGAAGGAGGAGCTGGCCTACCTGAAGAAGAACCACGAGGAGGAGATGAATGCCCTGAGAGGCCAGGTG
GGTGGAGATGTCAATGTGGAGATGGACGCTGCACCTGGCGTGGACCTGAGCCGCATTCTGAACGAGATGCGTGACCA
GTATGAGAAGATGGCAGAGAAGAACCGCAAGGATGCCGAGGAATGGTTCTTCACCAAGACAGAGGAGCTGAACCGCG
AGGTGGCCACCAACAGCGAGCTGGTGCAGAGCGGCAAGAGCGAGATCTCGGAGCTCCGGCGCACCATGCAGAACCTG
GAGATTGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGAACAGCCTGGAGGAGACCAAAGGTCGCTACTGC
ATGCAGCTGGCCCAGATCCAGGAGATGATTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTCCGCTGCGAGATGGAGCA
GCAGAACCAGGAGTACAAGATCCTGCTGGACGTGAAGACGCGGCTGGAGCAGGAGATCGCCACCTACCGCCGCCTGC
TGGAGGGCGAGGACGCCCACCTCTCCTCCTCCCAGTTCTCCTCTGGATCGCAGTCATCCAGAGATGTGACCTCCTCCAGC
CGCCAAATCCGCACCAAGGTCATGGATGTGCACGATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCACCAAG
AACTGAGGCTGCCCAGCCCCGCTCAGGCCTAGGAGGCCCCCCGTGTGGACACAGATCCCACTGGAAGATCCCCTCTCCT
GCCCAAGCACTTCACAGCTGGACCCTGCTTCACCCTCACCCCCTCCTGGCAATCAATACagcttcattatctgagt
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>VIRT7678
MQNLNDRLASYLDKVRALEEANADLEVKIRDWYQRQRPAEIKDYSPYFKTIEDLRNKILT
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IESLKEELAYLKKNHEEEMNALRGQVGGDVNVEMDAAPGVDLSRILNEMRDQYEKMAEKN
RKDAEEWFFTKTEELNREVATNSELVQSGKSEISELRRTMQNLEIELQSQLSMKASLENS
LEETKGRYCMQLAQIQEMIGSVEEQLAQLRCEMEQQNQEYKILLDVKTRLEQEIATYRRL
LEGEDAHLSSSQFSSGSQSSRDVTSSSRQIRTKVMDVHDGKVVSTHEQVLRTKN
```

