

**Department of Integrated Biosciences**

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**Master's Thesis**

**Evolutionary conservation and disruption of umami-sweet  
taste receptor gene family in ecologically diverse platyrrhine  
primates**

(多様な生態を示す広鼻猿類における  
旨味-甘味受容体遺伝子群の進化的保存性の検証)

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## Abstract

### Evolutionary conservation and disruption of umami-sweet taste receptor gene family in ecologically diverse platyrrhine primates

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## Introduction

Taste plays a vital role in an animal's fitness by helping them make decisions about ingesting beneficial foods and avoiding harmful substances in their daily life. The umami and sweet taste perception is initiated by the umami-sweet taste receptors (TAS1Rs); umami by TAS1R1-TAS1R3 heterodimer and sweet by TAS1R2-TAS1R3 heterodimer. Although these senses could be considered to be conserved, recent research has revealed diversity of these receptor genes across vertebrate species. However, much information has largely relied on whole-genome assembly (WGA) data which are often incomplete with shallow sequencing depth, especially for multigene families. Platyrrhine primates (monkeys of Americas) are suitable for understanding the evolutionary conservation and diversity of umami-sweet taste receptor gene family because of their remarkable diversity in color vision and diets. This study aims to clarify the compositions of *TAS1R* gene family among platyrrhines by applying targeted capture (TC) with high-depth short-read massive parallel sequencing ("Next-Generation" sequencing: NGS) and to examine if conservation/diversity of the genes is associated with color vision or dietary ecology of the monkeys.

## Materials and Methods

I examined 18 species, one individual for each, of platyrrhines from all three Families (Cebidae, Atelidae, Pitheciidae). Probes for the three genes, *TAS1R1*, *TAS1R2* and *TAS1R3*, were designed from available WGA databases of platyrrhines. As references of selective neutrality and single-copy sequencing depth, 85 single-copy non-protein-coding sequences (82 autosomal and 3 X-non-pseudoautosomal) were used. Sequencing reads were mapped to the gene/region sequences and assembled three rounds for accuracy. The sequencing depths and the density of single-nucleotide polymorphism (SNP) sites were evaluated. *TAS1R* genes were

further evaluated for the length of open-reading frame (ORF) and capability of forming 7-transmembrane (7-TM) structure to judge whether the genes were intact, disrupted, or intact-disrupted heterozygous.

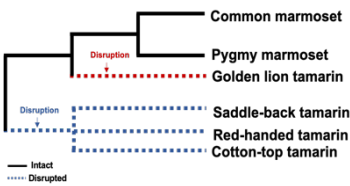
Results

Sequences depth compared between TC and WGA

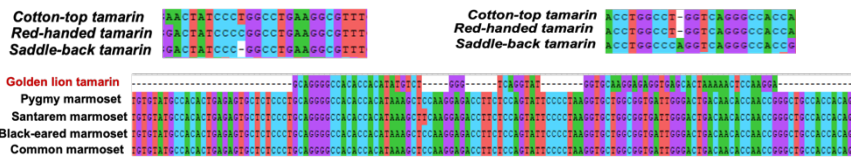
Genus	Name	Targeted Capture	WGA
Cebidae	Common marmoset	469	63
	Black-eared marmoset	790	NA
	Santarem marmoset	419	35
	Pygmy marmoset	546	35
	Golden Lion Tamarin	804	78
	Red-handed tamarin	472	53
	Cotton-top tamarin	487	55
	Saddle-back tamarin	448	NA
	Azara's night monkey	416	35
	Tufted capuchin	579	43
	White-faced capuchin	762	81
	Bolivian squirrel monkey	439	111
	mantled howler	496	43
Atelidae	black-handed spider monkey	508	57
	Common woolly monkey	480	35
	duky titi	470	35
Pitheciidae	Bearded saki	518	NA
	Pale-faced saki	588	79
	Average	538	56

The average sequence depths per nucleotide site of 18 platyrrhine species using targeted capture was 538 and data depth obtained from WGA was 56. On average, the depth of targeted capture was roughly ten times greater than that of WGA (Table left).

TASIR gene composition revealed by TC



The umami receptor *TASIR1* was disrupted in lion tamarin and tamarins. The phylogenetic tree (Figure left) indicates that lion tamarins and tamarins belong to separate branches, and their disruption patterns (Figure below) are notably distinct. Consequently, based on these observations, I inferred that these disruptions occurred independently. On the other hand, according to the comparison of the non-synonymous and synonymous nucleotide substitutions, other *TASIR* genes of lion tamarin and tamarins and the *TASIR* genes of other platyrrhine species appeared to be under natural selection to conserve their function.



Discussion

The much higher sequencing depth achieved with targeted capture than with WGA enabled significant improvement of sequencing reliability. The disruption of *TASIR1* gene in tamarins and lion tamarins was also confirmed in WGA databases of other tamarin species. The disruption of *TASIR1* in tamarins and loin tamarins implies their loss of umami sensation. While the loss does not seem to be associated with color vision, this might be related to their tree-sap feeding habit. Data obtained from targeted capture and WGA are complementary, providing a more comprehensive understanding when used together. Further analyses are required to determine the ecological factors influencing the evolution of the *TASIR* gene family.

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# 1 Introduction

## 1.1 Senses

Animals rely on their senses to find food, identify mates, recognize territories, avoid danger, and interpret social signals. These sensory abilities are essential for survival and reproduction, and they have coevolved with the anatomy, physiology, and behavior of animals, including humans (Kawamura and Melin, 2017). It is generally accepted that there are five senses, sight, smell, taste, hearing, and touch, which can be categorized as senses that perceive physical and chemical stimuli. Visual, auditory, and cutaneous senses perceive physical stimuli such as light, sound, temperature, and mechanical stimuli, while taste and smell represent the chemical senses which respond to chemical compounds.

## 1.2 Taste perception

In contrast to touch, vision, hearing, or smell, which operate across a variety of behavioral contexts, the sense of taste has specifically evolved to play a crucial role as the primary regulator and driver of feeding behavior (Yarmolinsky et al., 2009). Taste is responsible for assessing the nutritional content of food and preventing the consumption of toxic substances. In general, there are five basic tastes, umami, sweet, bitter, sour, and salty. Umami allows for the recognition of amino acids, sweet taste enables the identification of energy-rich nutrients, bitter and sour tastes warn against the ingestion of potentially harmful or poisonous chemicals, and salt taste ensures proper dietary electrolyte balance (Chandrashekar et al., 2006). Among them, umami, sweetness, and bitterness are mediated by the G-protein-coupled receptors while the sourness and saltiness are mediated by ion-channels (Chandrashekar et al., 2006; Yarmolinsky et al., 2009). The anatomical structures responsible for taste detection are taste-receptor cells (TRCs), which are organized into taste buds. These taste buds are distributed across different types of papillae on the tongue and the palate epithelium (Chandrashekar et al., 2006).

### 1.3 Umami-sweet taste receptor (TAS1Rs)

Taste receptor type 1 (TAS1R), a G protein-coupled receptor family, consists of three members, namely TAS1R1, TAS1R2 and TAS1R3, respectively, and act as umami or sweet receptors (Li et al., 2002). *TAS1R1*, *TAS1R2* and *TAS1R3* genes are single-copy genes, respectively, which contain six exons and five introns. The TAS1R1/TAS1R3 heterodimer serves as an umami taste receptor in mammals, detecting L-amino acids and 5'-ribonucleotides while the TAS1R2/TAS1R3 heterodimer functions as a sweet taste receptor (Li et al., 2002; Nelson et al., 2002; Toda et al., 2021).

The number of *TAS1R* genes as three appears to be conservative among vertebrates. Although the conservation of the number of *TAS1R* genes would imply their core role in detecting crucial nutrients like amino acids, nucleic acids, and sugars, recent research has revealed significant diversity across mammalian species.

For instance, the umami-sensory *TAS1R1* gene in giant pandas has become pseudogenized, coinciding with their shift in diet from carnivorous to bamboo-consuming (Zhao et al., 2010). In addition, the carnivorous domestic cat (*Felis silvestris catus*) has pseudogenized sweet-sensory *TAS1R2* gene (Li et al., 2005). In behavioral experiments, cats do not respond to sugar water, and comparison of *TAS1R1* nucleotide sequences with other felids revealed a common deletion within *TAS1R1* coding region. This suggests that pseudogenization of *TAS1R1* gene had already occurred in the common ancestor of felids.

Furthermore, among closely related species the taste receptor genes exhibit diversity possibly influenced by dietary differences among the animals. Notably in marine mammals, feeding behavior has been suspected to influence the composition of taste receptor genes. In carnivorous pinnipeds such as the California sea lion (*Zalophus californianus*) and the South American sea lion (*Otaria flavescens*), *TAS1R2* gene is pseudogenized. In the case of the California sea lion, *TAS1R3* gene is also pseudogenized (Jiang et al., 2012). Moreover, nearly all cetaceans may have lost

all taste modalities except for that of salt. This is thought to be related to their particular way of eating, which is to swallow food whole (Zhu et al., 2014).

#### 1.4 Evolutionary diversity of TAS1Rs for primates

High sensitivity to L-glutamate (L-Glu) is a characteristic of human umami receptor TAS1R1-TAS1R3, but the TAS1R1-TAS1R3 of other vertebrates does not consistently show this L-Glu response (Nelson et al., 2002; Oike et al., 2007). The mouse TAS1R1-TAS1R3 responds more strongly to other L-amino acids than to L-Glu. The amino acid responses in human and mouse TAS1R1-TAS1R3 are strongly enhanced by 5'-ribonucleotides (Nelson et al., 2002; Zhang et al., 2008), such as inosine monophosphate (IMP) and guanosine 5'-monophosphate (GMP). Toda et al. (2013) identified three key amino acid sites (170, 302, 379) in the TAS1R1 amino acid sequence responsible for receiving L-glutamate (L-Glu) and/or 5'-ribonucleotides. Toda et al. (2021) showed that the L-Glu sensitivity of TAS1R1-TAS1R3 is a derived state that has evolved repeatedly in large primates that rely on leaves as protein sources, after their divergence from insectivorous ancestors whose TAS1R1-TAS1R3 is more sensitive to 5'-ribonucleotides. Receptor expression experiments by Toda et al. (2021) showed that common amino acid substitutions at the three key amino acid sites that render TAS1R1-TAS1R3 sensitive to L-Glu occur independently at least three times in primate evolution, while TAS1R1-TAS1R3 senses 5'-ribonucleotides as opposed to L-Glu in several mammalian species, including insectivorous primates (Toda et al. 2021). The chemical analysis by Toda et al. (2021) also revealed that L-Glu is one of the major free amino acids in primate diets and that insects, but not leaves, contain large amounts of free 5'-ribonucleotides. These studies suggest that the ancestral type of primate TAS1R1-TAS1R3 was sensitive to nucleotides of insects and the TAS1R1-TAS1R3 of large primates evolved to detect L-Glu found in folivorous diets, overcoming bitter and aversive tastes of leaves by L-Glu preference.



More in detail, Toda et al. (2021) examined 18 species of primates, together with five species of non-primate mammals to investigate TAS1R1 evolution. They found that humans, macaques, and baboons [belonging to the Suborder Anthropoidea, Infraorder Catarrhini: humans and apes (the Superfamily Hominoidea), and African/Asian monkeys (the Family Cercopithecidae)], which showed high L-Glu sensitivity, had uncharged residues (Ala or Gly) at both positions 170 and 302 of TAS1R1. In contrast, squirrel monkeys (belonging to the Suborder Anthropoidea, the Infraorder Platyrrhini: monkeys of Americas) and mice, which showed low L-Glu sensitivity, had acidic residues at one or both positions. Moreover, they discovered that all tested catarrhines, as well as spider monkeys (a platyrrhine) and ring-tailed lemurs (belonging to the Suborder Strepsirrhini, Infraorder Lemuriformes), which obtain protein more from leaves than from insects, have uncharged residues at both 170 and 302. Other platyrrhine monkeys, except for cebids, exhibit significant L-Glu responses but have an acidic residue at 302. Several studies have proposed that the common ancestor of anthropoids had a larger body size and relied more on non-insect foods (Steiper and Seiffert, 2012; Wu et al., 2017). Considering that a single mutation in the spider monkey (TAS1R1-A302D) resulted in a reduced but still significant L-Glu response, it is likely that ancestral anthropoids initially gained small L-Glu sensitivity through a mutation to alanine at position 170. Subsequently, primary leaf-eaters might have independently evolved additional substitutions to enhance their L-Glu sensitivity.

This result is related to the structure of TAS1R1-TAS1R3 heterodimer, each of them contains an extracellular “Venus flytrap” domain (VFTD) connected to a smaller cysteine-rich domain (CRD) and a seven-transmembrane (7-TM) domain. The VFTD consists of two lobes with the ligand binding site located in the hinge region between these lobes (Kunishima et al., 2000; Muto et al., 2007). It has been elucidated that the hinge region of the VFTD in TAS1R1/TAS1R3 hosts the L-Glu binding site (López Cascales et al., 2010; Zhang et al., 2008), whereas the IMP-binding site is

situated near the entrance of the VFTD in TAS1R1 (Zhang et al., 2008). Toda et al. (2013) reported that loss-of-charge mutations at amino acid residues 170 and 302 in human TAS1R1 conferred a high affinity for L-Glu due to the elimination of electrostatic repulsion at the ligand binding pocket. This finding aligns with Roura et al. (2011), who proposed that Arg-307 in the human TAS1R1 is critical for amino acid recognition. They suggested that the presence of Thr (a neutral polar residue) in the rodent TAS1R1 at this position, instead of Arg (a charged polar residue), allows a wider range of L-amino acids to enter and interact with the orthosteric ligand binding site. Their results also suggest that residue 379, which exists at the outer side of the ligand binding pocket, influences both amino acid and 5'-ribonucleotide sensitivities.

Liu et al. (2014) conducted another comprehensive investigation into the natural selection on the *TAS1R* genes in catarrhine primates. They found significant relaxation of selective constraints on the sweet taste gene *TAS1R2* in the ancestral branch of the Subfamily Colobinae, likely related to their unique leaf ingestion and digestion. Additionally, they identified positive selection for the umami taste gene *TAS1R1* in the Family Cercopithecidae lineages, *TAS1R2* in the Subfamily Cercopithecinae, current Colobinae, and the Family Hylobatidae lineages, and *TAS1R3* in the genus *Macaca* lineages. This study also highlighted several mutations in Cercopithecidae, Colobinae, and the genus *Pygathrix* that were previously shown to alter receptor sensitivity. Most of the positively selected sites are located in the extracellular region of TAS1Rs. Molecular modeling identified two critical amino acid sites for TAS1R1 and four critical amino acid sites for TAS1R2 in the extracellular region, responsible for binding specific sweet and umami taste molecules. This study suggests that episodic and differentiated adaptive evolution of *TAS1R* genes has been pervasive in catarrhine primates, particularly concentrated in the extracellular region of these receptors.

These findings highlight the intricate relationship between diet, genetic mutations, and taste receptor evolution in primates, suggesting that research is needed to further investigate on these genetic adaptations for broader implications in primate evolution.

#### 1.4 Platyrrhines

In this study, I focused on platyrrhine primates as they are suitable for understanding the composition of umami-sweet taste receptor gene family in relation to other senses or feeding ecology because of their remarkable diversity in color vision and diets.

Species of the Infraorder Platyrrhini inhabit Mexico, Central America and South America. They comprise of three Families, Cebidae, Atelidae and Pitheciidae (Fleagle 2013). The Cebidae comprises of three Subfamilies, Cebinae (including capuchins and squirrel monkeys), Callitrichinae (including tamarins and marmosets) and Aotinae (owl monkeys). The Atelidae comprises of two Subfamilies, Alouattinae (howler monkeys) and Atelinae (including spider monkeys and woolly monkeys). The Pitheciidae comprises of two Subfamilies, Callicebinae (titis) and Pitheciinae (including sakis and uakaris).

Platyrrhines are diverse in feeding habits (Fleagle 2013). Cebids are overall omnivorous, primarily consuming fruits and insects, but also incorporating nuts, flowers, buds, seeds, leaves, plant gums, exudates, various invertebrates, and some vertebrate prey into their diet. Squirrel monkeys (genus *Saimiri*), which require higher protein levels, obtain this by consuming a significant amount of animal prey. Capuchins (genera *Cebus* and *Sapajus*) often manipulate food, such as using rocks to open oysters or smashing nuts and fruits to soften or open them to access the seeds. Callitrichines eat a substantial amount of plant gums and exudates in their diet and may also consume nectar. Additionally, some marmoset and tamarin species eat fungi and capture insects fleeing from army ant swarms (Gold, K. and Hutchins, 2004; Nowak, 1991, 1991). Owl monkeys (genus *Aotus*) are the only one nocturnal genus

among anthropoid primates. They are omnivorous, feeding on insects, fruits, leaves, seeds, bark, flowers, gums, bird eggs, and small vertebrates (Nowak, 1991). This dietary flexibility allows cebid monkeys to utilize alternative food sources during seasons when ripe fruits are scarce.

Atelids are primarily frugivorous but also consume varying amounts of leaves, flowers, nectar, plant gums, new shoots, and insects. Among them, howler monkeys (genus *Alouatta*) are the most folivorous. Their diet varies both geographically and seasonally, with a higher consumption of fruits when they are available, and leaves becoming more important when fruits are scarce or in disturbed forests. Atelines are characteristic with their long and prehensile tails, which can support their entire body weight while feeding (Nowak, 1991; Villavicencio, 2017). The spider monkey mainly feed on ripe fruit and less frequently leaves and flowers. They may also eat some nuts, seeds, insects, arachnids, and eggs (Chapman, 1987). The Diet of woolly monkey consists mainly of fruits, supplemented by leaves, seeds, and some insects. Consumption of leafy material accounts for probably less than 20% of their diet. A large part of their feeding time is spent eating ripe fruit (Peres, 1994).

Pitheciids are specialized for consuming large, hard fruits, often to access the seeds inside. Callicebines consume more fruit pulp compared to other genera. Pitheciines primarily eat large, indehiscent fruits with few large seeds, such as Brazil nuts. Pitheciid species also supplement their diet with leaves and insects.

Platyrrhines are also known with their extensive inter- and intraspecies variation of color vision (Kawamura, 2018). Howler monkeys attained the sex-independent trichromacy through duplication of the spectrally differentiated L/M opsin genes (Dulai et al., 1999; Jacobs et al., 1996a). On the other extreme, owl monkeys, the sole nocturnal anthropoid primates, are the cone monochromacy due to the loss of functional S opsin gene (Jacobs et al., 1996b, 1993; Levenson et al., 2007; Wikler and Rakic, 1990). Other platyrrhine species are reported to have allelic polymorphism of the single-locus X-linked L/M opsin gene and exhibit color vision

variation, a mixed population of female and male dichromats and female trichromats (Jacobs, 2007; Matsumoto et al., 2014).

Above all, the diverse dietary habits and color vision of platyrrhines prompted me to investigate their taste receptor gene family composition and functionalities which could provide insights into how they have evolved in response to their environment.

### 1.5 Whole-genome assembly (WGA) data and targeted capture

In bioinformatics, sequence assembly involves aligning and merging short sequencing reads to a longer DNA sequence to reconstruct the original sequences. This process is necessary because DNA sequencing technology cannot typically 'read' entire genomes in a single pass; instead, it reads shorter fragments ranging from ~20 to ~30,000 bases, depending on the technology used. These short fragments usually result from shotgun sequencing of genomic DNA or gene transcripts. Whole-genome assembly (WGA) utilizes these sequence assembly techniques to reconstruct entire genomes from these short fragments, providing a comprehensive view of the organism's genetic makeup. So, it has gradually become an alternative choice of low-cost but high-labor PCR. However, when investigating a specific gene or gene family using publicly available WGA databases, especially those of non-model organisms, accuracy is often a concern regarding DNA sequences and the composition of multigene families. This is possibly due to the poor assembly of shallow-depth, short-sequencing reads from massive parallel sequencing ("Next-Generation" sequencing: NGS) in many WGA databases. Also, many platyrrhines databases are still not available. Therefore, in this study, I applied targeted capture to investigate the *TASIR* gene family composition of 18 platyrrhine species with high-depth short-read NGS.

Targeted capture involves designing custom RNA or DNA baits that specifically hybridize with the genomic regions of interest, hybridizing these baits with the targeted genomic DNA fragments while minimizing hybridization with contaminant sequences, amplifying the targeted fragments using PCR via adaptor tags to enrich the

sample, and then performing NGS on the enriched sample to analyze the captured DNA fragments (Andermann et al., 2020). Targeted capture can improve the sequencing depth and enhance the reliability which is a more suitable method in this study.

#### 1.6 Purpose of this study

Our understanding on the relationship between taste receptor genes and diet in various primates remains elusive. Additionally, environmental information provided by color vision also may influence foraging behavior. Thus, analyzing the composition of *TAS1R* genes from the perspectives of diet and color vision could facilitate our understanding of the evolution of chemosensory systems. This study focuses on platyrrhine primates, which exhibit diverse diets and color vision. Although genomic databases have been increasingly enriched in recent years, complete genome data for platyrrhines are available for only a few species, and WGA databases tend to have shallow sequencing depth. Therefore, I used targeted capture and NGS, combined with information from the whole-genome assembly (WGA) database to study 18 platyrrhine species, including all three Families and all seven Subfamilies, to reveal evolutionary conservation and diversity of the *TAS1R* gene family in platyrrhine primates.

## 2 Materials and Methods

### 2.1 Genomic DNA samples

In this study, one individual each from 18 platyrrhine species were examined. These species cover all three Families (Cebidae, Atelidae and Pitheciidae), all seven Subfamilies (Callitrichinae, Aotinae, Cebinae, Alouattinae, Atelinae, Callicebinae and Pitheciinae), and 15 genera (*Callithrix*, *Mico*, *Cebuella*, *Leontopithecus*, *Saguinus*, *Aotus*, *Sapajus*, *Cebus*, *Saimiri*, *Alouatta*, *Ateles*, *Lagothrix*, *Callicebus*, *Chiropotes*, and *Pithecia*). The common name, scientific name, sample ID, sex, DNA source and providers of the platyrrhine samples are shown in Table 1.

Table 1 Sources of platyrrhine primates examined for *TAS1R* genes by targeted capture in this study.

Common Name	Scientific Name	Sample ID	Sex	DNA source	Provided from
					Central Institute for Experimental
Common marmoset	<i>Callithrix jacchus</i>	Cja61	female	Brain	Animals, individual ID H, through Dr. Yoshikuni Tanioka
Black-eared marmoset	<i>Callithrix penicillata</i>	Cpen6601	female	Muscle	Japan Monkey Center
Santarem marmoset	<i>Mico humeralifer</i>	Mhum6555	male	Liver	Japan Monkey Center
Pygmy marmoset	<i>Cebuella pygmaea</i>	Cpyg6460	male	Muscle	Japan Monkey Center
					Hamamatsu City Zoo, through Dr.
Golden Lion Tamarin	<i>Leontopithecus rosalia</i>	Lros7	male	Muscle	Hayakawa at Primate Research Institute, Kyoto University
Red-handed tamarin	<i>Saguinus midas</i>	Smid6595	female	Muscle	Japan Monkey Center
Cotton-top tamarin	<i>Saguinus oedipus</i>	Soe10	male	Liver	Primate Research Institute, Kyoto University
					Primate Research Institute, Kyoto
Saddle-back tamarin	<i>Saguinus fuscicollis</i>	Sfu9	unknown	Liver	University through Dr. Osamu Takenaka

Azara's night monkey	<i>Aotus azarae</i>	Aaz41	male	Blood	Primate Research Institute, Kyoto University
Tufted capuchin	<i>Sapajus apella</i>	Sap104	female	Blood	Primate Research Institute, Kyoto University
White-faced capuchin	<i>Cebus imitator</i>	Ccap9	male	Blood	Costa Rica, collected by Dr. Amanda Melin, Univ Calgary,
Bolivian squirrel monkey	<i>Saimiri boliviensis</i>	Sbol45	female	Blood	Japan Monkey Center
Mantled howler	<i>Alouatta palliata</i>	KSTR199	female	Blood	Univ Calgary, Melin Lab
Black-handed spider monkey	<i>Ateles geoffroyi yucatanensis</i>	Age319	female	Muscle	Mono Puma, collected at Punta Laguna, Yucatan, Mexico, by Dr. Filippo Aureli in 2013/6/18
Common woolly monkey	<i>Lagothrix lagotricha</i>	Llag6202	male	Muscle	Japan Monkey Center
Dusky titi	<i>Callicebus moloch</i>	Cmo4	unknown	Liver	Primate Research Institute, Kyoto University through Dr. Osamu Takenaka
Bearded saki	<i>Chiropotes satanas</i>	Csat6549	female	Muscle	Japan Monkey Center, Higashiyama Zoo
Pale-faced saki	<i>Pithecia pithecia</i>	Ppit5605	female	Muscle	Japan Monkey Center

## 2.2 Design of probes

The nucleotide sequence information of *TASIR* genes were taken by a past Kawamura lab student, Masahiro Hayashi, from the publicly available WGA databases of squirrel monkey (SaiBol1.0), common marmoset (calJac3), and Nancy Ma's owl monkey (Anan\_2.0) (Hayashi 2017 Master thesis) (Table 2). Probes covered all six exons and five introns as well as 100-bp 5'- and 3' flanking regions.



Table 2 Detailed information of the probe sequence source.

Orthologous Gene Group	Species	Sequence Name	Genome Database ID	Chromosome/ Scaffold	Probed Length	Strand
<i>TAS1R1</i>	<i>Saimiri boliviensis</i>	TAS1R1_Sbo	SaiBol1.0	JH378221	17,356	-
<i>TAS1R1</i>	<i>Callithrix jacchus</i>	TAS1R1_Cja	calJac3	Chr7	23,840	+
<i>TAS1R1</i>	<i>Aotus nancymae</i>	TAS1R1_Ana	Anan_2.0	Scaffold139	24,870	-
<i>TAS1R2</i>	<i>Saimiri boliviensis</i>	TAS1R2_Sbo	SaiBol1.0	JH378173	21,051	+
<i>TAS1R2</i>	<i>Callithrix jacchus</i>	TAS1R2_Cja	calJac3	Chr7	26,276	-
<i>TAS1R2</i>	<i>Aotus nancymae</i>	TAS1R2_Ana	Anan_1.0	Scaffold6	26,057	+
<i>TAS1R3</i>	<i>Saimiri boliviensis</i>	TAS1R3_Sbo	SaiBol1.0	JH378221	3,313	-
<i>TAS1R3</i>	<i>Callithrix jacchus</i>	TAS1R3_Cja	calJac3	Chr7	3,982	+
<i>TAS1R3</i>	<i>Aotus nancymae</i>	TAS1R3_Ana	Anan_2.0	Scaffold654.3	3,938	+

### 2.3 Design of neutral reference

A previous study by Kawamura lab (Akhtar et al. 2022) chose 85 single-locus non protein-coding sequences (82 autosomal and three X-nonpseudoautosomal) from the human reference genome hg19 using the Neutral Region Explorer (Arbiza et al. 2012) to use them as references of selective neutrality and of single-copy sequencing depth. The criteria of choosing these regions were (1) the regions did not contain repeat sequences, (2) each length was longer than 1.0kb, (3) distance was greater than 0.2 centimorgans (cM) from the nearest gene on autosomes or 0.1 cM on the X chromosome, and (4) minimum recombination rate was 0.9 cM/Mb as determined by the Neutral Region Explorer.

The Master thesis by Hayashi (2017) retrieved most of the orthologous sequences to these human sequences from the WGA data base of the squirrel monkey SaiBol1.0 (Table S1). For four regions not found in SaiBol1.0, sequences were retrieved from the common marmoset calJac3 (Table S1). For one region, the human sequence (hg19\_NR18) was used (Table S1).

## 2.4 Probe synthesis, targeted capture, and NGS

The synthesis of in-solution biotinylated RNA baits (myBaits®) was outsourced to Biodiscovery, LLC (Ann Arbor, MI) for targeted capture probes (Gnirke et al. 2009). Following probe design by Kawamura lab, each bait was synthesized with 120-nucleotides (nt) in length, overlapped adjacent baits by 60 nt. The baits in introns and flanking regions that contained repetitive sequences were eliminated.

The targeted capture and NGS were outsourced to the Centre for Health Genomics and Informatics and UCDNA Service at the University of Calgary, Canada. The DNA sequencing library was created by fragmenting genomic DNA into approximately 500 bp fragments and attaching adaptor oligonucleotides to the fragmented DNA. Genomic DNA samples with adaptors were heat-denatured in the presence of adapter-specific blocking oligonucleotides, and then lowered to the hybridization temperature to allow blockers to hybridize to the library adaptors. Biotinylated RNA baits were introduced and allowed to hybridize to targets for several hours. Bait-target hybrids were isolated from the solution using streptavidin-coated magnetic beads, which were stringently washed multiple times to remove non-hybridized and non-specifically hybridized molecules. This hybridization and washing conditions allowed up to ~10% mismatch, according to the manufacturer's protocol. The captured DNA library was released from the beads and amplified by polymerase chain reaction (PCR) using complementary adaptors. The massive parallel sequencer employed in this study was the Illumina NextSeq with 300 cycle and 150-bp paired end sequencing.

## 2.5 Quality control of NGS reads

The PRINSEQ tool was employed to ensure the quality of the raw NGS reads (Schmieder and Edwards, 2011). In the FASTQ-formatted reads, obtained from the Illumina sequencer, nucleotide positions with a quality score below 20 at either end of a read were removed. Additionally, reads with a mean quality score lower than 20 or shorter than 10 nucleotides were filtered out.

## 2.6 Reference sequences for the first-round mapping of NGS reads

For short reads to be as accurately mapped as possible, the principle I took was to choose the WGA databases of the phylogenetically closest species to the study species as the reference of first-round mapping. At the time I did the mapping, ten of the eighteen study platyrrhine species WGA databases were available. Among them, *TASIR* gene sequences from the WGA databases information of three species (golden lion tamarin, red-handed tamarin and mantled howler monkey) were incomplete. Therefore, I used the remaining seven species sequences of *TASIR* genes as reference for the first-round mapping (Table 3) [Bolivian squirrel monkey (*Saimiri boliviensis*), common marmoset (*Callithrix jacchus*), Nancy Ma's owl monkey (*Aotus azarae*), white-faced capuchin (*Cebus imitator*), tufted capuchin (*Sapajus apella*), black-handed spider monkey (*Ateles geoffroyi yucatanensis*) and pale-faced saki (*Pithecia pithecia*)].

