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Supplementary information

Ancient genomes reveal insights into ritual life at Chichén Itzá

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Ancient genomes reveal insights into ritual life at Chichén Itzá

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Supplementary Material

Supplementary text: Archaeological context of Chichén Itzá.

Contact researchers: Rodrigo Barquera, Oana del Castillo-Chávez, Kathrin Nägele, Patxi Pérez-Ramallo, Diana Iraíz Hernández-Zaragoza, and Christina Warinner.

Chichén Itzá became the dominant political centre of the northern Maya lowlands during the Terminal Classic (AD 800-1000), a period characterized by long-distance political and social connections – first to the Puuc Maya in the western Yucatan and later to the city of Tula in Central Mexico; the latter being associated with an ambitious new building program in an architectural style variously described as "International" or "Toltec"[1,2]. *El Castillo*, also known as the Temple of Kukulkán because of the elaborately carved feathered serpent columns adorning its façade, the massive pyramidal structure was constructed in a foreign Central Mexican style honouring the mythical ruler or deity Quetzalcoatl (known as K'uk'ulkan in Mayan), and other distinctive architecture from this period such as colonnades, a large ballcourt and structures explicitly associated with ritual sacrifice[3,4], including a *tzompantli* (skull rack) and anthropomorphic stone sculptures known as *chacmools*.

Evidence of ritual killing is extensive throughout the site of Chichén Itzá, and includes both the physical remains of sacrificed individuals, as well as representations in monumental art[5]. Elite activity at Chichén Itzá declined during the 11th century AD, with a last inscribed calendar date of AD 998[6,7], but the site continued to be a prominent ritual and pilgrimage centre through the colonial period and beyond[8–10]. Male adult crania obtained through ritual violence have been found adorning buildings at Chichén Itzá's Las Monjas complex and along the platform of the Caracol structure, as well as at later sites under Itzá control, such as Ixlú, where shared dental traits suggest at least some of these males were related[11].

Situated on a karst plain in one of the most densely settled regions of the Maya lowlands[12], Chichén Itzá enjoyed ready access to fertile agricultural lands and the resource-rich coastal zone[7], as well as abundant water from its extensive system of *cenotes* (sinkholes), *aguadas* (rainwater reservoirs), and human-made *chultunes* (underground cisterns)[1,13,14]. Throughout Mesoamerica, caves, cenotes, and chultunes have long been associated with water, rain, and child sacrifice[15–17], and such subterranean features are widely viewed as access points to the Maya underworld[18,19]. The chultún analysed in the present work was discovered adjacent to a small structure, perhaps an altar, when a local airstrip was built in the 1960s. Over one hundred human individuals were excavated from the chultún, which was constructed as an artificial cave in the shape of a bottle[15,20].

Supplementary methods: Stable isotopes analyses.

Contact researchers: Patxi Pérez-Ramallo, Adam Benjamin Rohrlach, Mary Lucas, Christina Warinner and Patrick Roberts.

The reconstruction of past human and faunal diets using stale carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope analysis is common and well-established in multidisciplinary archaeological research[21], with its application extending back to the 1970s[22,23]. Direct insights into dietary trends among past populations enables the investigation of connections between diet and social status, cultural customs linked to food, environmental impacts on subsistence, and individual mobility during the course of their life history[24,25]. Bone collagen $\delta^{13}C$ and $\delta^{15}N$ measurements primarily reflect the protein component of an individual's diet during the period of tissue formation and, to a lesser extent, the lipid and carbohydrate sources[26].

The $\delta^{13}C$ variability in terrestrial ecosystems is driven by differences in the two dominant photosynthetic pathways with regards to their discrimination against ^{13}C during CO_2 fixation[27]. C_3 plants (e.g., trees, shrubs, or wheat) have lower $\delta^{13}C$ values ranging from c. -24 to -36‰ (global mean -26.5‰). By contrast, C_4 plants (e.g., maize, millet, sugar cane, or sorghums) have higher $\delta^{13}C$ values, oscillating between c. -9 to -17‰ (global mean -12‰)[27–29]. The $\delta^{13}C$ values of marine plants, which draw CO_2 from a different source, sit towards the range of C_4 plants, while crassulacean acid metabolism (CAM) plants (e.g., succulents) occupy an intermediate position[30,31]. These distinctions are tracked into the tissues of consumers of these plants with an enrichment in $\delta^{13}C$ of approximately 5‰ between dietary plants and consumers, 1-2‰ in subsequent trophic level steps among omnivores and carnivores[21].[13]

Trophic level plays a major role in the variation of $\delta^{15}N$ values measured for animals in both terrestrial and aquatic ecosystems. $\delta^{15}N$ increase of between +3-6‰ from plants to herbivores, and from herbivores to carnivores have been observed in a variety of different ecological settings[30,32]. This trophic effect is most likely linked to the disproportionate loss of ^{15}N-depleted excretion products at each stage in the foodchain[33], although diet-tissue distinctions are highly variable between animals[34]. Marine consumers are, on average, higher in $\delta^{15}N$ compared with terrestrial consumers as a result of longer foodchains and different sources of nitrogen. Meanwhile freshwater consumers often demonstrate higher $\delta^{15}N$ although $\delta^{13}C$ is far more variable[35,36].

Here, we analysed bone collagen from the temporal and petrous bone used to conduct the radiocarbon dating and aDNA analysis on individuals sampled in this study. The samples analysed consisted of approximately 1 g of bone. Collagen was then extracted using a standard procedure[37]. The bone fragments were demineralized in 10 mL aliquots of 0.5M HCl at 4°C. The acid was changed until CO_2 stopped evolving. The residue was rinsed three times in deionized water before being gelatinized in pH 3 HCl at 75°C for 48 hours. The resulting solution was filtered, with the supernatant then being lyophilised over a period of 24 hours. After calculating the collagen yield for each sample, 0.5 mg of purified collagen sample were weighed into tin capsules to be analysed in duplicate, using a Thermo Fisher Elemental

Analyzer (Thermo Fisher Scientific Inc., Waltham, Massachusetts, U.S.) coupled to a Thermo Fisher Delta V Advantage Mass Spectrometer (Thermo Fisher Scientific Inc., Waltham, Massachusetts, U.S.) via a ConFlo IV system (Thermo Fisher Scientific Inc., Waltham, Massachusetts, U.S.) at the Max Planck Institute of Geoanthropology (formerly for the Science of Human History), Jena, Germany.

Isotopic values are reported as the ratio of the heavier isotope to the lighter isotope ($^{13}C/^{12}C$ or $^{15}N/^{14}N$) as δ values in parts per mill (‰) relative to international standards, Vienna Pee Dee Belemnite (VPDB) for $\delta^{13}C$ and atmospheric N_2 (AIR) for $\delta^{15}N$. Results were corrected using a two-point calibration against international standards (IAEA-CH-6 Sucrose, IAEA-N-2 Ammonium Sulphate and USGS40 L-Glutamic Acid); USGS40 $^{13}C_{raw}$ = -26.4 ± 0.1, $^{13}C_{true}$ = -26.4 ± 0.0, $^{15}N_{raw}$ = -4.4 ± 0.1, $^{15}N_{true}$ = -4.5 ± 0.2; IAEA N2 $^{15}N_{raw}$ = 20.2 ± 0.1, $^{15}N_{true}$ = 20.3 ± 0.2; IAEA C6 $^{13}C_{raw}$ = -10.9 ± 0.1, $^{13}C_{true}$ = -10.8 ± 0.0. Replicate analyses of standards suggest that machine measurement error is c. ± 0.2‰ for $\delta^{13}C$ and ± 0.1‰ for $\delta^{15}N$. Overall measurement precision was studied through the measurement of repeat extracts from a fish gelatine standard (n=20, ± 0.1‰ for $\delta^{13}C$ and ± 0.1‰ for $\delta^{15}N$).

The bioarchaeological results obtained from the human sacrifices discovered in the Midnight Terror cave in Belize[38] suggest that the Classic Maya preferred to select outsiders for sacrifice rather than locals. The observed standard deviation of the $\delta^{15}N$ values (SD=1.5) obtained from the individuals analysed at Chichén Itzá (Fig. S3) is the highest of all the Late Classic and Terminal Classic Maya sites analysed to date (see Table S1 and Fig. S4). The overall picture from the reconstruction of palaeodiet in this study reveals the consumption of significant amounts of maize, but with geographic variations reflected in microenvironmental differences in available foods and variability in trade networks[39,40]. Perhaps, as in the case of the Midnight Terror Cave, most of the individuals sacrificed at Chichén Itzá were non-local Maya. On the other hand, other studies have shown that the diet of the Classic Maya elite tends to be more variable than that of the general population over time[41], reflected also in $\delta^{13}C$ and $\delta^{15}N$ standard deviations observed elsewhere (e.g., Altun Ha or Baking Pot; see Table S1 and Fig. S4). Therefore, the differences in protein intake observed in the Chichén Itzá individuals studied could also indicate variations in social status.

Randomisation tests for isotope values for related vs. unrelated individuals

To test the difference between $\delta^{15}N$ and $\delta^{13}C$ values for the related and unrelated individuals, we began by calculating the pairwise differences in the values for all pairs, denoted n_{ij} and c_{ij}, respectively. We then calculated the observed W-statistic from a Wilcoxon Rank Sum test, denoted W_N and W_C. Due to the repeated measures inherent in comparing pairwise values, the assumption of independence between samples was not satisfied. Hence, we performed randomisation tests by randomly reassigning the *related* and *unrelated labels,* and reperforming and recalculating the W-statistic (for 100,000 replications, seed=12345). We then calculated a two-sided empirical *p*-value[42] for both W_N and W_C.

We found that both of the average $\delta^{15}\mathrm{N}$ and $\delta^{13}\mathrm{C}$ values were significantly lower for the related group when compared to the unrelated group ($p = 0.00439$ and $p = 0.00212$, respectively) indicating that related individuals share more similar $\delta^{15}\mathrm{N}$ and $\delta^{13}\mathrm{C}$ values than would be expected by random chance.

Table S1. Collagen $\delta^{15}N$ (‰) and $\delta^{13}C$ (‰) data and radiocarbon determinations calibrated using OxCal. v4.4.4 and the IntCal20 atmospheric curve[43].

Sample name	Radiocarbon years BP	Calibrated calendar date (AD, 95.4%)	MAMS reference	$\delta^{15}N$ (‰) (Air)	$\delta^{13}C$ (‰) (VPDB)	%N	%C	C/N ratio
YCH063	1437±17	595-650	35832	9.6	-10.2	13.10	36.12	3.2
YCH037	1289±22	665-775	35824	9.7	-8.9	13.49	37.15	3.2
YCH007	1228±22	700-885	35811	5.9	-9.0	14.66	42.70	3.4
YCH036	1224±22	700-885	35823	11.8	-9.1	15.36	42.33	3.2
YCH060	1210±17	770-885	35831	8.2	-9.0	15.16	41.29	3.2
YCH056	1198±23	770-895	35829	10.4	-13.4	15.13	43.90	3.4
YCH018	1188±24	770-945	35816	8.4	-9.9	15.09	42.68	3.3
YCH030	1178±22	770-950	35820	8.3	-8.9	15.63	43.21	3.2
YCH003	1177±24	770-950	35810	8.5	-9.7	12.67	35.58	3.3
YCH034	1157±23	770-980	35822	9.6	-9.2	15.54	42.91	3.2
YCH024	1157±21	770-980	35818	10.1	-13.3	14.92	41.93	3.3
YCH001	1156±22	770-980	35808	-	-10.5	-	-	3.2
YCH002	1154±21	770-980	35809	8.1	-10.4	14.91	43.09	3.4
YCH048	1144±23	770-990	35826	10.9	-9.1	15.60	43.06	3.2
YCH033	1100±22	890-995	35821	10.0	-8.1	13.32	38.80	3.4
YCH011	1098±21	890-995	35813	10.5	-8.1	14.26	40.90	3.3
YCH054	1091±23	890-1020	35828	10.1	-7.6	14.45	41.70	3.4
YCH016	1083±23	890-1025	35815	9.9	-9.5	14.57	40.73	3.3
YCH020	1070±24	895-1025	35817	9.1	-11.2	15.44	42.29	3.2
YCH040	1065±23	895-1025	35825	8.2	-10.3	13.66	40.01	3.4
YCH058	1060±22	995-1030	35830	11.2	-9.5	15.05	42.00	3.3
YCH012	1058±23	895-1030	35814	8.4	-9.3	15.94	43.28	3.2
YCH010	1054±23	895-1030	35812	11.3	-8.4	14.42	41.23	3.3
YCH027	1044±21	975-1035	35819	9.2	-8.5	16.26	44.16	3.2
YCH051	970±17	1025-1155	56233	8.2	-9.3	15.72	43.54	3.2
YCH004	-	-	-	12.1	-11.5	15.67	43.41	3.2
YCH005	-	-	-	8.6	-9.8	13.22	38.58	3.4
YCH006	-	-	-	8.4	-9.1	15.70	43.14	3.2
YCH008	-	-	-	12.1	-10.9	13.78	39.40	3.3
YCH009	-	-	-	8.9	-10.7	14.91	40.79	3.2
YCH015	-	-	-	8.5	-7.9	14.12	40.18	3.3
YCH017	-	-	-	9.6	-9.2	9.97	28.90	3.4
YCH022	-	-	-	9.9	-13.0	6.69	20.84	3.6
YCH023	-	-	-	12.2	-11.2	12.61	38.64	3.6
YCH025	-	-	-	10.4	-8.0	11.43	31.29	3.2
YCH029	-	-	-	10.6	-9.5	13.88	38.69	3.3
YCH031	-	-	-	9.4	-8.2	15.87	44.58	3.3

Sample name	Radiocarbon years BP	Calibrated calendar date (AD, 95.4%)	MAMS reference	$\delta^{15}N$ (‰) (Air)	$\delta^{13}C$ (‰) (VPDB)	%N	%C	C/N ratio
YCH032	-	-	-	14.0	-10.5	15.16	42.85	3.3
YCH038	-	-	-	10.6	-10.5	8.37	23.81	3.3
YCH039	-	-	-	11.7	-11.9	14.01	38.35	3.2
YCH041	-	-	-	9.5	-9.4	13.68	38.38	3.3
YCH042	-	-	-	8.8	-8.5	12.04	35.85	3.5
YCH043	-	-	-	8.4	-8.8	14.31	41.14	3.4
YCH045	-	-	-	11.4	-8.9	14.54	40.23	3.2
YCH046	-	-	-	8.6	-13.9	13.79	40.47	3.4
YCH047	-	-	-	11.0	-12.1	9.99	28.61	3.3
YCH049	-	-	-	8.0	-9.1	13.15	36.48	3.2
YCH050	-	-	-	9.8	-10.9	13.69	40.09	3.4
YCH053	-	-	-	8.6	-10.5	10.75	29.84	3.2
YCH055	-	-	-	9.3	-7.6	15.44	43.48	3.3
YCH059	-	-	-	8.4	-10.2	10.56	29.84	3.3
YCH061	-	-	-	11.1	-11.6	12.51	34.43	3.2
YCH062	-	-	-	11.1	-10.8	5.97	17.37	3.4
YCH064	-	-	-	9.8	-9.3	12.97	36.17	3.3

MAMS: Radiocarbon Lab, CEZA, Mannheim, Germany laboratory number; AMS: accelerator mass spectrometry. BP: before present.

Table S2. Collagen $\delta^{15}N$ and $\delta^{13}C$ mean values, SD, and number of samples for Late and Terminal Classic Maya individuals, excluding those potentially influenced by breastfeeding**.** Original citations to published studies are provided in the column "Reference".

Site	n	$\delta^{13}C$ (‰) (VPDB)	SD	n	$\delta^{15}N$ (‰) (Air)	SD	Reference
Chichén Itzá	53	-9.9	1.5	53	9.7	1.5	Present Study
Aguateca	5	-9.9	0.7	4	9.1	0.9	[44]
Altar de Sacrificios	22	-8.9	1.1	22	8.8	1.1	[44]
Altun Ha	47	-11.9	2.0	47	10.4	0.6	[45]
Baking Pot	9	-11.0	1.1	9	9.2	1.3	[46]
Barton Ramie	31	-11.2	1.2	31	8.9	0.4	[46]
Cahal Pech	9	-10.0	1.7	9	9.5	0.8	[47–49]
Caledonia	22	-9.9	1.9	22	9.1	1.1	[50]
Caracol	14	-9.6	1.3	14	9.3	1.1	[49]
Chac Balam	10	-8.5	1.5	10	11.5	0.7	[51]
Chau Hiix	18	-12.0	1.9	18	10.9	0.8	[52]
Chinikihá	7	-9.9	0.4	7	9.1	0.8	[53]
Copán	16	-10.0	1.0	15	7.6	0.7	[46]
Copán Valley	23	-10.3	0.8	22	7.5	0.8	[46]
Dos Pilas	19	-9.1	1.0	19	9.6	1.1	[44]
Holmul	2	-9.0	0.0	2	9.1	0.4	[46]
Itzán	4	-9.2	0.4	4	8.1	1.0	[44]
Lamanai	10	-14.8	1.1	8	10.0	0.4	[54]
Lower Dover	1	-11.9	-	1	10.6	-	[49]
Marco González	31	-7.9	1.3	31	10.2	1.1	[55]
Mayapán	68	-9.8	0.7	68	8.6	0.5	[56,57]
Minanha	24	-10.9	1.7	24	9.0	0.8	[58]
Pacbitun	19	-10.3	1.6	19	9.3	0.7	[49,59]
Peligroso (Chalillo)	1	-10.4	-	1	10.4	-	[49]
Piedras Negras	35	-9.2	0.8	35	8.9	0.9	[60]
Pook's Hill	6	-11.4	0.7	6	8.4	0.3	[49]
Ramonal (Chalillo)	1	-11.1	-	1	8.9	-	[49]
San Juan	3	-8.6	0.2	4	11.1	1.0	[51]
San Lorenzo	1	-12.2	-	1	9.5	-	[49]

Site	n	$\delta^{13}C$ (‰) (VPDB)	SD	n	$\delta^{15}N$ (‰) (Air)	SD	Reference
San Pedro	20	-6.8	1.1	20	9.7	0.5	[55]
Seibal	26	-9.6	1.4	26	9.3	1.0	[46]
Uaxactún	5	-10.3	0.9	5	9.4	1.0	[46]
Xunantunich	6	-10.8	1.8	6	9.7	0.9	[49,50]
Yaxuná	2	-12.4	0.8	2	7.0	0.5	[61]

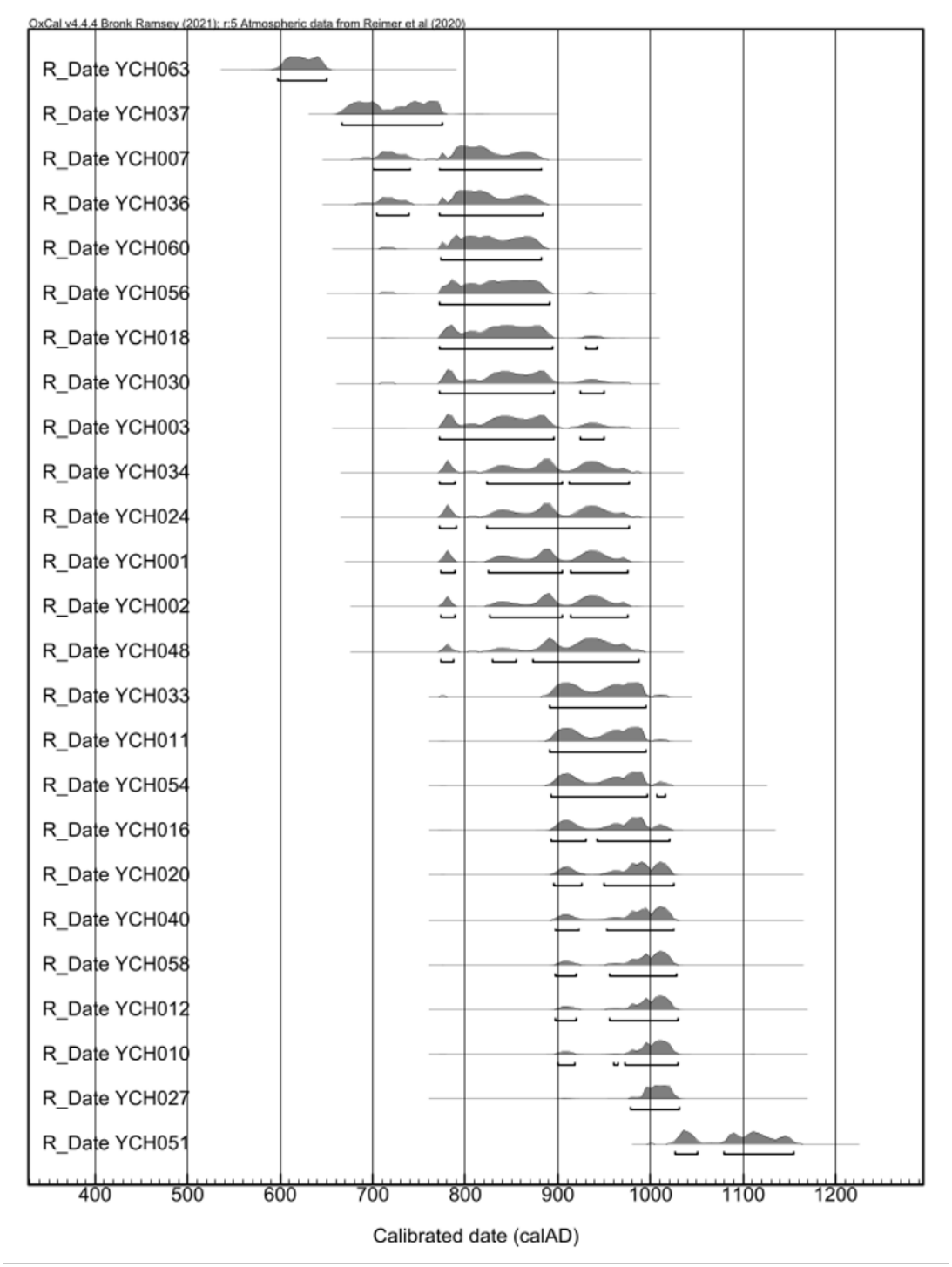

Figure S1. Radiocarbon dating results calibrated using OxCal. v4.4.4[62], and the IntCal20 atmospheric curve[43].

Supplementary methods: Genetic pairwise mismatch rate and genetic kin relationships.

Contact researchers: Rodrigo Barquera, Kathrin Nägele, Adam Benjamin Rohrlach and Christina Warinner.

We employed a method for statistically testing the genetic relatedness between individuals called BREADR (v.1.0.1) to estimating the pairwise-mismatch rate PMR for a pair of individuals based on the assumption of a binomial distribution for the PMR, for pseudo-haploid data, available. Here, for individuals *i* and *j*, we thinned the data such that all sites were at least 200K bases apart to best satisfy the assumption of independence. We also used the median PMR as a baseline for the expected PMR of two unrelated individuals. For a full description of the method, see Rohrlach et al., 2023[63].

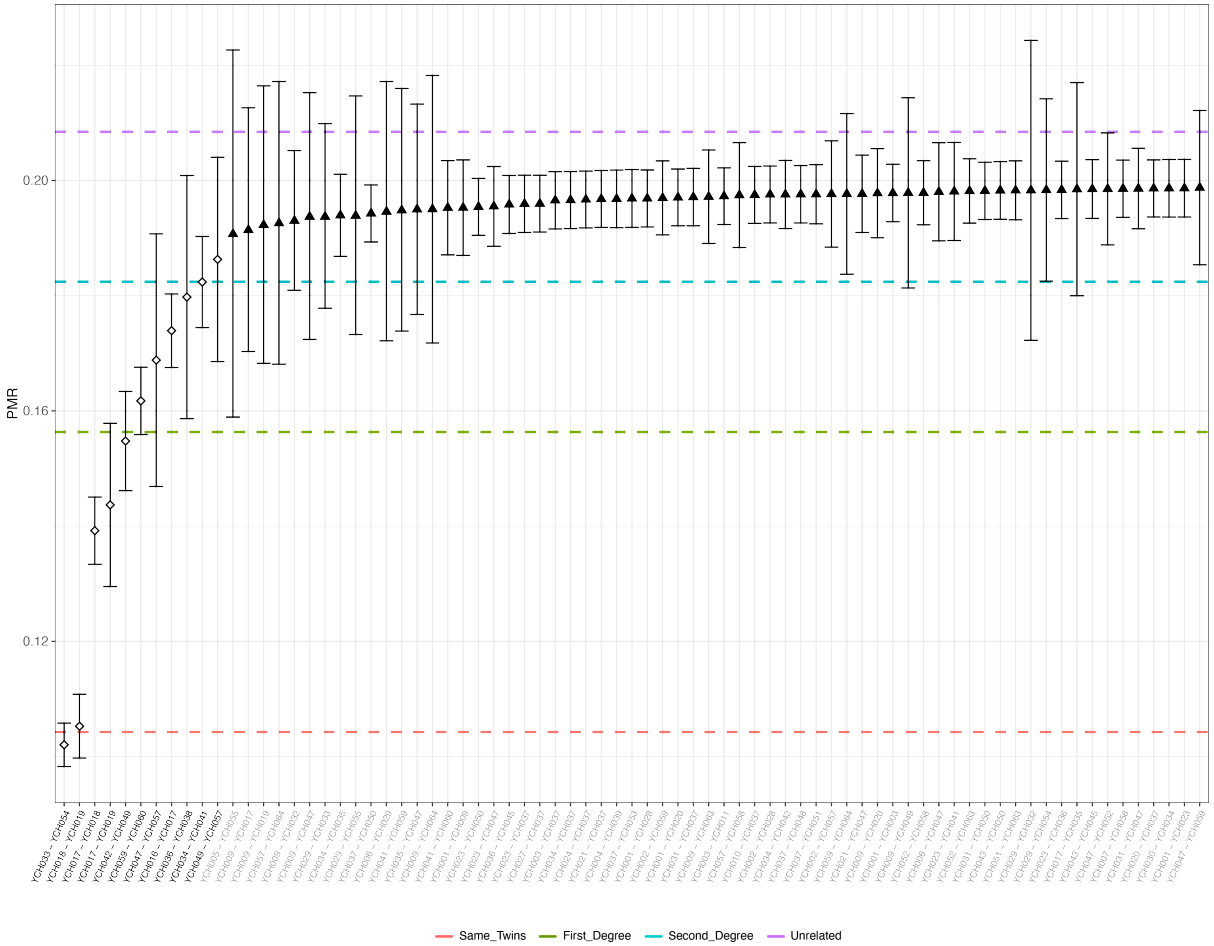

Figure S2. Genetic pairwise mismatch rate (PMR) for child pairs within the chultún identifies eleven close relative pairs (hollow diamonds, black text), including two pairs of monozygotic twins. A low overall PMR for unrelated individuals (black triangles, grey text) confirms low genetic diversity in the population; only pairs with a PMR significantly <0.20 are visualized in the plot.

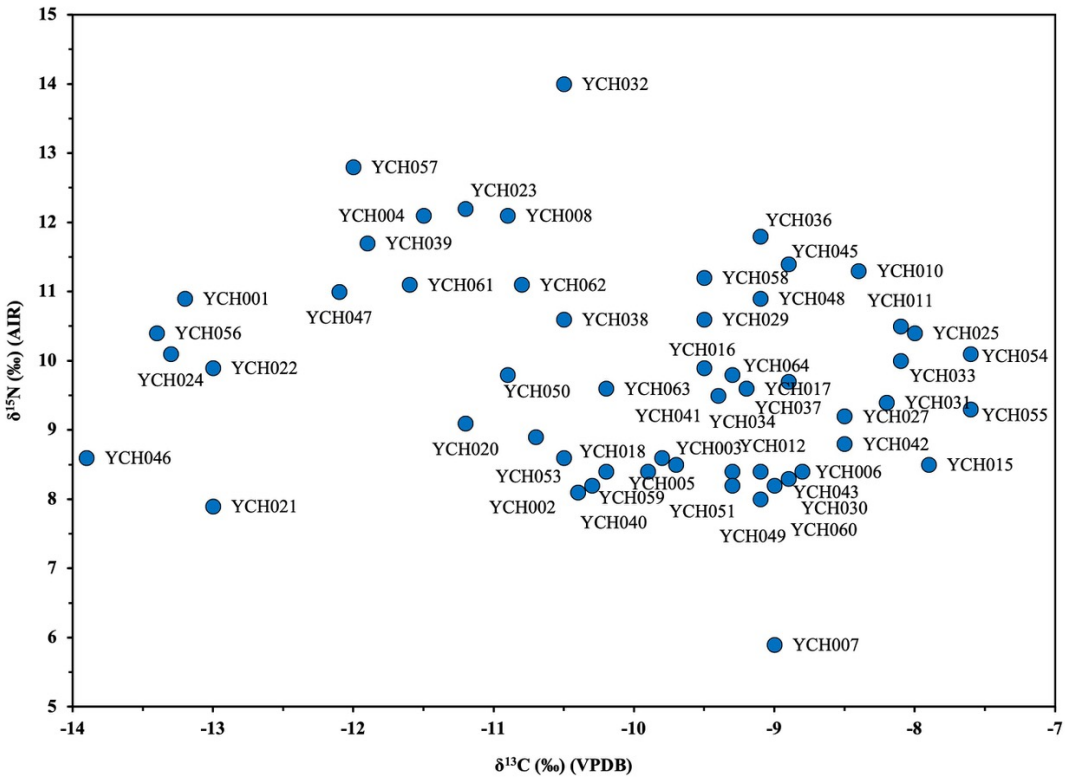

Figure S3. Enhanced view of human bone collagen isotopic $\delta^{13}C$ and $\delta^{15}N$ values from the present study.

