Unveiling the Mystery of the Petroleum Genome Archive: Paleofauna Activities, Geological History, and aDNA Identification Methods in Nanyang Oilfield

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Abstract: Specific macromolecules in petroleum, preserved through geological processes from ancient organisms, are recognized as molecular fossils or geochemical markers (GMs). Our selected GMs indicate that the source rocks of Nanyang Oilfield formed in an anoxic, saline, and stratified lacustrine environment with marine influence. Contrary to science fiction notions that oil originates from ancient large animals, mainstream academia has consistently asserted that oil is derived from the organic matter of lower life forms, formed over extended geological processes, with intact DNA no longer persisting in oil post-formation. However, this study successfully extracted 3,159,020 DNA fragments from the petroleum samples using the nanoparticle affinity bead technology, followed by sequencing and classification via the mega screen method. These fragments, categorized as original *in situ* DNA (oriDNA), recent environmental DNA (preDNA), and paleo-environmental DNA (paeDNA), exhibit a "Genome Accumulated over Time" (GAT) pattern of "old-less, new-many". This aligns with findings from GMs while offering more specific genetic information. The analysis reveals evidence of historical events, including animal extinctions, marine invasions, ancient bird species presence, Asian *Homo erectus* activities, and modern human influences in preDNA. Notably, the mitogenomic data positions Asian *Homo erectus* closer to modern humans than to chimpanzees at the maternal basis. The absence of deamination in petroleum ancient DNA (aDNA) fragments is likely due to the anaerobic, anhydrous environment and the screening process that excludes degraded fragments. Consequently, the authenticity criteria and scope of application of traditional aDNA methods require reevaluation. Surprisingly, the near-absence of oriDNA has impeded our efforts to determine the specific biological origins of the oil. These findings position petroleum as a novel, non-skeletal source of aDNA, offering insights into ancient animal activities, geological changes, and human origins while underscoring its potential as an untapped resource for studying genetic preservation across geological timescales.

Keywords: nanoparticle affinity bead, petroleum, DNA, the mega screen method, marine, bird, *Homo erectus*

Introduction

Petroleum, a fossil fuel, is widely recognized as originating from fossilized organic matter, such as plankton and bacteria, which accumulated alongside sediments in ancient oceans or lakes and transformed into petroleum under thermal pressure[1,2]. GMs, also termed molecular fossils or biomarkers, are organic compounds preserved in geological samples like sediments, rocks, crude oils, and coals. These molecules, exhibiting minimal structural alteration from their biological precursors in living organisms, offer valuable insights into past biological and environmental conditions. As such, they serve as tools for addressing challenges in exploration, development, production, environmental studies, and archeological or paleontological research [3]. Prior studies indicate that the primary source rocks of the Biyang Sag oil field in the Nanxiang Basin lie within the third member (Eh_3) of the Paleogene Hetaoyuan Formation [4,5,6,7,8]. The organic matter in these Eh_3 shales predominantly derives from phytoplankton, bacteria, and benthic algae, with minor contributions from animal and higher plant material. Furthermore, the presence of 24-n-propylcholestanes, indicative of marine organisms, suggests episodes of marine incursion in the Nanxiang Basin [6,7,8].

Paleontologists have claimed the ability to extract oriDNA from certain fossils dating back 1 million years (Ma) [9]. However, fossil distributions are often sparse, geographically scattered, and temporally fragmented. Expanding the range of aDNA sources could significantly advance paleontological research. Experimental evidence has demonstrated that vegetable oil refined at 400°C retains amplifiable DNA fragments [10,11,12,13], suggesting that small quantities of DNA may persist in the deoxygenated and dehydrated environment. In contrast, petroleum formation involves the maturation of organic matter in source rocks, with hydrocarbon generation typically occurring at temperatures between 60°C and 180°C [1]. This questions whether the oil DNA, including the oriDNA and environmental DNA (eDNA) from surrounding contexts, could be extracted and amplified. Such a success could provide critical insights into the genetic information preserved during petroleum's formation, migration, accumulation, and long-term storage.

Employing nanoparticle affinity bead technology, we successfully extracted DNA from petroleum sourced from the Nanyang Oilfield, constructed DNA libraries, and recovered 3,159,020 DNA fragments. Using the mega screen method, we classified the petroleum DNA (pDNA) according to their origins, distinguishing preDNA from paeDNA. The paeDNA proved instrumental in validating key local historical events, including marine invasions, activities of unclassified *Homo species*, and the presence of ancient bird species. Contrary to expectations, oriDNA from the petroleum was virtually undetectable, hindering attempts to determine the specific species contributing to the oil formation. Nonetheless, this discovery positions petroleum as an innovative reservoir for retrieving aDNA fragments from non-skeletal materials, providing a valuable avenue for investigating the evolutionary trajectory of ancient regional life within the context of local paleontology and geological development. Notably, most petroleum aDNA fragments exhibited "non-deaminated" characteristics, challenging the scope and validity of Pääbo's team's reliance on deamination as a primary indicator of aDNA authenticity. This discovery underscores the need for a global pDNA database, which could serve as a transformative platform for interdisciplinary research spanning geology, industrial genomics, and paleontology.

Results and Discussion

I. Petroleum Geology of the Nanyang area

During the Early to Middle Triassic, the Nanyang Oilfield was situated within a trough in the Qinling region of southern China. This area subsequently consolidated into a cohesive landmass following the collision of the Sino-Indian Plate in the Middle to Late Triassic [14]. The oil wells are situated in the Biyang Depression between the North China and the Yangtze Plates. The source rocks of these studied crude oil samples were deposited under a high-salinity and strongly reduced environment with a stratified water column. Geochemical studies on Eh_3 shales, the most favorable hydrocarbon source rock in the oil fields, have revealed an average organic matter abundance of 2.96 % (wt%), indicating low to mature stages of maturity, with prevalent type I to type II kerogen dominance [15]. The organic matter in source rocks primarily consists of bacteria, algae, and a small amount of higher plants from land.

The reservoirs are buried at depths of 90 to 1000 m, with oil layer thicknesses ranging from 1 to 4 m and assemblage thicknesses ranging from 2 to 15 m. The petroleum reservoirs in the Nanyang Oilfield experienced a complex filling history, including an early oil filling, significant uplift, a second phase of filling, and late-stage biodegradation. Therefore, the oils with a burial depth of less than 1100 m are characterized by higher density, higher viscosity, and depletion of light hydrocarbon fraction [16,17,18]. The significant uplift of stratum and erosion made the reservoired oil susceptible to incorporation into the earth's surface organisms. Fossil evidence suggests that the region was inhabited by Asian *Homo erectus* and a variety of mammals during the Middle Pleistocene dating back 0.5 Ma [19]. This region has been densely populated since the arrival of modern agricultural civilization.

II. Geochemical Markers as Indicators of Biological Origins

GMs exhibit limited ability to distinguish specific species contributing to organic inputs due to frequent overlap in their distributions across different species. However, certain GMs serve as reliable indicators of specific biological sources. In this study, β-carotene is associated with cyanobacteria or algae, while 3β-methylhopanes denote methanotrophic bacteria. Conversely, gammacerane, present in oil and sedimentary organic matter, derives from tetrahymanol produced by ciliates that feed on bacteria. Low pristane/phytane ratios and elevated gammacerane abundance typically correlate with anoxic, saline, and stratified water bodies [3]. Similarly, a reduced pristane-to-phytane ratio paired with a higher gammacerane index suggests a predominant contribution from aquatic organisms, with minimal input from higher plants, in a saline lacustrine basin. The prominence of tricyclic terpanes (TT) with the high frequency of C_{23}TT points to a marine or saline lacustrine depositional environment [20]. Our GM findings posit that most petroleum molecules originate from lower plants and plankton, a perspective aligned with the prevailing scholarly views, as depicted in Figures S1 and S2.

III. Extraction of DNA and Analysis via the Mega Screen Method

Using the nanoparticle affinity bead technology, the pDNA was extracted and sequenced, the 3,159,020 pDNA sequences were categorized for further analysis via the mega screen method (Materials and Methods). These sequences, derived from diverse species and sources, were broadly classified into oriDNA, paeDNA, and preDNA.

1. Establishing lineage subsets for pDNA fragments

Non-discriminatory alignment was performed without predefined target genomes using the Best E-value mode (BE mode), aligning over 3.15 million total sequences (TS) with the NCBI database (Materials and Methods). These sequences were subsequently categorized into lineage subsets: 51.29% (1,620,178 fragments) were assigned to bacteria, 33.16% (1,047,532 fragments) to the human genome, 3.85% (121,735 fragments) to the fungal genome, and 0.29% (9,252 fragments) to the avian genome. Additionally, 0.15% (4,785 fragments) corresponded to non-primate mammals and 1.11% (35,108 fragments) to non-human primates (MHPs). A minimal fraction (5 fragments) was attributed to algae, excluding red or brown algae (Figure 1). Notably, these DNA-based findings differ from the above

GM studies, as the species distribution and frequency indicated by DNA contrast with those inferred from GMs.

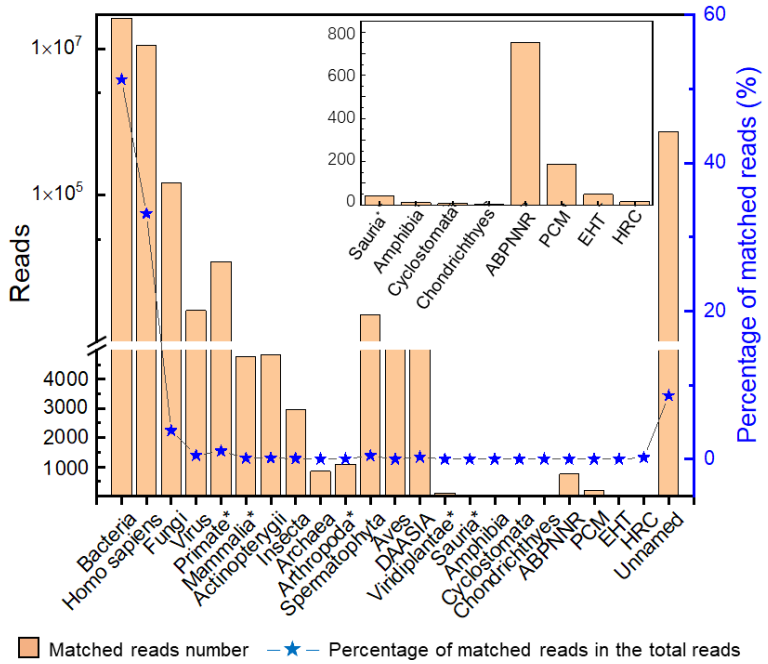

Figure 1. Analysis of pDNA sequences corresponding to different lineages

The bars represent the number of pDNA sequences that match a lineage, while the lines represent the percentage of pDNA fragments in that lineage compared to the total number of pDNA fragments. The abbreviations used are as follows: ABPNNR (Rotifera, Nemertea, Nematoda, Platyhelminthes, Annelida, and Bryozoa), PCM (Porifera, Cnidaria, and Mollusca), EHT (Hemichordata and Tunicata), HRC (Haptophyta, Rhodophyta, Cryptophyceae), and DAASIA (Discoba, Apusozoa, Amoebozoa, Sar, Ichthyosporea, and Apicomplexa). It's important to note that Viridiplantae* excludes Spermatophyta, Arthropoda* excludes Insecta, Sauria* excludes Aves, Primates* excludes *Homo*, and Mammalia* excludes Primates*. Additional details are provided in Tables S1 and S11.

2. Identify the unique lineage source of each sequence

We employed the MS mode (Materials and Methods) to determine the specific species fragments (SSFs) and their lineage origin. Through this approach, at least 400 pDNA sequences have been successfully identified as SSFs and categorized into nine groups based on their morphological characteristics and habitat (Table 1), including lower plants (Group G), marine organisms (Group M), primates (Groups C, P, and T), and birds (Group L). Although these sequences cannot trace major oil-forming species, they provide valuable data reflecting local geology, history, and evolution, an unexplored reservoir for investigating local geological and species evolution. Due to the lack of genome data for certain lower species, some pDNA sequences could not be genealogically determined.

3. Investigating local geological changes through algal distribution

We identified three sequences matching Chlorophyta and five aligning with Streptophyta (Table S1). Sequences ID_1G, ID_2G, and ID_3G display unique profiles distinct from known genomes, hinting at their potential classification as aDNA. Morphological evidence from core samples of the Hetaoyuan Formation (37.5 Ma) indicates a marine invasion, with preserved skeletons of red algae (Rhodophyta) and brown algae (Ochrophyta) reported by previous studies [6,7]. In contrast, our data detected no DNA from these algal groups, implying a significant loss of algal DNA in the reservoir since early times. The small size of these organisms likely renders them prone to rapid dissolution and rupture upon incorporation into the oil, resulting in the release and subsequent degradation of their DNA.

