

GWAS OF HUMAN BITTER TASTE PERCEPTION IDENTIFIES NEW LOCI AND REVEALS ADDITIONAL COMPLEXITY OF BITTER TASTE GENETICS

SUPPLEMENTARY DATA

Mirko Ledda, Zoltán Kutalik, Maria C. Souza Destito, Milena M. Souza, Cintia A. Cirillo, Amabilene Zamboni, Nathalie Martin, Edgard Morya, Koichi Sameshima, Jacques S. Beckmann, Johannes le Coutre, Sven Bergmann, Ulrich K. Genick

Figure S1. The study panel represents a continuous admixture of diverse genetic ancestries. A scatter plot of principal components one (PC1) and two (PC2) of study participants' genotype data show the admixed nature of the study population's genetic ancestries. Comparison to HAPMAP population data sets (not shown) indicate that PC1 represents the African-European axis while PC2 represents the European-Asian axis.

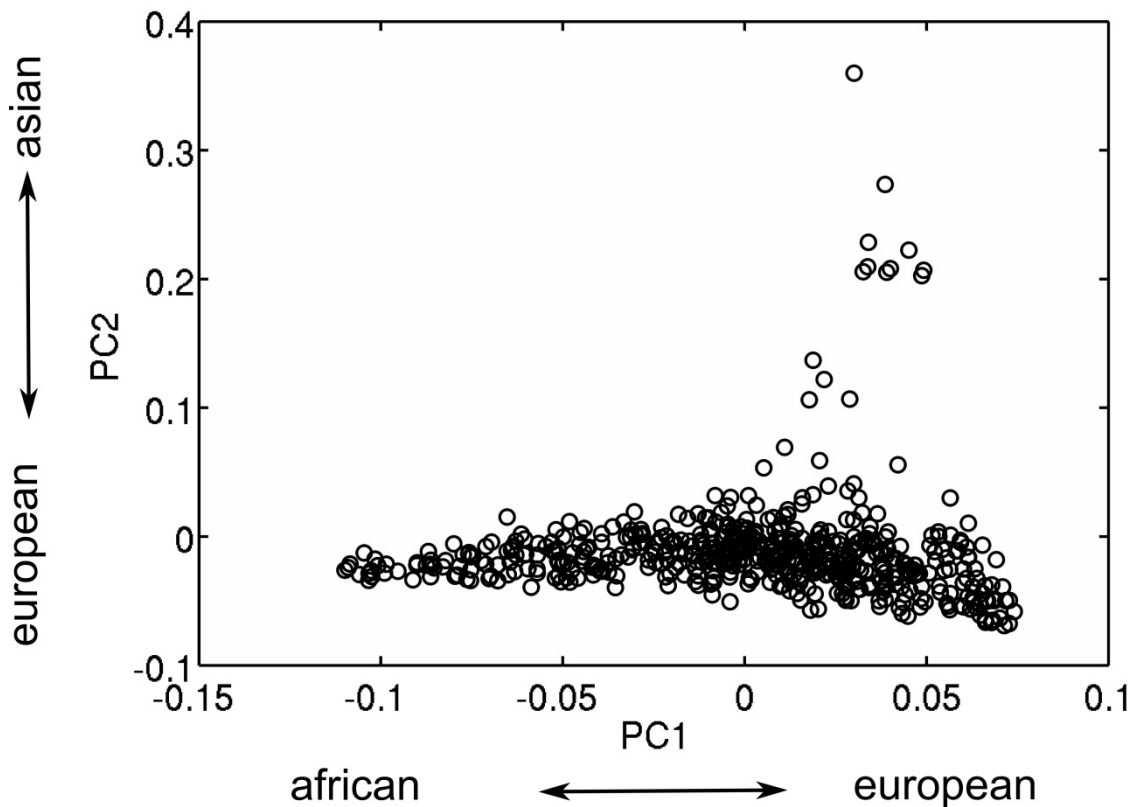


Figure S2. Graphical representation of the overall taste sensitivity parameter concept. Taste detection thresholds tend to be log-normally distributed. Detection thresholds are therefore log-transformed prior to the subsequent steps (note log-scale of x-axis). Panel (a) shows distributions of the detection thresholds for three different taste compounds (red, green and blue). The detection thresholds of one selected individual for these three taste compounds are shown by large dots. (b) The distribution curves are aligned along the x-axis so that their peaks fall onto the zero position. (c) The distributions are now stretched along the x-axis so that they all have unit width. This step converts the x-axis values into z-scores. The individual's overall taste sensitivity is then computed as the average of the z-scores for the three compounds.