```
>NM_000526.4 Homo sapiens keratin 14 (KRT14), mRNA
ACCCGAGCACCTTCTCTTCACTCAGCCAACTGCTCGCTCGCTCACCTCCCTCCTCTGCACCATGACCACC
TGCAGCCGCCAGTTCACCTCCTCCAGCTCCATGAAGGGCTCCTGCGGCATCGGGGGCGGCATCGGGGGCG
GCTCCAGCCGCATCTCCTCCGTCCTGGCCGGAGGGTCCTGCCGCGCCCCCAGCACCTACGGGGGCGGCCT
GTCTGTCTCATCCTCCCGCTTCTCCTCTGGGGGAGCCTACGGGCTGGGGGGCGGCTATGGCGGTGGCTTC
AGCAGCAGCAGCAGCAGCTTTGGTAGTGGCTTTGGGGGAGGATATGGTGGTGGCCTTGGTGCTGGCTTGG
GTGGTGGCTTTGGTGGTGGCTTTGCTGGTGGTGATGGGCTTCTGGTGGGCAGTGAGAAGGTGACCATGCA
GAACCTCAATGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGCTCTGGAGGAGGCCAACGCCGACCTG
GAAGTGAAGATCCGTGACTGGTACCAGAGGCAGCGGCCTGCTGAGATCAAAGACTACAGTCCCTACTTCA
AGACCATTGAGGACCTGAGGAACAAGATTCTCACAGCCACAGTGGACAATGCCAATGTCCTTCTGCAGAT
TGACAATGCCCGTCTGGCCGCGGATGACTTCCGCACCAAGTATGAGACAGAGTTGAACCTGCGCATGAGT
GTGGAAGCCGACATCAATGGCCTGCGCAGGGTGCTGGACGAACTGACCCTGGCCAGAGCTGACCTGGAGA
TGCAGATTGAGAGCCTGAAGGAGGAGCTGGCCTACCTGAAGAAGAACCACGAGGAGGAGATGAATGCCCT
GAGAGGCCAGGTGGGTGGAGATGTCAATGTGGAGATGGACGCTGCACCTGGCGTGGACCTGAGCCGCATT
CTGAACGAGATGCGTGACCAGTATGAGAAGATGGCAGAGAAGAACCGCAAGGATGCCGAGGAATGGTTCT
TCACCAAGACAGAGGAGCTGAACCGCGAGGTGGCCACCAACAGCGAGCTGGTGCAGAGCGGCAAGAGCGA
GATCTCGGAGCTCCGGCGCACCATGCAGAACCTGGAGATTGAGCTGCAGTCCCAGCTCAGCATGAAAGCA
TCCCTGGAGAACAGCCTGGAGGAGACCAAAGGTCGCTACTGCATGCAGCTGGCCCAGATCCAGGAGATGA
TTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTCCGCTGCGAGATGGAGCAGCAGAACCAGGAGTACAAGAT
CCTGCTGGACGTGAAGACGCGGCTGGAGCAGGAGATCGCCACCTACCGCCGCCTGCTGGAGGGCGAGGAC
GCCCACCTCTCCTCCTCCCAGTTCTCCTCTGGATCGCAGTCATCCAGAGATGTGACCTCCTCCAGCCGCC
AAATCCGCACCAAGGTCATGGATGTGCACGATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCAC
CAAGAACTGAGGCTGCCCAGCCCCGCTCAGGCCTAGGAGGCCCCCCGTGTGGACACAGATCCCACTGGAA
GATCCCCTCTCCTGCCCAAGCACTTCACAGCTGGACCCTGCTTCACCCTCACCCCCTCCTGGCAATCAAT
ACAGCTTCATTATCTGAGTTGCATAAAAAAAAAAAAAAAAAAA
```

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>NP_000517.2 keratin, type I cytoskeletal 14 [Homo sapiens]
MTTCSRQFTSSSSMKGSCGIGGGIGGGSSRISSVLAGGSCRAPSTYGGGLSVSSSRFSSGGAYGLGGGYG
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ADLEVKIRDWYQRQRPAEIKDYSPYFKTIEDLRNKILTATVDNANVLLQIDNARLAADDFRTKYETELNL
RMSVEADINGLRRVLDELTLARADLEMQIESLKEELAYLKKNHEEEMNALRGQVGGDVNVEMDAAPGVDL
```

```
SRILNEMRDQYEKMAEKNRKDAEEWFFTKTEELNREVATNSELVQSGKSEISELRRTMQNLEIELQSQLS
MKASLENSLEETKGRYCMQLAQIQEMIGSVEEQLAQLRCEMEQQNQEYKILLDVKTRLEQEIATYRRLLE
GEDAHLSSSQFSSGSQSSRDVTSSSRQIRTKVMDVHDGKVVSTHEQVLRTKN
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i1_HQ_samplec9816d|c11199/f3p18/1241      ------------------------------------------------------------          0
NM_000526.4                               ACCCGAGCACCTTCTCTTCACTCAGCCAACTGCTCGCTCGCTCACCTCCCTCCTCTGCAC          60
i1_HQ_samplec9816d|c41519/f7p0/1143       ------------------------------------------------------------          0
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      ------------------------------------------------------------          0
NM_000526.4                               CATGACCACCTGCAGCCGCCAGTTCACCTCCTCCAGCTCCATGAAGGGCTCCTGCGGCAT          12
i1_HQ_samplec9816d|c41519/f7p0/1143       ------------------------------------------------------------          0
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      ------------------------------------------------------------          0
NM_000526.4                               CGGGGGCGGCATCGGGGGCGGCTCCAGCCGCATCTCCTCCGTCCTGGCCGGAGGGTCCTG          18
i1_HQ_samplec9816d|c41519/f7p0/1143       ------------------------------------------------------------          0
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      ------------------------------------------------------------          0
NM_000526.4                               CCGCGCCCCCAGCACCTACGGGGGCGGCCTGTCTGTCTCATCCTCCCGCTTCTCCTCTGG          24
i1_HQ_samplec9816d|c41519/f7p0/1143       ------------------------------------------------------------          0
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      ------------------------------------------------------------          0
NM_000526.4                               GGGAGCCTACGGGCTGGGGGGCGGCTATGGCGGTGGCTTCAGCAGCAGCAGCAGCAGCTT          30
i1_HQ_samplec9816d|c41519/f7p0/1143       ------------------------------------------------------------          0
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      ------------------------------------------------------------          0
NM_000526.4                               TGGTAGTGGCTTTGGGGGAGGATATGGTGGTGGCCTTGGTGCTGGCTTGGGTGGTGGCTT          36
i1_HQ_samplec9816d|c41519/f7p0/1143       ------------------------------------------------------------          0
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      ----------------------------CTTCTGGTGGGCAGTGAGAAGGTGACCATGCA          32
NM_000526.4                               TGGTGGTGGCTTTGCTGGTGGTGATGGGCTTCTGGTGGGCAGTGAGAAGGTGACCATGCA          42
i1_HQ_samplec9816d|c41519/f7p0/1143       --------AGACCAAAGGTCGCTACTGCATGCAGCT------------GGCCCAGATCCA          40
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      GAACCTCAACGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGCTCTGGAGGAGGCCAA          92
NM_000526.4                               GAACCTCAATGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGCTCTGGAGGAGGCCAA          48
i1_HQ_samplec9816d|c41519/f7p0/1143       GGAGATGATTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTCCGCTGCGAGATGGAGCAGCA          10
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      CGCCGACCTGGAAGTGAAGATCCGTGACTGGTACCAGAGGCAGCGGCCTGCTGAGATCAA          15
NM_000526.4                               CGCCGACCTGGAAGTGAAGATCCGTGACTGGTACCAGAGGCAGCGGCCTGCTGAGATCAA          54
i1_HQ_samplec9816d|c41519/f7p0/1143       ---GAACCAGGAGTACAAGATCCTGCTGGACGTGAAGACGCGGCTGGAGCAGGAGATCGC          15
i0_HQ_samplec9816d|c8457/f2p5/954         ------------------------------------------------------------          0

i1_HQ_samplec9816d|c11199/f3p18/1241      AGACTACAGTCCCTACTTCAAGACCATTGAGGACCTGAGGAACAAGATTCTCACAGCCAC          21
NM_000526.4                               AGACTACAGTCCCTACTTCAAGACCATTGAGGACCTGAGGAACAAGATTCTCACAGCCAC          60
i1_HQ_samplec9816d|c41519/f7p0/1143       CACCTACCGCCGCCTGCTGGAGGGCGAGGACGCCC-------------------------          19
i0_HQ_samplec9816d|c8457/f2p5/954         -----------------------------atgccc-------------------------          6
                                                                       * * **

i1_HQ_samplec9816d|c11199/f3p18/1241      AGTGGACAATGCCAATGTCCTTCTG-CAGATTGACAATGCCCGTCTGGCCGCGGATGACT          27
NM_000526.4                               AGTGGACAATGCCAATGTCCTTCTG-CAGATTGACAATGCCCGTCTGGCCGCGGATGACT          65
i1_HQ_samplec9816d|c41519/f7p0/1143       AGTGAGTCTTGGCCCTCCCCTTAGTCCGCGCCCCCCATGGCAC----------TCTCACG          24
i0_HQ_samplec9816d|c8457/f2p5/954         aaTGAGTCTTGGCCCTCCCCTTAGTCCG-CCCCCCCATGGCAC----------TCTCACG          55
                                          * **     ** *  *  ****    *       * *** *              * **

i1_HQ_samplec9816d|c11199/f3p18/1241      TCCGCACCAAGTATGAGACAGAGTTGAACCTGCGCATGAGTGTGGAAGCCGACATCAATG          33
NM_000526.4                               TCCGCACCAAGTATGAGACAGAGTTGAACCTGCGCATGAGTGTGGAAGCCGACATCAATG          71
i1_HQ_samplec9816d|c41519/f7p0/1143       GCCCCACCATGTATCTAATG------ATCCTGTCCTTTTCTATTTTCACAGCC-----TC          29
i0_HQ_samplec9816d|c8457/f2p5/954         GCCCCACCATGTATCTAATG------ATCCTGC-CTTTTCTATTTTCACAGCC-----TC          10
                                           ** ***** ****   *        * ****  * *   * *     * * *     *

i1_HQ_samplec9816d|c11199/f3p18/1241      GCCTGCGCAGGGTGCTGGACGAACTGACCCTGGCCAGAGCTGACCTGGAGATGCAGATTG          39
NM_000526.4                               GCCTGCGCAGGGTGCTGGACGAACTGACCCTGGCCAGAGCTGACCTGGAGATGCAGATTG          77
i1_HQ_samplec9816d|c41519/f7p0/1143       TCCTCCTCCCAGTTCTCCT----------CTGGATCGCAGTCATCCAGAGATGGTAAGAC          34
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```
i0_HQ_samplec9816d|c8457/f2p5/954         TCCTCCTCCCAGTTCTCCT----------CTGGATCGCAGTCATCCAGAGATGGTAAGAC          15
                                           *** * *   ** **             ****   *   * * *  ******   *

i1_HQ_samplec9816d|c11199/f3p18/1241      AGAGCCTGAAGGAGGAGCTGGCCTAC----CTGAAGAAGAACCACGAGGAGGAGAT-GAA          44
NM_000526.4                               AGAGCCTGAAGGAGGAGCTGGCCTAC----CTGAAGAAGAACCACGAGGAGGAGAT-GAA          83
i1_HQ_samplec9816d|c41519/f7p0/1143       CCTCCTCCTCTGCAGGCCTGGGCTCCAGGCCACCCTCTGTACCCCAAGCAGGTCTAGGCA          40
i0_HQ_samplec9816d|c8457/f2p5/954         CCTCCTCCTCTGCAGGCCTGGGCTCCAGGCCACCCTCTGTACCCCAAGCAGGTCTAGGCA          21
                                              *      *  *  **** ** *    *       * *** * ** ***     * *

i1_HQ_samplec9816d|c11199/f3p18/1241      TGCCCTGAGAGGCCAGGTGGGTGGAGATGTCAATGTGGAGATGGACGCTGCACCTGGCGT          50
NM_000526.4                               TGCCCTGAGAGGCCAGGTGGGTGGAGATGTCAATGTGGAGATGGACGCTGCACCTGGCGT          89
i1_HQ_samplec9816d|c41519/f7p0/1143       TTGGCTA-GGGGCTCCGTGAGGGGCTGAGCTCTAGTGCTGTCACC--CAGTTTCCCTTGT          45
i0_HQ_samplec9816d|c8457/f2p5/954         TTGGCTA-GGGGCTCCGTGAGGGGCTGAGCTCTAGTGCTGTCACC--CAGTTTCCCTTGT          27
                                          *   **  * ***   *** * **    *     ***  *       * *   *    **

i1_HQ_samplec9816d|c11199/f3p18/1241      GGACCTGAGCCGCATTCTGAACGAGATGCGTGACCAGTATGAGAAGATGGCAGAGAAGAA          56
NM_000526.4                               GGACCTGAGCCGCATTCTGAACGAGATGCGTGACCAGTATGAGAAGATGGCAGAGAAGAA          95
i1_HQ_samplec9816d|c41519/f7p0/1143       GAACCTCCTTGGGTGGAAGAAGCTATTTTCTAAACCCTCCTTAGGGCTAGGAGAGGCAGC          51
i0_HQ_samplec9816d|c8457/f2p5/954         GAACCTCCTTGGGTGGAAGAAGCTATTTTCTAAACCCTCCTTAGGGCTAGGAGAGGCAGC          33
                                          * ****     *      ***     *   * * *  *       * * * ****

i1_HQ_samplec9816d|c11199/f3p18/1241      CCGCAA-GGATGCCGAGGAATGGTTCTTCACCAAGACAGAGGAGCTGAACCGCGAGGTGG          62
NM_000526.4                               CCGCAA-GGATGCCGAGGAATGGTTCTTCACCAAGACAGAGGAGCTGAACCGCGAGGTGG          10
i1_HQ_samplec9816d|c41519/f7p0/1143       CCCCACCTCTTGCTTCTACGTGGTGTCT----GTGGCAGATCCTATTGCTGTTGTGGTCA          57
i0_HQ_samplec9816d|c8457/f2p5/954         CCCCACCTCTTGCTTCTACGTGGTGTCT----GTGGCAGATCCTATTGCTGTTGTGGTCA          38
                                          ** **     ***       ****   *      * ****     *       * ***

i1_HQ_samplec9816d|c11199/f3p18/1241      CCACCAACAGCGAGCTGGTGCAGAGCGGCAAGAGCGAGATCTCGGAGCTCCGGCGCACCA          68
NM_000526.4                               CCACCAACAGCGAGCTGGTGCAGAGCGGCAAGAGCGAGATCTCGGAGCTCCGGCGCACCA          10
i1_HQ_samplec9816d|c41519/f7p0/1143       GCACCATGAACAGGGCCCTACA-------------GGGCTCTTCCCACTGA---GACCAC          61
i0_HQ_samplec9816d|c8457/f2p5/954         GCACCATGAACAGGGCCCTACA-------------GGGCTCTTCCCACTGA---GACCAC          43
                                           *****  * *  *    * **             * * ***     **     *  *

i1_HQ_samplec9816d|c11199/f3p18/1241      TGCAGAACCTGGAGATTGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGAACA          74
NM_000526.4                               TGCAGAACCTGGAGATTGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGAACA          11
i1_HQ_samplec9816d|c41519/f7p0/1143       TCCATTGGGTGAATATGGATGG----AACCAGCCAGGTGTGAGC-----TCTTAGGAAGC          66
i0_HQ_samplec9816d|c8457/f2p5/954         TCCATTGGGTGAATATGGATGG----AACCAGCCAGGTGTGAGC-----TCTTAGGAAGC          48
                                          * **     ** * ** **         *****   *  ***        **   ***

i1_HQ_samplec9816d|c11199/f3p18/1241      GCCTGGAGGAGACCAAAG---GTCGCTACTGCATGCAGCTGGC-CCAGATCCAGGAGATG          80
NM_000526.4                               GCCTGGAGGAGACCAAAG---GTCGCTACTGCATGCAGCTGGC-CCAGATCCAGGAGATG          11
i1_HQ_samplec9816d|c41519/f7p0/1143       TCTAATCTGAGGGCAAAGACTCTGTCTCTGACCTTTGGGAGCCCTCGTCTGAAAGAAATG          72
i0_HQ_samplec9816d|c8457/f2p5/954         TCTAATCTGAGGGCAAAGACTCTGTCTCTGACCTTTGGGAGCCCTCGTCTGAAAGAAATG          54
                                           *      ***  *****    *  **    * *   *  * *  *   *  * ** ***

i1_HQ_samplec9816d|c11199/f3p18/1241      ATTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTCCGCTGCGAGATGGAGCAGCAGAACCAG          86
NM_000526.4                               ATTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTCCGCTGCGAGATGGAGCAGCAGAACCAG          12
i1_HQ_samplec9816d|c41519/f7p0/1143       TGT----T---------------------GATGGTATCAGTGCTTGGGCAACAGCAGGGA          76
i0_HQ_samplec9816d|c8457/f2p5/954         TGT----T---------------------GATGGTATCAGTGCTTGGGCAACAGCAGGGA          57
                                            *                          * *    *  * * * * *** *** *

i1_HQ_samplec9816d|c11199/f3p18/1241      GAGTACAAGATCCTGCTGGACGTGAAGACGCGGCTGGAGCAGGAGATCGCCACCTACCGC          92
NM_000526.4                               GAGTACAAGATCCTGCTGGACGTGAAGACGCGGCTGGAGCAGGAGATCGCCACCTACCGC          13
i1_HQ_samplec9816d|c41519/f7p0/1143       GTGAAGCAGTAATCAGGGGAGAGGGCAATGGGGAGCCAGTTTGAGTTTCCTCACCTTCTT          82
i0_HQ_samplec9816d|c8457/f2p5/954         GTGAAGCAGTAATCAGGGGAGAGGGCAATGGGGAGCCAGTTTGAGTTTCCTCACCTTCTT          63
                                          * * *  **        ***   *   * * **    **   *** *  *   *   *

i1_HQ_samplec9816d|c11199/f3p18/1241      CGCCTGCTGGAGGGCGAGGACGCCCACCTCTCCTCCTCCCAGTTCTCCTCTGGATCGCAG          98
NM_000526.4                               CGCCTGCTGGAGGGCGAGGACGCCCACCTCTCCTCCTCCCAGTTCTCCTCTGGATCGCAG          13
i1_HQ_samplec9816d|c41519/f7p0/1143       GGCCTCCTTACTCCTGATTAGTCCATT--GTCTGTCCACCTCTGGTAACGTCCTCTTCCC          88
i0_HQ_samplec9816d|c8457/f2p5/954         GGCCTCCTTACTCCTGATTAGTCCATT--GTCTGTCCACCTCTGGTAACGTCCTCTTCCC          69
                                           **** **       **  *  **      **   *  **  *  *    *      *

