Priscilla Samayoa

Kristine Vidal

Brittany Puebla

Fan Ding

Notice that a match to the forward primer (nucleotides 1–42), and a match to the reverse primer (nucleotides 44–68) are within the same *Accession.* Also notice that position 43 of the forward primer is missing. What does this mean?

That’s where the SNP is.

Size of amplified DNA fragment: 5405-5185+1: 221 units

What does the *E- value* of *6e-12* mean?

It has a high probability that the hit is related to the query because it is a very low E-value.

Note the names of any *significant alignments* that have *E-values* less than 0.1. Do they make sense? What do they have in common?

Yes they make sense, what they have in common is that they all related to genes that control bitter taste receptor.

Size of amplified DNA fragment for homo sapiens non-taster and tasters:

321-101+1: 221

Non-taster sequence of amplified DNA: ccttcgtttt cttggtgaat ttttgggatg tagtgaagag gcaggcactg agcaacagtg attgtgtgct gctgtgtctc agcatcagcc ggcttttcct gcatggactg ctgttcctga gtgctatcca gcttacccac ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg attgcaaaccaagccaacctc

Taster sequence of amplified DNA: ccttcgtttt cttggtgaat ttttgggatg tagtgaagag gcagccactg agcaacagtg attgtgtgct gctgtgtctc agcatcagcc ggcttttcct gcatggactg ctgttcctga gtgctatcca gcttacccac ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg attgcaaacc aagccaacct c

Landed on chromosome 7

Genes found on either side of TAS2R38: [CLEC5A](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=retrieve&dopt=full_report&list_uids=23601) and [MGAM](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=retrieve&dopt=full_report&list_uids=8972)

Structures differ in that MGAM codes for an enzyme that plays a role the final steps of digestion of starch. CLEC5A plays a role in cell activation.

They are the same in that they are receptors mostly dealing with taste receptors and olfactory receptors.

You can conclude that genes that code for bitter taste receptors are on the same chromosome.

Bonobo/ Pan Paniscus:

1 atgttgactc taactcgcat ccacactgtg tcctatgaag tcaggagtac atttctgttc 61 atttcagtcc tggagttcgc agtggggttt ctgaccaatg ccttcgtttt cttggtgaat 121 ttttgggatg tagtgaagag gcagccactg agcaacagtg attgtgtgct gctgtgtctc 181 agcatcagcc ggcttttcct gcatggactg ctgttcctga gtgctatcca gcttacccac 241 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcaacat gctatggatg 301 attgcaaacc aagccaacct ctggcttgct gcctgcctca gcctgcttta ctgctccaag 361 ctcatccgtt tctctcacac cttcctgatc tgcttggcaa gctgggtctc caggaagatc 421 tcccagatgc tcctgggtat tattctttgc tcctgcatct gcactgtcct ctgtgtttgg 481 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca 541 aggctcaact ggcagattaa agatctcaac ttattttatt cctttctctt ctgctatctg 601 tggtctgtgc ctcctttcct attgtttctg gtttcttctg ggatgctgac tgtctccctg 661 ggaaggcaca tgaggacaat gaaggtctat accagagact ctcgtgaccc cagcctggag 721 gcccacatta aggccctcaa gtctcttgtc tcctttttct gcttctttgt gatatcatcc 781 tgtgctgcct tcatctctgt gcccctactg attctgtggc gtgacaaaat aggggtgatg 841 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagctgtcct gatctcaggc 901 aatgccaagt tgaggagagc tgtgacgacc attctgctct gggctcagag cagcctgaag 961 gtaagagccg accacaaggc agattcccgg acactgtgct ga

Gorilla:

