

# SUPPLEMENTAL FILE 2

Sequence variations in *CSH2*, *CSH1*, and *CSHL1* genes in gibbons compared to human reference gene sequence

gibbon 1 TGACAAGCCAGGAGGCATGATCCAGCATGTGTGGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCATCAGTGGCCCCAGGCCATAAA  
CSH2 1 -----

gibbon 91 CGTGCAGAGAAAACAGGTGGGAGAAAGCAGCGAGAGAGAAAGGGCCAGGGTATAAAAAAGGGCCACAAGAGACCAGCTCCAGGATCCCAAG  
CSH2 1 -----CAGCGAGAGAGAACTGGCCAGGGTATAAAAAAGGGCCACAAGAGACCAGCTCCAGGATCCCAAG

gibbon 181 GCCCAACTCCCCAAACCACTCAGGGTCTGTGGACAGCTCACCTAGCCGCATGAGCTGCAGGTAAGCGCCCTAAAATCCCTTTGGGCAC  
CSH2 65 GCCCAACTCCCCAAACCACTCAGGGTCTGTGGACAGCTCACCTAGCCGCATGAGCTGCAGGTAAGCGCCCTAAAATCCCTTTGGGCAC

gibbon 271 ACTGTGTCCCAAGGGGAGAAAGCGCTCCCTGTAGATGGGACGGGGGCACTAACCGTCAGGTTTGGGGCTCCTGAATGTGAATATCGCCAT  
CSH2 155 AACGTGTCCCAAGGGGAGAAAGCGCGCTCCCTGTAGATGGGACGGGGGCACTAACCGTCAGGTTTGGGGCTCCTGAATGTGAATATCGCCAT

gibbon 361 CGAAGTTCAGATATTTGGCCAATCTCTGAATGTTCCTGGTCCCGGAGGGAAGGAGAGAGAGAAAAACAACAGCTCCTGGAACAGGG  
CSH2 245 CTAAAGTTCAGATATTTGGCCAATCTCTGAATGTTCCTGGTCCCGGAGGGAAGGAGAGAGAGAAAAACAACAGCTCCTGGAACAGGG

gibbon 451 AGAGTGTGGCTCCTGGTCTCCGGCTCCCTCCTTTGCCCTCCGGTTCCTCCCAAGGCTCCCGATGTCCCTGCTCCTGGCTTTTGGCCCT  
CSH2 335 AGAGTGTGGCTCCTGGTCTCCGGCTCCCTCCTTTGCCCTCCGGTTCCTCCCAAGGCTCCCGATGTCCCTGCTCCTGGCTTTTGGCCCT

gibbon 541 GCTCTGCTGCCCTGGCTTCAAGAGGCTGTGCGGTCCAAACCGTTCCCTTAGCCAGGCTTTTGAAGAGACTATGTTCCAAGCCCATCG  
CSH2 425 GCTCTGCTGCCCTGGCTTCAAGAGGCTGTGCGGTCCAAACCGTTCCCTTAGCCAGGCTTTTGAAGAGACTATGTTCCAAGCCCATCG

gibbon 631 CGCGCACCAGCTGGCCATTGACACCTACCAGGAGTTTGTAAAGTCTTTGGGGAATGGGTCAGGGTCAGGGTGGCAAGAACGGGTGACTTT  
CSH2 515 CGCGCACCAGCTGGCCATTGACACCTACCAGGAGTTTGTAAAGTCTTTGGGGAATGGGTCAGGGTCAGGGTGGCAAGAACGGGTGACTTT

gibbon 721 CCCCCACTGGGGAAGTAATGGGAGGAGACTAAGAGAGCTCAGGGTTTCTTCTGAGCGAAAATGCAGGCAGATGAGCATAGGCTGAGCCA  
CSH2 605 CCCCCACTGGGGAAGTAATGGGAGGAGACTAAGAGAGCTCAGGGTTTCTTCTGAGCGAAAATGCAGGCAGATGAGCATAGGCTGAGCCA

gibbon 811 GGTTCCCAGAAAAGTAACAATGAGAGCTGGTCTCCAGCATAGAAAAGCAGCTTCTCTCTGGGGGGGGGCTCTCTCTAGGAAGAAA  
CSH2 695 GGTTCCCAGAAAAGTAACAATGAGAGCTGGTCTCCAGCATAGAAAAGCAGCAGTCTCTCTGGGGGGGGGCTCTCTCTAGGAAGAAA