i1_HQ_samplec9816d|c11199/f3p18/1241      TCATCCAGAGATGTGACCTCCTCCAGCCGCCAAATCCGCACCAAGGTCATGGATGTGCAC          10
NM_000526.4                               TCATCCAGAGATGTGACCTCCTCCAGCCGCCAAATCCGCACCAAGGTCATGGATGTGCAC          14
i1_HQ_samplec9816d|c41519/f7p0/1143       ACCTCTTCCCCAGTGACCTCCTCCAGCCGCCAAATCCGCACCAAGGTCATGGATGTGCAC          94
i0_HQ_samplec9816d|c8457/f2p5/954         ACCTCTTCCCCAGTGACCTCCTCCAGCCGCCAAATCCGCACCAAGGTCATGGATGTGCAC          75
                                           * **       ************************************************

i1_HQ_samplec9816d|c11199/f3p18/1241      GATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCACCAAGAACTGAGGCTGCCCA          11
NM_000526.4                               GATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCACCAAGAACTGAGGCTGCCCA          14
i1_HQ_samplec9816d|c41519/f7p0/1143       GATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCACCAAGAACTGAGGCTGCCCA          10
i0_HQ_samplec9816d|c8457/f2p5/954         GATGGCAAGGTGGTGTCCACCCACGAGCAGGTCCTTCGCACCAAGAACTGAGGCTGCCCA          81
                                          ************************************************************

i1_HQ_samplec9816d|c11199/f3p18/1241      GCCCCGCTCAGGCCTAGGAGGCCCCCCGTGTGGACACAGATCCCACTGGAAGATCCCCTC          11
NM_000526.4                               GCCCCGCTCAGGCCTAGGAGGCCCCCCGTGTGGACACAGATCCCACTGGAAGATCCCCTC          15
i1_HQ_samplec9816d|c41519/f7p0/1143       GCCCCGCTCAGGCCTAGGAGGCCCCCCGTGTGGACACAGATCCCACTGGAAGATCCCCTC          10
i0_HQ_samplec9816d|c8457/f2p5/954         GCCCCGCTCAGGCCTAGGAGGC-CCCCGTGTGGACACAGATCCCACTGGAAGATCCCCTC          87
                                          ********************** *************************************

i1_HQ_samplec9816d|c11199/f3p18/1241      TCCTGCCCAAGCACTTCACAGCTGGACCCTGCTTCACCCTCACCCCCTCCTGGCAATCAA          12
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```
NM_000526.4                                 TCCTGCCCAAGCACTTCACAGCTGGACCCTGCTTCACCCTCACCCCCTCCTGGCAATCAA            16
i1_HQ_samplec9816d|c41519/f7p0/1143         TCCTGCCCAAGCACTTCACAGCTGGACCCTGCTTCACCCTCACCCCCTCCTGGCAAtcaa            11
i0_HQ_samplec9816d|c8457/f2p5/954           TCCTGCCCAAGCACTTCACAGCTGGACCCTGCTTCACCCTCACCCCCTCCTggcaatcaa            93
                                            ************************************************************

i1_HQ_samplec9816d|c11199/f3p18/1241        TACagcttcattatctgagt------------------------      1241
NM_000526.4                                 TACAGCTTCATTATCTGAGTTGCATAAAAAAAAAAAAAAAAAAA      1653
i1_HQ_samplec9816d|c41519/f7p0/1143         tacagcttcattatctgagtt-----------------------      1143
i0_HQ_samplec9816d|c8457/f2p5/954           tacagcttcattatctgagtt-----------------------      954
                                            ********************
```

```
VIRT6606            ------------------------------------------------------------    0
VIRT5673            ------------------------------------------------------------    0
VIRT7678            ------------------------------------------------------------    0
NP_000517.2         MTTCSRQFTSSSSMKGSCGIGGGIGGGSSRISSVLAGGSCRAPSTYGGGLSVSSSRFSSG    60

VIRT6606            ------------------------------------------------------------    0
VIRT5673            ------------------------------------------------------------    0
VIRT7678            ----------------------------------------------------------MQ    2
NP_000517.2         GAYGLGGGYGGGFSSSSSSFGSGFGGGYGGGLGAGLGGGFGGGFAGGDGLLVGSEKVTMQ    120

VIRT6606            ------------------------------------------------------------    0
VIRT5673            ------------------------------------------------------------    0
VIRT7678            NLNDRLASYLDKVRALEEANADLEVKIRDWYQRQRPAEIKDYSPYFKTIEDLRNKILTAT    62
NP_000517.2         NLNDRLASYLDKVRALEEANADLEVKIRDWYQRQRPAEIKDYSPYFKTIEDLRNKILTAT    180

VIRT6606            ----------------------------------------------MCTMA---------    5
VIRT5673            -----------MALSRPHHVSNDPVLFYFHSLSSSQFSSGSQS-----------------    32
VIRT7678            VDNANVLLQIDNARLAADDFRTKYETELNLRMSVEADINGLRRVLDELTLARADLEMQIE    122
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VIRT6606            ------------------------------------------------------------    5
VIRT5673            ------------------------------------------------------------    32
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VIRT6606            --RWCPPTSRSFAPRTEAAQPRSGLGGPRVDT----------------------------    35
VIRT5673            --SRDGKTLLLCRPGLQATLCTPSRSRH--------------------------------    58
VIRT7678            DAEEWFFTKTEELNREVATNSELVQSGKSEISELRRTMQNLEIELQSQLSMKASLENSLE    242
NP_000517.2         DAEEWFFTKTEELNREVATNSELVQSGKSEISELRRTMQNLEIELQSQLSMKASLENSLE    360
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VIRT6606            --------DPTGRSPLLPKHFTAGPCFTLTPSWQSIQLHYLS----------   69
VIRT5673            WLGAP-----------------------------------------------   63
VIRT7678            GEDAHLSSSQFSSGSQSSRDVTSSSRQIRTKVMDVHDGKVVSTHEQVLRTKN   354
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KRT16

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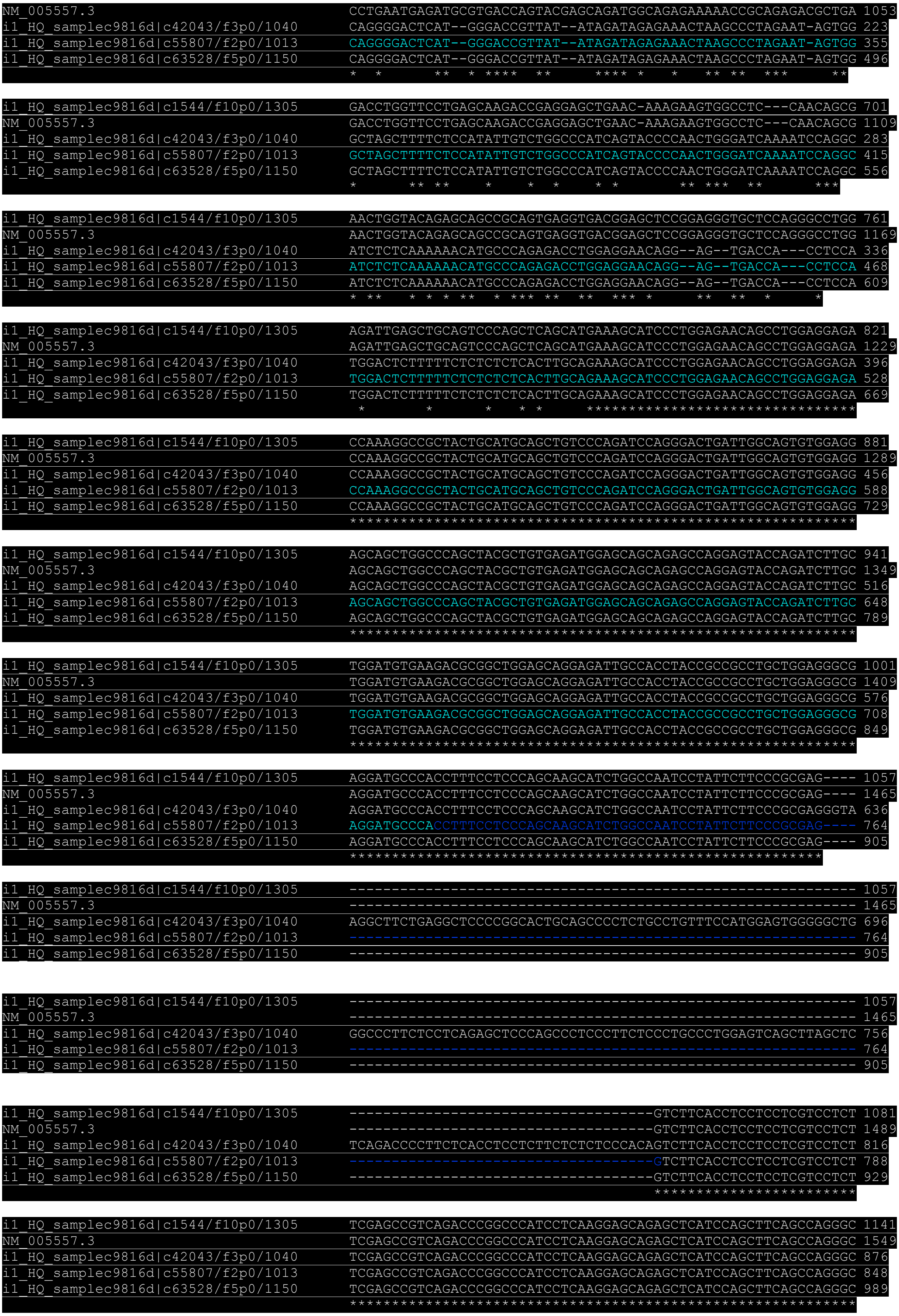

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NM_005557.3                              GACCTGGTTCCTGAGCAAGACCGAGGAGCTGAAC-AAAGAAGTGGCCTC---CAACAGCG 1109
i1_HQ_samplec9816d|c42043/f3p0/1040      GCTAGCTTTTCTCCATATTGTCTGGCCCATCAGTACCCCAACTGGGATCAAAATCCAGGC 283
i1_HQ_samplec9816d|c55807/f2p0/1013      GCTAGCTTTTCTCCATATTGTCTGGCCCATCAGTACCCCAACTGGGATCAAAATCCAGGC 415
i1_HQ_samplec9816d|c63528/f5p0/1150      GCTAGCTTTTCTCCATATTGTCTGGCCCATCAGTACCCCAACTGGGATCAAAATCCAGGC 556
                                         *      ** **    *    *  *    * *       ** ***  **      ***

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NM_005557.3                              AACTGGTACAGAGCAGCCGCAGTGAGGTGACGGAGCTCCGGAGGGTGCTCCAGGGCCTGG 1169
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i1_HQ_samplec9816d|c55807/f2p0/1013      ATCTCTCAAAAAACATGCCCAGAGACCTGGAGGAACAGG--AG--TGACCA---CCTCCA 468
i1_HQ_samplec9816d|c63528/f5p0/1150      ATCTCTCAAAAAACATGCCCAGAGACCTGGAGGAACAGG--AG--TGACCA---CCTCCA 609
                                         * **   * * * **  * *** **  **  *** *     **  **  *     *

i1_HQ_samplec9816d|c1544/f10p0/1305      AGATTGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGAACAGCCTGGAGGAGA 821
NM_005557.3                              AGATTGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGAACAGCCTGGAGGAGA 1229
i1_HQ_samplec9816d|c42043/f3p0/1040      TGGACTCTTTTTCTCTCTCTCACTTGCAGAAAGCATCCCTGGAGAACAGCCTGGAGGAGA 396
i1_HQ_samplec9816d|c55807/f2p0/1013      TGGACTCTTTTTCTCTCTCTCACTTGCAGAAAGCATCCCTGGAGAACAGCCTGGAGGAGA 528
i1_HQ_samplec9816d|c63528/f5p0/1150      TGGACTCTTTTTCTCTCTCTCACTTGCAGAAAGCATCCCTGGAGAACAGCCTGGAGGAGA 669
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i1_HQ_samplec9816d|c1544/f10p0/1305      CCAAAGGCCGCTACTGCATGCAGCTGTCCCAGATCCAGGGACTGATTGGCAGTGTGGAGG 881
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i1_HQ_samplec9816d|c42043/f3p0/1040      CCAAAGGCCGCTACTGCATGCAGCTGTCCCAGATCCAGGGACTGATTGGCAGTGTGGAGG 456
i1_HQ_samplec9816d|c55807/f2p0/1013      CCAAAGGCCGCTACTGCATGCAGCTGTCCCAGATCCAGGGACTGATTGGCAGTGTGGAGG 588
i1_HQ_samplec9816d|c63528/f5p0/1150      CCAAAGGCCGCTACTGCATGCAGCTGTCCCAGATCCAGGGACTGATTGGCAGTGTGGAGG 729
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i1_HQ_samplec9816d|c1544/f10p0/1305      AGCAGCTGGCCCAGCTACGCTGTGAGATGGAGCAGCAGAGCCAGGAGTACCAGATCTTGC 941
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i1_HQ_samplec9816d|c42043/f3p0/1040      AGCAGCTGGCCCAGCTACGCTGTGAGATGGAGCAGCAGAGCCAGGAGTACCAGATCTTGC 516
i1_HQ_samplec9816d|c55807/f2p0/1013      AGCAGCTGGCCCAGCTACGCTGTGAGATGGAGCAGCAGAGCCAGGAGTACCAGATCTTGC 648
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NM_005557.3                              TGGATGTGAAGACGCGGCTGGAGCAGGAGATTGCCACCTACCGCCGCCTGCTGGAGGGCG 1409
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i1_HQ_samplec9816d|c55807/f2p0/1013      TGGATGTGAAGACGCGGCTGGAGCAGGAGATTGCCACCTACCGCCGCCTGCTGGAGGGCG 708
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NM_005557.3                              AGGATGCCCACCTTTCCTCCCAGCAAGCATCTGGCCAATCCTATTCTTCCCGCGAG---- 1465
i1_HQ_samplec9816d|c42043/f3p0/1040      AGGATGCCCACCTTTCCTCCCAGCAAGCATCTGGCCAATCCTATTCTTCCCGCGAGGGTA 636
i1_HQ_samplec9816d|c55807/f2p0/1013      AGGATGCCCACCTTTCCTCCCAGCAAGCATCTGGCCAATCCTATTCTTCCCGCGAG---- 764
i1_HQ_samplec9816d|c63528/f5p0/1150      AGGATGCCCACCTTTCCTCCCAGCAAGCATCTGGCCAATCCTATTCTTCCCGCGAG---- 905
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i1_HQ_samplec9816d|c1544/f10p0/1305      ------------------------------------------------------------ 1057
NM_005557.3                              ------------------------------------------------------------ 1465
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i1_HQ_samplec9816d|c55807/f2p0/1013      ------------------------------------------------------------ 764
i1_HQ_samplec9816d|c63528/f5p0/1150      ------------------------------------------------------------ 905


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NM_005557.3                              ------------------------------------------------------------ 1465
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i1_HQ_samplec9816d|c55807/f2p0/1013      ------------------------------------------------------------ 764
i1_HQ_samplec9816d|c63528/f5p0/1150      ------------------------------------------------------------ 905


i1_HQ_samplec9816d|c1544/f10p0/1305      ------------------------------------GTCTTCACCTCCTCCTCGTCCTCT 1081
NM_005557.3                              ------------------------------------GTCTTCACCTCCTCCTCGTCCTCT 1489
i1_HQ_samplec9816d|c42043/f3p0/1040      TCAGACCCCTTCTCACCTCCTCTTCTCTCTCCCACAGTCTTCACCTCCTCCTCGTCCTCT 816
i1_HQ_samplec9816d|c55807/f2p0/1013      ------------------------------------GTCTTCACCTCCTCCTCGTCCTCT 788
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NM_005557.3                              TCGAGCCGTCAGACCCGGCCCATCCTCAAGGAGCAGAGCTCATCCAGCTTCAGCCAGGGC 1549
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i1_HQ_samplec9816d|c55807/f2p0/1013      TCGAGCCGTCAGACCCGGCCCATCCTCAAGGAGCAGAGCTCATCCAGCTTCAGCCAGGGC 848
i1_HQ_samplec9816d|c63528/f5p0/1150      TCGAGCCGTCAGACCCGGCCCATCCTCAAGGAGCAGAGCTCATCCAGCTTCAGCCAGGGC 989
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i1_HQ_samplec9816d|c55807/f2p0/1013      CAGAGCTCCTAGAACTGAGCTGCCTCTACCACAGCCTCCTGCCCACCAGCTGGCCTCACC 908
i1_HQ_samplec9816d|c63528/f5p0/1150      CAGAGCTCCTAGAACTGAGCTGCCTCTACCACAGCCTCCTGCCCACCAGCTGGCCTCACC 1049
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i1_HQ_samplec9816d|c1544/f10p0/1305      TCCTGAAGGCCCGGGTCAGGACCCTGCTCTCCTGGCGCAGTTCCCAGCTATCTCCCCTGC 1261
NM_005557.3                              TCCTGAAGGCCCGGGTCAGGACCCTGCTCTCCTGGCGCAGTTCCCAGCTATCTCCCCTGC 1669
i1_HQ_samplec9816d|c42043/f3p0/1040      TCCTGAAGGCCCGGGTCAGGACCCTGCTCTCCTGGCGCAGTTCCCAGCTATCTCCCCTGC 996
i1_HQ_samplec9816d|c55807/f2p0/1013      TCCTGAAGGCCCGGGTCAGGACCCTGCTCTCCTGGCGCAGTTCCCAGCTATCTCCCCTGC 968
i1_HQ_samplec9816d|c63528/f5p0/1150      TCCTGAAGGCCGGGTCAGGAC-CCTGCTCTCCAG-CGCAGTTCCCA-GCTGTCTCCCTGC 1106
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VIRT39978        --------ASEAPRHCSPSACFHGVGAGPFSSELPALPSPCP-GVSLALRPLLTSSSLSH     152
VIRT34198        ------------------------------------------------------------     0
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VIRT41599        IEGLKEELAYLRKNHEEEMLALRGQTGGDVNVEMDAAPGVDLSRILNEMRDQYEQMAEKN     62
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VIRT39978        SLHLLLVLFEPSDPAHPQGAELIQLQ--------------PGPEL------LELSCLYHS     192
VIRT34198        -------------------------------------------MDSFSLSHLQKASLENS     17
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VIRT41599        RRDAETWFLSKTEELNKEVASNSELVQSSRSEVTELRRVLQGLEIELQSQLSMKASLENS     122
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VIRT34198        LEETKGRYCMQLSQIQGLIGSVEEQLAQLRCEMEQQSQEYQILLDVKTRLEQEIATYRRL     77
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VIRT41599        LEETKGRYCMQLSQIQGLIGSVEEQLAQLRCEMEQQSQEYQILLDVKTRLEQEIATYRRL     182
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VIRT39978        ------------ADFLVD------------------------------------------ 235
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VIRT41599        LEGEDAHLSSQQASGQSYSSREVFTSSSSSSSRQTRPILKEQSSSSFSQGQSS 235
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KRT17

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GGAGATAGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGGGCAACCTGGCGGAGACAGAGAAC
CGCTACTGCGTGCAGCTGTCCCAGATCCAGGGGCTGATTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTTC
GCTGCGAGATGGAGCAGCAGAACCAGGAATACAAAATCCTGCTGGATGTGAAGACGCGGCTGGAGCAGGA
GATTGCCACCTACCGCCGCCTGCTGGAGGGAGAGGATGCCCACCTGACTCAGTACAAGAAAGAACCGGTG
ACCACCCGTCAGGTGCGTACCATTGTGGAAGAGGTCCAGGATGGCAAGGTCATCTCCTCCCGCGAGCAGG
TCCACCAGACCACCCGCTGAGGACTCAGCTACCCCGGCCGGCCACCCAGGAGGCAGGGAGGCAGCCGCCC
CATCTGCCCCACAGTCTCCGGCCTCTCCAGCCTCAGCCCCCTGCTTCAGTCCCTTCCCCATGCTTCCTTG
CCTGATGACAATAAAGCTTGTTGACTCAGCTATG
```

```
>NP_000413.1 keratin, type I cytoskeletal 17 [Homo sapiens]
MTTSIRQFTSSSSIKGSSGLGGGSSRTSCRLSGGLGAGSCRLGSAGGLGSTLGGSSYSSCYSFGSGGGYG
SSFGGVDGLLAGGEKATMQNLNDRLASYLDKVRALEEANTELEVKIRDWYQRQAPGPARDYSQYYRTIEE
LQNKILTATVDNANILLQIDNARLAADDFRTKFETEQALRLSVEADINGLRRVLDELTLARADLEMQIEN
LKEELAYLKKNHEEEMNALRGQVGGEINVEMDAAPGVDLSRILNEMRDQYEKMAEKNRKDAEDWFFSKTE
ELNREVATNSELVQSGKSEISELRRTMQALEIELQSQLSMKASLEGNLAETENRYCVQLSQIQGLIGSVE
EQLAQLRCEMEQQNQEYKILLDVKTRLEQEIATYRRLLEGEDAHLTQYKKEPVTTRQVRTIVEEVQDGKV
ISSREQVHQTTR
```