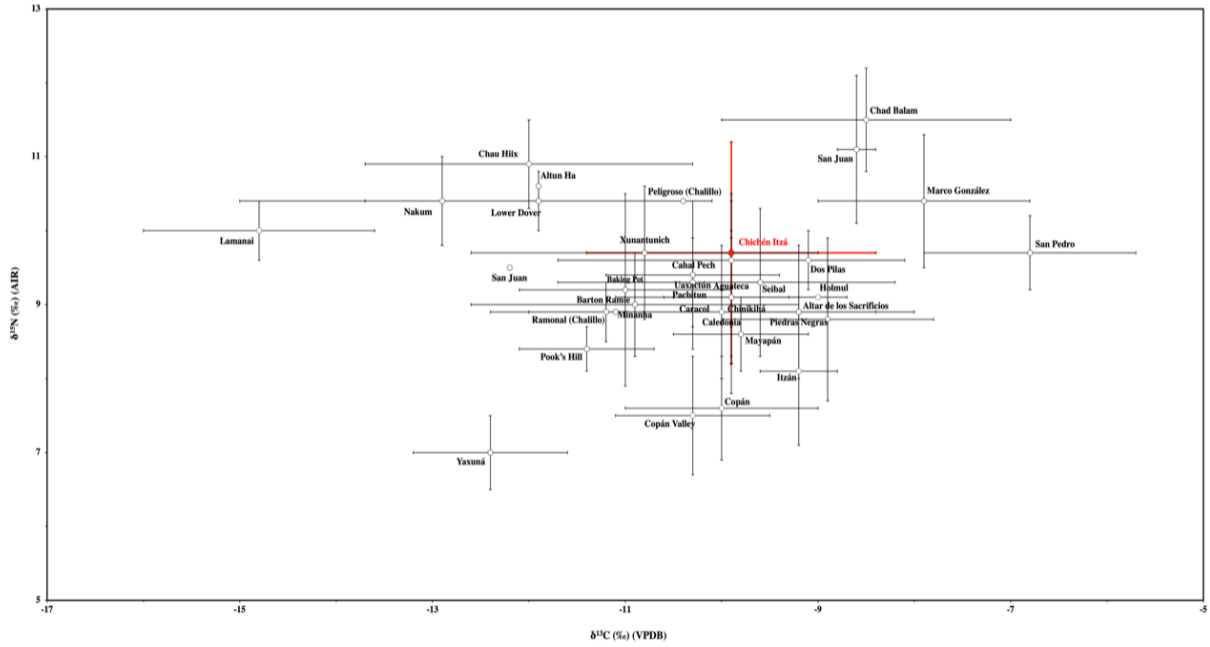

Figure S4. Collagen $\delta^{13}C$ and $\delta^{15}N$ mean values and SD for Late and Terminal Classic Maya from the present study and other Maya populations. See Table S2 for citations.

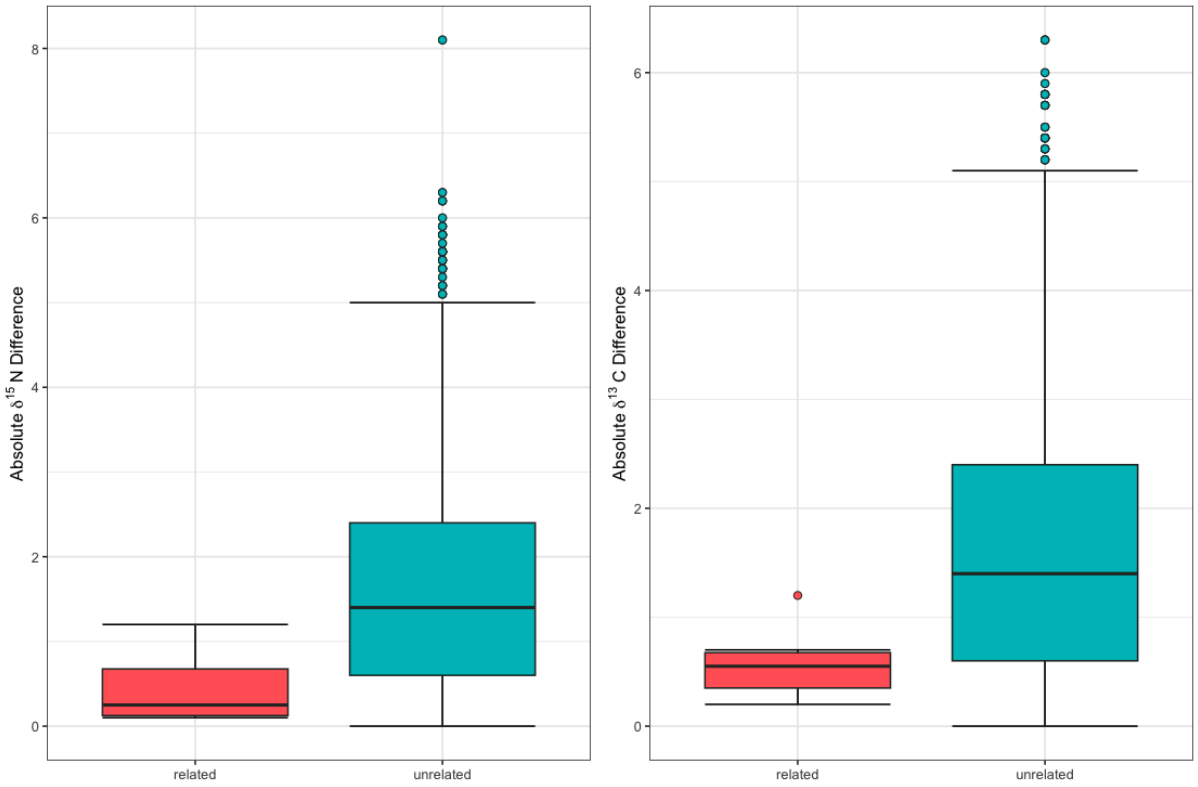

Figure S5. Difference between $\delta^{15}N$ and $\delta^{13}C$ values for the related and unrelated individuals found in the chultún.

Supplementary methods: Preparation of single stranded libraries.

Contact researchers: Rodrigo Barquera & Raffaela Angelina Bianco.

We built single-stranded, UDG-half treated libraries using a protocol implemented for the automated library preparation[64,65] on the Bravo-B NGS Workstation (Agilent Technologies, Inc., Santa Clara CA, USA) for the extracts for which not enough data could be obtained from the double-stranded, UDG-half treated libraries. Briefly, DNA fragments present in the extract are dephosphorylated at the 5′ and 3′ ends and separated into single strands by heat denaturation. 3′-biotinylated adapter molecules are attached to the 3′ ends of the DNA fragments using T4 DNA ligase and a splinter oligonucleotide carrying a stretch of six random nucleotides (marked as "N"). Following the immobilization of the ligation products on streptavidin-coated beads, the splinter oligonucleotide is removed by a bead wash at elevated temperature. Synthesis of the second strand is carried out using the Klenow fragment of *Escherichia coli* DNA polymerase I. Not incorporated primers are removed through a bead wash at elevated temperature. Following the blunt-end ligation of the second adapter, the final synthesised strand is released from the beads by heat denaturation.

Supplementary methods: Genetic continuity testing.

Contact researchers: Rodrigo Barquera, Pablo Librado & Adam Benjamin Rohrlach.

In order to formally assess whether TIX descends from CHI, we employed the direct ancestry test developed by J. Schraiber[66]. To prepare the input file as required, we began by mapping the sequence data from the YCH and TIX individuals to the *Pan troglodytes* reference genome (release: GCF_028858775.1-RS_2023_03)[67], to polarise the alleles as ancestral or derived. We then calculated the allele frequencies for chromosomes 1-22 for the TIX individuals, and the allele counts for the YCH and TIX individuals, using angsd[68] with -minQ 20. We then took the set of all 664,145,998 genomic sites covered by the YCH and TIX individuals and filtered these such that the site was covered by at least two individuals from YCH, were covered by at least 50 from TIX, and such that the site was not at fixation for TIX. This yielded a total of 23,904,864 sites which were analysed for continuity, 930,464 of which representing nucleotide transversions that segregated at MAF > 1%. Using this subset of genomic sites, we then produced genotype data using Plink[69] on the filtered genomic sites from above. The second step focused then on the ancient YCH specimens, to compute the number of reads that support each allele, at these specific 930,464 positions (-doCounts 1 and -dumpCounts 4). These read counts were subsequently categorized, for each SNP and YCH individual, as derived, ancestral or other allele. All SNPs showing an abnormal sequencing depth were filtered out (95% confidence interval), following the recommendation of the developer (possibly representing hidden structural variation). This last filter yielded a final panel of 883,941 high-quality nucleotide transversions, a SNP set representing an excellent trade-off between SNP quality and density, especially when considering that the method assumes linkage equilibrium and pruning is recommended. Using in-house scripts, the results from both steps were finally merged, and formatted according to the specifications.

Based on this input file, we next contrasted two competing population models: the null hypothesis assumes that YCH and TIX are the same population evolving over time (direct ancestry model), while the alternative one posits that YCH was instead sister to the true ancestral population (ancient but not ancestral model). The likelihood of both models and the underlying parameters were found indistinguishable, for each individual, and consequently the likelihood ratio tests returned *p*-values close to one. The null hypothesis of genetic continuity, therefore, cannot be rejected. Given the high sensitivity of this test, these results establish that TIX unequivocally descends from YCH.

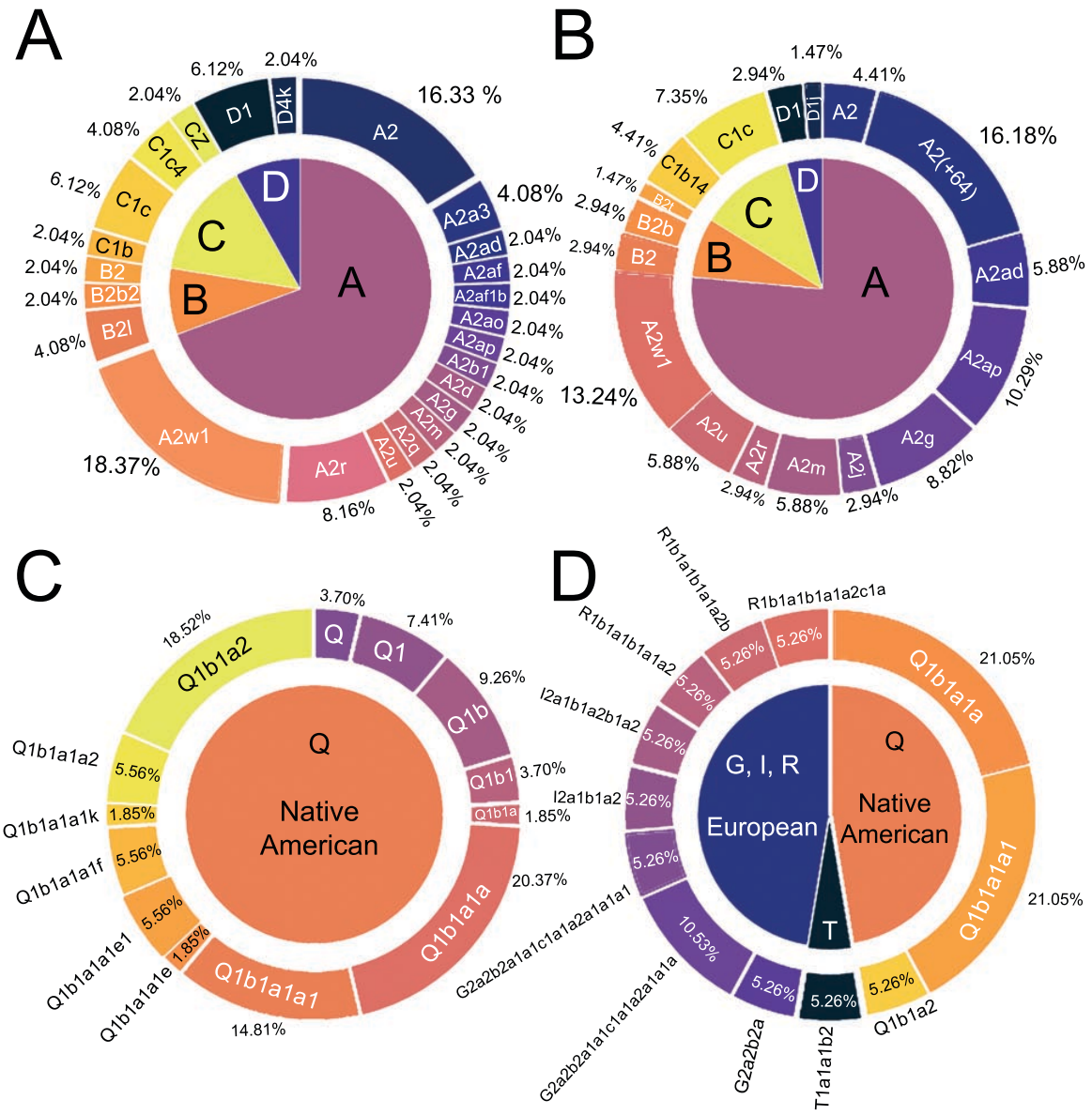

Figure S6. The diversity of uniparental markers in ancient Mayans from Chichén Itzá (YCH) and present-day Mayans from Tixcacaltuyub (TIX). **A.** Mitochondrial DNA (mtDNA) diversity in YCH. Inner circle represents the proportions of each of the main haplogroups found in the YCH group (N=64). Outer circle represents the high resolution mtDNA haplogroup diversity found in this group. **B.** The diversity of mtDNA lineages in TIX. Inner circle represents the proportions of each of the main haplogroups found in the TIX group (N=68). Outer circle represents the high resolution mtDNA haplogroup diversity found in this group. **C.** Y chromosome (Y-Chr) diversity in YCH. Inner circle represents the family of Y-Chr lineages found in the YCH group (N=64; they all belonged to haplotype Q). Outer circle represents the highest resolution available for the Y-Chr diversity found in this group. **D.** The diversity of Y-Chr haplogroups in TIX. Inner circle represents the proportions of each of the main continental origin for the Y-Chr haplotype lineages found in the TIX group (N=19). Outer circle represents the highest resolution available for the Y-Chr diversity found in this group. For the individual mtDNA and Y-Chr genotypes, please refer to Tables S9 & S10.

Table S3. Top lipid metabolism-associated genes for YCH.

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
rs988832	1	formin 2	FMN2	Body Mass Index	FMN2	
rs7542755	1	NULL	NULL	Body Mass Index, Lithium clearance adjusted for clinical predictors	COX6A1P1, RPL7P10	
rs1805152	1	chloride voltage-gated channel Ka	CLCNKA	Cholesterol, ClinVar: phenotype not specified, Bartter disease type 4B	CLCNKA, LOC106501712, CLCNKA	benign
rs7517847	1	interleukin 23 receptor	IL23R	Inflammatory Bowel Diseases, Plasma omega-6 polyunsaturated fatty acid levels (linoleic acid), Crohn's disease vs rheumatoid arthritis ordinary least squares OLS, Crohn's disease, Chronic inflammatory diseases (ankylosing spondylitis Crohn's disease psoriasis primary sclerosing cholangitis ulcerative colitis) (pleiotropy)	IL23R	
rs10925809	1	NULL	NULL	Lipoproteins	RPL39P10, CHRM3	
rs17321999	2	LBH regulator of WNT signaling pathway	LBH	Apolipoprotein A1 levels, Systemic lupus erythematosus	LBH	
rs1864430	2	interferon induced with helicase C domain 1	IFIH1	Cholesterol	IFIH1	
rs10490002	2	WD repeat, sterile alpha motif and U-box domain containing 1	WDSUB1	Cholesterol HDL	WDSUB1	
rs2118507	2	NULL	NULL	Cholesterol LDL	BIN1, CYP27C1	
rs6706926	2	fibroblast activation protein alpha	FAP	Cholesterol, Echocardiography	FAP	
rs2338545	2	phospholipase B1	PLB1	Diabetes mellitus type 2	PLB1	
rs4404290	2	NULL	NULL	Triglycerides	GLULP6, SLC39A10	
rs10199914	2	NULL	NULL	Triglycerides	intergenic	
rs1371555	2	NULL	NULL	Triglycerides	GLULP6, SLC39A10	
rs2419407	2	NULL	NULL	Waist-hip ratio		
rs10488961	4	calcium/calmodulin dependent protein kinase II delta	CAMK2D	Body Mass Index	CAMK2D	
rs1363396	5	NULL	NULL	Body Mass Index	PRR16, RPL23AP44	
rs6580146	5	NULL	NULL	Body Mass Index	KIF4B,P PIGP1	
rs162307	5	NULL	NULL	Cholesterol LDL	FAM170A, PRR16	
rs1822489	5	MCC regulator of WNT signaling pathway	MCC	Gamma glutamyl transferase levels, Waist-hip ratio		
rs1432723	5	NULL	NULL	Obesity-related traits	SGCD	
rs9275393	6	NULL	NULL	Cholesterol total		
rs9275371	6	NULL	NULL	Cholesterol total		
rs9275418	6	NULL	NULL	Cholesterol total		

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
rs2293289	6	1-acylglycerol-3-phosphate O-acyltransferase 4	AGPAT4	Lipoprotein (a) - cholesterol levels	AGPAT4	
rs1488	6	mitogen-activated protein kinase kinase kinase 4	MAP3K4	Lipoproteins	MAP3K4	
rs10952650	7	contactin associated protein 2	CNTNAP2	Diabetes Mellitus	CNTNAP2	
rs2971760	7	NULL	NULL	Type 2 diabetes		
rs4737384	8	staufen double-stranded RNA binding protein 2	STAU2	Body Mass Index, Body Weight Changes	RDH10,STAU2	
rs2169385	8	NULL	NULL	Cholesterol total, High-density lipoprotein cholesterol		
rs12546198	8	NULL	NULL	Cholesterol total, High-density lipoprotein cholesterol, Cake icing liking		
rs4620259	8	NULL	NULL	LDL cholesterol levels	TRHR	
rs12546225	8	NULL	NULL	Waist-hip ratio	RPL26P26, UBXN2B	
rs3861048	10	NULL	NULL	Body Fat Distribution, Body Mass Index, Body Weight, Waist circumference	GAPDHP21, ZWINT	
rs10509165	10	NULL	NULL	Cholesterol HDL, Receptors Tumor Necrosis Factor Type II	ARID5B, RTKN2	
rs10509138	10	NULL	NULL	Cholesterol LDL	ANK3	
rs2393726	10	AT-rich interaction domain 5B	ARID5B	Serum metabolite levels	ARID5B	
rs2254069	10	NULL	NULL	Waist-hip ratio, Waist-to-hip ratio adjusted for BMI		
rs174601	11	fatty acid desaturase 2	FADS2	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	C11orf9, C11orf10,FEN1, FADS1,FADS2, RAB3IL1,DAG LA,BEST1	
rs174570	11	fatty acid desaturase 2	FADS2	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS2, FADS3	
rs174574	11	fatty acid desaturase 2	FADS2	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS2, FADS1	
rs11041816	11	NULL	NULL	Fasting blood glucose (BMI interaction), Fasting blood glucose	LMO1	
rs174583	11	fatty acid desaturase 2	FADS2	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS2, C11orf10, C11orf9,FADS1, FEN1, FADS3, FADS1	
rs174576	11	fatty acid desaturase 2	FADS2	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS2,FADS1, FADS3, FADS2,C11orf9, C11orf10,FEN1	
rs102275	11	transmembrane protein 258	TMEM258	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels,	C11orf10, FADS1,FADS2, FEN1FADS3, TMEM258, FTH1,INCENP,	

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
				Trans fatty acid levels, Triglycerides	SCGB2A1,SCGB1D1,SCGB2A2,RAB3IL1,AHNAK,C11orf9,DAGLA,SYT7,BEST1, MYRF	
rs174556	11	fatty acid desaturase 1	FADS1	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS1, FADS2	
rs1535	11	fatty acid desaturase 2	FADS2	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS2, FEN,FADS1, FADS3	
rs174546	11	fatty acid desaturase 1	FADS1	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS1, FADS2, FADS3	
rs174537	11	myelin regulatory factor	MYRF	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	C11orf9, MYRF,FADS1,FADS2,FADS3, FEN1	
rs174550	11	fatty acid desaturase 1	FADS1	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS1,FADS2, C11orf10,C11orf9,FEN1,RAB3IL1, FTH1,INCENP, FADS1,SCGB1D1,SCGB2A1,DAGLA,RAB3IL, FADS3,SYT7,BEST1,SCGB1D2, BEST1	
rs174535	11	myelin regulatory factor	MYRF	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	MYRF, C11orf9,C11orf10,FADS2,FADS1,FEN1	benign
rs174549	11	fatty acid desaturase 1	FADS1	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS2, FADS1,C11orf9, C11orf10,FEN1, FADS3	
rs174536	11	myelin regulatory factor	MYRF	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FEN1,FADS2,TMEM258,MYRF,C11orf9	benign
rs174547	11	fatty acid desaturase 1	FADS1	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS1,FADS2, FADS3, C11orf10,C11orf9,FEN1, FTH1,C11orf9,DAGLA,RAB3IL1,BEST1, FTH1,INCENP, SCGB2A1,SCGB1D1,SCGB2A2,AHNAK,SYT7,	

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
rs174541	11	NULL	NULL	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	VRK2,FANCL, FEN1,FADS1, C11orf10,C11orf 9,FADS2, FEN1, FADS3, MAP2	
rs174548	11	fatty acid desaturase 1	FADS1	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS1, FEN1, FADS2	
rs174450	11	fatty acid desaturase 3	FADS3	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS3	
rs108499	11	myelin regulatory factor	MYRF	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	MYRF	benign
rs174534	11	myelin regulatory factor	MYRF	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	MYRF	benign
rs174538	11	NULL	NULL	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	ALPK1,NEURO G2,C4orf21,LA RP7, TMEM258, C11orf10, MYRF,TMEM2 58,FEN1,FADS2 , FADS1	
rs7115739	11	fatty acid desaturase 3	FADS3	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides		
rs198462	11	myelin regulatory factor	MYRF	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides		
rs174448	11	NULL	NULL	Cholesterol total, High-density lipoprotein cholesterol, Red blood cell fatty acid levels, Fatty acid levels, Total cholesterol levels, Trans fatty acid levels, Triglycerides	FADS3	
rs2732494	12	NULL	NULL	Body Fat Distribution, Body Mass Index, Body Weight, Waist circumference	PGBD3P3,TME M132C	
rs7138792	12	NULL	NULL	Body Fat Distribution, Body Weight	PGBD3P3,TME M132C	
rs2701248	12	NULL	NULL	Body Fat Distribution, Body Weight	PGBD3P3,TME M132C	
rs10744625	12	NULL	NULL	Homeostasis model assessment of insulin resistance (dietary factor interaction), Fasting insulin (dietary factor interaction)	EFCAB4B,PAR P11	
rs7309378	12	G protein-coupled receptor 19	GPR19	Protein levels in obesity		
rs7989336	13	heparan sulfate 6-O-sulfotransferase 3	HS6ST3	Obesity	HS6ST3	

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
rs5008128	13	NULL	NULL	Waist circumference	KLF12	
rs3848	14	neuronal PAS domain protein 3	NPAS3	Body Composition, Body Mass Index	NPAS3	
rs1041857	14	NULL	NULL	Cholesterol HDL	SALL2,OR10G3	
rs10484197	14	MAM domain containing glycosylphosphatidylinositol anchor 2	MDGA2	Cholesterol LDL	MDGA2	
rs10518907	15	NULL	NULL	Body Weights and Measures	TCF12,CGNL1	
rs737008	16	protamine 1	PRM1	Obesity-related traits, ClinVar: phenotype not specified	PRM1	benign
rs9330248	17	acetyl-CoA carboxylase alpha	ACACA	Body Mass Index, Age at menopause	ACACA,	
rs9330248	17	NULL	NULL	Body Mass Index, Age at menopause	ACACA,	
rs797973	17	NULL	NULL	Type 2 diabetes		
rs12104221	19	NULL	NULL	Obesity-related traits	MATK	
rs138354	22	X-prolyl aminopeptidase 3	XPNPEP3	Apolipoprotein B levels	XPNPEP3	
rs733381	22	trinucleotide repeat containing adaptor 6B	TNRC6B	Body Mass Index, Waist-hip ratio		
rs2076674	22	solute carrier family 25 member 17	SLC25A17	Low density lipoprotein cholesterol levels	SLC25A17	

SNP: Single Nucleotide Polymorphism identifier; Chr: Chromosome number.

Table S4. Top lipid metabolism-associated genes for TIX.

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
rs11102002	1	EPS8 like 3	EPS8L3	Apolipoprotein B levels		
rs1165226	1	ubiquitin specific peptidase 24	USP24	Cholesterol total		
rs7551981	1	NULL	NULL	Cholesterol total		
rs11102002	1	EPS8 like 3	EPS8L3	Low density lipoprotein cholesterol levels		
rs1165226	1	ubiquitin specific peptidase 24	USP24	Low-density lipoprotein cholesterol		
rs6719729	2	raftlin family member 2	RFTN2	Body Fat Distribution	RFTN2	
rs10497870	2	neurobeachin like 1	NBEAL1	Body Mass Index	NA	
rs3755157	2	ATP binding cassette subfamily B member 11	ABCB11	Fasting Glucose		benign
rs3755157	2	NULL	NULL	Fasting Glucose		benign
rs7645613	3	NULL	NULL	Type 2 diabetes		
rs4833079	4	NULL	NULL	Body Mass Index		
rs4833079	4	NULL	NULL	Body Mass Index	FLJ13197	
rs6876835	5	NULL	NULL	Body Fat Distribution	NSUN2	
rs12652687	5	F-box and leucine rich repeat protein 17	FBXL17	Body Mass Index	FBXL17	
rs3776717	5	ADP ribosylation factor like GTPase 15	ARL15	Body mass index and HDL-C pairwise	ARL15	
rs3776717	5	ADP ribosylation factor like GTPase 15	ARL15	Body mass index and type 2 diabetes pairwise	ARL15	
rs4460176	5	NULL	NULL	Cholesterol HDL	MAN2A1,TMEM232	
rs2963826	5	phosphodiesterase 4D	PDE4D	Obesity-related traits	PDE4D	
rs4916749	5	NULL	NULL	Waist circumference adjusted for body mass index	MEF2C-AS1	
rs7752021	6	NULL	NULL	Cholesterol total		
rs9275524	6	NULL	NULL	Cholesterol total		
rs9275555	6	NULL	NULL	Cholesterol total		
rs9275578	6	NULL	NULL	Cholesterol total		
rs9275595	6	NULL	NULL	Cholesterol total		
rs434841	6	notch receptor 4	NOTCH4	Diabetes mellitus type 1	NOTCH4	benign
rs434841	6	NULL	NULL	Diabetes mellitus type 1	NOTCH4	benign
rs12214416	6	NULL	NULL	Lp a levels	LPAL2	
rs434841	6	notch receptor 4	NOTCH4	Waist-to-hip ratio adjusted for BMI	NOTCH4	benign
rs434841	6	NULL	NULL	Waist-to-hip ratio adjusted for BMI	NOTCH4	benign
rs2040369	7	NULL	NULL	Body Weight	TRBV5-6, TRBV7-6	
rs4719818	7	NULL	NULL	Hip circumference adjusted for BMI	AC003090.1	
rs4719818	7	NULL	NULL	Hip index	AC003090.1	
rs1528036	7	inner mitochondrial	IMMP2L	Lipoproteins	IMMP2L	

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
		membrane peptidase subunit 2				
rs10487878	7	semaphorin 3C	SEMA3C	Lipoproteins VLDL	SEMA3C	
rs10950840	7	NULL	NULL	Obesity-related traits	ASS1P11	
rs9987000	7	NULL	NULL	Waist-hip ratio		
rs822318	8	NULL	NULL	Cholesterol HDL	MRPL49P2, FGF20	
rs4876361	8	NULL	NULL	Hip circumference adjusted for BMI	EIF3H	
rs4994	8	adrenoceptor beta 3	ADRB3	Obesity	ADRB3	benign, risk factor
rs4876361	8	NULL	NULL	Waist circumference adjusted for body mass index	EIF3H	
rs7858161	9	NULL	NULL	Hip circumference adjusted for BMI	YBX1P6	
rs1458495	9	NULL	NULL	Waist circumference	ANXA1, RORB	
rs7039360	9	NULL	NULL	Waist circumference	TLE4, RPS19P6	
rs4506565	10	transcription factor 7 like 2	TCF7L2	Body Mass Index	NA	
rs4506565	10	transcription factor 7 like 2	TCF7L2	Fasting blood glucose	TCF7L2	
rs4506565	10	transcription factor 7 like 2	TCF7L2	Fasting Glucose		
rs4506565	10	transcription factor 7 like 2	TCF7L2	Fasting Glucose	TCF7L2	
rs1937353	10	NULL	NULL	Hip	ST8SIA6,PTPLA	
rs4506565	10	transcription factor 7 like 2	TCF7L2	Type 2 diabetes	TCF7L2	
rs4506565	10	transcription factor 7 like 2	TCF7L2	Type 2 diabetes		
rs4938362	11	proprotein convertase subtilisin/kexin type 7	PCSK7	Apolipoprotein A1 levels		
rs4938362	11	proprotein convertase subtilisin/kexin type 7	PCSK7	Apolipoprotein B levels		
rs1003081	11	NULL	NULL	Body Mass Index	NA	
rs10502222	11	SIK family kinase 3	SIK3	Cholesterol total		
rs4938362	11	proprotein convertase subtilisin/kexin type 7	PCSK7	Low density lipoprotein cholesterol levels		
rs4938362	11	proprotein convertase subtilisin/kexin type 7	PCSK7	Total cholesterol levels		
rs4938362	11	proprotein convertase subtilisin/kexin type 7	PCSK7	Triglyceride levels		
rs2728641	12	NULL	NULL	BMI at 3 months old		
rs2728641	12	NULL	NULL	BMI at 6 months old		
rs17201502	12	Fas apoptotic inhibitory molecule 2	FAIM2	Body Mass Index		
rs7302017	12	NULL	NULL	Waist circumference	PPM1H	
rs10149366	14	NULL	NULL	Lipids	RPL3P3,EXOC5	
rs10149366	14	NULL	NULL	Triglycerides	RPL3P3,EXOC5	
rs242105	14	NULL	NULL	Type 2 diabetes		

SNP	Chr	Gene	Gene symbol	Phenotype	Assoc. genes	Clinical Significance
rs8037818	15	Rho GTPase activating protein 11A	ARHGAP11A	Obesity-related traits	ARHGAP11A,SCG5	
rs8037818	15	NULL	NULL	Obesity-related traits	ARHGAP11A,SCG5	
rs9939973	16	FTO alpha-ketoglutarate dependent dioxygenase	FTO	Body Mass Index		
rs9939973	16	FTO alpha-ketoglutarate dependent dioxygenase	FTO	Hip circumference	FTO	
rs11152166	18	collagen and calcium binding EGF domains 1	CCBE1	Body Mass Index	CCBE1	
rs1865063	19	dedicator of cytokinesis 6	DOCK6	HDL cholesterol levels	ANGPTL8	
rs166988	19	NULL	NULL	Obesity-related traits	KCTD15	

SNP: Single Nucleotide Polymorphism identifier; Chr: Chromosome number.

Table S5. Top lipid metabolism-associated genes comparison for YCH and TIX.

YCH	TIX
ACACA	ABCB11
AGPAT4	ADRB3
ARID5B	ARHGAP11A
CAMK2D	ARL15
CLCNKA	CCBE1
CNTNAP2	DOCK6
FADS1	EPS8L3
FADS2	FAIM2
FADS3	FBXL17
FAP	FTO
FMN2	IMMP2L
GPR19	NBEAL1
HS6ST3	NOTCH4
IFIH1	PCSK7
IL23R	PDE4D
LBH	RFTN2
MAP3K4	SEMA3C
MCC	SIK3
MDGA2	TCF7L2
MYRF	USP24
NPAS3	
PLB1	
PRM1	
SLC25A17	
STAU2	
TMEM258	
TNRC6B	
WDSUB1	
XPNPEP3	

Table S6. GoWinda enrichment analysis results for YCH.