Table 3 Reference sequences used for 1st mapping of NGS reads

Family	1 <sup>st</sup> mapping reference	Study species common name	Study species scientific name	Sample ID
Cebidae	<i>Callithrix jacchus</i>	Common marmoset	<i>Callithrix jacchus</i>	Cja61
		Black-eared marmoset	<i>Callithrix penicillata</i>	Cpen6601
		Santarem marmoset	<i>Mico humeralifer</i>	Mhum6555
		Pygmy marmoset	<i>Cebuella pygmaea</i>	Cpyg6460
		Golden Lion Tamarin	<i>Leontopithecus rosalia</i>	Lros7
		Red-handed tamarin	<i>Saguinus midas</i>	Smid6595
		Cotton-top tamarin	<i>Saguinus oedipus</i>	Soe10
		Saddle-back tamarin	<i>Saguinus fuscicallis</i>	Sfu9
	<i>Aotus azarae</i>	Azara's night monkey	<i>Aotus azarae</i>	Aaz41
	<i>Sapajus apella</i>	Tufted capuchin	<i>Sapajus apella</i>	Sap104
	<i>Cebus imitator</i>	White-faced capuchin	<i>Cebus imitator</i>	Ccap9
	<i>Saimiri boliviensis</i>	Bolivian squirrel monkey	<i>Saimiri boliviensis</i>	Sbol45
Atelidae	<i>Ateles geoffroyi yucatanensis</i>	Mantled howler	<i>Alouatta palliata</i>	KSTR199
		Black-handed spider monkey	<i>Ateles geoffroyi yucatanensis</i>	Age319
		Common woolly monkey	<i>Lagothrix lagotricha</i>	Llag6202
Pitheciidae	<i>Pithecia pithecia</i>	Dusky titi	<i>Callicebus moloch</i>	Cmo4
		Bearded saki	<i>Chiropotes satanas</i>	Csat6549
		Pale-faced saki	<i>Pithecia pithecia</i>	Ppit5605

## 2.7 The processing of NGS data

I conducted mapping procedure following Hou et al. (2024) and included three times mapping to ensure the reliability of results as far as possible. Figure 1 indicates the detailed process of processing the raw data to get consensus sequences of the platyrrhine primates in the study.

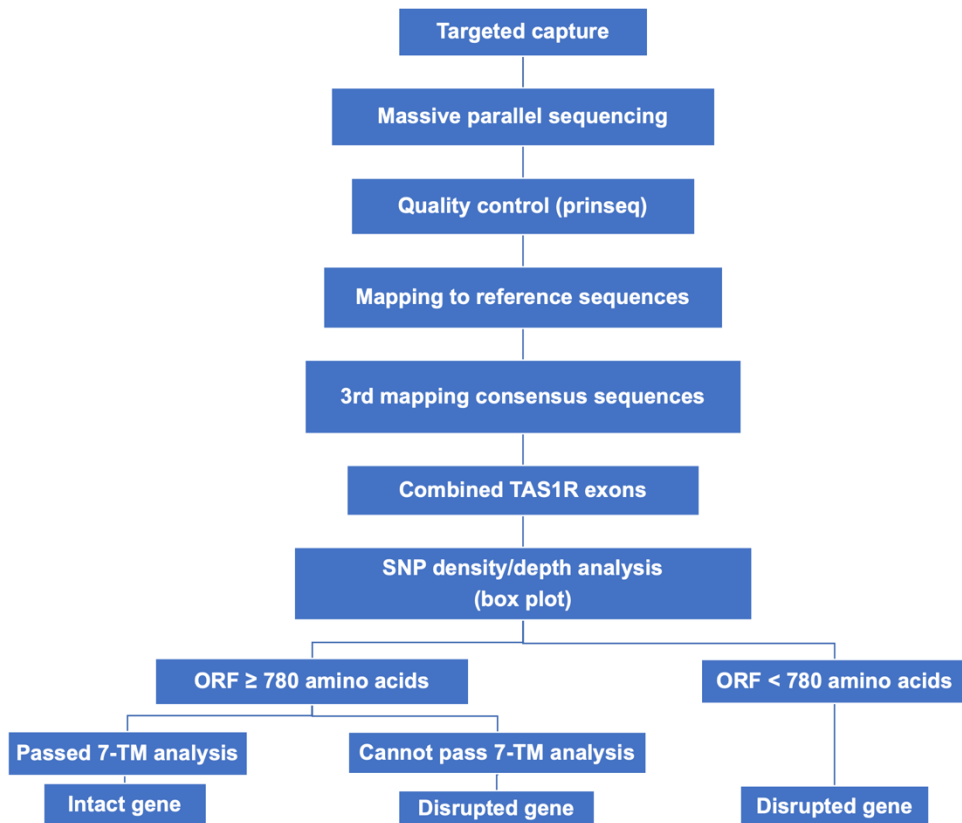


Figure 1 A general workflow of targeted capture data analysis

### 2.7.1 The first-round mapping

In the first mapping, Burrows-Wheeler-Alignment Tool (BWA-MEM) tool was used to map the qualified reads to the reference sequence. It is an alignment algorithm for aligning sequence reads or long query sequences against a large reference genome. It automatically chooses between local and end-to-end alignments, supports paired end reads and performs chimeric alignment (Li H, 2013). Then, the MarkDuplicates tool in the Genome Analysis Toolkit (GATK) (McKenna et al., 2010) was used to detect read pairs likely stemming from duplicates of the same DNA fragments due to

artificial processes like PCR amplification. In this study, only a single read pair from each set of duplicates was selected for further analyses to avoid biased results. Next, the HaplotypeCaller from GATK was used to assemble the mapped reads, identify insertion/deletion (indel) sites and single-nucleotide polymorphism (SNP) sites, and determine the haplotype phase among these polymorphic sites based on their physical linkage in a sequencing read. An indel site was defined as a location where an insertion or deletion of a nucleotide was detected among sequencing reads relative to the reference sequence while an SNP site was defined as a location where two or more nucleotide types were present among sequencing reads. We did not count a site as an SNP if only one nucleotide type was detected among the reads, even if this nucleotide differed from the reference sequence at that site (Hou et al., 2024). Following this, I used the GenotypeGVCFs function of GATK to combine all variant calls into a single Variant Call Format (VCF) file. Finally, the genotype VCF files were filtered by the VariantFiltration function to filter out any variant sites with a genotype quality (GQ) score less than 20 to generate the final filtered VCF files for subsequent variant analyses and studies. Finally, consensus sequences of both haplotypes of the sample were constructed by using bcftools consensus algorithm.

### 2.7.2 The second-round mapping

The second-round mapping is conducted to identify regions that remained unmapped after the first mapping process. By using one of the potential consensus sequences derived from the sample's haplotypes as reference, I aimed to enhance mapping specificity, thereby increasing confidence in identifying the true genomic composition. In the final step of the first-round mapping, bcftools marks allelic deletions with an asterisk marker. The consensus sequence with fewer asterisks was selected to serve as the reference. The second-round mapping followed a similar procedure to the first, with the exception that, in the second round, I employed mpileup (Li, 2011) which can provide information of unmapped sites or regions.

Also, in the final consensus sequence generation step, command was applied to mark all unmapped sites with 'N's.'

Finally, samtools bedcov(Danecek et al., 2021) was applied to evaluate the mapping depth information which can be one of the metrics to measure the quality of sequencing. Genes or genome regions with average depth lower than 10 were regarded as being absent and are removed from the third-round mapping to enhance the specificity.

### 2.7.3 The third-round mapping

Following the same criteria in 2<sup>nd</sup> mapping process, the consensus sequence generated from 2<sup>nd</sup> mapping with less asterisks which means less allelic deletion was chosen as the 3<sup>rd</sup> mapping's reference. The steps for mapping are basically the same as the previous time, except for the last step of obtaining consensus sequences. For the third mapping, the "1plu" and "2plu" options were used to determine both alleles, designated as H1 and H2, for phased genotypes and International Union of Pure and Applied Chemistry (IUPAC) degenerate code were generated for unphased SNP sites with more than one nucleotide kinds. 'N' sites were removed from the generated sequences, which makes the final consensus sequences consisting of only the sample's own sequences.

After 3 times mapping, samtools bedcov ((Danecek et al., 2021) was used to calculate the depth per site.

## 2.8 Visualization of mapping results

Data visualization is a crucial aspect of genomic data analysis. The Integrative Genomics Viewer (IGV) (Thorvaldsdottir et al., 2013), a high-performance tool designed to efficiently manage large, diverse data sets, was used to visualize the mapping results from the BAM files. IGV can clearly illustrated the mapping quality through the mapped reads depth. In addition, IGV can highlight single nucleotide

polymorphisms (SNPs) and insertions/deletions (indels) within the aligned reads detect variant which enhance the analysis and interpretation of genomic data.

## 2.9 Calculation of the sequence depth and SNP density

Depth referred to the average number of reads mapped per nucleotide site which is a crucial metric for assessing the quality of mapping. The depth was calculated from the total length of the sequences region (L) with only coding regions which in *TAS1Rs* mean only exons, the total number of reads (N) among coding regions as  $N/L$  by using the samtools bedcov tool. Vcftools were used to evaluate SNP density which referred to the number of SNP sites (not including indels) per 1000 bp (Danecek et al., 2011).

## 2.10 Determination of intact and disrupted gene

After got the final mapping consensus sequences, for each sample, both allele consensus sequences were analyzed. To predict the open reading frame (ORF) and 7-TM domain for *TAS1R* sequences with IUPAC degenerate nucleotide codes at SNP sites, where haplotype phases are indeterminable, I used a systematic replacement approach (Table 4). For each pair of H1 and H2 sequences, I substituted the IUPAC code (e.g., R for A/G) in H1 with one nucleotide in alphabetical order (A for H1-1) and the other nucleotide (G) in H2 (H2-1). Conversely, I made another replacement where G was in H1 (H1-2) and A in H2 (H2-2). This method accounts for potential disruptions in ORF and 7-TM domains due to single amino acid changes, regardless of haplotype phases. As the number of degenerate sites increases, so does the exponential growth in possible nucleotide combinations. Rather than exhaustive testing, I systematically evaluated these two pairs (H1-1/H2-1 and H1-2/H2-2) across all degenerate sites to ensure consistency in this study (Hou et al., 2024).



Table 4 Degenerate code substitution schemes

Degenerate Code	Substitution Scheme	
	Scheme 1	Scheme 2
R	A	G
M	A	C
W	A	T
S	C	G
Y	C	T
K	G	T

For the *TASIR* genes which include 6 exons and introns, I analyzed them by extracting only 6 exons and merging them into a whole sequence. Then, I used EMBOSS getorf (Rice et al., 2000) to find its open reading frame. I regarded any *TASIR* sequence with maximum ORF < 780 bp (encoding < 260 amino acids long) as disrupted because such a sequence is unlikely to have 7-transmembrane structure (7-TM). After obtaining consensus sequences with substituted degenerate codes using EMBOSS getorf, I generated the amino acid sequences of possible intact sequences. To further examine if all those possible intact sequences could make a functional 7-TM which is a typical characteristic of GPCRs to confirm being functional, amino acid sequence information was put into the DeepTMHMM (v1.0.18) designed by Technical University of Denmark (Hallgren et al., 2022) to predict 7-TM structure. To conclude, sequences which ORF is over 780bp with a 7-TM domain will be considered as intact genes. Otherwise, the sequences will be considered as disrupted genes.

## 2.11 Molecular evolutionary analysis.

### 2.11.1 Reconstruction of phylogenetic tree

After got the consensus sequences, I did the alignment using MUSCLE (Edgar,

2004). Tamura-Nei model (Tamura and Nei, 1993) was used to estimate the number of nucleotide substitutions per nucleotide site between *TASIR* consensus sequences with gap sites excluded in pairwise deletion. Phylogenetic trees were reconstructed for *TASIR* exons, *TASIR* introns, and neutral reference (NR) using the neighbor-joining method (Saitou and Nei, 1987). The reliability of these trees was assessed through bootstrap resampling with 1000 replications (Saitou and Nei, 1987). Specifically, for the phylogenetic tree involving the NR and *TASIR* introns, I aligned the NR sequences and introns separately before concatenating them to build the tree. All of the above procedures were ran under the platform of MEGA11 (Tamura et al., 2021).

#### 2.11.2 Test of difference between nonsynonymous and synonymous substitution rates

The nonsynonymous/synonymous substitution rate ratio test, also known as the  $d_N/d_S$  test, is a method used to detect natural selection on protein-coding genes. In this test,  $d_N$  represents the rate of nonsynonymous substitutions (changes that alter the amino acid sequence of a protein), while  $d_S$  represent the rate of synonymous substitutions (changes that do not alter the amino acid sequence). The ratio  $d_N/d_S$  is used to infer the type of selection acting on the gene: a ratio of 1 suggests neutral evolution, a ratio less than 1 indicates purifying (negative) selection, and a ratio greater than 1 suggests positive selection. This test is widely used in evolutionary biology to study the adaptive evolution of genes and to understand the evolutionary forces shaping the genetic diversity of species. In this study, instead of  $d_N/d_S$  ratio, I evaluated whether  $d_S - d_N$  is larger, smaller or equivalent with 0 for purifying selection, positive selection or neutrality, respectively. I used codon-based Z test of selection for purifying selection, positive selection and neutrality of *TASIRs* among 18 platyrrhine including both TC and WGA sequences in MEGA11 (Nei and Gojobor, 1986; Tamura et al., 2021). In order to eliminate the effects of frame shifts and obtain more comprehensive information on selection, I removed any site with an insertion from all species whenever an insertion was present in any one species.

### 2.11.3 Evolutionary rate test

The relative rate test compares genetic mutation and evolutionary rates between two closely related species (ingroups) and a distant reference species (outgroup) (Kumar, 2005). It evaluates how these ingroup species diverge from their common ancestor with the outgroup, without pinpointing the exact divergence time (Steiper and Seiffert, 2012). Following the selection test, some species pairs may show relaxed selection pressure. To confirm variations in evolutionary rates and explore functional and adaptive changes, Tajima's relative rate test in MEGA11 was employed in this study (Tajima, 1993; Tamura et al., 2021).

### 3 Results

#### 3.1 Sequencing depth information and SNP density

Depth per site represents the number of short reads averaged over nucleotide sites. Figure 2 shows that the average sequencing depth of three *TASIR* genes and neutral references for the three platyrrhine families is approximately the same. This suggests that despite designing probes from only Cebidae species, the mapping results still show comparable depth for the other two families.

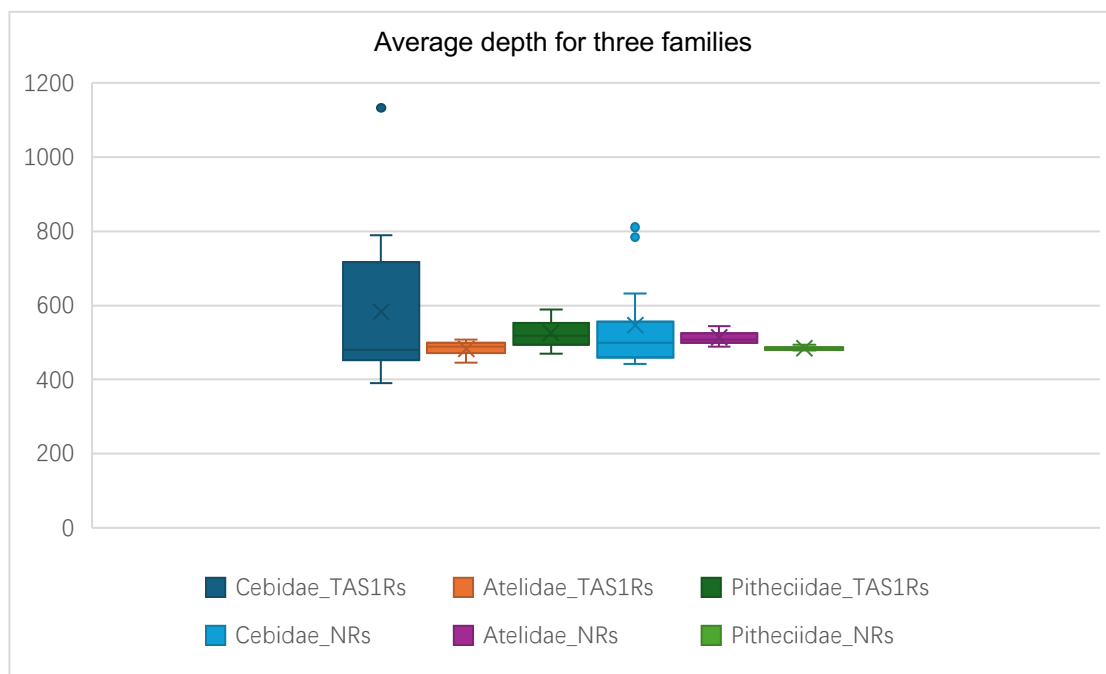


Figure 2 Average depth for three *TASIR* genes and neutral references for three families of platyrrhines, including Cebidae, Atelidae, Pitheciidae.

Also, the sequencing depth per site for the X-chromosomal neutral references (NR\_X) was approximately half that of the autosomal neutral references (NR\_A) in the samples from male individuals (golden lion tamarin, white-faced capuchin, common woolly monkey pygmy marmoset, Santarem marmoset, cotton-top tamarin and Azara's night monkey) (Figure S1). Conversely, in the samples from female individuals (bearded saki, pale-faced saki, Bolivian squirrel monkey, red-handed

tamarin, black-eared marmoset, common marmoset, tufted capuchin, black-handed spider monkey, and mantled howler monkey), the depth of the NR\_X was comparable to that of the NR\_A (Figure S1). These observations support that the sequencing depth well reflects differences in gene ploidy difference among samples. While the sex of saddle-back tamarin and dusky titi is unknown, the box plots imply that the two study species are likely to be female.

The average sequence depths per nucleotide site of 18 platyrrhine species by using targeted capture and data obtained from WGA are listed in Table 5. The depth achieved from targeted capture for all species was much higher than that from WGA. In 18 targeted captured platyrrhines, the minimum per-site sequencing depth in *TASIRs* was 416 and the maximum was 804. In contrast, the minimum depth from WGA was 35 and the maximum was 111. On average, the depth of targeted capture was roughly ten times greater than that of WGA, indicating that the results from targeted capture are more reliable than those from WGA.

Table 5 Sequencing depth comparison between TC and WGA.

Genus	Name	Targeted Capture	WGA
Cebidae	Common marmoset	469	63
	Black-eared marmoset	790	NA
	Santarem marmoset	419	35
	Pygmy marmoset	546	35
	Golden Lion Tamarin	804	78
	Red-handed tamarin	472	53
	Cotton-top tamarin	487	55
	Saddle-back tamarin	448	NA
	Azara's night monkey	416	35
	Tufted capuchin	579	43
	White-faced capuchin	762	81
	Bolivian squirrel monkey	439	111
Atelidae	Mantled howler	496	43
	Black-handed spider monkey	508	57
	Common woolly monkey	480	35
Pitheciidae	Dusky titi	470	35
	Bearded saki	518	NA
	Pale-faced saki	588	79
Average		538	56

I also counted the number of the SNP sites throughout exons and then calculated the SNP density (Table 6), i.e., the number of SNP sites (not including indels) per 1000 bp. Then I drew the box plots to compare the SNP density between disrupted gene and intact gene. As Figure 3 shows that the average SNP density of disrupted gene is higher than that of intact genes.

Table 6 SNP density for TAS1Rs of each platyrrhines

Common Name	TAS1R1			TAS1R2			TAS1R3		
	S	L	s	S	L	s	S	L	s
Common marmoset	1	2526	0.40	0	2505	0.00	0	2559	0.00
Black-eared marmoset	1	2526	0.40	1	2505	0.40	0	2559	0.00
Santarem marmoset	0	2526	0.00	3	2505	1.20	0	2559	0.00
Pygmy marmoset	2	2526	0.79	4	2505	1.60	5	2559	1.95
Golden Lion Tamarin	1	2242	0.45	0	2505	0.00	0	2559	0.00
Red-handed tamarin	10	2525	3.96	3	2505	1.20	0	2559	0.00
Cotton-top tamarin	1	2525	0.40	0	2505	0.00	0	2559	0.00
Saddle-back tamarin	2	2526	0.79	2	2505	0.80	1	2559	0.39
Azara's night monkey	8	2526	3.17	8	2505	3.19	1	2559	0.39
Tufted capuchin	0	2526	0.00	0	2505	0.00	0	2560	0.00
White-faced capuchin	0	2526	0.00	6	2505	2.40	0	2560	0.00
Bolivian squirrel monkey	0	2526	0.00	1	2505	0.40	0	2559	0.00
Mantled howler	0	2526	0.00	0	2505	0.00	0	2559	0.00
Black-handed spider monkey	6	2526	2.38	4	2505	1.60	4	2559	1.56
Common woolly monkey	2	2526	0.79	15	2505	5.99	1	2559	0.39
Dusky titi	0	2526	0.00	5	2508	1.99	0	2559	0.00
Bearded saki	2	2526	0.79	1	2505	0.40	0	2559	0.00
Pale-faced saki	0	2526	0.00	0	2505	0.00	1	2559	0.39

Notes: S: the number of SNP sites in the protein coding region

L: the length of coding sequence

s: SNP density (the number of SNP sites per 1000 bp in the coding region)

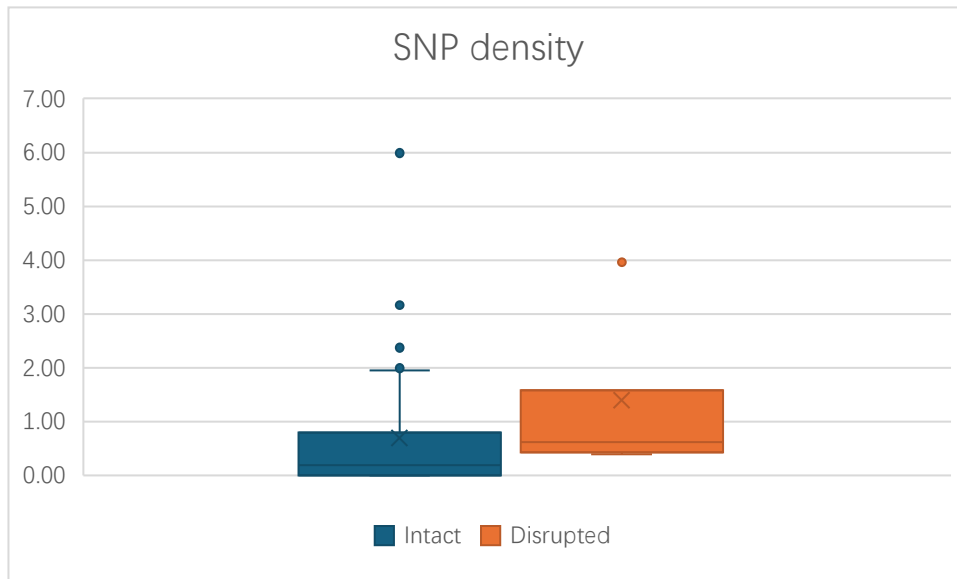


Figure 3 Box plot comparing the SNP density between intact and disrupted TAS1R genes. (TAS1R1 of golden lion tamarin and three tamarin species, including the red-handed tamarin, cotton-top tamarin, and saddle-back tamarin, are disrupted, other genes are all intact)

### 3.2 Comparison of gene compositions between TC and WGA

After the open reading frame (ORF) and 7-Transmembrane (7-TM) analysis, the *TAS1R1* in the golden lion tamarin and three tamarin species, including the red-handed tamarin, cotton-top tamarin, and saddle-back tamarin, was found to be a disrupted gene (Table 7).



Table 7 Intact and disrupted information of TAS1Rs for platyrrhines

Family	Name	<i>TAS1R1</i>	<i>TAS1R2</i>	<i>TAS1R3</i>
Cebidae	Common marmoset	Intact	Intact	Intact
	Black-eared marmoset	Intact	Intact	Intact
	Pygmy marmoset	Intact	Intact	Intact
	Santarem marmoset	Intact	Intact	Intact
	Golden Lion Tamarin	Disrupted	Intact	Intact
	Saddle-back tamarin	Disrupted	Intact	Intact
	Red-handed tamarin	Disrupted	Intact	Intact
	Cotton-top tamarin	Disrupted	Intact	Intact
	Azara's owl monkey	Intact	Intact	Intact
	White-faced capuchin	Intact	Intact	Intact
	Bolivian squirrel monkey	Intact	Intact	Intact
	Tufted capuchin	Intact	Intact	Intact
Atelidae	Mantled howler	Intact	Intact	Intact
	Black-handed spider monkey	Intact	Intact	Intact
	Common woolly monkey	Intact	Intact	Intact
Pitheciidae	Dusky titi	Intact	Intact	Intact
	Bearded saki	Intact	Intact	Intact
	Pale-faced saki	Intact	Intact	Intact

Table 8 records the exon length information for each species. For the disrupted ones, the *TAS1R1* sequence in the lion tamarin exhibited large deletions, whereas the tamarin species showed small deletions (Figure 5). These disruptions appeared to follow different patterns. Furthermore, based on the phylogenetic tree, lion tamarins and tamarins belonged to different branches, indicating that the disruptions in these two groups were independent events that occurred in their common ancestors respectively (Figure 4). For *TAS1R2* and *TAS1R3*, all species exhibited consistent

exon lengths except for the three species: tufted capuchin, white-faced capuchin and dusky titi. In dusky titi, the *TASIR2* has a three-nucleotide insertion in the third exon, which did not cause a frameshift. In *TASIR3* of tufted capuchin, white-faced capuchin, there was a three-nucleotide insertion in the C-terminal region, resulting only in the loss of the last amino acid. Although these insertions occurred, they did not appear to significantly alter the open reading frame length or the seven-transmembrane structure. Therefore, I considered that these changes were unlikely to impact the functionality of the *TASIR2* and *TASIR3*, which were supported by subsequent d<sub>N</sub>-d<sub>S</sub> analyses shown later.

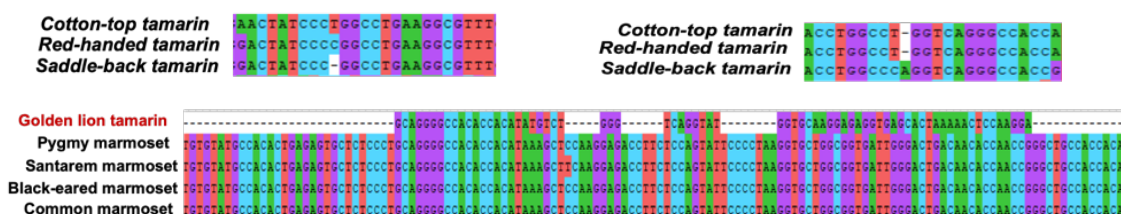


Figure 5 Alignment results of lion tamarin and tamarins

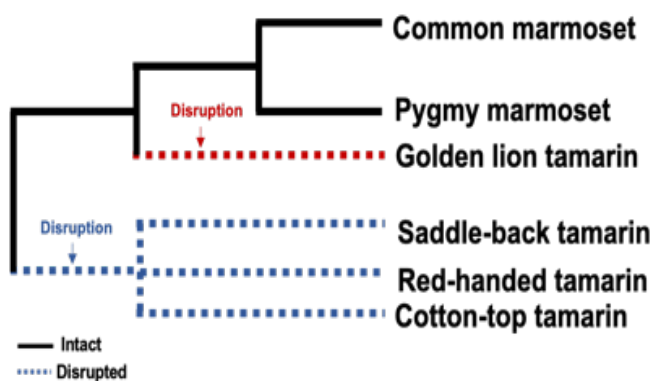


Figure 4 Phylogenetic tree of lion tamarin and tamarins

Table 8 Exon length information for 18 platyrrhine species

ID	TAS1R1						TAS1R2						TAS1R3					
	exon1	exon2	exon3	exon4	exon5	exon6	exon1	exon2	exon3	exon4	exon5	exon6	exon1	exon2	exon3	exon4	exon5	exon6
Aaz41	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Cja61	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Cpen6601	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Cpyg6460	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Lros7	188	72	718	217	121	926	182	301	759	210	124	929	191	301	783	204	121	959
Mhum6555	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Sfu9	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Smid6595	191	307	761	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Soe10	191	307	762	212	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Ccap9	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	960
Sbol45	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Sap104	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	960
KSTR199	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Age319	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Llag6202	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Cmo4	191	307	762	213	121	932	182	301	762	210	124	929	191	301	783	204	121	959
Csat6549	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959
Ppit5605	191	307	762	213	121	932	182	301	759	210	124	929	191	301	783	204	121	959

I also conducted ORF and 7-TM analyses on sequences obtained from WGA databases, as detailed in Table 9. In addition to identifying disrupted genes consistent with my TC results, I observed numerous genes are incomplete in the WGA data but found to be intact in my TC results. This confirmed the incompleteness of WGA data. This suggests that targeted capture can effectively complement WGA, thereby enhancing the accuracy and reliability of genomic analyses.

Table 9 ORF and 7-TM analysis results of platyrrhines' available WGA data.

Common name	TAS1R1		TAS1R2		TAS1R3	
	ORF	7-TM	ORF	7-TM	ORF	7-TM
Common marmoset	2533	7	2502	7	2556	7
Black-eared marmoset			NA			
Santarem marmoset	2523	7	2502	7	2556	7
Pygmy marmoset	1211	7	2502	7	2333	7
Golden Lion Tamarin	1211	-	2502	7	2556	7
Red-handed tamarin	1385	-	2502	7	2556	7
Cotton-top tamarin	998	-	2502	7	2556	7
Saddle-back tamarin			NA			
Azara's night monkey			NA			
Tufted capuchin	2523	7	2502	7	2553	7
White-faced capuchin	2520	7	2502	7	2553	7
Bolivian squirrel monkey	2523	7	2502	7	2556	7
Mantled howler	2523	7	2502	7	2556	7
Black-handed spider monkey	2523	7	2502	7	2556	7
Common woolly monkey	2523	7	2502	7	2329	7
sky titi	2523	7	2315	7	2556	7
Bearded saki			NA			
Pale-faced saki	2523	7	2502	7	2556	7

### 3.3 Reconstruction of phylogenetic tree

For the exon portion of *TAS1R* genes, I extracted sequence data of 6 exons from the short-read assembly and combined them into a contiguous sequence without introns or flanking regions. Using nucleotide sequence data from 18 platyrrhines obtained via targeted capture and 15 platyrrhines with available WGA databases, I

reconstructed neighbor-joining phylogenetic trees for *TASIR1*, *TASIR2*, and *TASIR3*, respectively (Figure S2-S4).

For the intron portion of *TASIR* genes, I included upstream and downstream flanking regions along with five introns. I aligned each segment separately before combining them to construct a phylogenetic tree. Additionally, I included human sequences of these genes as an outgroup to create a rooted tree. However, introns are much longer than exons, and there were many insertions or deletions among them. After reviewing the alignment results, I found that the alignment of the first intron of *TASIR1* was very patchy and unreliable. Figure S5-S7 show the intron-based phylogenetic trees of *TASIRs*.