Table 1. Summary of the SSFs in pDNA sequences matched genomes

Group	Target	ID	Lineages	pDNA Count	Affinity	
					Average	SD
G	Plastid + Nuclear DNA	1G-8G	*Chlorophyta, Streptophyta*	8	90.23%	16.05%
H	Primate mtDNA	1H-40H	*Home sapiens*	40	96.12%	15.44%
N	Non-primate mtDNA	1N	*Gallus gallus, Galliformes*	1	99.32%	-
		2N	*Sus scrofa, Artiodactyla*	1	99.48%	-
		3N-5N	*Mylopharyngodon piceus, Cypriniformes*	3	100.00%	-
T	Primate nuclear gene	1T-275T	*Pan troglodytes*	275	96.91%	4.47%
P		21P-28P	*Pan paniscus*	8	98.23%	2.15%
		29P-36P	*Gorilla gorilla*	8	98.42%	2.03%
		6P-20P	*Cercopithecidae* (Old World monkeys)	15	94.31%	2.42%
		2P-5P	*Platyrrhini* (New World monkeys)	4	94.31%	5.80%
		1P	*Carlito syrichta* (*Tarsiiformes*)	1	70.67%	-
C		1C-9C	Primate protein-coding sequences	9	92.11%	4.04%
A	Nuclear gene of non-indigenous organism	1A-7A	*Bos mutus, Artiodactyla*	7	93.67%	5.51%
		8A-15A	*Meleagris gallopavo, Galliformes*	8	92.06%	8.02%
M	Nuclear gene of marine organisms	1M	*Scyliorhinus canicula, Chondrichthyes*	1	50%	-
		2M-5M	*Mercenaria mercenaria, Mollusca*	4	70.89%	17.23%
		6M-10M	Marine fishes, *Actinopterygii*	5	57.79%	18.61%
L	Others	1L-4L	*Matches with very low similarity*	4	< 50%	-

Note: The sequences between 7C and 28P, and between 8C and 4P, are identical.

4. Evidence of marine organisms' DNA signature

The analysis identified sequences containing genetic signatures of marine organisms, including Chondrichthyes, Actinopterygii, Tunicata, and Mollusca (Table S2), indicating the occurrence of local marine transgressions. Four sequences correspond to ray-finned fish species, with two sequences attributed to Scombriformes and two to Eupercaria. These marine fishes emerged during the mid-to-late Cretaceous period [22], suggesting a marine invasion occurred after this age. This evidence lends circumstantial support to Xia's view [6].

5. Evidence of ancient animals' migration and continental drift

Fragments associated with non-native species, such as yaks in the northern Himalayan foothills, turkeys in the Americas, and kiwi birds in the South Pacific Islands, were discovered (Table S3). It is proposed that these species are descendants of ancient Pangaea ancestors who migrated and reproduced in their local habitats due to continental drift. Their eventual disappearance left molecular evidence underground, offering new insights into the theory of continental drift.

6. Unveiling species intermediate forms in avian ancestry

The Late Mesozoic strata underlying the Hetaoyuan Formation are thought to date back to an era marked by dinosaur reproduction and the emergence of early birds. The ID_1L fragment aligns with avian genomes, showing a 61.91 affinity value to the mRNA transcript sequence of *Calidris pugnax*, suggesting it derives from an ancient bird (Table S4). This sequence includes the protein-coding regions of exon 3, exon 4, and part of exon 5 but lacks introns, indicating its role as a pseudogene. Detailed analysis reveals a composite structure: the initial 25 base pairs upstream closely resemble the intergenic sequence of *Podarcis lilfordi* (Figure 2), pointing to a genomic blend of avian and reptilian origins. This combination of dinosaurian and avian traits may represent the first molecular evidence of transitional species within Darwin's evolutionary framework. The lack of an exact match to modern bird sequences

could reflect either the extinction of the host species or significant genomic divergence in its descendants. This discovery further corroborates the hypothesis that the Nanyang Basin was an ancestral habitat for early birds.

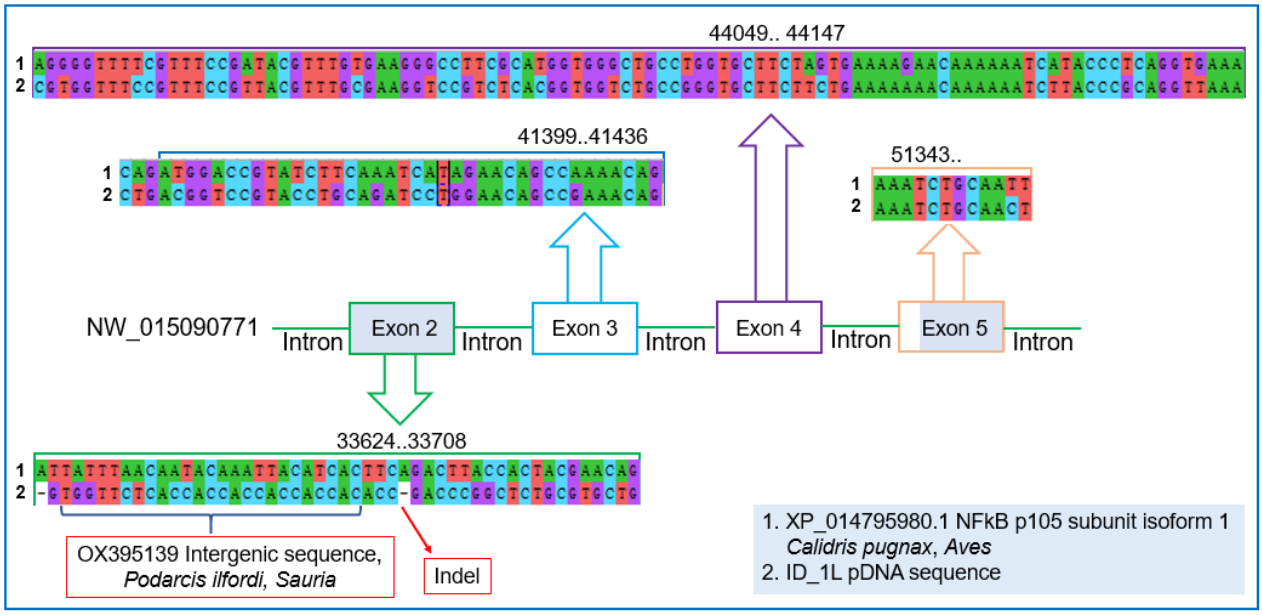

Figure 2. The Schematic diagram of *NFκB* p105 subunit-like DNA sequence (ID_1L)

7. Discovery of unclassified *Homo* species via mitogenomes

We utilized the MS mode to analyze a subset of 1,047,532 human-related sequences (Figure 1) and discovered five non-primate mitogenomic sequences (Table S5) without non-human primate mitogenomic sequences. Of these, 845 sequences exhibiting 100% affinity to the human mitogenomes were excluded for further analysis. Additionally, 41 sequences showed divergent affinity values to the human mitogenome, ranging from 91.48% to 99.5%. Given that comprehensive human mitogenome data are available and potential misclassifications arising from minor unknown loci variations are rarely ruled out, these sequences are likely of ancient origin (Table S6).

Closer examination of two sequences, ID_17H and ID_20H, revealed 100% mutual coverage but distinct identities of 96.98% and 99.50%, respectively, suggesting they derive from separate maternal lineages. The pDNA fragment ID_18H, with an affinity value of 96.80%, was positioned via phylogenetic analysis on a node with *Homo sapiens*, hinting at a possible origin from an unrecognized species within the genus *Homo* (Figure S3, top). Fragment ID_19H, displaying an affinity value of 83.85% to human ND4, was phylogenetically placed between the human and chimpanzee genera, potentially representing the earliest local *Homo species*; RelTime-ML analysis estimated its divergence from humans at 0.49 Ma (Figure S3, middle & bottom). Notably, these pDNA sequences are absent from the modern human genome, indicating that the ancient humans bearing these fragments are likely extinct.

8. Discovery of unclassified *Homo* species via nuclear genomes

In the pDNA, a large number of SSFs (with low affinities) aligned with nuclear sequences of non-human primates (NHPs) at varying frequencies: 1 with the Tarsiidae family, 4 with Platyrrhini (New World monkeys), 15 with *Macaca* (Old World monkeys), 8 with gorillas, 8 with pygmy chimpanzees (Table S7), and 271 with chimpanzees (Table S8). Among the 271 chimpanzee-aligned sequences, the second-hit species were modern humans in 241 cases (88.93%), other primates in 29 (10.70%), and non-primates in the remaining instances. Given the local fossil evidence of *Homo erectus* and the absence of non-human primate fossils in the region, we propose that these sequences may be linked to Asian *Homo erectus*, particularly in light of the genomic relationships between modern humans and NHPs.

9. Human activities and local eDNA

Unlike non-human apes, human burial practices have effectively slowed DNA decomposition, facilitating its preservation and accumulation in the environment surrounding burial sites. Fossils of *Homo erectus*, dated to approximately 0.5 Ma, have been uncovered in Nanzhao County near Nanyang oilfield [19]. Based on this, we infer that the ID_19H pDNA fragment analyzed in this study, along with the majority of the 271 pDNA fragments previously noted, likely originated from Late Asian *Homo erectus*. Given that these DNA fragments are considerably "younger" than the 37.5 Ma age of the source rock, they are classified as paeDNA.

10. Summary of the DNA Signatures of Late Asian *Homo erectus*

This study reveals that the mitogenomic divergence between Asian *Homo erectus* and modern humans is markedly smaller than that between Asian *Homo erectus* and chimpanzees. The study suggests that Asian *Homo erectus* are more closely related to humans on a maternal basis than to chimpanzees. They retained conservative skeletal traits, such as thick skulls and low foreheads, akin to Early African *Homo erectus*, with their extinction regarded as an "evolutionary dead end" [23,24,25,26]. Previous studies indicate that ancient human populations experienced significant population bottlenecks and limited mitochondrial haplogroup diversity, organizing into small, female-centered clan tribes with strong kinship bonds [27,28,29]. Determining the precise timing of reproductive isolation resulting from the genomic divergence between humans and chimpanzees remains a critical scientific question deserving further investigation.

Many SSFs matched the nuclear genes of non-human great apes (Table 1); however, central China is not a habitat for them. Consequently, these fragments likely originate from their closest relatives, Asian *Homo erectus*. The presence of a substantial number of NHP SSFs in oil samples is striking, suggesting a significant population of Asian *Homo erectus* during a prolonged period of residence in this region. Also, petroleum serves as an effective medium for preserving GAT genomes.

IV. Hypothesized Pattern of DNA migration and preservation in oil reservoirs

DNA is predominantly water-soluble, with limited solubility in lipids. The lipid envelopes encasing cells and organelles facilitate their entry into oil reservoirs. Upon rupture of these envelopes, DNA intermingles with alkane molecules but is subsequently extracted into the aqueous phase at the water-oil interface upon contact with water. We hypothesize that tissues or cells, particularly fat tissue, adipocytes, or casein fragments, can readily infiltrate petroleum reservoirs. In more extensive remains, multiple layers of fat tissue may become encapsulated by oil, resulting in "oil immersion preservation". This process enables a gradual release of DNA from tissues adjacent to the oil phase, with successive layers contributing DNA as degradation progresses until the organism is fully dissolved. In addition, fat tissues containing DNA can liquefy, allowing DNA to flow into the reservoir, resulting in a prolonged, slow, and continuous release. In contrast, smaller entities like algae and plankton possess cells that rupture rapidly, quickly releasing their DNA into the reservoir. Consequently, pDNA experiences ongoing loss over time (Figure 1). This raises an intriguing question: Do the hosts of eDNA, including paeDNA and preDNA, also contribute to oil formation? Though their input may appear minor, the evidence suggests a positive response.

Research has noted a decline in oriDNA and an increase in eDNA, predominantly from microorganisms such as bacteria, in bone fossils [30]. Over time, oriDNA and paeDNA in reservoirs undergo continuous degradation and loss, as eDNA persistently infiltrates the oil, creating a distribution of “old-less, new-many” for GAT genomes. Human activities, such as urban settlement, burial practices, and extensive cultivation of angiosperm crops, have further contributed to eDNA resources (Figure 3). The origins of oriDNA and paeDNA from the distant past remain inconclusive in this study due to a limited understanding of ancient paleoenvironments. In contrast, GMs are primarily oil-soluble, exhibiting minimal solubility in water. As a result, there is minimal concern regarding the loss of GMs from oil reservoirs, enhancing the effectiveness of their detection patterns in tracing the molecular origins of oil and gas. Although some environmental GMs may be continually incorporated, the “old-less, new-many” pattern observed in pDNA does not apply to GMs.