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:2000113	133.14	210	0.00014269	82	1069	1371	negative regulation of cellular macromolecule biosynthetic process
GO:2000112	359.48	474	0.00014269	197	3081	3826	regulation of cellular macromolecule biosynthetic process
GO:2000116	25.09	54	0.00014269	15	190	237	regulation of cysteine-type endopeptidase activity
GO:0035150	5.55	25	0.00014269	5	47	58	regulation of tube size
GO:0072126	0.77	7	0.00014269	1	5	5	positive regulation of glomerular mesangial cell proliferation
GO:0006636	3.32	24	0.00014269	5	39	50	unsaturated fatty acid biosynthetic process
GO:0032927	0.56	6	0.00014269	2	8	14	positive regulation of activin receptor signaling pathway
GO:0019941	25.20	64	0.00014269	19	314	406	modification-dependent protein catabolic process
GO:1901215	21.39	49	0.00014269	16	159	186	negative regulation of neuron death
GO:1901214	36.85	68	0.00014269	21	237	286	regulation of neuron death
GO:0006633	8.83	26	0.00014269	6	80	101	fatty acid biosynthetic process
GO:0006631	24.86	52	0.00014269	21	254	289	fatty acid metabolic process
GO:0048477	3.33	17	0.00014269	2	27	29	oogenesis
GO:0006689	0.46	7	0.00014269	1	5	6	ganglioside catabolic process
GO:0016010	4.04	20	0.00014269	3	14	15	dystrophin-associated glycoprotein complex
GO:0006690	6.38	20	0.00014269	9	78	92	icosanoid metabolic process
GO:0043632	25.75	64	0.00014269	19	318	410	modification-dependent macromolecule catabolic process
GO:0042311	2.53	12	0.00014269	3	19	22	vasodilation
GO:0098793	11.17	31	0.00014269	9	50	58	presynapse
GO:0043651	1.00	20	0.00014269	2	15	17	linoleic acid metabolic process
GO:0031668	16.35	37	0.00014269	11	163	200	cellular response to extracellular stimulus
GO:0031669	14.38	37	0.00014269	11	140	167	cellular response to nutrient levels
GO:0031667	32.90	83	0.00014269	27	309	363	response to nutrient levels
GO:0016032	40.25	73	0.00014269	28	414	517	viral process
GO:0043615	0.37	7	0.00014269	1	4	8	astrocyte cell migration
GO:0060179	0.31	7	0.00014269	1	4	5	male mating behavior
GO:0060180	1.06	13	0.00014269	1	4	7	female mating behavior
GO:0031594	11.82	30	0.00014269	13	40	46	neuromuscular junction
GO:0000422	5.03	21	0.00014269	4	22	25	mitophagy
GO:0030282	3.13	17	0.00014269	5	31	39	bone mineralization
GO:0030275	2.39	14	0.00014269	2	14	18	LRR domain binding
GO:0000460	0.50	6	0.00014269	1	7	8	maturation of 5.8S rRNA
GO:0035112	2.00	14	0.00014269	3	11	13	genitalia morphogenesis
GO:0050709	12.99	32	0.00014269	5	94	139	negative regulation of protein secretion
GO:0060255	571.60	680	0.00014269	296	4684	5767	regulation of macromolecule metabolic process
GO:0060205	24.41	48	0.00014269	21	282	379	cytoplasmic membrane-bounded vesicle lumen
GO:0050880	5.46	25	0.00014269	5	46	56	regulation of blood vessel size
GO:0050896	486.92	575	0.00014269	252	4122	5595	response to stimulus
GO:0060211	1.00	8	0.00014269	1	8	9	regulation of nuclear-transcribed mRNA poly(A) tail shortening
GO:0006750	0.88	12	0.00014269	1	13	14	glutathione biosynthetic process
GO:0060213	1.00	8	0.00014269	1	8	9	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
GO:0090090	21.07	58	0.00014269	13	142	180	negative regulation of canonical Wnt signaling pathway
GO:0090091	0.93	8	0.00014269	2	6	7	positive regulation of extracellular matrix disassembly
GO:0006749	1.60	12	0.00014269	1	35	45	glutathione metabolic process
GO:1901165	0.28	5	0.00014269	1	6	6	positive regulation of trophoblast cell migration
GO:0042383	19.78	43	0.00014269	12	79	87	sarcolemma
GO:0042398	2.86	12	0.00014269	1	41	46	cellular modified amino acid biosynthetic process
GO:0048519	562.40	656	0.00014269	273	3923	4898	negative regulation of biological process
GO:0048523	526.03	632	0.00014269	262	3674	4581	negative regulation of cellular process
GO:0050815	0.34	5	0.00014269	1	4	5	phosphoserine binding
GO:0000280	2.71	14	0.00014269	6	48	55	nuclear division
GO:0036293	40.73	74	0.00014269	23	244	276	response to decreased oxygen levels
GO:0006403	0.98	8	0.00014269	2	10	12	RNA localization
GO:0051851	6.85	22	0.00014269	5	52	71	modification by host of symbiont morphology or physiology
GO:0048227	0.52	6	0.00014269	1	8	8	plasma membrane to endosome transport
GO:0019752	76.82	133	0.00014269	53	725	821	carboxylic acid metabolic process
GO:0018401	2.00	14	0.00014269	1	5	5	peptidyl-proline hydroxylation to 4-hydroxy-L-proline
GO:0048285	9.60	26	0.00014269	8	71	79	organelle fission

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0005164	2.15	14	0.00014269	5	26	46	tumor necrosis factor receptor binding
GO:0031418	3.75	16	0.00014269	2	20	20	L-ascorbic acid binding
GO:0019787	32.31	74	0.00014269	19	300	345	ubiquitin-like protein transferase activity
GO:0044703	12.84	34	0.00014269	11	116	147	multi-organism reproductive process
GO:0044706	11.19	30	0.00014269	9	102	124	multi-multicellular organism process
GO:0044705	4.96	22	0.00014269	3	23	27	multi-organism reproductive behavior
GO:0031406	27.06	68	0.00014269	22	181	206	carboxylic acid binding
GO:0043374	0.30	10	0.00014269	2	6	7	CD8-positive, alpha-beta T cell differentiation
GO:0031331	28.56	58	0.00014269	14	310	369	positive regulation of cellular catabolic process
GO:0070979	5.16	24	0.00014269	3	24	28	protein K11-linked ubiquitination
GO:0031327	144.84	225	0.00014269	87	1179	1522	negative regulation of cellular biosynthetic process
GO:0031326	385.31	492	0.00014269	204	3314	4127	regulation of cellular biosynthetic process
GO:0031390	0.36	7	0.00014269	1	6	6	Ctf18 RFC-like complex
GO:0014823	6.74	26	0.00014269	6	50	59	response to activity
GO:0017080	5.34	17	0.00014269	6	22	24	sodium channel regulator activity
GO:0030046	1.75	11	0.00014269	2	5	5	parallel actin filament bundle assembly
GO:0070936	7.92	27	0.00014269	6	43	54	protein K48-linked ubiquitination
GO:0051817	10.97	36	0.00014269	11	84	107	modification of morphology or physiology of other organism involved in symbiotic interaction
GO:0000209	23.84	67	0.00014269	16	233	284	protein polyubiquitination
GO:0001573	1.67	11	0.00014269	3	15	20	ganglioside metabolic process
GO:0050685	2.57	15	0.00014269	3	28	33	positive regulation of mRNA processing
GO:0050680	13.97	32	0.00014269	8	101	124	negative regulation of epithelial cell proliferation
GO:0006520	33.47	68	0.00014269	25	306	342	cellular amino acid metabolic process
GO:0006534	0.60	12	0.00014269	1	8	10	cysteine metabolic process
GO:1903506	328.15	430	0.00014269	181	2776	3476	regulation of nucleic acid-templated transcription
GO:1903507	121.47	185	0.00014269	76	952	1236	negative regulation of nucleic acid-templated transcription
GO:0006511	24.92	64	0.00014269	19	309	401	ubiquitin-dependent protein catabolic process
GO:1903508	185.93	245	0.00014269	99	1270	1562	positive regulation of nucleic acid-templated transcription
GO:0006508	113.19	173	0.00014269	67	974	1208	proteolysis
GO:0044849	1.55	13	0.00014269	4	14	14	estrous cycle
GO:0006575	16.88	39	0.00014269	11	168	196	cellular modified amino acid metabolic process
GO:0043523	24.68	53	0.00014269	15	159	190	regulation of neuron apoptotic process
GO:0006536	2.07	15	0.00014269	2	24	26	glutamate metabolic process
GO:0032813	3.16	15	0.00014269	6	39	60	tumor necrosis factor receptor superfamily binding
GO:0019852	1.10	12	0.00014269	1	10	10	L-ascorbic acid metabolic process
GO:0031545	2.33	14	0.00014269	1	6	6	peptidyl-proline 4-dioxygenase activity
GO:0031543	2.78	14	0.00014269	1	9	9	peptidyl-proline dioxygenase activity
GO:0044827	4.13	19	0.00014269	3	12	13	modulation by host of viral genome replication
GO:0044829	0.30	5	0.00014269	1	7	7	positive regulation by host of viral genome replication
GO:0042133	3.93	18	0.00014269	6	24	34	neurotransmitter metabolic process
GO:0042136	2.87	15	0.00014269	4	14	21	neurotransmitter biosynthetic process
GO:0031461	6.65	29	0.00014269	6	101	110	cullin-RING ubiquitin ligase complex
GO:0030130	1.61	10	0.00014269	1	6	6	clathrin coat of trans-Golgi network vesicle
GO:0030123	0.60	9	0.00014269	2	7	7	AP-3 adaptor complex
GO:0030125	1.77	10	0.00014269	1	9	9	clathrin vesicle coat
GO:0032787	44.72	85	0.00014269	33	427	485	monocarboxylic acid metabolic process
GO:0031442	1.25	11	0.00014269	2	15	17	positive regulation of mRNA 3'-end processing
GO:0044764	40.85	73	0.00014269	28	427	534	multi-organism cellular process
GO:0043436	91.76	149	0.00014269	61	822	925	oxoacid metabolic process
GO:0044770	18.95	44	0.00014269	12	218	251	cell cycle phase transition
GO:0030175	14.76	35	0.00014269	10	58	71	filopodium
GO:0030178	28.34	59	0.00014269	14	169	211	negative regulation of Wnt signaling pathway
GO:0044772	18.68	44	0.00014269	12	211	243	mitotic cell cycle phase transition
GO:0097267	0.41	7	0.00014269	3	9	9	omega-hydroxylase P450 pathway
GO:0031490	4.77	18	0.00014269	3	47	64	chromatin DNA binding
GO:0030163	24.38	60	0.00014269	18	285	354	protein catabolic process
GO:0030162	70.61	112	0.00014269	38	629	797	regulation of proteolysis
GO:0044788	4.73	19	0.00014269	3	21	22	modulation by host of viral process
GO:0001666	40.16	72	0.00014269	22	237	267	response to hypoxia
GO:0001676	8.65	35	0.00014269	10	79	90	long-chain fatty acid metabolic process
GO:0001678	5.36	20	0.00014269	6	59	63	cellular glucose homeostasis
GO:0051900	2.05	13	0.00014269	2	18	19	regulation of mitochondrial depolarization
GO:0071242	8.13	26	0.00014269	6	31	42	cellular response to ammonium ion
GO:0034284	12.30	34	0.00014269	13	121	139	response to monosaccharide
GO:0071230	7.62	27	0.00014269	5	46	61	cellular response to amino acid stimulus
GO:0005766	0.74	7	0.00014269	1	10	11	primary lysosome
GO:1901699	66.45	106	0.00014269	37	383	456	cellular response to nitrogen compound

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GO:0016458	6.56	21	0.00014269	6	70	111	gene silencing
GO:0042737	1.19	12	0.00014269	4	12	16	drug catabolic process
GO:0042738	1.11	12	0.00014269	4	10	12	exogenous drug catabolic process
GO:0042765	0.23	6	0.00014269	1	5	5	GPI-anchor transamidase complex
GO:0090329	4.14	17	0.00014269	3	39	45	regulation of DNA-dependent DNA replication
GO:0010265	1.01	18	0.00014269	1	4	5	SCF complex assembly
GO:0060548	95.59	142	0.00014269	59	775	952	negative regulation of cell death
GO:0060509	1.88	13	0.00014269	1	4	5	Type I pneumocyte differentiation
GO:0035578	5.21	17	0.00014269	9	75	104	azurophil granule lumen
GO:1901605	23.73	62	0.00014269	21	219	244	alpha-amino acid metabolic process
GO:0071372	2.11	14	0.00014269	2	11	11	cellular response to follicle-stimulating hormone stimulus
GO:0071371	2.75	14	0.00014269	2	17	18	cellular response to gonadotropin stimulus
GO:1900262	0.36	7	0.00014269	1	6	6	regulation of DNA-directed DNA polymerase activity
GO:1900264	0.36	7	0.00014269	1	6	6	positive regulation of DNA-directed DNA polymerase activity
GO:0003254	8.10	29	0.00014269	7	37	42	regulation of membrane depolarization
GO:0071333	4.66	20	0.00014269	6	51	54	cellular response to glucose stimulus
GO:0071331	4.81	20	0.00014269	6	54	57	cellular response to hexose stimulus
GO:0071322	6.28	21	0.00014269	7	60	63	cellular response to carbohydrate stimulus
GO:0071326	4.84	20	0.00014269	6	55	58	cellular response to monosaccharide stimulus
GO:0016567	52.93	96	0.00014269	30	583	720	protein ubiquitination
GO:1901568	6.38	20	0.00014269	9	78	92	fatty acid derivative metabolic process
GO:0004563	0.55	7	0.00014269	1	5	5	beta-N-acetylhexosaminidase activity
GO:0030897	0.53	6	0.00014269	2	6	6	HOPS complex
GO:0016597	16.05	37	0.00014269	11	94	112	amino acid binding
GO:0009313	0.77	9	0.00014269	3	10	20	oligosaccharide catabolic process
GO:0009311	3.98	17	0.00014269	8	43	56	oligosaccharide metabolic process
GO:0010389	15.07	34	0.00014269	7	161	204	regulation of G2/M transition of mitotic cell cycle
GO:0071315	0.36	7	0.00014269	1	2	7	cellular response to morphine
GO:0071317	0.36	7	0.00014269	1	2	7	cellular response to isoquinoline alkaloid
GO:0005828	0.62	7	0.00014269	1	6	6	kinetochore microtubule
GO:0033057	4.29	20	0.00014269	2	17	21	multicellular organismal reproductive behavior
GO:0060359	16.43	37	0.00014269	9	75	94	response to ammonium ion
GO:1900151	1.03	8	0.00014269	1	11	14	regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
GO:1900153	1.03	8	0.00014269	1	11	14	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
GO:2001234	17.63	37	0.00014269	11	171	208	negative regulation of apoptotic signaling pathway
GO:1902750	6.31	23	0.00014269	3	83	109	negative regulation of cell cycle G2/M phase transition
GO:0034097	45.55	78	0.00014269	37	414	503	response to cytokine
GO:0016255	0.33	6	0.00014269	1	7	7	attachment of GPI anchor to protein
GO:0016236	11.21	33	0.00014269	7	95	110	macroautophagy
GO:0030522	22.21	46	0.00014269	15	148	182	intracellular receptor signaling pathway
GO:0001959	19.91	42	0.00014269	13	135	178	regulation of cytokine-mediated signaling pathway
GO:0001961	6.20	22	0.00014269	6	38	49	positive regulation of cytokine-mediated signaling pathway
GO:0022010	0.47	7	0.00014269	1	8	12	central nervous system myelination
GO:0048609	45.91	91	0.00014269	32	429	558	multicellular organismal reproductive process
GO:0009057	57.69	102	0.00014269	41	673	868	macromolecule catabolic process
GO:0009064	4.94	23	0.00014269	6	57	68	glutamine family amino acid metabolic process
GO:0009069	2.58	13	0.00014269	2	32	36	serine family amino acid metabolic process
GO:0035329	4.38	18	0.00014269	3	26	29	hippo signaling
GO:1902679	122.24	187	0.00014269	77	961	1261	negative regulation of RNA biosynthetic process
GO:1900019	2.13	11	0.00014269	2	4	5	regulation of protein kinase C activity
GO:1902680	186.77	245	0.00014269	99	1291	1584	positive regulation of RNA biosynthetic process
GO:1900020	2.13	11	0.00014269	2	4	5	positive regulation of protein kinase C activity
GO:0006974	55.28	90	0.00014269	30	586	737	cellular response to DNA damage stimulus
GO:0060479	3.26	14	0.00014269	2	20	21	lung cell differentiation
GO:0034162	1.06	8	0.00014269	4	12	15	toll-like receptor 9 signaling pathway
GO:0006950	246.48	320	0.00014269	124	2302	3024	response to stress
GO:2001141	328.74	430	0.00014269	181	2790	3502	regulation of RNA biosynthetic process
GO:1903976	0.34	7	0.00014269	1	4	5	negative regulation of glial cell migration
GO:0003018	10.78	32	0.00014269	8	72	89	vascular process in circulatory system
GO:0005654	293.58	370	0.00014269	172	2721	3336	nucleoplasm
GO:0006979	36.76	66	0.00014269	18	300	351	response to oxidative stress
GO:0005663	0.37	7	0.00014269	1	6	6	DNA replication factor C complex
GO:0030669	3.27	19	0.00014269	4	25	71	clathrin-coated endocytic vesicle membrane
GO:0031983	25.09	49	0.00014269	22	283	380	vesicle lumen

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GO:1900087	4.34	15	0.00014269	4	22	31	positive regulation of G1/S transition of mitotic cell cycle
GO:0042582	0.74	7	0.00014269	1	10	11	azurophil granule
GO:0042594	13.93	36	0.00014269	11	140	168	response to starvation
GO:0061726	5.03	21	0.00014269	4	22	25	mitochondrion disassembly
GO:1903935	0.04	3	0.00014269	1	3	9	response to sodium arsenite
GO:1903936	0.04	3	0.00014269	1	3	8	cellular response to sodium arsenite
GO:0006914	20.54	45	0.00014269	13	182	212	autophagy
GO:0006919	10.43	30	0.00014269	6	73	86	activation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0016881	2.09	12	0.00014269	1	20	20	acid-amino acid ligase activity
GO:0004887	1.23	13	0.00014269	1	7	7	thyroid hormone receptor activity
GO:0039528	0.29	5	0.00014269	1	5	7	cytoplasmic pattern recognition receptor signaling pathway in response to virus
GO:1903008	6.24	21	0.00014269	4	39	44	organelle disassembly
GO:1990247	0.29	5	0.00014269	1	7	8	N6-methyladenosine-containing RNA binding
GO:0051253	125.81	194	0.00014269	81	1000	1307	negative regulation of RNA metabolic process
GO:0051254	190.79	259	0.00014269	103	1340	1638	positive regulation of RNA metabolic process
GO:0051252	337.51	453	0.00014269	192	2899	3629	regulation of RNA metabolic process
GO:0009749	11.63	33	0.00014269	12	111	129	response to glucose
GO:0010715	1.86	13	0.00014269	5	14	19	regulation of extracellular matrix disassembly
GO:0009743	14.91	35	0.00014269	14	138	158	response to carbohydrate
GO:0009746	11.83	33	0.00014269	12	116	134	response to hexose
GO:0019005	2.51	25	0.00014269	3	27	30	SCF ubiquitin ligase complex
GO:0007026	2.05	14	0.00014269	2	15	20	negative regulation of microtubule depolymerization
GO:0010639	34.53	64	0.00014269	21	262	305	negative regulation of organelle organization
GO:0051172	146.90	230	0.00014269	91	1217	1564	negative regulation of nitrogen compound metabolic process
GO:0051171	396.49	514	0.00014269	217	3430	4253	regulation of nitrogen compound metabolic process
GO:0019048	7.36	25	0.00014269	7	32	36	modulation by virus of host morphology or physiology
GO:1990234	41.36	78	0.00014269	24	459	543	transferase complex
GO:0070324	1.30	13	0.00014269	1	6	6	thyroid hormone binding
GO:0060992	0.53	6	0.00014269	1	6	6	response to fungicide
GO:0034698	4.13	16	0.00014269	3	26	29	response to gonadotropin
GO:0032020	0.66	8	0.00014269	1	4	6	ISG15-protein conjugation
GO:0044068	6.13	23	0.00014269	6	26	28	modulation by symbiont of host cellular process
GO:0019054	5.74	23	0.00014269	6	22	24	modulation by virus of host process
GO:0045324	0.52	6	0.00014269	2	5	5	late endosome to vacuole transport
GO:0044003	8.12	25	0.00014269	7	41	47	modification by symbiont of host morphology or physiology
GO:0046685	1.42	22	0.00014269	4	24	31	response to arsenic-containing substance
GO:0046686	3.28	19	0.00014269	5	48	62	response to cadmium ion
GO:0004842	30.85	71	0.00014269	18	280	322	ubiquitin-protein transferase activity
GO:0019098	5.18	22	0.00014269	3	24	28	reproductive behavior
GO:0051305	1.45	10	0.00014269	1	6	6	chromosome movement towards spindle pole
GO:0070482	42.62	82	0.00014269	25	262	301	response to oxygen levels
GO:0001071	98.48	143	0.00014269	55	787	987	nucleic acid binding transcription factor activity
GO:0010823	7.99	25	0.00014269	6	43	50	negative regulation of mitochondrion organization
GO:0010821	22.76	49	0.00014269	17	208	249	regulation of mitochondrion organization
GO:0009889	391.14	495	0.00014269	206	3373	4194	regulation of biosynthetic process
GO:0007141	1.13	8	0.00014269	3	21	23	male meiosis I
GO:0007126	2.71	14	0.00014269	6	48	55	meiotic nuclear division
GO:0007127	1.34	10	0.00014269	4	26	28	meiosis I
GO:0034711	0.11	5	0.00014269	1	4	5	inhibin binding
GO:0051295	1.75	11	0.00014269	2	4	5	establishment of meiotic spindle localization
GO:0034774	23.87	47	0.00014269	20	269	362	secretory granule lumen
GO:1901987	34.35	62	0.00014269	19	344	429	regulation of cell cycle phase transition
GO:0071774	2.93	18	0.00014269	4	28	37	response to fibroblast growth factor
GO:1901990	32.09	61	0.00014269	18	315	393	regulation of mitotic cell cycle phase transition
GO:1901991	12.80	30	0.00014269	7	165	209	negative regulation of mitotic cell cycle phase transition
GO:0019184	0.93	12	0.00014269	1	14	15	nonribosomal peptide biosynthetic process
GO:0004977	0.67	8	0.00014269	1	5	6	melanocortin receptor activity
GO:0045454	5.47	20	0.00014269	5	53	64	cell redox homeostasis
GO:0004985	0.84	8	0.00014269	1	8	9	opioid receptor activity
GO:0071496	23.44	56	0.00014269	16	228	270	cellular response to external stimulus
GO:0071453	19.13	42	0.00014269	14	117	129	cellular response to oxygen levels
GO:0071455	1.00	8	0.00014269	2	6	7	cellular response to hyperoxia
GO:0038003	0.84	8	0.00014269	1	8	9	opioid receptor signaling pathway
GO:0022402	80.95	124	0.00014269	46	879	1026	cell cycle process
GO:0009410	0.64	15	0.00014269	3	10	13	response to xenobiotic stimulus

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GO:1901800	8.23	29	0.00014269	5	69	83	positive regulation of proteasomal protein catabolic process
GO:0010468	400.64	496	0.00014269	216	3368	4226	regulation of gene expression
GO:0035728	1.65	15	0.00014269	2	14	15	response to hepatocyte growth factor
GO:0035729	1.45	15	0.00014269	2	12	13	cellular response to hepatocyte growth factor stimulus
GO:0060760	6.46	27	0.00014269	7	41	54	positive regulation of response to cytokine stimulus
GO:1901858	1.79	12	0.00014269	3	5	6	regulation of mitochondrial DNA metabolic process
GO:0071417	63.67	99	0.00014269	35	354	413	cellular response to organonitrogen compound
GO:0010498	17.44	52	0.00014269	13	215	271	proteasomal protein catabolic process
GO:0060759	20.58	47	0.00014269	14	141	187	regulation of response to cytokine stimulus
GO:0072738	0.04	3	0.00014269	1	2	6	cellular response to diamide
GO:0071407	53.12	88	0.00014269	31	318	381	cellular response to organic cyclic compound
GO:0072737	0.04	3	0.00014269	1	2	6	response to diamide
GO:1901796	15.53	45	0.00014269	14	158	192	regulation of signal transduction by p53 class mediator
GO:0009628	117.93	167	0.00014269	59	881	1032	response to abiotic stimulus
GO:0010629	146.18	226	0.00014269	89	1179	1534	negative regulation of gene expression
GO:0010604	343.01	418	0.00014269	169	2491	3062	positive regulation of macromolecule metabolic process
GO:0010605	247.02	320	0.00014269	135	1949	2471	negative regulation of macromolecule metabolic process
GO:0008239	0.48	6	0.00014269	4	8	8	dipeptidyl-peptidase activity
GO:0075044	0.65	11	0.00014269	2	5	5	autophagy of host cells involved in interaction with symbiont
GO:0035821	11.60	36	0.00014269	11	112	150	modification of morphology or physiology of other organism
GO:0060828	33.30	65	0.00014269	16	209	261	regulation of canonical Wnt signaling pathway
GO:0075071	0.65	11	0.00014269	2	5	5	autophagy involved in symbiotic interaction
GO:0051051	58.22	94	0.00014269	33	390	506	negative regulation of transport
GO:0033206	1.70	11	0.00014269	2	6	6	meiotic cytokinesis
GO:0010556	365.84	474	0.00014269	197	3171	3951	regulation of macromolecule biosynthetic process
GO:0010558	138.71	215	0.00014269	85	1130	1458	negative regulation of macromolecule biosynthetic process
GO:0008250	1.25	11	0.00014269	3	9	11	oligosaccharyltransferase complex
GO:0010564	57.24	91	0.00014269	29	607	762	regulation of cell cycle process
GO:0008298	0.74	8	0.00014269	2	4	5	intracellular mRNA localization
GO:0016717	0.78	20	0.00014269	2	5	5	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
GO:0016705	17.45	55	0.00014269	12	128	145	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
GO:1901724	0.83	7	0.00014269	1	7	7	positive regulation of cell proliferation involved in kidney development
GO:0051603	28.28	70	0.00014269	23	346	446	proteolysis involved in cellular protein catabolic process
GO:0036037	0.30	10	0.00014269	2	6	11	CD8-positive, alpha-beta T cell activation
GO:0000096	3.46	15	0.00014269	2	29	33	sulfur amino acid metabolic process
GO:0019511	3.02	14	0.00014269	1	14	14	peptidyl-proline hydroxylation
GO:0085020	4.17	16	0.00014269	2	7	8	protein K6-linked ubiquitination
GO:0007584	14.48	39	0.00014269	15	141	158	response to nutrient
GO:0006167	0.43	6	0.00014269	1	5	6	AMP biosynthetic process
GO:0044433	118.86	170	0.00014269	73	952	1242	cytoplasmic vesicle part
GO:0031111	2.70	14	0.00014269	2	24	29	negative regulation of microtubule polymerization or depolymerization
GO:0031114	2.14	14	0.00014269	2	16	21	regulation of microtubule depolymerization
GO:0032446	58.43	106	0.00014269	34	654	799	protein modification by small protein conjugation
GO:0021782	6.05	19	0.00014269	3	39	56	glial cell development
GO:0019471	2.41	15	0.00014269	2	11	12	4-hydroxyproline metabolic process
GO:0032436	7.71	29	0.00014269	5	56	67	positive regulation of proteasomal ubiquitin-dependent protein catabolic process
GO:1902075	0.05	3	0.00014269	1	4	9	cellular response to salt
GO:0032486	1.06	11	0.00014269	2	9	10	Rap protein signal transduction
GO:0045732	19.10	48	0.00014269	12	222	282	positive regulation of protein catabolic process
GO:0044403	40.25	73	0.00014269	28	414	517	symbiosis, encompassing mutualism through parasitism
GO:0031146	3.80	25	0.00014269	3	61	85	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
GO:0044419	51.26	89	0.00014269	38	529	662	interspecies interaction between organisms
GO:0006189	0.23	6	0.00014269	1	6	7	'de novo' IMP biosynthetic process
GO:0080135	77.25	118	0.00014269	46	688	823	regulation of cellular response to stress

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0003950	1.86	13	0.00014269	4	20	21	NAD+ ADP-ribosyltransferase activity
GO:0043161	16.89	51	0.00014269	12	206	261	proteasome-mediated ubiquitin-dependent protein catabolic process
GO:0043177	27.10	68	0.00014269	22	182	207	organic acid binding
GO:0043186	1.10	8	0.00014269	4	14	16	P granule
GO:2000489	0.63	12	0.00014269	1	6	6	regulation of hepatic stellate cell activation
GO:0036109	1.23	21	0.00014269	3	11	13	alpha-linolenic acid metabolic process
GO:0051726	90.28	132	0.00014269	47	904	1122	regulation of cell cycle
GO:0045924	1.06	13	0.00014269	1	4	6	regulation of female receptivity
GO:1903364	13.23	32	0.00014269	7	155	196	positive regulation of cellular protein catabolic process
GO:0045935	211.28	277	0.00014269	111	1534	1866	positive regulation of nucleobase-containing compound metabolic process
GO:0045934	137.85	217	0.00014269	87	1113	1448	negative regulation of nucleobase-containing compound metabolic process
GO:0006355	326.78	430	0.00014269	181	2755	3450	regulation of transcription, DNA-templated
GO:0006357	194.41	273	0.00014269	107	1510	1871	regulation of transcription from RNA polymerase II promoter
GO:0045892	118.74	182	0.00014269	74	921	1198	negative regulation of transcription, DNA-templated
GO:0045893	185.93	245	0.00014269	99	1270	1562	positive regulation of transcription, DNA-templated
GO:0097067	1.21	14	0.00014269	2	14	16	cellular response to thyroid hormone stimulus
GO:0097066	1.81	15	0.00014269	3	23	25	response to thyroid hormone
GO:0097068	0.51	12	0.00014269	1	5	5	response to thyroxine
GO:0006271	0.51	7	0.00014269	1	6	7	DNA strand elongation involved in DNA replication
GO:0043200	11.90	32	0.00014269	8	92	112	response to amino acid
GO:0045862	38.45	74	0.00014269	20	326	395	positive regulation of proteolysis
GO:0051704	103.43	160	0.00014269	65	1021	1321	multi-organism process
GO:0051702	7.04	22	0.00014269	5	55	75	interaction with symbiont
GO:0043280	13.96	35	0.00014269	8	105	130	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0043281	19.71	54	0.00014269	15	169	207	regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0000151	15.52	47	0.00014269	11	177	202	ubiquitin ligase complex
GO:0051409	0.68	16	0.00014269	2	7	8	response to nitrosative stress
GO:0002475	0.61	6	0.00014269	1	5	17	antigen processing and presentation via MHC class Ib
GO:1903265	3.81	16	0.00014269	3	6	6	positive regulation of tumor necrosis factor-mediated signaling pathway
GO:0009991	34.91	83	0.00014269	27	333	398	response to extracellular stimulus
GO:1903203	5.99	20	0.00014269	4	20	23	regulation of oxidative stress-induced neuron death
GO:1903204	5.72	20	0.00014269	4	15	18	negative regulation of oxidative stress-induced neuron death
GO:0010972	5.28	22	0.00014269	2	72	97	negative regulation of G2/M transition of mitotic cell cycle
GO:0007341	0.56	9	0.00014269	2	7	7	penetration of zona pellucida
GO:0008641	0.57	7	0.00014269	1	6	9	small protein activating enzyme activity
GO:0019219	373.07	500	0.00014269	209	3212	3995	regulation of nucleobase-containing compound metabolic process
GO:0009892	272.78	350	0.00014269	145	2166	2737	negative regulation of metabolic process
GO:0009890	147.13	225	0.00014269	87	1200	1544	negative regulation of biosynthetic process
GO:0009896	34.78	66	0.00014269	17	363	435	positive regulation of catabolic process
GO:0009894	80.73	129	0.00014269	47	713	853	regulation of catabolic process
GO:0007292	4.32	17	0.00014269	2	37	43	female gamete generation
GO:0046827	1.31	11	0.00014269	3	17	20	positive regulation of protein export from nucleus
GO:0007276	32.00	62	0.00014269	25	332	447	gamete generation
GO:0033554	131.91	185	0.00014269	65	1226	1511	cellular response to stress
GO:0033559	7.70	37	0.00014269	12	89	106	unsaturated fatty acid metabolic process
GO:0007281	16.69	38	0.00014269	11	123	140	germ cell development
GO:0032291	0.47	7	0.00014269	1	8	12	axon ensheathment in central nervous system
GO:0070555	10.06	27	0.00014269	7	60	85	response to interleukin-1
GO:0003700	98.48	143	0.00014269	55	787	987	transcription factor activity, sequence-specific DNA binding
GO:0002438	0.94	8	0.00014269	1	7	8	acute inflammatory response to antigenic stimulus
GO:0044248	94.62	147	0.00014269	62	1038	1282	cellular catabolic process
GO:0044265	40.92	77	0.00014269	28	555	727	cellular macromolecule catabolic process
GO:0070534	6.48	26	0.00014269	4	27	42	protein K63-linked ubiquitination
GO:0080090	565.21	671	0.00014269	292	4699	5776	regulation of primary metabolic process
GO:0051580	5.02	17	0.00014269	3	12	14	regulation of neurotransmitter uptake
GO:0045649	3.13	13	0.00014269	2	17	20	regulation of macrophage differentiation
GO:0046974	0.43	6	0.00014269	1	4	10	histone methyltransferase activity (H3-K9 specific)
GO:0046976	0.43	6	0.00014269	1	3	8	histone methyltransferase activity (H3-K27 specific)
GO:0045651	2.64	13	0.00014269	2	10	13	positive regulation of macrophage differentiation