gibbon 901 CCTATATCCCAAAGGACCAGAAGTATTCATTCCTGCATAACCCAGACTTCCTTCTGCTTCTCAGACTCTATTCCGACACCCCTCCAACA  
CSH2 783 CCTATATCCCAAAGGACCAGAAGTATTCATTCCTGCATGACTCCAGACTTCCTTCTGCTTCTCAGACTCTATTCCGACACCCCTCCAACA

gibbon 991 GGAAGGAAACACAGCAGAAATCCGTGAGTGGATGCCCTTCTCCCG-AGGTGGGATGGGGGAGACCTGTGGTCAGAGCCCGGGCAGCAC  
CSH2 873 TGGAAGGAAACACAGCAGAAATCCGTGAGTGGATGCCCTTCTCCCGTAGGCGGGATGGGGGAGACCTGTGGTCAGAGCCCGGGCAGCAC

gibbon 1080 AGCCACTGTCCGTCTCCCTGCAGAACTTAGAGCTGCTCCGCATCTCCCTGGCGTCACTGAGTCTGGCTGGAGCCCGTGCCTTCC  
CSH2 963 AGCCACTGTCCGTCTCCCTGCAGAACTTAGAGCTGCTCCGCATCTCCCTGGCGTCACTGAGTCTGGCTGGAGCCCGTGCCTTCC

gibbon 1170 TCAGGAGTATCTTCAACAACGACCTGGTGTATGACACCTCGGACAGCGATGACTATCACCTCTAAAGGACCTAGAAAGGAGCATCCAAA  
CSH2 1053 TCAGGAGTATCTTCCCAACAACCTGGTGTATGACACCTCGGACAGCGATGACTATCACCTCTAAAGGACCTAGAAAGGAGCATCCAAA

gibbon 1260 CGCTGATGGGGGTGAGGGTGGCCAGGGGTCGCCAATCCTGGGGCCCCACTGGCTTCAAGGCTGGGGGAGAGAAACTGTGCCTC  
CSH2 1143 CGCTGATGGGGGTGAGGGTGGCCAGGGGTCGCCAATCCTGGGCCCCACTGGCTTCAAGGCTGGGGGAGAGAAACTGTGCCTC

gibbon 1350 TTTGTAGCAGTCAGGGCTGACCCAAGAGAAGCTCACCTTATCTTCAATTTCCCTGCGAATCCTCAGGGCTTTCTCTACACCCTGAAG  
CSH2 1233 TTTGTAGCAGTCAGGGCTGACCCAAGAGAAGCTCACCTTATCTTCAATTTCCCTGCGAATCCTCAGGGCTTTCTCTACACCCTGAAG

gibbon 1440 GGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCAAAGCGCTTGGCTCTCCTTCTCTTCTTCACTTTGAGAGGGCTG  
CSH2 1323 GGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCAAAGCGCTTGGCTCTCCTTCTCTTCTTCACTTTGAGAGGGCTG

gibbon 1530 GAAGATGGCAGCCCCAGACTGGCAGACTCTCAAGCAGACCTATAACAAGTTTGACACAAACTCCACAACCATGACGCAGTCTCAAG  
CSH2 1413 GAAGATGGCAGCCCCAGACTGGCAGACTCTCAAGCAGACCTATAACAAGTTTGACACAACTCCACAACCATGACGCAGTCTCAAG

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gibbon 1620 AACTACGGGCTGCCACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGGCATCGTGCACTGCCGCTCTGTGAGGGCAGC
CSH2 1503 AACTACGGGCTGCCACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGGCATCGTGCACTGCCGCTCTGTGAGGGCAGC

gibbon 1710 TGTGGCTTCTAGGTGCCCGCTGGCATCCTGTGACC-----CCTCCCACTGCCTCTCTGGCCCGGAAGGTGCCACTCCAGTGCCCAAC
CSH2 1593 TGTGGCTTCTAGGTGCCCGCTGGCATCCTGTGACCACCCCTCCCACTGCCTCTCTGGCCCGGAAGGTGCCACTCCAGTGCCCAAC

gibbon 1796 AGCCTTGTCTAATAAAATAAAGTTGTATCATTTCCTGACCAGGTGCTCTCTATAATATTATGGGGTGGAAAGTGGTGGTATGGAGC
CSH2 1683 AGCCTTGTCTAATAAAATAAAGTTGTATCATTTC-----

gibbon 1886 AAGGGCAGTGGGAAGACGACCTGGAGGGCCTTCAGGGTCTATTGGGAAGTAGGCTGCTGAAATATAAGAGGTTTGGCTGTTCTGGGC
CSH2 -----

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Alignment of human (NM\_020991) and gibbon *CSH2* genes sequences extracted from BAC AC198149. The green line demarcates the signal peptide sequence and the red box shows the start codon