Two examples highlight the "old-less, new-many" pattern of the GAT genome. First, DNA from lower life forms in crude oil has almost entirely disappeared, whereas DNA from modern species has progressively increased (Figure 1). Second, among 886 human mitogenome sequences, 845 from modern humans (preDNA) display a 100% affinity value, whereas 41 sequences from ancient *Homo species* (paeDNA) show varying degrees of divergence from the human mitogenome (Table S6).

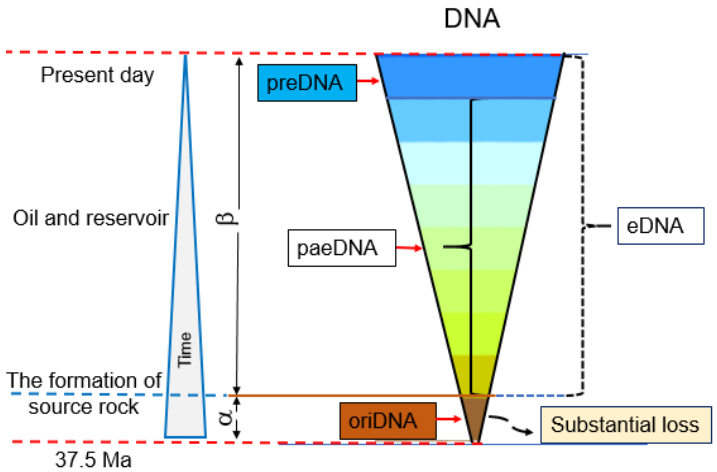

Figure 3. Preservation Patterns of DNA in Petroleum

V. Challenges to aDNA authenticity criteria

In this study, many pDNA fragments within the GAT genome exhibited no signs of fragmental deamination. We propose several explanations for this observation. First, eDNA encapsulated in lipids enters the reservoir, an anaerobic and anhydrous environment that may inhibit deamination. Second, DNA deamination typically requires water as a critical component, which is scarce in this context. Third, fragments displaying severe deamination may have been excluded during the selection process of the mega screen method. Deamination is a critical marker for authenticating aDNA in the Pääbo method [31, 32, 33]. However, Pääbo's team rarely encounters material like petroleum in this study. Consequently, this primary indicator of aDNA authenticity does not apply to pDNA studies, highlighting the need to reassess the scope of applicability of this method.

VI. Significance and outlook

Scientific Importance: Genetic information derived from DNA is essential for elucidating species relationships, life histories, and evolutionary mechanisms. This study marks the first successful extraction of DNA from petroleum, expanding the scope of molecular biology and challenging established disciplinary boundaries. It overturns the long-standing misconception that petroleum lacks DNA and provides the first molecular evidence demonstrating that Asian *Homo erectus* is more closely related to modern humans than to Chimpanzees in maternal side. Additionally, it contributes to geological theory by offering molecular evidence supporting marine invasion events in the Nanyang region. While Xia's evidence based on the algae alone has been deemed insufficient to confirm such events and remains not widely accepted, our findings bolster this hypothesis [6,7]. Moreover, this study facilitates the detection of intermediate animals, such as the ID_1L fragment mentioned before, which suggests activities of local avian ancestors (possibly Archaeopteryx?). This evidence significantly aids in addressing Darwin's puzzle, the scarcity of intermediate species in the fossil record, revealing that molecular evolution may exhibit greater diversity than previously recognized.

Petroleum as an SSF Reservoir: DNA sequences show remarkable similarities across different species. For example, humans and chimpanzees share over 98% of their genomic sequence. This closeness highlights the importance of using SSFs for accurate identification. Although SSFs represent only a little portion of a genome, just a few pieces from a sample are enough to confirm the presence of a particular species while also functioning as valuable geological markers. Petroleum SSFs are indicators for exploring ancient animal activity patterns, spanning lower life forms, birds, and advanced mammals. As a significant amount of SSFs was identified in the fragments of the petroleum GAT genome, this quantity significantly exceeds that found in other sample types (e.g., fossils, rocks), highlighting petroleum's role as a storage medium and an untapped reservoir for aDNA. Likewise, using the SSFs, we revealed traces of ancient animal activities from locally extinct species, such as yaks, Kiwi birds, sea fishes, and shellfish, laying the groundwork for reconstructing paleoenvironments and paleoecology.

Future Directions: Looking ahead, we aim to extract aDNA from petroleum, fossils, and source rocks to establish an integrated trinity of global aDNA libraries. This endeavor will pave the way for an innovative aDNA resource, enhancing our understanding of evolutionary and geological histories.

Methods

I. The geochemical survey

The oils were deasphalted with petroleum ether and then fractionated by column chromatography using a 2:1 (v/v) mixture of silica gel and alumina. The fractions were separated into saturated, aromatic, and resin components by sequential elution with 60 mL of petroleum ether, 40 mL of a dichloromethane/petroleum ether mixture (2:1, v/v), and 30 mL of a dichloromethane/methanol solution (93:7, v/v), respectively.

Gas chromatography (GC) analysis was conducted on the saturated fractions using an Agilent Model 6890 gas chromatograph installed with a silica column (HP-1, 30 mm × 0.25 mm i.d.). The oven temperature was programmed to increase from 100°C to 300°C for 10 minutes at a rate of 4°C/min. Helium was employed as the carrier gas.

Gas chromatography-mass spectrometry (GC-MS) analysis of the saturated and aromatic fractions was performed using an Agilent Model 6890 gas chromatograph coupled to a DB-5MS capillary column. The temperature program for the saturated fraction was as follows: the initial temperature was set at 100°C for 1 minute, followed by a ramp of 4°C per minute to 220°C, and then increased to 300°C at a rate of 3°C per minute and held for 15 minutes. The mass spectrometer was operated in electron impact mode, with an ionization energy of 70 eV and a scan range of 50-600 Da. The biomarker parameters of the saturated and aromatic hydrocarbons were determined by integrating the peak areas on the mass chromatograms.

II. DNA extraction, DNA library construction, sequencing, and NCBI nucleotide BLAST

The procedure was conducted in a BSL-2 industrial laboratory (Biosafety Level 2), following rigorous ancient DNA extraction protocols[29]. The process involved the UV sterilization of all items used and the utilization of Geobio® DNA Remover (Jiaxing Jiesai Biotechnology Co., Ltd., Jiaxing, China) on clean benches and solid equipment. It is important to note that this laboratory has never been exposed to fish, NHPs, or plant samples before this work.

To extract DNA from petroleum samples, we followed the recommended protocol of the Geobio® DPPS-PMNP DNA extraction kit developed by Jiaxing Jiesai Biotechnology Co [34]. Due to various long-term factors, some pDNA molecules are cross-linked with other macromolecules, forming complexes. To estimate the extract concentration, we measured the optical density (OD) at the UV 260 nm peak of the DNA mix, containing DNA complexes and free DNA molecules. We performed the extraction experiments on the samples five times, and the results were consistent (Table S9), providing sufficient DNA (Table S10). We used NEB PreCR®Mix for DNA repair.

The NGS DNA library construction followed the SSDLSP standard procedure (Sangon Biotech, CORP). Sequencing was conducted on Illumina NovaSeq 6000 (S-4 Reagent Kit) using the "Dual index sequencing" standard procedure, and the reads met the quality control standards with satisfactory quality distribution. Sometimes, it's necessary to manually remove extra adapter sequences at both ends of the read to obtain accurate information. After merging the forward and reverse reads, we performed local NCBI Nucleotide BLAST, Size 11, using the database (Version 5, Nucleotide sequence Database), identifying 3,159,020 valid sequences. The sequences were classified according to their biological characteristics, and their lengths were measured (Table S11). It is important to note that the processes of secondary oil collection may inadvertently lead to the loss of many aDNA fragments.

The mega screen method

First, we employed the Best E-value mode to group sequences by aligning fossil DNA with all known sequences from the NCBI database (Version 5, Nucleotide Sequence Database). We applied an E-value cutoff below 1E-07 to filter for qualified sequences (QS) and identify the best match at a taxonomic level.

In the second step, we used the MS mode by selecting the "exclude" option and conducting a search that omitted the first result. If the E-value difference between two searches is less than 1E-02 (meaning the quotient of the first E-value divided by the second one is ≤ 0.01), the fragment is considered specific to the first match, confirming its specificity. Conversely, if the difference exceeds the established threshold (1E-02), the fragment is not confirmed as originating from a single one. In this scenario, we cannot determine the fragment's origin.

The whole process involves the following steps:

1) Nucleotide Blast is employed to align sequences to the entire NCBI database without any limitation.

2) Creation of subsets for sorting the sequences: Using the Best E-value mode, results are matched, and sequence fragments are grouped into the appropriate subsets, determining the total number of sequences (TS). Subsequently, an E-value threshold of < 1E-07 is established to filter for qualified sequences (QS).

3) The subset primarily containing aDNA is selected.

4) Each sequence within this subset is screened individually using the MS mode to identify those originating from a single species, categorizing the "unique" sequences (SSFs).

5) Considering various factors, including local climate shifting, geological changes, and evolutionary principles of the host species, we can ascertain if the sequence is oriDNA.

Sequence affinity (Affinity): The metrics we set up to assess the similarity relationship between subject sequences and hit genomes were obtained by multiplying the two values of Identity and Cover obtained from NCBI BLAST and then converted to percentages (Identity × Cover × 100%). Mutations in the genomic and mitogenomic sequences occur continuously during the evolutionary process, leading to significant sequence differences between ancient and modern species. However, this variation is lower in conserved sequences than in non-conserved sequences. A high-affinity value indicates that the sequence is highly coherent and related to the genome of the modern species, which is likely to be either a conserved sequence or a modern eDNA. A low-affinity value indicates a low similarity, and the sequence may be from a distantly related species either has or has not yet been sequenced. It is necessary to consider various factors, including the sequence composition and conservation, host species information, host genome sequencing data, etc., rather than relying on the Affinity value alone when determining whether a sequence is an oriDNA.

Data and software availability

The sequencing data have been deposited in the NCBI BioProject (PRJNA1091869). The pDNA sequences utilized in this manuscript are listed in the Appendix (Table S12). In this study, MEGA11 was used to construct the RelTime-ML local timetree [36].

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Author contribution

The study was conceptualized and designed by W.Q.Z. and Y.Q.G., Y.Q.G., T.C.Q., and W.Q.Z. supervised the transportation of oil samples. M.J.L. performed the geochemical marker analysis. Geographical and paleogeological data analysis, as well as map creation, were conducted by F.L. and H.Y.Z. Petroleum DNA extraction from the samples was carried out by W.Q.Z., C.Y.Z., and J.Y.Y. Alignment between the sequences and present genomes was completed by Z.Y.G. and M.J.C. DNA laboratory analysis, interpretations, taxonomic profiling, and annotation were conducted by Z.Y.G., Z.Y.T., S.J.Z, L.J.Z, and W.Q.Z. The statistical analyses were performed and finished by G.Q.C., X.G.Z., R.C., and J.H.Z. Phylogenetic analyses of mitogenomic DNA sequences were performed by J.H.G., under the supervision of G.Q.C. and W.Q.Z. Figures were designed and finished by R.C., J.H.Z., L.Y.Q., and M.R.S. The manuscript was written by W.Q.Z. and corrected by Z.Y.T., M.J.L., and L.Y.Q. The Project Coordinator was T.C.Q.

Competing interests

The authors declare that they have no competing interests.

Data and materials availability

All data are available in the main text or the supplementary materials.