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GO:0044344	2.14	15	0.00014269	3	22	30	cellular response to fibroblast growth factor stimulus
GO:0006082	94.68	155	0.00014269	62	838	942	organic acid metabolic process
GO:1903046	10.01	31	0.00014269	10	120	139	meiotic cell cycle process
GO:1904386	0.51	12	0.00014269	1	5	5	response to L-phenylalanine derivative
GO:1903052	12.62	32	0.00014269	7	143	181	positive regulation of proteolysis involved in cellular protein catabolic process
GO:0032354	3.35	16	0.00014269	3	16	17	response to follicle-stimulating hormone
GO:0019373	0.63	7	0.00014269	3	11	11	epoxygenase P450 pathway
GO:0031047	3.65	20	0.00014269	5	40	53	gene silencing by RNA
GO:0070647	71.84	121	0.00014269	44	815	1020	protein modification by small protein conjugation or removal
GO:0042340	0.82	7	0.00026985	1	11	11	keratan sulfate catabolic process
GO:0097202	12.70	30	0.00026985	6	81	94	activation of cysteine-type endopeptidase activity
GO:0031329	65.26	105	0.00026985	40	614	739	regulation of cellular catabolic process
GO:0019842	11.45	28	0.00026985	7	76	82	vitamin binding
GO:0042176	41.77	73	0.00026985	21	350	435	regulation of protein catabolic process
GO:0035547	0.32	5	0.00026985	1	4	6	regulation of interferon-beta secretion
GO:0016595	2.79	12	0.00026985	1	10	10	glutamate binding
GO:0030662	15.07	34	0.00026985	11	111	183	coated vesicle membrane
GO:0030666	16.12	36	0.00026985	11	123	225	endocytic vesicle membrane
GO:0030665	11.40	28	0.00026985	8	76	126	clathrin-coated vesicle membrane
GO:0042692	14.65	35	0.00026985	13	80	90	muscle cell differentiation
GO:0046631	7.49	21	0.00026985	4	34	43	alpha-beta T cell activation
GO:0051303	3.86	14	0.00026985	2	58	62	establishment of chromosome localization
GO:0046479	0.79	7	0.00026985	1	8	10	glycosphingolipid catabolic process
GO:0005922	0.34	5	0.00026985	2	14	21	connexon complex
GO:0046514	0.83	7	0.00026985	1	9	11	ceramide catabolic process
GO:0018126	3.74	14	0.00026985	1	23	23	protein hydroxylation
GO:0043154	4.98	16	0.00026985	6	65	79	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0000178	0.70	7	0.00026985	2	16	18	exosome (RNase complex)
GO:1903313	3.50	15	0.00026985	3	41	48	positive regulation of mRNA metabolic process
GO:0007631	7.79	22	0.00026985	8	61	81	feeding behavior
GO:0046914	119.97	165	0.00026985	63	887	1091	transition metal ion binding
GO:0019377	0.81	7	0.00026985	1	10	12	glycolipid catabolic process
GO:0016053	25.13	49	0.00037914	18	215	253	organic acid biosynthetic process
GO:0098852	33.43	59	0.00037914	29	299	411	lytic vacuole membrane
GO:0098858	30.08	56	0.00037914	16	117	139	actin-based cell projection
GO:1903708	18.03	37	0.00037914	13	136	182	positive regulation of hemopoiesis
GO:0036295	1.18	8	0.00037914	2	11	14	cellular response to increased oxygen levels
GO:1902305	11.71	29	0.00037914	7	42	46	regulation of sodium ion transmembrane transport
GO:0098588	267.98	335	0.00037914	153	2150	2630	bounding membrane of organelle
GO:1901028	3.29	13	0.00037914	6	41	47	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
GO:0031440	1.86	11	0.00037914	2	27	34	regulation of mRNA 3'-end processing
GO:0002933	0.16	4	0.00037914	1	6	7	lipid hydroxylation
GO:0005765	33.43	59	0.00037914	29	299	411	lysosomal membrane
GO:0042698	3.58	14	0.00037914	5	22	22	ovulation cycle
GO:0046394	25.13	49	0.00037914	18	215	253	carboxylic acid biosynthetic process
GO:0046329	5.99	18	0.00037914	2	31	32	negative regulation of JNK cascade
GO:0005506	16.24	37	0.00037914	11	126	159	iron ion binding
GO:0072330	16.72	35	0.00037914	11	140	168	monocarboxylic acid biosynthetic process
GO:1902749	16.66	35	0.00037914	8	178	222	regulation of cell cycle G2/M phase transition
GO:0030539	2.67	12	0.00037914	3	14	17	male genitalia development
GO:1902741	0.41	5	0.00037914	1	6	7	positive regulation of interferon-alpha secretion
GO:1902739	0.41	5	0.00037914	1	6	7	regulation of interferon-alpha secretion
GO:0042593	12.50	31	0.00037914	11	141	153	glucose homeostasis
GO:1902617	0.75	7	0.00037914	1	5	5	response to fluoride
GO:0071673	1.01	7	0.00037914	1	3	8	positive regulation of smooth muscle cell chemotaxis
GO:1900748	2.24	11	0.00037914	2	5	5	positive regulation of vascular endothelial growth factor signaling pathway
GO:0010803	6.89	20	0.00037914	5	47	62	regulation of tumor necrosis factor-mediated signaling pathway
GO:0034453	3.26	13	0.00037914	2	37	40	microtubule anchoring
GO:0005930	11.58	28	0.00037914	10	71	74	axoneme
GO:0044446	870.48	979	0.00037914	460	7410	9166	intracellular organelle part
GO:0033500	12.50	31	0.00037914	11	141	153	carbohydrate homeostasis
GO:0044283	38.02	67	0.00037914	30	383	456	small molecule biosynthetic process
GO:0043069	86.25	126	0.00037914	54	707	876	negative regulation of programmed cell death
GO:0050765	1.00	7	0.0004864	2	15	16	negative regulation of phagocytosis
GO:0035278	1.16	8	0.0004864	1	11	11	miRNA mediated inhibition of translation

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GO:1901163	0.43	5	0.0004864	1	9	11	regulation of trophoblast cell migration
GO:0031325	339.76	412	0.0004864	168	2502	3044	positive regulation of cellular metabolic process
GO:0031323	575.05	666	0.0004864	296	4750	5846	regulation of cellular metabolic process
GO:0045974	1.16	8	0.0004864	1	11	11	regulation of translation, ncRNA-mediated
GO:0097179	0.51	7	0.0004864	3	5	5	protease inhibitor complex
GO:0040033	1.16	8	0.0004864	1	11	11	negative regulation of translation, ncRNA-mediated
GO:0097677	0.38	5	0.0004864	2	5	6	STAT family protein binding
GO:0060487	3.20	13	0.0004864	1	19	20	lung epithelial cell differentiation
GO:0010822	17.36	36	0.0004864	12	153	184	positive regulation of mitochondrion organization
GO:0007223	7.23	20	0.0004864	4	34	36	Wnt signaling pathway, calcium modulating pathway
GO:1901988	13.94	31	0.0004864	8	183	229	negative regulation of cell cycle phase transition
GO:0015301	2.30	11	0.0004864	4	22	25	anion:anion antiporter activity
GO:0009408	9.51	25	0.0004864	4	80	100	response to heat
GO:0009636	14.56	32	0.0004864	11	120	140	response to toxic substance
GO:0032395	0.85	7	0.0004864	3	7	53	MHC class II receptor activity
GO:0005452	1.62	9	0.00059176	3	15	15	inorganic anion exchanger activity
GO:0048522	604.78	693	0.00059176	288	4172	5143	positive regulation of cellular process
GO:2001020	12.61	29	0.00059176	13	153	184	regulation of response to DNA damage stimulus
GO:0045060	2.72	12	0.00059176	3	10	10	negative thymic T cell selection
GO:1902808	4.69	15	0.00059176	4	28	40	positive regulation of cell cycle G1/S phase transition
GO:0022616	0.90	7	0.00059176	1	11	12	DNA strand elongation
GO:0032095	1.29	8	0.00059176	1	14	18	regulation of response to food
GO:0008542	6.22	19	0.00059176	4	45	50	visual learning
GO:0050000	4.09	14	0.00059176	2	60	64	chromosome localization
GO:0010765	6.02	18	0.00059176	4	26	29	positive regulation of sodium ion transport
GO:0044422	909.97	1015	0.00059176	475	7619	9401	organelle part
GO:1903202	7.69	20	0.00059176	4	36	42	negative regulation of oxidative stress-induced cell death
GO:0008654	22.61	44	0.00059176	17	226	281	phospholipid biosynthetic process
GO:0003714	21.26	42	0.00059176	14	171	205	transcription corepressor activity
GO:0061458	3.04	12	0.000685	3	18	21	reproductive system development
GO:0006996	225.41	284	0.000685	117	1910	2253	organelle organization
GO:0007005	24.70	46	0.000685	15	234	286	mitochondrion organization
GO:0010458	0.88	7	0.000685	1	10	11	exit from mitosis
GO:0005902	8.57	22	0.000685	5	51	60	microvillus
GO:0038092	0.66	6	0.000685	2	7	9	nodal signaling pathway
GO:1900408	7.70	20	0.000685	4	37	44	negative regulation of cellular response to oxidative stress
GO:0007520	6.07	18	0.000685	3	17	19	myoblast fusion
GO:0019369	3.03	12	0.000685	6	39	42	arachidonic acid metabolic process
GO:0031638	13.32	30	0.000685	6	98	114	zymogen activation
GO:1903747	15.65	34	0.000685	11	113	140	regulation of establishment of protein localization to mitochondrion
GO:0015296	5.23	16	0.000685	4	39	42	anion:cation symporter activity
GO:0051173	223.14	280	0.000685	114	1626	1985	positive regulation of nitrogen compound metabolic process
GO:0008186	0.95	7	0.000685	3	22	34	RNA-dependent ATPase activity
GO:0002162	1.02	7	0.000685	1	7	9	dystroglycan binding
GO:0043383	2.95	12	0.00090392	3	11	12	negative T cell selection
GO:0009056	135.78	185	0.00090392	86	1327	1630	catabolic process
GO:0000777	6.23	18	0.00090392	7	80	91	condensed chromosome kinetochore
GO:0044437	51.04	80	0.00090392	41	471	641	vacuolar part
GO:0070848	42.66	70	0.00090392	28	250	283	response to growth factor
GO:0097062	2.61	11	0.00090392	1	10	10	dendritic spine maintenance
GO:0051879	3.95	14	0.00100244	6	29	33	Hsp90 protein binding
GO:0070987	1.06	7	0.00100244	1	18	19	error-free translesion synthesis
GO:0031324	245.53	306	0.00100244	134	1970	2493	negative regulation of cellular metabolic process
GO:0035032	0.44	5	0.00100244	1	5	5	phosphatidylinositol 3-kinase complex, class III
GO:0043900	39.07	64	0.00100244	27	358	466	regulation of multi-organism process
GO:1900736	0.73	6	0.00100244	1	5	6	regulation of phospholipase C-activating G-protein coupled receptor signaling pathway
GO:0002042	3.18	12	0.00100244	3	15	16	cell migration involved in sprouting angiogenesis
GO:0070734	0.73	6	0.00100244	1	9	16	histone H3-K27 methylation
GO:0048149	1.49	8	0.00100244	1	8	9	behavioral response to ethanol
GO:0008610	54.24	84	0.00100244	35	485	594	lipid biosynthetic process
GO:1902308	0.45	5	0.00110314	1	4	6	regulation of peptidyl-serine dephosphorylation
GO:0045061	3.40	13	0.00110314	4	17	17	thymic T cell selection
GO:0002039	6.72	19	0.00110314	8	54	74	p53 binding
GO:0071547	0.46	5	0.00110314	2	5	5	piP-body
GO:0044249	358.69	430	0.00110314	192	3473	4277	cellular biosynthetic process

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GO:0017144	2.82	12	0.00120093	4	31	35	drug metabolic process
GO:0015294	10.46	25	0.00120093	8	79	86	solute:cation symporter activity
GO:0034124	0.11	3	0.00120093	1	4	5	regulation of MyD88-dependent toll-like receptor signaling pathway
GO:1901797	4.71	15	0.00120093	4	23	32	negative regulation of signal transduction by p53 class mediator
GO:0031110	5.61	16	0.00120093	3	56	67	regulation of microtubule polymerization or depolymerization
GO:0046825	2.71	11	0.00120093	3	27	31	regulation of protein export from nucleus
GO:1901030	3.19	12	0.0012761	5	35	38	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
GO:0071260	7.28	19	0.0012761	5	70	75	cellular response to mechanical stimulus
GO:0090241	0.28	4	0.0012761	1	5	5	negative regulation of histone H4 acetylation
GO:0010628	225.28	280	0.0012761	116	1578	1954	positive regulation of gene expression
GO:0009607	51.36	80	0.0012761	35	604	810	response to biotic stimulus
GO:0031214	5.87	17	0.0012761	5	62	74	biomineral tissue development
GO:0043014	4.84	15	0.0012761	4	24	29	alpha-tubulin binding
GO:0042276	1.07	7	0.0012761	1	17	18	error-prone translesion synthesis
GO:0043566	6.62	18	0.0012761	3	65	86	structure-specific DNA binding
GO:0051865	7.45	20	0.0012761	5	47	55	protein autoubiquitination
GO:0030027	36.68	61	0.0012761	18	152	175	lamellipodium
GO:0051701	16.87	34	0.0012761	15	130	151	interaction with host
GO:0043066	83.43	119	0.0012761	53	695	863	negative regulation of apoptotic process
GO:0043679	8.56	22	0.00135519	6	43	52	axon terminus
GO:0015185	0.74	6	0.00135519	1	4	5	gamma-aminobutyric acid transmembrane transporter activity
GO:0005829	547.77	630	0.00135519	268	4208	5076	cytosol
GO:0019079	3.25	12	0.00135519	4	21	25	viral genome replication
GO:0032094	1.41	8	0.00135519	1	13	16	response to food
GO:0003677	189.14	241	0.00135519	104	1872	2326	DNA binding
GO:0018208	4.39	14	0.00135519	1	47	50	peptidyl-proline modification
GO:2000649	10.01	24	0.00135519	6	31	35	regulation of sodium ion transmembrane transporter activity
GO:0045944	126.40	168	0.00135519	67	881	1087	positive regulation of transcription from RNA polymerase II promoter
GO:0010948	18.85	37	0.00135519	9	255	339	negative regulation of cell cycle process
GO:0014874	2.83	11	0.00144495	3	14	15	response to stimulus involved in regulation of muscle adaptation
GO:0050684	6.82	19	0.00144495	7	91	114	regulation of mRNA processing
GO:0032873	6.56	18	0.00144495	2	39	41	negative regulation of stress-activated MAPK cascade
GO:0030877	0.79	6	0.00144495	3	9	10	beta-catenin destruction complex
GO:0070303	6.56	18	0.00144495	2	39	41	negative regulation of stress-activated protein kinase signaling cascade
GO:0010557	204.20	256	0.00144495	104	1476	1821	positive regulation of macromolecule biosynthetic process
GO:0051589	5.43	16	0.00144495	2	12	14	negative regulation of neurotransmitter transport
GO:0070989	1.47	8	0.00165073	4	11	13	oxidative demethylation
GO:0023057	159.47	205	0.00165073	72	1059	1262	negative regulation of signaling
GO:0016725	0.50	5	0.00165073	2	8	8	oxidoreductase activity, acting on CH or CH2 groups
GO:0018024	6.57	18	0.00165073	4	39	45	histone-lysine N-methyltransferase activity
GO:0072124	1.13	7	0.00174155	1	8	8	regulation of glomerular mesangial cell proliferation
GO:0060136	0.11	3	0.00174155	1	4	6	embryonic process involved in female pregnancy
GO:1902254	4.26	14	0.00174155	3	15	22	negative regulation of intrinsic apoptotic signaling pathway by p53 class mediator
GO:0042755	3.31	12	0.00174155	3	22	27	eating behavior
GO:0044306	10.05	24	0.00174155	8	57	68	neuron projection terminus
GO:0005243	0.27	4	0.00181965	1	8	12	gap junction channel activity
GO:0010648	161.36	207	0.00181965	74	1075	1281	negative regulation of cell communication
GO:0071456	17.03	34	0.00181965	12	99	106	cellular response to hypoxia
GO:0007632	7.10	19	0.00181965	4	50	55	visual behavior
GO:1903320	23.56	43	0.00181965	13	255	316	regulation of protein modification by small protein conjugation or removal
GO:0007346	46.64	73	0.00181965	24	484	602	regulation of mitotic cell cycle
GO:0033599	1.98	9	0.00181965	1	12	16	regulation of mammary gland epithelial cell proliferation
GO:0018026	0.84	6	0.00181965	1	9	9	peptidyl-lysine monomethylation
GO:0048490	0.83	6	0.0019009	1	13	16	anterograde synaptic vesicle transport
GO:0003229	0.84	6	0.0019009	2	5	6	ventricular cardiac muscle tissue development
GO:0016879	6.02	17	0.0019009	5	47	51	ligase activity, forming carbon-nitrogen bonds

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:1900740	2.84	11	0.0019009	4	28	30	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
GO:1900739	2.84	11	0.0019009	4	28	30	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
GO:1904781	1.17	7	0.0019009	2	5	6	positive regulation of protein localization to centrosome
GO:0032434	16.39	33	0.0019009	7	108	133	regulation of proteasomal ubiquitin-dependent protein catabolic process
GO:0055093	1.54	8	0.0019009	2	18	23	response to hyperoxia
GO:2000104	2.43	10	0.00198869	2	16	19	negative regulation of DNA-dependent DNA replication
GO:0097237	5.73	16	0.00198869	5	22	25	cellular response to toxic substance
GO:1902253	4.32	14	0.00198869	3	20	28	regulation of intrinsic apoptotic signaling pathway by p53 class mediator
GO:0052547	39.97	65	0.00198869	22	328	422	regulation of peptidase activity
GO:0035865	0.55	5	0.00198869	2	8	8	cellular response to potassium ion
GO:0045639	9.87	23	0.00198869	7	67	87	positive regulation of myeloid cell differentiation
GO:1901570	2.42	10	0.00206708	4	29	38	fatty acid derivative biosynthetic process
GO:0046456	2.42	10	0.00206708	4	29	38	icosanoid biosynthetic process
GO:0007275	38.93	63	0.00206708	27	350	427	multicellular organismal development
GO:0044281	179.77	230	0.00206708	107	1508	1733	small molecule metabolic process
GO:0046040	0.83	6	0.00214836	1	9	11	IMP metabolic process
GO:0001967	1.27	7	0.00214836	3	11	13	suckling behavior
GO:0007200	7.50	19	0.00214836	5	46	51	phospholipase C-activating G-protein coupled receptor signaling pathway
GO:0006188	0.83	6	0.00214836	1	9	11	IMP biosynthetic process
GO:0032201	1.60	8	0.00214836	2	24	25	telomere maintenance via semi-conservative replication
GO:0035194	1.56	8	0.00221991	1	17	17	posttranscriptional gene silencing by RNA
GO:0098531	11.84	26	0.00221991	6	45	54	transcription factor activity, direct ligand regulated sequence-specific DNA binding
GO:0043312	38.58	62	0.00221991	30	419	548	neutrophil degranulation
GO:0006505	1.22	7	0.00221991	2	18	24	GPI anchor metabolic process
GO:0005774	35.74	59	0.00221991	29	322	437	vacuolar membrane
GO:0009058	378.97	448	0.00221991	206	3634	4479	biosynthetic process
GO:0004879	11.84	26	0.00221991	6	45	54	RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding
GO:1903311	8.50	21	0.00221991	9	108	134	regulation of mRNA metabolic process
GO:0031396	21.52	40	0.00230055	10	232	292	regulation of protein ubiquitination
GO:1901983	6.00	17	0.00230055	5	52	66	regulation of protein acetylation
GO:0001829	0.59	5	0.00233693	2	12	22	trophectodermal cell differentiation
GO:0030207	1.25	7	0.00233693	1	12	14	chondroitin sulfate catabolic process
GO:0030120	3.44	12	0.00233693	2	35	35	vesicle coat
GO:0006986	6.64	18	0.00233693	6	43	55	response to unfolded protein
GO:1904259	1.21	7	0.00233693	1	5	5	regulation of basement membrane assembly involved in embryonic body morphogenesis
GO:1904261	1.21	7	0.00233693	1	5	5	positive regulation of basement membrane assembly involved in embryonic body morphogenesis
GO:0016840	0.73	6	0.00233693	1	9	9	carbon-nitrogen lyase activity
GO:0045180	1.26	7	0.00233693	1	5	5	basal cortex
GO:0045744	3.34	12	0.00233693	3	26	31	negative regulation of G-protein coupled receptor protein signaling pathway
GO:0071229	23.01	42	0.00233693	11	163	190	cellular response to acid chemical
GO:0031996	0.53	5	0.00233693	2	9	11	thioesterase binding
GO:1900746	2.90	11	0.00233693	2	13	15	regulation of vascular endothelial growth factor signaling pathway
GO:0008970	0.86	6	0.00233693	3	9	9	phosphatidylcholine 1-acylhydrolase activity
GO:0061136	17.84	35	0.00233693	8	138	170	regulation of proteasomal protein catabolic process
GO:1903146	6.14	17	0.00233693	5	38	43	regulation of mitophagy
GO:0003823	3.44	12	0.00233693	4	50	155	antigen binding
GO:0090032	0.52	5	0.00248159	1	5	5	negative regulation of steroid hormone biosynthetic process
GO:0051881	7.31	19	0.00248159	5	41	53	regulation of mitochondrial membrane potential
GO:0044699	1359.12	1467	0.00248159	670	9732	11942	single-organism process
GO:0035631	0.57	5	0.00248159	2	11	11	CD40 receptor complex
GO:0031944	0.52	5	0.00248159	1	5	5	negative regulation of glucocorticoid metabolic process
GO:0031947	0.52	5	0.00248159	1	5	5	negative regulation of glucocorticoid biosynthetic process

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GO:0007191	1.63	8	0.00248159	1	7	8	adenylate cyclase-activating dopamine receptor signaling pathway
GO:0045930	18.95	36	0.00248159	11	224	292	negative regulation of mitotic cell cycle
GO:0006282	7.96	20	0.00248159	8	82	90	regulation of DNA repair
GO:0022898	47.64	73	0.00248159	23	180	200	regulation of transmembrane transporter activity
GO:0032098	1.63	8	0.00248159	1	16	20	regulation of appetite
GO:0032412	46.82	72	0.00248159	22	174	194	regulation of ion transmembrane transporter activity
GO:2000064	0.55	5	0.0026263	1	6	6	regulation of cortisol biosynthetic process
GO:0045055	41.33	65	0.0026263	31	447	584	regulated secretory pathway
GO:0000731	5.17	15	0.0026263	3	36	37	DNA synthesis involved in DNA repair
GO:0000086	12.20	26	0.0026263	5	117	139	G2/M transition of mitotic cell cycle
GO:0016491	65.58	96	0.0026263	32	573	687	oxidoreductase activity
GO:0051017	8.17	20	0.0026263	6	39	48	actin filament bundle assembly
GO:0009968	144.38	186	0.0026263	68	966	1153	negative regulation of signal transduction
GO:0010952	21.86	40	0.0026263	11	145	175	positive regulation of peptidase activity
GO:0032727	0.93	6	0.00278752	2	17	21	positive regulation of interferon-alpha production
GO:0035966	6.89	18	0.00278752	6	47	62	response to topologically incorrect protein
GO:0002028	15.43	31	0.00278752	9	63	67	regulation of sodium ion transport
GO:0005921	0.84	6	0.00278752	1	14	18	gap junction
GO:0007517	17.36	34	0.00278752	11	98	109	muscle organ development
GO:1904779	1.25	7	0.00278752	2	6	7	regulation of protein localization to centrosome
GO:0052548	38.41	62	0.00286484	20	311	401	regulation of endopeptidase activity
GO:0071295	2.10	9	0.00294056	4	18	20	cellular response to vitamin
GO:0080134	148.71	192	0.00294056	83	1294	1633	regulation of response to stress
GO:1903201	8.35	20	0.00294056	4	50	59	regulation of oxidative stress-induced cell death
GO:0043534	4.23	13	0.0030032	4	19	25	blood vessel endothelial cell migration
GO:0009065	2.24	9	0.0030032	3	21	28	glutamine family amino acid catabolic process
GO:0042613	1.15	7	0.0030032	3	11	77	MHC class II protein complex
GO:0010463	1.67	8	0.0030032	4	15	17	mesenchymal cell proliferation
GO:0009605	129.18	170	0.0030032	69	1061	1330	response to external stimulus
GO:0036294	17.51	34	0.00307962	12	105	113	cellular response to decreased oxygen levels
GO:0042054	7.44	19	0.00307962	5	51	57	histone methyltransferase activity
GO:0016571	9.42	22	0.00307962	6	80	91	histone methylation
GO:0051705	22.95	41	0.00307962	9	64	83	multi-organism behavior
GO:0045648	1.77	8	0.00307962	3	20	25	positive regulation of erythrocyte differentiation
GO:0036296	1.72	8	0.00315947	2	23	30	response to increased oxygen levels
GO:0044839	12.27	26	0.00315947	5	119	141	cell cycle G2/M phase transition
GO:0031644	14.51	29	0.00322793	7	62	72	regulation of neurological system process
GO:0031527	3.59	12	0.00322793	3	14	20	filopodium membrane
GO:2001258	5.32	15	0.00322793	3	26	33	negative regulation of cation channel activity
GO:0090193	1.28	7	0.00322793	1	8	10	positive regulation of glomerulus development
GO:0000768	7.09	18	0.00322793	3	24	28	syncytium formation by plasma membrane fusion
GO:0008374	4.64	14	0.00322793	7	41	65	O-acyltransferase activity
GO:2000117	5.97	16	0.00329667	6	70	86	negative regulation of cysteine-type endopeptidase activity
GO:0006487	4.15	13	0.00329667	4	43	50	protein N-linked glycosylation
GO:2001056	18.33	35	0.00329667	8	120	145	positive regulation of cysteine-type endopeptidase activity
GO:0003013	17.01	33	0.00329667	9	113	133	circulatory system process
GO:0042060	12.94	27	0.00335858	13	70	78	wound healing
GO:1901698	96.39	131	0.00335858	50	635	749	response to nitrogen compound
GO:0002283	39.23	62	0.00335858	30	423	555	neutrophil activation involved in immune response
GO:0051145	1.32	7	0.00335858	3	19	19	smooth muscle cell differentiation
GO:0070507	14.55	29	0.00335858	7	145	168	regulation of microtubule cytoskeleton organization
GO:0031090	322.11	383	0.00335858	179	2745	3362	organelle membrane
GO:0043524	17.73	34	0.00342582	10	114	134	negative regulation of neuron apoptotic process
GO:1901575	118.49	157	0.00342582	74	1217	1501	organic substance catabolic process
GO:0031005	3.14	11	0.00342582	3	12	13	filamin binding
GO:0061512	2.19	9	0.00348124	3	22	24	protein localization to cilium
GO:0030008	2.24	9	0.00348124	2	10	11	TRAPP complex
GO:0006949	7.18	18	0.00348124	3	25	29	syncytium formation
GO:0009597	0.61	5	0.00348124	1	5	5	detection of virus
GO:1901722	1.31	7	0.00348124	1	12	12	regulation of cell proliferation involved in kidney development
GO:0061061	17.76	34	0.00348124	11	100	111	muscle structure development
GO:0033655	0.96	6	0.00348124	1	5	5	host cell cytoplasm part
GO:0000785	26.59	46	0.00357115	23	271	337	chromatin
GO:0016604	75.67	107	0.00357115	47	638	810	nuclear body
GO:0030149	1.36	7	0.00365548	1	16	19	sphingolipid catabolic process
GO:0018027	0.97	6	0.00365548	1	12	18	peptidyl-lysine dimethylation
GO:0044728	6.06	16	0.00371956	7	56	72	DNA methylation or demethylation