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i1_HQ_samplec9816d|c24577/f2p18/1511      ------------------------------------------------------------    0
NM_000422.2                               ---------ATCGCTACGCCCACTTGGTGGCCTATAAAGGAAGCGGGCGAACCCCGGCAG    51
i1_HQ_samplec9816d|c41456/f18p0/1500      aagaaccgcaaggatgccgaggattggttcttcagcaagacagaggaactgaaccgcgag    60
i1_HQ_samplec9816d|c64385/f12p0/1166      ------------------------------------------------------------    0

i1_HQ_samplec9816d|c24577/f2p18/1511      --ctaca-caacttggggcccctctcctctccagcccttctcctgtgtgcCTGCCTGC--    55
NM_000422.2                               CCCTACA-CAACTTGGGGCCCCTCTCCTCTCCAGCCCTTCTCCTGTGTGCCTGCCTCCTG    110
i1_HQ_samplec9816d|c41456/f18p0/1500      gtgGCCACCAACAGTGAGCTGGTG-------CAGAGTGGCAAGAGTGAGATCTCGGAGCT    113
i1_HQ_samplec9816d|c64385/f12p0/1166      ------------------------------------------------------------    0

i1_HQ_samplec9816d|c24577/f2p18/1511      -CGCCGCCACCATGACCACCTCCATCCGCCAGTTCACCTCCTCCAGCTCCATCAAGGGCT    114
NM_000422.2                               CCGCCGCCACCATGACCACCTCCATCCGCCAGTTCACCTCCTCCAGCTCCATCAAGGGCT    170
i1_HQ_samplec9816d|c41456/f18p0/1500      -CCGGCGCACCATGCAGGCCTTGGAGATAGAGCTGCAGTCCCAGCTCAGCATGAAAGCAT    172
i1_HQ_samplec9816d|c64385/f12p0/1166      ------------------------------------------------------------    0

i1_HQ_samplec9816d|c24577/f2p18/1511      CCTCC------GGCCTGGGGGGCGGCTCGTCCCGCACCTCCTGCCGGCTGTCTGGCGGCC    168
NM_000422.2                               CCTCC------GGCCTGGGGGGCGGCTCGTCCCGCACCTCCTGCCGGCTGTCTGGCGGCC    224
i1_HQ_samplec9816d|c41456/f18p0/1500      CCCTGGAGGGCAACCTGGCGGAGACAGAGAACCGCTACTGCGTGCAGCTGTCCCAGATCC    232
i1_HQ_samplec9816d|c64385/f12p0/1166      ------------------------------------------------------------    0

i1_HQ_samplec9816d|c24577/f2p18/1511      TGGGTGCCGGCT-------------CCTGCAGGCTGGGATCTGCTGGCGGCCTGGGCAGC    215
NM_000422.2                               TGGGTGCCGGCT-------------CCTGCAGGCTGGGATCTGCTGGCGGCCTGGGCAGC    271
i1_HQ_samplec9816d|c41456/f18p0/1500      AGGGGCTGATTGGCAGCGTGGAGGAGCAGCTGGCCCAGCTTCGCTGCGAGATGGAGCAGC    292
i1_HQ_samplec9816d|c64385/f12p0/1166      ------------------------------------------------------------    0

i1_HQ_samplec9816d|c24577/f2p18/1511      ACCCTCGGGGGTAGCAGCTACTCCAGCTGCTACAGCTTTGGCTCTGGTGGTGGCTATGGC    275
NM_000422.2                               ACCCTCGGGGGTAGCAGCTACTCCAGCTGCTACAGCTTTGGCTCTGGTGGTGGCTATGGC    331
i1_HQ_samplec9816d|c41456/f18p0/1500      AGAACCAGGAATACAAAATCCTGCTGGATGTGAAGACGCGGCTGGAGCAGGAGATTGCCA    352
i1_HQ_samplec9816d|c64385/f12p0/1166      -------------------------------------------gggctctcagacccaca    17
                                                                                              *

i1_HQ_samplec9816d|c24577/f2p18/1511      AGCAGCTTTGGGGGTGTTGATGGGCTGCTGGCTGGAGGTGAGAAGGCCACCATGCAGAAC    335
NM_000422.2                               AGCAGCTTTGGGGGTGTTGATGGGCTGCTGGCTGGAGGTGAGAAGGCCACCATGCAGAAC    391
i1_HQ_samplec9816d|c41456/f18p0/1500      CCTACCGCCGCCTGCTGGAGGGAGAGGATGCC---CACCTGACTCAGTACAAGAAAGAAC    409
i1_HQ_samplec9816d|c64385/f12p0/1166      tctaatttcctctctgtttttttttttctttc---agcctgactcagtacAAGAAAGAAC    74
                                             *                        *  *                ** *   *****

i1_HQ_samplec9816d|c24577/f2p18/1511      CTCAATGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGCCCTGGAGGAGGCCAACACT    395
NM_000422.2                               CTCAATGACCGCCTGGCCTCCTACCTGGACAAGGTGCGTGCCCTGGAGGAGGCCAACACT    451
i1_HQ_samplec9816d|c41456/f18p0/1500      GTAAGTATCTGCGTGGCTTCGGCCCTGGGGGTTGG-------------------------    444
i1_HQ_samplec9816d|c64385/f12p0/1166      GTAAGTATCTGCGTGGCTTCGGCCCTGGGGGTTGG-------------------------    109
                                           * * *  * ** **** **   *****     *

i1_HQ_samplec9816d|c24577/f2p18/1511      GAGCTGGAGGTGAAGATCCGTGACTGGTACCAGAGGCAGGCCCCGGGGCCCGCCCGTGAC    455
NM_000422.2                               GAGCTGGAGGTGAAGATCCGTGACTGGTACCAGAGGCAGGCCCCGGGGCCCGCCCGTGAC    511
i1_HQ_samplec9816d|c41456/f18p0/1500      --------------------------GTGCATGGGACAGGCAGCC-CACCTGCACGTTGC    477
i1_HQ_samplec9816d|c64385/f12p0/1166      --------------------------GTGCATGGGACAGGCAGCC-CACCTGCCACGTGC    142
                                                                    ** *  * * *****  *    ** **      *

i1_HQ_samplec9816d|c24577/f2p18/1511      TACAGCCAGTACTACAGGACAATTGAGGAGCTGCAGAACAAGATCCTC-ACAGCCACCGT    514
```

```
NM_000422.2                               TACAGCCAGTACTACAGGACAATTGAGGAGCTGCAGAACAAGATCCTC-ACAGCCACCGT    570
i1_HQ_samplec9816d|c41456/f18p0/1500      TGGGGCAGGGTCC----------CCAGGAGCTCCAGGAGTTGATGGCTGTCCCTCAGCAG    527
i1_HQ_samplec9816d|c64385/f12p0/1166      TG-GGCAGGGTCC----------CCAGGAGCTCCAGGAGTTGATGGCTGTCCCTCAGCAG    191
                                          *   **  *  *             ******* *** *   ***      *   ** *

i1_HQ_samplec9816d|c24577/f2p18/1511      G-GACAATGCCAACATCCTGCTACAGATTGACAATGCCCGTCTGGCTGC-TG-----ATG    567
NM_000422.2                               G-GACAATGCCAACATCCTGCTACAGATTGACAATGCCCGTCTGGCTGC-TG-----ATG    623
i1_HQ_samplec9816d|c41456/f18p0/1500      GGAGAAGTGACTCATTAGCACTGAGGATTGATACTCAGGAAAAGAGCAAATGAGAGAGAC    587
i1_HQ_samplec9816d|c64385/f12p0/1166      GGAGAAGTGACTCATTAGCACTGAGGATTGATACTCAGGAAAAGATCAAATGAGAGAGAC    251
                                          *    * ** *    *    **   ****** * *        *      **

i1_HQ_samplec9816d|c24577/f2p18/1511      ACTTCCGCACCAAGTTTGAGACAGAGCAGGCCCTGCGCCTGAGTGTGGAGGCCGACATCA    627
NM_000422.2                               ACTTCCGCACCAAGTTTGAGACAGAGCAGGCCCTGCGCCTGAGTGTGGAGGCCGACATCA    683
i1_HQ_samplec9816d|c41456/f18p0/1500      ACTGTCTGGTCTGATGGGGGTGGGGCAGGGAACTGGTCCTTACCTTGGAGATCCTAGTCT    647
i1_HQ_samplec9816d|c64385/f12p0/1166      ACTGTCTGGTCTGATGGGGGTGGGGCAGGGAACTGGTCCTTACCTTGGAGATCCTAGTCT    311
                                          ***  *    *   *  * *   *    **  ***  *** *   *****  *    **

i1_HQ_samplec9816d|c24577/f2p18/1511      ATGGCCTGCGCAGGGTGCTGGATGAGCTGACCCTGGCCAGAGCCGACCTGGAGATGCAGA    687
NM_000422.2                               ATGGCCTGCGCAGGGTGCTGGATGAGCTGACCCTGGCCAGAGCCGACCTGGAGATGCAGA    743
i1_HQ_samplec9816d|c41456/f18p0/1500      GATGGAGGAGACAGGTCCCAGCTCTGGAGATTGTCATCTGA-----------TGGGAAGA    696
i1_HQ_samplec9816d|c64385/f12p0/1166      GATGGAGGAGACAGGTCCCAGCTCTGGAGATTGTCATCTGA-----------TGGGAAGA    360
                                             *   * *   *** *  * *  *  **   *   * **              * ***

i1_HQ_samplec9816d|c24577/f2p18/1511      TTGAGAACCTCAAGGAGGAGCTGGCCTACCTGAAGAAGAACCACGAGGAGGAGATGAACG    747
NM_000422.2                               TTGAGAACCTCAAGGAGGAGCTGGCCTACCTGAAGAAGAACCACGAGGAGGAGATGAACG    803
i1_HQ_samplec9816d|c41456/f18p0/1500      TAGGAACATGGTCTCATGATCTTTGCTCTTGACAGCTTTTGGATGAGCAAAAACAGTCCT    756
i1_HQ_samplec9816d|c64385/f12p0/1166      TAGGAACATGGTCTCATGATCTTTGCTCTTGACAGCTTTTGGATGAGCAAAAACAGTCCT    420
                                          * *  *         * ** **   **      **       * *** *  *   *  *

i1_HQ_samplec9816d|c24577/f2p18/1511      CCCTGCGAGGCCAGGTGGGTGGTGAGATCAATGTGGAGATGGACGCTGCCCCAGGCGTGG    807
NM_000422.2                               CCCTGCGAGGCCAGGTGGGTGGTGAGATCAATGTGGAGATGGACGCTGCCCCAGGCGTGG    863
i1_HQ_samplec9816d|c41456/f18p0/1500      GTCTCTGGGGTCTGTAGCCTGATGGGAG--ATAGGGACATGGTCCTTGTCCTCCAAATTC    814
i1_HQ_samplec9816d|c64385/f12p0/1166      GTCTCTGGGGTCTGTAGCCTGATGGGAG--ATAGGGACATGGTCCTTGTCCTCCAAATTC    478
                                            **  * ** * *  *  ** ** **   **  *** **** *  ** **      *

i1_HQ_samplec9816d|c24577/f2p18/1511      ACCTGAGCCGCATCCTCAACGAGATGCGTGACCAGTATGAGAAGATGGCAGAGAAGAACC    867
NM_000422.2                               ACCTGAGCCGCATCCTCAACGAGATGCGTGACCAGTATGAGAAGATGGCAGAGAAGAACC    923
i1_HQ_samplec9816d|c41456/f18p0/1500      CAATCTGATGG-------AGAATATATGATCCTAGCCTTAGGG---TTCCTAGTCTAAT-    863
i1_HQ_samplec9816d|c64385/f12p0/1166      CAATCTGATGG-------AGAATATATGATCCTAGCCTTAGGG---TTCCTAGTCTAAT-    527
                                             *  *  *        *  * **  *   * **  * **       *  **   **

i1_HQ_samplec9816d|c24577/f2p18/1511      GCAAGGATGCCGAGGATTGGTTCTTCAGCAAGACAGAG-GAACTGAACCGCGAGGTGGCC    926
NM_000422.2                               GCAAGGATGCCGAGGATTGGTTCTTCAGCAAGACAGAG-GAACTGAACCGCGAGGTGGCC    982
i1_HQ_samplec9816d|c41456/f18p0/1500      -GGAGGAGATAGGGGCCTGGTTTTTGTCTTGGCGATCCCAGTCTGATGGGGGAGATGGTA    922
i1_HQ_samplec9816d|c64385/f12p0/1166      -GGAGGAGATAGGGGCCTGGTTTTTGTCTTGGCGATCCCAGTCTGATGGGGGAGATGGTA    586
                                             ****    * **  ***** **      *  *       ****   * *** ***

i1_HQ_samplec9816d|c24577/f2p18/1511      ACCAACAGTGAGCTGGTGCAGAGTGGCAAGAGTGAGATCTCGGAGCTCCGGCGCACCATG    986
NM_000422.2                               ACCAACAGTGAGCTGGTGCAGAGTGGCAAGAGTGAGATCTCGGAGCTCCGGCGCACCATG    1042
i1_HQ_samplec9816d|c41456/f18p0/1500      GA--AAATCTATGTCCTAGAGACTGCAGAGAAATGGAGA-CGGATTTCATGG--AGTCTA    977
i1_HQ_samplec9816d|c64385/f12p0/1166      GA--AAATCTATGTCCTAGAGACTGCAGAGAAATGGAGA-CGGATTTCATGG--AGTCTA    641
                                              * *   *  *  *  *** **   ***    **   ****  **  *   *   *

i1_HQ_samplec9816d|c24577/f2p18/1511      CAGGCCTTGGAGATAGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGGGCAAC    1046
NM_000422.2                               CAGGCCTTGGAGATAGAGCTGCAGTCCCAGCTCAGCATGAAAGCATCCCTGGAGGGCAAC    1102
i1_HQ_samplec9816d|c41456/f18p0/1500      CATGGCTCCTCCCTGG-CAGGACACACTGGATCAGAATCAAATAACCCATCTGGGGAGGC    1036
i1_HQ_samplec9816d|c64385/f12p0/1166      CATGGCTCCTCCCTGG-CAGGACACACTGGATCAGAATCAAATAACCCATCTGGGGAGGC    700
                                          ** * **      * *    *     *  * **** ** ***  * ** *   ***   *

i1_HQ_samplec9816d|c24577/f2p18/1511      CTGGCGGAGACAGAGAACCGCTACTGCGTGCAGCTGTCCCAGATCCAGGGGCTG-ATTGG    1105
NM_000422.2                               CTGGCGGAGACAGAGAACCGCTACTGCGTGCAGCTGTCCCAGATCCAGGGGCTG-ATTGG    1161
i1_HQ_samplec9816d|c41456/f18p0/1500      AAGACTCACACAGGGC--------CACCGGCAGAGGGATGGGATGGAAGGGAGGTGGTGG    1088
i1_HQ_samplec9816d|c64385/f12p0/1166      AAGACTCACACAGGGC--------CACCGGCAGAGGGATGGGATGGAAGGGAGGTGGTGG    752
                                            * *  * **** *           *  ****  *     ***  * ***  *   ***