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CSH1 1 -----
Gibbon 1 TGACAAGCCAGGAGGCATGATCCAGCATGTGTGGGAGGAGCTTCTAAATTATCCATTAGCACAAGCCCATCAGTGGCCCCAGGCCATAAA

CSH1 1 -----GCAGCGAGAGAGAACTGGCCAGGGTATAAAAAAGGCCCAAGAGACCGGCTCTAGGATCCCAAG
Gibbon 91 CGTGCAGAGAAACAGGTGGGGAGAAGCAGCGAGAGAGAAAGGGCCAGGGTATAAAAAAGGCCCAAGAGACCGGCTCTAGGATCCCAAG

CSH1 66 GCCCAACTCCCCAACCACCTCAGGGTCTGTGGACAGCTCACCTAGTGGCATTGCTCCAGGTAAGCGCCCTAAAATCCCTTTGGGCAC
Gibbon 181 GCCCAACTCCCCAACCACCTCAGGGTCTGTGGACAGCTCACCTAGTGGCATTGCTCCAGGTAAGCGCCCTAAAATCCCTTTGGGCAC

CSH1 156 AACTGTGCTCCAGGGGAGAGGCGCCCTCTGTAGATGGGACGGGGGCCTAACCCCTCAGGTTTGGGGCTTATGAATGTGATATCGCCAT
Gibbon 271 AACTGTGCTCCAGGGGAGAGGCGCCCTCTGTAGATGGGACGGGGGCCTAACCCCTCAGGTTTGGGGCTTATGAATGTGATATATCGCCAT

CSH1 246 CTAAGCCAGATATTTGGCCAATCTCTGAATGTTCTGGTCTCTGGAGGATGGAGAGAGAGAAAAAACAACAGCTCCTGGACAGG
Gibbon 361 CTAAGCCAGATATTTGGCCAATCTCTGAATGTTCTGGTCTCTGGAGGATGGAGAGAGAGAAAAAACAACAGCTCCTGGACAGG

CSH1 336 GAGAGCGCTGGCTCTTCTCTCCGGTCCCTCAATTGGCCCTCCGGTTTCTCCCAAGGCTCCCGAGCGTCCCTGCTCCTGGCTTTTGCC
Gibbon 450 GAGAGCGCTGGCTCTTCTCTCCGGTCCCTCAATTGGCCCTCCGGTTTCTCCCAAGGCTCCCGAGCGTCCCTGCTCCTGGCTTTTGCC

CSH1 426 TGCTCTGCCTGCCTGGCTTCAAGAGGCTGGTCCCGTCCAAACCGTTCCTTATCCAGGCTTTTGAAGCAGCTATGTTCCAAGCCCATC
Gibbon 540 TGCTCTGCCTGCCTGGCTTCAAGAGGCTGGTCCCGTCCAAACCGTTCCTTATCCAGGCTTTTGAAGCAGCTATGTTCCAAGCCCATC

CSH1 516 GCGGCACCAGCTGGCCATTGACACCTACCAGGAGTTTGTAACTCTTGGGGAATGGGTCCGGTCCAGGGTGGCAAGAACGGGTGACTT
Gibbon 630 GCGGCACCAGCTGGCCATTGACACCTACCAGGAGTTTGTAACTCTTGGGGAATGGGTCCGGTCCAGGGTGGCAAGAACGGGTGACTT

CSH1 606 TCCCCACTGGGGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTCTTCTGAAAGCGAAAATGCAGGCAGATGAGCATAGGCTGAGCC
Gibbon 720 TCCCCACTGGGGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTCTTCTGAAAGCGAAAATGCAGGCAGATGAGCATAGGCTGAGCC