For the NR, similar to the introns, I aligned each NR sequence separately and then merged the alignments to draw a phylogenetic tree (Figure S8). Not only the species which sequences from TC and WGA are clustered together and the nucleotide-based trees for exons, introns and NRs were all consistent with species tree.

### 3.4 Genetic variation tests of *TASIR* genes

To further understand the adaptive and genetic characteristics of the species, I conducted  $d_N-d_S$  test of natural selection for purifying selection, positive selection and neutrality with not only my targeted capture results but also WGA information.

In the purifying selection test of *TASIR1*, the p-values among the three tamarin species, red-handed tamarin, cotton-top tamarin, and saddle-back tamarin, were over 0.05, which indicated that the purifying selective pressure in these tamarins were relaxed. For species observed with the in-frame insertions in their exons, tufted capuchin, white-faced capuchin and dusky titi, the p-values were all less than 0.05. This indicates that these species are under significant purifying selection, suggesting that these *TASIR1* remains functional. For species within Atelidae, purifying selection was not supported. No results supported positive selection or neutrality. Selection test results are shown in Table S2-10.

Then, I conducted Tajima's relative rate test (Tajima, 1993; Tamura et al., 2021) for *TASIRI* gene of a tamarin vs. common marmoset and for the lion tamarin vs common marmoset using the Bolivian squirrel monkey as an outgroup. The results indicated that all tamarins and the lion tamarin exhibit significantly faster evolutionary rates than the common marmoset. Additionally, the evolutionary rate of *TASIRI* of the lion tamarin was significantly faster than that of the tamarins, supporting that the disruptions in tamarins and the lion tamarin were independent events and that the latter disruption was older in evolutionary history. For other species, the results revealed no significant differences in evolutionary rates. The results are shown in Table 10.

Table 10 Tajima's relative rate test

A	B	Outgroup	P value
Golden lion tamarin	Common marmoset	Bolivian squirrel monkey	0.00000
Red-handed tamarin			0.03781
Cotton-top tamarin			0.01030
Saddle-back tamarin			0.02218
Red-handed tamarin	Cotton-top tamarin		0.53161
	Saddle-back tamarin		0.46580
Cotton-top tamarin			0.77283
Golden lion tamarin	Red-handed tamarin		0.00001
black-handed spider monkey	Mantled howler		0.72181
	Lagothrix lagotricha		0.39614
Mantled howler			0.72181

### 3.5 Validation of three key sites responsible for L-Glutamate and/or nucleotide detection

As mentioned before, Toda et al. (2021) identified three key sites, 170, 302 and 379, which were responsible for detecting L-glutamate and/or nucleotides. In my study, I also got the residues information of these three sites among 18 study platyrrhine species. Figure 6 shows a phylogenetic tree with the detailed information of three sites for all my study species.

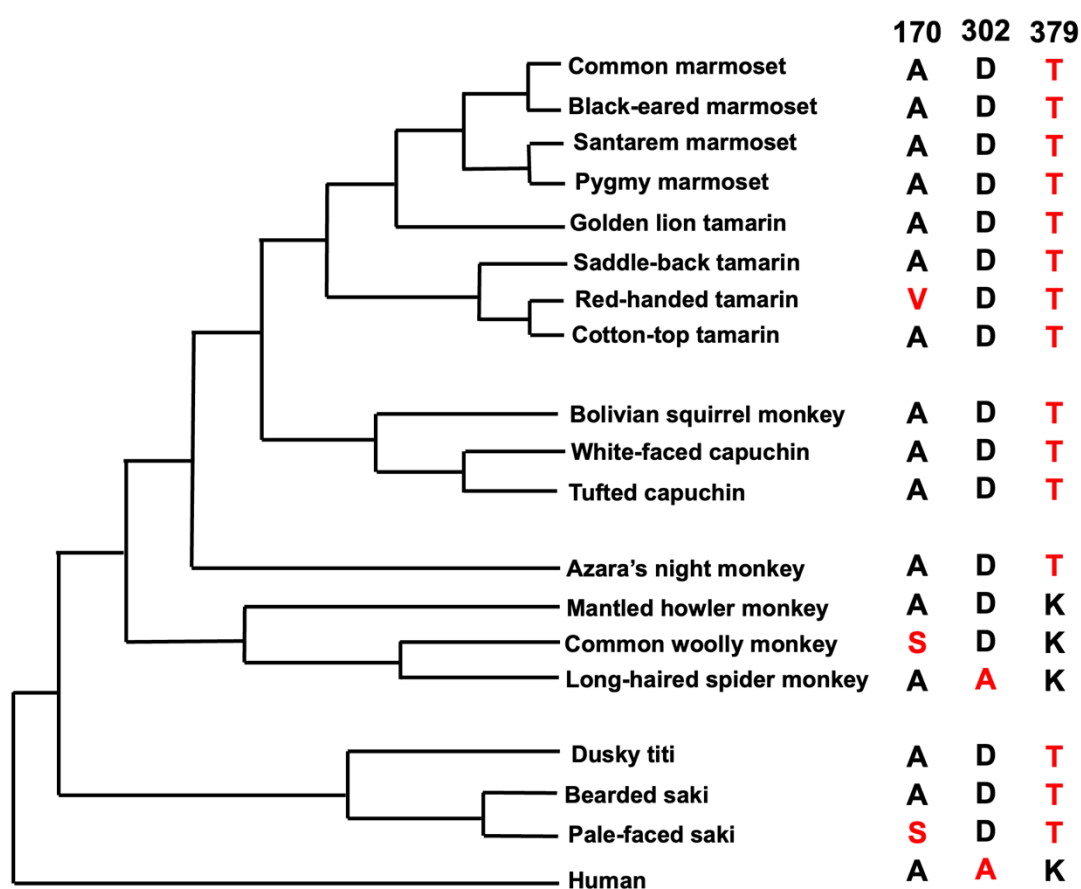


Figure 6 A phylogenetic tree which marked three key sites, 170, 302 and 379, of TAS1R1 gene among platyrrhine species. Human was used as an outgroup. The composition of the last common ancestor (LCA) of Anthroipoidea was inferred to be 170A, 302D, and 379K.

For the Cebidae family and two species of Pitheciidae (dusky titi and bearded saki), three key site composition was uniformed among them except for red-handed tamarin which are found to have disrupted *TAS1R1*. Other than red-handed tamarin, Cebidae Family have the composition of 170A, 302D and 379K while for red-handed tamarin

have V at 170. Different from bearded saki, pale-faced saki have the combination of 170S, 302D and 379T. For the Atelidae family, they all have K at 379, but have A or S at 170 and A or D at 379.



## 4 Discussion

In this study, targeted capture was employed to specifically probe the *TASIR* genes and the autosomal and X-chromosomal neutral reference regions from genomic DNA samples of 18 platyrrhine primates including three Family and seven Subfamilies with diverse feeding habits and color vision. The targeted capture was followed by short-read and high-depth NGS. The sequencing depth of TC was much higher than WGA which indicated that my targeted capture was highly reliable. By conducting ORF and 7-TM domain analysis, I found that the *TASIR1* is disrupted in tamarins and lion tamarins. Additionally, the *TASIR2* in dusky titi and the *TASIR3* in both white-faced capuchin and tufted capuchin showed insertions in their exons which may not largely affect the gene function.

*TASIR* genes are relatively conserved in evolution and that the *TASIR* gene composition remains virtually constant in size across most vertebrates (Shi and Zhang, 2006). This could indicate the essential role of both sweet and umami tastes and the consistent presence and variety of these taste compounds in many vertebrates. As the selection test indicated, most of the studied platyrrhine species exhibited significant purifying selection. These species had intact *TASIR* genes, supporting that their umami-sweet taste sensation was functional. This is consistent with their diverse diets, which include fruits, leaves, tree sap, insects, and so on.

Notably, the *TASIR1* in tamarins and lion tamarins were found to be disrupted, indicating a loss of the umami taste sensation in these species. According to the Tajima's relative rate test, tamarins seemed to evolve at similar rate, but exhibited a different rate with lion tamarins. The alignment results revealed distinct disruption patterns between the two species: lion tamarin exhibited large deletions in exon 2, whereas tamarins showed shared small insertions or deletions of 1-2 base pairs. In the phylogenetic tree, these two species belong to different branches. Based on these observations, I inferred that the disruptions in the *TASIR1* occurred independently in tamarins' common ancestor and lion tamarin.

Lion tamarins (Callitrichidae: *Leontopithecus*) are small frugivores and faunivores, primarily consuming ripe fruit, nectar, insects, and small vertebrates, with gums rarely included in their diet. They feed on a wide variety of plants, encompassing at least 79 different species from 32 families (Raboy and Dietz, 2004). Among *Saguinus* genus, many species show a preference for consuming reproductive parts of plants, with fruits and flowers making up over 70% of their diet (Botton-Divet and Nyakatura, 2021). For instance, the cotton-top tamarin's diet consists of 48.6% fruits (including arils, fruits, and seeds), with a variation between dry and wet seasons (28.1% in dry season and 59.9% in wet season). Exudates make up 24% of their diet (44.9% in dry season and 14.9% in wet season), and nectar contributes 15% (2.1% in dry season and 16.9% in wet season), among other dietary items (García-Castillo and Defler, 2018). Similarly, the red-handed tamarin is predominantly frugivorous, with insects and exudates playing lesser roles in their diet (Fleagle, 2013). The saddle-back tamarin shows a seasonal dietary variation: during the wet season, they primarily consume small, widely dispersed fruits, whereas in the dry season, when fruits are rare, their herbivorous intake mainly comprises nectar. Also, Insects account for nearly half of their daily feeding time (Fleagle, 2013).

In conclusion, lion tamarin and other tamarins predominantly feed on fruits and nectar, although the saddle-back tamarin incorporates insects into its diet, fruits remain a significant component. Therefore, the observed disruption of *TASIRI* in lion tamarins and other tamarins may be linked to their fruit-reliant feeding habits.

Additionally, based on the  $d_N-d_S$  test of purifying selection test for *TASIRI*, the p-value of Atelidae family shows over 0.05 which indicated they were not under strict purifying selection. Based on these results, I hypothesize that the selection pressure on *TASIRI* among them may be relaxed, potentially associated with their feeding habits.

Moreover, Tajima's relative rate test among them indicated no significant difference in their evolutionary rate. Additionally, the branches of the Atelidae family in phylogenetic trees appear slightly longer compared to other species, suggesting

greater genetic divergence from a common ancestor. This could imply a recent relaxation of selection pressure, which requires more time for the accumulation of genetic changes or mutations detectable in evolutionary tests. Atelidae Family are primarily frugivorous but also consume a variety of plant materials and insects, with diet variability seasonally and geographically. The relaxation of their *TAS1R1* may be linked to an increasing dependence on leaves over time.

Furthermore, the higher SNP density in disrupted genes compared to intact genes can be attributed to several factors. Disrupted genes are under relaxed purifying selection, meaning that deleterious mutations are less likely to be eliminated because the gene is already non-functional or less functional. This allows SNPs to accumulate at a higher rate. In contrast, intact genes are under stronger purifying selection to maintain their functional integrity, leading to lower SNP density. Additionally, disrupted genes may have undergone more historical mutations before becoming non-functional, resulting in a higher overall SNP density.

Another notable aspect is no apparent relationship between the disruption and color vision in platyrrhines. This study identified *TAS1R1* disruption in saddle-back tamarins (sex unspecified), female red-handed tamarins, male cotton-top tamarins, and male golden lion tamarins. These platyrrhine species exhibit a mix of male and female dichromats, alongside female trichromats. In contrast, species like howler monkeys, with sex-independent trichromacy, and owl monkeys, displaying cone monochromacy, retain all three *TAS1R* genes intact. Additionally, other platyrrhines with polymorphic color vision, varying by sex, also maintain intact *TAS1R* genes. Thus, it suggests that there is no apparent trade-off between the acquisition of trichromacy and the loss of umami taste function.

On the other hand, Toda et al. (2021) identified three key sites, 170, 302 and 379, which responsible for detecting L-glutamate and/or nucleotides. The common ancestor of Catarrhine and Platyrrhine have 170A, 302D and 379K. As predicted, Atelidae family, which have larger body sizes, were found to have loss-of-charge

mutations at amino acid residues 170 and 302. These mutations result in a high affinity for L-Glu, consistent with their increased reliance on the diet primarily composed of leaves.

In the Cebidae Family, the composition of the three key sites was consistent except in the red-handed tamarin, which has a disrupted *TASIRI*. Cebidae Family, which generally has smaller body sizes and a diet primarily consisting of insects, has acidic residues at one or both positions 170 and 302. This results in low L-Glu sensitivity and increased sensitivity to 5-ribonucleotides. Further analysis is required to determine the role and relationship of these three key sites in detecting L-glutamate and/or nucleotides.

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## 6 References

- Akhtar, M.S., Ashino, R., Oota, H., Ishida, H., Niimura, Y., Touhara, K., Melin, A.D., Kawamura, S., 2022. Genetic variation of olfactory receptor gene family in a Japanese population. *AS* 130, 93–106. <https://doi.org/10.1537/ase.211024>
- Andermann, T., Torres Jiménez, M.F., Matos-Maraví, P., Batista, R., Blanco-Pastor, J.L., Gustafsson, A.L.S., Kistler, L., Liberal, I.M., Oxelman, B., Bacon, C.D., Antonelli, A., 2020. A Guide to Carrying Out a Phylogenomic Target Sequence Capture Project. *Front. Genet.* 10, 1407. <https://doi.org/10.3389/fgene.2019.01407>
- Arbiza, L., Zhong, E., Keinan, A., 2012. NRE: a tool for exploring neutral loci in the human genome. *BMC Bioinformatics* 13, 301. <https://doi.org/10.1186/1471-2105-13-301>
- Botton-Divet, L., Nyakatura, J.A., 2021. Vertical clinging and leaping induced evolutionary rate shifts in postcranial evolution of tamarins and marmosets (Primates, Callitrichidae). *BMC Ecol Evo* 21, 132. <https://doi.org/10.1186/s12862-021-01848-z>
- Chandrashekar, J., Hoon, M.A., Ryba, N.J.P., Zuker, C.S., 2006. The receptors and cells for mammalian taste. *Nature* 444, 288–294. <https://doi.org/10.1038/nature05401>
- Chapman, C., 1987. Flexibility in Diets of Three Species of Costa Rican Primates. *IJFP* 49, 90–105. <https://doi.org/10.1159/000156311>
- Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., McVean, G., Durbin, R., 1000 Genomes Project Analysis Group, 2011. The variant call format and VCFtools. *Bioinformatics* 27, 2156–2158. <https://doi.org/10.1093/bioinformatics/btr330>
- Danecek, P., Bonfield, J.K., Liddle, J., Marshall, J., Ohan, V., Pollard, M.O., Whitwham, A., Keane, T., McCarthy, S.A., Davies, R.M., Li, H., 2021. Twelve years of SAMtools and BCFtools. *GigaScience* 10, giab008. <https://doi.org/10.1093/gigascience/giab008>
- Dulai, K.S., Von Dornum, M., Mollon, J.D., Hunt, D.M., 1999. The Evolution of Trichromatic Color Vision by Opsin Gene Duplication in New World and Old World Primates. *Genome Res.* 9, 629–638. <https://doi.org/10.1101/gr.9.7.629>
- Edgar, R.C., 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32, 1792–1797. <https://doi.org/10.1093/nar/gkh340>

Felsenstein, J., 1985. CONFIDENCE LIMITS ON PHYLOGENIES: AN APPROACH USING THE BOOTSTRAP. *Evolution* 39, 783–791.  
<https://doi.org/10.1111/j.1558-5646.1985.tb00420.x>

Fleagle JG. Primate adaptation and evolution. New York: Wiley; 2013

Gnirke, A., Melnikov, A., Maguire, J., Rogov, P., LeProust, E.M., Brockman, W., Fennell, T., Giannoukos, G., Fisher, S., Russ, C., Gabriel, S., Jaffe, D.B., Lander, E.S., Nusbaum, C., 2009. Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. *Nat Biotechnol* 27, 182–189.  
<https://doi.org/10.1038/nbt.1523>

Gold, K., B., Hutchins, M. (Eds.), 2004. *New World Monkeys I: Squirrel monkeys and capuchins.*, 2. ed. ed. Gale, Detroit.

Hallgren, J., Tsirigos, K.D., Pedersen, M.D., Almagro Armenteros, J.J., Marcatili, P., Nielsen, H., Krogh, A., Winther, O., 2022. DeepTMHMM predicts alpha and beta transmembrane proteins using deep neural networks.  
<https://doi.org/10.1101/2022.04.08.487609>

Hou, M., Akhtar, M.S., Hayashi, M., Ashino, R., Matsumoto-Oda, A., Hayakawa, T., Ishida, T., Melin, A.D., Imai, H., Kawamura, S., 2024. Reduction of bitter taste receptor gene family in folivorous colobine primates relative to omnivorous cercopithecine primates. *Primates*. <https://doi.org/10.1007/s10329-024-01124-w>

Jacobs, G.H., 2007. New World Monkeys and Color. *Int J Primatol* 28, 729–759.  
<https://doi.org/10.1007/s10764-007-9168-y>

Jacobs, G.H., Deegan, J.F., Neitz, J., Crognale, M.A., Neitz, M., 1993. Photopigments and color vision in the nocturnal monkey, *Aotus*. *Vision Research* 33, 1773–1783.  
[https://doi.org/10.1016/0042-6989\(93\)90168-V](https://doi.org/10.1016/0042-6989(93)90168-V)

Jacobs, G.H., Neitz, M., Deegan, J.F., Neitz, J., 1996a. Trichromatic colour vision in New World monkeys. *Nature* 382, 156–158. <https://doi.org/10.1038/382156a0>

Jacobs, G.H., Neitz, M., Neitz, J., 1996b. Mutations in S-Cone Pigment Genes and the Absence of Colour Vision in Two Species of Nocturnal Primate. *Proceedings: Biological Sciences* 263, 705–710.

Jiang, P., Josue, J., Li, X., Glaser, D., Li, W., Brand, J.G., Margolskee, R.F., Reed, D.R., Beauchamp, G.K., 2012. Major taste loss in carnivorous mammals. *Proc. Natl. Acad. Sci. U.S.A.* 109, 4956–4961. <https://doi.org/10.1073/pnas.1118360109>

Kawamura, S., 2018. Colour Vision Genetics Learned from New World Monkeys in Santa Rosa, Costa Rica, in: Kalbitzer, U., Jack, K.M. (Eds.), *Primate Life Histories, Sex Roles, and Adaptability, Developments in Primatology: Progress and Prospects*. Springer International Publishing, Cham, pp. 257–277. [https://doi.org/10.1007/978-3-319-98285-4\\_13](https://doi.org/10.1007/978-3-319-98285-4_13)

Kawamura, S., Melin, A.D., 2017. Evolution of Genes for Color Vision and the Chemical Senses in Primates, in: Saitou, N. (Ed.), *Evolution of the Human Genome I, Evolutionary Studies*. Springer Japan, Tokyo, pp. 181–216. [https://doi.org/10.1007/978-4-431-56603-8\\_10](https://doi.org/10.1007/978-4-431-56603-8_10)

Kumar, S., 2005. Molecular clocks: four decades of evolution. *Nat Rev Genet* 6, 654–662. <https://doi.org/10.1038/nrg1659>

Kunishima, N., Shimada, Y., Tsuji, Y., Sato, T., Yamamoto, M., Kumasaka, T., Nakanishi, S., Jingami, H., Morikawa, K., 2000. Structural basis of glutamate recognition by a dimeric metabotropic glutamate receptor. *Nature* 407, 971–977. <https://doi.org/10.1038/35039564>

Levenson, D.H., Fernandez-duque, E., Evans, S., Jacobs, G.H., 2007. Mutational changes in S-cone opsin genes common to both nocturnal and cathemeral *Aotus* monkeys. *American J Primatol* 69, 757–765. <https://doi.org/10.1002/ajp.20402>

Li, H., 2011. A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. *Bioinformatics* 27, 2987–2993. <https://doi.org/10.1093/bioinformatics/btr509>

Li H. (2013) Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv:1303.3997v2 [q-bio.GN]

Li, X., Li, W., Wang, H., Cao, J., Maehashi, K., Huang, L., Bachmanov, A.A., Reed, D.R., Legrand-Defretin, V., Beauchamp, G.K., Brand, J.G., 2005. Pseudogenization of a Sweet-Receptor Gene Accounts for Cats' Indifference toward Sugar. *PLoS Genet* 1, e3. <https://doi.org/10.1371/journal.pgen.0010003>

Li, X., Staszewski, L., Xu, H., Durick, K., Zoller, M., Adler, E., 2002. Human receptors for sweet and umami taste. *Proc. Natl. Acad. Sci. U.S.A.* 99, 4692–4696. <https://doi.org/10.1073/pnas.072090199>

Liu, G., Walter, L., Tang, S., Tan, X., Shi, F., Pan, H., Roos, C., Liu, Z., Li, M., 2014. Differentiated adaptive evolution, episodic relaxation of selective constraints, and



pseudogenization of umami and sweet taste genes TAS1Rs in catarrhine primates. *Front Zool* 11, 79. <https://doi.org/10.1186/s12983-014-0079-4>

López Cascales, J.J., Oliveira Costa, S.D., De Groot, B.L., Walters, D.E., 2010. Binding of glutamate to the umami receptor. *Biophysical Chemistry* 152, 139–144. <https://doi.org/10.1016/j.bpc.2010.09.001>

Masahiro Hayashi. Master thesis 2017

Matsumoto, Y., Hiramatsu, C., Matsushita, Y., Ozawa, N., Ashino, R., Nakata, M., Kasagi, S., Di Fiore, A., Schaffner, C.M., Aureli, F., Melin, A.D., Kawamura, S., 2014. Evolutionary renovation of L / M opsin polymorphism confers a fruit discrimination advantage to ateline New World monkeys. *Molecular Ecology* 23, 1799–1812. <https://doi.org/10.1111/mec.12703>

McKenna, A., Hanna, M., Banks, E., Sivachenko, A., Cibulskis, K., Kernytsky, A., Garimella, K., Altshuler, D., Gabriel, S., Daly, M., DePristo, M.A., 2010. The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res.* 20, 1297–1303. <https://doi.org/10.1101/gr.107524.110>

Muto, T., Tsuchiya, D., Morikawa, K., Jingami, H., 2007. Structures of the extracellular regions of the group II/III metabotropic glutamate receptors. *Proc. Natl. Acad. Sci. U.S.A.* 104, 3759–3764. <https://doi.org/10.1073/pnas.0611577104>

Nei, M., Gojobor, T., 1986. Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Molecular Biology and Evolution*. <https://doi.org/10.1093/oxfordjournals.molbev.a040410>

Nelson, G., Chandrashekar, J., Hoon, M.A., Feng, L., Zhao, G., Ryba, N.J.P., Zuker, C.S., 2002. An amino-acid taste receptor. *Nature* 416, 199–202. <https://doi.org/10.1038/nature726>

Nowak, R., 1991. Walker's Mammals of the World,. *Journal of Mammalogy* Vol. 1, 115–133. <https://doi.org/10.2307/1381225>

Oike, H., Nagai, T., Furuyama, A., Okada, S., Aihara, Y., Ishimaru, Y., Marui, T., Matsumoto, I., Misaka, T., Abe, K., 2007. Characterization of Ligands for Fish Taste Receptors. *J. Neurosci.* 27, 5584–5592. <https://doi.org/10.1523/JNEUROSCI.0651-07.2007>

- Peres, C.A., 1994. Diet and Feeding Ecology of Gray Woolly Monkeys (*Lagothrix lagotricha cana*) in Central Amazonia: Comparisons with Other Atelines.
- Raboy, B.E., Dietz, J.M., 2004. Diet, foraging, and use of space in wild golden-headed lion tamarins. *American J Primatol* 63, 1–15.  
<https://doi.org/10.1002/ajp.20032>
- Rice, P., Longden, I., Bleasby, A., 2000. EMBOSS: The European Molecular Biology Open Software Suite.
- Saitou, N., Nei, M., 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*.  
<https://doi.org/10.1093/oxfordjournals.molbev.a040454>
- Schmieder, R., Edwards, R., 2011. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* 27, 863–864. <https://doi.org/10.1093/bioinformatics/btr026>
- Shi, P., Zhang, J., 2006. Contrasting Modes of Evolution Between Vertebrate Sweet/Umami Receptor Genes and Bitter Receptor Genes. *Molecular Biology and Evolution* 23, 292–300. <https://doi.org/10.1093/molbev/msj028>
- Steiper, M.E., Seiffert, E.R., 2012. Evidence for a convergent slowdown in primate molecular rates and its implications for the timing of early primate evolution. *Proc. Natl. Acad. Sci. U.S.A.* 109, 6006–6011. <https://doi.org/10.1073/pnas.1119506109>
- Tajima, F., 1993. Simple methods for testing the molecular evolutionary clock hypothesis. *Genetics* 135, 599–607. <https://doi.org/10.1093/genetics/135.2.599>
- Tamura, K., Nei, M., 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution*. <https://doi.org/10.1093/oxfordjournals.molbev.a040023>
- Tamura, K., Stecher, G., Kumar, S., 2021. MEGA11: Molecular Evolutionary Genetics Analysis Version 11. *Molecular Biology and Evolution* 38, 3022–3027.  
<https://doi.org/10.1093/molbev/msab120>
- Thorvaldsdottir, H., Robinson, J.T., Mesirov, J.P., 2013. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Briefings in Bioinformatics* 14, 178–192. <https://doi.org/10.1093/bib/bbs017>
- Toda, Y., Hayakawa, T., Itoigawa, A., Kurihara, Y., Nakagita, T., Hayashi, M., Ashino, R., Melin, A.D., Ishimaru, Y., Kawamura, S., Imai, H., Misaka, T., 2021.

Evolution of the primate glutamate taste sensor from a nucleotide sensor. *Current Biology* 31, 4641-4649.e5. <https://doi.org/10.1016/j.cub.2021.08.002>

Villavicencio, J.E.S., 2017. Taxonomy of the genus *Brachyteles* Spix, 1823 and its phylogenetic position within the subfamily *Atelinae* Gray, 1825 (Mestrado em Sistemática, Taxonomia Animal e Biodiversidade). Universidade de São Paulo, São Paulo. <https://doi.org/10.11606/D.38.2017.tde-16112016-150803>

Wikler, K., Rakic, P., 1990. Distribution of photoreceptor subtypes in the retina of diurnal and nocturnal primates. *J. Neurosci.* 10, 3390–3401. <https://doi.org/10.1523/JNEUROSCI.10-10-03390.1990>

Wu, J., Yonezawa, T., Kishino, H., 2017. Rates of Molecular Evolution Suggest Natural History of Life History Traits and a Post-K-Pg Nocturnal Bottleneck of Placentals. *Current Biology* 27, 3025-3033.e5. <https://doi.org/10.1016/j.cub.2017.08.043>

Yarmolinsky, D.A., Zuker, C.S., Ryba, N.J.P., 2009. Common Sense about Taste: From Mammals to Insects. *Cell* 139, 234–244. <https://doi.org/10.1016/j.cell.2009.10.001>

Zhang, F., Klebansky, B., Fine, R.M., Xu, H., Pronin, A., Liu, H., Tachdjian, C., Li, X., 2008. Molecular mechanism for the umami taste synergism. *Proc. Natl. Acad. Sci. U.S.A.* 105, 20930–20934. <https://doi.org/10.1073/pnas.0810174106>

Zhao, H., Yang, J.-R., Xu, H., Zhang, J., 2010. Pseudogenization of the Umami Taste Receptor Gene *Tas1r1* in the Giant Panda Coincided with its Dietary Switch to Bamboo. *Molecular Biology and Evolution* 27, 2669–2673. <https://doi.org/10.1093/molbev/msq153>

Zhu, K., Zhou, X., Xu, S., Sun, D., Ren, W., Zhou, K., Yang, G., 2014. The loss of taste genes in cetaceans. *BMC Evol Biol* 14, 218. <https://doi.org/10.1186/s12862-014-0218-8>

## 7 Supplementary

Table S1 Detail information of neutral references

Species	Sequence Name	Genome Database ID	Probed Length
<i>Saimiri boliviensis</i>	saiBol1_NR1	saiBol1	2,520
<i>Saimiri boliviensis</i>	saiBol1_NR2	saiBol1	7,969
<i>Saimiri boliviensis</i>	saiBol1_NR3	saiBol1	1,592
<i>Saimiri boliviensis</i>	saiBol1_NR4	saiBol1	1,422
<i>Saimiri boliviensis</i>	saiBol1_NR5	saiBol1	6,205
<i>Saimiri boliviensis</i>	saiBol1_NR6	saiBol1	1,372
<i>Saimiri boliviensis</i>	saiBol1_NR7	saiBol1	2,280
<i>Saimiri boliviensis</i>	saiBol1_NR8	saiBol1	3,317
<i>Saimiri boliviensis</i>	saiBol1_NR9	saiBol1	1,375
<i>Saimiri boliviensis</i>	saiBol1_NR10	saiBol1	1,338
<i>Saimiri boliviensis</i>	saiBol1_NR11	saiBol1	1,441
<i>Saimiri boliviensis</i>	saiBol1_NR12	saiBol1	1,861
<i>Saimiri boliviensis</i>	saiBol1_NR13	saiBol1	2,416
<i>Saimiri boliviensis</i>	saiBol1_NR14	saiBol1	2,553
<i>Saimiri boliviensis</i>	saiBol1_NR15	saiBol1	1,764
<i>Saimiri boliviensis</i>	saiBol1_NR16	saiBol1	1,170
<i>Saimiri boliviensis</i>	saiBol1_NR17	saiBol1	10,451
<i>Saimiri boliviensis</i>	saiBol1_NR19	saiBol1	1,643
<i>Saimiri boliviensis</i>	saiBol1_NR20	saiBol1	4,647
<i>Saimiri boliviensis</i>	saiBol1_NR21	saiBol1	1,520
<i>Saimiri boliviensis</i>	saiBol1_NR22	saiBol1	5,214
<i>Saimiri boliviensis</i>	saiBol1_NR23	saiBol1	5,565
<i>Saimiri boliviensis</i>	saiBol1_NR24	saiBol1	1,435
<i>Saimiri boliviensis</i>	saiBol1_NR25	saiBol1	3,149
<i>Saimiri boliviensis</i>	saiBol1_NR26	saiBol1	1,329