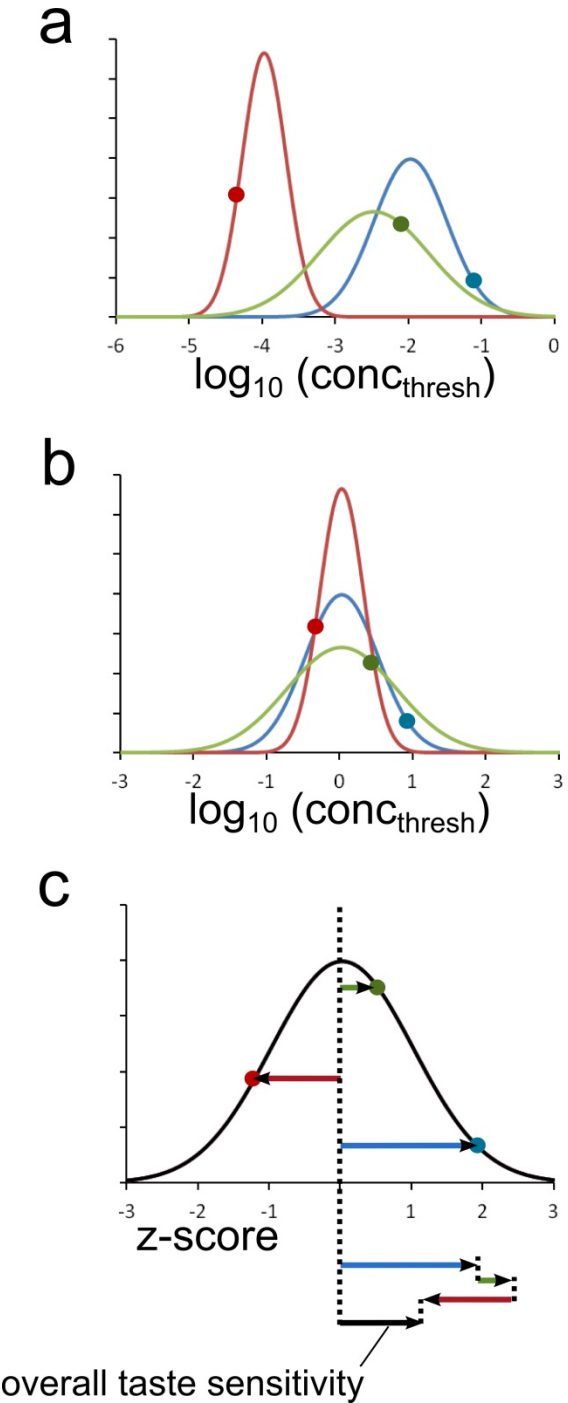


Figure S3. Effect of OTS correction on GWAS p-values for PROP, quinine and caffeine detection thresholds. The panels show scatter plots in which the changes in p-value resulting from OTS correction ($\Delta p = p_{\text{OTS corrected}} - p_{\text{non-corrected}}$) are plotted against the respective p-value prior to correction for each of the SNPs included in the GWAS. Positive Δp -values indicate an association that is strengthened as a result of OTS correction. The dotted line represents the threshold for genome-wide significance and highlighted in red are SNPs showing genome-wide significance after OTS correction. The plots were generated using the results from the discovery cohort (504 subjects). Panels **a,b** and **c** show the results of this analysis for PROP, quinine and caffeine detection threshold respectively. Panel **d** shows the results of a bootstrapping test to determine if the observed boost for highly associated p-values could occur by chance. For this we randomly shuffled caffeine detection thresholds across subjects followed by a GWAS with both uncorrected and OTS corrected randomized thresholds. This procedure was repeated 100 times and all p-values were plotted.