Supplementary Materials

Figures. S1 to S4; Tables S1 to S12

Supplementary Materials for

Uncovering Ancient DNA in Petroleum: Insights into Earth's Hidden Life Events and Geological History

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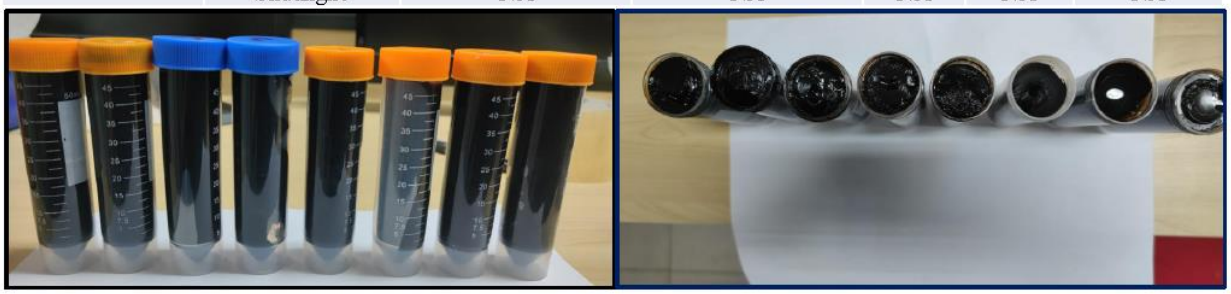
The PDF file includes:

Figures S1 to S4；Tables S1 to S12

A

Physical properties of the petroleum fluids						
Oilfields	Sample Number	Density (g/cm^3)	Colloid Asphaltene (%)	Wax (%)	Sulfur (%)	Viscosity (cP)
Gucheng Well number：51215	1	0.863	39.3	14.5	0.084	15.5
	2	0.865	39.9	15.4	0.085	15.7
	3	0.867	38.1	14.8	0.083	15.2
	4	0.871	39.1	15.2	0.084	15.4
Storage depots 20210301	Gucheng	NA	NA	NA	NA	NA
	Jinglou	NA	NA	NA	NA	NA
	Shuanglou	NA	NA	NA	NA	NA
	Shuanghe	NA	NA	NA	NA	NA



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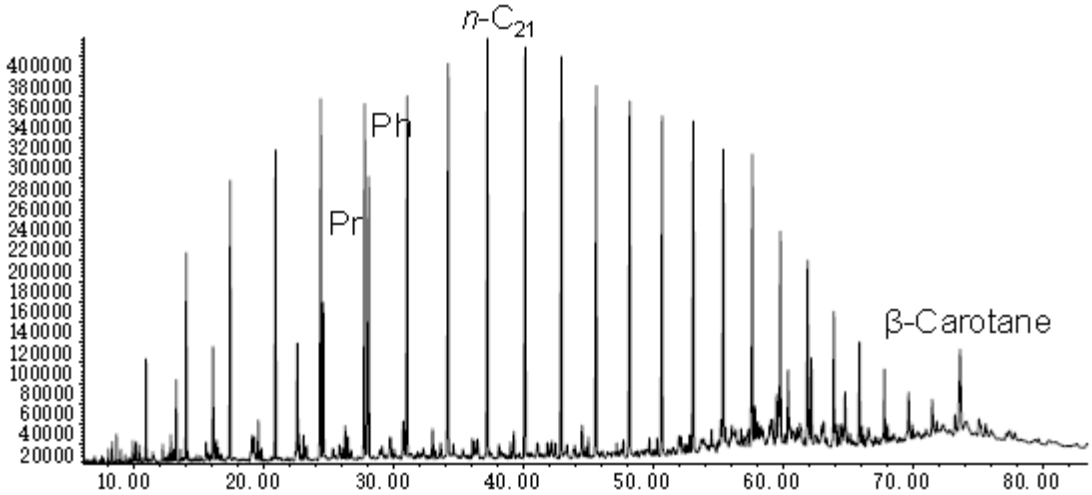

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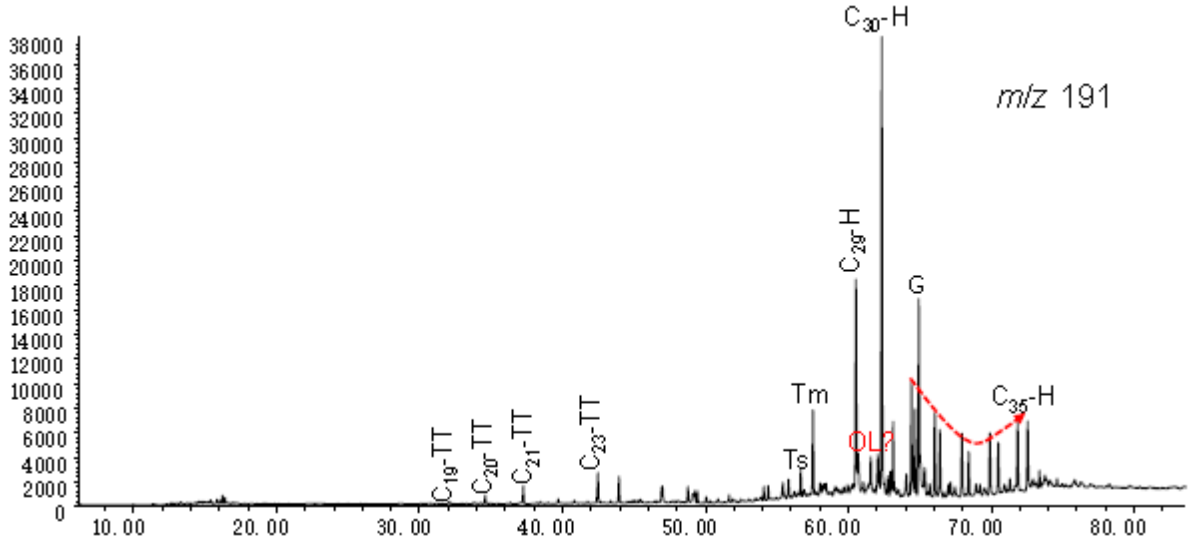
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C29-H
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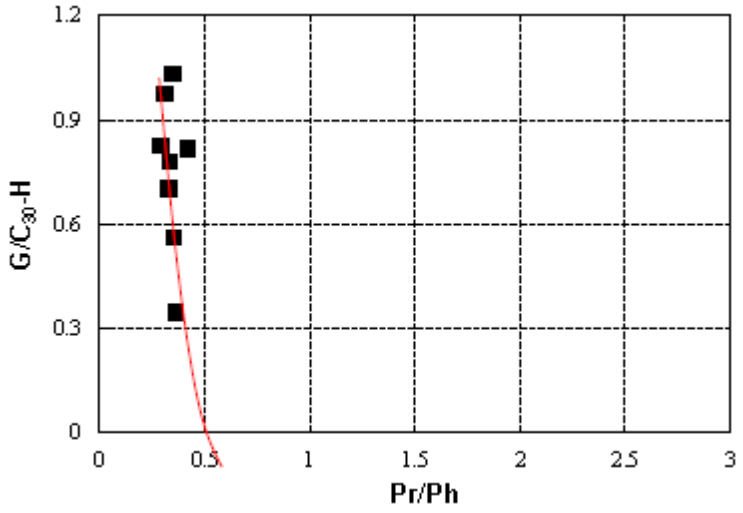
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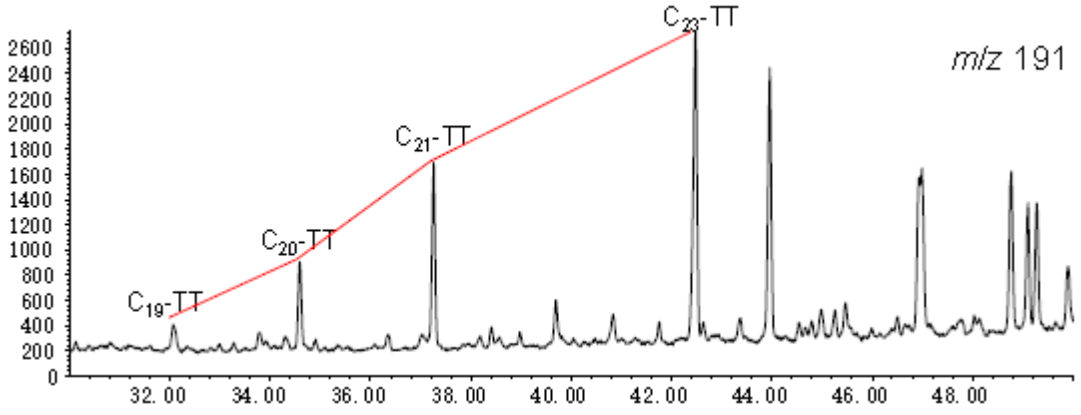
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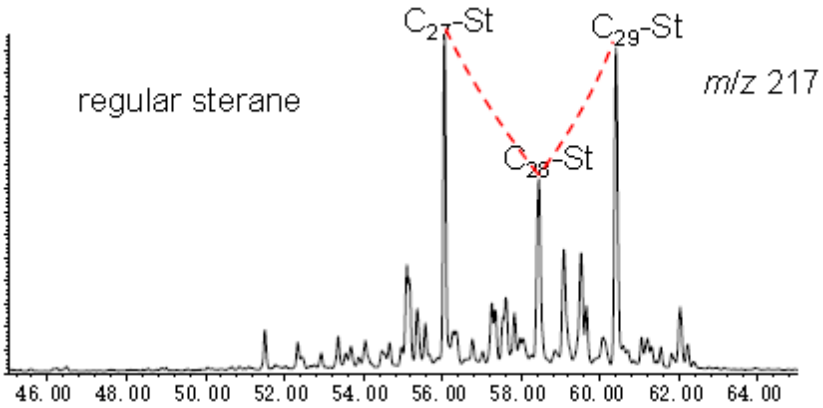

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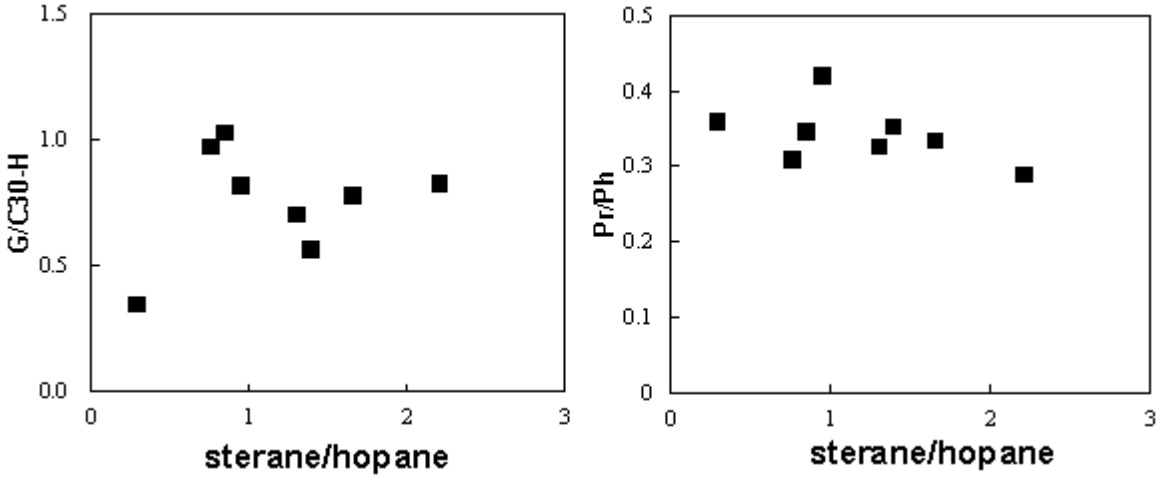

Figure S1. Geochemical analysis of petroleum samples

A, the buk geochemical characteristics of the petroleum used in this study. **B**, the distribution of *n*-alkanes and isoprenoids in the petroleum used in this study. **C**, the distribution of hopanes in the petroleum used in this study. **D**, the distribution of hopanes-gammacerane in the petroleum used in this study. **E**, the distribution of tricyclic terpanes in the petroleum used in this study. **F**, the distribution of sterane in the petroleum used in this study. **G**, the distribution of sterane in the petroleum used in this study.