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GO:0030119	2.18	9	0.00371956	2	33	37	AP-type membrane coat adaptor complex
GO:0016416	0.37	4	0.00371956	1	5	5	O-palmitoyltransferase activity
GO:0061013	2.65	10	0.00371956	3	24	29	regulation of mRNA catabolic process
GO:0098743	2.69	10	0.00378529	1	18	20	cell aggregation
GO:0001502	2.68	10	0.00378529	1	17	19	cartilage condensation
GO:0007020	1.32	7	0.00378529	1	14	16	microtubule nucleation
GO:0033646	0.99	6	0.00378529	1	6	7	host intracellular part
GO:0048245	0.36	4	0.00391525	1	7	12	eosinophil chemotaxis
GO:1901606	9.97	22	0.00391525	10	91	102	alpha-amino acid catabolic process
GO:0005643	2.76	10	0.00391525	5	43	47	nuclear pore
GO:0031946	0.62	5	0.00391525	1	7	7	regulation of glucocorticoid biosynthetic process
GO:0032353	0.62	5	0.00391525	1	7	7	negative regulation of hormone biosynthetic process
GO:0003073	4.34	13	0.00398586	3	22	32	regulation of systemic arterial blood pressure
GO:0032409	49.16	74	0.00398586	24	193	213	regulation of transporter activity
GO:0034620	5.34	15	0.00405521	3	7	11	cellular response to unfolded protein
GO:1902589	155.92	198	0.00411391	82	1342	1599	single-organism organelle organization
GO:0006305	4.39	13	0.00411391	5	43	57	DNA alkylation
GO:0006306	4.39	13	0.00411391	5	43	57	DNA methylation
GO:0044238	835.91	925	0.00411391	446	7207	8768	primary metabolic process
GO:0042339	2.75	10	0.00414149	3	31	32	keratan sulfate metabolic process
GO:0031943	0.64	5	0.00414149	1	8	9	regulation of glucocorticoid metabolic process
GO:0032109	9.06	21	0.00414149	4	58	63	positive regulation of response to nutrient levels
GO:0032106	9.06	21	0.00414149	4	58	63	positive regulation of response to extracellular stimulus
GO:0010519	1.35	7	0.00414149	2	6	7	negative regulation of phospholipase activity
GO:0051567	0.97	6	0.00414149	1	9	15	histone H3-K9 methylation
GO:0043531	4.30	13	0.00414149	2	28	38	ADP binding
GO:0051716	276.13	330	0.00414149	138	2198	2655	cellular response to stimulus
GO:0007254	4.91	14	0.00414149	3	42	57	JNK cascade
GO:0014877	2.30	9	0.00426545	2	9	10	response to muscle inactivity involved in regulation of muscle adaptation
GO:0014894	2.30	9	0.00426545	2	9	10	response to denervation involved in regulation of muscle adaptation
GO:1902230	1.39	7	0.00426545	3	23	31	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage
GO:0009267	10.50	23	0.00426545	6	112	136	cellular response to starvation
GO:1900034	6.10	16	0.00426545	6	74	80	regulation of cellular response to heat
GO:0015929	1.42	7	0.00426545	1	13	15	hexosaminidase activity
GO:0032232	7.51	18	0.00426545	2	19	22	negative regulation of actin filament bundle assembly
GO:0044255	102.97	139	0.00426545	68	821	984	cellular lipid metabolic process
GO:0006506	0.97	6	0.00432556	1	17	21	GPI anchor biosynthetic process
GO:0010035	53.25	79	0.00432556	29	389	465	response to inorganic substance
GO:0007224	8.48	20	0.00432556	7	60	69	smoothened signaling pathway
GO:2001243	7.97	19	0.00438999	5	74	90	negative regulation of intrinsic apoptotic signaling pathway
GO:0035770	14.01	28	0.00438999	10	152	199	ribonucleoprotein granule
GO:1990511	0.16	3	0.00438999	1	3	5	piRNA biosynthetic process
GO:0044711	115.15	152	0.00452964	72	1072	1278	single-organism biosynthetic process
GO:1901576	372.24	435	0.00452964	200	3566	4398	organic substance biosynthetic process
GO:0034058	1.01	6	0.00458545	2	8	8	endosomal vesicle fusion
GO:0045141	0.36	4	0.00458545	1	9	9	meiotic telomere clustering
GO:0043299	39.59	62	0.00458545	30	434	571	leukocyte degranulation
GO:0046470	7.32	18	0.0046395	12	68	85	phosphatidylcholine metabolic process
GO:0014870	2.35	9	0.0046395	2	10	11	response to muscle inactivity
GO:1902883	8.73	20	0.0046395	4	39	46	negative regulation of response to oxidative stress
GO:0031670	2.22	9	0.00475608	4	22	24	cellular response to nutrient
GO:0005109	2.78	10	0.00475608	1	20	26	frizzled binding
GO:1903975	1.41	7	0.00475608	1	7	8	regulation of glial cell migration
GO:0015630	10.99	23	0.00475608	6	110	120	microtubule cytoskeleton
GO:0019222	683.48	763	0.00475608	334	5407	6639	regulation of metabolic process
GO:0044237	817.98	904	0.00475608	438	7162	8739	cellular metabolic process
GO:0071947	0.04	2	0.00475608	1	1	8	protein deubiquitination involved in ubiquitin-dependent protein catabolic process
GO:0048806	5.40	15	0.00480754	4	30	38	genitalia development
GO:0045786	43.01	66	0.00480754	24	447	571	negative regulation of cell cycle
GO:0043207	47.89	72	0.00480754	33	579	770	response to external biotic stimulus
GO:0000122	83.37	114	0.00480754	48	619	780	negative regulation of transcription from RNA polymerase II promoter
GO:0016868	0.67	5	0.00487561	3	8	10	intramolecular transferase activity, phosphotransferases
GO:0010635	4.93	14	0.00487561	2	9	9	regulation of mitochondrial fusion

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GO:0002526	4.14	13	0.00487561	4	53	63	acute inflammatory response
GO:0015106	1.40	7	0.00495243	1	11	11	bicarbonate transmembrane transporter activity
GO:0072677	0.39	4	0.00501314	1	8	13	eosinophil migration
GO:0010469	43.14	66	0.00501314	24	410	576	regulation of receptor activity
GO:0031072	11.94	25	0.00501314	7	94	118	heat shock protein binding
GO:0090169	0.65	5	0.00508222	1	15	19	regulation of spindle assembly
GO:0051026	0.38	4	0.00508222	1	5	6	chiasma assembly
GO:0042119	39.97	62	0.00515755	30	430	564	neutrophil activation
GO:0031328	217.52	265	0.00521783	110	1579	1942	positive regulation of cellular biosynthetic process
GO:0035967	5.54	15	0.00521783	3	10	16	cellular response to topologically incorrect protein
GO:1903706	36.85	58	0.00527792	23	357	486	regulation of hemopoiesis
GO:1903053	4.48	13	0.00534353	5	32	38	regulation of extracellular matrix organization
GO:0097165	0.18	3	0.00539527	1	5	5	nuclear stress granule
GO:0043507	8.00	19	0.00539527	7	58	78	positive regulation of JUN kinase activity
GO:0045202	65.09	93	0.00539527	40	196	239	synapse
GO:0044428	417.07	481	0.00539527	228	3668	4485	nuclear part
GO:2001032	0.70	5	0.00545669	2	13	15	regulation of double-strand break repair via nonhomologous end joining
GO:0061631	1.91	8	0.00552214	1	23	27	ubiquitin conjugating enzyme activity
GO:0051136	1.47	7	0.00558991	2	6	6	regulation of NK T cell differentiation
GO:0046545	0.71	5	0.00558991	1	3	5	development of primary female sexual characteristics
GO:0070840	1.90	8	0.00558991	2	21	23	dynein complex binding
GO:0006766	12.74	26	0.00567489	7	110	122	vitamin metabolic process
GO:0043217	1.48	7	0.00573876	1	12	12	myelin maintenance
GO:0016441	1.88	8	0.00577578	1	19	19	posttranscriptional gene silencing
GO:0034397	0.40	4	0.00577578	1	10	10	telomere localization
GO:0033043	116.21	152	0.00577578	62	976	1142	regulation of organelle organization
GO:0090220	0.40	4	0.00577578	1	10	10	chromosome localization to nuclear envelope involved in homologous chromosome segregation
GO:0006297	1.50	7	0.00577578	1	22	23	nucleotide-excision repair, DNA gap filling
GO:1900372	4.50	13	0.00581658	3	22	31	negative regulation of purine nucleotide biosynthetic process
GO:0030809	4.50	13	0.00581658	3	22	31	negative regulation of nucleotide biosynthetic process
GO:0000989	56.53	82	0.00581658	34	470	558	transcription factor activity, transcription factor binding
GO:0000988	56.53	82	0.00581658	34	470	558	transcription factor activity, protein binding
GO:0034587	1.05	6	0.00581658	3	15	19	piRNA metabolic process
GO:0004859	0.69	5	0.00588249	2	9	11	phospholipase inhibitor activity
GO:0051050	128.51	166	0.00588249	67	854	1019	positive regulation of transport
GO:0050700	1.28	7	0.00593468	3	13	14	CARD domain binding
GO:0036230	40.18	62	0.00593468	30	432	570	granulocyte activation
GO:0061650	1.94	8	0.00597363	1	24	28	ubiquitin-like protein conjugating enzyme activity
GO:0032107	19.21	35	0.00597363	11	176	216	regulation of response to nutrient levels
GO:0032104	19.21	35	0.00597363	11	176	216	regulation of response to extracellular stimulus
GO:0014070	93.66	126	0.00597363	50	656	777	response to organic cyclic compound
GO:1903050	22.86	40	0.00597363	11	217	278	regulation of proteolysis involved in cellular protein catabolic process
GO:0045069	8.79	20	0.00604125	4	77	92	regulation of viral genome replication
GO:0061572	8.95	20	0.00609374	6	41	51	actin filament bundle organization
GO:0045010	3.44	11	0.00609374	4	21	27	actin nucleation
GO:0016279	7.47	18	0.00609374	4	51	58	protein-lysine N-methyltransferase activity
GO:0042221	277.76	329	0.00614433	145	2058	2480	response to chemical
GO:0061014	1.89	8	0.00614433	1	20	23	positive regulation of mRNA catabolic process
GO:0010243	92.45	124	0.00625759	48	594	694	response to organonitrogen compound
GO:0016579	20.21	36	0.00625759	14	230	314	protein deubiquitination
GO:0016278	7.48	18	0.00625759	4	52	59	lysine N-methyltransferase activity
GO:0045137	0.74	5	0.00625759	1	4	6	development of primary sexual characteristics
GO:0051099	18.83	34	0.00634315	17	137	158	positive regulation of binding
GO:0061640	6.84	17	0.00641311	4	52	57	cytoskeleton-dependent cytokinesis
GO:0044794	0.75	5	0.00647322	1	13	13	positive regulation by host of viral process
GO:0070301	5.11	14	0.00647322	4	52	60	cellular response to hydrogen peroxide
GO:1901374	0.40	4	0.00652304	2	4	10	acetate ester transport
GO:0046676	6.96	17	0.00652304	2	33	38	negative regulation of insulin secretion
GO:0015695	1.51	7	0.00652304	3	18	24	organic cation transport
GO:0023026	1.10	6	0.00659605	2	16	47	MHC class II protein complex binding
GO:0035666	1.10	6	0.00666291	2	25	30	TRIF-dependent toll-like receptor signaling pathway
GO:1902494	70.17	98	0.00673157	35	725	888	catalytic complex
GO:0051052	29.29	48	0.00673157	21	327	389	regulation of DNA metabolic process
GO:0000790	19.61	35	0.00679964	15	172	211	nuclear chromatin
GO:0044724	6.39	16	0.00687201	9	76	105	single-organism carbohydrate catabolic process
GO:0034045	1.14	6	0.0070081	2	14	14	pre-autophagosomal structure membrane

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0060192	1.50	7	0.00706435	2	12	15	negative regulation of lipase activity
GO:0006903	2.54	9	0.00706435	2	14	15	vesicle targeting
GO:0017166	1.95	8	0.00712845	1	9	10	vinculin binding
GO:0060742	1.14	6	0.00712845	3	7	8	epithelial cell differentiation involved in prostate gland development
GO:0098586	1.56	7	0.00727148	2	26	31	cellular response to virus
GO:0022414	125.72	161	0.00732391	68	1099	1341	reproductive process
GO:0001101	34.21	54	0.00732391	16	274	317	response to acid chemical
GO:0016055	49.79	73	0.00734978	22	288	349	Wnt signaling pathway
GO:1904063	11.74	24	0.00734978	7	51	62	negative regulation of cation transmembrane transport
GO:0015101	1.13	6	0.00734978	2	14	14	organic cation transmembrane transporter activity
GO:0035580	5.81	15	0.00734978	5	52	80	specific granule lumen
GO:0051276	23.48	40	0.00734978	17	340	420	chromosome organization
GO:0045505	1.14	6	0.00747764	1	8	8	dynein intermediate chain binding
GO:0019985	2.50	9	0.00751782	2	37	40	translesion synthesis
GO:0033132	3.54	11	0.00751782	1	4	5	negative regulation of glucokinase activity
GO:1903300	3.54	11	0.00751782	1	4	5	negative regulation of hexokinase activity
GO:0019915	2.05	8	0.00774758	2	23	30	lipid storage
GO:0005126	13.01	26	0.00774758	12	174	234	cytokine receptor binding
GO:1903689	1.56	7	0.00780924	1	6	6	regulation of wound healing, spreading of epidermal cells
GO:0090407	41.63	63	0.00786965	28	406	495	organophosphate biosynthetic process
GO:0055102	0.76	5	0.00786965	2	13	16	lipase inhibitor activity
GO:0045637	22.57	39	0.00786965	14	182	249	regulation of myeloid cell differentiation
GO:0016052	7.14	17	0.00822922	10	81	111	carbohydrate catabolic process
GO:0045058	4.65	13	0.0082726	4	24	25	T cell selection
GO:0035973	0.45	4	0.0082726	1	5	6	aggrephagy
GO:2001021	3.56	11	0.00833096	5	53	71	negative regulation of response to DNA damage stimulus
GO:0070120	0.45	4	0.00840568	1	5	5	ciliary neurotrophic factor-mediated signaling pathway
GO:2000779	4.13	12	0.0086051	5	47	52	regulation of double-strand break repair
GO:0048562	13.90	27	0.00868963	12	101	122	embryonic organ morphogenesis
GO:0015747	1.18	6	0.00868963	1	5	5	urate transport
GO:0010994	3.64	11	0.00868963	1	4	5	free ubiquitin chain polymerization
GO:0032351	0.79	5	0.00868963	1	8	8	negative regulation of hormone metabolic process
GO:0009314	40.94	62	0.00876218	26	367	424	response to radiation
GO:0035519	3.59	11	0.00879376	1	4	5	protein K29-linked ubiquitination
GO:0070646	20.64	36	0.00879376	14	243	327	protein modification by small protein removal
GO:0042611	1.52	7	0.00882936	3	16	101	MHC protein complex
GO:0033131	3.63	11	0.00882936	1	7	9	regulation of glucokinase activity
GO:0009891	219.93	265	0.00882936	110	1600	1969	positive regulation of biosynthetic process
GO:0043401	11.95	24	0.00894433	5	51	59	steroid hormone mediated signaling pathway
GO:0008134	50.01	73	0.00894433	34	428	511	transcription factor binding
GO:0006471	1.59	7	0.00897723	3	20	21	protein ADP-ribosylation
GO:0042733	9.10	20	0.00897723	7	51	58	embryonic digit morphogenesis
GO:1903377	3.62	11	0.00897723	1	4	5	negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway
GO:0043687	54.08	78	0.00902577	30	376	463	post-translational protein modification
GO:0070842	3.61	11	0.00902577	1	4	8	aggresome assembly
GO:0048029	7.91	18	0.00907047	4	62	65	monosaccharide binding
GO:0043648	8.58	19	0.00919914	5	83	86	dicarboxylic acid metabolic process
GO:1902510	0.21	3	0.00941453	1	6	7	regulation of apoptotic DNA fragmentation
GO:0090192	1.63	7	0.00941453	1	11	13	regulation of glomerulus development
GO:0044424	1432.29	1528	0.00954113	710	11426	14183	intracellular part
GO:0032924	1.15	6	0.00968625	2	18	22	activin receptor signaling pathway
GO:0033147	1.67	7	0.00968625	3	11	14	negative regulation of intracellular estrogen receptor signaling pathway
GO:0015701	3.04	10	0.00968625	4	33	36	bicarbonate transport
GO:0070585	5.92	15	0.00968625	3	42	55	protein localization to mitochondrion
GO:0055114	80.70	109	0.00975156	44	750	892	oxidation-reduction process
GO:0051494	18.55	33	0.00975156	7	101	116	negative regulation of cytoskeleton organization
GO:0023023	1.21	6	0.00980001	2	17	50	MHC protein complex binding
GO:0043388	7.37	17	0.0098467	6	41	49	positive regulation of DNA binding
GO:0000910	7.24	17	0.0098467	4	58	64	cytokinesis
GO:0097602	3.64	11	0.00991074	1	9	11	cullin family protein binding
GO:0004497	9.19	20	0.00995754	8	80	95	monooxygenase activity
GO:1990381	4.21	12	0.00995754	2	15	21	ubiquitin-specific protease binding
GO:0071671	1.67	7	0.01008223	1	6	11	regulation of smooth muscle cell chemotaxis
GO:1902018	0.82	5	0.01008223	1	9	9	negative regulation of cilium assembly

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GO:1903299	3.69	11	0.01008223	1	8	10	regulation of hexokinase activity
GO:0051224	20.96	36	0.01012243	8	171	232	negative regulation of protein transport
GO:1903321	9.98	21	0.01012243	6	138	179	negative regulation of protein modification by small protein conjugation or removal
GO:0014854	2.66	9	0.01026956	2	13	14	response to inactivity
GO:0015696	9.94	21	0.01026956	7	53	65	ammonium transport
GO:0010566	1.64	7	0.01026956	2	13	13	regulation of ketone biosynthetic process
GO:0005789	93.14	125	0.01031114	57	794	957	endoplasmic reticulum membrane
GO:0016706	7.30	17	0.01036564	3	37	39	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors
GO:0012506	82.59	111	0.01041474	49	602	780	vesicle membrane
GO:0030154	198.34	241	0.01041474	106	1353	1651	cell differentiation
GO:0012505	8.68	19	0.01045298	8	47	54	endomembrane system
GO:0061734	3.67	11	0.01045298	1	4	5	parkin-mediated mitophagy in response to mitochondrial depolarization
GO:0007015	27.73	45	0.01048546	17	144	175	actin filament organization
GO:1901880	6.12	15	0.01048546	3	47	54	negative regulation of protein depolymerization
GO:0018119	0.80	5	0.01048546	1	5	6	peptidyl-cysteine S-nitrosylation
GO:0017014	0.80	5	0.01048546	1	5	6	protein nitrosylation
GO:0019904	85.23	114	0.01082923	39	566	693	protein domain specific binding
GO:0072393	1.24	6	0.01095426	1	9	10	microtubule anchoring at microtubule organizing center
GO:0097413	3.72	11	0.01101217	1	5	5	Lewy body
GO:0044314	3.73	11	0.01113954	1	4	5	protein K27-linked ubiquitination
GO:0051354	4.86	13	0.01126205	2	17	22	negative regulation of oxidoreductase activity
GO:2000483	0.51	4	0.01130406	1	6	7	negative regulation of interleukin-8 secretion
GO:1902307	3.23	10	0.01147227	2	14	17	positive regulation of sodium ion transmembrane transport
GO:0046466	1.73	7	0.01168848	1	20	23	membrane lipid catabolic process
GO:0030742	2.67	9	0.0117367	4	20	23	GTP-dependent protein binding
GO:0050764	9.54	20	0.01178107	7	61	88	regulation of phagocytosis
GO:0008637	5.60	14	0.01178107	3	47	52	apoptotic mitochondrial changes
GO:0070841	3.78	11	0.01182274	1	5	10	inclusion body assembly
GO:0034452	1.71	7	0.01196273	2	11	12	dynactin binding
GO:0044828	3.83	11	0.01199735	1	5	5	negative regulation by host of viral genome replication
GO:0010950	20.33	35	0.01199735	8	134	163	positive regulation of endopeptidase activity
GO:0016866	0.87	5	0.01203055	3	13	16	intramolecular transferase activity
GO:0034968	8.13	18	0.01203055	4	63	73	histone lysine methylation
GO:0043506	8.78	19	0.01205675	7	71	92	regulation of JUN kinase activity
GO:1904264	3.77	11	0.01205675	1	11	18	ubiquitin protein ligase activity involved in ERAD pathway
GO:0043242	6.23	15	0.01205675	3	50	63	negative regulation of protein complex disassembly
GO:0002437	2.19	8	0.01217953	1	18	28	inflammatory response to antigenic stimulus
GO:0033643	1.28	6	0.01217953	1	9	11	host cell part
GO:0048518	682.35	753	0.01221971	321	4744	5866	positive regulation of biological process
GO:0098779	3.78	11	0.01226184	1	7	8	mitophagy in response to mitochondrial depolarization
GO:0044233	0.84	5	0.01226184	2	9	11	ER-mitochondrion membrane contact site
GO:0016192	150.54	187	0.01235923	88	1240	1500	vesicle-mediated transport
GO:0000776	8.13	18	0.01235923	7	108	121	kinetochore
GO:0032590	2.24	8	0.01235923	1	13	14	dendrite membrane
GO:1903376	3.81	11	0.01260118	1	7	8	regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway
GO:0005346	0.26	3	0.01263803	1	5	6	purine ribonucleotide transmembrane transporter activity
GO:0000295	0.26	3	0.01263803	1	5	6	adenine nucleotide transmembrane transporter activity
GO:1903362	26.50	43	0.01263803	13	238	302	regulation of cellular protein catabolic process
GO:0006513	7.62	17	0.0126847	5	49	65	protein monoubiquitination
GO:0051588	12.41	24	0.01273272	9	57	63	regulation of neurotransmitter transport
GO:1904469	0.90	5	0.01284421	1	9	11	positive regulation of tumor necrosis factor secretion
GO:2001242	10.83	22	0.01289394	7	124	148	regulation of intrinsic apoptotic signaling pathway
GO:0000791	1.29	6	0.01292973	3	23	30	euchromatin
GO:0003676	294.83	344	0.01292973	160	3102	3882	nucleic acid binding
GO:0036120	2.18	8	0.01306076	2	18	20	cellular response to platelet-derived growth factor stimulus
GO:0051403	6.31	15	0.01310577	4	62	77	stress-activated MAPK cascade
GO:0004111	0.25	3	0.0131573	1	6	6	creatine kinase activity
GO:0044723	54.22	79	0.0131573	35	468	559	single-organism carbohydrate metabolic process

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GO:0071420	2.28	8	0.0131573	4	8	8	cellular response to histamine
GO:0043267	6.87	16	0.0131573	5	24	28	negative regulation of potassium ion transport
GO:0071704	876.03	954	0.01319302	464	7537	9182	organic substance metabolic process
GO:2000045	13.83	26	0.01329932	10	123	154	regulation of G1/S transition of mitotic cell cycle
GO:0046632	5.67	14	0.01332468	3	30	33	alpha-beta T cell differentiation
GO:0015812	1.77	7	0.01332468	2	7	8	gamma-aminobutyric acid transport
GO:0055015	0.55	4	0.01332468	1	10	10	ventricular cardiac muscle cell development
GO:0042165	1.77	7	0.01338462	2	12	13	neurotransmitter binding
GO:0090141	3.86	11	0.01343074	1	14	14	positive regulation of mitochondrial fission
GO:0005876	2.25	8	0.0136248	2	34	41	spindle microtubule
GO:0090494	3.87	11	0.01371017	1	4	5	dopamine uptake
GO:0090493	3.87	11	0.01371017	1	4	5	catecholamine uptake
GO:0051048	25.98	42	0.01371017	12	160	224	negative regulation of secretion
GO:0043046	1.77	7	0.01371017	4	20	20	DNA methylation involved in gamete generation
GO:0008276	8.86	19	0.01377423	5	77	84	protein methyltransferase activity
GO:0032092	13.19	25	0.01392364	10	81	90	positive regulation of protein binding
GO:0031016	2.81	9	0.01392364	5	18	21	pancreas development
GO:0012507	4.43	12	0.01392364	5	40	104	ER to Golgi transport vesicle membrane
GO:0010637	3.87	11	0.01392364	1	6	6	negative regulation of mitochondrial fusion
GO:1902916	3.85	11	0.01392364	1	9	10	positive regulation of protein polyubiquitination
GO:0032413	12.51	24	0.01392364	7	51	59	negative regulation of ion transmembrane transporter activity
GO:0031397	9.68	20	0.01396659	5	131	169	negative regulation of protein ubiquitination
GO:0003211	0.55	4	0.01402638	2	9	10	cardiac ventricle formation
GO:0044444	1026.62	1109	0.01415051	510	7964	9722	cytoplasmic part
GO:0033121	0.91	5	0.01430756	1	6	6	regulation of purine nucleotide catabolic process
GO:1903749	10.92	22	0.01447022	9	100	126	positive regulation of establishment of protein localization to mitochondrion
GO:1901985	4.51	12	0.01450486	3	28	35	positive regulation of protein acetylation
GO:1901203	1.78	7	0.01452151	1	9	9	positive regulation of extracellular matrix assembly
GO:0005737	422.43	479	0.01452151	207	2879	3500	cytoplasm
GO:0006767	9.02	19	0.01481476	5	75	85	water-soluble vitamin metabolic process
GO:0034063	1.32	6	0.01481476	1	11	14	stress granule assembly
GO:0001965	2.25	8	0.01481476	1	17	18	G-protein alpha-subunit binding
GO:0071877	0.90	5	0.01486501	1	4	6	regulation of adrenergic receptor signaling pathway
GO:0051301	35.76	54	0.01495937	14	364	409	cell division
GO:1902229	1.77	7	0.01506546	3	31	39	regulation of intrinsic apoptotic signaling pathway in response to DNA damage
GO:0002693	1.75	7	0.01506546	1	11	14	positive regulation of cellular extravasation
GO:0006607	1.83	7	0.01508802	5	14	15	NLS-bearing protein import into nucleus
GO:0061630	14.78	27	0.01508802	7	115	143	ubiquitin protein ligase activity
GO:0003406	1.79	7	0.01508802	2	4	6	retinal pigment epithelium development
GO:0044793	3.98	11	0.01520076	1	8	8	negative regulation by host of viral process
GO:0035520	0.55	4	0.01523566	1	7	9	monoubiquitinated protein deubiquitination
GO:0006304	7.06	16	0.01523566	7	76	94	DNA modification
GO:0002020	13.93	26	0.01528694	13	102	145	protease binding
GO:0030336	49.65	71	0.01552776	24	203	249	negative regulation of cell migration
GO:0032344	0.92	5	0.01552776	1	6	6	regulation of aldosterone metabolic process
GO:0032347	0.92	5	0.01552776	1	6	6	regulation of aldosterone biosynthetic process
GO:0030118	3.42	10	0.01581447	1	14	14	clathrin coat
GO:0016098	0.28	3	0.01586756	2	5	7	monoterpenoid metabolic process
GO:0019903	15.45	28	0.01596254	12	108	121	protein phosphatase binding
GO:0035864	0.93	5	0.01596254	2	14	14	response to potassium ion
GO:0005779	0.91	5	0.0160005	3	15	16	integral component of peroxisomal membrane
GO:0031231	0.91	5	0.0160005	3	15	16	intrinsic component of peroxisomal membrane
GO:2000146	51.51	73	0.01601967	25	216	266	negative regulation of cell motility
GO:0003207	0.58	4	0.01601967	2	10	11	cardiac chamber formation
GO:0030818	3.37	10	0.01601967	2	17	26	negative regulation of cAMP biosynthetic process
GO:0043274	4.60	12	0.01609421	2	12	15	phospholipase binding
GO:0030803	3.38	10	0.01617513	2	19	28	negative regulation of cyclic nucleotide biosynthetic process
GO:1902547	4.06	11	0.01654089	2	14	16	regulation of cellular response to vascular endothelial growth factor stimulus
GO:0000423	4.01	11	0.01654089	1	12	13	macromitophagy
GO:1903599	3.97	11	0.01654089	1	7	7	positive regulation of mitophagy
GO:0043067	165.30	202	0.01663588	86	1200	1468	regulation of programmed cell death
GO:0006622	1.36	6	0.01675344	1	16	18	protein targeting to lysosome
GO:0006955	61.89	85	0.01686161	45	684	1131	immune response
GO:0051059	1.82	7	0.01686161	3	25	28	NF-kappaB binding
GO:0044427	51.94	73	0.01699062	35	601	780	chromosomal part
GO:0097300	1.36	6	0.01711415	3	20	20	programmed necrotic cell death