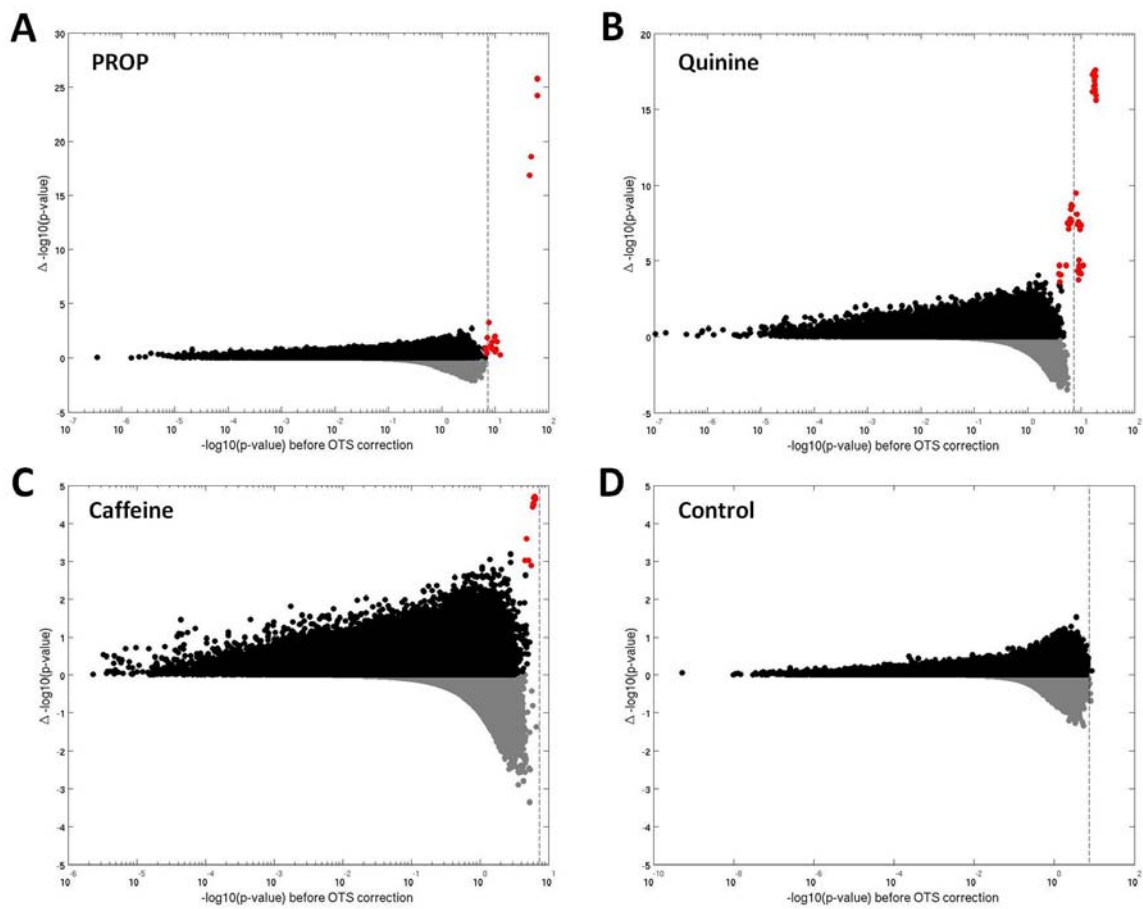


Table S1. GWAS results with log₁₀-transformed caffeine and quinine thresholds for all sequenced SNPs in the bitter taste receptor cluster on chromosome 12 (104 subjects). Associations are filtered for MAF > 5%, p_{HW} > 10⁻⁵ and call rates > 0.90.

MAF : Minor allele frequency ; p_{HW} : Hardy-Weinberg p-value

* Based on human genome build 36.1

SNP name	Chr*	Position*	MAF	p _{HW}	Call rate	Caffeine		Quinine		Function	Functional class
						p	r ²	p	r ²		
NRC932	12	11081963	7.0%	3.5E-01	0.91	4.5E-01	0.6%	1.4E-01	2.4%	intron	neutral
NRC65	12	11129812	8.9%	2.2E-01	0.91	9.5E-01	0.0%	5.4E-04	12.1%	intron	
NRC415	12	11066845	9.5%	1.9E-01	0.91	3.3E-01	1.1%	8.0E-03	7.5%		
NRC795	12	11142550	10.1%	1.6E-01	0.91	9.6E-01	0.0%	3.6E-01	1.0%	intron	
NRC2065	12	11142551	11.4%	1.1E-01	0.91	9.7E-01	0.0%	7.2E-01	0.1%	missense	
rs35972994	12	11081079	13.3%	5.4E-02	0.91	8.0E-01	0.1%	1.6E-01	2.2%	intron	
NRC204	12	11081594	16.5%	1.3E-02	0.91	4.3E-02	4.5%	1.0E-02	7.0%		
NRC1789	12	11129152	19.6%	2.2E-03	0.91	4.8E-01	0.6%	6.9E-01	0.2%	intron	
rs11054160	12	11053800	26.6%	1.0E-05	0.91	5.7E-02	4.0%	1.1E-02	6.9%	intron	
rs7135941	12	11042236	29.1%	4.3E-05	0.91	5.1E-02	4.2%	8.6E-03	7.3%	intron	
rs2888682	12	11093467	38.0%	1.5E-02	0.91	4.1E-01	0.8%	6.6E-06	18.9%	intron	
rs2600333	12	11142297	39.2%	1.0E-02	0.91	5.0E-01	0.5%	4.1E-05	16.2%		
rs2255156	12	11110793	49.4%	8.3E-04	0.91	2.3E-01	1.6%	4.7E-02	4.3%	missense	
rs2255155	12	11110795	49.4%	8.3E-04	0.91	2.3E-01	1.6%	4.7E-02	4.3%	intron	
NRC1768	12	11076728	5.0%	5.1E-01	0.92	3.8E-01	0.9%	2.8E-01	1.3%	intron	
NRC1974	12	11066827	9.4%	1.9E-01	0.92	6.5E-01	0.2%	1.1E-02	7.0%		