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<i>Saimiri boliviensis</i>	saiBol1_NR27	saiBol1	810
<i>Saimiri boliviensis</i>	saiBol1_NR28	saiBol1	2,056
<i>Saimiri boliviensis</i>	saiBol1_NR29	saiBol1	6,807
<i>Saimiri boliviensis</i>	saiBol1_NR30	saiBol1	1,452
<i>Saimiri boliviensis</i>	saiBol1_NR31	saiBol1	4,936
<i>Saimiri boliviensis</i>	saiBol1_NR32	saiBol1	1,207
<i>Saimiri boliviensis</i>	saiBol1_NR33	saiBol1	6,467
<i>Saimiri boliviensis</i>	saiBol1_NR34	saiBol1	1,521
<i>Saimiri boliviensis</i>	saiBol1_NR35	saiBol1	1,403
<i>Saimiri boliviensis</i>	saiBol1_NR36	saiBol1	3,454
<i>Saimiri boliviensis</i>	saiBol1_NR37	saiBol1	1,995
<i>Saimiri boliviensis</i>	saiBol1_NR38	saiBol1	1,668
<i>Saimiri boliviensis</i>	saiBol1_NR39	saiBol1	5,252
<i>Saimiri boliviensis</i>	saiBol1_NR40	saiBol1	1,354
<i>Saimiri boliviensis</i>	saiBol1_NR41	saiBol1	2,809
<i>Saimiri boliviensis</i>	saiBol1_NR42	saiBol1	1,917
<i>Saimiri boliviensis</i>	saiBol1_NR43	saiBol1	3,160
<i>Saimiri boliviensis</i>	saiBol1_NR44	saiBol1	3,036
<i>Saimiri boliviensis</i>	saiBol1_NR45	saiBol1	19,145
<i>Saimiri boliviensis</i>	saiBol1_NR46	saiBol1	6,472
<i>Saimiri boliviensis</i>	saiBol1_NR47	saiBol1	3,055
<i>Saimiri boliviensis</i>	saiBol1_NR48	saiBol1	2,779
<i>Saimiri boliviensis</i>	saiBol1_NR49	saiBol1	4,976
<i>Saimiri boliviensis</i>	saiBol1_NR50	saiBol1	2,299
<i>Saimiri boliviensis</i>	saiBol1_NR51	saiBol1	4,014
<i>Saimiri boliviensis</i>	saiBol1_NR52	saiBol1	2,570
<i>Saimiri boliviensis</i>	saiBol1_NR53	saiBol1	1,504
<i>Saimiri boliviensis</i>	saiBol1_NR54	saiBol1	1,361

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<i>Saimiri boliviensis</i>	saiBol1_NR55	saiBol1	2,104
<i>Saimiri boliviensis</i>	saiBol1_NR56	saiBol1	2,713
<i>Saimiri boliviensis</i>	saiBol1_NR57	saiBol1	1,751
<i>Saimiri boliviensis</i>	saiBol1_NR58	saiBol1	1,878
<i>Saimiri boliviensis</i>	saiBol1_NR59	saiBol1	1,724
<i>Saimiri boliviensis</i>	saiBol1_NR60	saiBol1	1,347
<i>Saimiri boliviensis</i>	saiBol1_NR61	saiBol1	1,731
<i>Saimiri boliviensis</i>	saiBol1_NR62	saiBol1	2,186
<i>Saimiri boliviensis</i>	saiBol1_NR63	saiBol1	2,251
<i>Saimiri boliviensis</i>	saiBol1_NR64	saiBol1	11,562
<i>Saimiri boliviensis</i>	saiBol1_NR65	saiBol1	2,478
<i>Saimiri boliviensis</i>	saiBol1_NR66	saiBol1	1,580
<i>Saimiri boliviensis</i>	saiBol1_NR67	saiBol1	2,584
<i>Saimiri boliviensis</i>	saiBol1_NR68	saiBol1	1,443
<i>Saimiri boliviensis</i>	saiBol1_NR69	saiBol1	1,693
<i>Saimiri boliviensis</i>	saiBol1_NR70	saiBol1	4,706
<i>Saimiri boliviensis</i>	saiBol1_NR71	saiBol1	1,641
<i>Saimiri boliviensis</i>	saiBol1_NR72	saiBol1	6,174
<i>Saimiri boliviensis</i>	saiBol1_NR73	saiBol1	15,301
<i>Saimiri boliviensis</i>	saiBol1_NR74	saiBol1	12,628
<i>Saimiri boliviensis</i>	saiBol1_NR75	saiBol1	12,846
<i>Saimiri boliviensis</i>	saiBol1_NR76	saiBol1	3,571
<i>Saimiri boliviensis</i>	saiBol1_NR77	saiBol1	3,121
<i>Saimiri boliviensis</i>	saiBol1_NR78	saiBol1	1,501
<i>Saimiri boliviensis</i>	saiBol1_NR79	saiBol1	1,366
<i>Saimiri boliviensis</i>	saiBol1_NR80	saiBol1	1,452
<i>Saimiri boliviensis</i>	saiBol1_NR81	saiBol1	2,249
<i>Saimiri boliviensis</i>	saiBol1_NR82	saiBol1	697

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<i>Saimiri boliviensis</i>	saiBol1_NR83	saiBol1	1,722
<i>Saimiri boliviensis</i>	saiBol1_NR84	saiBol1	2,360
<i>Saimiri boliviensis</i>	saiBol1_NR85	saiBol1	2,342
<i>Callithrix jaccahus</i>	carJac3_NR14	calJac3	1,918
<i>Callithrix jaccahus</i>	carJac3_NR17	calJac3	6,388
<i>Callithrix jaccahus</i>	carJac3_NR74	calJac3	14,512
<i>Callithrix jaccahus</i>	carJac3_NR78	calJac3	1,356
<i>Homo sapiens</i>	hg19_NR18	hg19	2,289

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Table S2 Purifying selection test of TAS1R1

	Hosa	Cja_WGA	Cja	Open	Mhum_WGA	Mhum	Cpyrg_WGA	Cpyrg	Lrs_WGA	Lrs	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Lliq_WGA	Lliq	KSTR_WGA	KSTR	Omo_WGA	Omo	Csat	Pp1t_WGA	Pp1t	
Hosa		6.48E+00	6.40E+00	6.84E+00	6.78E+00	6.75E+00	6.25E+00	6.25E+00	5.62E+00	5.26E+00	6.98E+00	6.92E+00	6.85E+00	6.85E+00	6.63E+00	5.60E+00	5.67E+00	5.46E+00	5.70E+00	5.61E+00	6.91E+00	6.91E+00	5.29E+00	5.25E+00	5.32E+00	5.27E+00	5.38E+00	5.38E+00	5.40E+00	5.31E+00	5.28E+00	5.24E+00	5.26E+00	
Cja_WGA	1.06E-09		0.00E+00	1.00E+00	2.63E+00	2.43E+00	1.82E+00	2.23E+00	1.96E+00	1.82E+00	4.88E+00	4.85E+00	4.68E+00	4.57E+00	4.01E+00	4.81E+00	4.81E+00	4.85E+00	5.02E+00	4.92E+00	6.59E+00	6.59E+00	5.00E+00	4.85E+00	5.43E+00	5.38E+00	4.75E+00	4.75E+00	5.26E+00	5.03E+00	5.74E+00	5.74E+00		
Cja	1.57E-09	1.00E+00		1.00E+00	2.43E+00	2.23E+00	1.58E+00	1.58E+00	1.96E+00	1.78E+00	4.78E+00	4.75E+00	4.57E+00	4.46E+00	3.90E+00	4.71E+00	4.70E+00	4.54E+00	4.82E+00	4.81E+00	6.51E+00	6.51E+00	4.90E+00	4.75E+00	5.33E+00	5.28E+00	4.65E+00	4.65E+00	5.17E+00	5.06E+00	5.64E+00	5.64E+00		
Cpyr	1.06E-09	1.59E-01	1.59E-01		2.01E+00	1.82E+00	1.82E+00	2.37E+00	2.10E+00	1.88E+00	4.85E+00	4.86E+00	4.68E+00	4.57E+00	4.01E+00	4.81E+00	4.85E+00	5.02E+00	4.92E+00	6.59E+00	6.59E+00	5.00E+00	4.85E+00	5.43E+00	5.38E+00	4.75E+00	4.75E+00	5.07E+00	4.96E+00	5.03E+00	5.74E+00	5.74E+00		
Cpyr	1.06E-09	1.59E-01	1.59E-01		2.23E+00	2.23E+00	1.58E+00	2.37E+00	2.10E+00	1.88E+00	4.85E+00	4.86E+00	4.68E+00	4.57E+00	4.01E+00	4.81E+00	4.85E+00	5.02E+00	4.92E+00	6.59E+00	6.59E+00	5.00E+00	4.85E+00	5.43E+00	5.38E+00	4.75E+00	4.75E+00	5.07E+00	4.96E+00	5.03E+00	5.74E+00	5.74E+00		
Mhum_WGA	2.43E+00	4.88E-03	8.20E-03	1.38E-02			1.00E+00	2.73E+00	2.73E+00	2.87E+00	2.59E+00	5.33E+00	5.15E+00	5.14E+00	5.04E+00	4.43E+00	5.26E+00	5.06E+00	5.27E+00	5.16E+00	6.89E+00	6.89E+00	5.16E+00	5.02E+00	5.58E+00	5.53E+00	4.82E+00	4.82E+00	5.13E+00	5.20E+00	5.39E+00	6.07E+00	6.07E+00	
Mhum	3.60E+00	8.20E-03	1.38E-02	2.35E-02			1.59E-01	2.55E+00	2.55E+00	2.74E+00	2.48E+00	5.23E+00	5.05E+00	5.03E+00	4.93E+00	4.32E+00	5.16E+00	4.98E+00	4.80E+00	5.17E+00	5.08E+00	6.81E+00	6.81E+00	5.07E+00	4.82E+00	5.44E+00	5.44E+00	4.82E+00	4.82E+00	5.04E+00	5.10E+00	5.29E+00	5.98E+00	5.98E+00
Cpyrg_WGA	3.18E-09	3.55E-02	6.04E-02	3.55E-02	3.60E-03	5.99E-03		0.00E+00	2.00E+00	1.74E+00	4.56E+00	4.48E+00	4.34E+00	4.22E+00	3.65E+00	4.62E+00	4.69E+00	4.53E+00	4.91E+00	4.80E+00	6.58E+00	6.58E+00	4.82E+00	4.68E+00	5.28E+00	4.58E+00	4.58E+00	4.99E+00	4.98E+00	4.85E+00	5.58E+00	5.56E+00		
Cpyrg	3.18E-09	3.55E-02	6.04E-02	3.55E-02	3.60E-03	5.99E-03	1.00E+00		2.00E+00	1.74E+00	4.56E+00	4.48E+00	4.34E+00	4.22E+00	3.65E+00	4.62E+00	4.69E+00	4.53E+00	4.91E+00	4.80E+00	6.58E+00	6.58E+00	4.82E+00	4.68E+00	5.28E+00	4.58E+00	4.58E+00	4.99E+00	4.98E+00	4.85E+00	5.58E+00	5.56E+00		
Lrs_WGA	6.98E-08	1.39E-02	1.39E-02	9.65E-03	2.39E-03	3.52E-03	2.39E-02	2.39E-02		0.00E+00	3.45E+00	3.24E+00	3.01E+00	2.98E+00	2.81E+00	3.51E+00	3.77E+00	3.72E+00	4.10E+00	3.96E+00	4.85E+00	4.85E+00	4.24E+00	3.98E+00	4.45E+00	4.39E+00	3.41E+00	3.41E+00	3.33E+00	3.41E+00	3.98E+00	4.29E+00	4.29E+00	
Lrs	3.19E-07	2.63E-02	2.63E-02	1.90E-02	5.40E-03	7.67E-03	4.18E-02	4.18E-02	1.00E+00		3.18E+00	2.97E+00	2.75E+00	2.83E+00	2.55E+00	3.19E+00	3.50E+00	3.45E+00	3.83E+00	3.72E+00	4.57E+00	4.57E+00	3.92E+00	3.66E+00	4.08E+00	4.02E+00	3.11E+00	3.11E+00	2.99E+00	3.07E+00	3.57E+00	3.97E+00	3.97E+00	
Smid_WGA	8.90E-11	1.62E-06	2.51E-06	1.62E-06	2.32E-07	3.59E-07	6.28E-06	6.28E-06	3.92E-04	9.45E-04						6.39E-01	6.71E-01	7.78E-01	1.79E+00	5.20E+00	5.35E+00	5.11E+00	5.45E+00	5.35E+00	6.50E+00	6.50E+00	5.12E+00	5.08E+00	5.76E+00	5.81E+00	5.74E+00	5.80E+00	5.80E+00	
Smid	1.21E+10	1.84E-08	2.87E-08	1.84E-08	5.13E-07	7.97E-07	9.29E-06	9.29E-06	7.73E-04	1.83E-03	2.82E-01					2.89E-02	2.89E-02	2.89E-02	1.48E+00	5.01E+00	5.12E+00	4.86E+00	5.22E+00	5.12E+00	6.34E+00	6.34E+00	5.09E+00	5.01E+00	5.84E+00	5.80E+00	5.79E+00	5.82E+00	5.82E+00	
Soe_WGA	4.67E+10	3.67E-06	6.02E-06	3.67E-06	5.50E-07	8.52E-07	1.52E-05	1.52E-05	1.57E-03	3.43E-03	2.52E-01	4.88E-01				1.29E+00	5.09E+00	5.29E+00	5.00E+00	5.36E+00	5.24E+00	6.45E+00	6.45E+00	4.97E+00	4.82E+00	5.75E+00	5.70E+00	4.78E+00	4.78E+00	5.70E+00	5.69E+00	5.71E+00	5.73E+00	5.73E+00
Soe	3.95E+10	5.99E-06	9.32E-06	5.99E-06	8.47E-07	1.31E-06	2.34E-05	2.34E-05	2.28E-03	4.82E-03	2.19E-01	4.88E-01	1.00E+00			1.08E+00	5.00E+00	5.16E+00	4.91E+00	5.26E+00	5.16E+00	6.37E+00	6.37E+00	5.01E+00	4.87E+00	5.66E+00	5.61E+00	4.80E+00	4.80E+00	5.61E+00	5.60E+00	5.73E+00	5.76E+00	5.76E+00
Sfu	5.12E+10	5.21E-05	8.00E-05	5.21E-05	1.04E-05	1.60E-05	1.98E-04	1.98E-04	2.92E-03	6.00E-03	3.83E-02	7.40E-02	1.00E-01	1.41E-01		4.70E+00	4.87E+00	4.61E+00	4.97E+00	4.87E+00	6.21E+00	6.21E+00	4.88E+00	4.83E+00	5.67E+00	5.62E+00	4.62E+00	4.62E+00	5.48E+00	5.47E+00	5.61E+00	6.01E+00	6.01E+00	
Aaz	6.83E-08	2.21E-06	3.42E-06	2.21E-06	3.21E-07	4.95E-07	4.94E-06	4.94E-06	3.16E-04	8.97E-04	4.19E-07	9.59E-07	6.57E-07	1.00E-06	3.45E-06		3.63E+00	3.81E+00	4.22E+00	4.10E+00	5.58E+00	5.58E+00	3.74E+00	3.68E+00	4.00E+00	3.94E+00	3.07E+00	3.07E+00	4.36E+00	4.25E+00	4.12E+00	4.50E+00	4.50E+00	
Sap_WGA	5.01E-08	2.21E-06	3.44E-06	2.21E-06	7.55E-07	1.17E-06	3.62E-06	3.62E-06	1.30E-04	3.28E-04	2.11E-07	5.94E-07	3.26E-07	4.99E-07	1.72E-06	2.11E-04		1.15E+00	1.58E+00	1.29E+00	5.23E+00	5.23E+00	3.84E+00	3.82E+00	4.06E+00	4.00E+00	3.99E+00	3.99E+00	4.00E+00	3.99E+00	4.03E+00	4.59E+00	4.59E+00	
Sap104	1.29E-07	4.38E-06	6.80E-06	4.37E-06	1.49E-06	2.32E-06	7.13E-06	7.13E-06	1.54E-04	3.83E-04	6.22E-07	1.77E-06	9.70E-07	1.48E-06	5.10E-06	1.11E-04	1.26E-01		8.34E-01	4.62E-01	5.18E+00	5.18E+00	3.63E+00	3.57E+00	4.22E+00	4.16E+00	3.76E+00	3.76E+00	3.95E+00	3.84E+00	3.86E+00	4.32E+00	4.32E+00	
Ccap_WGA	4.38E-08	9.00E-07	1.40E-06	8.99E-07	3.09E-07	4.80E-07	1.48E-06	1.48E-06	3.84E-05	1.04E-04	1.35E-07	3.79E-07	2.08E-07	3.19E-07	1.10E-06	2.41E-05	6.04E-02	2.03E-01		1.00E+00	5.43E+00	5.43E+00	3.90E+00	3.79E+00	4.38E+00	4.32E+00	3.82E+00	3.82E+00	4.34E+00	4.22E+00	4.26E+00	4.70E+00	4.70E+00	
Ccap	6.61E-08	1.41E-06	2.20E-06	1.41E-06	4.85E-07	7.53E-07	2.33E-06	2.33E-06	5.78E-05	1.52E-04	2.10E-07	5.92E-07	3.25E-07	4.97E-07	1.72E-06	3.75E-05	1.00E-01	3.22E-01	1.59E-01		5.43E+00	5.43E+00	3.79E+00	3.68E+00	4.27E+00	4.21E+00	3.81E+00	3.81E+00	4.22E+00	4.11E+00	4.14E+00	4.59E+00	4.59E+00	
Sbol_WGA	1.28E+10	6.14E-10	9.36E-10	6.12E-10	3.71E-10	5.65E-10	7.25E-10	7.25E-10	1.91E-06	5.85E-06	9.61E-10	2.05E-09	1.21E-09	1.83E-09	3.87E-09	8.34E-08	3.58E-07	4.55E-07	1.47E-07	1.49E-07		1.49E+07												
Sbol	1.28E+10	6.14E-10	9.36E-10	6.12E-10	3.71E-10	5.65E-10	7.25E-10	7.25E-10	1.91E-06	5.85E-06	9.61E-10	2.05E-09	1.21E-09	1.83E-09	3.87E-09	8.34E-08	3.58E-07	4.55E-07	1.47E-07	1.49E-07	1.00E+00													
Age_WGA	2.77E-07	1.01E-06	1.52E-06	1.01E-06	4.94E-07	7.47E-07	2.09E-06	2.09E-06	2.17E-05	7.36E-05	5.85E-07	7.79E-07	1.14E-06	9.50E-07	1.68E-06	1.43E-04	1.73E-04	2.07E-04	7.88E-05	1.19E-04	1.68E-06	1.68E-06												
Age	3.37E-07	1.86E-06	2.81E-06	1.86E-06	9.10E-07	1.38E-06	3.85E-06	3.85E-06	5.91E-05	1.81E-04	7.13E-07	9.50E-07	2.09E-06	1.74E-06	2.02E-06	1.76E-04	2.13E-04	2.54E-04	1.17E-04	1.77E-04	2.02E-06	2.02E-06	1.00E+00											
Lliq_WGA	2.42E-07	1.52E-07	2.30E-07	1.51E-07	7.45E-08	1.13E-07	2.90E-07	2.90E-07	9.73E-06	4.05E-05	3.29E-08	2.23E-08	3.48E-08	5.20E-08	4.99E-08	5.49E-05	4.37E-05	2.35E-05	1.27E-05	1.93E-05	8.09E-08	8.09E-08	4.69E-02	4.97E-02										
Lliq	3.11E-07	1.91E-07	2.89E-07	1.91E-07	9.37E-08	1.42E-07	3.65E-07	3.65E-07	1.24E-05	5.14E-05	4.16E-08	2.81E-08	4.40E-08	6.57E-08	6.29E-08	6.97E-05	5.54E-05	2.98E-05	1.60E-05	2.45E-05	1.54E-07	1.54E-07	5.82E-02	7.13E-02	1.00E+00									
KSTR_WGA	1.88E-07	2.85E-06	4.28E-06	2.85E-06	1.20E-06	5.78E-06	5.78E-06	5.78E-06	4.43E-04	1.17E-03	1.41E-06	1.30E-06	2.49E-06	2.30E-06	4.85E-06	1.32E-03	2.40E-04	1.31E-04	1.07E-04	1.09E-04	1.02E-06	1.02E-06	6.49E-02	7.81E-02	6.79E-03	8.54E-03								
KSTR	1.88E-07	2.85E-06	4.28E-06	2.85E-06	1.40E-06	2.10E-06	5.78E-06	5.78E-06	4.43E-04	1.17E-03	1.41E-06	1.30E-06	2.49E-06	2.30E-06	4.85E-06	1.32E-03	2.40E-04	1.31E-04	1.07E-04	1.09E-04	1.02E-06	1.02E-06	6.49E-02	7.81E-02	6.79E-03	8.54E-03	1.00E+00							
Omo_WGA	1.74E-07	3.15E-07	4.81E-07	7.34E-07	5.54E-07	8.42E-07	1.05E-06	1.05E-06	5.70E-04	1.97E-03	2.51E-06	4.88E-06	4.39E-06	6.59E-06	1.19E-07	1.37E-05	5.40E-05	6.57E-05	1.52E-05	2.34E-05	6.75E-08	6.75E-08	8.89E-04</											



Table S3 Positive selection test of TAS1R1

	Hsaa	Cja_WGA	Cja	Cpen	Mhum_WGA	Mhum	Cpyg_WGA	Cpyg	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Ltag_WGA	Ltag	KSTR_WGA	KSTR	Omo_WGA	Omo	Ocat	Ppil_WGA	Ppil	
Hsaa		-6.48	-6.40	-6.48	-6.78	-6.70	-6.25	-6.82	-6.26	-6.98	-6.92	-6.85	-6.88	-6.63	-6.60	-6.67	-6.46	-6.70	-6.61	-6.91	-6.91	-6.29	-6.25	-6.32	-6.27	-6.38	-6.38	-6.40	-6.31	-6.28	-6.28	-6.28	-6.28	
Cja_WGA	1.00		0.00	-1.00	-2.63	-2.43	-1.82	-1.82	-2.23	-1.96	-4.88	-4.85	-4.68	-4.57	-4.01	-4.81	-4.81	-4.65	-5.02	-4.92	-6.59	-6.59	-6.00	-4.85	-5.43	-5.38	-4.75	-4.75	-5.26	-5.16	-5.03	-5.74	-5.74	
Cja	1.00	1.00		-1.00	-2.43	-2.23	-1.56	-1.56	-2.23	-1.96	-4.78	-4.75	-4.57	-4.46	-3.90	-4.71	-4.70	-4.54	-4.92	-4.81	-6.51	-6.51	-4.90	-4.75	-5.33	-5.28	-4.65	-4.65	-5.17	-5.06	-4.93	-5.64	-5.64	
Cpen	1.00	1.00	1.00		-2.23	-2.01	-1.82	-1.82	-2.37	-2.10	-4.88	-4.85	-4.68	-4.57	-4.01	-4.81	-4.81	-4.65	-5.02	-4.92	-6.59	-6.59	-5.00	-4.85	-5.43	-5.38	-4.75	-4.75	-5.07	-4.96	-5.03	-5.74	-5.74	
Mhum_WGA	1.00	1.00	1.00	1.00		-1.00	-2.73	-2.73	-2.87	-2.59	-5.33	-5.15	-5.14	-5.04	-4.43	-5.26	-5.06	-4.90	-5.27	-5.16	-6.69	-6.69	-5.16	-5.02	-5.88	-5.53	-4.92	-4.92	-6.13	-5.20	-5.39	-6.07	-6.07	
Mhum	1.00	1.00	1.00	1.00	1.00		-2.55	-2.55	-2.74	-2.46	-5.23	-5.05	-5.03	-4.93	-4.32	-5.16	-4.96	-4.80	-5.17	-5.06	-6.61	-6.61	-5.07	-4.92	-5.49	-5.44	-4.82	-4.82	-5.04	-5.10	-5.29	-5.98	-5.98	
Cpyg_WGA	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-2.00	-1.74	-4.56	-4.46	-4.34	-4.22	-3.65	-4.62	-4.69	-4.53	-4.91	-4.80	-6.56	-6.56	-4.82	-4.68	-5.28	-5.23	-4.58	-4.58	-4.99	-4.98	-4.85	-5.56	-5.56	
Cpyg	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-2.00	-1.74	-4.56	-4.46	-4.34	-4.22	-3.65	-4.62	-4.69	-4.53	-4.91	-4.80	-6.56	-6.56	-4.82	-4.68	-5.28	-5.23	-4.58	-4.58	-4.99	-4.98	-4.85	-5.56	-5.56	
Lros_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-3.45	-3.24	-3.01	-2.89	-2.81	-3.51	-3.77	-3.72	-4.10	-3.99	-4.85	-4.85	-4.24	-3.98	-4.45	-4.39	-3.41	-3.41	-3.33	-3.41	-3.88	-4.29	-4.29	
Lros	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-3.18	-2.97	-2.75	-2.63	-2.55	-3.19	-3.50	-3.45	-3.83	-3.72	-4.57	-4.57	-3.92	-3.66	-4.08	-4.02	-3.11	-3.11	-2.99	-3.07	-3.57	-3.97	-3.97	
Smid_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-0.64	-0.67	-0.78	-1.79	-5.20	-5.35	-5.11	-5.45	-5.35	-6.50	-6.50	-5.12	-5.08	-5.76	-5.71	-4.92	-4.92	-5.82	-5.81	-5.74	-6.80	-6.80	
Smid	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-0.03	-0.03	-1.46	-5.01	-5.12	-4.86	-5.22	-5.12	-6.34	-6.34	-5.06	-5.01	-5.84	-5.80	-4.94	-4.94	-5.68	-5.63	-5.79	-6.82	-6.82	
Soe_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-1.29	-5.09	-5.25	-5.00	-5.36	-5.26	-6.45	-6.45	-4.97	-4.82	-5.75	-5.70	-4.78	-4.78	-5.70	-5.69	-5.71	-6.73	-6.73	
Soe	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-1.08	-5.00	-5.16	-4.91	-5.26	-5.16	-6.37	-6.37	-5.01	-4.87	-5.66	-5.61	-4.80	-4.80	-5.61	-5.60	-5.73	-6.76	-6.76
Sfu	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-4.70	-4.87	-4.81	-4.97	-4.87	-6.21	-6.21	-4.88	-4.83	-5.67	-5.62	-4.62	-4.62	-5.48	-5.47	-5.61	-6.01	-6.01
Aaz	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-3.63	-3.81	-4.22	-4.10	-5.56	-5.56	-3.74	-3.68	-4.00	-3.94	-3.07	-3.07	-4.36	-4.25	-4.12	-4.50	-4.50
Sap_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-1.15	-1.56	-1.29	-1.29	-5.23	-5.23	-3.68	-3.62	-4.06	-4.00	-3.59	-3.59	-4.00	-3.89	-4.03	-4.59	-4.59
Sap104	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-6.83	-6.46	-5.18	-5.18	-3.63	-3.57	-4.22	-4.16	-3.76	-3.76	-3.95	-3.84	-3.86	-4.32	-4.32	
Ccap_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-1.00	-5.43	-5.43	-3.90	-3.79	-4.38	-4.32	-3.82	-3.82	-4.34	-4.22	-4.26	-4.70	-4.70	
Ccap	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-5.43	-5.43	-3.79	-3.68	-4.27	-4.21	-3.81	-3.81	-4.22	-4.11	-4.14	-4.59	-4.59	
Sbol_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-4.88	-4.83	-5.57	-5.42	-4.99	-4.99	-5.61	-5.57	-5.94	-5.96	-5.96	
Sbol	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-4.88	-4.83	-5.57	-5.42	-4.99	-4.99	-5.61	-5.57	-5.94	-5.96	-5.96	
Age_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-1.76	-1.58	-1.53	-1.53	-3.20	-3.09	-3.45	-3.42	-3.42	
Age	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-1.66	-1.48	-1.43	-1.43	-3.07	-2.96	-3.27	-3.36	-3.36	
Ltag_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-2.51	-2.51	-3.70	-3.59	-3.95	-4.15	-4.15	
Ltag	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-2.42	-2.42	-3.63	-3.52	-3.88	-4.08	-4.08	
KSTR_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00	-3.38	-3.27	-4.04	-3.93	-3.93	
KSTR	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-3.38	-3.27	-4.04	-3.93	-3.93	
Omo_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		1.00		-1.56	-4.03	-4.02
Omo	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-3.91	-3.90	-3.90
Ocat	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		-2.65	-2.65
Ppil_WGA	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		0.00
Ppil	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Table S4 Evolutionary neutrality test of TAS1R