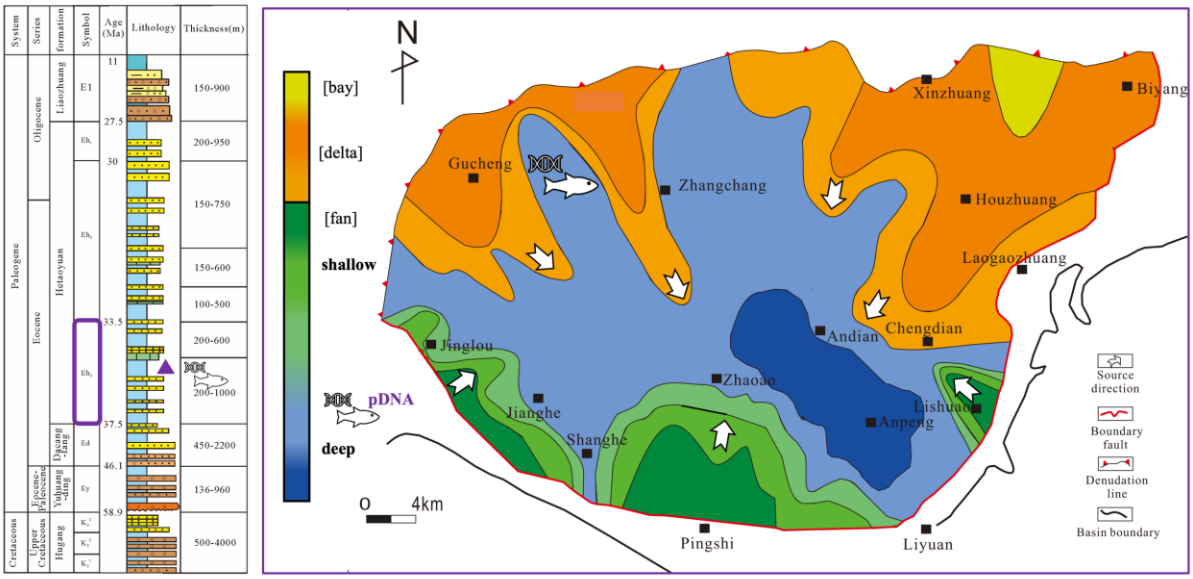

Figure S2. The lithostratigraphy of the Hetaoyuan Formation (left) and corresponding paleogeography in the Eocene ages (right) at the sample position. The paleogeographic map is modified from Li's work [1-3], based on the corrective information from Dong's work[4] and Xia[5].The samples are located in Member 3 of the Hetaoyuan Formation.

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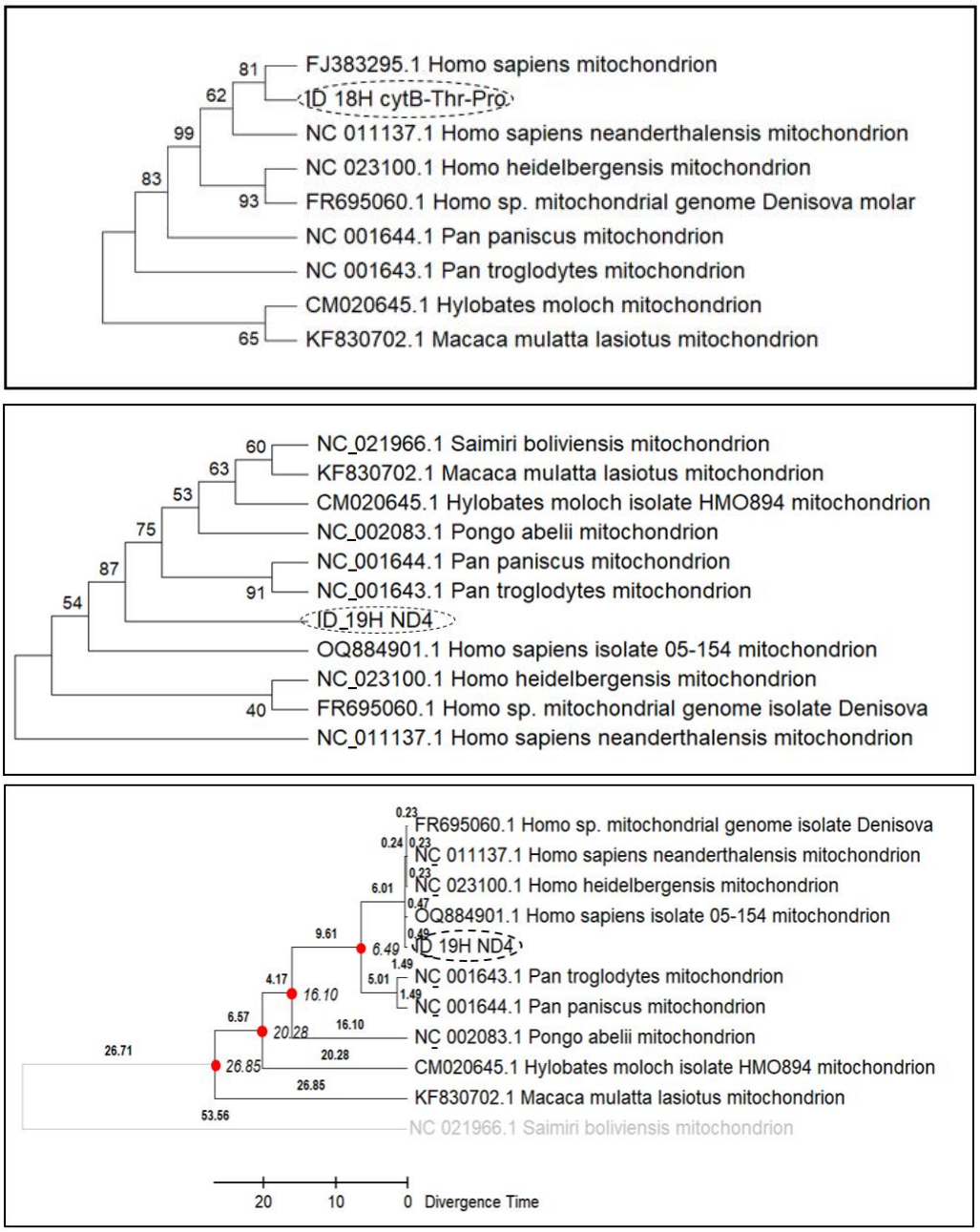

Figure S3. The phylogenetic analysis of the pDNA sequences

The phylogenetic analyses are established using primate mitogenomic sequences as references. The data is being examined utilizing the Maximum Likelihood method in MEGA11 on a locally installed computational platform. The divergences are evaluated in Bootstrap consensus trees through specific calculations with 1000 bootstrap replicates under the HKY+G model and a Timetree under RelTime-ML mode. In each context, ID_18H (shown in the top) and ID_19H (shown in the middle and the bottom) correspond to the human cytB+Thr+Pro and ND4 regions, respectively (OQ884901.1). The Bootstrap value of the node on the Bootstrap consensus tree and the divergence time near the node on the Timetree are numerically represented and displayed for analysis.

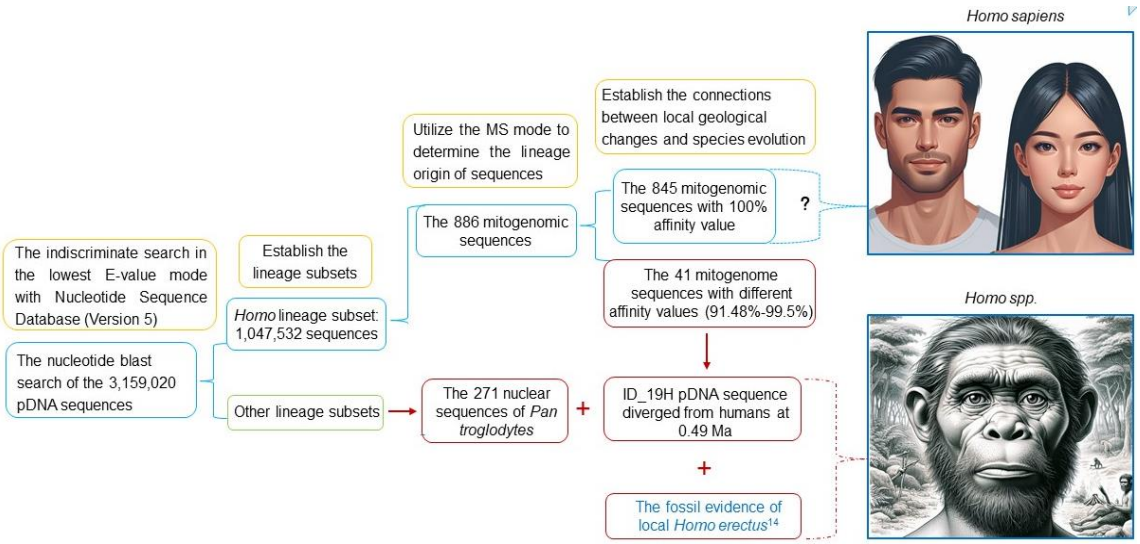

Figure S4. The molecular evidence for the presence of unclassified *Homo species*

Table S1. The pDNA sequences corresponding to low plant genomes

ID	Len	Taxo	Nucleotide ID	Target Description	Cover	Identity	E-value	Affinity
1G	75	*Chlorella desiccata*, Chlorophyta	OK569792.1	Mitochondrion	74%	100%	1.00E-18	74.00%
2G	103	*Picochlorum sp.*, Chlorophyta	CP120464.1	SENEW3 chromosome 10	99%	91.18%	6.00E-30	90.26%
3G	179	*Rhytidiadelphus loreus*, Streptophyta, Bryophyta, Hylocomiaceae	OX344761.1	Genome, chromosome 1	96%	83%	9.00E-38	79.32%
4G	83	*Ulva expansa*, Chlorophyta	MH730161.1	28S rDNA	100%	100%	3.00E-32	100.00%
5G	100	*Klebsormidium sp.*, Streptophyta, Klebsormidiaceae, Klebsormidium	OR168110.1	Plastid DNA	100%	100%	2.00E-41	100.00%
6G	141	*Klebsormidium sp.*, Streptophyta, Klebsormidiaceae, Klebsormidium	OR168110.1	Plastid DNA	100%	100%	2.00E-63	100.00%
7G	153	*Marchantia polymorpha*, Streptophyta, Embryophyta, Marchantiophyta	AP019866.1	Chloroplast DNA	100%	99%	4.00E-67	99.35%
8G	155	*Marchantia polymorpha*, Streptophyta, Embryophyta, Marchantiophyta	AP020202.1	Chloroplast DNA	100%	99.35%	3.00E-69	99.35%

Table S2. The pDNA sequences corresponding to the marine organisms' genomes

pDNA		Results of the Nucleotide Blast			
ID	Len	Taxo	Nucleotide	E-value	Affinity
1M	78	*Scyliorhinus canicula*, Chondrichthyes	LR744051.1	2.00E-06	50%
2M	80	*Mercenaria mercenaria*, Mollusca	XM_045350734.2	9.00E-18	83%
3M	92	*Nucula nucleus*, Mollusca	LC123061.1	5.00E-22	78%
4M	112	*Ruditapes philippinarum*, Mollusca	KU682310.1	2.00E-16	77%
5M	184	*Phorcus lineatus*, Mollusca	OV121097.1	2.00E-07	45%
6M	253	*Lateolabrax maculatus*, Actinopterygii	CP027279.1	2.00E-52	68%
7M	203	*Hyperoplus immaculatus*, Actinopterygii	OX442354.1	1.00E-29	44%
8M	187	*Thunnus maccoyii*, Actinopterygii	OU343202.1	8.00E-19	70%
9M	83	*Thunnus maccoyii*, Actinopterygii	OU343200.1	9.00E-12	72%
10M	131	*Aplidium turbinatum*, Tunicata	OU964919.12	3.00E-09	35%

Table S3. The 15 pDNA sequences corresponding to the genomes of non-indigenous organisms

pDNA		Results of the Nucleotide Blast			
ID	Len	Taxo	Nucleotide ID	E-value	Affinity
1A	117	*Bos mutus*	CP027076.1	3.00E-46	97.44%
2A	149	*Bos mutus*	CP027076.1	8.00E-55	92.98%
3A	144	*Bos mutus*	CP027076.1	2.00E-61	96.62%
4A	97	*Bos mutus*	CP027076.1	5.00E-23	81.66%
5A	162	*Bos mutus*	CP027078.1	3.00E-67	95.92%
6A	119	*Bos mutus*	CP027078.1	3.00E-46	96.64%
7A	140	*Bos mutus*	CP027087.1	9.00E-54	94.45%
8A	223	*Meleagris gallopavo*	OW982293.1	4.00E-93	92.34%
9A	151	*Meleagris gallopavo*	OW982293.1	2.00E-49	95.26%
10A	117	*Meleagris gallopavo*	OW982293.1	8.00E-41	97.20%
11A	198	*Meleagris gallopavo*	OW982293.1	5.00E-53	94.28%
12A	288	*Meleagris gallopavo*	OW982293.1	9.00E-128	97.20%
13A	92	*Meleagris gallopavo*	OW982297.1	2.00E-20	72.90%
14A	154	*Meleagris gallopavo*	OW982293.1	4.00E-53	95.26%
15A	103	*Apteryx mantelli*	LK358553.1	2.00E-08	39.05%