rs2597994	12	11097484	40.0%	3.5E-02	0.92	2.9E-01	1.3%	2.2E-05	17.2%	intron	
rs2599410	12	11110929	49.4%	5.0E-04	0.92	3.6E-01	1.0%	2.4E-03	9.6%		
rs2597977	12	11081128	15.4%	2.0E-02	0.93	1.2E-01	2.7%	9.5E-02	3.1%	missense	
rs10772398	12	11030856	24.1%	1.5E-01	0.93	1.0E-01	2.9%	4.7E-01	0.6%	intron	neutral
rs12311490	12	11038848	28.4%	2.4E-05	0.93	1.7E-01	2.1%	1.3E-02	6.6%	missense	
rs11054158	12	11053554	28.4%	2.4E-05	0.93	2.3E-01	1.6%	9.5E-03	7.2%	intron	
rs10772419	12	11064757	37.7%	1.9E-02	0.93	3.5E-01	1.0%	2.6E-05	16.9%	intron	
rs2599394	12	11092896	38.3%	3.7E-02	0.93	4.6E-01	0.6%	6.7E-06	18.9%		
rs2708363	12	11144422	41.4%	7.2E-03	0.93	3.0E-01	1.2%	3.4E-06	19.9%	intron	
rs10845298	12	11112695	49.4%	3.0E-04	0.93	2.5E-01	1.5%	7.2E-03	7.7%	intron	
NRC1323	12	11099244	9.8%	1.7E-01	0.94	3.6E-01	0.9%	5.2E-01	0.5%	intron	
NRC2107	12	11142729	13.4%	4.7E-02	0.94	6.6E-01	0.2%	1.6E-01	2.3%	intron	
rs12371085	12	11068028	15.2%	2.1E-02	0.94	2.4E-01	1.6%	8.2E-02	3.4%	intron	
rs3911150	12	11093515	15.9%	2.7E-01	0.94	2.4E-03	9.6%	9.8E-01	0.0%	intron	
rs9803044	12	11122809	17.1%	8.4E-03	0.94	4.3E-02	4.5%	1.4E-02	6.4%	intron	
rs7959172	12	11145474	18.3%	4.4E-01	0.94	5.6E-01	0.4%	2.8E-02	5.3%	intron	
NRC246	12	11083263	21.3%	5.1E-04	0.94	2.3E-02	5.6%	2.4E-02	5.5%	intron	
NRC2260	12	11135775	22.0%	3.2E-04	0.94	3.0E-01	1.2%	2.2E-01	1.7%	intron	
rs7304447	12	11055369	26.8%	5.0E-05	0.94	2.4E-01	1.5%	8.5E-03	7.4%	intron	
rs2597961	12	11149770	37.8%	4.5E-03	0.94	4.4E-01	0.7%	2.0E-05	17.3%	intron	
NRC2687	12	11093113	5.4%	4.6E-01	0.95	4.7E-01	0.6%	9.0E-01	0.0%	coding-synon	
NRC437	12	11143054	6.0%	4.1E-01	0.95	3.7E-01	0.9%	1.4E-01	2.4%	intron	
NRC2622	12	11099157	6.6%	3.6E-01	0.95	6.1E-01	0.3%	2.4E-02	5.6%	intron	