i1_HQ_samplec9816d|c24577/f2p18/1511      CAGCGTGGAGGAGCAGCTGGCCCAGCTTCGCTG--CGAGATGGAGCAGC----AGAACCA    1159
NM_000422.2                               CAGCGTGGAGGAGCAGCTGGCCCAGCTTCGCTG--CGAGATGGAGCAGC----AGAACCA    1215
i1_HQ_samplec9816d|c41456/f18p0/1500      CAGGG-------ACAGGAGGGATGTGTGTGCAGTGTGATGTCGAGGTGCCAGTGGAGGCA    1141
i1_HQ_samplec9816d|c64385/f12p0/1166      CAGGG-------ACAGGAGGGATGTGTGTGCAGTGTGATGTCGAGGTGCCAGTGGAGGCA    805
                                          *** *        ***  **      *  ** *   **  * ***  **     **  **

i1_HQ_samplec9816d|c24577/f2p18/1511      GGAATACAAAATCCTGCTGGATGTGA---AGACGCGGCTGGAGC-----AGGAGATTGCC    1211
NM_000422.2                               GGAATACAAAATCCTGCTGGATGTGA---AGACGCGGCTGGAGC-----AGGAGATTGCC    1267
i1_HQ_samplec9816d|c41456/f18p0/1500      CTCACAGCACCTGGGGGAGGATGAGGGAGAGAGCCGGCTCCTGTCCATGAGGGCTAGGGG    1201
i1_HQ_samplec9816d|c64385/f12p0/1166      CTCACAGCACCTGGGGGAGGATGAGGGAGAGAGCCGGCTCCTGTCCATGAGGGCTAGGGG    865
                                             * *  *  *   *  ***** *    ***  *****   *      ***     *

i1_HQ_samplec9816d|c24577/f2p18/1511      ACCTACCGCCGCCTGCTGGAGGGAGAGGATGCCCACCTGACTCAGTACAAGAAAGAACCG    1271
NM_000422.2                               ACCTACCGCCGCCTGCTGGAGGGAGAGGATGCCCACCTGACTCAGTACAAGAAAGAACCG    1327
i1_HQ_samplec9816d|c41456/f18p0/1500      GCAAGCGAGGGCCTCCTGGCCC---CTACCCACTTTAAATTGCCTGCTTCTCCTGCAGCG    1258
i1_HQ_samplec9816d|c64385/f12p0/1166      GCAAGCGAGGGCCTCCTGGCCC---CTACCCACTTTAAATTGCCTGCTTCTCCTGCAGCG    922
                                           *   *    **** ****             *         *           * * **

i1_HQ_samplec9816d|c24577/f2p18/1511      GTGACCACCCGTCAGGTGCGTACCATTGTGGAAGAGGTCCAGGATGGCAAGGTCATCTCC    1331
NM_000422.2                               GTGACCACCCGTCAGGTGCGTACCATTGTGGAAGAGGTCCAGGATGGCAAGGTCATCTCC    1387
i1_HQ_samplec9816d|c41456/f18p0/1500      GTGACCACCCGTCAGGTGCGTACCATTGTGGAAGAGGTCCAGGATGGCAAGGTCATCTCC    1318
i1_HQ_samplec9816d|c64385/f12p0/1166      GTGACCACCCGTCAGGTGCGTACCATTGTGGAAGAGGTCCAGGATGGCAAGGTCATCTCC    982
                                          ************************************************************

i1_HQ_samplec9816d|c24577/f2p18/1511      TCCCGCGAGCAGGTCCACCAGACCACCCGCTGAGGACTCAGCTACCCCGGCCGGCCACCC    1391
NM_000422.2                               TCCCGCGAGCAGGTCCACCAGACCACCCGCTGAGGACTCAGCTACCCCGGCCGGCCACCC    1447
i1_HQ_samplec9816d|c41456/f18p0/1500      TCCCGCGAGCAGGTCCACCAGACCACCCGCTGAGGACTCAGCTACCCCGGCCGGCCACCC    1378
i1_HQ_samplec9816d|c64385/f12p0/1166      TCCCGCGAGCAGGTCCACCAGACCACCCGCTGAGGACTCAGCTACCCCGGCCGGCCACCC    1042
                                          ************************************************************
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i1_HQ_samplec9816d|c24577/f2p18/1511      AGGAGGCAGGGAGGCAGCCGCCCCATCTGCCCCACAGTCTCCGGCCTCTCCAGCCTCAGC    1451
NM_000422.2                               AGGAGGCAGGGAGGCAGCCGCCCCATCTGCCCCACAGTCTCCGGCCTCTCCAGCCTCAGC    1507
i1_HQ_samplec9816d|c41456/f18p0/1500      AGGAGGCAGGGAGGCAGCCGCCCCATCTGCCCCACAGTCTCCGGCCTCTCCAGCCTCAGC    1438
i1_HQ_samplec9816d|c64385/f12p0/1166      AGGAGGCAGGGAGGCAGCCGCCCCATCTGCCCCACAGTCTCCGGCCTCTCCAGCCTCAGC    1102
                                          ************************************************************

i1 HQ samplec9816d|c24577/f2p18/1511      CCCCTGCTTCAGTCCCTTCCCCATGCTTCCTTGCCTGATgacaataaagcttgt--tgac    1509
NM_000422.2                               CCCCTGCTTCAGTCCCTTCCCCATGCTTCCTTGCCTGATGACAATAAAGCTTGT--TGAC    1565
i1_HQ_samplec9816d|c41456/f18p0/1500      CCCCTGCTTCAGTCCCTTCCCCATGCTTCCTTGCCTGATGACAATAaagc--ttgttgac    1496
i1_HQ_samplec9816d|c64385/f12p0/1166      CCCCTGCTTCAGTCCCTTCCCCATGCTTCCTTGCCTGATGGACAATTAAAGCTTGTTGac    1162
                                          ****************************************   *   *     *  ****