	Hosa	Cja_WGA	Cja	Open	Mhum_WGA	Mhum	Cpyg_WGA	Cpyg	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Llag_WGA	Llag	KSTR_WGA	KSTR	Cmo_WGA	Cmo	Coat	Pp1t_WGA	Pp1t
Hosa		-6.48E+00	-6.40E+00	-6.48E+00	-6.78E+00	-6.70E+00	-6.25E+00	-6.25E+00	-5.62E+00	-5.26E+00	-6.98E+00	-6.92E+00	-6.65E+00	-6.68E+00	-6.63E+00	-6.60E+00	-5.67E+00	-5.46E+00	-5.70E+00	-5.61E+00	-6.91E+00	-6.91E+00	-5.29E+00	-5.25E+00	-5.32E+00	-5.27E+00	-5.38E+00	-5.38E+00	-5.40E+00	-5.31E+00	-5.28E+00	-5.28E+00	
Cja_WGA	2.12E-09		0.00E+00	-1.00E+00	-2.63E+00	-2.43E+00	-1.82E+00	-1.82E+00	-2.23E+00	-1.96E+00	-4.88E+00	-4.85E+00	-4.68E+00	-4.57E+00	-4.01E+00	-4.81E+00	-4.81E+00	-4.65E+00	-5.02E+00	-4.92E+00	-6.59E+00	-6.59E+00	-5.00E+00	-4.85E+00	-5.43E+00	-5.38E+00	-4.75E+00	-4.75E+00	-5.26E+00	-5.16E+00	-5.03E+00	-5.74E+00	-5.74E+00
Cja	3.13E-09	1.00E+00		-1.00E+00	-2.43E+00	-2.23E+00	-1.58E+00	-1.58E+00	-2.23E+00	-1.96E+00	-4.78E+00	-4.75E+00	-4.46E+00	-3.90E+00	-4.71E+00	-4.70E+00	-4.84E+00	-4.92E+00	-4.92E+00	-6.51E+00	-6.51E+00	-4.90E+00	-4.75E+00	-5.33E+00	-5.29E+00	-4.85E+00	-4.85E+00	-5.17E+00	-5.06E+00	-4.93E+00	-5.84E+00	-5.84E+00	
Open	2.11E-09	3.19E-01	3.19E-01		-2.23E+00	-2.01E+00	-1.82E+00	-1.82E+00	-2.37E+00	-2.10E+00	-4.85E+00	-4.85E+00	-4.68E+00	-4.57E+00	-4.01E+00	-4.81E+00	-4.81E+00	-4.65E+00	-5.02E+00	-4.92E+00	-6.59E+00	-6.59E+00	-5.00E+00	-4.85E+00	-5.43E+00	-5.38E+00	-4.75E+00	-4.75E+00	-5.07E+00	-4.98E+00	-5.03E+00	-5.74E+00	-5.74E+00
Mhum_WGA	4.87E-10	9.76E-03	1.84E-02	2.77E-02		-1.00E+00	-2.73E+00	-2.73E+00	-2.87E+00	-2.59E+00	-5.33E+00	-5.15E+00	-5.14E+00	-5.04E+00	-4.43E+00	-5.26E+00	-5.06E+00	-4.90E+00	-5.27E+00	-5.16E+00	-6.69E+00	-6.69E+00	-5.16E+00	-5.02E+00	-5.58E+00	-5.53E+00	-4.92E+00	-4.92E+00	-5.13E+00	-5.20E+00	-5.39E+00	-6.07E+00	-6.07E+00
Mhum	7.21E-10	1.64E-02	2.77E-02	4.70E-02	3.19E-01		-2.55E+00	-2.55E+00	-2.74E+00	-2.46E+00	-5.23E+00	-5.05E+00	-5.03E+00	-4.93E+00	-4.32E+00	-5.16E+00	-4.96E+00	-4.80E+00	-5.17E+00	-5.06E+00	-6.61E+00	-6.61E+00	-5.07E+00	-4.92E+00	-5.49E+00	-5.44E+00	-4.82E+00	-4.82E+00	-5.04E+00	-5.10E+00	-5.29E+00	-5.98E+00	-5.98E+00
Cpyg_WGA	6.37E-09	7.10E-02	1.21E-01	7.10E-02	7.19E-03	1.20E-02		0.00E+00	-2.00E+00	-1.74E+00	-4.56E+00	-4.46E+00	-4.34E+00	-4.22E+00	-3.65E+00	-4.62E+00	-4.69E+00	-4.53E+00	-4.91E+00	-4.80E+00	-6.56E+00	-6.56E+00	-4.82E+00	-4.68E+00	-5.28E+00	-5.23E+00	-4.58E+00	-4.58E+00	-4.99E+00	-4.98E+00	-4.85E+00	-5.56E+00	-5.56E+00
Cpyg	6.37E-09	7.10E-02	1.21E-01	7.10E-02	7.19E-03	1.20E-02	1.00E+00		-2.00E+00	-1.74E+00	-4.56E+00	-4.46E+00	-4.34E+00	-4.22E+00	-3.65E+00	-4.62E+00	-4.69E+00	-4.53E+00	-4.91E+00	-4.80E+00	-6.56E+00	-6.56E+00	-4.82E+00	-4.68E+00	-5.28E+00	-5.23E+00	-4.58E+00	-4.58E+00	-4.99E+00	-4.98E+00	-4.85E+00	-5.56E+00	-5.56E+00
Lros_WGA	1.28E-07	2.77E-02	2.77E-02	1.93E-02	4.76E-03	7.03E-03	6.75E-02	4.75E-02		0.00E+00	-3.45E+00	-3.18E+00	-2.97E+00	-2.75E+00	-2.63E+00	-2.55E+00	-3.19E+00	-3.50E+00	-3.45E+00	-3.83E+00	-3.72E+00	-4.57E+00	-4.57E+00	-3.92E+00	-3.66E+00	-4.08E+00	-4.02E+00	-3.11E+00	-3.11E+00	-2.99E+00	-3.07E+00	-3.97E+00	-3.97E+00
Lros	6.38E-07	5.25E-02	5.25E-02	3.80E-02	1.08E-02	1.53E-02	8.36E-02	8.36E-02	1.00E+00		-3.18E+00	-2.97E+00	-2.75E+00	-2.63E+00	-2.55E+00	-3.19E+00	-3.50E+00	-3.45E+00	-3.83E+00	-3.72E+00	-4.57E+00	-4.57E+00	-3.92E+00	-3.66E+00	-4.08E+00	-4.02E+00	-3.11E+00	-3.11E+00	-2.99E+00	-3.07E+00	-3.97E+00	-3.97E+00	
Smid_WGA	1.78E-10	3.24E-06	5.02E-06	3.23E-06	4.65E-07	7.19E-07	1.26E-05	1.26E-05	7.84E-04	1.89E-03		-6.39E-01	-6.71E-01	-7.78E-01	-1.79E+00	-5.20E+00	-5.35E+00	-5.11E+00	-6.45E+00	-5.35E+00	-6.50E+00	-6.50E+00	-5.12E+00	-5.08E+00	-5.76E+00	-5.71E+00	-4.92E+00	-4.92E+00	-5.82E+00	-5.81E+00	-5.74E+00	-5.80E+00	-5.80E+00
Smid	2.42E-10	3.68E-06	5.75E-06	3.68E-06	1.03E-06	1.59E-06	1.88E-05	1.88E-05	1.55E-03	3.65E-03	5.24E-01	-2.89E-02	-2.89E-02	-1.46E+00	-5.01E+00	-5.12E+00	-4.86E+00	-5.22E+00	-5.12E+00	-6.34E+00	-6.34E+00	-5.06E+00	-5.01E+00	-5.84E+00	-5.80E+00	-4.94E+00	-4.94E+00	-5.68E+00	-5.63E+00	-5.79E+00	-5.82E+00	-5.82E+00	
Soe_WGA	9.34E-10	7.74E-06	1.20E-05	7.74E-06	1.19E-06	1.70E-06	3.03E-05	3.03E-05	3.14E-03	6.86E-03	5.04E-01	9.77E-01		0.00E+00	-1.29E+00	-5.09E+00	-5.25E+00	-5.00E+00	-6.36E+00	-5.26E+00	-6.45E+00	-6.45E+00	-4.97E+00	-4.82E+00	-5.75E+00	-5.70E+00	-4.78E+00	-4.78E+00	-5.70E+00	-5.69E+00	-5.71E+00	-5.73E+00	-5.73E+00
Soe	7.90E-10	1.20E-05	1.86E-05	1.20E-05	1.69E-06	2.63E-06	4.68E-05	4.68E-05	4.65E-03	9.64E-03	4.38E-01	9.77E-01	1.00E+00		-1.08E+00	-5.00E+00	-5.16E+00	-4.91E+00	-5.26E+00	-5.16E+00	-6.37E+00	-6.37E+00	-5.01E+00	-4.87E+00	-5.66E+00	-5.61E+00	-4.80E+00	-4.80E+00	-5.61E+00	-5.60E+00	-5.73E+00	-5.76E+00	-5.76E+00
Sfu	1.02E-09	1.04E-04	1.61E-04	1.04E-04	2.07E-05	3.21E-05	3.91E-04	3.91E-04	5.85E-03	1.20E-02	7.65E-02	1.48E-01	2.00E-01	2.82E-01	-4.70E+00	-4.87E+00	-4.61E+00	-4.97E+00	-4.87E+00	-6.21E+00	-6.21E+00	-4.88E+00	-4.88E+00	-4.67E+00	-4.62E+00	-4.62E+00	-4.62E+00	-4.48E+00	-5.47E+00	-5.61E+00	-6.01E+00	-6.01E+00	
Aaz	1.37E-07	4.43E-06	6.84E-06	4.42E-06	6.42E-07	9.90E-07	9.89E-06	9.89E-06	6.32E-04	1.79E-03	8.38E-07	1.92E-06	1.31E-06	2.00E-06	6.90E-06	-3.63E+00	-3.81E+00	-4.22E+00	-4.10E+00	-5.56E+00	-5.56E+00	-3.74E+00	-3.68E+00	-4.00E+00	-3.94E+00	-3.07E+00	-3.07E+00	-4.25E+00	-4.12E+00	-4.50E+00	-4.50E+00	-4.50E+00	
Sap_WGA	1.00E-07	4.42E-06	6.87E-06	4.41E-06	1.51E-06	2.35E-06	7.25E-06	7.25E-06	2.59E-04	6.56E-04	4.22E-07	1.19E-06	6.53E-07	9.98E-07	3.45E-06	4.22E-04	-1.15E+00	-1.56E+00	-1.29E+00	-5.23E+00	-5.23E+00	-3.68E+00	-3.62E+00	-4.06E+00	-3.59E+00	-3.59E+00	-3.59E+00	-4.00E+00	-3.89E+00	-4.03E+00	-4.59E+00	-4.59E+00	
Sap104	2.58E-07	8.75E-06	1.36E-05	8.74E-06	2.99E-06	4.64E-06	1.43E-05	1.43E-05	3.98E-04	7.66E-04	1.24E-06	3.55E-06	1.94E-06	2.97E-06	1.02E-05	2.21E-04	2.52E-01		8.34E-01	-4.62E-01	-5.18E+00	-5.18E+00	-3.63E+00	-3.57E+00	-4.22E+00	-4.14E+00	-3.76E+00	-3.76E+00	-3.64E+00	-4.32E+00	-4.32E+00	-4.32E+00	
Ccap_WGA	8.71E-08	1.80E-06	2.80E-06	1.80E-06	6.19E-07	9.60E-07	2.96E-06	2.96E-06	7.67E-05	2.07E-04	2.69E-07	7.58E-07	4.17E-07	6.37E-07	2.20E-06	4.81E-05	1.21E-01	4.06E-01		-1.00E+00	-5.43E+00	-5.43E+00	-3.90E+00	-3.79E+00	-4.38E+00	-4.32E+00	-3.82E+00	-3.82E+00	-4.22E+00	-4.26E+00	-4.70E+00	-4.70E+00	
Ccap	1.32E-07	2.83E-06	4.40E-06	2.83E-06	9.70E-07	1.51E-06	4.65E-06	4.65E-06	1.15E-04	3.05E-04	4.20E-07	1.18E-06	6.50E-07	9.95E-07	3.43E-06	7.51E-05	2.01E-01	6.45E-01	3.19E-01	-1.00E+00	-5.43E+00	-5.43E+00	-3.79E+00	-3.68E+00	-4.27E+00	-4.21E+00	-3.81E+00	-3.81E+00	-4.22E+00	-4.11E+00	-4.14E+00	-4.59E+00	-4.59E+00
Sbol_WGA	2.56E-10	1.23E-09	1.87E-09	1.22E-09	7.41E-10	1.13E-09	1.45E-09	1.45E-09	3.81E-06	1.17E-05	1.92E-09	4.11E-09	2.42E-09	3.66E-09	7.75E-09	1.67E-07	7.16E-07	9.10E-07	2.95E-07	2.98E-07		0.00E+00	-4.88E+00	-4.83E+00	-5.57E+00	-5.42E+00	-4.99E+00	-4.99E+00	-5.61E+00	-5.57E+00	-5.94E+00	-5.96E+00	-5.96E+00
Sbol	2.56E-10	1.23E-09	1.87E-09	1.22E-09	7.41E-10	1.13E-09	1.45E-09	1.45E-09	3.81E-06	1.17E-05	1.92E-09	4.11E-09	2.42E-09	3.66E-09	7.75E-09	1.67E-07	7.16E-07	9.10E-07	2.95E-07	2.98E-07	1.00E+00	-4.88E+00	-4.83E+00	-5.57E+00	-5.42E+00	-4.99E+00	-4.99E+00	-5.61E+00	-5.57E+00	-5.94E+00	-5.96E+00	-5.96E+00	
Age_WGA	5.54E-07	2.02E-06	3.04E-06	2.01E-06	8.99E-07	1.49E-06	4.19E-06	4.19E-06	4.34E-05	1.47E-04	1.17E-06	1.56E-06	2.29E-06	1.90E-06	3.31E-06	2.87E-04	3.46E-04	4.13E-04	1.58E-04	2.39E-04	3.31E-06	3.31E-06	0.00E+00	-1.76E+00	-1.58E+00	-1.53E+00	-1.53E+00	-3.20E+00	-3.09E+00	-3.45E+00	-3.42E+00	-3.42E+00	
Age	6.73E-07	3.72E-06	5.62E-06	3.72E-06	1.82E-06	2.75E-06	7.71E-06	7.71E-06	1.18E-04	3.82E-04	1.43E-06	1.90E-06	4.18E-06	3.47E-06	4.04E-06	3.52E-04	4.23E-04	5.07E-04	2.35E-04	3.54E-04	4.05E-06	4.05E-06	1.00E+00	-1.66E+00	-1.48E+00	-1.43E+00	-1.43E+00	-3.07E+00	-2.96E+00	-3.27E+00	-3.36E+00	-3.36E+00	
Llag_WGA	4.85E-07	3.03E-07	4.60E-07	3.03E-07	1.04E-07	2.26E-07	5.79E-07	5.79E-07	1.95E-05	8.09E-05	6.58E-08	4.47E-08	6.96E-08	1.04E-07	9.97E-08	1.10E-04	8.74E-05	4.70E-05	2.53E-05	1.62E-07	1.62E-07	8.07E-02	9.94E-02		0.00E+00	-2.51E+00	-2.51E+00	-3.70E+00	-3.59E+00	-3.95E+00	-4.15E+00	-4.15E+00	
Llag	6.23E-07	3.82E-07	5.79E-07	3.81E-07	1.87E-07	2.84E-07	7.30E-07	7.30E-07	2.48E-05	1.03E-04	8.31E-08	5.62E-08	8.79E-08	1.31E-07	1.26E-07	1.39E-04	1.11E-04	5.96E-05	3.21E-05	4.90E-05	3.09E-07	3.09E-07	1.16E-01	1.43E-01	1.00E+00		-2.42E+00	-2.42E+00	-3.63E+00	-3.52E+00	-3.88E+00	-4.08E+00	-4.08E+00
KSTR_WGA	3.72E-07	5.70E-06	8.56E-06	5.69E-06	2.80E-06	4.20E-06	1.16E-05	1.16E-05	8.87E-04	2.35E-03	2.83E-06	2.60E-06	4.97E-06	4.60E-06	9.71E-06	2.63E-03	4.80E-04	2.61E-04	2.14E-04	2.17E-04	2.04E-06	2.04E-06	1.30E-01	1.56E-01	1.36E-02	1.71E-02		0.00E+00	-3.38E+00	-3.27E+00	-4.04E+00	-3.93E+00	-3.93E+00
KSTR	3.72E-07	5.70E-06	8.56E-06	5.69E-06	2.80E-06	4.20E-06	1.16E-05	1.16E-05	8.87E-04	2.35E-03	2.83E-06	2.60E-06	4.97E-06	4.60E-06	9.71E-06	2.63E-03	4.80E-04	2.61E-04	2.14E-04	2.17E-04	2.04E-06	2.04E-06	1.30E-01	1.56E-01	1.36E-02	1.71E-02	1.00E+00	-3.38E+00	-3.27E+00	-4.04E+00	-3.93E+00	-3.93E+00	
Cmo_WGA	3.48E-07	6.31E-07																															

Table S5 Purifying selection test of TAS1R2

	Hosa	Cja_WGA	Cja	Cpen	Mhum_WGA/Mhum	Cpyg	Cpyg_WGA	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Llag_WGA	Llag	KSTR_WGA	KSTR	Cmo_WGA	Cmo	Csat	Ppht_WGA	Ppht		
Hosa		5.69E+00	5.69E+00	5.61E+00	5.92E+00	5.65E+00	5.86E+00	6.06E+00	5.84E+00	5.83E+00	5.57E+00	5.67E+00	5.67E+00	6.74E+00	5.38E+00	5.03E+00	5.03E+00	4.85E+00	4.92E+00	5.48E+00	5.52E+00	5.31E+00	6.27E+00	5.21E+00	5.08E+00	4.98E+00	4.89E+00	5.57E+00	5.66E+00	5.50E+00	6.15E+00	5.98E+00		
Cja_WGA	4.52E-08		1.42E+00	1.42E+00	3.92E+00	3.50E+00	4.55E+00	4.88E+00	5.53E+00	5.01E+00	5.12E+00	5.32E+00	5.32E+00	6.49E+00	6.30E+00	5.45E+00	5.45E+00	5.26E+00	5.11E+00	5.53E+00	5.49E+00	6.25E+00	6.13E+00	6.38E+00	6.18E+00	5.83E+00	5.92E+00	6.68E+00	6.56E+00	6.31E+00	6.55E+00	6.47E+00		
Cja	4.52E-08	7.96E-02		0.00E+00	3.65E+00	3.20E+00	4.31E+00	4.66E+00	5.34E+00	4.80E+00	4.91E+00	5.12E+00	5.12E+00	6.31E+00	6.12E+00	5.26E+00	5.26E+00	5.26E+00	5.11E+00	5.35E+00	5.30E+00	6.07E+00	5.95E+00	6.21E+00	6.00E+00	5.65E+00	5.74E+00	6.51E+00	6.39E+00	6.31E+00	6.55E+00	6.47E+00		
Cpen	6.58E-08	7.96E-02	1.00E+00		3.51E+00	3.04E+00	4.18E+00	4.54E+00	5.24E+00	4.78E+00	4.69E+00	4.80E+00	5.02E+00	5.02E+00	6.22E+00	6.03E+00	5.26E+00	5.26E+00	5.16E+00	5.11E+00	5.25E+00	5.20E+00	5.99E+00	5.86E+00	6.12E+00	5.91E+00	5.56E+00	5.66E+00	6.43E+00	6.39E+00	6.22E+00	6.47E+00	6.38E+00	
Mhum_WGA	1.60E-08	7.34E-05	1.95E-04	3.21E-04		1.74E+00	4.26E+00	4.62E+00	4.78E+00	4.26E+00	4.49E+00	4.83E+00	4.83E+00	5.69E+00	5.87E+00	5.19E+00	5.19E+00	5.19E+00	5.24E+00	5.08E+00	5.03E+00	5.81E+00	5.68E+00	5.94E+00	5.83E+00	5.28E+00	5.37E+00	6.28E+00	6.32E+00	6.39E+00	6.64E+00	6.55E+00		
Mhum	5.38E-08	3.23E-04	8.78E-04	1.45E-03	4.25E-02		3.87E+00	4.26E+00	4.44E+00	4.44E+00	3.95E+00	4.20E+00	4.36E+00	4.56E+00	5.30E+00	5.87E+00	4.89E+00	4.89E+00	4.88E+00	4.93E+00	4.77E+00	5.33E+00	5.38E+00	5.87E+00	5.84E+00	4.99E+00	5.08E+00	5.92E+00	5.97E+00	6.12E+00	6.42E+00	6.33E+00		
Cpyg	2.08E-08	6.59E-06	1.71E-05	2.76E-05	2.05E-05	8.92E-05		5.36E+00	5.36E+00	4.83E+00	4.72E+00	4.83E+00	4.83E+00	6.17E+00	6.49E+00	5.51E+00	5.50E+00	5.50E+00	5.45E+00	5.40E+00	6.17E+00	6.05E+00	6.30E+00	6.19E+00	5.59E+00	5.89E+00	6.80E+00	6.75E+00	6.44E+00	6.69E+00	6.80E+00			
Cpyg_WGA	7.93E-09	1.62E-06	4.14E-06	6.63E-06	4.90E-06	2.06E-05	1.59E-01		5.60E+00	5.60E+00	5.15E+00	5.04E+00	5.25E+00	5.25E+00	6.43E+00	6.75E+00	5.64E+00	5.83E+00	5.64E+00	5.69E+00	5.72E+00	5.67E+00	6.43E+00	6.30E+00	6.55E+00	6.45E+00	5.85E+00	5.94E+00	6.85E+00	6.81E+00	6.64E+00	6.88E+00	6.80E+00	
Lros_WGA	2.32E-08	9.36E-08	2.27E-07	3.53E-07	2.50E-06	9.88E-06	2.02E-07	6.96E-08		0.00E+00	5.00E+00	4.67E+00	5.11E+00	5.11E+00	5.94E+00	6.17E+00	5.69E+00	5.69E+00	5.69E+00	5.74E+00	5.39E+00	5.34E+00	6.47E+00	6.43E+00	6.07E+00	6.04E+00	5.66E+00	5.76E+00	6.05E+00	6.14E+00	6.08E+00	6.50E+00	6.33E+00	
Lros	2.32E-08	9.36E-08	2.27E-07	3.53E-07	2.50E-06	9.88E-06	2.02E-07	6.96E-08	1.00E+00		5.00E+00	4.67E+00	5.11E+00	5.11E+00	5.94E+00	6.17E+00	5.69E+00	5.69E+00	5.69E+00	5.74E+00	5.39E+00	5.34E+00	6.47E+00	6.43E+00	6.07E+00	6.04E+00	5.66E+00	5.76E+00	6.05E+00	6.14E+00	6.08E+00	6.50E+00	6.33E+00	
Smid_WGA	2.38E-08	9.34E-07	2.32E-06	3.64E-06	2.07E-05	6.52E-05	2.02E-06	5.20E-07	9.95E-07	9.95E-07		1.42E+00	3.02E+00	3.02E+00	5.10E+00	6.05E+00	5.54E+00	5.35E+00	5.32E+00	5.37E+00	5.11E+00	5.08E+00	5.83E+00	5.79E+00	5.49E+00	5.46E+00	5.01E+00	5.10E+00	6.20E+00	6.29E+00	6.59E+00	6.75E+00	6.58E+00	
Smid	7.76E-08	5.94E-07	1.47E-06	2.31E-06	8.15E-06	2.54E-05	3.20E-06	8.19E-07	3.96E-06	3.96E-06	7.96E-02		2.46E+00	2.46E+00	4.99E+00	5.77E+00	5.25E+00	5.05E+00	5.02E+00	5.07E+00	4.80E+00	4.75E+00	5.79E+00	5.75E+00	5.45E+00	5.42E+00	4.91E+00	5.01E+00	6.33E+00	6.42E+00	6.51E+00	6.67E+00	6.50E+00	
Soe_WGA	5.11E-08	2.40E-07	5.90E-07	9.24E-07	2.02E-06	6.22E-06	2.01E-06	3.28E-07	6.26E-07	6.26E-07	1.53E-03	7.62E-03		5.21E+00	6.05E+00	5.45E+00	5.25E+00	5.22E+00	5.27E+00	5.01E+00	4.96E+00	5.92E+00	5.89E+00	5.78E+00	5.75E+00	5.11E+00	5.20E+00	6.46E+00	6.55E+00	6.68E+00	6.84E+00	6.87E+00		
Soe	5.11E-08	2.40E-07	5.90E-07	9.24E-07	2.02E-06	6.22E-06	2.01E-06	3.28E-07	6.26E-07	6.26E-07	1.53E-03	7.62E-03	1.00E+00		5.21E+00	6.05E+00	5.45E+00	5.25E+00	5.22E+00	5.27E+00	5.01E+00	4.96E+00	5.92E+00	5.89E+00	5.78E+00	5.75E+00	5.11E+00	5.20E+00	6.46E+00	6.55E+00	6.68E+00	6.84E+00	6.87E+00	
Sfu	2.96E-10	1.01E-09	2.39E-09	3.68E-09	4.48E-08	1.10E-07	4.84E-09	1.34E-09	1.43E-08	1.43E-08	6.43E-07	1.02E-06	4.04E-07	4.04E-07		6.84E+00	6.80E+00	6.63E+00	6.60E+00	6.65E+00	6.51E+00	6.47E+00	7.10E+00	7.06E+00	7.13E+00	7.11E+00	6.26E+00	6.35E+00	7.41E+00	7.37E+00	6.68E+00	7.33E+00	7.17E+00	
Aaz	1.85E-07	2.59E-09	6.11E-09	9.33E-09	1.98E-08	2.00E-08	9.91E-10	2.85E-10	4.78E-09	4.78E-09	8.64E-09	3.21E-08	8.56E-09	8.56E-09	1.77E-10		4.64E+00	4.74E+00	4.41E+00	4.47E+00	4.56E+00	4.72E+00	5.03E+00	4.99E+00	5.18E+00	5.04E+00	4.35E+00	4.45E+00	5.84E+00	5.83E+00	4.83E+00	5.60E+00	5.41E+00	
Sap_WGA	8.62E-07	1.35E-07	3.19E-07	3.16E-07	4.32E-07	1.61E-06	1.06E-07	5.71E-08	4.50E-08	4.50E-08	8.93E-08	3.31E-07	1.37E-07	1.37E-07	2.16E-10	4.54E-06		2.01E+00	2.87E+00	2.80E+00	3.92E+00	3.98E+00	4.85E+00	4.80E+00	4.43E+00	4.49E+00	4.37E+00	4.47E+00	5.23E+00	5.09E+00	5.15E+00	5.52E+00	5.33E+00	
Sap104	8.62E-07	1.35E-07	3.19E-07	3.16E-07	4.32E-07	1.61E-06	6.86E-08	2.42E-08	4.50E-08	4.50E-08	2.14E-07	7.96E-07	3.28E-07	3.28E-07	5.03E-10	2.91E-06	2.35E-02		3.20E+00	3.14E+00	3.92E+00	3.98E+00	4.85E+00	4.80E+00	4.43E+00	4.49E+00	4.42E+00	4.42E+00	5.09E+00	4.94E+00	5.17E+00	5.54E+00	5.35E+00	
Ccap_WGA	1.91E-06	3.24E-07	3.24E-07	4.93E-07	4.38E-07	1.84E-06	1.07E-07	5.80E-08	4.57E-08	4.57E-08	2.46E-07	9.14E-07	3.77E-07	3.77E-07	5.89E-10	1.14E-05	2.43E-03	8.79E-04		3.20E+00	3.14E+00	3.92E+00	3.98E+00	4.85E+00	4.80E+00	4.43E+00	4.49E+00	4.42E+00	4.42E+00	5.09E+00	4.94E+00	5.17E+00	5.54E+00	5.35E+00
Ccap	1.37E-06	6.16E-07	6.16E-07	6.16E-07	3.50E-07	1.31E-06	8.55E-08	4.62E-08	3.63E-08	3.63E-08	1.96E-07	7.28E-07	3.00E-07	3.00E-07	4.62E-10	9.06E-06	2.99E-03	1.07E-03	1.00E+00		3.89E+00	3.82E+00	4.48E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00	4.43E+00
Sbol_WGA	1.18E-07	9.34E-08	2.19E-07	3.32E-07	7.06E-07	2.61E-06	1.40E-07	4.01E-08	1.82E-07	1.82E-07	6.14E-07	2.27E-06	9.39E-07	9.39E-07	9.17E-10	6.17E-06	7.42E-05	7.42E-05	1.30E-04	8.37E-05		2.01E+00	4.56E+00	4.51E+00	4.61E+00	4.56E+00	3.84E+00	3.95E+00	5.57E+00	5.58E+00	5.29E+00	5.65E+00	5.46E+00	
Sbol	1.01E-07	1.16E-07	2.72E-07	4.14E-07	8.79E-07	3.26E-06	1.73E-07	4.97E-08	2.27E-07	2.27E-07	7.62E-07	2.83E-06	1.17E-06	1.17E-06	1.12E-09	3.21E-06	5.97E-05	5.97E-05	1.63E-04	1.05E-04	2.35E-02		4.50E+00	4.45E+00	4.56E+00	4.51E+00	4.10E+00	4.21E+00	5.53E+00	5.53E+00	5.23E+00	5.60E+00	5.41E+00	
Age_WGA	2.05E-07	3.24E-09	7.54E-09	1.14E-08	2.63E-08	9.64E-08	4.71E-09	1.38E-09	1.12E-09	1.12E-09	2.40E-08	2.91E-08	1.54E-08	1.54E-08	4.88E-11	8.54E-07	1.88E-06	1.88E-06	6.96E-06	8.64E-06	6.30E-06	7.89E-06		6.48E-01	3.16E+00	2.79E+00	3.55E+00	3.42E+00	5.10E+00	5.15E+00	5.48E+00	5.84E+00	5.66E+00	
Age	3.05E-07	5.90E-09	1.37E-08	2.08E-08	4.83E-08	1.78E-07	8.59E-09	2.50E-09	1.33E-09	1.33E-09	2.86E-08	3.48E-08	1.84E-08	1.84E-08	5.72E-11	1.03E-06	2.28E-06	2.28E-06	8.46E-06	1.05E-05	7.64E-06	9.57E-06	2.59E-01		3.09E+00	2.71E+00	3.49E+00	3.36E+00	5.25E+00	5.30E+00	5.44E+00	5.80E+00	5.62E+00	
Llag_WGA	3.98E-07	1.73E-09	4.01E-09	6.05E-09	1.39E-08	5.08E-08	2.51E-09	7.37E-10	7.70E-09	7.70E-09	1.12E-07	1.37E-07	3.05E-08	3.05E-08	4.18E-11	4.57E-07	1.04E-05	1.04E-05	1.81E-05	1.08E-05	5.04E-06	6.32E-06	1.07E-03	1.25E-03		3.95E+00	3.83E+00	5.25E+00	5.29E+00	5.89E+00	5.39E+00	5.80E+00		
Llag	7.13E-07	4.56E-09	1.06E-08	1.61E-08	2.44E-08	8.99E-08	4.32E-09	1.26E-09	8.74E-09	8.74E-09	1.28E-07	1.58E-07	3.47E-08	3.47E-08	4.54E-11	8.10E-07	8.20E-06	8.20E-06	1.97E-05	1.29E-05	6.11E-06	7.85E-06	3.08E-03	3.86E-03	1.00E+00		3.71E+00	3.71E+00	5.01E+00	5.07E+00	5.77E+00	5.86E+00	5.87E+00	
KSTR_WGA	1.08E-06	2.35E-08	5.41E-08	8.13E-08	2.93E-07	1.05E-06	7.35E-08	2.19E-08	5.15E-08	5.15E-08	9.64E-07	1.48E-06	6.23E-07	6.23E-07	3.09E-09	1.46E-05	1.34E-05	1.09E-05	1.19E-05	9.80E-06	1.00E-04	3.73E-05	2.77E-04	3.40E-04	3.40E-04	6.74E-05	1.02E-04		1.00E+00	4.41E+00	5.06E+00	5.22E+00	5.52E+00	5.33E+00
KSTR	1.58E-06	1.55E-08	3.56E-08	5.35E-08	1.93E-07	6.92E-07	4.83E-08	1.44E-08	3.38E-08	3.38E-08	6.31E-07	9.65E-07	4.07E-07	4.07E-07	2.03E-09	9.51E-06	8.81E-06	7.16E-06	7.85E-06	6.45E-06	6.70E-05	2.47E-05	4.24E-04	1.03E-04	1.57E-04	1.59E-01		4.31E+00	4.37E+00	5.32E+00	5.61E+00	5.42E+00		
Cmo_WGA																																		