NRC1191	12	11135737	7.2%	3.2E-01	0.95	3.8E-01	0.9%	1.7E-02	6.1%	intron	
NRC342	12	11093513	8.4%	2.4E-01	0.95	4.4E-01	0.7%	5.8E-01	0.4%	intron	
NRC1309	12	11135750	8.4%	2.4E-01	0.95	5.9E-01	0.3%	5.7E-02	4.0%	intron	
NRC1526	12	11030814	9.6%	1.7E-01	0.95	4.5E-01	0.7%	4.8E-01	0.6%	intron	
NRC542	12	11082011	10.2%	1.4E-01	0.95	4.9E-01	0.5%	2.0E-02	5.9%	intron	
NRC1651	12	11106661	11.4%	9.6E-02	0.95	8.6E-01	0.0%	4.3E-01	0.7%	intron	
rs3553142	12	11081113	13.9%	3.8E-02	0.95	4.1E-01	0.8%	2.3E-01	1.6%		
rs2418305	12	11109820	16.3%	1.2E-02	0.95	4.6E-02	4.4%	6.2E-01	0.3%	intron	
NRC2566	12	11135645	20.5%	1.7E-05	0.95	3.2E-01	1.1%	2.5E-02	5.4%	intron	
rs7311538	12	11055064	27.7%	1.3E-05	0.95	1.9E-01	1.9%	8.3E-03	7.4%	intron	
rs7301234	12	11042151	29.5%	1.7E-05	0.95	1.4E-01	2.4%	5.4E-03	8.2%	intron	
rs2708366	12	11142361	39.8%	1.2E-02	0.95	3.2E-01	1.1%	1.8E-06	20.8%	intron	
NRC12	12	11122800	46.4%	7.4E-02	0.95	3.5E-01	1.0%	1.5E-02	6.4%	intron	
rs3983334	12	11109786	48.2%	1.0E-03	0.95	1.9E-01	2.0%	3.6E-02	4.8%	intron	
NRC1634	12	11090715	5.4%	4.6E-01	0.97	7.1E-01	0.2%	9.4E-01	0.0%	intron	
NRC554	12	11099170	6.5%	3.6E-01	0.97	3.7E-01	0.9%	1.3E-01	2.6%	intron	
rs58622223	12	11055359	7.1%	2.6E-04	0.97	2.9E-01	1.3%	4.2E-01	0.7%	intron	
NRC73	12	11055706	7.1%	2.6E-04	0.97	3.0E-01	1.2%	4.1E-01	0.8%		
NRC941	12	11081998	8.9%	2.0E-01	0.97	1.8E-01	2.0%	1.5E-03	10.4%	intron	neutral
NRC593	12	11133701	10.7%	1.2E-01	0.97	7.5E-02	3.5%	7.8E-01	0.1%	intron	
NRC103	12	11138363	13.1%	5.1E-02	0.97	6.7E-01	0.2%	1.6E-01	2.3%	intron	
NRC1920	12	11069804	13.7%	4.0E-02	0.97	5.8E-01	0.3%	6.6E-01	0.2%	intron	
rs11612527	12	11072815	14.3%	1.1E-01	0.97	9.9E-01	0.0%	1.2E-02	6.8%		
rs7315455	12	11076336	17.3%	5.9E-01	0.97	5.2E-01	0.5%	1.2E-02	6.8%	coding-synon	
NRC2316	12	11093523	18.5%	3.4E-03	0.97	4.5E-01	0.6%	2.5E-01	1.5%	intron	
rs10431300	12	11109681	19.0%	2.3E-03	0.97	6.5E-02	3.8%	1.6E-02	6.3%	intron	
rs2708381	12	11105412	20.8%	2.1E-01	0.97	5.7E-01	0.4%	7.9E-03	7.5%	intron	
NRC230	12	11083519	21.4%	4.1E-04	0.97	3.3E-02	5.0%	3.0E-02	5.2%	intron	
rs11054152	12	11050779	28.0%	3.3E-05	0.97	2.1E-01	1.7%	8.0E-03	7.5%	intron	
rs2597963	12	11149278	39.9%	1.9E-02	0.97	4.2E-01	0.7%	2.3E-06	20.4%	intron	
rs2708358	12	11149520	39.9%	2.8E-03	0.97	3.8E-01	0.9%	1.7E-06	20.8%	intron	
NRC319	12	11091336	5.9%	4.2E-01	0.98	7.1E-01	0.2%	7.4E-01	0.1%	intron	
rs56985810	12	11066344	7.1%	2.3E-04	0.98	2.8E-01	1.3%	4.7E-01	0.6%	utr-3	
NRC892	12	11136001	8.2%	2.4E-01	0.98	8.3E-01	0.1%	7.9E-02	3.4%	intron	
NRC2651	12	11107247	9.4%	1.8E-01	0.98	5.8E-01	0.3%	9.6E-01	0.0%	intron	
NRC2161	12	11109780	10.6%	1.2E-01	0.98	7.7E-01	0.1%	1.6E-02	6.3%	utr-5	
NRC874	12	11083465	15.3%	1.9E-02	0.98	6.8E-01	0.2%	5.3E-02	4.1%	missense	
rs7296803	12	11143041	15.3%	1.9E-02	0.98	7.3E-01	0.1%	7.2E-03	7.7%	missense	
NRC1621	12	11135393	17.6%	4.0E-04	0.98	6.9E-01	0.2%	1.1E-03	10.9%		
rs4763611	12	11056384	19.4%	7.8E-02	0.98	6.1E-01	0.3%	3.7E-03	8.8%	intron	
rs11560811	12	11110637	19.4%	1.7E-03	0.98	4.2E-02	4.5%	1.0E-02	7.1%	utr-3	
rs3983335	12	11109802	20.0%	1.1E-03	0.98	1.7E-01	2.1%	8.4E-02	3.3%	intron	
NRC1550	12	11083314	20.6%	7.2E-04	0.98	6.2E-02	3.9%	3.2E-02	5.0%	missense	neutral
NRC801	12	11083336	20.6%	7.2E-04	0.98	3.0E-02	5.1%	1.4E-02	6.5%	intron	
NRC939	12	11083575	21.2%	4.6E-04	0.98	4.1E-02	4.6%	1.9E-02	5.9%	intron	
NRC670	12	11093748	24.1%	3.4E-05	0.98	4.7E-01	0.6%	2.2E-01	1.7%	missense	