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GO:0071287	3.99	11	0.01715248	1	7	9	cellular response to manganese ion
GO:0030594	9.84	20	0.01724015	8	53	65	neurotransmitter receptor activity
GO:0051937	5.85	14	0.01726224	2	10	12	catecholamine transport
GO:0008188	7.09	16	0.01726224	4	30	38	neuropeptide receptor activity
GO:0089720	0.29	3	0.01726224	1	7	20	caspase binding
GO:0051087	10.47	21	0.01734631	9	78	92	chaperone binding
GO:0016763	6.57	15	0.01753194	5	41	45	transferase activity, transferring pentosyl groups
GO:1903624	0.28	3	0.01782227	1	7	9	regulation of DNA catabolic process
GO:0008170	9.13	19	0.01782227	5	77	86	N-methyltransferase activity
GO:0030214	2.38	8	0.01786236	2	15	16	hyaluronan catabolic process
GO:0044710	433.03	489	0.01798923	236	3598	4337	single-organism metabolic process
GO:0007610	116.68	147	0.01817045	53	452	536	behavior
GO:0016747	12.71	24	0.01822693	15	141	193	transferase activity, transferring acyl groups other than amino-acyl groups
GO:0006464	340.38	390	0.01824045	176	2525	3029	cellular protein modification process
GO:0036211	340.38	390	0.01824045	176	2525	3029	protein modification process
GO:0043229	890.29	965	0.01827775	443	7527	9229	intracellular organelle
GO:1902235	5.31	13	0.01830369	2	26	30	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway
GO:0042605	1.30	6	0.01830369	2	15	58	peptide antigen binding
GO:0006497	28.16	44	0.01848568	16	108	141	protein lipidation
GO:0051246	287.55	334	0.01851995	137	2183	2644	regulation of protein metabolic process
GO:0051926	5.22	13	0.0185704	4	44	61	negative regulation of calcium ion transport
GO:0003006	58.75	81	0.0185704	31	499	589	developmental process involved in reproduction
GO:0032962	0.60	4	0.0185704	1	5	5	positive regulation of inositol trisphosphate biosynthetic process
GO:0006479	11.39	22	0.0185704	6	121	136	protein methylation
GO:0061647	1.37	6	0.0185704	1	13	19	histone H3-K9 modification
GO:0002275	42.68	62	0.0185704	30	445	585	myeloid cell activation involved in immune response
GO:0008213	11.39	22	0.0185704	6	121	136	protein alkylation
GO:0061659	15.08	27	0.01860419	7	120	148	ubiquitin-like protein ligase activity
GO:1903531	21.88	36	0.01869807	9	145	203	negative regulation of secretion by cell
GO:0008089	1.40	6	0.01872284	1	21	26	anterograde axon cargo transport
GO:0071546	0.59	4	0.01880255	2	7	7	pi-body
GO:0048232	28.98	45	0.019175	23	309	410	male gamete generation
GO:0009063	11.54	22	0.01925357	10	103	115	cellular amino acid catabolic process
GO:0004601	4.07	11	0.01925357	1	32	40	peroxidase activity
GO:0090201	4.12	11	0.01929576	1	14	17	negative regulation of release of cytochrome c from mitochondria
GO:0034384	1.41	6	0.01932116	3	8	15	high-density lipoprotein particle clearance
GO:1902930	6.67	15	0.01950098	5	73	85	regulation of alcohol biosynthetic process
GO:0032886	17.45	30	0.01967837	8	168	192	regulation of microtubule-based process
GO:0051010	1.92	7	0.01967837	1	12	12	microtubule plus-end binding
GO:0030111	52.16	73	0.0197202	22	277	340	regulation of Wnt signaling pathway
GO:0019841	0.61	4	0.01989258	1	13	14	retinol binding
GO:0034618	0.99	5	0.02003419	1	6	6	arginine binding
GO:0016874	16.54	29	0.02008847	10	150	168	ligase activity
GO:0003264	0.62	4	0.02033191	2	6	8	regulation of cardioblast proliferation
GO:0003266	0.62	4	0.02033191	2	6	8	regulation of secondary heart field cardioblast proliferation
GO:0046328	27.73	43	0.02057155	13	144	176	regulation of JNK cascade
GO:0006623	1.44	6	0.0206075	1	17	19	protein targeting to vacuole
GO:0001818	16.57	29	0.0206075	12	208	281	negative regulation of cytokine production
GO:0022829	0.62	4	0.02069037	1	17	22	wide pore channel activity
GO:1902806	14.47	26	0.02070561	10	133	169	regulation of cell cycle G1/S phase transition
GO:1900407	10.04	20	0.02070561	4	60	77	regulation of cellular response to oxidative stress
GO:0090199	5.35	13	0.02074539	2	39	45	regulation of release of cytochrome c from mitochondria
GO:0006301	3.00	9	0.02090961	2	43	47	postreplication repair
GO:0003712	51.53	72	0.02090961	30	421	503	transcription cofactor activity
GO:0010506	30.64	47	0.02118789	17	256	303	regulation of autophagy
GO:0006776	1.91	7	0.02120792	2	8	8	vitamin A metabolic process
GO:0090140	5.39	13	0.02128778	2	22	25	regulation of mitochondrial fission
GO:0070050	4.78	12	0.02159259	2	8	8	neuron cellular homeostasis
GO:0015216	0.32	3	0.02159259	1	6	7	purine nucleotide transmembrane transporter activity
GO:0046033	1.46	6	0.02159259	1	10	11	AMP metabolic process
GO:0007212	3.02	9	0.02196051	2	18	25	dopamine receptor signaling pathway
GO:0048585	189.32	227	0.02199633	86	1241	1520	negative regulation of response to stimulus
GO:0071897	8.03	17	0.02202702	4	93	98	DNA biosynthetic process
GO:0036464	13.68	25	0.02205588	9	143	189	cytoplasmic ribonucleoprotein granule
GO:0034464	1.02	5	0.02205588	1	8	8	BBSome
GO:0001768	1.98	7	0.02227373	1	5	6	establishment of T cell polarity

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0009893	422.67	476	0.02227373	196	3000	3658	positive regulation of metabolic process
GO:0003707	13.03	24	0.02227373	5	50	59	steroid hormone receptor activity
GO:0010833	2.51	8	0.02236881	2	43	49	telomere maintenance via telomere lengthening
GO:0002376	176.25	212	0.02244308	111	1692	2391	immune system process
GO:0016684	4.18	11	0.02244308	1	35	43	oxidoreductase activity, acting on peroxide as acceptor
GO:0043954	5.44	13	0.02262042	2	31	33	cellular component maintenance
GO:0010042	4.18	11	0.02272828	1	12	16	response to manganese ion
GO:0043414	16.85	29	0.02282317	10	192	222	macromolecule methylation
GO:0009060	1.49	6	0.02282317	1	16	20	aerobic respiration
GO:0072666	1.48	6	0.02301858	1	18	20	establishment of protein localization to vacuole
GO:0019538	433.44	487	0.02304528	222	3335	4052	protein metabolic process
GO:1902260	2.53	8	0.02307915	2	7	7	negative regulation of delayed rectifier potassium channel activity
GO:0015872	4.22	11	0.02307915	1	7	8	dopamine transport
GO:0016485	24.50	39	0.02314886	12	174	204	protein processing
GO:0097164	19.92	33	0.02314886	17	149	181	ammonium ion metabolic process
GO:1904385	1.99	7	0.02332494	2	11	11	cellular response to angiotensin
GO:1901992	9.49	19	0.02336199	6	51	63	positive regulation of mitotic cell cycle phase transition
GO:0004623	2.53	8	0.02336199	5	31	33	phospholipase A2 activity
GO:0044389	30.23	46	0.02349756	21	232	301	ubiquitin-like protein ligase binding
GO:0008152	910.51	983	0.02360793	481	7887	9618	metabolic process
GO:0009635	0.10	2	0.02367303	1	6	6	response to herbicide
GO:1900543	7.47	16	0.02379442	5	41	53	negative regulation of purine nucleotide metabolic process
GO:2000271	1.04	5	0.02387669	2	6	7	positive regulation of fibroblast apoptotic process
GO:0032872	30.39	46	0.02398525	15	180	215	regulation of stress-activated MAPK cascade
GO:0032647	1.52	6	0.0240446	2	23	30	regulation of interferon-alpha production
GO:1900825	1.99	7	0.0240446	2	3	5	regulation of membrane depolarization during cardiac muscle cell action potential
GO:0043618	8.86	18	0.02405966	3	96	130	regulation of transcription from RNA polymerase II promoter in response to stress
GO:0040029	16.78	29	0.02417562	13	161	232	regulation of gene expression, epigenetic
GO:0010569	2.00	7	0.02464128	3	22	25	regulation of double-strand break repair via homologous recombination
GO:0044271	277.46	321	0.02464128	141	2702	3364	cellular nitrogen compound biosynthetic process
GO:0006887	65.66	88	0.02486193	44	616	786	exocytosis
GO:2000378	7.51	16	0.02486193	3	43	51	negative regulation of reactive oxygen species metabolic process
GO:0001773	3.65	10	0.02496375	3	20	25	myeloid dendritic cell activation
GO:0015844	6.84	15	0.02499057	3	18	20	monoamine transport
GO:1902176	4.27	11	0.02503392	1	16	19	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway
GO:1903047	46.82	66	0.02513616	25	549	651	mitotic cell cycle process
GO:0015866	0.33	3	0.02513616	1	6	9	ADP transport
GO:1903055	2.54	8	0.02517418	2	17	19	positive regulation of extracellular matrix organization
GO:2000269	1.47	6	0.02520714	3	15	16	regulation of fibroblast apoptotic process
GO:0032648	3.12	9	0.0254832	3	38	51	regulation of interferon-beta production
GO:0050866	16.91	29	0.02562218	11	146	194	negative regulation of cell activation
GO:0050905	21.45	35	0.02562218	9	63	78	neuromuscular process
GO:0045184	119.67	149	0.02573649	57	990	1184	establishment of protein localization
GO:0009620	1.53	6	0.02575451	3	35	47	response to fungus
GO:0030176	7.58	16	0.02582999	6	88	180	integral component of endoplasmic reticulum membrane
GO:0090370	0.33	3	0.02582999	1	4	5	negative regulation of cholesterol efflux
GO:0043412	353.19	401	0.02585628	183	2665	3199	macromolecule modification
GO:0051213	9.60	19	0.0259796	5	74	85	dioxygenase activity
GO:0045980	7.56	16	0.02605498	5	42	55	negative regulation of nucleotide metabolic process
GO:0001767	2.06	7	0.02605498	1	6	7	establishment of lymphocyte polarity
GO:0014002	3.73	10	0.02628847	1	17	27	astrocyte development
GO:0045059	2.04	7	0.0263431	1	8	8	positive thymic T cell selection
GO:0006541	1.06	5	0.02639847	3	19	21	glutamine metabolic process
GO:0005344	3.16	11	0.02657754	1	9	14	oxygen transporter activity
GO:0032410	13.32	24	0.02684482	7	59	67	negative regulation of transporter activity
GO:1903541	4.35	11	0.02684482	1	16	16	regulation of exosomal secretion
GO:0015671	3.17	11	0.02684482	1	10	15	oxygen transport
GO:0007283	28.10	43	0.02691529	22	307	408	spermatogenesis
GO:0031098	6.93	15	0.02702131	4	67	82	stress-activated protein kinase signaling cascade
GO:1902107	16.36	28	0.02725976	9	111	151	positive regulation of leukocyte differentiation

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GO:0071556	1.48	6	0.0272844	2	19	85	integral component of lumenal side of endoplasmic reticulum membrane
GO:0043522	1.10	5	0.02732503	1	8	12	leucine zipper domain binding
GO:0006672	6.24	14	0.02740138	4	63	74	ceramide metabolic process
GO:0043620	8.99	18	0.02746844	3	100	136	regulation of DNA-templated transcription in response to stress
GO:2001033	0.35	3	0.02746844	1	5	6	negative regulation of double-strand break repair via nonhomologous end joining
GO:1903817	2.62	8	0.02756954	2	8	8	negative regulation of voltage-gated potassium channel activity
GO:0090030	1.10	5	0.02759264	1	9	9	regulation of steroid hormone biosynthetic process
GO:0006656	3.15	9	0.02782708	5	30	45	phosphatidylcholine biosynthetic process
GO:0051247	174.53	209	0.02784814	86	1288	1564	positive regulation of protein metabolic process
GO:1903214	12.53	23	0.02784814	7	82	106	regulation of protein targeting to mitochondrion
GO:0070302	30.75	46	0.02788213	15	181	216	regulation of stress-activated protein kinase signaling cascade
GO:1902115	14.11	25	0.02790987	10	130	157	regulation of organelle assembly
GO:0034776	2.61	8	0.02795824	4	10	11	response to histamine
GO:0018022	9.01	18	0.02815771	4	74	85	peptidyl-lysine methylation
GO:0017034	1.56	6	0.02835996	2	5	5	Rap guanyl-nucleotide exchange factor activity
GO:0072488	2.59	8	0.02839638	4	20	23	ammonium transmembrane transport
GO:0008347	2.09	7	0.02839638	1	14	20	glial cell migration
GO:1904467	1.12	5	0.02846358	1	15	18	regulation of tumor necrosis factor secretion
GO:0070265	1.56	6	0.02860496	3	21	21	necrotic cell death
GO:0006296	2.08	7	0.02867212	1	33	44	nucleotide-excision repair, DNA incision, 5'-to lesion
GO:0015605	1.11	5	0.02872181	2	18	21	organophosphate ester transmembrane transporter activity
GO:0009755	13.46	24	0.02880966	5	78	97	hormone-mediated signaling pathway
GO:0051258	6.99	15	0.02884034	3	46	58	protein polymerization
GO:0035067	0.69	4	0.02893847	1	13	16	negative regulation of histone acetylation
GO:0015293	14.85	26	0.02943504	9	114	123	symporter activity
GO:0005544	5.02	12	0.02943504	5	24	25	calcium-dependent phospholipid binding
GO:0043201	2.07	7	0.02963347	2	10	10	response to leucine
GO:0030131	1.59	6	0.0296907	1	22	24	clathrin adaptor complex
GO:0050717	0.36	3	0.0297093	1	4	5	positive regulation of interleukin-1 alpha secretion
GO:0032730	0.36	3	0.0297093	1	4	7	positive regulation of interleukin-1 alpha production
GO:0036119	2.61	8	0.03016499	2	19	21	response to platelet-derived growth factor
GO:0045945	1.60	6	0.03028334	2	10	11	positive regulation of transcription from RNA polymerase III promoter
GO:2000427	0.36	3	0.0304497	1	4	19	positive regulation of apoptotic cell clearance
GO:1900117	2.11	7	0.03049542	4	21	23	regulation of execution phase of apoptosis
GO:0032480	2.64	8	0.03100368	2	39	52	negative regulation of type I interferon production
GO:0030659	81.27	105	0.03121272	47	586	762	cytoplasmic vesicle membrane
GO:0010677	7.08	15	0.03121272	4	30	37	negative regulation of cellular carbohydrate metabolic process
GO:0035025	3.21	9	0.03150848	1	13	14	positive regulation of Rho protein signal transduction
GO:0061608	0.37	3	0.03153442	3	9	10	nuclear import signal receptor activity
GO:0010523	1.59	6	0.03153442	2	6	7	negative regulation of calcium ion transport into cytosol
GO:0001756	3.82	10	0.03165255	1	34	40	somitogenesis
GO:0021591	2.67	8	0.03168861	3	12	22	ventricular system development
GO:0015867	0.36	3	0.03190223	1	8	11	ATP transport
GO:1902236	4.46	11	0.03251271	1	16	18	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway
GO:0030575	1.16	5	0.03264501	3	10	11	nuclear body organization
GO:0006644	44.03	62	0.03273098	31	352	416	phospholipid metabolic process
GO:0016198	4.43	11	0.03301113	2	6	6	axon choice point recognition
GO:0034766	13.53	24	0.03302501	7	69	84	negative regulation of ion transmembrane transport
GO:0045502	1.64	6	0.0330418	1	17	19	dynein binding
GO:0036503	4.45	11	0.03312169	1	17	24	ERAD pathway
GO:0042981	162.31	195	0.03318441	85	1188	1453	regulation of apoptotic process
GO:0043226	1071.35	1144	0.03337241	538	8790	10801	organelle
GO:0033273	9.18	18	0.03340459	10	78	83	response to vitamin
GO:0005351	1.63	6	0.03376985	1	10	11	sugar:proton symporter activity
GO:0005402	1.63	6	0.03376985	1	10	11	cation:sugar symporter activity
GO:0070742	1.65	6	0.03384394	1	11	21	C2H2 zinc finger domain binding
GO:0070330	1.16	5	0.0339174	2	19	24	aromatase activity
GO:0044441	42.67	60	0.03435593	24	318	354	ciliary part
GO:0005942	1.15	5	0.03437212	1	11	12	phosphatidylinositol 3-kinase complex
GO:0042415	4.55	11	0.03464883	1	6	9	norepinephrine metabolic process
GO:0051184	1.17	5	0.03464883	2	15	18	cofactor transporter activity

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GO:0005355	1.63	6	0.03477995	1	14	15	glucose transmembrane transporter activity
GO:0050433	7.13	15	0.03497438	4	34	41	regulation of catecholamine secretion
GO:0033683	2.18	7	0.03531689	1	35	47	nucleotide-excision repair, DNA incision
GO:2001233	34.26	50	0.0354671	17	315	378	regulation of apoptotic signaling pathway
GO:0015669	3.47	11	0.0354671	1	14	19	gas transport
GO:0033209	7.82	16	0.03553746	6	108	160	tumor necrosis factor-mediated signaling pathway
GO:0015149	1.65	6	0.0359503	1	15	16	hexose transmembrane transporter activity
GO:0032612	0.37	3	0.0359503	1	4	5	interleukin-1 production
GO:0032611	0.37	3	0.0359503	1	4	5	interleukin-1 beta production
GO:1990776	2.20	7	0.03596362	2	13	14	response to angiotensin
GO:1902931	1.18	5	0.03596362	1	16	18	negative regulation of alcohol biosynthetic process
GO:0044432	136.60	167	0.03596362	76	1108	1378	endoplasmic reticulum part
GO:0033138	12.94	23	0.03612741	10	76	91	positive regulation of peptidyl-serine phosphorylation
GO:0072520	0.74	4	0.03632153	1	9	12	seminiferous tubule development
GO:0004622	2.23	7	0.0367358	5	19	19	lysophospholipase activity
GO:1901989	10.06	19	0.03680121	6	62	77	positive regulation of cell cycle phase transition
GO:0046929	4.58	11	0.03680121	1	10	11	negative regulation of neurotransmitter secretion
GO:0046683	17.51	29	0.037043	11	117	129	response to organophosphorus
GO:0071243	0.40	3	0.03712357	1	11	17	cellular response to arsenic-containing substance
GO:0051604	26.30	40	0.03736539	13	194	229	protein maturation
GO:0009987	1469.91	1549	0.03737271	723	11284	13780	cellular process
GO:0008306	10.06	19	0.03740041	4	63	73	associative learning
GO:2000573	4.53	11	0.03740041	5	47	61	positive regulation of DNA biosynthetic process
GO:0009084	0.78	4	0.03755671	2	10	13	glutamine family amino acid biosynthetic process
GO:0090279	2.12	7	0.03755671	4	25	37	regulation of calcium ion import
GO:1902017	5.21	12	0.03757876	4	41	42	regulation of cilium assembly
GO:0072006	0.75	4	0.03762416	1	7	9	nephron development
GO:1903409	3.95	10	0.03762416	3	21	30	reactive oxygen species biosynthetic process
GO:0006283	3.37	9	0.03821249	3	66	81	transcription-coupled nucleotide-excision repair
GO:0001505	21.46	34	0.03821249	12	79	94	regulation of neurotransmitter levels
GO:0034763	13.73	24	0.03821512	7	77	92	negative regulation of transmembrane transport
GO:0008285	90.92	115	0.03824024	48	572	701	negative regulation of cell proliferation
GO:0032183	1.21	5	0.03839375	1	13	17	SUMO binding
GO:1902175	4.61	11	0.03839375	1	23	27	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway
GO:0032839	4.62	11	0.0387362	2	22	23	dendrite cytoplasm
GO:0055069	4.59	11	0.03911883	1	13	14	zinc ion homeostasis
GO:0035577	5.24	12	0.03915508	8	52	58	azurophil granule membrane
GO:0005975	58.82	80	0.03915508	36	544	647	carbohydrate metabolic process
GO:1900449	10.06	19	0.03915508	6	35	37	regulation of glutamate receptor signaling pathway
GO:0000723	5.95	13	0.03931513	3	75	98	telomere maintenance
GO:0045907	2.77	8	0.03932299	3	22	25	positive regulation of vasoconstriction
GO:0007568	24.70	38	0.03932299	13	201	241	aging
GO:0071363	38.70	55	0.03945202	25	222	250	cellular response to growth factor stimulus
GO:0031579	3.99	10	0.03945202	3	17	21	membrane raft organization
GO:0098902	2.24	7	0.03945202	2	4	6	regulation of membrane depolarization during action potential
GO:0046638	4.65	11	0.03945282	5	33	38	positive regulation of alpha-beta T cell differentiation
GO:0051293	4.62	11	0.03945602	2	30	31	establishment of spindle localization
GO:0044260	635.23	693	0.03945602	325	5541	6783	cellular macromolecule metabolic process
GO:0045333	2.82	8	0.03960556	2	35	39	cellular respiration
GO:0044451	94.43	119	0.0396288	56	873	1084	nucleoplasm part
GO:0005871	1.22	5	0.03972054	1	18	19	kinesin complex
GO:0010603	0.40	3	0.03980437	1	6	6	regulation of cytoplasmic mRNA processing body assembly
GO:0045920	6.60	14	0.04000007	4	26	32	negative regulation of exocytosis
GO:0072559	0.40	3	0.04007753	1	4	6	NLRP3 inflammasome complex
GO:0016746	16.16	27	0.04013628	17	173	226	transferase activity, transferring acyl groups
GO:0090278	8.68	17	0.04025989	2	36	42	negative regulation of peptide hormone secretion
GO:2000310	6.62	14	0.04041365	5	16	18	regulation of N-methyl-D-aspartate selective glutamate receptor activity
GO:0007218	7.99	16	0.04049104	4	50	72	neuropeptide signaling pathway
GO:0070888	2.79	8	0.04058854	3	28	34	E-box binding
GO:0015980	8.70	17	0.04062535	9	88	104	energy derivation by oxidation of organic compounds
GO:0031641	9.50	18	0.04064314	6	32	35	regulation of myelination
GO:0031227	8.05	16	0.04090165	6	92	184	intrinsic component of endoplasmic reticulum membrane
GO:0002792	8.71	17	0.04090165	2	37	43	negative regulation of peptide secretion

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GO:0042826	11.63	21	0.04100749	7	85	103	histone deacetylase binding
GO:0007528	9.46	18	0.04105777	6	22	26	neuromuscular junction development
GO:0032838	4.68	11	0.04116932	2	24	25	cell projection cytoplasm
GO:0043623	35.63	51	0.04132566	14	299	383	cellular protein complex assembly
GO:1903351	4.67	11	0.04144578	1	11	15	cellular response to dopamine
GO:1903350	4.67	11	0.04144578	1	11	15	response to dopamine
GO:0035065	5.34	12	0.04167737	4	42	52	regulation of histone acetylation
GO:0051503	0.42	3	0.0416977	1	10	13	adenine nucleotide transport
GO:0015868	0.42	3	0.0416977	1	10	14	purine ribonucleotide transport
GO:0002753	2.29	7	0.04174332	3	30	36	cytoplasmic pattern recognition receptor signaling pathway
GO:0044273	2.81	8	0.04174332	2	39	47	sulfur compound catabolic process
GO:0046885	2.28	7	0.04205247	2	17	18	regulation of hormone biosynthetic process
GO:0045646	2.83	8	0.04220368	3	33	41	regulation of erythrocyte differentiation
GO:0070403	1.23	5	0.04222247	2	13	14	NAD+ binding
GO:0032182	10.95	20	0.04222247	5	85	104	ubiquitin-like protein binding
GO:0044232	1.24	5	0.04222247	2	13	15	organelle membrane contact site
GO:0007033	7.39	15	0.04227162	5	74	82	vacuole organization
GO:0032438	1.73	6	0.04230231	1	18	23	melanosome organization
GO:0030433	5.31	12	0.04250867	2	48	66	ER-associated ubiquitin-dependent protein catabolic process
GO:0003062	1.26	5	0.04256022	1	5	6	regulation of heart rate by chemical signal
GO:0061462	1.74	6	0.04318245	1	23	26	protein localization to lysosome
GO:0042608	2.28	7	0.04337331	1	6	10	T cell receptor binding
GO:0021987	14.83	25	0.04361102	9	52	60	cerebral cortex development
GO:0043271	20.99	33	0.04361102	12	105	131	negative regulation of ion transport
GO:0044267	356.16	400	0.04366048	179	2759	3356	cellular protein metabolic process
GO:0048709	5.39	12	0.04400058	4	24	26	oligodendrocyte differentiation
GO:0042220	4.75	11	0.04402821	3	27	33	response to cocaine
GO:2001022	6.72	14	0.04409399	7	68	73	positive regulation of response to DNA damage stimulus
GO:0007143	0.43	3	0.04431272	1	8	10	female meiotic division
GO:0031528	1.77	6	0.044595	4	20	25	microvillus membrane
GO:0005776	5.42	12	0.04482625	3	52	63	autophagosome
GO:0061418	6.78	14	0.044915	1	72	95	regulation of transcription from RNA polymerase II promoter in response to hypoxia
GO:0003008	207.63	242	0.04495726	97	1047	1233	system process
GO:0002682	132.08	160	0.04497605	77	1197	1731	regulation of immune system process
GO:0005775	15.56	26	0.04530668	16	145	200	vacuolar lumen
GO:1900426	0.43	3	0.04530668	2	8	9	positive regulation of defense response to bacterium
GO:0030815	4.10	10	0.04543792	2	21	30	negative regulation of cAMP metabolic process
GO:0030117	5.40	12	0.04556002	2	46	47	membrane coat
GO:0051969	2.88	8	0.04558371	2	12	15	regulation of transmission of nerve impulse
GO:1901679	0.43	3	0.04580246	1	11	12	nucleotide transmembrane transport
GO:0001504	4.73	11	0.04596102	1	11	11	neurotransmitter uptake
GO:0070887	190.49	223	0.04628908	100	1309	1543	cellular response to chemical stimulus
GO:0030800	4.11	10	0.04629919	2	23	32	negative regulation of cyclic nucleotide metabolic process
GO:1902116	2.91	8	0.04635625	3	28	32	negative regulation of organelle assembly
GO:0010906	13.31	23	0.04635625	8	81	97	regulation of glucose metabolic process
GO:0032200	6.12	13	0.04635625	3	79	111	telomere organization
GO:0005938	26.83	40	0.04641969	14	116	125	cell cortex
GO:0090184	3.50	9	0.04644444	3	33	41	positive regulation of kidney development
GO:0010269	0.15	2	0.04646787	1	4	6	response to selenium ion
GO:0035082	3.41	9	0.04689062	5	25	25	axoneme assembly
GO:0002053	2.91	8	0.04691013	5	26	28	positive regulation of mesenchymal cell proliferation
GO:2000757	0.83	4	0.04699005	1	16	20	negative regulation of peptidyl-lysine acetylation
GO:0060455	0.15	2	0.04792232	1	2	6	negative regulation of gastric acid secretion
GO:0008083	14.88	25	0.04792232	9	123	147	growth factor activity
GO:0005720	1.30	5	0.04802303	2	25	39	nuclear heterochromatin
GO:0048738	5.43	12	0.04822555	4	21	24	cardiac muscle tissue development
GO:2000756	5.47	12	0.0482897	4	45	57	regulation of peptidyl-lysine acetylation
GO:0071248	20.36	32	0.04831301	12	128	155	cellular response to metal ion
GO:0010038	41.03	57	0.04831959	22	277	326	response to metal ion
GO:0045912	7.53	15	0.04841457	4	38	46	negative regulation of carbohydrate metabolic process
GO:0035282	4.16	10	0.04848376	1	35	42	segmentation
GO:0042439	9.63	18	0.04853833	12	90	109	ethanolamine-containing compound metabolic process
GO:0008270	93.69	117	0.04860615	45	674	836	zinc ion binding
GO:0032922	6.86	14	0.04862608	4	47	56	circadian regulation of gene expression
GO:0034622	52.20	70	0.04913809	23	525	737	cellular macromolecular complex assembly

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0032270	166.74	197	0.04924155	80	1205	1451	positive regulation of cellular protein metabolic process
GO:0008094	6.22	13	0.04924155	4	44	54	DNA-dependent ATPase activity
GO:0050662	22.03	34	0.04924155	13	168	191	coenzyme binding
GO:0001016	1.28	5	0.04924155	1	4	5	RNA polymerase III regulatory region DNA binding
GO:0042572	3.54	9	0.04924155	4	27	30	retinol metabolic process
GO:0048753	2.34	7	0.04924155	2	19	24	pigment granule organization
GO:0033691	0.85	4	0.04924155	2	8	9	sialic acid binding
GO:0044390	5.47	12	0.04925865	2	18	19	ubiquitin-like protein conjugating enzyme binding
GO:0017147	4.85	11	0.04971424	2	21	25	Wnt-protein binding
GO:0031466	0.45	3	0.04991748	2	5	6	Cul5-RING ubiquitin ligase complex
GO:0010225	0.85	4	0.04995983	2	13	13	response to UV-C
GO:0005996	14.14	27	0.04997778	12	160	192	monosaccharide metabolic process

GO: Gene ontology; ANG: Average number of genes involved; Can.: Number of candidate genes; FDR: *p*-value adjusted for false discovery rate (only FDR values <0.05 were taken as statistically significant); Unique: Unique genes detected; Max: Maximum possible number of genes detected; Total: total number of genes detected.

Table S7. GoWinda enrichment analysis results for TIX.