i1_HQ_samplec9816d|c24577/f2p18/1511      tc-------        1511
NM_000422.2                               TCAGCTATG        1574
i1_HQ_samplec9816d|c41456/f18p0/1500      tcag-----        1500
i1_HQ_samplec9816d|c64385/f12p0/1166      tcag-----        1166
                                          **
```

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VIRT65337        ------------------------------------MAPPWQ-DTLDQNQITHLGRQDSHR     24
NP_000413.1      MTTSIRQFTSSSSIKGSSGLGGGSSRTSCRLSGGLGAGSCRLGSAGGLGSTLGGSSYSSC     60
VIRT63810        ------------------------------------------------------------     0
VIRT66411        MTTSIRQFTSSSSIKGSSGLGGGSSRTSCRLSGGLGAGSCRLGSAGGLGSTLGGSSYSSC     60

VIRT65337        ---ATGRGMGWKGGGG--RDRRDV------------------------------------     43
NP_000413.1      YSFGSGGGYGSSFGGVDGLLAGGEKATMQNLNDRLASYLDKVRALEEANTELEVKIRDWY     120
VIRT63810        ------------------------------------------------------------     0
VIRT66411        YSFGSGGGYGSSFGGVDGLLAGGEKATMQNLNDRLASYLDKVRALEEANTELEVKIRDWY     120

VIRT65337        ------------------------------------------------------------     43
NP_000413.1      QRQAPGPARDYSQYYRTIEELQNKILTATVDNANILLQIDNARLAADDFRTKFETEQALR     180
VIRT63810        ------------------------------------------------------------     0
VIRT66411        QRQAPGPARDYSQYYRTIEELQNKILTATVDNANILLQIDNARLAADDFRTKFETEQALR     180

VIRT65337        ------------------------------------------------------------     43
NP_000413.1      LSVEADINGLRRVLDELTLARADLEMQIENLKEELAYLKKNHEEEMNALRGQVGGEINVE     240
VIRT63810        ------------------------------------------------------------     0
VIRT66411        LSVEADINGLRRVLDELTLARADLEMQIENLKEELAYLKKNHEEEMNALRGQVGGEINVE     240

VIRT65337        ------------------------------------------------------------     43
NP_000413.1      MDAAPGVDLSRILNEMRDQYEKMAEKNRKDAEDWFFSKTEELNREVATNSELVQSGKSEI     300
VIRT63810        ------------------------------------------------------------     0
VIRT66411        MDAAPGVDLSRILNEMRDQYEKMAEKNRKDAEDWFFSKTEELNREVATNSELVQSGKSEI     300

VIRT65337        ------------------------------------------------------------     43
NP_000413.1      SELRRTMQALEIELQSQLSMKASLEGNLAETENRYCVQLSQIQGLIGSVEEQLAQLRCEM     360
VIRT63810        ------MQALEIELQSQLSMKASLEGNLAETENRYCVQLSQIQGLIGSVEEQLAQLRCEM     54
VIRT66411        SELRRTMQALEIELQSQLSMKASLEGNLAETENRYCVQLSQIQGLIGSVEEQLAQLRCEM     360

VIRT65337        ------------------------------------------------------------     43
NP_000413.1      EQQNQEYKILLDVKTRLEQEIATYRRLLEGEDAHLTQYKKEPVTTRQVRTIVEEVQDGKV     420
VIRT63810        EQQNQEYKILLDVKTRLEQEIATYRRLLEGEDAHLTQYKKERKYLRGFGPGGWVHGTGSP     114
VIRT66411        EQQNQEYKILLDVKTRLEQEIATYRRLLEGEDAHLTQYKKEPVTTRQVRTIVEEVQDGKV     420

VIRT65337        ---CAV--------    46
NP_000413.1      ISSREQVHQTTR--    432
VIRT63810        PARCWGRVPRSSRS    128
VIRT66411        ISSREQVHQTTR--    432
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SPAG7

Sequence	**Header**	**AA Seq**
Present	i1_HQ_samplec9816d|c12681/f2p0/1109	
Absent	i0_HQ_samplec9816d|c625/f16p11/997	
NCBI	NM_004890	

>i1_HQ_samplec9816d|c12681/f2p0/1109
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GCATACTACATGATGTGGTGGAAGTGGCTGGCCTGACATCCTTCTCCTTTGGGGAAGATGATGACTGTCGCTATGTCAT
GATCTTCAAAAAGGAGTTTGCACCCTCAGATGAAGAGCTAGACTCTTACCGTCGTGGAGAGGAATGGGACCCCCAGAA
GGCTGAGGAGAAGCGGAAGCTGAAGGAGCTGGCCCAGAGGCAAGAGGAGGAGGCAGCCCAGCAGGGGCCTGTGGT
GGTGAGCCCTGCCAGCGACTACAAGGACAAGTACAGCCACCTCATCGGCAAGGGAGCAGCCAAAGACGCAGCCCACA
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GTGGCAGGAGGGCAGTGGAGGCTGAGGTACGGATTTCTAGGCCCGCCTACCCTCCTCTCTGCCCCTAGTGCCCGTGGC
CAATAAGAGGGACACACGCTCCATTGAAGAGGCTATGAATGAGATCAGAGCCAAGAAGCGTCTGCGGCAGAGTGGGG
AAGAGTTGCCGCCAACCTCCTAGGCGCCCCGCCCAGCTCCCTTTGACCCCTGGGGCAGGGCAGGGGGCAGGGAGAGA
CAAGGCTGCTGCTATTAGAGCCCATCCTGGAGCCCCACCTCTGAACCACCTCCTACCAGCTGTCCCTCAGGCTGGGGGA
AAACAGGTGTTTGATTTGTCACCGTTGGAGCTTGGATATGTGCGTGGCATGTGTGTGTGTGTGTGAGAGTGTGAATGC
ACAGGTGGGTATTTAATCTGTATTATTCCCCGTTCTTGGAATTTTCTTCCCCATGGGGctggggtactttacattcaataaatactgt
tt
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>VIRT83091
MADLLGSILSSMEKPPSLGDQETRRKAREQAARLKKLQEQEKQQKVEFRKRMEKEVSDFI
QDSGQIKKKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYVMIFKKEFAPSDEELDS
YRRGEEWDPQKAEEKRKLKELAQRQEEEAAQQGPVVVSPASDYKDKYSHLIGKGAAKDAA
HMLQANKTYGCGEATVRLGVAGRGA
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AGATCGAGAGGAGCATACTACATGATGTGGTGGAAGTGGCTGGCCTGACATCCTTCTCCTTTGGGGAAGATGATGACT
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GGACCCCCAGAAGGCTGAGGAGAAGCGGAAGCTGAAGGAGCTGGCCCAGAGGCAAGAGGAGGAGGCAGCCCAGCA
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ACGCAGCCCACATGCTACAGGCCAATAAGACCTACGGCTGTGTGCCCGTGGCCAATAAGAGGGACACACGCTCCATTG
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>VIRT85203
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YRRGEEWDPQKAEEKRKLKELAQRQEEEAAQQGPVVVSPASDYKDKYSHLIGKGAAKDAA
HMLQANKTYGCVPVANKRDTRSIEEAMNEIRAKKRLRQSGEELPPTS
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AGAAGCCACCCAGCCTCGGTGACCAGGAGACTCGGCGCAAGGCCCGAGAACAGGCCGCCCGCCTGAAGAA
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CAGAAGGCTGAGGAGAAGCGGAAGCTGAAGGAGCTGGCCCAGAGGCAAGAGGAGGAGGCAGCCCAGCAGG
GGCCTGTGGTGGTGAGCCCTGCCAGCGACTACAAGGACAAGTACAGCCACCTCATCGGCAAGGGAGCAGC
CAAAGACGCAGCCCACATGCTACAGGCCAATAAGACCTACGGCTGTGTGCCCGTGGCCAATAAGAGGGAC
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```

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TGCCGCCAACCTCCTAGGCGCCCCGCCCAGCTCCCTTTGACCCCTGGGGCAGGGCAGGGGGCAGGGAGAG
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GGCTGGGGGAAAACAGGTGTTTGATTTGTCACCGTTGGAGCTTGGATATGTGCGTGGCATGTGTGTGTGT
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>NP_004881.2 sperm-associated antigen 7 [Homo sapiens]
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LAQRQEEEAAQQGPVVVSPASDYKDKYSHLIGKGAAKDAAHMLQANKTYGCVPVANKRDTRSIEEAMNEI
RAKKRLRQSGEELPPTS
i1_HQ_samplec9816d|c12681/f2p0/1109     ------------------------actcccaagatggcggacctactgggctccatcctg     36
i0_HQ_samplec9816d|c625/f16p11/997      ------------------------ACTCCCAAGATGGCGGACCTACTGGGCTCCATCCTG     36
NM_004890.2                             AAGACGCACCGCCCCCTCTCAGTCACTCCCAAGATGGCGGACCTACTGGGCTCCATCCTG     60
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i1_HQ_samplec9816d|c12681/f2p0/1109     agctccatggagaagccacccagcCTCGGTGACCAGGAGACTCGGCGCAAGGCCCGAGAA     96
i0_HQ_samplec9816d|c625/f16p11/997      AGCTCCATGGAGAAGCCACCCAGCCTCGGTGACCAGGAGACTCGGCGCAAGGCCCGAGAA     96
NM_004890.2                             AGCTCCATGGAGAAGCCACCCAGCCTCGGTGACCAGGAGACTCGGCGCAAGGCCCGAGAA     120
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i1_HQ_samplec9816d|c12681/f2p0/1109     CAGGCCGCCCGCCTGAAGAAACTACAAGAGCAAGAGAAACAACAGAAAGTGGAGTTTCGT     156
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NM_004890.2                             CAGGCCGCCCGCCTGAAGAAACTACAAGAGCAAGAGAAACAACAGAAAGTGGAGTTTCGT     180
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i1_HQ_samplec9816d|c12681/f2p0/1109     AAAAGGATGGAGAAGGAGGTGTCAGATTTCATTCAAGACAGTGGGCAGATCAAGAAAAAG     216
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i1_HQ_samplec9816d|c12681/f2p0/1109     TTTCAGCCAATGAACAAGATCGAGAGGAGCATACTACATGATGTGGTGGAAGTGGCTGGC     276
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i1_HQ_samplec9816d|c12681/f2p0/1109     CTGACATCCTTCTCCTTTGGGGAAGATGATGACTGTCGCTATGTCATGATCTTCAAAAAG     336
i0_HQ_samplec9816d|c625/f16p11/997      CTGACATCCTTCTCCTTTGGGGAAGATGATGACTGTCGCTATGTCATGATCTTCAAAAAG     336
NM_004890.2                             CTGACATCCTTCTCCTTTGGGGAAGATGATGACTGTCGCTATGTCATGATCTTCAAAAAG     360
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NM_004890.2                             GAGTTTGCACCCTCAGATGAAGAGCTAGACTCTTACCGTCGTGGAGAGGAATGGGACCCC     420
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i1_HQ_samplec9816d|c12681/f2p0/1109     CAGAAGGCTGAGGAGAAGCGGAAGCTGAAGGAGCTGGCCCAGAGGCAAGAGGAGGAGGCA     456
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i1_HQ_samplec9816d|c12681/f2p0/1109     GCCCAGCAGGGGCCTGTGGTGGTGAGCCCTGCCAGCGACTACAAGGACAAGTACAGCCAC     516
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NM_004890.2                             GGCTGT------------------------------------------------------     606
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NM_004890.2                             ------------------------------------------------------------     606


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i0_HQ_samplec9816d|c625/f16p11/997      -GTGCCCGTGGCCAATAAGAGGGACACACGCTCCATTGAAGAGGCTATGAATGAGATCAG     641
NM_004890.2                             -GTGCCCGTGGCCAATAAGAGGGACACACGCTCCATTGAAGAGGCTATGAATGAGATCAG     665
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i1_HQ_samplec9816d|c12681/f2p0/1109     AGCCAAGAAGCGTCTGCGGCAGAGTGGGGAAGAGTTGCCGCCAACCTCCTAGGCGCCCCG     816
i0_HQ_samplec9816d|c625/f16p11/997      AGCCAAGAAGCGTCTGCGGCAGAGTGGGGAAGAGTTGCCGCCAACCTCCTAGGCGCCCCG     701
NM_004890.2                             AGCCAAGAAGCGTCTGCGGCAGAGTGGGGAAGAGTTGCCGCCAACCTCCTAGGCGCCCCG     725
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i1_HQ_samplec9816d|c12681/f2p0/1109     CCCAGCTCCCTTTGACCCCTGGGGCAGGGCAGGGGGCAGGGAGAGACAAGGCTGCTGCTA     876
i0_HQ_samplec9816d|c625/f16p11/997      CCCAGCTCCCTTTGACCCCTGGGGCAGGGCAGGGGGCAGGGAGAGACAAGGCTGCTGCTA     761
NM_004890.2                             CCCAGCTCCCTTTGACCCCTGGGGCAGGGCAGGGGGCAGGGAGAGACAAGGCTGCTGCTA     785
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i1_HQ_samplec9816d|c12681/f2p0/1109     TTAGAGCCCATCCTGGAGCCCCACCTCTGAACCACCTCCTACCAGCTGTCCCTCAGGCTG     936
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i1_HQ_samplec9816d|c12681/f2p0/1109     GGGGAAAACAGGTGTTTGATTTGTCACCGTTGGAGCTTGGATATGTGCGTGGCATGTGTG     996
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NP_004881.2      MADLLGSILSSMEKPPSLGDQETRRKAREQAARLKKLQEQEKQQKVEFRKRMEKEVSDFI      60
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VIRT83091        QDSGQIKKKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYVMIFKKEFAPSDEELDS      120
VIRT85203        QDSGQIKKKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYVMIFKKEFAPSDEELDS      120
NP_004881.2      QDSGQIKKKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYVMIFKKEFAPSDEELDS      120
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VIRT83091        YRRGEEWDPQKAEEKRKLKELAQRQEEEAAQQGPVVVSPASDYKDKYSHLIGKGAAKDAA      180
VIRT85203        YRRGEEWDPQKAEEKRKLKELAQRQEEEAAQQGPVVVSPASDYKDKYSHLIGKGAAKDAA      180
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VIRT83091        HMLQANKTYGCGEATVRLGVAGRGA----------------------      205
VIRT85203        HMLQANKTYGCVPVANKRDTRSIEEAMNEIRAKKRLRQSGEELPPTS      227
NP_004881.2      HMLQANKTYGCVPVANKRDTRSIEEAMNEIRAKKRLRQSGEELPPTS      227
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RPS11

Sequence	Header	AA Seq
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Absent	i0_HQ_samplec9816d|c92306/f20p24/550	
NCBI	NM_001015	

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GGGACCTGACCTATGATCGGCCCCCGCTCCTAGGCGTGGTGACCAAGATGAAGATGCAGAGGACCATTGTCATCCGCC
GAGACTATCTGCACTACATCCGCAAGTACAACCGCTTCGAGAAGCGCCACAAGAACATGTCTGTACACCTGTCCCCCTG
CTTCAGGGACGTCCAGATCGGTGACATCGTCACAGTGGGCGAGTGCCGGCCTCTGAGCAAGACAGTGCGCTTCAACGT
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>VIRT97525
MTMVLCIFILVTTPERIRPRMDTLPVKGHFLSM
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>NM_001015.4 Homo sapiens ribosomal protein S11 (RPS11), mRNA
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TGGTAATGTGTCCATTCGAGGGCGGATCCTCTCTGGCGTGGTGACCAAGATGAAGATGCAGAGGACCATT
GTCATCCGCCGAGACTATCTGCACTACATCCGCAAGTACAACCGCTTCGAGAAGCGCCACAAGAACATGT
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>NP_001006.1 40S ribosomal protein S11 [Homo sapiens]
MADIQTERAYQKQPTIFQNKKRVLLGETGKEKLPRYYKNIGLGFKTPKEAIEGTYIDKKCPFTGNVSIRG
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NVLKVTKAAGTKKQFQKF