NRC1123	12	11135723	27.1%	1.2E-02	0.98	8.4E-01	0.0%	3.0E-02	5.1%	intron
rs7304936	12	11055749	27.6%	2.4E-05	0.98	1.9E-01	2.0%	6.7E-03	7.8%	
rs2597975	12	11144064	32.4%	1.9E-05	0.98	2.9E-02	5.2%	2.1E-01	1.8%	utr-3
NRC2694	12	11135657	37.1%	2.7E-01	0.98	3.0E-01	1.2%	6.3E-03	7.9%	intron
rs2443739	12	11149713	39.4%	2.1E-03	0.98	4.4E-01	0.7%	2.4E-06	20.4%	intron
rs10743937	12	11064722	40.6%	1.5E-03	0.98	3.1E-01	1.2%	2.4E-06	20.3%	intron
rs2600334	12	11142972	40.6%	1.1E-02	0.98	3.4E-01	1.0%	1.2E-06	21.3%	missense
rs12313469	12	11066354	41.2%	3.7E-03	0.98	3.3E-01	1.1%	6.4E-06	19.0%	intron
NRC581	12	11121610	47.1%	8.2E-02	0.98	4.9E-01	0.5%	4.4E-04	12.4%	intron
NRC2081	12	11090850	5.2%	4.7E-01	0.99	7.4E-01	0.1%	6.5E-02	3.8%	intron
NRC1249	12	11100769	5.2%	4.7E-01	0.99	1.9E-01	2.0%	6.9E-01	0.2%	intron
NRC1272	12	11083138	5.8%	4.2E-01	0.99	9.5E-01	0.0%	1.7E-01	2.2%	intron
NRC2032	12	11090836	10.5%	1.3E-01	0.99	5.8E-01	0.4%	3.4E-02	4.9%	intron
rs2708379	12	11106296	10.5%	1.3E-01	0.99	1.9E-01	1.9%	9.3E-01	0.0%	intron
rs55748583	12	11030979	14.5%	1.5E-01	0.99	9.6E-04	11.1%	7.7E-01	0.1%	intron
NRC982	12	11149337	14.5%	2.6E-02	0.99	6.6E-01	0.2%	1.9E-01	1.9%	intron
NRC239	12	11029834	15.7%	1.5E-02	0.99	6.3E-01	0.3%	4.9E-01	0.5%	intron neutral
rs11054149	12	11046217	17.4%	5.1E-01	0.99	5.7E-01	0.4%	8.9E-03	7.3%	intron
NRC1381	12	11103640	17.4%	5.6E-03	0.99	5.6E-01	0.4%	6.2E-02	3.8%	intron
NRC1241	12	11083478	18.6%	2.7E-03	0.99	9.3E-02	3.1%	3.1E-02	5.1%	intron
NRC1553	12	11093692	18.6%	2.7E-03	0.99	2.1E-02	5.8%	6.9E-01	0.2%	intron
NRC1089	12	11105627	18.6%	3.3E-01	0.99	5.2E-01	0.5%	6.9E-03	7.7%	intron
rs11533164	12	11110698	18.6%	2.7E-03	0.99	8.5E-02	3.3%	1.3E-02	6.6%	intron
rs35860793	12	11147923	18.6%	3.3E-01	0.99	5.2E-01	0.5%	6.9E-03	7.7%	missense
NRC1833	12	11083608	19.2%	1.8E-03	0.99	5.3E-02	4.1%	7.6E-03	7.6%	missense
rs7136962	12	11032237	20.3%	1.8E-01	0.99	6.6E-01	0.2%	3.6E-03	8.9%	
rs12581501	12	11045061	20.3%	1.8E-01	0.99	6.4E-01	0.3%	4.2E-03	8.6%	neutral
rs2597990	12	11094726	20.3%	2.2E-02	0.99	3.8E-03	8.8%	6.1E-01	0.3%	intron
rs11531976	12	11110607	20.3%	1.4E-01	0.99	4.5E-02	4.4%	2.5E-03	9.5%	intron
NRC1311	12	11100785	22.1%	2.0E-04	0.99	2.7E-01	1.4%	3.0E-01	1.2%	utr-5
NRC913	12	11092349	23.3%	7.1E-05	0.99	8.7E-01	0.0%	1.0E-01	3.0%	intron
NRC2721	12	11092361	23.3%	7.1E-05	0.99	4.4E-01	0.7%	3.5E-02	4.9%	intron
NRC1551	12	11099328	24.4%	2.3E-05	0.99	1.4E-01	2.4%	4.1E-01	0.8%	intron
rs10845284	12	11049566	27.3%	1.8E-05	0.99	2.5E-01	1.5%	4.9E-03	8.4%	intron
rs10732561	12	11062104	32.6%	6.9E-04	0.99	2.6E-02	5.4%	2.8E-01	1.3%	intron
rs2597984	12	11091001	32.6%	4.4E-05	0.99	3.1E-02	5.1%	2.4E-01	1.5%	intron
rs2708377	12	11107582	32.6%	6.9E-04	0.99	3.6E-02	4.8%	2.1E-01	1.8%	intron
rs2597981	12	11083557	38.4%	1.3E-01	0.99	3.5E-01	1.0%	9.2E-07	21.7%	intron
rs2708319	12	11092308	39.0%	5.8E-02	0.99	4.1E-01	0.8%	8.2E-07	21.8%	intron
rs2443094	12	11142205	41.3%	6.3E-03	0.99	3.6E-01	0.9%	6.3E-07	22.2%	intron
rs2597973	12	11144393	41.3%	6.3E-03	0.99	3.7E-01	0.9%	3.7E-07	22.9%	intron
rs2708361	12	11147927	41.3%	6.3E-03	0.99	3.6E-01	0.9%	6.0E-07	22.3%	
NRC958	12	11135699	46.5%	1.1E-01	0.99	1.2E-01	2.6%	7.0E-03	7.7%	intron
rs9777856	12	11094589	5.2%	4.7E-01	1.00	6.7E-01	0.2%	5.3E-02	4.1%	
NRC1821	12	11105566	5.2%	4.7E-01	1.00	4.7E-01	0.6%	1.3E-01	2.6%	intron
NRC869	12	11110575	5.2%	4.7E-01	1.00	1.0E-01	3.0%	3.3E-01	1.1%	intron