Table S4. The pDNA sequences exhibiting low affinity values

pDNA		Results of the Nucleotide Blast				
ID	Len	Taxo	Loci/Protein	Nucleotide	E-value	Affinity
1L	250	*Calidris pugnax*, Aves	NFKB1	XM_014940504.1	2.00E-32	61.91
2L	250	*Myotis daubentoniid,* Mammalia	Chromosome 13	OY725372.1	3.00E-38	59.8
3L	273	*Aquila chrysaetos*, *Aves*	Chromosome 13	LR606193.1	7.00E-19	45.46
4L	250	None				

Table S5. The 5 pDNA sequences corresponding to non-primate mitogenomes

pDNA		Results of the Nucleotide Blast				
ID	Len	Taxo	Nucleotide	Range/Area	E-value	Affinity
1N	146	*Gallus gallus,* Galliformes	OP740918.1	503-648; 12S	2.00E-66	99.3200%
2N	193	*Sus scrofa,* Artiodactyla	MN124249.1	344-536; COX1	2.00E-92	99.4800%
3N	81	*Mylopharyngodon piceus,* Cypriniformes	MF687133.1	13586-13666; ND5	3.00E-32	100.0000%
4N	203	*Ctenopharyngodon Idella,* Cypriniformes	MG827396.1	10382-10582; ND4	6.00E-97	100.0000%
5N	113	*Ctenopharyngodon Idella,* Cypriniformes	MG827396.1	400-288; 12S	2.00E-48	100.0000%

Table S6. The 41 pDNA sequences corresponding to human mitogenome

pDNA		Results of the Nucleotide Blast				
ID	Len	Taxo	Nucleotide ID	Mito Range/Area	E-value	Affinity
1H	249	*Home sapiens*	OR182493.1	13856-14104; ND5	2.00E-125	99.60%
2H	238	*Home sapiens*	ON422324.1	8347-8584; ATP8+ATP6	2.00E-119	99.58%
3H	216	*Home sapiens*	MH449153.1	9787-10002; COX3+trnG	3.00E-107	99.54%
4H	215	*Home sapiens*	OQ388438.1	47-261; D-loop	1.00E-106	99.53%
5H	212	*Home sapiens*	ON946746.1	765-554; D-loop	5.00E-105	99.53%
6H	194	*Home sapiens*	MH449153.1	9974-9781; COX3	5.00E-95	99.48%
7H	186	*Home sapiens*	MG660585.1	8790-8975; ATP6	1.00E-90	99.46%
8H	176	*Home sapiens*	JQ664512.1	4404-4578; trnM+ND2	5.00E-85	98.44%
9H	164	*Home sapiens*	MN503417.1	11624-11787; trnH+trnS+trnL+ND5	2.00E-76	99.39%
10H	153	*Home sapiens*	MN207699.1	652-804; D-loop:	2.00E-72	99.35%
11H	111	*Home sapiens*	OR182493.1	13525-13415; ND5	3.00E-49	99.10%
12H	200	*Home sapiens*	LS997688.1	28-227; D-loop:	1.00E-96	99.00%
13H	280	*Home sapiens*	MF362729.1	11759-12038; ND4	7.00E-140	98.93%
14H	245	*Home sapiens*	OQ707209.1	8658-8902; ATP6	6.00E-120	98.78%
15H	199	*Home sapiens*	MG660585.1	7993-8191; COX2:	1.00E-92	98.49%
16H	189	*Home sapiens*	KF162400.1	8394-8206; ATP8	2.00E-89	98.41%

17H	199		*Home sapiens*	OR182493.1	13537-13735; ND5	2.00E-89	96.98%
18H	250		*Home sapiens*	FJ383295.1	16068-15820; CYTB+trnT+trnP	1.00E-113	96.80%
19H	177		*Home sapiens*	OQ884901.1	11485-11325; ND4	5.00E-60	83.85%
20H	199		*Home sapiens*	OR182493.1	13537-13735; ND5	8.00E-98	99.50%
21H	189		*Home sapiens*	OR182493.1	15872-15684; CYTB	3.00E-92	99.47%
22H	188		*Home sapiens*	OR159678.1	3294-3481; trnL-ND1	1.00E-91	99.47%
23H	179		*Home sapiens*	OR182493.1	14442-14620; ND6	1.00E-86	99.44%
24H	175		*Home sapiens*	OR159678.1	4656-4482; ND2	2.00E-84	99.43%
25H	137		*Home sapiens*	OR159678.1	3223-3359; 16S+trnL+ND1	2.00E-63	99.27%
26H	128		*Home sapiens*	OQ707209.1	10974-10847; ND4	1.00E-58	99.22%
27H	128		*Home sapiens*	LC733705.1	10847-10974; ND4	1.00E-58	99.22%
28H	127		*Home sapiens*	OR182493.1	11643-11769; ND4	5.00E-58	99.21%
29H	123		*Home sapiens*	OR182493.1	3674-3796; ND1	8.00E-56	99.19%
30H	118		*Home sapiens*	OR182493.1	3430-3547; ND1	5.00E-53	99.15%
31H	106		*Home sapiens*	OR182493.1	14567-14672; ND6	2.00E-46	99.06%
32H	199		*Home sapiens*	OR182493.1	15529-15727; CYTB	4.00E-96	98.99%
33H	99		*Home sapiens*	OR182493.1	13226-13128; ND5	1.00E-42	98.99%
34H	83		*Home sapiens*	OR182493.1	11867-11785; ND4	8.00E-34	98.80%
35H	173		*Home sapiens*	OR182493.2	3320-3148; 16S+trnL+ND1	4.00E-80	98.27%
36H	200		*Home sapiens*	OR182493.1	12487-12288; trnL+ND5	2.00E-93	98.00%
37H	259		*Home sapiens*	OR182493.1	14124-14382; trnL+ND5	5.00E-121	97.30%
38H	143		*Home sapiens*	OR182493.1	13614-13754; ND5	2.00E-67	98.00%
39H	152		*Home sapiens*	MG660585.1	7949-8040/COX2:	4.00E-65	96.71%
40H	225		*Home sapiens*	ON422324.1	8367-8589/ATP8-ATP6	5.00E-81	90.57%
41H	123		*Home sapiens*	OR182493.1	3674-3796/ND1	8.00E-56	99.19%

Table S7. The 36 pDNA sequences aligning with non-human primate nuclear sequences

pDNA		Results of the Nucleotide Blast			
ID	Len	Taxo	Nucleotide	E-value	Affinity
1P	150	*Carlito syrichta*	XM_021713054.1	3.00E-20	70.67%
2P	122	*Sapajus apella*	XR_004259191.1	8.00E-41	92.62%
3P	63	*Callithrix jacchus*	AC188585.3	5.00E-19	96.83%
4P	160	*Sapajus apella*	XM_032273219.1	1.00E-47	84.12%
5P	164	*Aotus nancymaae*	XM_012443881.1	1.00E-68	95.96%
6P	166	*Macaca thibetana*	XM_050789932.1	4.00E-66	95.18%
7P	187	*Macaca mulatta*	AC188451.1	1.00E-86	99.47%
8P	93	*Macaca mulatta*	AC187507.2	1.00E-29	93.55%
9P	178	*Macaca mulatta*	AC214608.1	3.00E-67	93.82%
10P	121	*Macaca mulatta*	AC279264.1	4.00E-45	95.87%
11P	150	*Macaca mulatta*	AC211796.4	3.00E-61	96.67%
12P	262	*Macaca mulatta*	AC204076.9	1.00E-99	92.37%
13P	118	*Macaca mulatta*	OM502028.1	3.00E-40	97.17%
14P	139	*Macaca thibetana*	XM_050772658.1	2.00E-48	90.72%
15P	149	*Macaca nemestrina*	XR_003018358.1	7.00E-56	94.63%
16P	118	*Macaca mulatta*	AC280286.1	5.00E-43	95.00%
17P	196	*Macaca mulatta*	AC197276.3	6.00E-71	91.33%
18P	140	*Macaca mulatta*	AC202605.16	3.00E-53	95.00%
19P	250	*Macaca mulatta*	AB128049.1	4.00E-94	91.67%
20P	121	*Macaca nemestrina*	XR_996760.2	7.00E-42	92.24%
21P	71	*Pan paniscus*	XM_034938079.2	1.00E-21	95.77%
22P	146	*Pan paniscus*	AC280336.1	3.00E-66	100.00%
23P	141	*Pan paniscus*	AC280342.1	2.00E-63	100.00%
24P	163	*Pan paniscus*	XM_055115310.1	6.00E-70	97.55%
25P	148	*Pan paniscus*	AC280341.1	3.00E-67	100.00%
26P	153	*Pan paniscus*	XM_008974855.5	3.00E-67	98.71%
27P	173	*Pan paniscus*	AC280344.1	4.00E-79	99.42%

28P	139	*Pan paniscus*	XM034963660.2	1.00E-52	94.37%
29P	97	*Gorilla gorilla*	AC270505.1	3.00E-38	98.97%
30P	97	*Gorilla gorilla*	AC270505.1	5.00E-41	100.00%
31P	135	*Gorilla gorilla*	AC275387.1	3.00E-60	99.26%
32P	103	*Gorilla gorilla*	AC145355.3	2.00E-44	100.00%
33P	209	*Gorilla gorilla*	AC145852.3	3.00E-81	93.78%
34P	163	*Gorilla gorilla*	AC280153.1	9.00E-71	97.55%
35P	150	*Gorilla gorilla*	AC275724.1	6.00E-67	98.67%
36P	114	*Gorilla gorilla*	AC280262.1	1.00E-48	99.12%

Table S8. The 271 pDNA sequences matching the nuclear sequences of *Pan troglodyte*

pDNA		Results of the Nucleotide Blast			
ID	Len	Taxo	Accession	E-Value	Affinity
1T	109	*Pan troglodytes*	AC183379.3	1.00E-44	99.00%
2T	129	*Pan troglodytes*	AC183666.2	2.00E-55	99.22%
3T	110	*Pan troglodytes*	AC194549.3	7.00E-47	100.00%
4T	127	*Pan troglodytes*	AC190233.5	5.00E-56	100.00%
5T	182	*Pan troglodytes*	AC188551.3	3.00E-75	96.15%
6T	210	*Pan troglodytes*	AC192764.3	1.00E-93	97.62%
8T	145	*Pan troglodytes*	AC186180.3	3.00E-60	97.28%
9T	164	*Pan troglodytes*	AC142339.1	3.00E-74	99.39%
10T	146	*Pan troglodytes*	AC142339.1	2.00E-69	99.32%
12T	86	*Pan troglodytes*	BS000075.1	5.00E-34	100.00%
13T	153	*Pan troglodytes*	AC157217.2	3.00E-64	96.18%
14T	150	*Pan troglodytes*	AC161061.2	1.00E-66	99.33%
15T	154	*Pan troglodytes*	AC183961.2	2.00E-70	100.00%
16T	225	*Pan troglodytes*	AC183961.2	4.00E-110	99.56%
17T	146	*Pan troglodytes*	AC183768.2	9.00E-68	98.63%
18T	247	*Pan troglodytes*	AC146269.3	2.00E-99	94.33%

19T	150	*Pan troglodytes*	AC211714.3	2.00E-68	96.67%
20T	225	*Pan troglodytes*	AC183684.3	5.00E-115	99.56%
21T	286	*Pan troglodytes*	AC192151.3	7.00E-85	86.23%
22T	91	*Pan troglodytes*	AC200162.4	2.00E-34	97.80%
23T	120	*Pan troglodytes*	AC275774.1	1.00E-33	91.74%
24T	133	*Pan troglodytes*	AC145864.2	4.00E-59	99.25%
25T	217	*Pan troglodytes*	XM_016920966.2	4.00E-112	100.00%
26T	156	*Pan troglodytes*	AC200710.3	1.00E-44	89.87%
27T	163	*Pan troglodytes*	AC200710.3	1.00E-59	93.33%
28T	171	*Pan troglodytes*	BS000063.1	6.00E-77	97.08%
29T	198	*Pan troglodytes*	AC188570.3	3.00E-88	97.51%
30T	191	*Pan troglodytes*	AC192066.3	3.00E-75	93.35%
31T	108	*Pan troglodytes*	AC192447.3	4.00E-44	99.07%
32T	150	*Pan troglodytes*	AC188569.4	2.00E-68	100.00%
33T	200	*Pan troglodytes*	AC279071.1	3.00E-88	97.04%
34T	200	*Pan troglodytes*	AC279071.1	1.00E-86	96.55%
35T	208	*Pan troglodytes*	AC279071.1	9.00E-87	96.55%
36T	101	*Pan troglodytes*	BS000130.1	1.00E-37	97.03%
37T	146	*Pan troglodytes*	AC190214.5	8.00E-61	96.69%
38T	148	*Pan troglodytes*	AC190214.5	5.00E-64	98.01%
39T	195	*Pan troglodytes*	AC193038.3	4.00E-90	98.46%
40T	163	*Pan troglodytes*	AC195663.3	2.00E-72	98.16%
41T	183	*Pan troglodytes*	AC186383.2	3.00E-81	97.81%
42T	101	*Pan troglodytes*	AC192189.4	6.00E-40	98.02%
43T	188	*Pan troglodytes*	AC188419.3	3.00E-81	97.34%
44T	98	*Pan troglodytes*	AC187371.2	9.00E-39	98.98%
45T	196	*Pan troglodytes*	AC146236.3	7.00E-89	98.47%
46T	166	*Pan troglodytes*	AC146236.3	5.00E-81	99.40%
47T	99	*Pan troglodytes*	AC187746.3	1.00E-35	90.00%
48T	211	*Pan troglodytes*	AC198057.3	2.00E-97	98.05%