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i1_HQ_samplec9816d|c27462/f2p0/1054      gcggccgggaagatggcggacattcagactgagcgtgcctaccaaaagcagCCGACCATC    60
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NM_001015.4                              ------------------------------------------------------------    0

i1_HQ_samplec9816d|c27462/f2p0/1054      TTTTCAAAACAAGAAGAGGGTCCTGCTGGGAGAAACTGGCAAGGAGAAGCTCCCGCGGTA    120
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NM_001015.4                              ------------------------------------------------------------    0

i1_HQ_samplec9816d|c27462/f2p0/1054      CTACAAGAACATCGGTCTGGGCTTCAAGACACCCAAGGAGGTGCGGGGAACCTCAGAAGA    180
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i1_HQ_samplec9816d|c27462/f2p0/1054      AAGAAGGGGAACCTGGCGTTCCTGCACGTGTGCCCACGACGAGTTGCCCTGCCTGCATCT    240
i0_HQ_samplec9816d|c92306/f20p24/550     ------------------------------------------------------------    0
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i1_HQ_samplec9816d|c27462/f2p0/1054      AAGTGGCTTCTGGGGCTGCTGGGAATTGTAGTTGCTTCCCTGAGGCCACGCCCCTGGCTC    300
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NM_001015.4                              ------------------------------------------------------------    0

i1_HQ_samplec9816d|c27462/f2p0/1054      TTTTAAGGAACCGCCCGCCCAAGGCTCACTCCTTTATCTTTCCTATCCTTTCAGGCTATT    360
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i0_HQ_samplec9816d|c92306/f20p24/550     ------------------------------------------------------------    0
NM_001015.4                              ----------------------------------TCTCCTTACGT----------CAC    14

i1_HQ_samplec9816d|c27462/f2p0/1054      ATCCTCTCTGGTAAGTGCGGGAGTTACTGGTGTCTGGGGCCTGAAATACTGAAAGAAGGG    480
i0_HQ_samplec9816d|c92306/f20p24/550     ------------------------------------------------------------    0
NM_001015.4                              TTCCTCTCCAGCCCCTG------------------CGTAAT-CGATAAGGAAACCCGGA    54

i1_HQ_samplec9816d|c27462/f2p0/1054      TCTTGGGGCCCAGACTCCTGGGTCCTGGGTGAGAGGGGTGGTTAGGAATGCAAACTTG-T    539
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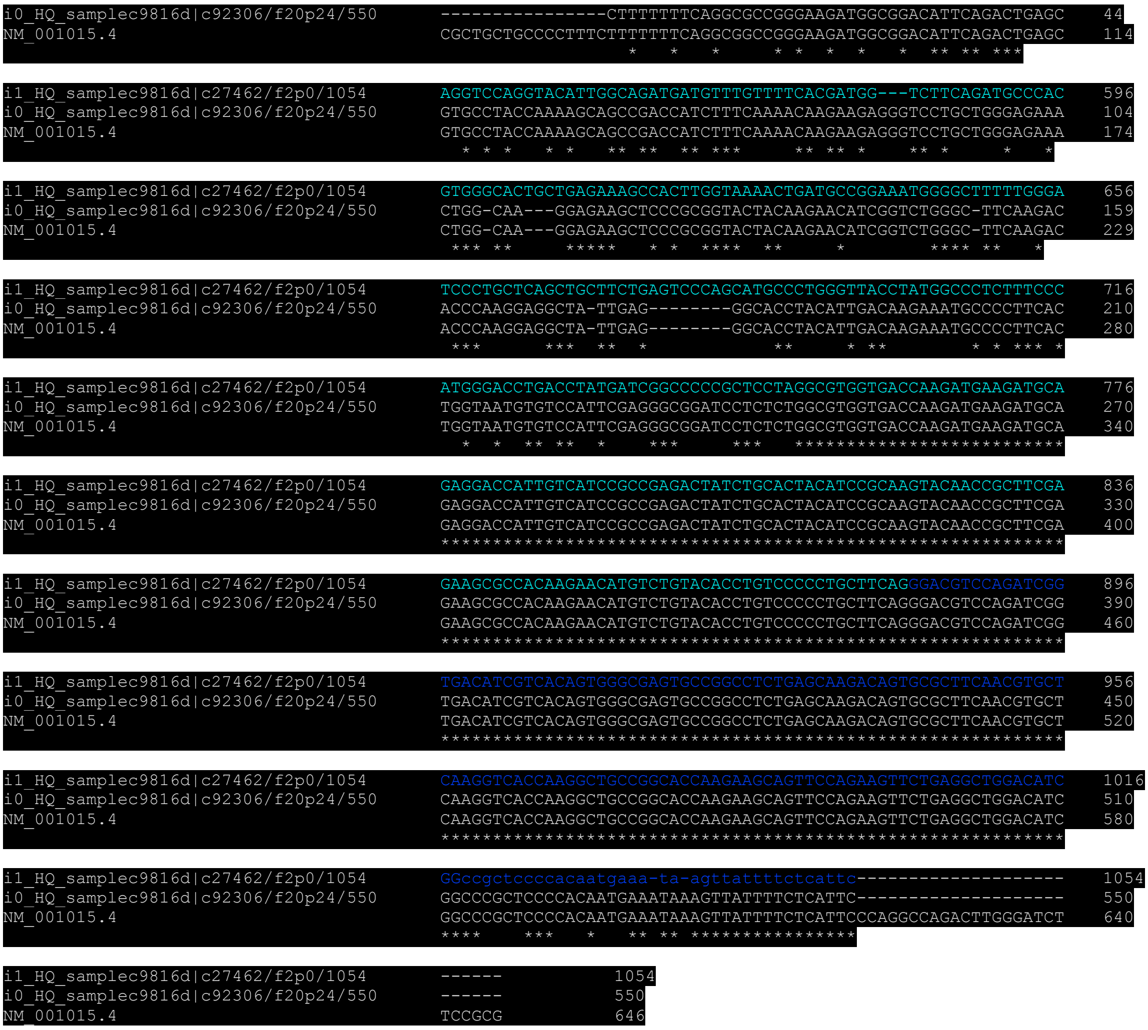

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                                                            *   *   *     * *  *  *   *  ** ** ***

i1_HQ_samplec9816d|c27462/f2p0/1054       AGGTCCAGGTACATTGGCAGATGATGTTTGTTTTCACGATGG---TCTTCAGATGCCCAC    596
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NM_001015.4                               GTGCCTACCAAAAGCAGCCGACCATCTTTCAAAACAAGAAGAGGGTCCTGCTGGGAGAAA    174
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i1_HQ_samplec9816d|c27462/f2p0/1054       GTGGGCACTGCTGAGAAAGCCACTTGGTAAAACTGATGCCGGAAATGGGGCTTTTTGGGA    656
i0_HQ_samplec9816d|c92306/f20p24/550      CTGG-CAA---GGAGAAGCTCCCGCGGTACTACAAGAACATCGGTCTGGGC-TTCAAGAC    159
NM_001015.4                               CTGG-CAA---GGAGAAGCTCCCGCGGTACTACAAGAACATCGGTCTGGGC-TTCAAGAC    229
                                           *** **     *****   * *  ****  **     *        **** **   *

i1_HQ_samplec9816d|c27462/f2p0/1054       TCCCTGCTCAGCTGCTTCTGAGTCCCAGCATGCCCTGGGTTACCTATGGCCCTCTTTCCC    716
i0_HQ_samplec9816d|c92306/f20p24/550      ACCCAAGGAGGCTA-TTGAG--------GGCACCTACATTGACAAGAAATGCCCCTTCAC    210
NM_001015.4                               ACCCAAGGAGGCTA-TTGAG--------GGCACCTACATTGACAAGAAATGCCCCTTCAC    280
                                           ***      ***  **  *            **     * **        * * *** *

i1_HQ_samplec9816d|c27462/f2p0/1054       ATGGGACCTGACCTATGATCGGCCCCCGCTCCTAGGCGTGGTGACCAAGATGAAGATGCA    776
i0_HQ_samplec9816d|c92306/f20p24/550      TGGTAATGTGTCCATTCGAGGGCGGATCCTCTCTGGCGTGGTGACCAAGATGAAGATGCA    270
NM_001015.4                               TGGTAATGTGTCCATTCGAGGGCGGATCCTCTCTGGCGTGGTGACCAAGATGAAGATGCA    340
                                            *  *  ** **  *    ***     ***   **************************

i1_HQ_samplec9816d|c27462/f2p0/1054       GAGGACCATTGTCATCCGCCGAGACTATCTGCACTACATCCGCAAGTACAACCGCTTCGA    836
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i1_HQ_samplec9816d|c27462/f2p0/1054       GAAGCGCCACAAGAACATGTCTGTACACCTGTCCCCCTGCTTCAGGGACGTCCAGATCGG    896
i0_HQ_samplec9816d|c92306/f20p24/550      GAAGCGCCACAAGAACATGTCTGTACACCTGTCCCCCTGCTTCAGGGACGTCCAGATCGG    390
NM_001015.4                               GAAGCGCCACAAGAACATGTCTGTACACCTGTCCCCCTGCTTCAGGGACGTCCAGATCGG    460
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i0_HQ_samplec9816d|c92306/f20p24/550      TGACATCGTCACAGTGGGCGAGTGCCGGCCTCTGAGCAAGACAGTGCGCTTCAACGTGCT    450
NM_001015.4                               TGACATCGTCACAGTGGGCGAGTGCCGGCCTCTGAGCAAGACAGTGCGCTTCAACGTGCT    520
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NM_001015.4                               CAAGGTCACCAAGGCTGCCGGCACCAAGAAGCAGTTCCAGAAGTTCTGAGGCTGGACATC    580
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i1_HQ_samplec9816d|c27462/f2p0/1054       GGccgctccccacaatgaaa-ta-agttattttctcattc--------------------    1054
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NM_001015.4                               GGCCCGCTCCCCACAATGAAATAAAGTTATTTTCTCATTCCCAGGCCAGACTTGGGATCT    640
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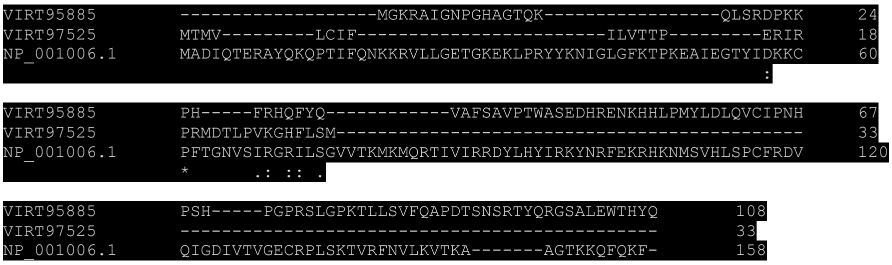

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VIRT97525        MTMV---------LCIF------------------------ILVTTP---------ERIR     18
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VIRT95885        PH-----FRHQFYQ------------VAFSAVPTWASEDHRENKHHLPMYLDLQVCIPNH     67
VIRT97525        PRMDTLPVKGHFLSM---------------------------------------------     33
NP_001006.1      PFTGNVSIRGRILSGVVTKMKMQRTIVIRRDYLHYIRKYNRFEKRHKNMSVHLSPCFRDV     120
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VIRT95885        PSH-----PGPRSLGPKTLLSVFQAPDTSNSRTYQRGSALEWTHYQ       108
VIRT97525        ----------------------------------------------       33
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NAA10

Sequence	**Header**	**AA Seq**
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Absent	i0_HQ_samplec9816d|c92336/f66p39/908	
NCBI	NM_001256119	
	NM_003491	

>i1_HQ_samplec9816d|c63491/f3p24/1053
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CATGCAGCACTGCAACCTCCTCTGCCTGCCCGAGAACTACCAGATGAAATACTACTTCTACCATGGCCTTTCCTGGCCCC
AGCTCTCTTACATTGCTGAGGACGAGAATGGGAAGATTGTGGGGTATGTCCTGGCCAAAATGGAAGAGGACCCAGATG
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CTGCACCTCTATTCCAACACCCTCAACTTTCAGATCAGTGAAGTGGAGCCCAAATACTATGCAGATGGGGAGGACGCCT
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CGTGGTGCTGGGTGCCATCGAGAACAAGGTGGAGAGCAAAGGCAATTCACCTCCGAGCTCAGGAGAGGCCTGTCGCG
AGGAGAAGGGCCTGGCTGCCGAGGATAGTGGTGGGGACAGCAAGGACCTCAGCGAGGTCAGCGAGACCACAGAGAG
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>VIRT111589
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EVEPKYYADGEDAYAMKRDLTQMADELRRHLELKEKGRHVVLGAIENKVESKGNSPPSSG
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>VIRT112564

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>NM_001256119.1 Homo sapiens N(alpha)-acetyltransferase 10, NatA catalytic subunit (NAA10), transcript variant 2, mRNA
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CTAATGAACATGCAGCACTGCAACCTCCTCTGCCTGCCCGAGAACTACCAGATGAAATACTACTTCTACC
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CACCGGCGCCTCGGTCTGGCTCAGAAACTGATGGACCAGGCCTCTCGAGCCATGATAGAGAACTTCAATG
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GGACGCCTATGCCATGAAGCGGGACCTCACTCAGATGGCCGACGAGCTGAGGCGGCACCTGGAGCTGAAA
GAGAAGGGCAGGCACGTGGTGCTGGGTGCCATCGAGAACAAGGTGGAGAGCAAAGGCAATTCACCTCCGA
GCTCAGGAGAGGCCTGTCGCGAGGAGAAGGGCCTGGCTGCCGAGGATAGTGGTGGGGACAGCAAGGACCT
CAGCGAGGTCAGCGAGACCACAGAGAGCACAGATGTCAAGGACAGCTCAGAGGCCTCCGACTCAGCCTCC
TAGAGCCTGCCCCATCCCCTCCTCACCCCACGAGCTTTCACAATAAATTCGCTCCGTGGCACTGGGGAAC
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>NP_001243048.1 N-alpha-acetyltransferase 10 isoform 2 [Homo sapiens]
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1, mRNA
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CCTTCACGATCCGCTGGGACCCGCGAGCCCCGCCGCCGTTATGAACATCCGCAATGCGAGGCCAGAGGAC
CTAATGAACATGCAGCACTGCAACCTCCTCTGCCTGCCCGAGAACTACCAGATGAAATACTACTTCTACC
ATGGCCTTTCCTGGCCCCAGCTCTCTTACATTGCTGAGGACGAGAATGGGAAGATTGTGGGGTATGTCCT
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CACCGGCGCCTCGGTCTGGCTCAGAAACTGATGGACCAGGCCTCTCGAGCCATGATAGAGAACTTCAATG
CCAAATATGTCTCCCTGCATGTCAGGAAGAGTAACCGGGCCGCCCTGCACCTCTATTCCAACACCCTCAA
CTTTCAGATCAGTGAAGTGGAGCCCAAATACTATGCAGATGGGGAGGACGCCTATGCCATGAAGCGGGAC
CTCACTCAGATGGCCGACGAGCTGAGGCGGCACCTGGAGCTGAAAGAGAAGGGCAGGCACGTGGTGCTGG
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AAAAAAAAAAAAAAAA
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i1_HQ_samplec9816d|c63491/f3p24/1053      GCGGGGCCGGGGCTGCGATTCCCTCCTGTTTGCGTGATGTCGGGCCTCCGTTGGGTGGGC    120
NM_001256119.1                            GCTGGCCTGT-CCCGCGCATTGGCCAAGCGGCCGGGAGGACGGGCCCGGCGGCCGTGCAC    90
i0_HQ_samplec9816d|c92336/f66p39/908      ------------------------------------------------------------    0
NM_003491.3                               GCTGGCCTGT-CCCGCGCATTGGCCAAGCGGCCGGGAGGACGGGCCCGGCGGCCGTGCAC    90

i1_HQ_samplec9816d|c63491/f3p24/1053      -----TCCGGGGACCTCCGGGGCGCCCACTCCTGTTCCTGTGCTCCGGGCGTTGTGCAAA    175
NM_001256119.1                            TTCCGGCCGGTGGCCGGCCCGGCGCGCACCGCCCCTTCCGCCGT-----CGCCCAGCGAG    145
i0_HQ_samplec9816d|c92336/f66p39/908      ----------------gcccggcgcgcaccgccccttccGCCGT-----CGCCCAGCGAG    39
NM_003491.3                               TTCCGGCCGGTGGCCGGCCCGGCGCGCACCGCCCCTTCCGCCGT-----CGCCCAGCGAG    145
                                                           *  ***** ***  *   * * *   *     **    ** *

i1_HQ_samplec9816d|c63491/f3p24/1053      GTCAGATCGTCACAGTGCCTGCCCAGCCCCGAGGGAGGGGGGCCGAGCAGACCGACGGGG    235
NM_001256119.1                            CCCAGCTCCGGTCCCAGCCCCGGCCGTCCCGGCGTCGCTTC--GGAGCGCGGCGGCAGC-    202
i0_HQ_samplec9816d|c92336/f66p39/908      CCCAGCTCCGGTCCCAGCCCCGGCCGTCCCGGCGTCGCTTC--GGAGCGCGGCGGCAGC-    96
NM_003491.3                               CCCAGCTCCGGTCCCAGCCCCGGCCGTCCCGGCGTCGCTTC--GGAGCGCGGCGGCAGC-    202
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i1_HQ_samplec9816d|c63491/f3p24/1053      AGCAGGCTTCTCACCCGTGGTCACCGCCGCCTTAGACTGAGCGCGTTCCACTGCCCTCCT    295
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i0_HQ_samplec9816d|c92336/f66p39/908      TGACTGCGCCTTCACGATCCGCTGGGACCCGCGAGCCCCGCCGCCGTTATGAACATCCGC    156
NM_003491.3                               TGACTGCGCCTTCACGATCCGCTGGGACCCGCGAGCCCCGCCGCCGTTATGAACATCCGC    262
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i1_HQ_samplec9816d|c63491/f3p24/1053      TCCCTGCAGCCAGAGGACCTAATGAACATGCAGCACTGCAACCTCCTCTGCCTGCCCGAG    355
NM_001256119.1                            AATGCGAGGCCAGAGGACCTAATGAACATGCAGCACTGCAACCTCCTCTGCCTGCCCGAG    322
i0_HQ_samplec9816d|c92336/f66p39/908      AATGCGAGGCCAGAGGACCTAATGAACATGCAGCACTGCAACCTCCTCTGCCTGCCCGAG    216
NM_003491.3                               AATGCGAGGCCAGAGGACCTAATGAACATGCAGCACTGCAACCTCCTCTGCCTGCCCGAG    322
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i1_HQ_samplec9816d|c63491/f3p24/1053      AACTACCAGATGAAATACTACTTCTACCATGGCCTTTCCTGGCCCCAGCTCTCTTACATT    415
NM_001256119.1                            AACTACCAGATGAAATACTACTTCTACCATGGCCTTTCCTGGCCCCAGCTCTCTTACATT    382
i0_HQ_samplec9816d|c92336/f66p39/908      AACTACCAGATGAAATACTACTTCTACCATGGCCTTTCCTGGCCCCAGCTCTCTTACATT    276
NM_003491.3                               AACTACCAGATGAAATACTACTTCTACCATGGCCTTTCCTGGCCCCAGCTCTCTTACATT    382
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NM_001256119.1                            GCTGAGGACGAGAATGGGAAGATTGTGGGGTATGTCCTGGCCAAAATGGAAGAGGACCCA    442
i0_HQ_samplec9816d|c92336/f66p39/908      GCTGAGGACGAGAATGGGAAGATTGTGGGGTATGTCCTGGCCAAAATGGAAGAGGACCCA    336
NM_003491.3                               GCTGAGGACGAGAATGGGAAGATTGTGGGGTATGTCCTGGCCAAAATGGAAGAGGACCCA    442