Table S6 Positive selection test of TAS1R2

	Hosa	Cja_WGA	Cja	Cpen	Mhum_WGA	Mhum	Cpyg	Cpyg_WGA	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Llag_WGA	Llag	KSTR_WGA	KSTR	Cmo_WGA	Cmo	Csat	Ppit_WGA	Ppit	
Hosa		-5.692																																
Cja_WGA	1.000		-1.417	-1.417	-3.922	-3.504	-4.545	-4.884	-5.534	-5.534	-5.013	-5.118	-5.325	-5.325	-6.491	-6.297	-5.452	-5.452	-5.256	-5.110	-5.534	-5.486	-6.250	-6.126	-6.380	-6.180	-5.834	-5.923	-6.683	-6.557	-6.306	-6.552	-6.466	
Cja	1.000	1.000		0.000	-3.648	-3.200	-4.306	-4.659	-5.336	-5.336	-4.799	-4.907	-5.120	-5.120	-6.313	-6.119	-5.260	-5.260	-5.256	-5.110	-5.345	-5.296	-6.074	-5.948	-6.207	-6.002	-5.654	-5.744	-6.514	-6.388	-6.306	-6.552	-6.466	
Cpen	1.000	1.000	1.000		-3.505	-3.040	-4.182	-4.544	-5.237	-5.237	-4.690	-4.800	-5.016	-5.016	-6.224	-6.030	-5.262	-5.262	-5.161	-5.110	-5.251	-5.201	-5.987	-5.859	-6.121	-5.914	-5.565	-5.656	-6.432	-6.390	-6.222	-6.471	-6.383	
Mhum_WGA	1.000	1.000	1.000	1.000			-1.736	-4.259	-4.616	-4.781	-4.781	-4.257	-4.493	-4.831	-4.831	-5.694	-5.870	-5.191	-5.191	-5.188	-5.239	-5.078	-5.027	-5.809	-5.678	-5.945	-5.825	-5.279	-5.373	-6.281	-6.325	-6.390	-6.550	
Mhum	1.000	1.000	1.000	1.000	1.000			-3.869	-4.258	-4.444	-4.444	-3.954	-4.204	-4.550	-4.560	-5.497	-5.868	-4.885	-4.885	-4.882	-4.934	-4.771	-4.717	-5.527	-5.391	-5.667	-5.542	-4.986	-5.083	-5.924	-6.970	-6.124	-6.422	-6.334
Cpyg	1.000	1.000	1.000	1.000	1.000	1.000			-1.001	-5.362	-5.362	-4.832	-4.722	-4.833	-4.833	-6.167	-6.494	-5.507	-5.602	-5.503	-5.553	-5.445	-5.397	-6.173	-6.047	-6.304	-6.191	-5.587	-5.678	-6.796	-6.754	-6.441	-6.687	-6.601
Cpyg_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000			-5.599	-5.599	-5.149	-5.044	-5.254	-5.254	-6.433	-6.746	-5.642	-5.827	-5.638	-5.688	-5.719	-5.672	-6.427	-6.304	-6.554	-6.445	-5.849	-5.938	-6.847	-6.805	-6.640	-6.881	-6.796
Lros_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		0.000	-4.999	-4.670	-5.106	-5.106	-5.939	-6.170	-5.693	-5.693	-5.690	-5.740	-5.386	-5.337	-6.469	-6.434	-6.070	-6.043	-5.664	-5.755	-6.054	-6.142	-6.079	-6.503	-6.330	
Lros	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000			-4.999	-4.670	-5.106	-5.106	-5.939	-6.170	-5.693	-5.693	-5.690	-5.740	-5.386	-5.337	-6.469	-6.434	-6.070	-6.043	-5.664	-5.755	-6.054	-6.142	-6.079	-6.503	-6.330
Smid_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000			-1.417	-3.023	-3.023	-5.100	-6.046	-5.544	-5.350	-5.318	-5.370	-5.110	-5.061	-5.829	-5.791	-5.493	-5.463	-5.006	-5.104	-6.199	-6.287	-6.593	-6.755	-6.584
Smid	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000			-2.462	-2.462	-4.992	-5.767	-5.251	-5.050	-5.018	-5.071	-4.804	-4.751	-5.787	-5.749	-5.449	-5.418	-4.906	-5.006	-6.333	-6.420	-6.508	-6.671	-6.499
Soe_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		0.000	-5.206	-6.048	-5.450	-5.254	-5.222	-5.274	-5.012	-4.961	-5.924	-5.886	-5.778	-5.750	-5.107	-5.204	-6.462	-6.548	-6.680	-6.841	-6.671	
Soe	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		-5.206	-6.048	-5.450	-5.254	-5.222	-5.274	-5.012	-4.961	-5.924	-5.886	-5.778	-5.750	-5.107	-5.204	-6.462	-6.548	-6.680	-6.841	-6.671	
Sfu	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		-6.840	-6.801	-6.631	-6.600	-6.648	-6.510	-6.469	-7.096	-7.064	-7.126	-7.109	-6.260	-6.347	-7.414	-7.373	-6.681	-7.331	-7.168	
Aaz	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		-4.637	-4.745	-4.409	-4.466	-4.562	-4.721	-5.034	-4.990	-5.178	-5.044	-4.346	-4.454	-5.836	-5.834	-4.828	-5.600	-5.410	
Sap_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		-2.007	-2.870	-2.799	-3.919	-3.978	-4.848	-4.803	-4.431	-4.491	-4.367	-4.473	-5.233	-5.089	-5.148	-5.517	-5.329	
Sap104	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		-3.200	-3.138	-3.919	-3.978	-4.848	-4.803	-4.431	-4.491	-4.420	-4.525	-5.087	-4.941	-5.172	-5.540	-5.352	
Ccap_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		1.000	-3.764	-3.700	-4.532	-4.483	-4.322	-4.270	-4.398	-4.502	-4.987	-5.038	-4.600	-4.991	-4.792	
Ccap	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.160		-3.886	-3.824	-4.478	-4.429	-4.427	-4.379	-4.447	-4.551	-5.034	-4.987	-4.344	-4.746
Sbol_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Sbol	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Age_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Age	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Llag_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Llag	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
KSTR_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
KSTR	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Cmo_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Cmo	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Csat	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Ppit_WGA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	
Ppit	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	

Table S7 Evolutionary neutrality test of TAS1R2

	Hosa	Cja_WGA	Cja	Cpen	Mhum_WGA	Mhum	Cpyg	Cpyg_WGA	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Lliag_WGA	Lliag	KSTR_WGA	KSTR	Cmo_WGA	Cmo	Csat	Ppil_WGA	Ppil	
Hosa		-5.69E+00	-5.69E+00	-5.61E+00	-5.92E+00	-5.65E+00	-5.86E+00	-6.06E+00	-5.84E+00	-5.84E+00	-5.83E+00	-5.57E+00	-5.67E+00	-5.67E+00	-6.74E+00	-5.38E+00	-5.03E+00	-5.03E+00	-4.85E+00	-4.92E+00	-5.48E+00	-5.52E+00	-5.31E+00	-5.27E+00	-5.21E+00	-5.08E+00	-4.98E+00	-4.89E+00	-5.57E+00	-5.66E+00	-5.50E+00	-6.15E+00	-5.98E+00	
Cja_WGA	9.65E-08		-1.42E+00	-3.92E+00	-3.30E+00	-4.85E+00	-4.88E+00	-5.53E+00	-5.33E+00	-5.01E+00	-5.12E+00	-5.32E+00	-5.32E+00	-4.49E+00	-6.30E+00	-5.45E+00	-5.45E+00	-5.26E+00	-5.11E+00	-5.53E+00	-5.49E+00	-6.25E+00	-6.13E+00	-6.38E+00	-6.18E+00	-5.83E+00	-5.92E+00	-6.68E+00	-6.56E+00	-6.31E+00	-6.55E+00	-6.47E+00		
Cja	9.05E-08	1.59E-01		0.00E+00	-3.85E+00	-3.20E+00	-4.31E+00	-4.66E+00	-5.34E+00	-4.80E+00	-4.91E+00	-5.12E+00	-5.12E+00	-6.31E+00	-5.12E+00	-5.26E+00	-5.26E+00	-5.11E+00	-5.35E+00	-5.30E+00	-6.07E+00	-5.95E+00	-6.21E+00	-6.00E+00	-5.65E+00	-5.74E+00	-6.39E+00	-6.39E+00	-6.55E+00	-6.31E+00	-6.55E+00	-6.47E+00		
Cpen	1.32E-07	1.59E-01	1.00E+00		-3.51E+00	-3.04E+00	-4.19E+00	-4.54E+00	-5.24E+00	-5.24E+00	-4.69E+00	-4.80E+00	-5.02E+00	-5.02E+00	-6.22E+00	-6.03E+00	-5.28E+00	-5.26E+00	-5.16E+00	-5.11E+00	-5.25E+00	-5.20E+00	-5.99E+00	-5.88E+00	-6.12E+00	-5.91E+00	-5.56E+00	-5.66E+00	-6.43E+00	-6.39E+00	-6.22E+00	-6.47E+00	-6.38E+00	
Mhum_WGA	3.19E-08	1.47E-04	3.92E-04	6.42E-04		-1.74E+00	-4.28E+00	-4.62E+00	-4.78E+00	-4.78E+00	-4.26E+00	-4.49E+00	-4.83E+00	-4.83E+00	-5.69E+00	-5.87E+00	-5.19E+00	-5.19E+00	-5.19E+00	-5.24E+00	-5.08E+00	-5.03E+00	-5.81E+00	-5.68E+00	-5.94E+00	-5.83E+00	-5.28E+00	-5.37E+00	-6.28E+00	-6.32E+00	-6.39E+00	-6.64E+00	-6.55E+00	
Mhum	1.08E-07	6.45E-04	1.76E-03	2.91E-03	8.51E-02		-3.87E+00	-4.44E+00	-4.44E+00	-3.95E+00	-4.20E+00	-4.56E+00	-4.56E+00	-5.50E+00	-5.87E+00	-4.89E+00	-4.89E+00	-4.88E+00	-4.93E+00	-4.77E+00	-4.72E+00	-5.53E+00	-5.39E+00	-5.67E+00	-5.54E+00	-4.99E+00	-5.08E+00	-5.92E+00	-5.97E+00	-6.12E+00	-6.42E+00	-6.33E+00		
Cpyg	4.15E-08	1.32E-05	3.42E-05	5.53E-05	4.11E-05	1.78E-04		-1.00E+00	-5.36E+00	-4.83E+00	-4.72E+00	-4.83E+00	-5.25E+00	-5.25E+00	-6.43E+00	-6.17E+00	-5.49E+00	-5.50E+00	-5.50E+00	-5.55E+00	-5.45E+00	-5.40E+00	-6.17E+00	-6.05E+00	-6.30E+00	-6.19E+00	-5.59E+00	-5.68E+00	-6.80E+00	-6.75E+00	-6.44E+00	-6.69E+00	-6.60E+00	
Cpyg_WGA	1.59E-08	3.24E-06	8.29E-06	1.33E-05	9.79E-06	4.13E-05	3.19E-01		-5.60E+00	-5.15E+00	-5.04E+00	-5.25E+00	-5.25E+00	-6.43E+00	-6.17E+00	-5.49E+00	-5.50E+00	-5.50E+00	-5.55E+00	-5.45E+00	-5.40E+00	-6.17E+00	-6.05E+00	-6.30E+00	-6.19E+00	-5.59E+00	-5.68E+00	-6.80E+00	-6.75E+00	-6.44E+00	-6.69E+00	-6.60E+00		
Lros_WGA	4.65E-08	1.87E-07	4.55E-07	7.06E-07	5.00E-06	1.98E-05	4.05E-07	1.39E-07		0.00E+00	-5.00E+00	-4.67E+00	-5.11E+00	-5.11E+00	-5.94E+00	-6.17E+00	-5.69E+00	-5.69E+00	-5.69E+00	-5.74E+00	-5.39E+00	-5.34E+00	-6.47E+00	-6.43E+00	-6.07E+00	-6.04E+00	-5.66E+00	-5.76E+00	-6.05E+00	-6.14E+00	-6.08E+00	-6.50E+00	-6.33E+00	
Lros	4.65E-08	1.87E-07	4.55E-07	7.06E-07	5.00E-06	1.98E-05	4.05E-07	1.39E-07	1.00E+00		-5.00E+00	-4.67E+00	-5.11E+00	-5.11E+00	-5.94E+00	-6.17E+00	-5.69E+00	-5.69E+00	-5.69E+00	-5.74E+00	-5.39E+00	-5.34E+00	-6.47E+00	-6.43E+00	-6.07E+00	-6.04E+00	-5.66E+00	-5.76E+00	-6.05E+00	-6.14E+00	-6.08E+00	-6.50E+00	-6.33E+00	
Smid_WGA	4.76E-08	1.87E-06	4.64E-06	7.29E-06	4.14E-05	1.30E-04	4.04E-06	1.04E-06	1.99E-06	1.99E-06		-1.42E+00	-3.02E+00	-3.02E+00	-6.05E+00	-5.54E+00	-5.35E+00	-5.32E+00	-5.37E+00	-5.11E+00	-5.06E+00	-5.83E+00	-5.79E+00	-5.49E+00	-5.46E+00	-5.01E+00	-5.10E+00	-6.20E+00	-6.29E+00	-6.59E+00	-6.75E+00	-6.58E+00		
Smid	1.55E-07	1.19E-06	2.94E-06	4.62E-06	1.63E-05	5.08E-05	6.40E-06	1.64E-06	7.93E-06	7.93E-06	1.59E-01		-2.46E+00	-2.46E+00	-4.99E+00	-5.77E+00	-5.25E+00	-5.05E+00	-5.02E+00	-5.07E+00	-4.80E+00	-4.75E+00	-5.79E+00	-5.75E+00	-5.45E+00	-5.42E+00	-4.91E+00	-5.01E+00	-6.33E+00	-6.42E+00	-6.51E+00	-6.67E+00	-6.50E+00	
Soe_WGA	1.02E-07	4.79E-07	1.19E-06	1.85E-06	4.05E-06	1.24E-05	4.02E-06	6.56E-07	1.25E-06	1.25E-06	3.06E-03	1.52E-02		0.00E+00	-5.21E+00	-6.05E+00	-5.45E+00	-5.25E+00	-5.22E+00	-5.27E+00	-5.01E+00	-4.96E+00	-5.92E+00	-5.89E+00	-5.78E+00	-5.75E+00	-5.11E+00	-5.20E+00	-6.48E+00	-6.55E+00	-6.68E+00	-6.84E+00	-6.67E+00	
Soe	1.02E-07	4.79E-07	1.19E-06	1.85E-06	4.05E-06	1.24E-05	4.02E-06	6.56E-07	1.25E-06	1.25E-06	3.06E-03	1.52E-02	1.00E+00		-5.21E+00	-6.05E+00	-5.45E+00	-5.25E+00	-5.22E+00	-5.27E+00	-5.01E+00	-4.96E+00	-5.92E+00	-5.89E+00	-5.78E+00	-5.75E+00	-5.11E+00	-5.20E+00	-6.48E+00	-6.55E+00	-6.68E+00	-6.84E+00	-6.67E+00	
Sfu	5.91E-10	2.01E-09	4.79E-09	7.35E-09	8.96E-08	2.21E-07	6.89E-09	2.67E-09	2.87E-08	2.87E-08	1.73E-08	2.04E-06	8.09E-07	8.09E-07		-6.84E+00	-8.80E+00	-6.83E+00	-6.80E+00	-6.65E+00	-6.51E+00	-6.47E+00	-7.10E+00	-7.09E+00	-7.13E+00	-7.11E+00	-6.26E+00	-6.35E+00	-7.41E+00	-7.37E+00	-6.68E+00	-7.33E+00	-7.17E+00	
Aaz	3.71E-07	5.18E-09	1.22E-08	1.87E-08	3.96E-08	4.01E-08	1.98E-09	9.56E-09	9.56E-09	9.56E-09	6.42E-08	1.71E-08	1.71E-08	3.54E-10		-6.44E+00	-8.80E+00	-6.83E+00	-6.80E+00	-6.65E+00	-6.51E+00	-6.47E+00	-7.10E+00	-7.09E+00	-7.13E+00	-7.11E+00	-6.26E+00	-6.35E+00	-7.41E+00	-7.37E+00	-6.68E+00	-7.33E+00	-7.17E+00	
Sap_WGA	1.72E-06	2.70E-07	6.37E-07	6.32E-07	8.64E-07	3.23E-06	2.11E-07	1.14E-07	9.01E-08	9.01E-08	1.79E-07	6.62E-07	2.73E-07	4.31E-10	9.07E-06		-2.01E+00	-2.87E+00	-2.80E+00	-3.92E+00	-3.98E+00	-4.85E+00	-4.43E+00	-4.49E+00	-4.49E+00	-4.37E+00	-4.47E+00	-5.23E+00	-5.09E+00	-5.15E+00	-5.52E+00	-5.33E+00		
Sap104	1.72E-06	2.70E-07	6.37E-07	6.32E-07	8.64E-07	3.23E-06	2.11E-07	1.14E-07	9.01E-08	9.01E-08	1.79E-07	6.62E-07	2.73E-07	4.31E-10	9.07E-06	4.70E-02		-2.01E+00	-2.87E+00	-2.80E+00	-3.92E+00	-3.98E+00	-4.85E+00	-4.43E+00	-4.49E+00	-4.49E+00	-4.37E+00	-4.47E+00	-5.23E+00	-5.09E+00	-5.15E+00	-5.52E+00	-5.33E+00	
Ccap_WGA	3.81E-06	6.48E-07	6.48E-07	9.87E-07	8.77E-07	3.27E-06	2.15E-07	1.16E-07	9.14E-08	9.14E-08	4.93E-07	1.83E-06	7.55E-07	7.55E-07	1.17E-09	2.28E-05	4.85E-03	1.76E-03		-3.20E+00	-3.14E+00	-3.92E+00	-3.98E+00	-4.85E+00	-4.43E+00	-4.49E+00	-4.49E+00	-4.37E+00	-4.47E+00	-5.23E+00	-5.09E+00	-5.15E+00	-5.52E+00	-5.33E+00
Ccap	2.75E-06	1.23E-06	1.23E-06	1.23E-06	7.00E-07	2.62E-06	1.71E-07	9.25E-08	7.26E-08	7.26E-08	3.91E-07	1.48E-06	6.00E-07	6.00E-07	9.24E-10	1.81E-05	5.98E-03	2.14E-03	3.19E-01		-3.89E+00	-3.82E+00	-4.48E+00	-4.43E+00	-4.43E+00	-4.38E+00	-4.45E+00	-4.55E+00	-5.03E+00	-4.99E+00	-4.34E+00	-4.75E+00	-4.54E+00	
Sbol_WGA	2.38E-07	1.87E-07	4.37E-07	6.63E-07	1.41E-06	5.22E-06	2.79E-07	8.02E-08	3.65E-07	3.65E-07	1.23E-06	4.54E-06	1.88E-06	1.88E-06	1.83E-09	1.23E-05	1.48E-04	1.48E-04	2.60E-04	1.67E-04		-2.01E+00	-4.56E+00	-4.51E+00	-4.61E+00	-4.56E+00	-3.84E+00	-3.95E+00	-5.57E+00	-5.58E+00	-5.29E+00	-5.65E+00	-5.48E+00	
Sbol	2.02E-07	2.33E-07	5.45E-07	8.27E-07	1.76E-06	6.51E-06	3.47E-07	9.93E-08	4.54E-07	4.54E-07	1.52E-06	5.66E-06	2.33E-06	2.33E-06	2.24E-09	6.42E-06	1.19E-04	1.19E-04	3.26E-04	2.10E-04	4.70E-02		-4.50E+00	-4.45E+00	-4.51E+00	-4.10E+00	-4.21E+00	-5.53E+00	-5.53E+00	-5.23E+00	-5.60E+00	-5.41E+00		
Age_WGA	5.14E-07	6.49E-09	1.51E-08	2.28E-08	5.27E-08	1.93E-07	9.42E-09	2.76E-09	2.24E-09	2.24E-09	4.80E-08	5.83E-08	3.08E-08	3.08E-08	9.73E-11	1.71E-06	3.77E-06	3.77E-06	1.39E-05	1.73E-05	1.26E-05	1.59E-05		-6.48E-01	-3.16E+00	-2.79E+00	-3.55E+00	-3.42E+00	-5.10E+00	-5.15E+00	-4.88E+00	-5.84E+00	-5.66E+00	
Age	6.10E-07	1.18E-08	2.75E-08	4.16E-08	9.97E-08	3.55E-07	1.72E-08	5.00E-09	2.65E-09	2.65E-09	5.73E-08	6.97E-08	3.68E-08	3.68E-08	1.14E-10	2.06E-06	4.56E-06	4.56E-06	1.69E-05	2.10E-05	1.53E-05	1.91E-05	5.18E-01		-3.09E+00	-2.71E+00	-3.49E+00	-3.36E+00	-5.25E+00	-5.30E+00	-5.44E+00	-5.80E+00	-5.62E+00	
Lliag_WGA	7.96E-07	3.46E-09	8.01E-09	1.21E-08	2.79E-08	1.02E-07	5.01E-09	1.47E-09	1.54E-08	1.54E-08	2.25E-07	2.75E-07	8.10E-08	6.10E-08	8.36E-11	9.14E-07	2.09E-05	2.09E-05	3.21E-05	2.12E-05	1.01E-05	1.26E-05	2.01E-03	2.49E-03		0.00E+00	-3.95E+00	-3.83E+00	-5.25E+00	-5.29E+00	-5.89E+00	-5.98E+00	-5.80E+00	
Lliag	1.43E-06	9.11E-09	2.13E-08	3.23E-08	4.88E-08	1.80E-07	8.65E-09	2.51E-09	1.75E-08	1.75E-08	2.58E-07	3.15E-07	6.93E-08	6.93E-08	9.09E-11	1.64E-06	1.64E-05	1.64E-05	3.93E-05	2.56E-05	1.22E-05	1.53E-05	6.16E-03	7.71E-03	1.00E+00		-3.83E+00	-3.71E+00	-5.01E+00	-5.06E+00	-5.77E+00	-5.86E+00	-5.67E+00	
KSTR_WGA	2.17E-06	4.69E-08	1.08E-07	1.63E-07	5.87E-07	2.10E-06	1.47E-07	4.37E-08	1.03E-07	1.03E-07	1.93E-06	2.95E-06	1.25E-06	1.25E-06	6.19E-09	2.92E-05	2.68E-05	2.18E-05	2.38E-05	1.96E-05	2.01E-04	7.45E-05	5.54E-04	6.81E-04	1.35E-04	2.04E-04		-1.00E+00	-4.41E+00	-4.47E+00	-5.22E+00	-5.52E+00	-5.33E+00	
KSTR	3.17E-06	3.09E-08	7.13E-08	1.07E-07	3.86E-07	1.38E-06	9.67E-08	2.88E-08	6.77E-08	6.77E-08	1.26E-06	1.93E-06	8.14E-07	8.14E-07	4.06E-09	1.90E-05	1.76E-05	1.43E-05	1.57E-05	1.29E-05	1.34E-04	4.94E-05	8.49E-04	1.04E-03	2.07E-04	3.15E-04	3.19E-01		-4.31E+00	-4.37E+00	-5.32E+00	-5.61E+00	-5.42E+00	
Cmo_WGA	1																																	

Table S 8 Purifying selection test of TAS1R3

	Hosa	Cja_WGA	Cja	Cpen	Mhum_WGA	Mhum	Cpyg_WGA	Cpyg	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Llig_WGA	Llig	KSTR_WGA	KSTR	Omo_WGA	Omo	Ocat	Ppil_WGA	Ppil
Hosa		8.55E+00	8.55E+00	8.55E+00	8.12E+00	8.05E+00	8.99E+00	8.36E+00	8.08E+00	8.08E+00	7.66E+00	7.70E+00	7.87E+00	7.91E+00	7.52E+00	8.91E+00	6.70E+00	6.75E+00	6.50E+00	6.53E+00	7.42E+00	7.42E+00	6.59E+00	6.55E+00	6.86E+00	6.82E+00	6.67E+00	6.65E+00	7.44E+00	7.14E+00	7.25E+00	7.01E+00	6.92E+00
Cja_WGA	2.31E-14		0.00E+00	0.00E+00	3.68E+00	3.54E+00	4.17E+00	4.59E+00	6.18E+00	6.18E+00	6.97E+00	7.03E+00	6.86E+00	6.91E+00	6.27E+00	6.83E+00	7.22E+00	7.14E+00	7.24E+00	7.28E+00	8.12E+00	8.12E+00	7.33E+00	7.13E+00	7.28E+00	7.25E+00	6.45E+00	6.42E+00	7.29E+00	7.41E+00	7.87E+00	6.77E+00	6.69E+00
Cja	2.31E-14	1.00E+00		0.00E+00	3.68E+00	3.54E+00	4.17E+00	4.59E+00	6.18E+00	6.18E+00	6.97E+00	7.03E+00	6.86E+00	6.91E+00	6.27E+00	6.83E+00	7.22E+00	7.14E+00	7.24E+00	7.28E+00	8.12E+00	8.12E+00	7.33E+00	7.13E+00	7.28E+00	7.25E+00	6.45E+00	6.42E+00	7.29E+00	7.41E+00	7.87E+00	6.77E+00	6.69E+00
Open	2.31E-14	1.00E+00	1.00E+00		3.68E+00	3.54E+00	4.17E+00	4.59E+00	6.18E+00	6.18E+00	6.97E+00	7.03E+00	6.86E+00	6.91E+00	6.27E+00	6.83E+00	7.22E+00	7.14E+00	7.24E+00	7.28E+00	8.12E+00	8.12E+00	7.33E+00	7.13E+00	7.28E+00	7.25E+00	6.45E+00	6.42E+00	7.29E+00	7.41E+00	7.87E+00	6.77E+00	6.69E+00
Mhum_WGA	2.31E-13	1.77E-04	1.77E-04	1.77E-04																													
Mhum	3.34E-13	2.88E-04	2.88E-04	2.88E-04			1.59E-01																										
Cpyg_WGA	5.44E-14	2.92E-05	2.92E-05	2.92E-05	1.37E-05	2.22E-05																											
Cpyg	6.34E-14	5.41E-06	5.41E-06	5.41E-06	9.64E-06	1.55E-05	1.00E+00																										
Lros_WGA	2.83E-13	4.52E-09	4.52E-09	4.52E-09	2.29E-08	3.52E-08	2.81E-09	6.34E-10																									
Lros	2.83E-13	4.52E-09	4.52E-09	4.52E-09	2.29E-08	3.52E-08	2.81E-09	6.34E-10	1.00E+00																								
Smid_WGA	2.61E-12	9.04E-11	9.04E-11	9.04E-11	3.20E-10	4.87E-10	1.46E-11	9.85E-12	5.13E-08	5.13E-08																							
Smid	2.16E-12	6.93E-11	6.93E-11	6.93E-11	2.45E-10	3.72E-10	1.11E-11	7.58E-12	3.86E-08	3.86E-08	1.00E+00																						
Soe_WGA	8.89E-13	1.64E-10	1.64E-10	1.64E-10	2.53E-10	3.85E-10	1.31E-11	7.81E-12	1.88E-09	1.88E-09	4.98E-04	2.89E-04																					
Soe	7.28E-13	1.25E-10	1.25E-10	1.25E-10	1.92E-10	2.93E-10	1.31E-11	5.98E-12	1.41E-09	1.41E-09	2.89E-04	2.04E-04	1.00E+00																				
Sfu	5.42E-12	2.97E-09	2.97E-09	2.97E-09	8.68E-09	1.33E-08	6.62E-10	7.12E-10	1.95E-07	1.95E-07	1.66E-04	1.24E-04	1.96E-05	1.43E-05																			
Aaz	1.25E-10	1.55E-14	1.55E-14	1.55E-14	9.46E-14	1.40E-13	5.32E-15	3.81E-15	1.73E-11	1.73E-11	1.69E-11	1.33E-11	2.90E-12	2.28E-12	8.14E-11																		
Sap_WGA	3.50E-10	2.58E-11	2.58E-11	2.58E-11	1.58E-10	2.36E-10	3.50E-11	1.29E-11	1.02E-09	1.02E-09	4.53E-09	3.58E-09	5.19E-10	4.10E-10	2.43E-07	1.66E-08																	
Sap104	2.85E-10	3.81E-11	3.81E-11	3.81E-11	2.34E-10	3.49E-10	5.21E-11	1.90E-11	6.70E-10	6.70E-10	1.02E-08	8.09E-09	1.17E-09	9.24E-10	5.50E-07	1.09E-08	1.01E-01																
Ccap_WGA	9.91E-10	2.36E-11	2.36E-11	2.36E-11	1.43E-10	2.14E-10	2.10E-11	5.36E-12	4.24E-10	4.24E-10	4.11E-09	3.27E-09	4.87E-10	3.87E-10	2.13E-07	5.03E-09	1.41E-03	1.54E-03															
Ccap	8.23E-10	1.89E-11	1.89E-11	1.89E-11	1.15E-10	1.71E-10	1.66E-11	4.27E-12	3.35E-10	3.35E-10	3.27E-09	2.60E-09	3.85E-10	3.06E-10	1.71E-07	6.29E-09	1.04E-03	1.16E-03	1.00E+00														
Sbol_WGA	8.98E-12	2.29E-13	2.29E-13	2.29E-13	1.34E-12	1.98E-12	4.92E-13	1.33E-13	5.01E-12	5.01E-12	1.03E-10	8.16E-11	8.72E-12	6.92E-12	3.23E-10	4.04E-09	7.79E-09	5.10E-09	1.34E-08	1.68E-08													
Sbol	8.98E-12	2.29E-13	2.29E-13	2.29E-13	1.34E-12	1.98E-12	4.92E-13	1.33E-13	5.01E-12	5.01E-12	1.03E-10	8.16E-11	8.72E-12	6.92E-12	3.23E-10	4.04E-09	7.79E-09	5.10E-09	1.34E-08	1.68E-08	1.00E+00												
Age_WGA	6.07E-10	1.47E-11	1.47E-11	1.47E-11	1.33E-10	3.25E-11	1.07E-11	8.60E-11	8.60E-11	8.60E-11	3.45E-09	2.76E-09	4.43E-10	3.55E-10	2.82E-08	8.60E-08	1.12E-07	1.66E-07	2.34E-07	1.91E-07	1.08E-07	1.08E-07											
Age	7.58E-10	4.05E-11	4.05E-11	4.05E-11	3.70E-10	5.52E-10	4.04E-11	1.32E-11	1.52E-10	1.52E-10	6.20E-09	4.95E-09	7.90E-10	6.33E-10	5.09E-08	1.55E-07	3.04E-07	4.50E-07	6.29E-07	5.13E-07	1.59E-07	1.59E-07	2.70E-01										
Llig_WGA	1.61E-10	1.91E-11	1.91E-11	1.91E-11	7.72E-11	1.15E-10	1.26E-11	3.41E-12	5.09E-10	5.09E-10	2.81E-09	2.26E-09	3.69E-10	2.97E-10	4.52E-09	3.05E-08	5.75E-08	8.47E-08	5.38E-08	4.39E-08	1.72E-08	1.72E-08	1.90E-06	2.70E-06									
Llig	1.95E-10	2.27E-11	2.27E-11	2.27E-11	9.19E-11	1.37E-10	1.50E-11	4.04E-12	2.72E-10	2.72E-10	3.36E-09	2.70E-09	4.40E-10	3.54E-10	5.42E-09	3.67E-08	6.94E-08	1.02E-07	6.49E-08	5.28E-08	2.07E-08	2.07E-08	2.26E-06	3.21E-06	2.70E-01								
KSTR_WGA	4.22E-10	1.20E-09	1.20E-09	1.20E-09	1.49E-09	2.21E-09	8.78E-10	1.83E-10	1.23E-08	1.23E-08	1.16E-07	9.44E-08	1.08E-08	8.85E-09	1.81E-07	8.02E-06	4.93E-06	4.89E-06	4.26E-06	3.94E-06	1.38E-06	1.38E-06	9.76E-04	1.46E-03	1.87E-04	2.28E-04							
KSTR	4.56E-10	1.46E-09	1.46E-09	1.46E-09	1.81E-09	2.68E-09	1.07E-09	2.22E-10	1.49E-08	1.49E-08	1.40E-07	1.14E-07	1.32E-08	1.08E-08	2.18E-07	6.60E-06	4.04E-06	4.00E-06	3.50E-06	2.91E-06	1.13E-06	1.13E-06	1.16E-03	1.74E-03	2.26E-04	2.75E-04	1.00E+00						
Omo_WGA	8.32E-12	1.83E-11	1.83E-11	1.83E-11	2.28E-11	3.35E-11	2.17E-11	4.73E-12	2.56E-11	2.56E-11	1.80E-09	1.47E-09	1.84E-09	1.51E-09	9.30E-09	9.59E-10	6.96E-09	1.48E-08	2.36E-09	1.93E-09	1.42E-08	1.42E-08	2.21E-08	2.13E-08	5.62E-09	6.77E-09	2.51E-07	2.98E-07					
Omo	3.81E-11	9.80E-12	9.80E-12	9.80E-12	1.22E-11	1.79E-11	1.15E-11	3.02E-12	2.94E-11	2.94E-11	2.11E-09	1.71E-09	2.15E-09	1.76E-09	2.42E-08	2.45E-09	4.99E-09	1.07E-08	3.72E-09	3.04E-09	2.78E-08	2.78E-08	1.29E-07	1.26E-07	3.28E-08	3.96E-08	9.65E-07	1.15E-06	1.63E-02				
Ocat	2.22E-11	8.94E-13	8.94E-13	8.94E-13	2.37E-12	3.50E-12	3.38E-13	2.48E-13	2.70E-10	2.70E-10	7.98E-10	6.34E-10	1.01E-10	8.05E-11	1.37E-09	1.50E-09	5.62E-09	8.28E-09	3.15E-09	2.55E-09	5.76E-09	5.76E-09	1.09E-07	1.05E-07	1.86E-08	2.23E-08	6.99E-07	8.42E-07	1.18E-09	2.94E-09			
Ppil_WGA	7.68E-11	2.58E-10	2.58E-10	2.58E-10	3.18E-10	4.73E-10	9.13E-11	7.08E-11	2.33E-09	2.33E-09	2.18E-09	1.75E-09	3.20E-09	2.59E-09	1.82E-08	5.54E-09	3.20E-08	4.70E-08	1.77E-08	1.44E-08	1.01E-07	1.01E-07	1.10E-05	2.37E-05	2.95E-07	3.57E-07	4.61E-05	5.42E-05	4.42E-08	1.15E-07	1.37E-06		
Ppil	1.17E-10	3.79E-10	3.79E-10	3.79E-10	4.67E-10	6.95E-10	8.91E-11	1.04E-10	2.29E-09	2.29E-09	4.81E-09	3.85E-09	7.05E-09	5.66E-09	4.04E-08	1.22E-08	7.11E-08	1.05E-07	3.94E-08	3.19E-08	2.24E-07	2.24E-07	1.83E-05	3.94E-05	6.59E-07	7.97E-07	9.97E-05	1.17E-04	6.60E-08	1.72E-07	3.08E-06	1.93E-01	