NRC1757	12	11058487	5.7%	4.2E-01	1.00	5.5E-01	0.4%	1.2E-01	2.7%		
NRC988	12	11109747	5.7%	4.2E-01	1.00	2.7E-02	5.3%	6.1E-01	0.3%	intron	
NRC1727	12	11092430	6.3%	3.7E-01	1.00	5.7E-01	0.4%	3.5E-01	1.0%	intron	neutral
NRC1663	12	11110574	6.3%	3.7E-01	1.00	6.4E-02	3.8%	4.6E-01	0.6%	intron	
NRC673	12	11105713	6.9%	3.3E-01	1.00	6.3E-01	0.3%	6.6E-01	0.2%	intron	deleterious
NRC488	12	11074360	8.0%	2.5E-01	1.00	7.2E-01	0.1%	2.1E-01	1.8%		
NRC1341	12	11067579	9.8%	1.5E-01	1.00	3.6E-01	1.0%	7.1E-01	0.2%	intron	
NRC1900	12	11074336	9.8%	1.5E-01	1.00	7.6E-01	0.1%	8.0E-01	0.1%	intron	neutral
NRC2307	12	11099384	9.8%	1.5E-01	1.00	8.9E-01	0.0%	3.4E-01	1.0%	intron	
NRC1696	12	11147880	9.8%	1.5E-01	1.00	9.3E-01	0.0%	5.2E-01	0.5%	intron	
NRC663	12	11067557	10.3%	1.3E-01	1.00	3.3E-01	1.1%	7.6E-01	0.1%	intron	
NRC2184	12	11105889	10.3%	1.3E-01	1.00	3.4E-02	4.9%	9.3E-01	0.0%	intron	
NRC1102	12	11092390	10.9%	1.1E-01	1.00	6.8E-01	0.2%	8.2E-01	0.1%	intron	none
NRC2555	12	11099402	11.5%	8.7E-02	1.00	7.3E-01	0.1%	2.7E-01	1.4%	intron	
NRC647	12	11098032	12.1%	7.0E-02	1.00	4.9E-01	0.5%	3.2E-01	1.1%	intron	
NRC2182	12	11142997	12.1%	7.0E-02	1.00	4.1E-01	0.8%	2.2E-01	1.7%	utr-3	
NRC112	12	11058671	12.6%	5.6E-02	1.00	1.2E-02	6.8%	1.5E-01	2.3%	missense	
NRC2200	12	11041321	13.2%	5.0E-02	1.00	6.4E-01	0.3%	2.5E-01	1.5%	intron	
NRC273	12	11094917	13.8%	3.5E-02	1.00	8.7E-02	3.3%	7.5E-01	0.1%	intron	
NRC908	12	11065569	14.4%	2.7E-02	1.00	8.7E-01	0.0%	1.4E-01	2.5%	intron	neutral
NRC341	12	11074458	14.4%	1.4E-01	1.00	8.5E-04	11.4%	8.0E-01	0.1%	coding-synon	
NRC2591	12	11135912	14.9%	2.0E-02	1.00	4.5E-01	0.6%	4.6E-04	12.4%	coding-synon	
NRC868	12	11094932	16.1%	1.1E-02	1.00	1.5E-02	6.4%	3.7E-01	0.9%	intron	deleterious
NRC476	12	11030202	16.7%	5.2E-01	1.00	7.8E-03	7.5%	9.3E-01	0.0%		
NRC2154	12	11065639	16.7%	8.3E-03	1.00	3.8E-01	0.9%	5.5E-02	4.1%	intron	
rs7978808	12	11143651	17.2%	6.0E-03	1.00	2.9E-01	1.3%	1.9E-02	6.0%	utr-5	
rs10845294	12	11074553	17.8%	6.8E-02	1.00	5.2E-01	0.5%	4.8E-03	8.4%	intron	
NRC2401	12	11105295	17.8%	4.2E-03	1.00	5.5E-01	0.4%	9.5E-01	0.0%	intron	
rs10845289	12	11058493	18.4%	3.4E-01	1.00	4.6E-01	0.6%	8.9E-03	7.3%	coding-synon	
NRC328	12	11083774	18.4%	3.4E-01	1.00	4.6E-01	0.6%	8.9E-03	7.3%	intron	
rs10845288	12	11055798	19.0%	2.7E-01	1.00	4.7E-01	0.6%	9.5E-03	7.2%	intron	
rs7966304	12	11094968	19.0%	2.7E-01	1.00	4.9E-01	0.6%	7.1E-03	7.7%	intron	
NRC2621	12	11135992	19.0%	2.0E-03	1.00	6.0E-02	3.9%	7.3E-03	7.6%	intron	
rs11054148	12	11045311	19.5%	1.1E-01	1.00	7.5E-01	0.1%	2.6E-03	9.4%	intron	
NRC1374	12	11074957	19.5%	1.4E-03	1.00	2.0E-01	1.9%	6.6E-01	0.2%	intron	
rs34373072	12	11080752	19.5%	1.1E-01	1.00	7.5E-01	0.1%	2.6E-03	9.4%	intron	
rs35304582	12	11091123	19.5%	1.1E-01	1.00	7.5E-01	0.1%	2.6E-03	9.4%	intron	
rs35062230	12	11092677	19.5%	1.1E-01	1.00	7.5E-01	0.1%	2.6E-03	9.4%	intron	
rs7973242	12	11099772	19.5%	1.1E-01	1.00	7.5E-01	0.1%	2.6E-03	9.4%	intron	
NRC1681	12	11105653	19.5%	1.4E-03	1.00	2.1E-01	1.8%	9.1E-01	0.0%	intron	
rs61912112	12	11147851	19.5%	1.1E-01	1.00	7.5E-01	0.1%	2.6E-03	9.4%	intron	
rs35683753	12	11051659	20.1%	1.6E-01	1.00	6.8E-01	0.2%	3.5E-03	8.9%	intron	
rs12370363	12	11074779	20.1%	1.6E-01	1.00	6.8E-01	0.2%	3.5E-03	8.9%	intron	
NRC1750	12	11080220	20.7%	5.8E-04	1.00	6.5E-01	0.2%	4.6E-01	0.6%	intron	
NRC2115	12	11106124	20.7%	5.8E-04	1.00	3.7E-02	4.8%	7.3E-01	0.1%	intron	
rs35720106	12	11135433	20.7%	5.8E-04	1.00	4.5E-02	4.4%	1.5E-02	6.4%	intron	