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NM_001256119.1                              GATGATGTGCCCCATGGACATATCACCTCATTGGCTGTGAAGCGTTCCCACCGGCGCCTC     502
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NM_003491.3                                 GATGATGTGCCCCATGGACATATCACCTCATTGGCTGTGAAGCGTTCCCACCGGCGCCTC     502
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i0_HQ_samplec9816d|c92336/f66p39/908        GGTCTGGCTCAGAAACTGATGGACCAGGCCTCTCGAGCCATGATAGAGAACTTCAATGCC     456
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i1_HQ_samplec9816d|c63491/f3p24/1053        ACCCTCAACTTTCAGATCAGTGAAGTGGAGCCCAAATACTATGCAGATGGGGAGGACGCC     715
NM_001256119.1                              ---------------ATCAGTGAAGTGGAGCCCAAATACTATGCAGATGGGGAGGACGCC     637
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i1_HQ_samplec9816d|c63491/f3p24/1053        AATTCACCTCCGAGCTCAGGAGAGGCCTGTCGCGAGGAGAAGGGCCTGGCTGCCGAGGAT     895
NM_001256119.1                              AATTCACCTCCGAGCTCAGGAGAGGCCTGTCGCGAGGAGAAGGGCCTGGCTGCCGAGGAT     817
i0_HQ_samplec9816d|c92336/f66p39/908        AATTCACCTCCGAGCTCAGGAGAGGCCTGTCGCGAGGAGAAGGGCCTGGCTGCCGAGGAT     756
NM_003491.3                                 AATTCACCTCCGAGCTCAGGAGAGGCCTGTCGCGAGGAGAAGGGCCTGGCTGCCGAGGAT     862
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i0_HQ_samplec9816d|c92336/f66p39/908        AAGGACAGCTCAGAGGCCTCCGACTCAGCCTCCTAGAGCCTGCCCCATCCCCTCCTCACC     876
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NM_003491.3                                 CCACGAGCTTTCACAATAAATTCGCTCCGTGGCACTGGGGAACTTTGTGTGTGAGCGCGC     1042
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VIRT112564          MNIRNARPEDLMNMQHCNLLCLPENYQMKYYFYHGLSWPQLSYIAEDENGKIVGYVLAKM   60
NP_003482.1         MNIRNARPEDLMNMQHCNLLCLPENYQMKYYFYHGLSWPQLSYIAEDENGKIVGYVLAKM   60
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NP_001243048.1      EEDPDDVPHGHITSLAVKRSHRRLGLAQKLMDQASRAMIENFNAKYVSLHVRK-------   113
VIRT111589          EEDPDDVPHGHITSLAVKRSHRRLGLAQKLMDQASRAMIENFNAKYVSLHVRKSNRAALH   109
VIRT112564          EEDPDDVPHGHITSLAVKRSHRRLGLAQKLMDQASRAMIENFNAKYVSLHVRKSNRAALH   120
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VIRT112564          LYSNTLNFQISEVEPKYYADGEDAYAMKRDLTQMADELRRHLELKEKGRHVVLGAIENKV   180
NP_003482.1         LYSNTLNFQISEVEPKYYADGEDAYAMKRDLTQMADELRRHLELKEKGRHVVLGAIENKV   180
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EMC9

Sequence	Header	AA Seq
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Absent	i0_HQ_samplec9816d|c1265/f10p11/810	
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	NM_001346874	

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GCCGAACCGAAGCCTCGCTCGCCATGGGGGAGGTGGAGATCTCGGCCCTGGCCTACGTGAAGATGTGCCT
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>NP_057133.2 ER membrane protein complex subunit 9 isoform a [Homo sapiens]
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>NP_001333806.1 ER membrane protein complex subunit 9 isoform b precursor [Homo sapiens]
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NM_001346877.1                           GAAGGCGGGGCTCGGATGCAATCGGGACCT------CCTCCTGGACTGGGCCGGGGGCGG     80
NM_016049.3                              GAAGGCGGGGCTCGGATGCAATCGGGACCT------CCTCCTGGACTGGGCCGGGGGCGG     80
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NM_001346877.1                           ACTCCGGGACCCAGGGCGCCGGGAGCCGGCGGGCTACCTGCGAG--TCGAGTTAGCGTTG     138
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NM_001346877.1                           TCGCCGAACCGAAGTGAGAGGGCACGGGGAAGGGTCAAAGAGCGTGCCGA----------     188
NM_016049.3                              TCGCCGAACCGAAGCCTCGCTCGCCATGGGGGAGGTGGAGATCTCGGCCCTGGCCTACGT     198
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NM_001346874.1                           TCGCCGAACCGAAGCCTCGCTCGCCATGGGGGAGGTGGAGATCTCGGCCCTGGCCTACGT     198
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NM_001346877.1                           ------------------------------------------------------------     188
NM_016049.3                              GAAGATGTGCCTGCATGCTGCCCGGTACCCACACGCCGCAGTCAACGGGCTGTTTTTGGC     258
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NM_001346877.1                           --------------------------------------------------AGCGCTGGAG     198
NM_016049.3                              GCCAGCGCCGCGGTCTGGAGAATGCCTGTGCCTCACCGACTGTGTGCCCCTCTTCCACAG     318
i0_HQ_samplec9816d|c2150/f3p12/894       GCCAGCGCCGCGGTCTGGAGAATGCCTGTGCCTCACCGACTGTGTGCCCCTCTTCCACAG     245
NM_001346874.1                           GCCAGCGCCGCGGTCTGGAGAATGCCTGTGCCTCACCGACTGTGTGCCCCTCTTCCACAG     318
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NM_016049.3                              CCACCTGGCCCTGTCCGTCATGTTGGAGGTCGCCCTCAACCAGGTGGATGTGTGGGGAGC     378
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NM_001346877.1                           ACAGGCCGGTCTGGTGGTGGCTGGTTACTACCATGCCAATGCAGCTGTGAACGATCAGAG     318
NM_016049.3                              ACAGGCCGGTCTGGTGGTGGCTGGTTACTACCATGCCAATGCAGCTGTGAACGATCAGA-     437
i0_HQ_samplec9816d|c2150/f3p12/894       ACAGGCCGGTCTGGTGGTGGCTGGTTACTACCATGCCAATGCAGCTGTGAACGATCAGAG     365
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i0_HQ_samplec9816d|c2150/f3p12/894  CCAGCAGGCCCGATCCCCGCAGGCCACCTACAGGGAAAGGCCACAGCTGCGCCCACACCT    458
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i1_HQ_samplec9816d|c6322/f2p3/1046  ATGAGACCTGGGAGGCCCAGCTCAAATGGATGGGTTTTGCCCACAGTTGGCTCCTCACTC    631
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NM_001346877.1                      ATGAGACCTGGGAGGCCCAGCTCAAATGGATGGGTTTTGCCCACAGTTGGCTCCTCACTC    498
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i1_HQ_samplec9816d|c6322/f2p3/1046  CTCTGATCTTCCCTCTACACAGCCCTGGGCCCCTGGCCTTGAAAATTGCTGGGCGAATTG    691
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NM_001346877.1                      CTCTGATCTTCCCTCTACACAGCCCTGGGCCCCTGGCCTTGAAAATTGCTGGGCGAATTG    558
NM_016049.3                         ---------------------GCCCTGGGCCCCTGGCCTTGAAAATTGCTGGGCGAATTG    476
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NM_016049.3                         CAGAATTCTTCCCTGATGCAGTACTTATTATGTTGGATAATCAGAAACTGGTGCCTCAGC    536
i0_HQ_samplec9816d|c2150/f3p12/894  CAGAATTCTTCCCTGATGCAGTACTTATTATGTTGGATAATCAGAAACTGGTGCCTCAGC    599
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i1_HQ_samplec9816d|c6322/f2p3/1046  CTCGTGTGCCCCCGGTCATCGTCCTGGAGAACCAAGGTCTCCGCTGGGTCCCTAAGGATA    811
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i1_HQ_samplec9816d|c6322/f2p3/1046  AGAACTTAGTGATGTGGAGGGACTGGGAAGAGTCACGGCAGATGGTGGGAGCTCTACTGG    871
i0_HQ_samplec9816d|c1265/f10p11/810 AGAACTTAGTGATGTGGAGGGACTGGGAAGAGTCACGGCAGATGGTGGGAGCTCTACTGG    636
NM_001346877.1                      AGAACTTAGTGATGTGGAGGGACTGGGAAGAGTCACGGCAGATGGTGGGAGCTCTACTGG    738
NM_016049.3                         AGAACTTAGTGATGTGGAGGGACTGGGAAGAGTCACGGCAGATGGTGGGAGCTCTACTGG    656
i0_HQ_samplec9816d|c2150/f3p12/894  AGAACTTAGTGATGTGGAGGGACTGGGAAGAGTCACGGCAGATGGTGGGAGCTCTACTGG    719
NM_001346874.1                      AGAACTTAGTGATGTGGAGGGACTGGGAAGAGTCACGGCAGATGGTGGGAGCTCTACTGG    858
                                    ************************************************************

i1_HQ_samplec9816d|c6322/f2p3/1046  AAGATCGGGCCCACCAGCACCTTGTGGACTTTGACTGCCACCTTGATGACATCCGGCAGG    931
i0_HQ_samplec9816d|c1265/f10p11/810 AAGATCGGGCCCACCAGCACCTTGTGGACTTTGACTGCCACCTTGATGACATCCGGCAGG    696
NM_001346877.1                      AAGATCGGGCCCACCAGCACCTTGTGGACTTTGACTGCCACCTTGATGACATCCGGCAGG    798
NM_016049.3                         AAGATCGGGCCCACCAGCACCTTGTGGACTTTGACTGCCACCTTGATGACATCCGGCAGG    716
i0_HQ_samplec9816d|c2150/f3p12/894  AAGATCGGGCCCACCAGCACCTTGTGGACTTTGACTGCCACCTTGATGACATCCGGCAGG    779
NM_001346874.1                      AAGATCGGGCCCACCAGCACCTTGTGGACTTTGACTGCCACCTTGATGACATCCGGCAGG    918
                                    ************************************************************

i1_HQ_samplec9816d|c6322/f2p3/1046  ACTGGACCAACCAGCGGCTCAACACTCAAATCACCCAGTGGGTTGGTCCCACTAATGGAA    991
i0_HQ_samplec9816d|c1265/f10p11/810 ACTGGACCAACCAGCGGCTCAACACTCAAATCACCCAGTGGGTTGGTCCCACTAATGGAA    756
NM_001346877.1                      ACTGGACCAACCAGCGGCTCAACACTCAAATCACCCAGTGGGTTGGTCCCACTAATGGAA    858
NM_016049.3                         ACTGGACCAACCAGCGGCTCAACACTCAAATCACCCAGTGGGTTGGTCCCACTAATGGAA    776
i0_HQ_samplec9816d|c2150/f3p12/894  ACTGGACCAACCAGCGGCTCAACACTCAAATCACCCAGTGGGTTGGTCCCACTAATGGAA    839
NM_001346874.1                      ACTGGACCAACCAGCGGCTCAACACTCAAATCACCCAGTGGGTTGGTCCCACTAATGGAA    978
                                    ************************************************************

i1_HQ_samplec9816d|c6322/f2p3/1046  ATGGAAATGCCTGAGCCAGggccagcggggcccggttccaataaagagacttggg-----    1046
i0_HQ_samplec9816d|c1265/f10p11/810 ATGGAAATGCCTGAGCCAGGGCCAGCGGGGCCCGGTTCCAATAAAGAGACTTGG------    810
NM_001346877.1                      ATGGAAATGCCTGAGCCAGGGCCAGCGGGGCCCGGTTCCAATAAAGAGACTTGGGCTGA-    917
NM_016049.3                         ATGGAAATGCCTGAGCCAGGGCCAGCGGGGCCCGGTTCCAATAAAGAGACTTGGGCTGAA    836
i0_HQ_samplec9816d|c2150/f3p12/894  ATGGAAATGCCTGAGCCAGGGCCAGCGGGGCCCGGTTCCAATAAAGAGACTTGGG-----    894
NM_001346874.1                      ATGGAAATGCCTGAGCCAGGGCCAGCGGGGCCCGGTTCCAATAAAGAGACTTGGGCTGA-    1037
                                    ******************************************************

i1_HQ_samplec9816d|c6322/f2p3/1046  ------------------------------------------------------------    1046
i0_HQ_samplec9816d|c1265/f10p11/810 ------------------------------------------------------------    810
NM_001346877.1                      ------------------------------------------------------------    917
NM_016049.3                         AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA    896
i0_HQ_samplec9816d|c2150/f3p12/894  ------------------------------------------------------------    894
NM_001346874.1                      ------------------------------------------------------------    1037
```

```
VIRT130505          MGEVEISALAYVKMCLHAARYPHAAVNGLFLAPAPRSGECLCLTDCVPLFHSHLALSVML  60
VIRT147453          ------------------------------------------------------------  0
NP_001333806.1      ------------------------------------------------------------  0
NP_001333803.1      ------------------------------------------------------------  0
VIRT151133          MGEVEISALAYVKMCLHAARYPHAAVNGLFLAPAPRSGECLCLTDCVPLFHSHLALSVML  60
NP_057133.2         MGEVEISALAYVKMCLHAARYPHAAVNGLFLAPAPRSGECLCLTDCVPLFHSHLALSVML  60
```

```
VIRT130505          EVALNQVDVWGAQAGLVVAGYYHANAAVNDQSTQASSSRASSIQQARSPQAT-------- 112
VIRT147453          -------------MGF-AHSWLLTPLIFPLHSPGPLALKIAGRIAEFFPDAVLIMLDNQK 46
NP_001333806.1      -------------MGF-AHSWLLTPLIFPLHSPGPLALKIAGRIAEFFPDAVLIMLDNQK 46
NP_001333803.1      -------------MGF-AHSWLLTPLIFPLHSPGPLALKIAGRIAEFFPDAVLIMLDNQK 46
VIRT151133          EVALNQVDVWGAQAGLVVAGYYHANAAVNDQSPGPLALKIAGRIAEFFPDAVLIMLDNQK 120
NP_057133.2         EVALNQVDVWGAQAGLVVAGYYHANAAVNDQSPGPLALKIAGRIAEFFPDAVLIMLDNQK 120
                                  *: . .:  :   .  :*    : : :.      *:*.

VIRT130505          YRERPQLRPHL------------------------------------------------- 123
VIRT147453          LVPQPRVPPVIVLENQGLRWVPKDKNLVMWRDWEESRQMVGALLEDRAHQHLVDFDCHLD 106
NP_001333806.1      LVPQPRVPPVIVLENQGLRWVPKDKNLVMWRDWEESRQMVGALLEDRAHQHLVDFDCHLD 106
NP_001333803.1      LVPQPRVPPVIVLENQGLRWVPKDKNLVMWRDWEESRQMVGALLEDRAHQHLVDFDCHLD 106
VIRT151133          LVPQPRVPPVIVLENQGLRWVPKDKNLVMWRDWEESRQMVGALLEDRAHQHLVDFDCHLD 180
NP_057133.2         LVPQPRVPPVIVLENQGLRWVPKDKNLVMWRDWEESRQMVGALLEDRAHQHLVDFDCHLD 180
                       :*:: * :

VIRT130505          ----------------------------   123
VIRT147453          DIRQDWTNQRLNTQITQWVGPTNGNGNA   134
NP_001333806.1      DIRQDWTNQRLNTQITQWVGPTNGNGNA   134
NP_001333803.1      DIRQDWTNQRLNTQITQWVGPTNGNGNA   134
VIRT151133          DIRQDWTNQRLNTQITQWVGPTNGNGNA   208
NP_057133.2         DIRQDWTNQRLNTQITQWVGPTNGNGNA   208
```