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0035145	0.265	6	0.00127286	1	7	9	exon-exon junction complex
GO:0016174	0.532	7	0.00127286	2	5	6	NAD(P)H oxidase activity
GO:0050810	6.87	31	0.00127286	11	77	89	regulation of steroid biosynthetic process
GO:0061333	2.215	11	0.00127286	2	13	20	renal tubule morphogenesis
GO:1901678	0.568	10	0.00127286	2	8	11	iron coordination entity transport
GO:0016427	0.372	6	0.00127286	1	6	7	tRNA (cytosine) methyltransferase activity
GO:0016469	1.009	10	0.00127286	2	25	40	proton-transporting two-sector ATPase complex
GO:0016471	0.501	9	0.00127286	1	8	16	vacuolar proton-transporting V-type ATPase complex
GO:0072512	2.439	12	0.00127286	4	35	45	trivalent inorganic cation transport
GO:0015232	0.553	10	0.00127286	2	6	8	heme transporter activity
GO:0060323	0.839	9	0.00127286	1	5	9	head morphogenesis
GO:0048671	4.233	17	0.00127286	3	8	9	negative regulation of collateral sprouting
GO:0046148	4.716	17	0.00127286	3	38	46	pigment biosynthetic process
GO:0042632	5.976	20	0.00127286	5	57	67	cholesterol homeostasis
GO:0030670	4.612	17	0.00127286	7	55	105	phagocytic vesicle membrane
GO:1904251	1.506	20	0.00127286	3	12	12	regulation of bile acid metabolic process
GO:0051184	1.172	10	0.00127286	2	15	18	cofactor transporter activity
GO:0015682	2.439	12	0.00127286	4	35	45	ferric iron transport
GO:0071498	2.207	12	0.00127286	3	15	17	cellular response to fluid shear stress
GO:0038007	4.683	21	0.00127286	4	8	8	netrin-activated signaling pathway
GO:0033179	0.807	10	0.00127286	2	8	8	proton-transporting V-type ATPase, V0 domain
GO:0033177	0.862	10	0.00127286	2	11	14	proton-transporting two-sector ATPase complex, proton-transporting domain
GO:0033176	0.541	9	0.00127286	1	9	17	proton-transporting V-type ATPase complex
GO:0051055	3.392	28	0.00127286	8	43	47	negative regulation of lipid biosynthetic process
GO:0035850	2.479	12	0.00127286	3	8	9	epithelial cell differentiation involved in kidney development
GO:0010565	14.967	38	0.00127286	15	175	209	regulation of cellular ketone metabolic process
GO:0045833	5.589	29	0.00127286	9	71	84	negative regulation of lipid metabolic process
GO:0044429	59.181	95	0.00127286	58	794	975	mitochondrial part
GO:0015991	2.038	11	0.00127286	3	25	27	ATP hydrolysis coupled proton transport
GO:0015988	2.038	11	0.00127286	3	25	27	energy coupled proton transmembrane transport, against electrochemical gradient
GO:0045939	2.458	26	0.00127286	6	23	25	negative regulation of steroid metabolic process
GO:0005042	4.285	20	0.00127286	3	6	6	netrin receptor activity
GO:0097090	7.456	21	0.00127286	3	6	9	presynaptic membrane organization
GO:0043249	0.695	9	0.00127286	1	8	12	erythrocyte maturation
GO:0070857	1.342	20	0.00127286	3	10	10	regulation of bile acid biosynthetic process

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0010894	2.16	26	0.00127286	6	21	23	negative regulation of steroid biosynthetic process
GO:0046890	13.506	40	0.00127286	16	153	170	regulation of lipid biosynthetic process
GO:0019218	10.874	38	0.00127286	13	99	114	regulation of steroid metabolic process
GO:0033572	2.419	12	0.00127286	4	34	43	transferrin transport
GO:0015886	0.553	10	0.00127286	2	6	8	heme transport
GO:0055092	5.976	20	0.00127286	5	57	67	sterol homeostasis
GO:0015801	2.544	12	0.00127286	1	4	5	aromatic amino acid transport
GO:0042162	2.032	11	0.00223708	4	26	32	telomeric DNA binding
GO:0009226	2.175	11	0.00223708	4	16	20	nucleotide-sugar biosynthetic process
GO:0000777	6.226	19	0.00223708	8	80	91	condensed chromosome kinetochore
GO:0051181	2.09	10	0.00223708	2	22	30	cofactor transport
GO:0071705	63.573	101	0.00223708	37	425	523	nitrogen compound transport
GO:0055088	11.079	28	0.00223708	10	92	104	lipid homeostasis
GO:0006470	34.837	61	0.00311462	25	163	187	protein dephosphorylation
GO:0004721	31.176	55	0.00311462	21	142	165	phosphoprotein phosphatase activity
GO:0000096	3.462	14	0.00311462	5	29	33	sulfur amino acid metabolic process
GO:0043020	0.628	6	0.00311462	1	7	10	NADPH oxidase complex
GO:0050667	1.056	7	0.00361117	2	11	12	homocysteine metabolic process
GO:0030218	4.539	16	0.00361117	4	43	61	erythrocyte differentiation
GO:0031966	33.66	58	0.00361117	34	496	620	mitochondrial membrane
GO:0007185	7.2	20	0.00361117	3	6	6	transmembrane receptor protein tyrosine phosphatase signaling pathway
GO:0019198	15.678	34	0.00361117	7	15	16	transmembrane receptor protein phosphatase activity
GO:0051654	0.843	7	0.00361117	2	8	12	establishment of mitochondrion localization
GO:0005001	15.678	34	0.00361117	7	15	16	transmembrane receptor protein tyrosine phosphatase activity
GO:0007420	40.535	70	0.00361117	23	151	193	brain development
GO:0048670	5.642	17	0.00438339	3	17	20	regulation of collateral sprouting
GO:0090662	2.521	11	0.00438339	3	32	34	ATP hydrolysis coupled transmembrane transport
GO:0050673	14.991	32	0.00488299	10	71	87	epithelial cell proliferation
GO:0005640	3.94	14	0.00488299	5	18	24	nuclear outer membrane
GO:0090235	0.952	7	0.00488299	1	5	5	regulation of metaphase plate congression
GO:0004725	25.856	47	0.00488299	15	80	97	protein tyrosine phosphatase activity
GO:0061024	124.741	169	0.00488299	81	746	899	membrane organization
GO:0047497	0.673	6	0.00622486	1	6	8	mitochondrion transport along microtubule
GO:0034643	0.673	6	0.00622486	1	6	8	establishment of mitochondrion localization, microtubule-mediated
GO:0019673	1.463	8	0.00622486	1	6	8	GDP-mannose metabolic process
GO:0050775	12.754	28	0.00671548	4	28	33	positive regulation of dendrite morphogenesis

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0030488	1.015	7	0.00671548	2	18	19	tRNA methylation
GO:0008175	1.013	7	0.00671548	2	19	21	tRNA methyltransferase activity
GO:0043515	1.143	7	0.00718408	1	5	5	kinetochore binding
GO:0090383	2.12	10	0.00718408	2	26	34	phagosome acidification
GO:0016311	42.846	69	0.00718408	31	237	275	dephosphorylation
GO:2000977	0.086	3	0.00765	1	2	5	regulation of forebrain neuron differentiation
GO:0045851	2.541	11	0.00765	3	39	50	pH reduction
GO:0051452	2.541	11	0.00765	3	39	49	intracellular pH reduction
GO:0010467	1.571	8	0.00827838	2	5	14	gene expression
GO:0035335	26.885	48	0.00885716	16	83	98	peptidyl-tyrosine dephosphorylation
GO:0042438	3.324	12	0.01312553	1	11	13	melanin biosynthetic process
GO:0071480	1.225	7	0.01312553	2	22	28	cellular response to gamma radiation
GO:0019216	38.588	63	0.01312553	28	328	366	regulation of lipid metabolic process
GO:0033564	4.369	14	0.01312553	2	6	8	anterior/posterior axon guidance
GO:0033130	2.491	10	0.01363756	2	8	8	acetylcholine receptor binding
GO:0019068	0.285	4	0.01411414	1	10	11	virion assembly
GO:0050658	17.065	34	0.01475137	11	137	168	RNA transport
GO:0050657	17.065	34	0.01475137	11	137	168	nucleic acid transport
GO:0051236	17.065	34	0.01475137	11	137	168	establishment of RNA localization
GO:0044550	3.385	12	0.01475137	1	13	15	secondary metabolite biosynthetic process
GO:0016791	39.014	62	0.01475137	27	214	249	phosphatase activity
GO:0090305	16.193	33	0.01475137	22	224	283	nucleic acid phosphodiester bond hydrolysis
GO:0033162	3.45	12	0.01475137	1	11	12	melanosome membrane
GO:0097105	7.34	19	0.01475137	2	5	8	presynaptic membrane assembly
GO:0031968	15.068	31	0.01578021	17	149	180	organelle outer membrane
GO:0008173	1.683	8	0.0162773	3	36	42	RNA methyltransferase activity
GO:1902931	1.179	7	0.0162773	4	16	18	negative regulation of alcohol biosynthetic process
GO:0042554	0.888	6	0.0162773	1	10	13	superoxide anion generation
GO:0060850	3.034	11	0.0162773	4	14	18	regulation of transcription involved in cell fate commitment
GO:0048536	3.611	12	0.01757137	4	32	34	spleen development
GO:0006879	4.652	14	0.01757137	6	48	61	cellular iron ion homeostasis
GO:0090129	4.03	13	0.01776087	2	8	9	positive regulation of synapse maturation
GO:1900006	20.732	38	0.01776087	10	58	67	positive regulation of dendrite development
GO:0090128	4.096	13	0.0191617	2	10	11	regulation of synapse maturation
GO:0000794	1.693	8	0.0191617	3	21	25	condensed nuclear chromosome
GO:0002067	1.74	8	0.01994537	3	20	22	glandular epithelial cell differentiation
GO:0051028	8.826	21	0.01994537	8	117	144	mRNA transport
GO:0070129	0.905	6	0.020649	1	17	18	regulation of mitochondrial translation
GO:0010510	0.608	5	0.020649	2	10	13	regulation of acetyl-CoA biosynthetic process from pyruvate
GO:0071709	13.66	28	0.0230736	5	21	28	membrane assembly
GO:0019867	15.474	31	0.0238077	17	151	182	outer membrane
GO:0044802	97.039	131	0.0238077	58	587	723	single-organism membrane organization

GO Term	ANG	Can	FDR	Unique	Max	Total	Description
GO:0050664	1.372	7	0.02452175	2	10	14	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor
GO:0034497	0.366	4	0.02484557	2	5	5	protein localization to pre-autophagosomal structure
GO:0055072	7.767	19	0.02514802	7	66	82	iron ion homeostasis
GO:0016175	1.031	6	0.0259594	1	6	9	superoxide-generating NADPH oxidase activity
GO:0051453	3.76	12	0.02600521	4	52	64	regulation of intracellular pH
GO:0032353	0.619	5	0.02600521	3	7	7	negative regulation of hormone biosynthetic process
GO:0007219	13.249	27	0.0262065	10	94	118	Notch signaling pathway
GO:0033540	1.892	8	0.02917049	3	13	16	fatty acid beta-oxidation using acyl-CoA oxidase
GO:0009295	1.796	8	0.02917049	3	38	43	nucleoid
GO:0042645	1.796	8	0.02917049	3	38	43	mitochondrial nucleoid
GO:0008138	1.835	8	0.02935145	3	35	46	protein tyrosine/serine/threonine phosphatase activity
GO:0070567	1.043	6	0.0311	3	8	9	cytidylyltransferase activity
GO:1902369	1.016	6	0.03328087	1	7	10	negative regulation of RNA catabolic process
GO:0006582	3.942	12	0.03442866	1	12	14	melanin metabolic process
GO:0006826	3.974	12	0.03483992	4	49	66	iron ion transport
GO:0000776	8.129	19	0.03483992	8	108	121	kinetochore
GO:0097119	5.065	14	0.03483992	3	6	6	postsynaptic density protein 95 clustering
GO:0010332	2.929	10	0.03592412	4	46	53	response to gamma radiation
GO:0016836	4.534	13	0.03743394	3	44	47	hydro-lyase activity
GO:0009067	1.522	7	0.0374894	3	16	16	aspartate family amino acid biosynthetic process
GO:0016004	0.411	4	0.03875807	1	9	14	phospholipase activator activity
GO:0015931	19.24	35	0.03875807	12	168	204	nucleobase-containing compound transport
GO:0001510	1.928	8	0.03891934	3	39	45	RNA methylation
GO:0034405	4.073	12	0.04308577	3	30	33	response to fluid shear stress
GO:0009225	4.058	12	0.04406087	5	28	32	nucleotide-sugar metabolic process
GO:0061005	4.033	12	0.04553993	3	20	23	cell differentiation involved in kidney development
GO:0030641	4.083	12	0.04744207	4	55	68	regulation of cellular pH

GO: Gene ontology; ANG: Average number of genes involved; Can.: Number of candidate genes; FDR: *p*-value adjusted for false discovery rate (only FDR values <0.05 were taken as statistically significant); Unique: Unique genes detected; Max: Maximum possible number of genes detected; Total: total number of genes detected.

Table S8: SNP positions enriched in Chichén Itzá, Tixcacaltuyub and the SNPs reported by Lindo et al., 2016[17] for the HLA region.

Chichén Itzá (YCH)		Tixcacaltuyub (TIX)		Lindo et al., 2016	
SNP	Gene	SNP	Gene	SNP	Gene
rs1063349	*HLA-DQB1*	rs2647045	*HLA-DQA2, HLA-DQB1*	rs9272426	*HLA-DQA1*
rs1063355	*HLA-DQB1, HLA-DQB1, HLA-DRA, HLA-DQA1*	rs3130425	*HCG27, HLA-C*	rs3207966	*HLA-DQA1*
rs1071630	*HLA-DQA1*	rs6906021	*HLA-DQB1, HLA-DQA1*	rs3187964	*HLA-DQA1*
rs2394990	*DHFRP2, HLA-S*	rs7382297	*HLA-C, RPL3P2*	rs1047985	*HLA-DQA1*
rs3129304	*HLA-DOA*	rs7454108	*HLA-DQA2*	rs1047989	*HLA-DQA1*
rs34826728	*HLA-DQA1*	rs9275524	*HLA-DQB1*	rs1047993	*HLA-DQA1*
rs5000634	*HLA-DQB1, HLA-DQA2,*	rs9275595	*HLA-DQA2*	rs10093	*HLA-DQA1*
rs6928482	*HLA-DQB1*			rs1129765	*HLA-DQA1*
rs7745040	*HLA-DQA2, HLA-DRB1*			rs1142323	*HLA-DQA1*
rs9272484	*HLA-DQA1*				
rs9272547	*HLA-DQA1*				
rs9273373	*HLA-DQB1*				
rs9273479	*HLA-DQB1*				
rs9275141	*HLA-DQB1, HLA-DQA2*				
rs9469003	*MICA, HLA-X, HLA-B, HCP5*				

Table S9. HLA, mtDNA and Y-Chr genotypes for YCH.

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
YCH001	B2l	Q1b1a1a	A*68:01	B*52:01	C*03:03	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:06	B*40:02	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH002	A2w1	Q1b1a2	A*24:02	B*39:02	C*07:02	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*68:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH003	A2q	Q1b1a1a	A*31:01	B*35:01	C*04:01	DRB1*04:10	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*35:20	C*15:09	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH004	A2ap	Q1b1a1a	A*24:02	B*35:01	C*04:01	DRB1*14:06	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*05:01
			A*31:01	B*35:01	C*04:01	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*02:01	DPB1*04:02
YCH006	B2l	Q1b	A*24:02	B*39:06	C*07:02	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:01
			A*68:01	B*15:01	C*01:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:03	DPA1*01:03	DPB1*04:02
YCH007	A2u	Q1b1a1a	A*24:02	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:05	B*35:23	C*04:01	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH008	A2	Q1b1a1a1	A*02:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*03:01
			A*02:01	B*35:01	C*07:02	DRB1*08:02	NULL	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
YCH010	A2m	Q1b1a1a1g~	A*68:01	B*40:02	C*03:05	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH011	A2b1	Q1b1a1a1	A*24:02	B*35:01	C*04:01	DRB1*14:06	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*68:03	B*40:02	C*03:05	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH012	A2g	Q1b1a1a1	A*24:02	B*40:02	C*03:05	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*02:02	DPB1*05:01
			A*31:01	B*40:02	C*15:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH015	A2	Q1b1a1a	A*31:01	B*40:02	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*51:01	C*08:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:04	DPA1*01:03	DPB1*04:02
YCH016	A2w1	Q1b1a1a1	A*31:09	B*35:01	C*04:01	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*02:06	B*35:01	C*04:01	DRB1*08:02	NULL	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
YCH018	A2ad	Q1b1a1a1	A*02:01	B*35:17	C*04:01	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:02	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH020	A2d	Q1b1a1a	A*24:02	B*15:01	C*01:02	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:01
			A*31:01	B*40:02	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH021	A2r	Q1b1a1a1	A*68:01	B*40:08	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:02	C*07:02	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH022	A2ao	Q1b	A*68:01	B*35:01	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:03	DPA1*01:03	DPB1*04:02
			A*68:01	B*40:08	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH023	A2a3	Q1b1a1a	A*02:06	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*03:01
			A*68:03	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*05:03	DQB1*03:04	DPA1*01:03	DPB1*04:02
YCH024	C1c4	Q1b1a1a2b1~	A*02:01	B*35:17	C*04:01	DRB1*04:10	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:02	DPB1*05:01
			A*31:01	B*40:02	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*02:01	DPB1*03:01
YCH026	D1	Q1b1a2	A*24:02	B*40:02	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*35:20	C*04:01	DRB1*08:02	NULL	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
YCH027	B2b2	Q1b1a1a1	A*24:02	B*35:12	C*04:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*02:01	DPB1*14:01

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
			A*68:01	B*40:27	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH028	A2	Q1b1a1a1e1c~	A*68:01	B*35:20	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:02	C*03:04	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH030	A2w1	Q1b1a2a~	A*24:02	B*15:01	C*01:02	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*14:01
			A*24:02	B*35:17	C*04:01	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*04:02
YCH031	A2r	Q1b1a1a	A*02:06	B*35:01	C*04:01	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH032	D1	Q1b1	A*68:01	B*40:02	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:05	C*07:02	DRB1*14:02	DRB3*01:01	DQA1*05:01	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH033	A2	Q1b1a1a2b1~	A*68:01	B*40:02	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*68:01	B*40:08	C*03:04	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*02:01
YCH034	A2w1	Q1b1a2~	A*68:01	B*40:02	C*03:05	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:02	DPB1*04:02
			A*31:01	B*48:01	C*08:03	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*05:01
YCH036	A2	Q1b1a1a	A*24:02	B*35:01	C*04:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:02	C*03:05	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH037	A2a3	Q1b1a1a	A*31:01	B*35:01	C*04:01	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*04:02
			A*68:01	B*40:11	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*14:01
YCH039	A2r	Q1b1a1a	A*31:01	B*48:01	C*08:03	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:03	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:17	C*03:03	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH040	A2	Q1b1a1a	A*68:01	B*39:02	C*07:02	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*39:05	C*03:04	DRB1*08:02	NULL	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
YCH041	A2w1	Q1b1a1a1m	A*31:01	B*40:02	C*03:05	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*48:01	C*15:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH043	A2w1	Q1b1a1a	A*24:02	B*35:01	C*07:02	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*68:03	B*40:02	C*07:02	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:04	DPA1*01:03	DPB1*04:02
YCH045	C1c4	Q1b1a2	A*31:01	B*15:01	C*01:02	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*02:01
			A*24:02	B*35:01	C*04:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH046	A2g	Q1b1a1a2	A*02:01	B*40:02	C*03:05	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*15:01	C*01:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH048	A2	Q1b1a2a~	A*24:02	B*52:01	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:01	B*15:01	C*01:02	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH049	D1	Q1b1a1a1	A*24:02	B*35:01	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:02	C*03:04	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH050	C1c	Q1b1a1a	A*68:01	B*39:05	C*07:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:08	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
YCH051	N/D	Q1b1	A*24:02	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:02	C*03:05	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*02:01	DPB1*05:01
YCH052	A2af1b	Q1b1	A*68:03	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:06	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH053	A2w1	Q1b1a1a1e1c~	A*31:01	B*35:20	C*04:01	DRB1*04:10	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:08	C*03:04	DRB1*14:06	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
YCH055	A2w1	Q1b1a~	A*02:06	B*39:02	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*40:02	C*03:05	DRB1*04:17	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:02	DPB1*05:01

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
YCH056	A2w1	Q1b1a2~	A*24:02	B*35:01	C*03:04	DRB1*14:06	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*02:01	DPB1*14:01
			A*68:01	B*40:08	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH057	B2	Q1b1a2	A*24:02	B*35:17	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*31:01	B*40:02	C*04:01	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH058	C1b	Q1b1a1a	A*68:01	B*40:08	C*03:04	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*40:02	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
YCH059	A2af1b	Q1b1a1a1f	A*68:01	B*35:12	C*04:01	DRB1*08:02	NULL	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:02	C*07:02	DRB1*04:11	DRB4*01:03	DQA1*05:03	DQB1*03:01	DPA1*02:01	DPB1*05:01
YCH060	A2r	Q1b1a2a	A*68:01	B*40:02	C*03:05	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:01	C*04:01	DRB1*04:10	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
YCH063	C1c	Q1b1a2	A*24:02	B*35:01	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:01	B*35:01	C*04:01	DRB1*04:07	DRB4*01:01	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02

mtDNA: Mitochondrial DNA haplogroup; Y-Chr: Y chromosome haplotype; N/D: Not determined.

Table S10. HLA, mtDNA and Y-Chr genotypes for TIX.

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
TIX011	A2u	Q1b1a1a1	A*02:01	B*35:12	C*04:01	DRB1*08:02	Null	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX012	A2ap	-	A*68:03	B*39:02	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*02:01
			A*68:03	B*39:05	C*07:02	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX013	A2ad	Q1b1a1a	A*24:02	B*35:20	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX014	A2w1	-	A*24:02	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*15:01	C*01:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX015	C1b14	Q1b1a1a1	A*31:01	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX016	A2m	I2a1b1a2b1a2	A*68:01	B*35:12	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*40:08	C*03:04	DRB1*04:25	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX017	A2af1b	G2a2b2a1a1c1a1a2a1a1a	A*23:01	B*15:03	C*02:10	DRB1*01:01	Null	DQA1*01:01	DQB1*02:02	DPA1*03:01	DPB1*105:01
			A*31:01	B*15:01	C*04:01	DRB1*09:01	DRB4*01:01	DQA1*03:03	DQB1*05:01	DPA1*01:03	DPB1*04:01
TIX018	A2u	Q1b1a1a1	A*32:01	B*51:01	C*01:02	DRB1*16:01	DRB5*02:02	DQA1*01:02	DQB1*05:02	DPA1*02:01	DPB1*14:01
			A*68:01	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX019	A2	R1b1a1b1a1a2c1a	A*02:06	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:06	B*35:17	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX020	A2	-	A*68:01	B*35:12	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:20	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX021	A2w1	-	A*24:02	B*14:01	C*08:02	DRB1*13:03	DRB3*02:02	DQA1*02:01	DQB1*02:02	DPA1*01:03	DPB1*01:01
			A*32:01	B*53:01	C*04:01	DRB1*01:01	Null	DQA1*01:01	DQB1*05:01	DPA1*02:01	DPB1*04:01
TIX022	A2m	-	A*31:01	B*40:08	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*45:01	C*06:02	DRB1*04:05	DRB4*01:03	DQA1*03:03	DQB1*03:02	DPA1*02:01	DPB1*11:01
TIX023	B2b	T1a1a1b2	A*03:01	B*35:01	C*04:01	DRB1*11:01	DRB3*02:02	DQA1*05:05	DQB1*03:19	DPA1*01:03	DPB1*05:01
			A*31:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*105:01
TIX024	A2	-	A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX025	B2	-	A*68:03	B*40:02	C*04:01	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:01	B*35:01	C*07:02	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:04	DPA1*01:03	DPB1*04:02
TIX026	A2ap	-	A*31:01	B*35:01	C*07:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX027	A2	-	A*24:02	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*29:02	B*44:03	C*16:01	DRB1*11:03	DRB3*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX028	A2ap	-	A*68:03	B*39:02	C*07:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*02:01
			A*31:01	B*35:01	C*07:02	DRB1*16:02	DRB5*02:02	DQA1*05:05	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX029	A2w1	-	A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX030	A2ad	-	A*24:02	B*35:01	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*68:01	B*35:17	C*04:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:04	DPA1*01:03	DPB1*04:02
TIX031	B2b	-	A*11:01	B*40:01	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*06:01
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX032	A2j	-	A*24:02	B*35:20	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
			A*31:01	B*40:02	C*04:01	DRB1*13:02	DRB3*03:01	DQA1*01:02	DQB1*06:04	DPA1*01:03	DPB1*02:01
TIX033	C1c4	-	A*31:01	B*40:02	C*03:04	DRB1*08:02	Null	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*35:12	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX034	C1c4	Q1b1a1a	A*68:03	B*35:12	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX035	A2j	Q1b1a1a1	A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:02	DPB1*05:01
			A*31:01	B*40:02	C*03:04	DRB1*13:02	DRB3*03:01	DQA1*01:02	DQB1*06:04	DPA1*01:03	DPB1*02:01
TIX036	A2	-	A*02:01	B*35:12	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*40:08	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX037	A2u	-	A*68:01	B*48:01	C*08:03	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*80:01	B*57:02	C*18:02	DRB1*10:01	Null	DQA1*01:04	DQB1*05:01	DPA1*02:02	DPB1*01:01
TIX038	A2ap	-	A*24:02	B*35:20	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX039	A2	-	A*31:01	B*39:05	C*07:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:06	C*07:02	DRB1*14:06	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX040	A2m	-	A*31:01	B*40:08	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*35:12	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX041	A2w1	G2a2b2a	A*68:01	B*15:01	C*01:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX042	A2w1	-	A*68:01	B*39:05	C*07:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:01
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX043	A2	-	A*24:02	B*35:20	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX044	A2w1	-	A*31:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*31:01	B*40:02	C*03:04	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*05:01
TIX045	B2t	Q1b1a1a	A*26:01	B*35:01	C*04:01	DRB1*04:02	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*35:12	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX046	A2ad	-	A*31:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*05:01
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX047	A2	R1b1a1b1a1a2	A*26:01	B*45:01	C*06:02	DRB1*07:01	DRB4*01:01	DQA1*02:01	DQB1*02:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX048	C1c4	-	A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:06	C*07:02	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX049	A2	-	A*68:03	B*35:43	C*01:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*14:01
			A*24:02	B*40:02	C*04:01	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX050	A2r1	-	A*24:02	B*35:01	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*11:01	B*35:03	C*04:01	DRB1*15:01	DRB5*01:01	DQA1*01:02	DQB1*06:02	DPA1*01:03	DPB1*04:02
TIX051	A2r1	G2a2b2a1a1c1a1a2a1a1a1	A*11:01	B*35:03	C*04:01	DRB1*15:01	DRB5*01:01	DQA1*01:02	DQB1*06:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*39:06	C*07:02	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX052	A2w1	-	A*24:02	B*15:01	C*01:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*39:06	C*07:02	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX053	B2	I2a1b1a2	A*31:01	B*40:08	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX054	D1	-	A*24:02	B*35:20	C*03:05	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:02	C*03:04	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
TIX055	D1	-	A*24:02	B*40:02	C*03:05	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX056	A2g	-	A*24:02	B*40:02	C*03:05	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:02	C*03:05	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX057	C1b14	G2a2b2a1a1c1a1a2a1a1a	A*31:01	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX058	A2	-	A*68:01	B*35:12	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:20	C*04:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX059	A2g	-	A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:12	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*02:01	DPB1*14:01
TIX060	A2ap	-	A*31:01	B*35:01	C*07:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX062	A2ap	-	A*24:02	B*35:17	C*04:01	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX063	A2g	-	A*24:02	B*35:12	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:01	B*40:02	C*03:05	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX064	A2	-	A*68:01	B*35:12	C*04:01	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*08:02	Null	DQA1*04:01	DQB1*04:02	DPA1*01:03	DPB1*04:02
TIX065	A2ad	Q1b1a1a	A*24:02	B*35:20	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX066	A2w1	-	A*24:02	B*07:02	C*07:02	DRB1*03:01	DRB3*01:01	DQA1*05:01	DQB1*02:01	DPA1*01:03	DPB1*04:01
			A*31:01	B*35:20	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX067	A2w1	-	A*68:01	B*35:20	C*04:01	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:01	C*04:01	DRB1*04:25	DRB4*01:03	DQA1*03:03	DQB1*04:02	DPA1*01:03	DPB1*04:02
TIX068	C1c	Q1b1a2	A*68:01	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*48:01	C*08:03	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX069	A2m	-	A*31:01	B*40:08	C*03:04	DRB1*04:04	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*32:01	B*41:01	C*17:01	DRB1*03:01	DRB3*02:02	DQA1*05:01	DQB1*02:01	DPA1*01:03	DPB1*04:01
TIX070	D1j	-	A*02:06	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*11:01	B*35:01	C*04:01	DRB1*01:01	Null	DQA1*01:01	DQB1*05:01	DPA1*01:03	DPB1*02:01
TIX071	A2ap	-	A*24:02	B*40:08	C*03:04	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*51:01	C*15:09	DRB1*14:02	DRB3*01:01	DQA1*05:03	DQB1*03:01	DPA1*01:03	DPB1*04:02
TIX072	C1b14	-	A*68:01	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*35:01	C*04:01	DRB1*13:02	DRB3*03:01	DQA1*01:02	DQB1*05:01	DPA1*02:01	DPB1*131:01
TIX073	A2g	-	A*68:03	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX074	A2g	-	A*68:03	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX075	C1c4	R1b1a1b1a1a2b	A*24:02	B*39:06	C*07:02	DRB1*04:11	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*26:01	B*45:01	C*06:02	DRB1*07:01	DRB4*01:01	DQA1*02:01	DQB1*02:02	DPA1*01:03	DPB1*04:02
TIX076	A2	-	A*68:03	B*35:12	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*24:02	B*35:20	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX077	A2ag	-	A*68:03	B*35:43	C*01:02	DRB1*04:03	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
			A*02:01	B*35:12	C*04:01	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02
TIX078	A2g	-	A*68:01	B*35:01	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02

Sample	mtDNA	Y-Chr	*HLA-A*	*HLA-B*	*HLA-C*	*HLA-DRB1*	*HLA-DRB3/4/5*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DPA1*	*HLA-DPB1*
			A*68:03	B*39:05	C*07:02	DRB1*04:07	DRB4*01:03	DQA1*03:01	DQB1*03:02	DPA1*01:03	DPB1*04:02

mtDNA: Mitochondrial DNA haplogroup; Y-Chr: Y chromosome haplotype.