49T	135	*Pan troglodytes*	AC190196.3	8.00E-46	80.00%
50T	146	*Pan troglodytes*	AC163767.4	9.00E-68	98.63%
51T	200	*Pan troglodytes*	BS000037.1	4.00E-95	99.01%
52T	210	*Pan troglodytes*	AC270591.1	9.00E-102	99.52%
53T	127	*Pan troglodytes*	AC189685.3	2.00E-54	99.21%
54T	150	*Pan troglodytes*	AC145994.2	3.00E-65	98.00%
55T	120	*Pan troglodytes*	AC157954.2	3.00E-56	100.00%
56T	101	*Pan troglodytes*	AC183764.3	2.00E-45	100.00%
57T	135	*Pan troglodytes*	AC197161.3	1.00E-59	97.78%
58T	188	*Pan troglodytes*	CT737396.3	8.00E-84	97.34%
59T	142	*Pan troglodytes*	AC192120.4	7.00E-65	99.30%
60T	189	*Pan troglodytes*	AC188680.4	5.00E-74	94.18%
61T	109	*Pan troglodytes*	AL593856.8	3.00E-44	98.18%
63T	94	*Pan troglodytes*	AC216085.3	2.00E-41	100.00%
64T	255	*Pan troglodytes*	AC216085.3	1.00E-120	98.82%
65T	182	*Pan troglodytes*	AC216085.3	6.00E-83	98.90%
66T	145	*Pan troglodytes*	AC216085.3	1.00E-65	100.00%
67T	238	*Pan troglodytes*	AC187370.3	3.00E-112	98.32%
68T	267	*Pan troglodytes*	AC192481.1	3.00E-108	94.96%
69T	87	*Pan troglodytes*	AC192937.3	1.00E-30	96.63%
70T	154	*Pan troglodytes*	AC192196.4	8.00E-71	99.35%
71T	148	*Pan troglodytes*	AC187381.2	1.00E-63	96.98%
72T	153	*Pan troglodytes*	AC186877.3	2.00E-71	99.00%
73T	164	*Pan troglodytes*	XR_008537664.1	4.00E-69	96.95%
74T	107	*Pan troglodytes*	AC190156.3	3.00E-43	98.15%
75T	88	*Pan troglodytes*	AC193863.2	2.00E-33	98.86%
76T	121	*Pan troglodytes*	AC193907.3	2.00E-47	97.52%
77T	112	*Pan troglodytes*	AC193928.3	3.00E-45	98.21%
78T	159	*Pan troglodytes*	AC183417.2	1.00E-71	99.37%
79T	173	*Pan troglodytes*	AC183417.2	5.00E-78	98.84%

80T	139	*Pan troglodytes*	AC188669.3	2.00E-62	100.00%
81T	164	*Pan troglodytes*	AC142309.1	1.00E-65	94.12%
82T	241	*Pan troglodytes*	AC113436.28	1.00E-106	97.10%
83T	238	*Pan troglodytes*	AC190258.1	3.00E-113	99.16%
84T	113	*Pan troglodytes*	AC200161.3	3.00E-39	98.02%
85T	181	*Pan troglodytes*	AC194556.3	2.00E-82	98.90%
86T	207	*Pan troglodytes*	AC190228.3	2.00E-97	99.52%
87T	183	*Pan troglodytes*	AC186385.2	2.00E-84	99.45%
88T	150	*Pan troglodytes*	AC186385.2	3.00E-61	96.67%
89T	201	*Pan troglodytes*	AC187722.3	4.00E-80	93.60%
90T	182	*Pan troglodytes*	AC160651.2	3.00E-90	99.45%
91T	150	*Pan troglodytes*	LO018685.1	6.00E-36	87.06%
92T	107	*Pan troglodytes*	AC187607.2	1.00E-43	99.07%
93T	101	*Pan troglodytes*	AC146004.3	5.00E-42	100.00%
94T	219	*Pan troglodytes*	AC192564.2	3.00E-100	98.17%
95T	135	*Pan troglodytes*	AC092859.26	2.00E-56	98.52%
96T	148	*Pan troglodytes*	AC192953.2	1.00E-58	93.59%
97T	150	*Pan troglodytes*	AC192953.2	3.00E-65	98.00%
98T	218	*Pan troglodytes*	AC191970.3	1.00E-67	84.94%
99T	110	*Pan troglodytes*	AC214852.3	3.00E-45	99.09%
100T	81	*Pan troglodytes*	AC190217.3	3.00E-31	100.00%
101T	150	*Pan troglodytes*	AP023480.1	9.00E-42	86.38%
102T	247	*Pan troglodytes*	AC270562.1	2.00E-109	97.17%
103T	157	*Pan troglodytes*	AC214854.3	2.00E-70	99.36%
104T	157	*Pan troglodytes*	AC200159.3	5.00E-68	98.68%
105T	116	*Pan troglodytes*	AC200159.3	3.00E-52	99.14%
106T	137	*Pan troglodytes*	AC196938.3	3.00E-59	99.28%
107T	82	*Pan troglodytes*	AC211978.4	2.00E-26	95.12%
108T	225	*Pan troglodytes*	AC211978.4	1.00E-111	100.00%
109T	153	*Pan troglodytes*	AC193935.3	6.00E-67	98.04%

110T	235	*Pan troglodytes*	AC161620.5	3.00E-117	100.00%
111T	191	*Pan troglodytes*	AC184799.2	1.00E-79	96.34%
112T	109	*Pan troglodytes*	AC192408.3	9.00E-76	100.00%
113T	102	*Pan troglodytes*	AC186892.2	3.00E-38	97.06%
114T	223	*Pan troglodytes*	AC149092.6	3.00E-87	94.17%
115T	96	*Pan troglodytes*	AC149092.6	2.00E-39	100.00%
116T	97	*Pan troglodytes*	AC190234.6	7.00E-40	100.00%
117T	190	*Pan troglodytes*	AC186045.5	1.00E-90	99.47%
118T	189	*Pan troglodytes*	AC193895.4	9.00E-88	99.47%
119T	249	*Pan troglodytes*	AC145375.5	7.00E-116	98.02%
120T	72	*Pan troglodytes*	AC186387.2	2.00E-18	91.67%
121T	152	*Pan troglodytes*	AC190249.3	8.00E-68	99.34%
122T	138	*Pan troglodytes*	NG_013342.1	3.00E-59	98.55%
123T	123	*Pan troglodytes*	AC183376.4	3.00E-52	99.19%
124T	258	*Pan troglodytes*	AC146396.5	7.00E-116	96.58%
125T	172	*Pan troglodytes*	AC068196.4	7.00E-76	97.18%
126T	104	*Pan troglodytes*	AC192725.2	1.00E-41	100.00%
127T	186	*Pan troglodytes*	AC192725.2	4.00E-90	100.00%
128T	150	*Pan troglodytes*	CP068263.2	2.00E-53	93.88%
129T	115	*Pan troglodytes*	AC145378.2	3.00E-46	99.13%
130T	83	*Pan troglodytes*	AC145378.2	5.00E-30	97.59%
131T	253	*Pan troglodytes*	AC188550.3	7.00E-111	97.23%
132T	152	*Pan troglodytes*	AC196251.3	1.00E-66	98.68%
133T	173	*Pan troglodytes*	AC196251.3	3.00E-80	99.00%
134T	124	*Pan troglodytes*	AC147033.2	2.00E-48	96.06%
135T	238	*Pan troglodytes*	AC147978.3	4.00E-112	99.16%
136T	202	*Pan troglodytes*	AC198619.4	8.00E-95	99.50%
137T	171	*Pan troglodytes*	XM_024357983.2	2.00E-73	97.08%
138T	150	*Pan troglodytes*	CU464036.1	2.00E-68	100.00%
139T	168	*Pan troglodytes*	AC193856.2	2.00E-78	99.40%

140T	225		*Pan troglodytes*	AC146171.2	3.00E-75	87.56%
141T	156		*Pan troglodytes*	AC220072.5	1.00E-71	100.00%
142T	116		*Pan troglodytes*	AC193260.2	2.00E-46	97.41%
143T	236		*Pan troglodytes*	AC193885.4	2.00E-104	96.61%
144T	206		*Pan troglodytes*	XR_002942333.2	3.00E-96	98.55%
145T	146		*Pan troglodytes*	AC200342.3	5.00E-68	100.00%
146T	138		*Pan troglodytes*	AC172375.3	3.00E-49	94.20%
147T	93		*Pan troglodytes*	BS000211.1	7.00E-39	100.00%
148T	203		*Pan troglodytes*	AC006582.13	2.00E-69	86.60%
149T	135		*Pan troglodytes*	AC200459.2	1.00E-57	98.52%
150T	288		*Pan troglodytes*	AC190143.3	2.00E-135	97.92%
151T	124		*Pan troglodytes*	AC186185.2	7.00E-48	90.00%
152T	253		*Pan troglodytes*	AC186185.2	3.00E-120	98.21%
153T	150		*Pan troglodytes*	AC186185.2	2.00E-68	100.00%
154T	99		*Pan troglodytes*	AC186185.2	3.00E-39	98.99%
155T	210		*Pan troglodytes*	AC183773.2	2.00E-89	94.44%
156T	81		*Pan troglodytes*	AC217027.3	3.00E-30	97.00%
157T	125		*Pan troglodytes*	NG_009388.1	1.00E-44	94.09%
158T	126		*Pan troglodytes*	AC229904.2	2.00E-54	97.62%
159T	83		*Pan troglodytes*	AC147079.4	1.00E-31	97.59%
160T	221		*Pan troglodytes*	AC213062.4	6.00E-104	98.64%
161T	212		*Pan troglodytes*	AC192213.3	2.00E-99	98.58%
162T	146		*Pan troglodytes*	AC183271.3	2.00E-66	99.32%
163T	264		*Pan troglodytes*	AC159827.1	2.00E-128	98.86%
164T	156		*Pan troglodytes*	AC159827.1	1.00E-68	98.08%
165T	256		*Pan troglodytes*	AC182427.3	3.00E-112	95.51%
166T	110		*Pan troglodytes*	AC092033.4	3.00E-43	97.30%
167T	100		*Pan troglodytes*	AC192124.3	5.00E-41	99.00%
168T	179		*Pan troglodytes*	AC161386.4	1.00E-75	96.65%
169T	171		*Pan troglodytes*	AC188559.3	2.00E-78	98.83%