CSH1 696 AGGTTCACAGAAAAGCAACAATGGAGCTGGTCTCCAGCATAGAAAACAGCAGTCTCTCTGGT-----GGGGGTCTCTCTAGGAAGAA
Gibbon 810 AGGTTCACAGAAAAGCAACAATGGAGCTGGTCTCCAGCATAGAAAACAGCAGTCTCTCTGGT-----GGGGGTCTCTCTAGGAAGAA

CSH1 784 ACCTATATCCCAAAGGACCAGAAGTATTCATTCTGCATTAACCCAGACTCCTTCTGCTTCTCAGACTCTATTCGGACACCTCCAAC
Gibbon 900 ACCTATATCCCAAAGGACCAGAAGTATTCATTCTGCATTAACCCAGACTCCTTCTGCTTCTCAGACTCTATTCGGACACCTCCAAC

CSH1 874 ATGGAGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCTAGCGGGATGGGGAGACCTGTGGTCAGCGCTCCCGGCAGCA
Gibbon 990 ATGGAGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCTAGCGGGATGGGGAGACCTGTGGTCAGCGCTCCCGGCAGCA

CSH1 964 CAGCCACTGCGGTCTCTCCCTGCAGAACTTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCGTCCGGTTC
Gibbon 1079 CAGCCACTGCGGTCTCTCCCTGCAGAACTTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCGTCCGGTTC

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CSH1 1054 CTCAGGAGTATCTTCGCCAACACCTGGTGTATGACACCTCGGACAGCGATGACTATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAA  
Gibbon 1169 CTCAGGAGTATCTTCGCCAACACCTGGTGTATGACACCTCGGACAGCGATGACTATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAA

CSH1 1144 ACCTGATGGGGGTGAGGGTGGCCAGGGGTCCCAATCCTGGAAACCCACTGGCTTCAGGGCTGGGGAGAGAAACTGCTGCCCT  
Gibbon 1259 ACCTGATGGGGGTGAGGGTGGCCAGGGGTCCCAATCCTGGGGCCCACTGGCTTCAGGGCTGGGGAGAGAAACTGCTGCCCT

CSH1 1234 CTTTCTAGCAGTAAGGCGCTGACCCAGAGAACTACCTTATTCTTCATTTCCCTGGTGAATCCTCCAGGCCTTTCTCTACACCCTGAA  
Gibbon 1349 CTTTCTAGCAGTCAGGCGCTGACCCAGAGAACTACCTTATTCTTCATTTCCCTGGTGAATCCTCCAGGCCTTTCTCTACACCCTGAA

CSH1 1324 GGGGAGGAGGAAAATGGATAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCAGAGGC  
Gibbon 1439 GGGGAGGAGGAAAATGGATAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCAGAGGC

CSH1 1414 GGAAGACGGCAGCCCGCGACTGGCAGATCCCTCAAGCAGACCTAACAGCAAGTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAA  
Gibbon 1529 GGAAGATGGCAGCCCGCAGACTAGGCAGACCCTCAAGCAGACCTAACCAAGTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAA

CSH1 1504 GAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGTTCGAGACATTCCTGCGCATGGTGCAGTGCCGCTCTGTGGAGGCAG  
Gibbon 1619 GAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGTTCGAGACATTCCTGCGCATGGTGCAGTGCCGCTCTGTGGAGGCAG

CSH1 1594 CTGTGGCTTCTAGGTGCCCAAGTATGCATCCTGTGACCCCTCCCAAGTGCCTCTCCTGCCCTCAGAGGTGCCACTCCAGTGCCCAACAGC  
Gibbon 1709 CTGTGGCTTCTAGGTGCCCAAGTATGCATCCTGTGACCCCTCCCAAGTGCCTCTCCTGCCCTCAGAGGTGCCACTCCAGTGCCCAACAGC

CSH1 1683 CTGTCTTAATAAATAAAGTTGTATCATTTC-----  
Gibbon 1799 CTGTCTTAATAAATAAAGTTGTATCATTTCCTGTACCAGGTGTCTTCTATAATATTATGGGGTGGAAAGTGGTGGTATGGAGCAAG

CSH1  
Gibbon 1889 GGGCAGGTGGGAAGACGACCTGGAGGGCT

Alignment of human (NM\_001317) and gibbon *CSH1* genes sequences extracted from BAC AC198149. . The green line demarcates the signal peptide sequence and the red box shows the start codon