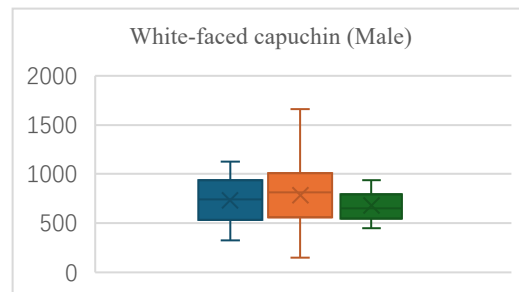
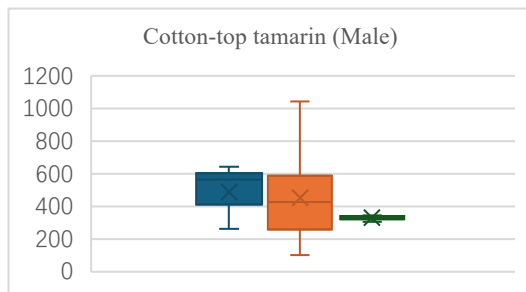
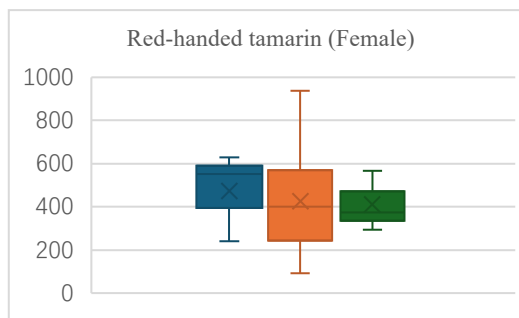
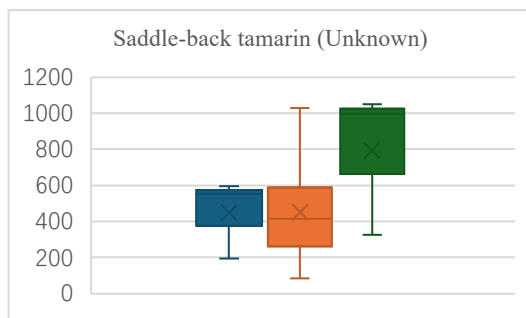
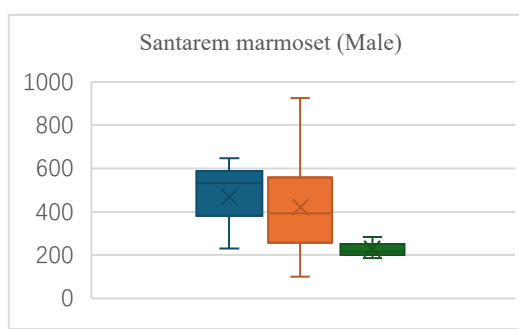
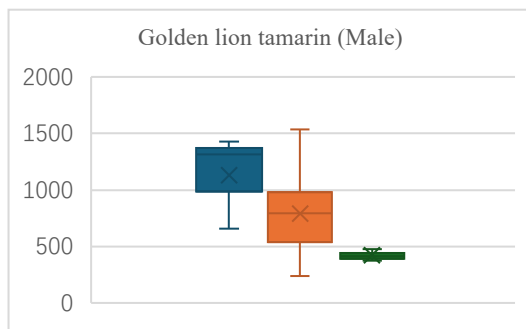
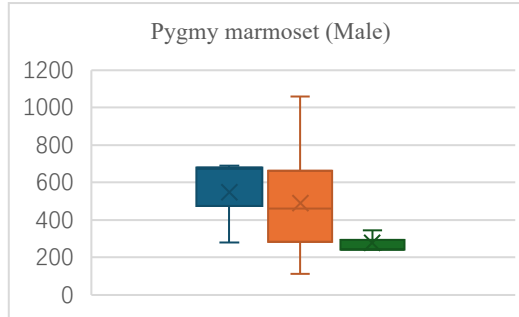
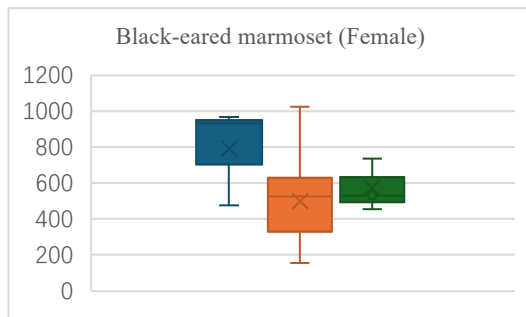
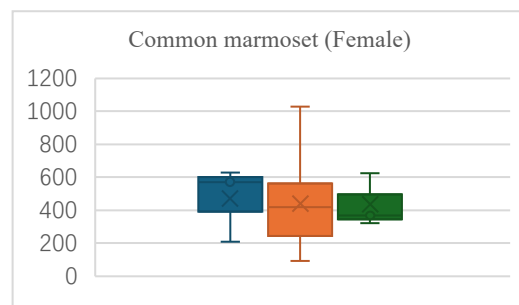
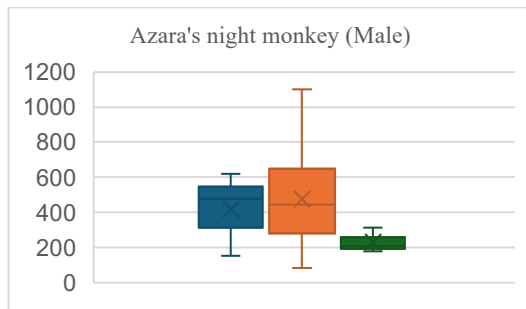
Table S9 Positive selection test of TAS1R3

	Hosa	Cpa_WGA	Cpa	Open	Mhum_WGA_Mhum	Cpyg_WGA	Cpyg	L80s	Lros	Smid_WGA	Smid	Soe_WGA	Sfu	Sap_WGA	Sap104	Casp_WGA	Casp	Sbol_WGA	Sbol	Age_WGA	Age	Age	Llag_WGA	Llag	KSTR_WGA	KSTR	Cmo_WGA	Cmo	Csat	PpIt_WGA	PpIt		
Hosa	1.0000	-8.5525	-8.5525	-8.5525	-8.1223	-8.0525	-8.3928	-8.3643	-8.0840	-7.6628	-7.6983	-7.8718	-7.9054	-7.5224	-6.9098	-6.7041	-6.7451	-6.4958	-6.5316	-7.2429	-7.2409	-6.5934	-6.5482	-6.8591	-6.8217	-6.6663	-6.6509	-7.4397	-7.1440	-7.2492	-7.0059	-6.9224	
Cpa	1.0000	0.0000	0.0000	0.0000	-3.6773	-3.5375	-4.1672	-4.5939	-6.1814	-6.1814	-6.9738	-7.0264	-6.8552	-6.9093	-6.2683	-6.8262	-7.2198	-7.1439	-7.2375	-7.2812	-6.1238	-6.1238	-7.3294	-7.1319	-7.2791	-7.2453	-6.4546	-6.4152	-7.2869	-7.4080	-6.8686	-6.7654	-6.6882
Cpyg	1.0000	1.0000	1.0000	1.0000	-3.6773	-3.5375	-4.1672	-4.5939	-6.1814	-6.1814	-6.9738	-7.0264	-6.8552	-6.9093	-6.2683	-6.8262	-7.2198	-7.1439	-7.2375	-7.2812	-6.1238	-6.1238	-7.3294	-7.1319	-7.2791	-7.2453	-6.4546	-6.4152	-7.2869	-7.4080	-6.8686	-6.7654	-6.6882
L80s	1.0000	1.0000	1.0000	1.0000	-3.6773	-3.5375	-4.1672	-4.5939	-6.1814	-6.1814	-6.9738	-7.0264	-6.8552	-6.9093	-6.2683	-6.8262	-7.2198	-7.1439	-7.2375	-7.2812	-6.1238	-6.1238	-7.3294	-7.1319	-7.2791	-7.2453	-6.4546	-6.4152	-7.2869	-7.4080	-6.8686	-6.7654	-6.6882
Lros	1.0000	1.0000	1.0000	1.0000	-3.6773	-3.5375	-4.1672	-4.5939	-6.1814	-6.1814	-6.9738	-7.0264	-6.8552	-6.9093	-6.2683	-6.8262	-7.2198	-7.1439	-7.2375	-7.2812	-6.1238	-6.1238	-7.3294	-7.1319	-7.2791	-7.2453	-6.4546	-6.4152	-7.2869	-7.4080	-6.8686	-6.7654	-6.6882
Smid_WGA	1.0000	1.0000	1.0000	1.0000	-1.0008	-4.3616	-4.4507	-5.8393	-5.8383	-6.7220	-6.7756	-6.7693	-6.8238	-6.0449	-8.2897	-6.8634	-6.7552	-6.8823	-6.9259	-7.7901	-7.7901	-6.8972	-6.6931	-7.0051	-6.9705	-6.4103	-6.3706	-7.2441	-7.3661	-6.8811	-6.7233	-6.6461	
Smid	1.0000	1.0000	1.0000	1.0000	-4.2384	-4.3308	-4.7467	-5.7467	-6.8378	-6.8916	-6.6852	-6.7401	-6.9542	-6.8167	-7.6782	-6.7045	-6.8026	-6.8475	-7.7155	-7.7155	-6.8177	-6.6124	-6.9269	-6.8300	-6.2901	-6.1689	-7.2912	-6.6011	-6.6346	-6.5657			
Cpyg_WGA	1.0000	1.0000	1.0000	1.0000	0.0000	0.0000	0.0000	0.0000	-6.2800	-6.2800	-7.3309	-7.3832	-7.3520	-7.3520	-6.5756	-6.8843	-7.1607	-7.0825	-7.2606	-7.3062	-7.9798	-7.9798	-7.7151	-7.1322	-7.3593	-7.3253	-6.5133	-6.4781	-7.2537	-7.3771	-6.9007	-6.9719	-6.9767
Cpyg	1.0000	1.0000	1.0000	1.0000	0.0000	0.0000	0.0000	0.0000	-6.5843	-6.5843	-7.4071	-7.4578	-7.4520	-7.5032	-6.5610	-6.8827	-7.3553	-7.2798	-7.5244	-7.5679	-8.2259	-8.2259	-7.3914	-7.1329	-7.6171	-7.5787	-6.8398	-6.7951	-7.5486	-7.6345	-6.1088	-7.0220	-6.9465
Soe_WGA	1.0000	1.0000	1.0000	1.0000	-3.5627	-3.5627	-4.4215	-4.4215	-6.0000	-6.0000	-7.3627	-7.4235	-7.4235	-7.4235	-6.3675	-6.6827	-6.7351	-6.6927	-6.8025	-7.4807	-7.4807	-6.6927	-6.5133	-6.9303	-6.9303	-6.7117	-6.6825	-7.5107	-7.5947	-6.7548	-6.7548	-6.3226	
Sfu	1.0000	1.0000	1.0000	1.0000	-6.6652	-6.7265	-6.3624	-6.4215	-5.3707	-7.2980	-6.4814	-6.5733	-6.6555	-6.7128	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	-5.7375	
Sap_WGA	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Sap104	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Casp_WGA	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Casp	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Sbol_WGA	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Sbol	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Age_WGA	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Age	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Llag_WGA	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
Llag	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
KSTR_WGA	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	
KSTR	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.00										

Table S10 Evolutionary neutrality test of TAS1R3

	Hosa	Cja_WGA	Gja	Cpen	Mhum_WGA	Mhum	Cpyg_WGA	Cpyg	Lros_WGA	Lros	Smid_WGA	Smid	Soe_WGA	Soe	Sfu	Aaz	Sap_WGA	Sap104	Ccap_WGA	Ccap	Sbol_WGA	Sbol	Age_WGA	Age	Lliag_WGA	Lliag	KSTR_WGA	KSTR	Cno_WGA	Cno	Caat	Ppt_WGA	Ppt
Hosa		-8.55E+00	4.65E+00	4.55E+00	-4.12E+00	-3.05E+00	-8.39E+00	-8.30E+00	-8.08E+00	-7.66E+00	-7.07E+00	-7.07E+00	-7.91E+00	-7.52E+00	-6.91E+00	-6.75E+00	-6.75E+00	-6.53E+00	-7.42E+00	-7.42E+00	-6.86E+00	-6.82E+00	-6.86E+00	-6.82E+00	-6.86E+00	-6.82E+00	-6.86E+00	-6.82E+00	-7.44E+00	-7.14E+00	-7.25E+00	-7.01E+00	-6.92E+00
Cja_WGA	4.62E-14		0.00E+00	0.00E+00	-3.68E+00	-3.54E+00	-4.17E+00	-4.59E+00	-6.18E+00	-6.18E+00	-6.97E+00	-7.03E+00	-6.86E+00	-6.91E+00	-6.27E+00	-6.63E+00	-7.22E+00	-7.14E+00	-7.24E+00	-7.28E+00	-8.12E+00	-8.12E+00	-7.33E+00	-7.13E+00	-7.28E+00	-7.25E+00	-6.45E+00	-6.42E+00	-7.29E+00	-7.41E+00	-7.87E+00	-6.77E+00	-6.69E+00
Gja	4.62E-14	1.00E+00		0.00E+00	-3.68E+00	-3.54E+00	-4.17E+00	-4.59E+00	-6.18E+00	-6.18E+00	-6.97E+00	-7.03E+00	-6.86E+00	-6.91E+00	-6.27E+00	-6.63E+00	-7.22E+00	-7.14E+00	-7.24E+00	-7.28E+00	-8.12E+00	-8.12E+00	-7.33E+00	-7.13E+00	-7.28E+00	-7.25E+00	-6.45E+00	-6.42E+00	-7.29E+00	-7.41E+00	-7.87E+00	-6.77E+00	-6.69E+00
Cpen	4.62E-14	1.00E+00	1.00E+00		-3.68E+00	-3.54E+00	-4.17E+00	-4.59E+00	-6.18E+00	-6.18E+00	-6.97E+00	-7.03E+00	-6.86E+00	-6.91E+00	-6.27E+00	-6.63E+00	-7.22E+00	-7.14E+00	-7.24E+00	-7.28E+00	-8.12E+00	-8.12E+00	-7.33E+00	-7.13E+00	-7.28E+00	-7.25E+00	-6.45E+00	-6.42E+00	-7.29E+00	-7.41E+00	-7.87E+00	-6.77E+00	-6.69E+00
Mhum_WGA	4.62E-13	3.54E-04	3.54E-04	3.54E-04		-1.00E+00	-4.36E+00	-4.45E+00	-5.84E+00	-5.84E+00	-6.72E+00	-6.78E+00	-6.77E+00	-6.82E+00	-6.04E+00	-8.29E+00	-8.86E+00	-6.79E+00	-6.88E+00	-6.93E+00	-7.79E+00	-7.79E+00	-6.90E+00	-6.69E+00	-7.01E+00	-6.97E+00	-6.41E+00	-6.37E+00	-7.24E+00	-7.37E+00	-7.68E+00	-6.72E+00	-6.65E+00
Mhum	6.69E-13	5.75E-04	5.75E-04	5.75E-04	3.19E-01		-4.24E+00	-4.33E+00	-5.75E+00	-5.75E+00	-6.64E+00	-6.69E+00	-6.69E+00	-6.74E+00	-5.95E+00	-8.22E+00	-8.78E+00	-6.70E+00	-6.80E+00	-6.85E+00	-7.72E+00	-7.72E+00	-6.82E+00	-6.61E+00	-6.93E+00	-6.89E+00	-6.33E+00	-6.29E+00	-7.17E+00	-7.29E+00	-7.61E+00	-6.64E+00	-6.57E+00
Cpyg_WGA	1.09E-13	5.85E-05	5.85E-05	5.85E-05	2.74E-05	4.45E-05		0.00E+00	-6.28E+00	-6.28E+00	-7.33E+00	-7.35E+00	-7.35E+00	-6.59E+00	-8.82E+00	-7.16E+00	-7.08E+00	-7.26E+00	-7.31E+00	-7.96E+00	-7.96E+00	-7.16E+00	-7.13E+00	-7.36E+00	-7.33E+00	-6.52E+00	-6.48E+00	-7.25E+00	-7.39E+00	-8.05E+00	-6.97E+00	-6.90E+00	
Cpyg	1.27E-13	1.08E-05	1.08E-05	1.08E-05	1.93E-05	3.10E-05	1.00E+00		-6.58E+00	-6.58E+00	-7.41E+00	-7.46E+00	-7.45E+00	-6.56E+00	-8.89E+00	-7.36E+00	-7.28E+00	-7.52E+00	-7.57E+00	-8.23E+00	-8.23E+00	-7.36E+00	-7.35E+00	-7.61E+00	-7.58E+00	-6.83E+00	-6.80E+00	-7.55E+00	-7.63E+00	-8.11E+00	-7.02E+00	-6.95E+00	
Lros_WGA	5.66E-13	9.04E-09	9.04E-09	9.04E-09	4.57E-08	7.04E-08	5.62E-09	1.27E-09		0.00E+00	-5.67E+00	-5.73E+00	-6.36E+00	-6.42E+00	-5.37E+00	-7.30E+00	-6.49E+00	-6.57E+00	-6.67E+00	-6.71E+00	-7.54E+00	-7.54E+00	-6.98E+00	-6.87E+00	-6.63E+00	-6.75E+00	-5.97E+00	-5.93E+00	-7.22E+00	-7.19E+00	-6.76E+00	-6.32E+00	-6.32E+00
Lros	5.66E-13	9.04E-09	9.04E-09	9.04E-09	4.57E-08	7.04E-08	5.62E-09	1.27E-09	1.00E+00		-5.67E+00	-5.73E+00	-6.36E+00	-6.42E+00	-5.37E+00	-7.30E+00	-6.49E+00	-6.57E+00	-6.67E+00	-6.71E+00	-7.54E+00	-7.54E+00	-6.98E+00	-6.87E+00	-6.63E+00	-6.75E+00	-5.97E+00	-5.93E+00	-7.22E+00	-7.19E+00	-6.76E+00	-6.32E+00	-6.32E+00
Smid_WGA	5.21E-12	1.81E-10	1.81E-10	1.81E-10	6.41E-10	9.74E-10	2.92E-11	1.97E-11	1.03E-07	1.03E-07		1.00E+00	-3.44E+00	-3.54E+00	-3.70E+00	-7.30E+00	-6.18E+00	-6.01E+00	-6.20E+00	-6.25E+00	-6.95E+00	-6.95E+00	-6.24E+00	-6.12E+00	-6.28E+00	-6.24E+00	-5.49E+00	-5.45E+00	-6.37E+00	-6.34E+00	-6.54E+00	-6.33E+00	-6.17E+00
Smid	4.33E-12	1.39E-10	1.39E-10	1.39E-10	4.90E-10	7.44E-10	2.23E-11	1.52E-11	7.73E-08	7.73E-08	3.19E-01		-3.54E+00	-3.64E+00	-3.78E+00	-7.35E+00	-6.23E+00	-6.06E+00	-6.25E+00	-6.30E+00	-6.99E+00	-6.99E+00	-6.28E+00	-6.16E+00	-6.33E+00	-6.29E+00	-5.53E+00	-5.49E+00	-6.41E+00	-6.38E+00	-6.58E+00	-6.38E+00	-6.21E+00
Soe_WGA	1.74E-12	3.29E-10	3.29E-10	3.29E-10	5.08E-10	7.69E-10	2.62E-11	1.56E-11	3.77E-09	3.77E-09	8.12E-04	5.78E-04		1.00E+00	4.27E+00	-7.64E+00	-6.62E+00	-6.46E+00	-6.64E+00	-6.68E+00	-7.43E+00	-7.43E+00	-6.66E+00	-6.84E+00	-6.69E+00	-6.66E+00	-6.00E+00	-5.96E+00	-6.37E+00	-6.34E+00	-6.95E+00	-6.25E+00	-6.09E+00
Soe	1.48E-12	2.50E-10	2.50E-10	2.50E-10	3.85E-10	5.85E-10	2.62E-11	1.20E-11	2.82E-09	2.82E-09	5.79E-04	4.08E-04	3.19E-01		-4.35E+00	-7.69E+00	-6.67E+00	-6.51E+00	-6.68E+00	-6.73E+00	-7.48E+00	-7.48E+00	-6.70E+00	-6.58E+00	-6.74E+00	-6.70E+00	-6.04E+00	-6.00E+00	-6.41E+00	-6.38E+00	-7.00E+00	-6.30E+00	-6.13E+00
Sfu	1.08E-11	5.95E-09	5.95E-09	5.95E-09	1.74E-08	2.67E-08	1.32E-09	1.42E-09	3.90E-07	3.90E-07	3.31E-04	2.48E-04	3.91E-05	2.86E-05	-6.99E+00	-5.32E+00	-5.14E+00	-5.35E+00	-5.40E+00	-6.72E+00	-6.72E+00	-5.79E+00	-5.67E+00	-6.18E+00	-6.14E+00	-5.39E+00	-5.35E+00	-6.03E+00	-5.83E+00	-6.43E+00	-5.89E+00	-5.72E+00	
Aaz	2.50E-10	3.10E-14	3.10E-14	3.10E-14	1.89E-13	2.79E-13	1.06E-14	7.63E-15	3.46E-11	3.46E-11	3.38E-11	2.65E-11	5.80E-12	4.56E-12	1.63E-10	-5.91E+00	-6.00E+00	-6.16E+00	-6.11E+00	-6.20E+00	-6.20E+00	-5.55E+00	-5.42E+00	-5.78E+00	-5.74E+00	-4.50E+00	-4.55E+00	-6.50E+00	-6.31E+00	-6.41E+00	-6.14E+00	-5.97E+00	
Sap_WGA	7.00E-10	5.17E-11	5.17E-11	5.17E-11	3.16E-10	4.72E-10	6.99E-11	2.57E-11	2.05E-09	2.05E-09	9.05E-09	7.16E-09	1.04E-09	8.21E-10	4.86E-07	3.32E-08		-1.28E+00	-3.05E+00	-3.15E+00	-6.07E+00	-6.07E+00	-5.49E+00	-5.27E+00	-5.64E+00	-5.60E+00	-4.62E+00	-4.67E+00	-6.09E+00	-6.16E+00	-6.14E+00	-5.77E+00	-5.59E+00
Sap104	5.71E-10	7.62E-11	7.62E-11	7.62E-11	4.67E-10	6.99E-10	1.04E-10	3.80E-11	1.34E-09	2.04E-08	1.62E-08	2.34E-09	1.85E-09	1.10E-06	2.18E-08	2.03E-01		-3.02E+00	-3.11E+00	-6.16E+00	-6.16E+00	-5.41E+00	-5.18E+00	-5.56E+00	-5.51E+00	-4.62E+00	-4.67E+00	-5.93E+00	-6.00E+00	-6.05E+00	-5.68E+00	-5.51E+00	
Ccap_WGA	1.96E-09	4.72E-11	4.72E-11	4.72E-11	2.87E-10	4.29E-10	4.19E-11	1.07E-11	8.49E-10	8.49E-10	8.22E-09	6.54E-09	9.74E-10	7.74E-10	4.26E-07	1.01E-08	2.81E-03	3.09E-03		1.00E+00	5.95E+00	5.95E+00	5.33E+00	5.10E+00	5.65E+00	5.61E+00	-4.65E+00	-4.70E+00	-6.32E+00	-6.22E+00	-6.26E+00	-6.59E+00	-5.72E+00
Ccap	1.65E-09	3.77E-11	3.77E-11	3.77E-11	2.29E-10	3.42E-10	3.32E-11	8.55E-12	6.71E-10	6.71E-10	6.12E-10	3.41E-07	1.26E-08	2.08E-03	2.32E-03	3.19E-01		-5.90E+00	-5.90E+00	-5.36E+00	-5.15E+00	-5.70E+00	-5.66E+00	-4.70E+00	-4.74E+00	-6.36E+00	-6.26E+00	-6.30E+00	-6.54E+00	-5.77E+00			
Sbol_WGA	1.80E-11	4.58E-13	4.58E-13	4.58E-13	2.67E-12	3.95E-12	9.83E-13	2.66E-13	1.00E-11	1.00E-11	2.06E-10	1.63E-10	1.74E-11	1.38E-11	6.46E-10	8.08E-09	1.56E-08	1.02E-08	2.67E-08	3.36E-08		0.00E+00	-5.50E+00	-5.42E+00	-5.90E+00	-5.86E+00	-4.92E+00	-4.97E+00	-5.94E+00	-5.80E+00	-6.13E+00	-5.52E+00	-5.34E+00
Sbol	1.80E-11	4.58E-13	4.58E-13	4.58E-13	2.67E-12	3.95E-12	9.83E-13	2.66E-13	1.00E-11	1.00E-11	2.06E-10	1.63E-10	1.74E-11	1.38E-11	6.46E-10	8.08E-09	1.56E-08	1.02E-08	2.67E-08	3.36E-08	1.00E+00		-5.50E+00	-5.42E+00	-5.90E+00	-5.86E+00	-4.92E+00	-4.97E+00	-5.94E+00	-5.80E+00	-6.13E+00	-5.52E+00	-5.34E+00
Age_WGA	1.21E-09	2.94E-11	2.94E-11	2.94E-11	2.66E-10	3.97E-10	6.49E-11	2.14E-11	1.72E-10	1.72E-10	6.90E-09	5.52E-09	8.87E-10	7.11E-10	5.65E-08	1.72E-07	2.25E-07	3.32E-07	4.69E-07	3.82E-07	2.17E-07	2.17E-07		-6.15E-01	-4.85E+00	-4.76E+00	-4.72E+00	-3.04E+00	-2.98E+00	-5.47E+00	-5.51E+00	-4.22E+00	-4.09E+00
Age	1.52E-09	8.10E-11	8.10E-11	8.10E-11	7.40E-10	1.10E-09	8.09E-11	2.65E-11	3.05E-10	1.24E-08	9.91E-09	1.58E-09	1.27E-09	1.02E-07	3.05E-07	6.09E-07	8.99E-07	1.26E-06	1.03E-06	3.17E-07	3.17E-07	3.90E-06	5.40E-06		-6.15E-01	-3.66E+00	-3.61E+00	-6.14E+00	-5.76E+00	-5.88E+00	-5.28E+00	-5.09E+00	
Lliag_WGA	3.22E-10	3.81E-11	3.81E-11	3.81E-11	1.54E-10	2.29E-10	2.52E-11	6.82E-12	1.02E-09	1.02E-09	5.62E-09	4.51E-09	7.39E-10	5.95E-10	9.03E-09	6.11E-08	1.19E-07	1.69E-07	1.08E-07	8.79E-08	3.44E-08	3.44E-08											
Lliag	3.89E-10	4.43E-11	4.43E-11	4.43E-11	1.84E-10	2.73E-10	3.00E-11	8.08E-12	5.44E-10	5.44E-10	6.73E-09	5.40E-09	8.80E-10	7.08E-10	1.08E-08	7.34E-08	1.39E-07	2.04E-07	1.30E-07	1.06E-07	4.14E-08	4.14E-08	4.53E-06	6.43E-06	5.40E-01								
KSTR_WGA	8.45E-10	2.40E-09	2.40E-09	2.40E-09	2.98E-09	4.41E-09	1.78E-09	3.86E-10	2.46E-08	2.46E-08	2.31E-07	1.89E-07	2.17E-08	1.77E-08	3.62E-07	1.60E-05	8.86E-06	9.79E-06	8.52E-06	7.09E-06	2.27E-06	2.27E-06	1.95E-03	2.92E-03	3.75E-04	4.56E-04							
KSTR	9.12E-10	2.91E-09	2.91E-09	2.91E-09	3.62E-09	5.35E-09	2.14E-09	4.45E-10	2.99E-08	2.99E-08	2.79E-07	2.28E-07	2.64E-08	2.15E-08	4.36E-07	1.32E-05	8.08E-06	8.01E-06	7.00E-06	5.82E-06	2.27E-06	2.27E-06	2.32E-03	3.47E-03	4.52E-04	5.49E-04	1.60E-01						
Cno_WGA	1.66E-11	3.66E-11	3.66E-11	3.66E-11	4.56E-11	6.70E-11	4.34E-11	9.45E-12	5.12E-11	5.12E-11	3.60E-09	2.93E-09	3.67E-09	3.01E-09	1.86E-08	1.92E-09	1.39E-08	2.97E-08	4.71E-09	3.86E-09	2.84E-08	2.84E-08	4.										