rs11526470	12	11074808	21.3%	3.7E-04	1.00	8.1E-01	0.1%	3.5E-06	19.8%	intron	
NRC2043	12	11105722	23.0%	8.2E-05	1.00	4.3E-01	0.7%	5.4E-01	0.4%	intron	
rs11054143	12	11041586	24.1%	9.5E-01	1.00	1.1E-01	2.8%	3.4E-02	4.9%	intron	
NRC251	12	11135461	24.1%	1.1E-03	1.00	2.2E-01	1.7%	1.2E-03	10.8%	intron	
NRC1933	12	11106137	24.7%	1.5E-05	1.00	1.4E-01	2.5%	5.9E-01	0.3%	intron	
rs12226919	12	11041300	28.7%	1.7E-05	1.00	1.6E-01	2.2%	2.2E-03	9.7%	intron	
rs1817043	12	11107119	32.2%	5.3E-04	1.00	3.0E-02	5.2%	2.5E-01	1.5%	intron	
rs2257110	12	11093789	32.8%	9.7E-05	1.00	3.2E-02	5.0%	2.4E-01	1.6%	intron	
rs2597974	12	11144112	32.8%	9.7E-05	1.00	3.2E-02	5.0%	2.4E-01	1.6%	intron	
NRC287	12	11121430	33.9%	5.0E-05	1.00	2.1E-01	1.8%	2.8E-04	13.2%	intron	neutral
rs1868769	12	11066020	34.5%	1.8E-03	1.00	3.8E-02	4.7%	2.1E-01	1.8%	intron	
rs2597991	12	11094910	36.2%	7.9E-01	1.00	4.2E-01	0.8%	7.4E-07	22.0%	intron	
rs11533168	12	11117688	36.2%	2.6E-03	1.00	7.9E-01	0.1%	1.1E-07	24.5%		
rs10845295	12	11075099	37.4%	1.2E-02	1.00	4.6E-01	0.6%	2.7E-06	20.2%	intron	
rs10772423	12	11074484	38.5%	4.7E-02	1.00	3.9E-01	0.8%	1.5E-06	21.1%	intron	
rs7134036	12	11076851	38.5%	4.7E-02	1.00	3.9E-01	0.8%	1.5E-06	21.1%	missense	
rs7134148	12	11076915	38.5%	4.7E-02	1.00	3.9E-01	0.8%	1.5E-06	21.1%	coding-synon	
rs2708380	12	11105479	38.5%	4.7E-02	1.00	4.7E-01	0.6%	2.8E-07	23.3%	intron	
NRC2023	12	11137838	38.5%	1.3E-02	1.00	6.2E-01	0.3%	9.5E-04	11.2%	intron	
rs6488334	12	11031711	39.1%	1.9E-05	1.00	7.2E-01	0.2%	4.3E-01	0.7%	intron	
rs10772418	12	11062010	39.1%	8.4E-02	1.00	3.9E-01	0.8%	1.9E-06	20.7%	intron	neutral
rs2597985	12	11092754	39.1%	8.4E-02	1.00	4.0E-01	0.8%	7.4E-07	22.0%	intron	
rs2044826	12	11099773	39.1%	8.4E-02	1.00	4.0E-01	0.8%	7.4E-07	22.0%	missense	neutral
rs2597997	12	11099817	39.1%	8.4E-02	1.00	4.0E-01	0.8%	7.4E-07	22.0%	missense	
NRC1005	12	11137826	40.2%	1.3E-04	1.00	6.5E-01	0.2%	3.3E-04	12.9%	coding-synon	
rs2599395	12	11143746	40.2%	1.9E-03	1.00	4.5E-01	0.6%	3.8E-07	22.9%	coding-synon	
rs10772420	12	11065543	40.8%	4.6E-03	1.00	3.5E-01	1.0%	1.1E-06	21.5%	coding-synon	
rs10845293	12	11074522	40.8%	4.6E-03	1.00	3.5E-01	1.0%	1.1E-06	21.5%	intron	
rs2443093	12	11142160	41.4%	1.0E-02	1.00	3.6E-01	1.0%	5.4E-07	22.4%		
rs2600335	12	11143187	41.4%	1.0E-02	1.00	3.6E-01	1.0%	5.4E-07	22.4%		
NRC1108	12	11121486	42.0%	6.7E-01	1.00	4.1E-01	0.8%	1.6E-03	10.3%		
NRC227	12	11135457	42.0%	2.9E-01	1.00	2.4E-01	1.6%	3.7E-06	19.8%	intron	
NRC55	12	11135416	43.1%	9.2E-01	1.00	3.0E-01	1.2%	1.8E-02	6.0%	intron	
NRC321	12	11121437	44.8%	3.6E-01	1.00	4.4E-01	0.7%	6.6E-04	11.8%		
rs10772408	12	11042866	48.3%	6.6E-01	1.00	8.8E-02	3.2%	5.2E-01	0.5%	intron	
NRC2130	12	11117757	48.9%	2.2E-02	1.00	1.3E-01	2.6%	3.4E-03	9.0%	utr-3	neutral
NRC1656	12	11121670	49.4%	1.4E-03	1.00	3.7E-01	0.9%	2.9E-03	9.3%		
rs6488335	12	11031750	50.0%	4.9E-02	1.00	1.5E-01	2.3%	1.0E-03	11.1%	intron	
NRC1312	12	11121636	50.0%	4.9E-04	1.00	2.5E-01	1.5%	4.1E-03	8.7%	intron	