Table S11. Frequencies of *HLA-A* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
A*02:01	7	0.0745	4	0.0299	0.2073	1.0000
A*02:06	6	0.0638	3	0.0224	0.1666	1.0000
A*03:01	0	0.0000	1	0.0075	1.0000	1.0000
A*11:01	0	0.0000	4	0.0299	0.1449	1.0000
A*23:01	0	0.0000	1	0.0075	1.0000	1.0000
A*24:02	33	0.3511	39	0.2910	0.3858	1.0000
A*26:01	0	0.0000	3	0.0224	0.2699	1.0000
A*29:02	0	0.0000	1	0.0075	1.0000	1.0000
A*31:01	18	0.1915	20	0.1493	0.4710	1.0000
A*31:09	1	0.0106	0	0.0000	0.4123	1.0000
A*32:01	0	0.0000	3	0.0224	0.2699	1.0000
A*68:01	23	0.2447	18	0.1343	0.0367	0.5508
A*68:03	5	0.0532	36	0.2687	0.0000	**0.0003**
A*68:05	1	0.0106	0	0.0000	0.4123	1.0000
A*80:01	0	0.0000	1	0.0075	1.0000	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S12. Frequencies of *HLA-B* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
B*07:02	0	0.0000	1	0.0075	1.0000	1.0000
B*14:01	0	0.0000	1	0.0075	1.0000	1.0000
B*15:01	6	0.0638	4	0.0299	0.3249	1.0000
B*15:03	0	0.0000	1	0.0075	1.0000	1.0000
B*35:01	25	0.2660	19	0.1418	0.0262	0.7062
B*35:03	0	0.0000	2	0.0149	0.5133	1.0000
B*35:12	2	0.0213	14	0.1045	0.0169	0.4573
B*35:17	5	0.0532	3	0.0224	0.2793	1.0000
B*35:20	4	0.0426	11	0.0821	0.2866	1.0000
B*35:23	1	0.0106	0	0.0000	0.4123	1.0000
B*35:43	0	0.0000	2	0.0149	0.5133	1.0000
B*39:02	6	0.0638	2	0.0149	0.0677	1.0000
B*39:05	5	0.0532	27	0.2015	0.0016	**0.0436**
B*39:06	1	0.0106	5	0.0373	0.4048	1.0000
B*40:01	0	0.0000	1	0.0075	1.0000	1.0000
B*40:02	23	0.2447	11	0.0821	0.0011	**0.0296**
B*40:08	8	0.0851	13	0.0970	0.8198	1.0000
B*40:11	1	0.0106	0	0.0000	0.4123	1.0000
B*40:27	1	0.0106	0	0.0000	0.4123	1.0000
B*41:01	0	0.0000	1	0.0075	1.0000	1.0000
B*44:03	0	0.0000	1	0.0075	1.0000	1.0000
B*45:01	0	0.0000	3	0.0224	0.2699	1.0000
B*48:01	3	0.0319	2	0.0149	0.4055	1.0000
B*51:01	1	0.0106	8	0.0597	0.0850	1.0000
B*52:01	2	0.0213	0	0.0000	0.1689	1.0000
B*53:01	0	0.0000	1	0.0075	1.0000	1.0000
B*57:02	0	0.0000	1	0.0075	1.0000	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S13. Frequencies of *HLA-C* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
C*01:02	6	0.0638	6	0.0448	0.5582	1.0000
C*02:10	0	0.0000	1	0.0075	1.0000	1.0000
C*03:03	2	0.0213	0	0.0000	0.1689	1.0000
C*03:04	26	0.2766	23	0.1716	0.0715	1.0000
C*03:05	10	0.1064	5	0.0373	0.0555	0.8877
C*04:01	25	0.2660	30	0.2239	0.5300	1.0000
C*06:02	0	0.0000	3	0.0224	0.2699	1.0000
C*07:02	19	0.2021	53	0.3955	0.0023	**0.0369**
C*08:01	1	0.0106	0	0.0000	0.4123	1.0000
C*08:02	0	0.0000	1	0.0075	1.0000	1.0000
C*08:03	2	0.0213	2	0.0149	1.0000	1.0000
C*15:02	2	0.0213	0	0.0000	0.1689	1.0000
C*15:09	1	0.0106	7	0.0522	0.1448	1.0000
C*16:01	0	0.0000	1	0.0075	1.0000	1.0000
C*17:01	0	0.0000	1	0.0075	1.0000	1.0000
C*18:02	0	0.0000	1	0.0075	1.0000	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S14. Frequencies of *HLA-DRB1* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
DRB1*01:01	0	0.0000	3	0.0224	0.2699	1.0000
DRB1*03:01	0	0.0000	2	0.0149	0.5133	1.0000
DRB1*04:02	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*04:03	7	0.0745	8	0.0597	0.7874	1.0000
DRB1*04:04	10	0.1064	13	0.0970	0.8266	1.0000
DRB1*04:05	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*04:07	22	0.2340	62	0.4627	0.0005	**0.0114**
DRB1*04:10	4	0.0426	0	0.0000	0.0278	0.6674
DRB1*04:11	18	0.1915	8	0.0597	0.0028	0.0662
DRB1*04:17	1	0.0106	0	0.0000	0.4123	1.0000
DRB1*04:25	0	0.0000	2	0.0149	0.5133	1.0000
DRB1*07:01	0	0.0000	2	0.0149	0.5133	1.0000
DRB1*08:02	5	0.0532	3	0.0224	0.2793	1.0000
DRB1*09:01	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*10:01	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*11:01	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*11:03	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*13:02	0	0.0000	3	0.0224	0.2699	1.0000
DRB1*13:03	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*14:02	15	0.1596	15	0.1119	0.3237	1.0000
DRB1*14:06	4	0.0426	1	0.0075	0.1623	1.0000
DRB1*15:01	0	0.0000	2	0.0149	0.5133	1.0000
DRB1*16:01	0	0.0000	1	0.0075	1.0000	1.0000
DRB1*16:02	8	0.0851	2	0.0149	0.0176	0.4227

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S15. Frequencies of *HLA-DRB3/4/5* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
DRB3*01:01	19	0.2021	17	0.1269	0.1420	0.4259
DRB3*02:02	0	0.0000	4	0.0299	0.1449	0.4347
DRB3*03:01	0	0.0000	3	0.0224	0.2699	0.8096
DRB4*01:01	1	0.0106	3	0.0224	0.6448	1.0000
DRB4*01:03	61	0.6489	95	0.7090	0.3858	0.7716
DRB5*01:01	0	0.0000	2	0.0149	0.5133	1.0000
DRB5*02:02	8	0.0851	3	0.0224	0.0547	0.1093
Null	5	0.0532	7	0.0522	1.0000	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S16. Frequencies of *HLA-DQA1* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
DQA1*01:01	0	0.0000	3	0.0224	0.2699	1.0000
DQA1*01:02	0	0.0000	6	0.0448	0.0438	0.4377
DQA1*01:04	0	0.0000	1	0.0075	1.0000	1.0000
DQA1*02:01	0	0.0000	3	0.0224	0.2699	1.0000
DQA1*03:01	48	0.5106	93	0.6940	0.0057	0.0575
DQA1*03:03	12	0.1277	3	0.0224	0.0022	**0.0218**
DQA1*04:01	5	0.0532	3	0.0224	0.2793	1.0000
DQA1*05:01	1	0.0106	2	0.0149	1.0000	1.0000
DQA1*05:03	20	0.2128	16	0.1194	0.0661	0.6615
DQA1*05:05	8	0.0851	4	0.0299	0.0771	0.7707

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S17. Frequencies of *HLA-DQB1* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
DQB1*02:01	0	0.0000	2	0.0149	0.5133	1.0000
DQB1*02:02	0	0.0000	4	0.0299	0.1449	1.0000
DQB1*03:01	25	0.2660	17	0.1269	0.0093	0.1115
DQB1*03:02	46	0.4894	94	0.7015	0.0015	**0.0177**
DQB1*03:03	3	0.0319	0	0.0000	0.0688	0.8251
DQB1*03:04	3	0.0319	2	0.0149	0.4055	1.0000
DQB1*03:19	0	0.0000	1	0.0075	1.0000	1.0000
DQB1*04:02	17	0.1809	4	0.0299	0.0001	**0.0016**
DQB1*05:01	0	0.0000	5	0.0373	0.0791	0.9496
DQB1*05:02	0	0.0000	1	0.0075	1.0000	1.0000
DQB1*06:02	0	0.0000	2	0.0149	0.5133	1.0000
DQB1*06:04	0	0.0000	2	0.0149	0.5133	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S18. Frequencies of *HLA-DPA1* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
DPA1*01:03	82	0.8723	122	0.9104	0.3861	1.0000
DPA1*02:01	8	0.0851	9	0.0672	0.6183	1.0000
DPA1*02:02	4	0.0426	2	0.0149	0.2329	0.9315
DPA1*03:01	0	0.0000	1	0.0075	1.0000	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Table S19. Frequencies of *HLA-DPB1* alleles in Chichén Itzá and Tixcacaltuyub.

HLA allele	Chichén Itzá		Tixcacaltuyub		Significance	
	n= (2N=94)	Frequency	n= (2N=134)	Frequency	raw *p* value	p_{corr}
DPB1*01:01	0	0.0000	2	0.0149	0.5133	1.0000
DPB1*02:01	2	0.0213	5	0.0373	0.7028	1.0000
DPB1*03:01	3	0.0319	0	0.0000	0.0688	0.7563
DPB1*04:01	2	0.0213	5	0.0373	0.7028	1.0000
DPB1*04:02	76	0.8085	110	0.8209	0.8630	1.0000
DPB1*05:01	7	0.0745	7	0.0522	0.5789	1.0000
DPB1*06:01	0	0.0000	1	0.0075	1.0000	1.0000
DPB1*11:01	0	0.0000	1	0.0075	1.0000	1.0000
DPB1*14:01	4	0.0426	3	0.0224	0.4507	1.0000
DPB1*105:01	0	0.0000	2	0.0149	0.5133	1.0000
DPB1*131:01	0	0.0000	1	0.0075	1.0000	1.0000

2N refers to the number of chromosomes analysed. p_{corr}: *p* values after correction. Significant p_{corr} values are in bold.

Supplementary methods: Non-overlapping HLA associations.

Contact researcher: Bridget Penman.

Here we present examples of individual non-overlapping HLA associations analyses, to further illustrate the results related to this test. In the first case (Fig. S7), we present patterns obtained for the class I genes *HLA-B* and *HLA-C,* for which f^*_{adj} is high in both YCH and TIX populations, as illustrated in figure 4 in the main text. *HLA-B* and *HLA-C* are so close together that non overlapping associations between them (whilst perhaps driven by pathogens) are also unsurprising. It can be seen in Fig. S7 that whilst the level of non-overlap between *HLA-B* and *HLA-C* is similar for YCH and TIX, the highest frequency allelic associations are different in the two populations.

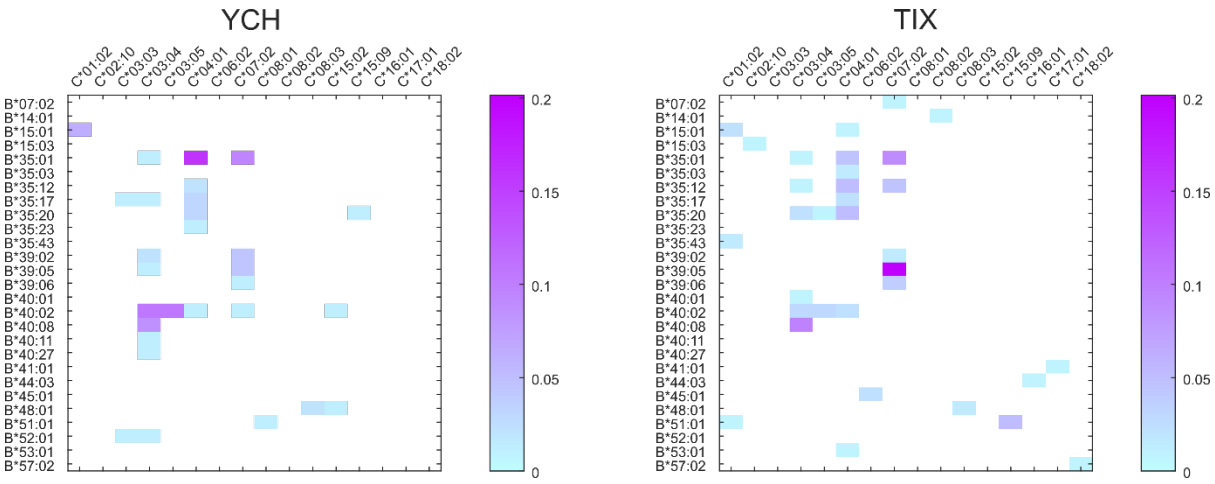

Figure S7. Frequencies of *HLA-B* and *HLA-C* associations in the ancient (YCH) and modern (TIX) populations.

Associations between *HLA-B* and *HLA-DRB1*, or between *HLA-B* and *HLA-DRB3*/*4*/*5* are relatively overlapping in the YCH population (lower f^*_{adj}) but non overlapping in the TIX population (higher f^*_{adj}), as shown in Fig. 4 of the main text. In Fig. S8, we show the specific allelic combinations present in the two populations, and use green ovals to highlight some of the features that are driving this pattern, i.e., high frequency alleles which share associations at relatively similar frequencies (overlap) in the YCH population, and high frequency alleles which do not share such associations, or where the shared associations are at very low frequencies (non-overlap) in the TIX population.

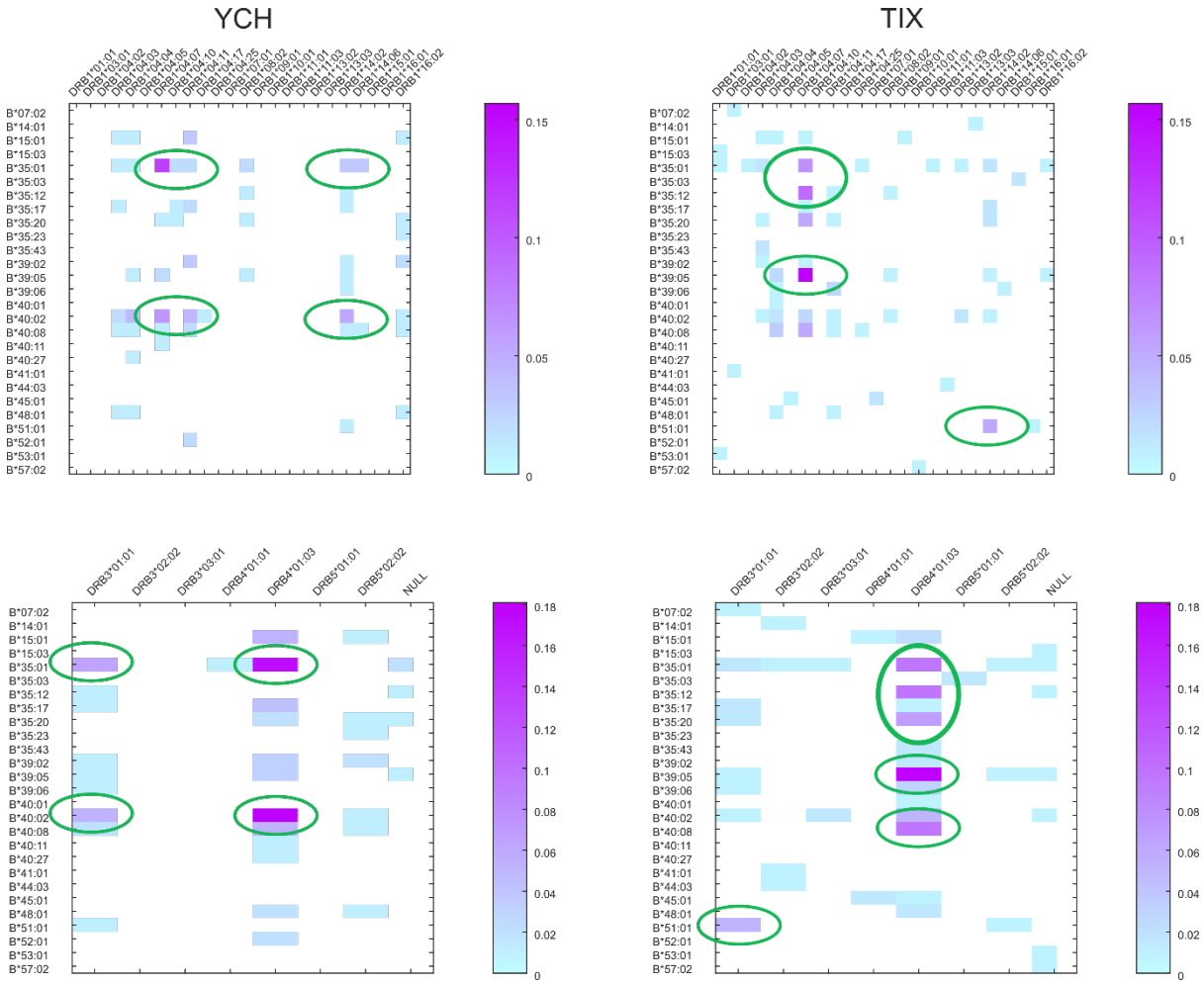

Figure S8. Frequencies of *HLA-B* and *HLA-DRB1* and *HLA-B* and *DRB3/4/5* associations in the ancient (YCH) and present day (TIX) populations.

Supplementary methods: *In-silico* binding prediction assays.

Contact researcher: Rodrigo Barquera.

Peptide-binding predictions between HLA molecules and peptides have been used previously to assess the role of HLA in the susceptibility or resistance to specific pathogens[70–72]. Here, we use this approach to analyse the binding strength of *Salmonella spp.* derived peptides to HLA class II alleles found in both ancient (YCH) and modern (TIX) Native Americans from the Maya region. For this test, we analysed the binding patterns of peptides (varying in length from 12-mers to 18-mers) derived from 18 proteins from *Salmonella spp.* against 25 HLA class II molecules. These proteins have been shown to produce an immunogenic response in the human body by means of the production of antibodies[73–79].

The sequence of the following proteins were extracted from the UniProt database[80] (primary UniProt accession number in parentheses) and included in our analyses: Secreted effector protein SseB (Q7BVH7), Flagellin (P06178), 60 kDa chaperonin (C0Q6A2), Outer membrane protein A (Q8Z7S0), Secreted effector protein SseJ (Q9FD10), Peptidoglycan-associated protein (A0A3Z2B3K0), Cytolysin A (B6E461), Nucleoside-specific channel-forming protein Tsx (P0A262), VacJ lipoprotein (C0PZX2), Outer membrane porin protein OmpD (Q5PHY0), Outer membrane protease OmpX (A0A3Y4CN55), Outer membrane protein W (Q8Z7E2), Outer membrane protein S1 (Q56110), Maltoporin (P26466), Sucrose porin (P22340), Outer membrane porin F (P37432), Outer membrane porin PhoE (P30705), and Outer membrane porin C (P0A264). This set of proteins was presented *in silico* against HLA molecules using netMHCIIpan 4.0[81]. The lengths of the peptides to be obtained were set to 12 to 18 residues, resulting in a set of 41,404 unique peptides. Due to the lack of inhibitory concentration (IC_{50}) values for some alleles, we used a ranking system as previously reported[72,81] to fairly compare all analysed alleles. For each HLA molecule, the percentile rank of the predicted binding score was used for detecting strong peptide binders and weak peptide binders by the recommended thresholds (%Rank < 2% for strong binders and 2% ≤ %Rank < 10% for weak binders, for HLA class II molecules).

Table S20. Binding prediction results for the *Salmonella enterica* peptides presented by HLA class II molecules.

HLA molecule	Strong binding		Weak binding	
	n=	%	n=	%
DRB1*04:03	355	9.96	1680	10.23
DRB1*04:04	187	5.25	1014	6.17
DRB1*04:05	150	4.21	1347	8.20
DRB1*04:07	542	15.21	2062	12.55
DRB1*04:10	226	6.34	1679	10.22
DRB1*04:11	274	7.69	1209	7.36
DRB1*04:17	421	11.81	1924	11.71
DRB1*08:02	220	6.17	1023	6.23
DRB1*14:02	561	15.74	1628	9.91
DRB1*14:06	196	5.50	926	5.64
DRB1*16:02	432	12.12	1936	11.78
HLA molecule				
DRB3*01:01	435	34.74	2312	41.28
DRB4*01:01	232	18.53	883	15.77
DRB4*01:03	197	15.73	908	16.21
DRB5*02:02	388	30.99	1498	26.75
HLA molecule				
HLA-DQA1*03:01/DQB1*03:01	859	11.78	2475	10.66
HLA-DQA1*03:01/DQB1*03:02	177	2.43	1566	6.75
HLA-DQA1*03:01/DQB1*03:03	917	12.57	2184	9.41
HLA-DQA1*03:03/DQB1*04:02	460	6.31	1919	8.27
HLA-DQA1*04:01/DQB1*04:02	206	2.82	1624	7.00
HLA-DQA1*05:01/DQB1*03:01	1192	16.34	4216	18.16
HLA-DQA1*05:01/DQB1*03:04	847	11.61	2454	10.57
HLA-DQA1*05:05/DQB1*03:01	824	11.30	2461	10.60
HLA-DQA1*05:05/DQB1*03:02	848	11.63	2121	9.14
HLA-DQA1*05:05/DQB1*03:03	964	13.22	2192	9.44

Strong binding: Rank value is on the top 2.0%. Weak binding: Rank value is between the top 2.0% and the top 10%. n: number of peptides presented by that specific allele. %: percentage of the total peptides presented by the HLA class II alleles studied, that are presented by that specific allele. Total number of peptides strongly bound to *HLA-DRB1* alleles: 3564. Total number of peptides strongly bound to *HLA-DRB3*/*4*/*5* alleles: 1252. Total number of peptides strongly bound to HLA-DQ molecules: 7294. Total number of peptides weakly bound to *HLA-DRB1* alleles: 16,428. Total number of peptides weakly bound to *HLA-DRB3*/*4*/*5* alleles: 5601. Total number of peptides weakly bound to HLA-DQ molecules: 23,212.

Supplementary Information: source populations for the population genetics analyses.

Category	Population or individual	Reference
Circum Arctic populations	Eskimo_ChaplinSireniki	82
	Eskimo_Naukan	83
	Greenland_Saqqaq.SG	84
	Aleut	82
	Alaskan_Athabskan.SG	85
	Canada_400BP.SG	86
	Canada_6000BP.SG	86
	Canada_BigBar_5700BP.SG	87
	Canada_MDorset_published	88
	Thule.SG	86
	Tlingit	82
	Tsimshian.SG	86
	USA_AK_Ancient_Athabaskan_1100BP	88
	USA_AK_NeoAleut_published	88
	USA_AK_PaleoAleut_published	88
	USA_AK_Prehistoric.SG	89
	USA_Alaska_TrailCreek_9000BP.SG	87
	USA_Ancient_Beringian.SG	90
	USA_Anzick_realigned.SG	91
SW USA	USA_CA_Early_SanNicolas.SG	85
	USA_CA_Late_SanNicolas.SG	85
	USA_Nevada_LovelockCave_1850BP.SG	87
	USA_Nevada_LovelockCave_600BP.SG	87
	USA_Nevada_SpiritCave_11000BP.SG	87
	USA_NM_Chaco	92
	USA_WA_Kennewick.SG	93
	Baja_Mexico.SG	85
	USA_CA_Late_SanNicolas.SG	85
	Island_Chumash_SanCruz.SG	85
	Island_Chumash_SanMiguel.SG	85
	Mainland_Chumash_NewCuyama.SG	85
	Mainland_Chumash.SG	85
Pima	Pima	94
Northern Mexico	Mexico_Pericues.SG	86
	Mexico_Pericues.SG_lc	86
	Mexico_PreColumbian_CH_MOM6.SG_lc	86
	Mexico_PreColumbian.SG_lc	86
Oaxaca	Mixe	82

Category	Population or individual	Reference
	Mixtec	82
Huichol	Huichol.SG	86
Mayan	Mayan	94
Mayan	Kaqchikel	95
Bahamas	Bahamas_AbacoIsl_Ceramic	96
	Bahamas_CrookedIsl_Ceramic	96
	Bahamas_EleutheraIsl_Ceramic	96
	Bahamas_LongIsl_Ceramic	96
	Bahamas_SouthAndros_Ceramic	96
	Bahamas_Taino.SG	97
Belize	Belize_EArchaic_published	98
Cuba	Cuba_CanimarAbajo_Archaic	99
	Cuba_CuevaCalero_Archaic	99
	Cuba_CuevaEsqueletos_Ceramic	99
	Cuba_CuevaPerico_Archaic	99
	Cuba_ElMorrillo_Ceramic	99
	Cuba_GuayaboBlanco_Archaic	99
	Cuba_LasCarolinas_Archaic	99
	Cuba_Manuelito_Archaic	99
	Cuba_PlayadelMango_Archaic	99
Curaçao	Curacao_deSavaan_Ceramic	96
	Curacao_SantaCruz_Ceramic	96
Dominican Republic	Dominican_Andres_Archaic	96
	Dominican_Andres_Ceramic	96
	Dominican_Atajadizo_Ceramic	96
	Dominican_Atajadizo_Ceramic_1d.rel.17903	96
	Dominican_Ceramic_JuanDolio	96
	Dominican_CuevaJuana_Ceramic	96
	Dominican_CuevaRoja_Archaic	96
	Dominican_EdilioCruz_Ceramic	96
	Dominican_ElFrances_Ceramic	96
	Dominican_ElSoco_Ceramic	96
	Dominican_LaCaleta_Ceramic	96
	Dominican_LaUnion_Ceramic	96
	Dominican_LomaPerenal_Ceramic	96
	Dominican_LosCorniel_Ceramic	96
	Dominican_LosMuertos_Ceramic	96
	Dominican_Macao_Ceramic	96

Category	Population or individual	Reference
Guadeloupe	Guadeloupe_AnseGourde_Ceramic	99
Haiti	Haiti_Diale1_Ceramic	96
St. Lucia	StLucia_Lavoutte_Ceramic	99
Puerto Rico	PuertoRico_CaboRojo11_Ceramic	96
	PuertoRico_CanasCollоresMonserrate_Ceramic	96
	PuertoRico_Collores_Ceramic	96
	PuertoRico_LosIndios_Ceramic	99
	PuertoRico_Monserrate_Ceramic	96
	PuertoRico_PasodelIndio_Ceramic	99
	PuertoRico_PuntaCandelero_Ceramic	99
	PuertoRico_SantaElena_Ceramic	96
	PuertoRico_Tibes_Ceramic	99
Venezuela	Venezuela_LasLocas_Ceramic	99
	Piapoco	94
Bolivia	Aymara.SG	86
	Bolivia_MH_Iroco_1050BP	100
	Bolivia_MH_Miraflores	100
	Bolivia_MH_Tiwanaku	100
	Bolivian	82
Peru	Peru_Campanayuq_MH_1000BP_lc	82
	Peru_Chanka_LIP	100
	Peru_Cuncaicha_3300BP	101
	Peru_Cuncaicha_4200BP	101
	Peru_Cuncaicha_9000BP	101
	Peru_EIP_Moche	100
	Peru_ElBrujo_EIP_1300BP	100
	Peru_Highlands_Chinchawas_MH	100
	Peru_Highlands_LIP_Chimu	100
	Peru_HuacaPrieta_LA_4500BP	100
	Peru_Kaillachuro_Unknown.SG	102
	Peru_LaGalgada_4100BP	101
	Peru_Laramate_900BP	101
	Peru_Lauricocha_3500BP	101
	Peru_Lauricocha_5800BP	101
	Peru_Lauricocha_8600BP	101
	Peru_LH_Inca	100
	Peru_Lima_EIP_1450BP	100
	Peru_Lima_LIP_650BP	100
	Peru_LimaCoast_MH_1000BP	100

Category	Population or individual	Reference
	Peru_LIP_La_Galgada_600BP	100
	Peru_LIP_Ychsma	100
	Peru_MH_LIP_ElBrujo_850BP	100
	Peru_MH_LIP_Lambayeque	100
	Peru_Palpa_LIP_550BP	100
	Peru_Palpa_MH_950BP	100
	Peru_Paracas_EH_2250BP	100
	Peru_RioUncallane_1800BP.SG	102
	Peru_SanSebastian_LH_500BP	100
	Peru_SanSebastian_LIP_600BP	100
	Peru_SoroMikayaPatjxa_6800BP.SG	102
	Peru_Ullujaya_EIP_1350BP	100
	Peru_Ullujaya_MH_950BP	100
	Peru_WariHighlands_MH_lc	100
	Quechua	82
Brazil	Karitiana	103
	Brazil_Botocudo.SG	104
	Brazil_Enoque_HG.SG	86
	Brazil_Jabuticabeira2_2100BP	101
	Brazil_LapaDoSanto_9600BP	101
	Brazil_Laranjal_6700BP	101
	Brazil_Moraes_5800BP	101
	Brazil_Sumidouro_10100BP.SG	87
Argentina	Argentina_Aconcagua_Inca_500BP.SG	87
	Argentina_ArroyoSeco2_7700BP	101
	Argentina_BeagleChannel_Yamana_100BP.SG	86
	Argentina_LagunaChica_1600BP	101
	Argentina_LagunaChica_6800BP_published	101
	Argentina_LagunaToro_2400BP	100
	Argentina_NorthTierradelFiego_Selknam_100BP.SG	86
	Argentina_NorthTierradelFuego_LaArcillosa2_6000BP	86
	Argentina_Tierra_del_Fuego_brother.I12367	86
Chile	Chile_CaletaHuelen_MH_1100BP	100
	Chile_Chinchorro_LA.SG_lc	86
	Chile_Conchali_700BP	101
	Chile_LIP_Pukara_600BP	101
	Chile_LIP_Pukara_700BP	101
	Chile_LosRieles_12000BP.SG	101
	Chile_LosRieles_5100BP	101

Category	Population or individual	Reference
	Chile_PicaOcho_700BP	101
	Chile_PuntaSantaAna_7300BP.SG	87
	Chile_StraitOfMagellan_Kaweskar_100BP.SG	86
	Chile_WesternArchipelago_Ayayema_4700BP.SG	87
	Chile_WesternArchipelago_Kaweskar_800BP.SG	105
	Chile_Yamana_BeagleChannel_800BP.SG	105
	Yamana_BeagleChannel_Grouped_1900-500BP	105
	Haush_MitrePeninsula_Grouped_700BP	100
	Selknam_FaroMendez_100BP	86
	Selknam_NorthTierradelFuego_Grouped_500BP	86
	Aonikenk_SouthContinent_CerroJohnny_400BP	100

Supplementary methods: Community engagement activities.

Contact researchers: Rodrigo Barquera, Oana del Castillo-Chávez, Julio César Lara-Riegos, María Ermila Moo-Mezeta, Julio César Torres-Romero, Christina Warinner.

In April and May, 2023, a group of local researchers was joined by Rodrigo Barquera, María Ermila Moo-Mezeta and Julio César Lara-Riegos to take part in different activities with the goal of delivering the results of the analyses done for the present work, as well as to collect information on the views of different communities from Yucatán, Mexico, about the results presented. Such activities involved the presentation of the results to the students and teachers at the Autonomous University of Yucatan (UADY), and to students (junior high and high school levels) and participants from Tixcacaltuyub. Among other activities, the group delivered an introduction to the field of archaeogenetics, explained what motivated their research in this context and shared the main findings of the present work. To keep a dynamic that would allow for the exchange of thoughts on the findings and how are they perceived by the community, different strategies were used. Among the activities carried out, reciting a poem expressing the meaning of identity for the author, both in Mayan and Spanish, storytelling about what drove researchers and collaborators to work for the joint project, the distribution among students of colouring books[106] (please see: https://ecoevocommunity.nature.com/posts/29206-adventures-in-archaeological-science-a-colouring-book-for-young-scientists, for further information) both in Spanish and Yucatan Mayan as an introduction to bioarchaeology and archaeogenetics, and asking the audience about their perceptions of the results, can be listed as the ones that qualitatively yielded the most engagement from the audience. Among the reported perceptions, we could record overall excitement from the participants and students about the genetic continuity between the ancient individuals from Chichén Itzá and the participants from the community of Tixcacaltuyub, and questions about whether this genetic signature from Chichén Itzá could be found in other communities (whether close to Chichén Itzá or not) were raised, which could be further explored in future collaborations. Another set of colouring books was shared with students visiting the facilities of the Centro INAH Yucatán (Mérida, Yucatán, Mexico), in this case with more emphasis on the archaeological implications for these studies, led by Oana del Castillo-Chávez.

But political aspects are also involved in the work with communities which have contributed to research. As María Ermila Moo-Mezeta points out, “Being a research professor of indigenous origin has allowed me to have a global vision without sectarianizing the social reality of the municipality where I was born, I have closely felt the contradictions of a reality that is lived in Mayan communities and a system that does not respond to what is necessary to guarantee the rights of each person. I had the opportunity to have grown in the Mayan worldview, being clear about the social processes that occur within it, the particular characteristics of this population to transmit their knowledge, their customs and the way to perpetuate culture, I am part of a historical and collective memory of the Mayan people, my biggest challenge has been to establish strategies that allow me a critical look, a deep analysis of the population to which I belong to be able to contribute to academia and generate knowledge of what yesterday was mere daily life.”

We consider that incorporating these views as part of our final results is fundamental, as these are the actual descendants from the people that once lived in these regions, and they are willing to reconcile our views and results with their own cosmogony: “In indigenous ways of knowing, we say that a thing cannot be understood until it is known by all four aspects of our being: mind, body, emotion and spirit”[107]. Inspired by the efforts of others[108,109], we translated (the translation is not peer-reviewed by the journal) the final version of the article into Spanish in order to make our research more accessible for communities involved in this and other research projects in the region.

Local researchers and collaborators leading the science communication activities: Oana del Castillo-Chávez (co-author), Julio Lara Riegos (co-author), María Ermila Moo-Mezeta (co-author), Pilar Márquez Vega (photographic documentation and logistic support), Mirna Canul Aké (translation of the colouring book into Yucatec Mayan); Margarita Zarco Salgado (Head of the Social Projects Unit, UADY; organisation, through those responsible for social projects developing in the community of Tixcacaltuyub, of the information delivered to the participants), Lifter Omar Ricalde Cab (responsible for the organisation of the delivery of information to students in the community), Miguel Güemez Pineda (responsible for the communication of information in the Mayan language to the adult participants of the study), Ramón Peniche Lara (research coordinator at UADY; management of resources for the trip to the community), José Esparza Bautista (community manager of Tixcacaltuyub; organisation with the commissioner of Tixcacaltuyub and municipal president of Yaxcabá of the meeting with the study participants), Marian Gabriel (social pedagogue; responsible for the intercultural dissemination strategy), and Lizbeth Carrillo Can (Mayan poet; declamation in Mayan and Spanish of the poem “Teen”/“Yo”/“I”).

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