CSHL1 1 -----  
Gibbon 1 CACAAGCCCATCAGTGGCCCCAGGCCATAACCTGTCAGAGAAACAGTGGGGAGAAGCAGCGAGAGAGAAGGGGCCAGGGTATAAAAAAGG

CSHL1 1 -----AGCATCCCAAGGCCCGACTCCCCACCACTCAGGGTCTGTGGACAGCTCACCTAGCGGCATGCTGCA  
Gibbon 91 CCCACAAGAGACAGCTCCAGGATCCCAAGGCCCACTCCCAACCACTCAGGGTCTGTGGACAGCTCACCTAGCGGCATGCTGCA

CSHL1 72 GGTAAGCGCCCTAAAATCCCTTTGGGCACACTGTGCTCAGGGGAGAGCGCGCCCTGCAGATGGGACGGGGCCTAACCTCAGG  
Gibbon 181 GGTAAAGCGCCCTAAAATCCCTTTGGGCACACTGTGCTCAGGGGAGAGCGCGCCCTGTAGATGGGACGGGGCCTAACCTCAGG

CSHL1 161 TTTGGGGCTTCTGAATGTGAATATCGCCATCTAAGCCAGATATTTGGCCAAATCTCTGAATGTTCCCTGGTCCCTGGAGGATGGAGAGAG  
Gibbon 271 TTTGGGGCTTCTGAATGTGAATATCGCCATCTAAGCCAGATATTTGGCCAAATCTCTGAATGTTCCCTGGTCCCTGGAGGATGGAGAGAG

CSHL1 251 AGAAAAAGAAAACAGCTCCTGGAACAGGGAGAGTGTGGCCTCTTCTCTCGGGCTCCCTCTTSCCCTCCGTTTCTCCCCAGGCTC  
Gibbon 361 AGAAAAAACAAACAGCTCCTGGAACAGGGAGAGTGTGGCCTCTTCTCTCGGGCTCCCTCTTTGCCCTCCGTTTCTCCCCAGGCTC

CSHL1 339 CCGACSTCCCTGCTCCTGGCTTTGCCCCTGCTCCTGCTGCCCTGGCTTCAAGAGGCTGTGCCGTCCAAACCGTTCCCTTATCCAGGCT  
Gibbon 451 CCGACTCCCTGCTCCTGGCTTTGCCCCTGCTCCTGCTGCCCTGGCTTCAAGAGGCTGTGCCGTCCAAACCGTTCCCTTATCCAGGCT

CSHL1 429 TTTTAAAGAGGCTATGCTCCAAGCCATCGCGCCACCACTGGCCATTGACACCTACCAGGAGTTTATAAGCTCTTGGGGAATGGGTGC  
Gibbon 541 TTTTAAAGAGACTATGCTCCAAGCCATCGCGCCACCACTGGCCATTGACACCTACCAGGAGTTTATAAGCTCTTGGGGAATGGGTGC

CSHL1 519 GGGTCAGGGTGGCAAGAACGGGTGACTTTCCCCCACTGGGGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTCTGAGCGAA  
Gibbon 631 GGGTCAGGGTGGCAAGAACGGGTGACTTTCCCCCACTGGGGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTTATACTGAGCGAA

CSHL1 609 AATGCAGGCAGATGAGCATAGGCTGAGCCAGGTTCCCAGAAAGTAACAATGGAGCTGGTCTCCAGCATAGAAAGCAGTGGTCTTCTCT  
Gibbon 721 AATGCAGGCAGATGAGCATAGGCTGAGCCAGGTTCCCAGAAAGTAACAATGGAGCTGGTCTCCAGCATAGAAAGCAGTGGTCTTCTCT

CSHL1 699 GGT--GGGGGTCTTC CCTAGGAAGAAGCCTATATCA CAAAGGAA CAGAAGTATTCATTCTGCATGACT CCCAGAC TCCTTCTGCT  
Gibbon 811 GGC GGGGGGTCTTC CCTAGGAAGAAGCCTATATCC CAAAGGAA CAGAAGTATTCATTCTGCATAAC CCCAGACT TCCTTCTGCT

CSHL1 787 TCTCAGACTCTATTCCGACAT CCTCCAACATGGAGGAAAC CAGCAGAAATCCGTGAGTGGATGCTCTCTCCCTAGGC GGGGATGGGG  
Gibbon 901 TCTCAGACTCTATTCCGACAC CCTCCAACAGCAGGAAAC CAGCAGAAATCCGTGAGTGGATGCTCTCTCCCTAGGC AGGT GGGGATGGGG