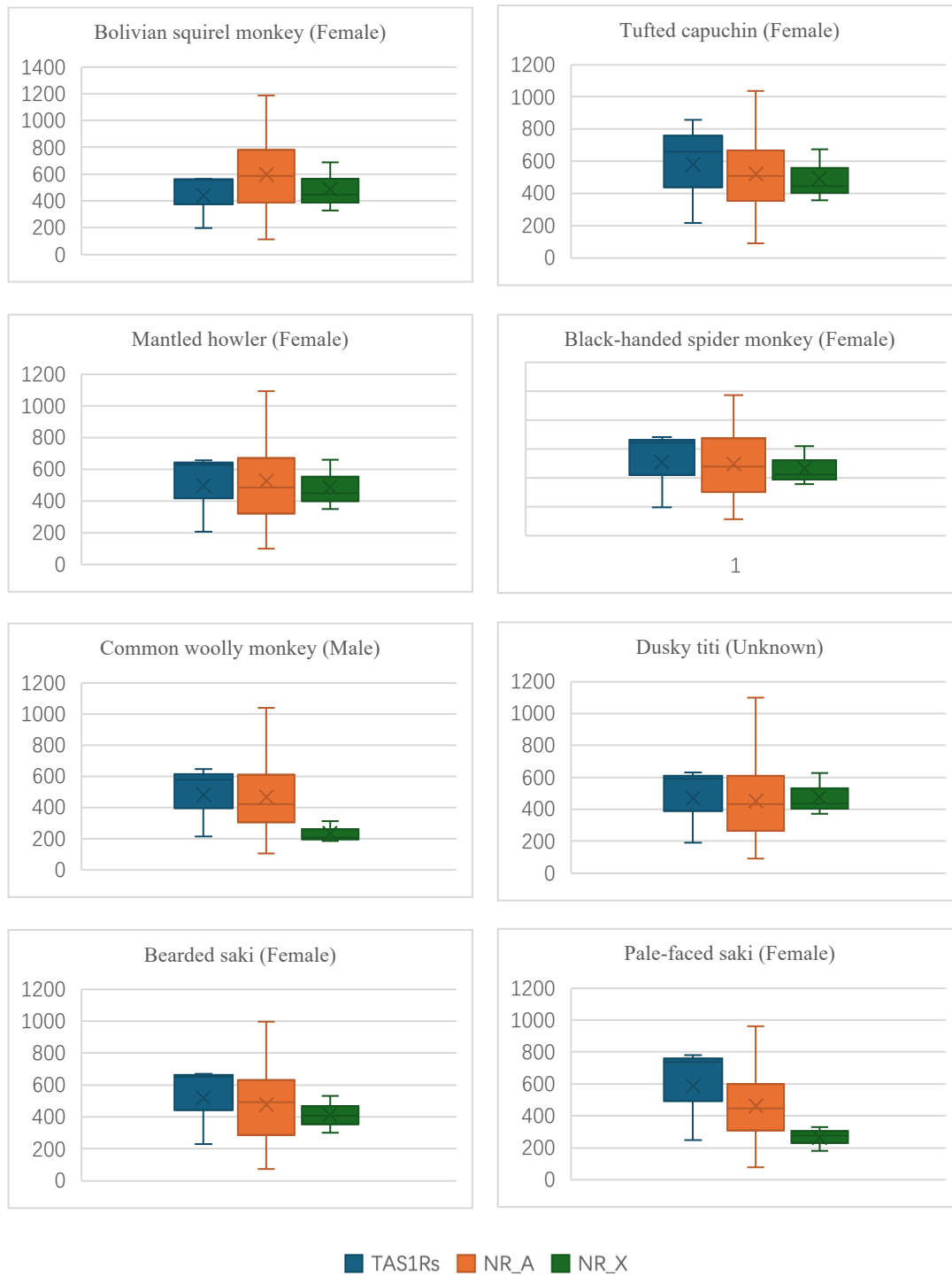


Figure S1 The range of the per-site sequencing depth of the TAS1R genes, that of autosomal neutral references (NR-A) and that of the X-chromosomal neutral references (NR-Xs) in each platyrrhine study specie, depicted by boxplots.

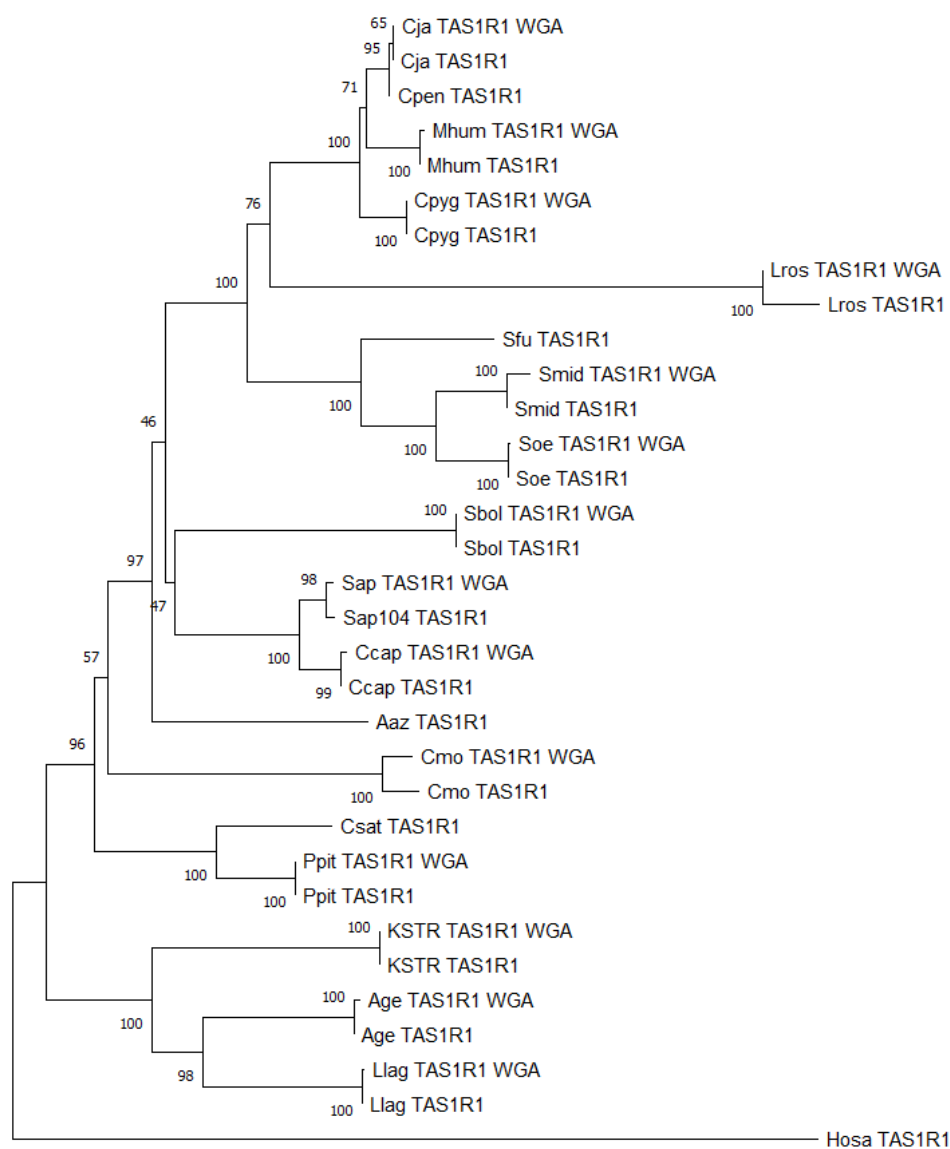


Figure S2 Phylogenetic tree reconstructed for TAS1R1 based on exons including both targeted capture and WGA sequences. Human was used as an outgroup.

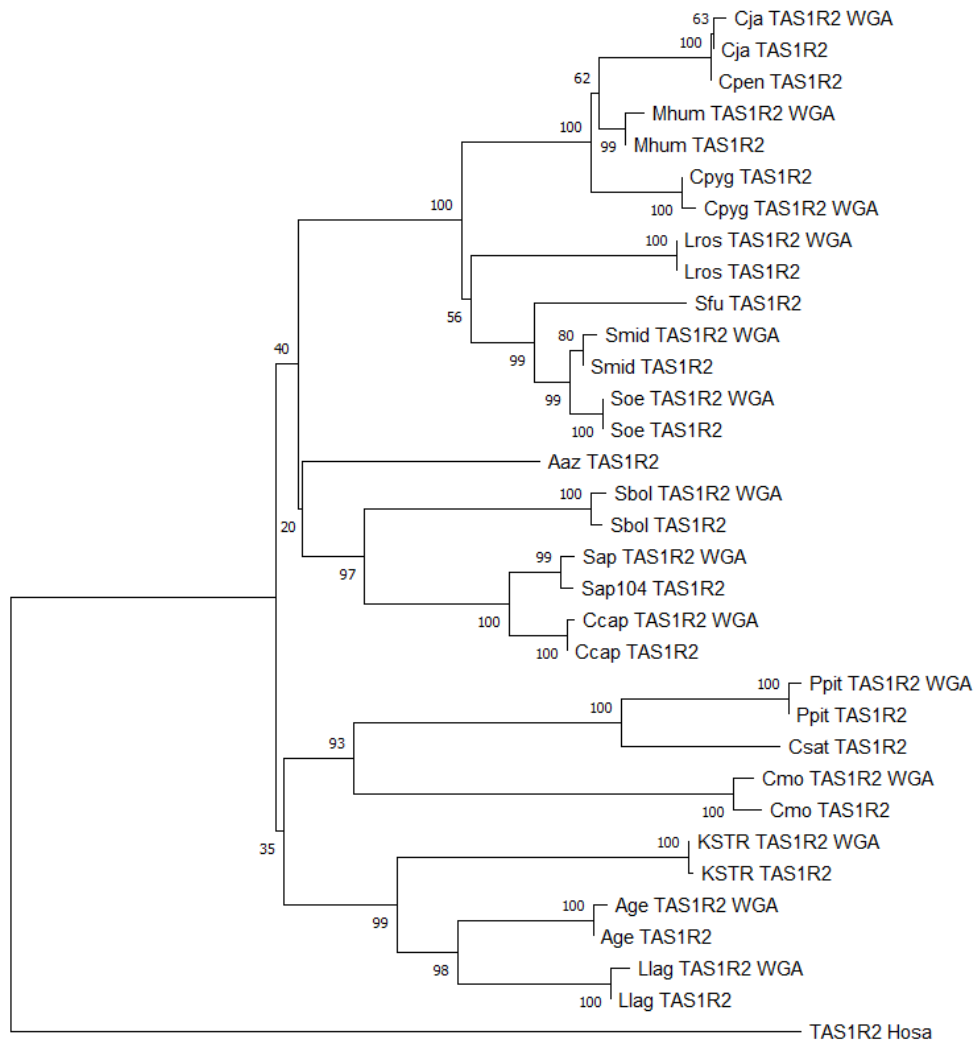


Figure S3 Phylogenetic tree reconstructed for TAS1R2 based on exons including both targeted capture and WGA sequences. Human was used as an outgroup.

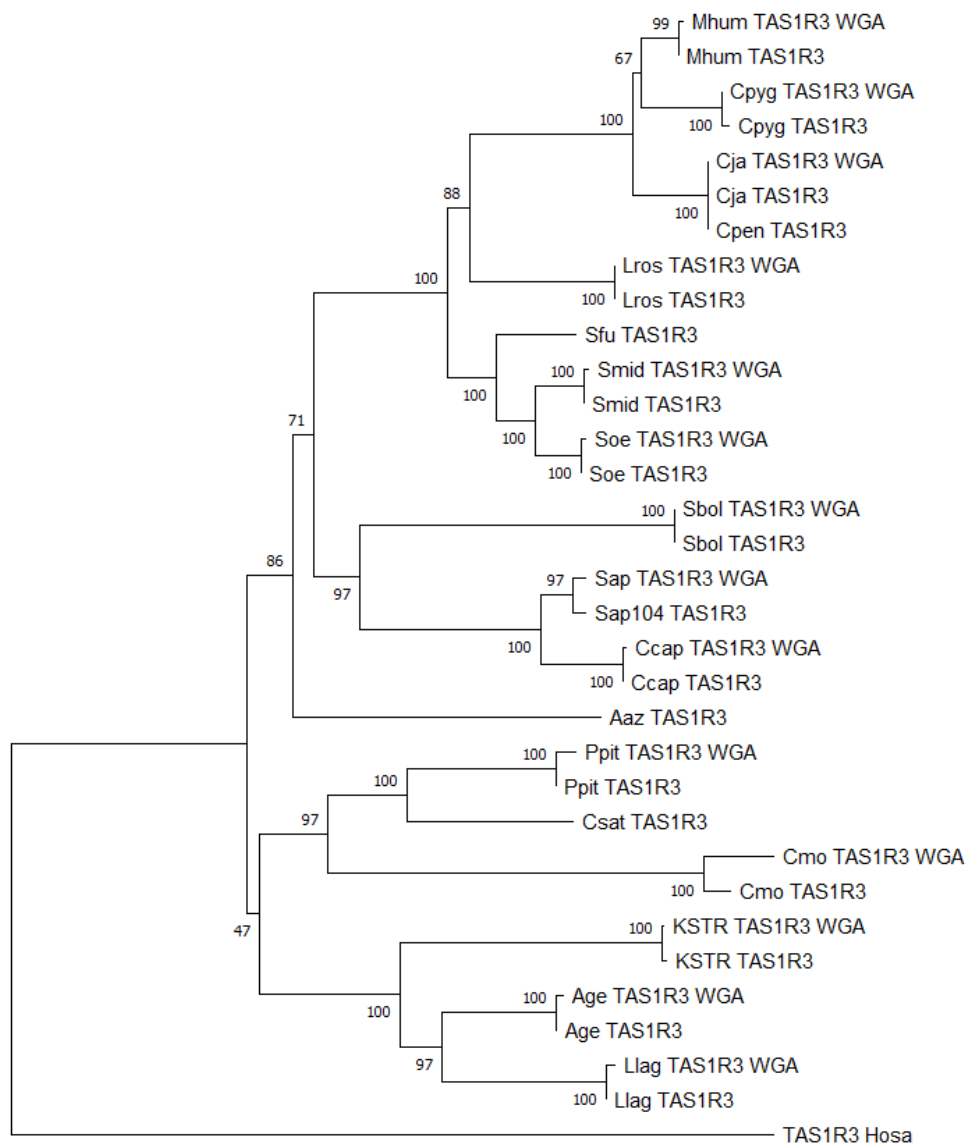


Figure S4 Phylogenetic tree reconstructed for TAS1R3 based on exons including both targeted capture and WGA sequences. Human was used as an outgroup.

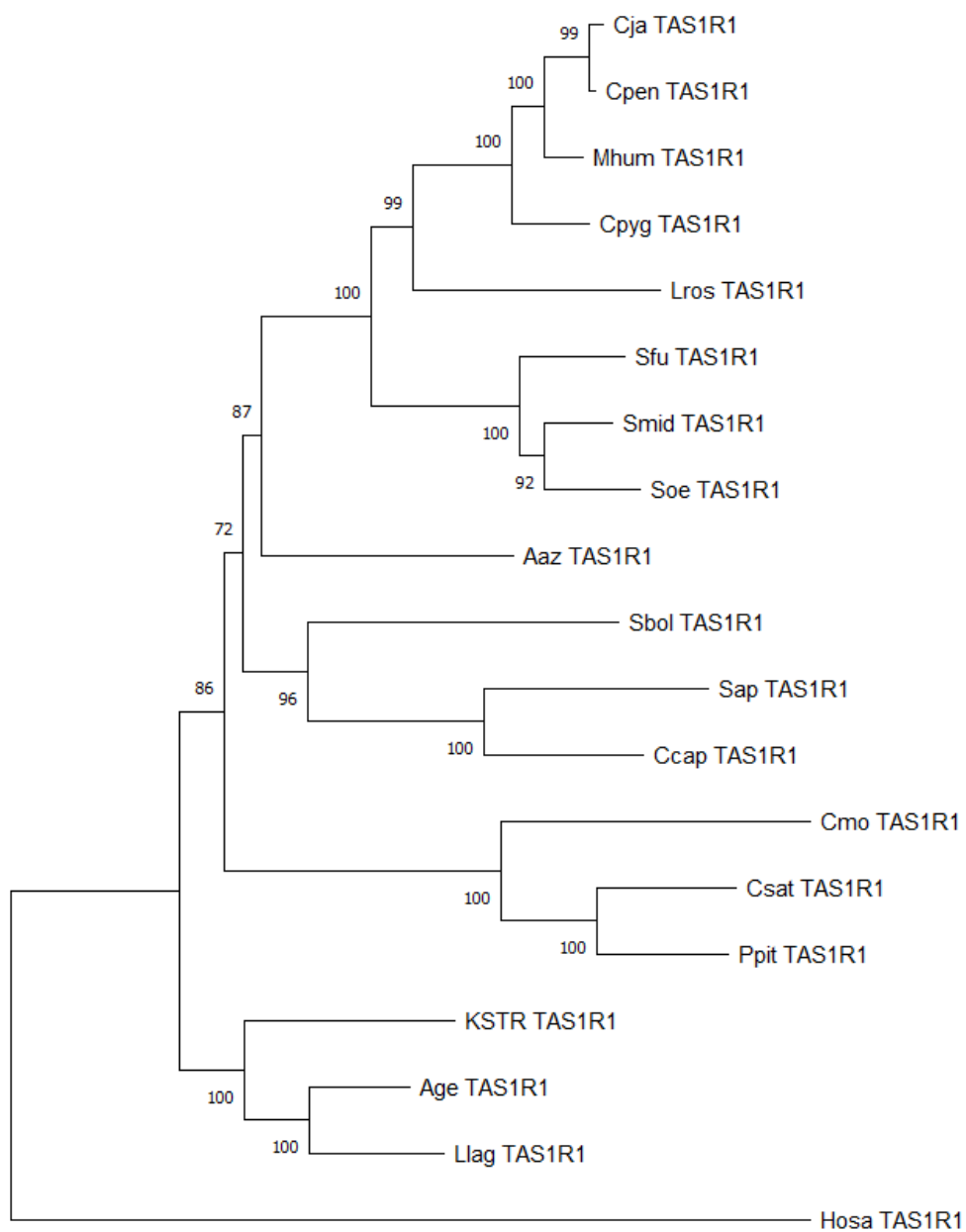


Figure S5 Phylogenetic tree reconstructed for TAS1R1 based on introns with the first intron removed. Human was used as an outgroup.

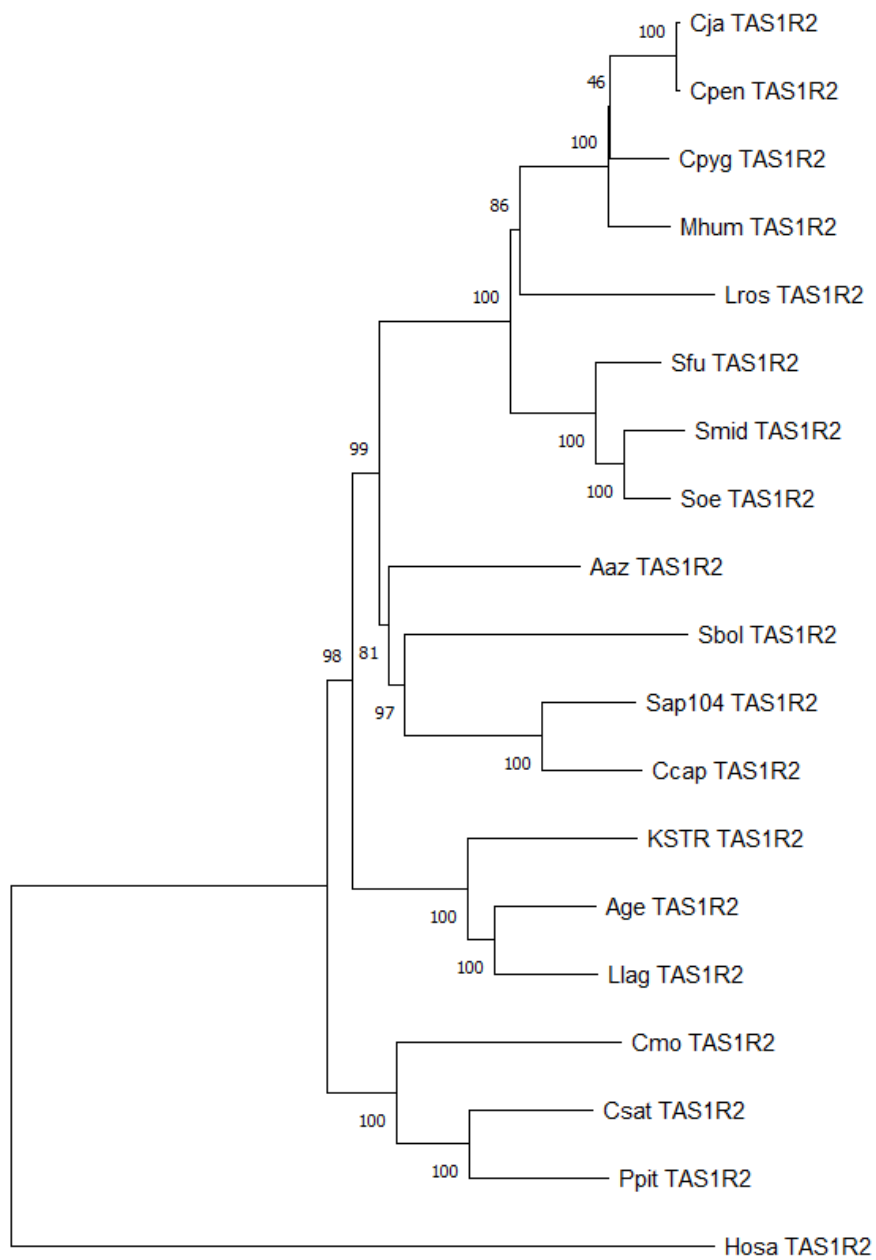


Figure S6 Phylogenetic tree reconstructed for TAS1R2 based on introns. Human was used as an outgroup.

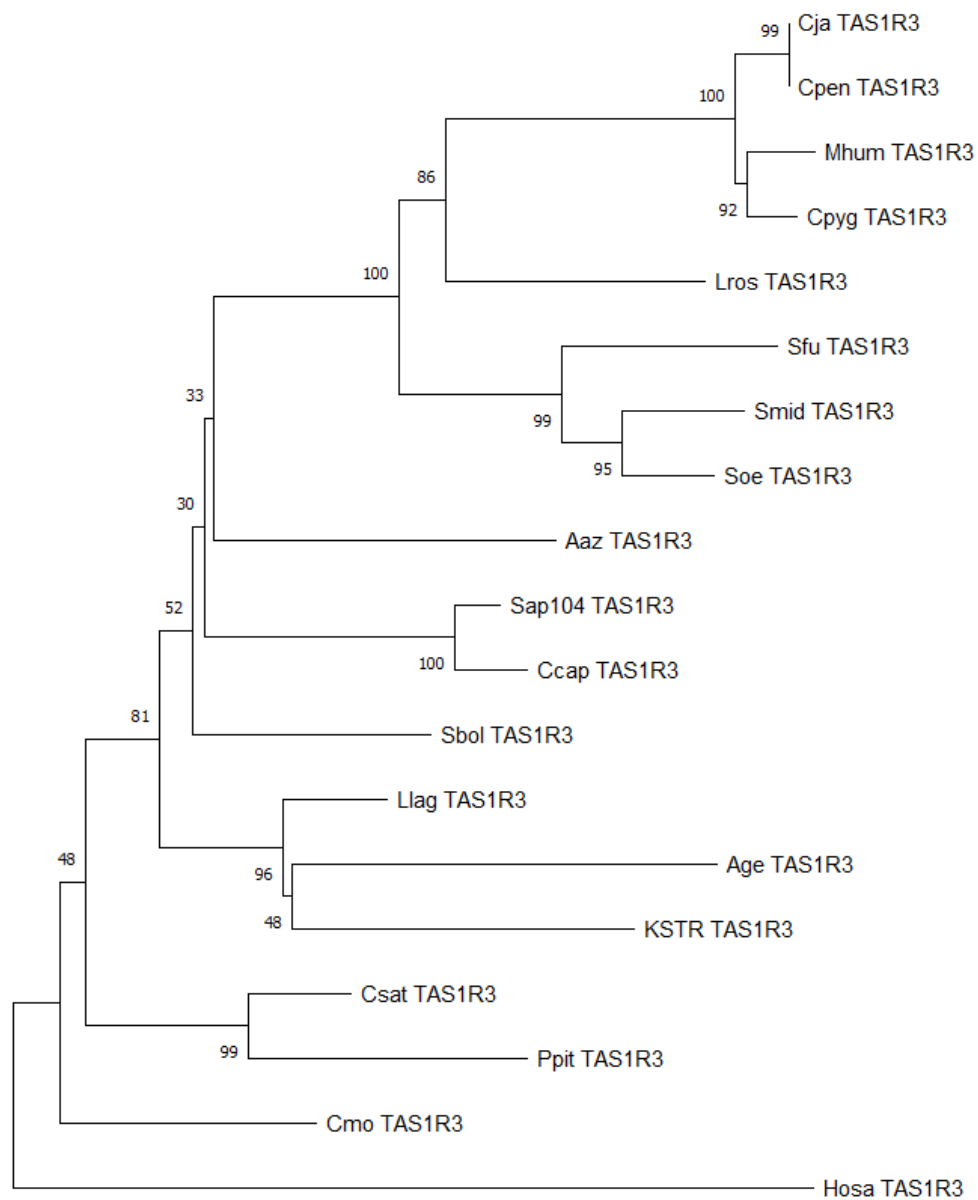


Figure S7 Phylogenetic tree reconstructed for TAS1R3 based on introns. Human was used as an outgroup.



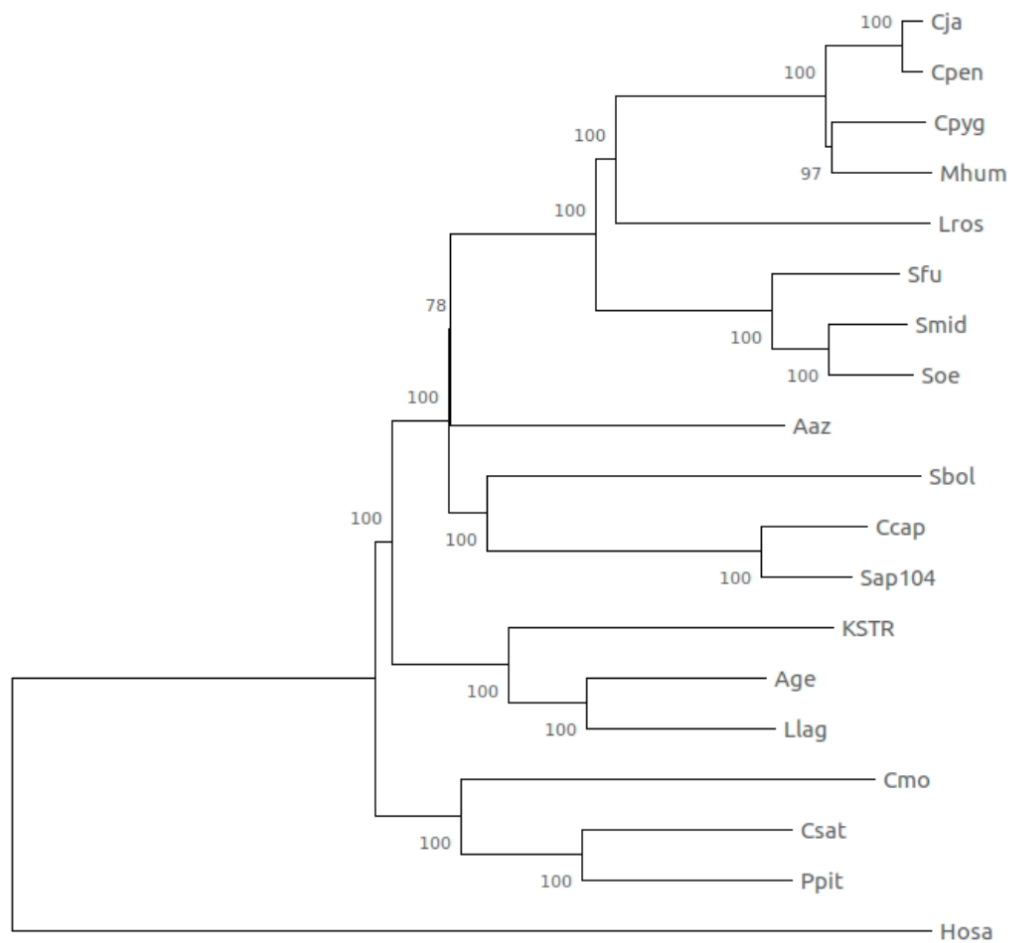


Figure S8 Phylogenetic tree for neutral references. Human was used as an outgroup.