1 atgttgactc taactcgcat ccgcactgtg tcctatgaag tcaggagtac atttctgttc 61 atttcagtcc tggagtttgc agtggggttt ctgaccaatg ccttcgtttt cttggtgaat 121 ttttgggatg tagtgaagag gcagccactg agcaacagtg attgtgtgct gctgtgtctc 181 agcatcagcc ggcttttcct gcatggactg ctgttcctga gtgctatcca gcttacccac 241 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 301 attgcaaacc aagccaacct ctggcttgct gcctgcctca gcctgcttta ctgctccaag 361 ctcatccgtt tctctcacac cttcctgatc tgcttggcaa gctgggtctc caggaagatc 421 tcccagatgc tcctgggtac tattctttgc tcctgcatct gcactgtcct ctgtgtttgg 481 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca 541 aggctcaact ggcagattaa agatctcaac ttattttatt cctttctctt ctgctatctg 601 tggtctgtgc ctcctttcct attgtttctg gtttcttctg ggatgctgac tgtctccctg 661 ggaaggcaca tgaggacaat gaaggtctat atcagagact ctcgtgaccc cagcctggag 721 gcccacatta aagccctcaa gtctcttgtc tcctttttct gcttctttgt gatatcatcc 781 tgtgctgcct tcatctctgt gcccctacyg attctgtggc gcgacaaaat aggggtgatg 841 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagccgtcct gatctcaggc 901 aatgccaagt tgaggagagc tgtgacaacc attctgctct gggctcagag crgcctgaag 961 gtaagagccg accacaaggc agattcccgg acaccgtgct ga

Chimpanzee:

1 atgttgactc taactcgcat ccacactgtg tcctatgaag tcaggagtac atttctgttc 61 atttcagtcc tggagtttgc agtggggttt ctgaccaatg ccttcgtttt cttggtgaat 121 ttttgggatg tagtgaagag gcagccactg agcaacagtg attgtgtgct gctgtgtctc 181 agcatcagcc ggcttttcct gcatggactg ctgttcctga gtgctatcca gcttacccac 241 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 301 attgcaaacc aagccaacct ctggcttgct gcctgcctca gcctgcttta ctgctccaag 361 ctcatccgtt tctctcacac cttcctgatc tgcttggcaa gctgggtctc caggaagatc 421 tcccagatgc tcstgggtat tattctttgc tcctgcatct gcactgtcct ctgtgtttgg 481 tgstttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca 541 aggctcaact ggcagattaa agatctcaac ttattttatt cctttctctt ctgctatctg 601 tggtctgtgc ctcctttcct attgtttstg gtttcttctg ggatgctgac tgtctccctg 661 ggaaggcaca tgaggacaat gaaggtctat accagagact ctcgtgaccc cagcctggag 721 gcccacatta aggccctcaa gtctcttgtc tcctttttct gcttctttgt gatatcatcc 781 tgtgctgcct tcatctctgt gcccctactg attctgtggc gtgacaaaat aggggtgatg 841 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagccgtcct gatctcaggc 901 aatgccaagt tgaggagagc tgtgacgacc attctgctct gggctcagag cagcctgaag 961 gtaagagcyg accacaaggc agattcccgg acactgtgct ga

G.The 221 base pair amplicon for taster is different by one base pair from the human PTC non-taster. The 221base pair amplicon for the non-taster is different by one base pair from the human PTC taster. The initial stretch of yellow shows the difference between the DNA base pairs. The SNP is at 45. They have different amino acids, the amino acids differ in that GGC encodes for glycine and GCC encodes for alanine.

H. Comparing human taster and non-taster: they differ in number 45 base pair. Non-taster have a G nucleotide, taster has a C.

I. Comparing all of the species humans (taster and non-taster), bonobo, chimpanzee and gorilla: from 1- 100 they all differ as well as in nucleotide 145, 287 and from 132 on. The ancestral state of this gene at nucleotide position 145, 785, 886 is that the mutation at 145 is that of non-tasters. At 785 and 886, there is no human sequence for us to evaluate. Other primates are tasters; they match up perfectly with the taster sequence. Bonobo does have a small base pair difference at 287 from both taster and non-taster. This suggests that bitter taste receptors are an evolutionary trait.

J. Comparing forward primer vs PTC human taster vs PTC non-taster: They differ by one base pair, 43. The forward primer stops matching up at 44, because that’s where it ends. The primer binds at the beginning of the sequence.