CSHL1 877 AGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGC CGGTCTTCCCTGCAGAACTTAGAGCTGCTCC CATCTCCCTGTGCTCA  
Gibbon 990 AGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGT CGGTCTTCCCTGCAGAACTTAGAGCTGCTCC CATCTCCCTGCGCTCA

CSHL1 967 TCGAGTCGC GGCTGGAGCCCGTGCCTTCCTCAGGAGTAC CTTCAACAA CACTGGTGTATGACACCTCGGACAGCGATGACTAT CACC  
Gibbon 1080 TCGAGTCGT GGCTGGAGCCCGTGCCTTCCTCAGGAGTAT CTTCAACAA CACTGGTGTATGACACCTCGGACAGCGATGACTAT GACC

CSHL1 1057 TCCTAAAGGACCTAGAG GAAGGCATCCAAATGCTGATGGGGTGAGGGTGGC CCAGGGGTCCCCAATCCTGGAAG CCCACTGGCTTCGA  
Gibbon 1170 TCCTAAAGGACCTAGAA GAAGGCATCCAAACGCTGATGGGGTGAGGGTGGCC CCAGGGGTCCCCAATCCTGGG GCG CCCACTGGCTTCGA

CSHL1 1147 GGGCTGGGGGAGAGAAACTGCTGCCCTCTTTCTAGCAGTCAGGCGCTGACCCAAGAGAACTACCTTATTCTTCATTTCCCTCTCTGA  
Gibbon 1260 GGGCTGGGGGAGAGAAACTGCTGCCCTCTTTCTAGCAGTCAGGCGCTGACCCAAGAGAACTACCTTATTCTTCATTTCCCTCTCTGA

CSHL1 1237 ATCTCCAGGCCTTTCTCTACACCCTGAAGGGGAGGAGGAAATGGAT AATGAGAGAGGGAGGGAAACAGTGCCCAAGCGCTTGGCTCTC  
Gibbon 1350 ATCTCCAGGCCTTTCTCTACACCCTGAAGGGGAGGAGGAAATGGAT AATGAGAGAGGGAGGGAAACAGTGCCCAAGCGCTTGGCTCTC

CSHL1 1327 TCCTTCTCTTGCCTTCACTTTGCAGAGGCTGGAAGACGGCAGCCACTGACTGGGCAGACCTCAAGCAGACCTACAGCAAGTTTGACACA  
Gibbon 1440 TCCTTCTCTTGCCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCACTGACTGGGCAGACCTCAAGCAGACCTATAACAAGTTTGACACA

CSHL1 1417 AACTCGCACAAACATGACGCACTGCTCAAGAACTACGGGCTGCTCCACTGCTCAGGAAGGACATGGACAAGGTGAGACATTCTCTGCGC  
Gibbon 1530 AACTCGCACAAACATGACGCACTGCTCAAGAACTACGGGCTGCTCCACTGCTCAGGAAGGACATGGACAAGGTGAGACATTCTCTGCGC

CSHL1 1507 ATGCTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGGGGCCCGGTGGCATCCTGTGACCCCTCCCCAGTGCCTCTCTGGCCC  
Gibbon 1620 ATGCTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGGGGCCCGGTGGCATCCTGTGACCCCTCCCCAGTGCCTCTCTGGCCC

CSHL1 1597 TGAAAGGTGCCACTCCAGTGCCACCAGCCTTGCTTAATAAAATTAAGTTGTATTCTT-----  
Gibbon 1710 CGAAAGGTGCCACTCCAGTGCCACCAGCCTTGCTTAATAAAATTAAGTTGTATTCTT-----

CSHL1  
Gibbon 1800 TGGGGTGAAAGTGGTGGTATGGAGCAAGGGGCAGGTGGGAAGACGACCTGGAGGGCCTCAGGGTCTATTGGGAACTAGGCTGCTGAAA

CSHL1  
Gibbon 1890 TATAAGAGGTTTGGCTGTTCTGGCCAGA

Alignment of human (NM\_022579) and gibbon *CSH2* genes sequences extracted from BAC AC198149. . The green line demarcates the signal peptide sequence and the red box shows the start codon