170T	158		*Pan troglodytes*	AC147058.3	1.00E-54	93.04%
171T	125		*Pan troglodytes*	AC191700.3	8.00E-55	99.20%
172T	226		*Pan troglodytes*	AC192996.2	2.00E-104	98.23%
173T	146		*Pan troglodytes*	XR_001716146.2	2.00E-66	99.32%
174T	214		*Pan troglodytes*	XM_055114440.2	3.00E-98	96.73%
175T	237		*Pan troglodytes*	AC146059.4	1.00E-115	99.16%
176T	98		*Pan troglodytes*	AC189686.4	1.00E-41	100.00%
177T	140		*Pan troglodytes*	AC192800.2	1.00E-59	97.86%
178T	154		*Pan troglodytes*	CT989257.3	8.00E-71	99.35%
179T	223		*Pan troglodytes*	AC275882.1	1.00E-95	96.41%
180T	239		*Pan troglodytes*	AC183992.2	2.00E-69	87.45%
181T	251		*Pan troglodytes*	XM_054669499.1	4.00E-126	100.00%
182T	167		*Pan troglodytes*	AC146242.3	1.00E-49	74.43%
183T	150		*Pan troglodytes*	AC146384.4	3.00E-65	98.00%
184T	74		*Pan troglodytes*	AC213065.4	2.00E-28	100.00%
185T	107		*Pan troglodytes*	AC213065.4	2.00E-45	98.13%
186T	161		*Pan troglodytes*	AC159020.3	2.00E-76	100.00%
187T	150		*Pan troglodytes*	AC187623.2	6.00E-67	98.67%
188T	228		*Pan troglodytes*	AC187732.3	1.00E-111	99.56%
189T	56		*Pan troglodytes*	AC188437.4	1.00E-18	100.00%
190T	105		*Pan troglodytes*	AC186388.3	2.00E-45	100.00%
191T	135		*Pan troglodytes*	AC196245.2	4.00E-58	98.52%
192T	117		*Pan troglodytes*	AC146132.3	5.00E-52	100.00%
193T	140		*Pan troglodytes*	XM_016934978.2	7.00E-61	96.60%
194T	151		*Pan troglodytes*	AC190144.3	2.00E-62	96.71%
195T	150		*Pan troglodytes*	AC194763.3	3.00E-70	100.00%
196T	112		*Pan troglodytes*	AC160143.4	4.00E-18	62.81%
197T	244		*Pan troglodytes*	AC191942.3	2.00E-89	93.03%
198T	69		*Pan troglodytes*	AC148317.3	3.00E-23	98.55%
199T	131		*Pan troglodytes*	AC202278.2	3.00E-47	93.89%

200T	97	*Pan troglodytes*	AC188802.3	5.00E-41	100.00%
201T	122	*Pan troglodytes*	AC198462.3	1.00E-43	93.44%
202T	198	*Pan troglodytes*	AC113435.14	1.00E-73	92.42%
203T	200	*Pan troglodytes*	AC279053.1	1.00E-30	77.76%
204T	150	*Pan troglodytes*	AC199715.3	1.00E-68	99.33%
205T	156	*Pan troglodytes*	AC192734.2	2.00E-63	96.20%
206T	195	*Pan troglodytes*	AC192834.3	8.00E-92	98.97%
207T	131	*Pan troglodytes*	AC199235.3	8.00E-57	98.48%
208T	193	*Pan troglodytes*	AC190232.2	8.00E-95	98.96%
209T	98	*Pan troglodytes*	AC275872.1	1.00E-43	100.00%
210T	145	*Pan troglodytes*	AC182425.3	5.00E-55	93.79%
211T	242	*Pan troglodytes*	AC142323.1	1.00E-126	100.00%
212T	249	*Pan troglodytes*	AC270583.1	3E-120	99.60%
213T	189	*Pan troglodytes*	AC192566.2	4E-90	99.47%
214T	201	*Pan troglodytes*	AC183962.3	9E-80	91.64%
215T	201	*Pan troglodytes*	AC183962.3	9E-87	96.52%
216T	95	*Pan troglodytes*	AC190197.3	8E-39	100.00%
217T	114	*Pan troglodytes*	AC149231.2	2E-50	100.00%
218T	153	*Pan troglodytes*	AC280209.1	1E-47	89.54%
219T	124	*Pan troglodytes*	AC182393.2	4E-48	96.77%
220T	117	*Pan troglodytes*	AC183622.3	8.00E-53	99.15%
221T	99	*Pan troglodytes*	AC192641.3	2.00E-42	98.99%
222T	221	*Pan troglodytes*	AC188594.3	1.00E-108	99.10%
223T	121	*Pan troglodytes*	AL954246.1	2.00E-53	98.35%
224T	150	*Pan troglodytes*	AC184876.2	1.00E-54	89.01%
225T	195	*Pan troglodytes*	AC223435.5	7.00E-88	97.44%
226T	114	*Pan troglodytes*	AC185967.2	2.00E-45	96.61%
227T	91	*Pan troglodytes*	NG_046914.3	3.00E-36	97.80%
228T	222	*Pan troglodytes*	AC226173.4	2.00E-97	96.85%
229T	150	*Pan troglodytes*	AC226173.4	2.00E-62	96.10%

230T	125		*Pan troglodytes*	AC161276.2	6.00E-51	97.60%
231T	148		*Pan troglodytes*	AC145882.3	2.00E-46	87.19%
232T	217		*Pan troglodytes*	AC142289.1	3.00E-102	98.62%
233T	184		*Pan troglodytes*	AC160566.2	1.00E-89	98.91%
234T	104		*Pan troglodytes*	CR937045.1	1.00E-43	98.08%
235T	140		*Pan troglodytes*	AC194569.3	2.00E-58	92.85%
236T	150		*Pan troglodytes*	CR937026.1	8.00E-72	99.33%
237T	226		*Pan troglodytes*	AC188603.5	7.00E-114	99.12%
238T	272		*Pan troglodytes*	AC201862.3	9.00E-133	98.90%
239T	194		*Pan troglodytes*	AC187629.3	7.00E-73	93.30%
240T	109		*Pan troglodytes*	AC190218.2	1.00E-47	100.00%
241T	151		*Pan troglodytes*	BS000098.1	3.00E-67	99.34%
242T	161		*Pan troglodytes*	AC195070.2	2.00E-76	100.00%
243T	147		*Pan troglodytes*	AC270731.1	9.00E-68	99.32%
244T	113		*Pan troglodytes*	AC279127.1	6.00E-46	98.23%
245T	113		*Pan troglodytes*	AC204684.4	3.00E-52	100.00%
246T	145		*Pan troglodytes*	AC147078.2	6.00E-63	98.62%
247T	205		*Pan troglodytes*	XR_001714532.2	2.00E-95	99.02%
248T	226		*Pan troglodytes*	AC194989.3	3.00E-94	94.69%
249T	246		*Pan troglodytes*	AC198805.2	7.00E-116	98.78%
250T	104		*Pan troglodytes*	AC188667.3	1.00E-43	100.00%
251T	172		*Pan troglodytes*	AC186553.1	3.00E-80	100.00%
252T	167		*Pan troglodytes*	AC152353.1	3.00E-68	92.21%
253T	231		*Pan troglodytes*	AC191699.3	9.00E-89	92.64%
254T	177		*Pan troglodytes*	AC184055.3	6.00E-77	97.75%
255T	197		*Pan troglodytes*	NG_029917.1	2.00E-63	88.34%
256T	150		*Pan troglodytes*	AC197160.3	5.00E-58	95.33%
257T	225		*Pan troglodytes*	AC158369.5	2.00E-104	98.67%
258T	158		*Pan troglodytes*	AC192128.3	5.00E-71	99.37%
259T	98		*Pan troglodytes*	AC190422.2	1.00E-37	98.96%

260T	135		*Pan troglodytes*	AL954234.1	4.00E-58	98.26%
261T	205		*Pan troglodytes*	AC214850.4	2.00E-95	99.02%
262T	223		*Pan troglodytes*	AC197403.3	3.00E-102	97.76%
263T	54		*Pan troglodytes*	AC275851.1	5.00E-17	100.00%
264T	282		*Pan troglodytes*	XM_054358264.1	3.00E-143	100.00%
265T	255		*Pan troglodytes*	AC192167.3	4.00E-61	77.39%
266T	159		*Pan troglodytes*	AC183378.2	8.00E-65	95.24%
267T	205		*Pan troglodytes*	AC188675.3	2.00E-81	94.15%
268T	100		*Pan troglodytes*	AC192137.3	7.00E-40	99.00%
270T	125		*Pan troglodytes*	AC198664.3	3.00E-53	99.20%
271T	285		*Pan troglodytes*	AC163769.4	9.00E-122	91.50%
272T	197		*Pan troglodytes*	AC163769.4	9.00E-122	91.50%
273T	144		*Pan troglodytes*	XM_054677932.1	3.00E-55	95.14%
274T	176		*Pan troglodytes*	XM_001155344.5	1.00E-75	97.16%
275T	239		*Pan troglodytes*	AC183528.2	4.00E-106	96.09%

Table S9. Quantification of DNA extraction for petroleum samples

Bench number	Sample ID	Extraction phase of petroleum oil well	Oil volume to DNA extraction	OD_{260}	pDNAmix （ng）
1	NY201905	First oil recovery	120 mL	0.082	205
2			120 mL	0.103	257.5
3			120 mL	0.115	287.5
4			120 mL	0.087	217.5
5			120 mL	0.113	282.5
6	NY202102	Secondary oil recovery (using hot water and surfactants)	120 mL	0.051	127.5
7			120 mL	0.215	537.5
8			120 mL	0.093	232.5
9			120 mL	0.089	222.5
10			120 mL	0.067	167.5

Table S10. Results of DNA extraction from petroleum and the illumina NovaSeq sequencing

Bench ID	Sample ID	Extraction phase of petroleum oil well	Oil volume to DNA extraction	OD_{260}	pDNAmix (ng)	Total reads amount	Sequences from non-indigenous species
1	NY201905	First oil extraction	720 mL	0.618	3708	3,159,002	Multiple
2	NY202102	Secondary oil recovery (using hot water and surfactants)	720 mL	0.675	4050	390,932	None

Table S11. The length of pDNAs and the Blast results

Taxo	Minimum (bp)	Maximum (bp)	Mean	SD	Number
Bacteria	50	290	159.73	48.12	1620178
Homo sapiens	50	290	150.55	46.05	1047532
Fungi	50	290	152.24453	48.2	121735
Virus	51	290	150.3744	22.26	16290
*Primate**	50	290	130.64	43.00	35108
*Mammalia**	50	290	129.24	48.69	4785
Actinopterygii	50	290	147.76691	41.01	4835
Insecta	50	290	161.15654	49.99	2945
Archaea	53	288	154.88	47.67	851
*Arthropoda**	50	285	139.90	43.87	1094
Spermatophyta	50	290	151.97439	45.78	15188
Aves	51	288	149.28199	10.42	9252
DAASIA	55	248	167.32	46.30	6988
*Viridiplantae**	60	276	156.03	48.86	117
sauria	61	288	157.40476	62.39	42
amphibia	95	181	140.75	38.35	4
Cyclostomata	83	272	181.50	80.47	7
Chondrichthyes	78	221	159.50	63.61	4
ABPNNR	59	267	187.17	88.41	752
PCM	68	298	197.20	85.64	187
EHT	77	219	186.34	92.41	49
HRC	61	247	163.72	80.79	15
Unnamed	88	296	157.26	49.87	271062
Total					3159020

Please note that the data in Viridiplantae* does not include Spermatophyta, the data in Arthropoda* excludes Insecta, the data in Sauria* does not include Aves, the data in Primates* does not include Homo sapiens, and the data in Mammalia* does not include Primates*.

Table S12. Appendix table of the pDNA sequences used in this research

ID	Bench ID	Sequences
1T	A00583:504:HM2HWDSXY:2:2677:15781:24095	CATCCTGGCTAACATGGTGAAACTCTGACTCTACTAAAAATACCAAAAATTAGCCAGGCGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAG
2T	A00583:504:HM2HWDSXY:2:2673:19443:6825	CACTGCACCCTAGCCTGGGCAACAGAGCAAGACTCCATCTCAAGAAAAAAGAAAAAAAAAGAAAAGAAAAGGAAAAAGAGAAGAGAAGAGAAAAGAAAAGAATAAAGAAAAGAGGCCTTTAGGAAATCC
7C	A00583:504:HM2HWDSXY:2:2672:18900:12555	CACACCCACTGCACTCCAGCCTGGTAACAGAGCGATACTCCGTCACCAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAGGAAATATCACCAGAACGGATATCACTGCACTCTTCACGAAAAAGAAAAAGAAAATACCAGA
28P	A00583:504:HM2HWDSXY:2:2672:18900:12555	ACACACCCACTGCACTCCAGCCTGGTAACAGAGCGATACTCCGTCACCAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAGGAAATATCACCAGAACGGATATCACTGCACTCTTCACGAAAAAGAAAAAGAAAATACCAGA
3T	A00583:504:HM2HWDSXY:2:2672:14823:26694	GGGTGACTTCGTTTTGATCAAAAATCCAAGGAAACAGAGGACTTGTTGGGTTGTGGGTTTCCTGATGGCTTGGTGCCAGCTATGGATTTAGTTGATAAGGCCCAGTTTCT
14A	A00583:504:HM2HWDSXY:2:2667:23845:4460	CCAATGCAGGACAATCAAGCTGCGTAATGCAAGCAGGAGAGCAGCACTACGCCCAATAATGGAAGAATGATGAACAAGGCAGAGCCATTTCTCTGCTCTTCCTGCAAGGCATGTACTCACTCTGCTTTCATCTTTTCTAATGGAAAAGGAAGCA
4T	A00583:504:HM2HWDSXY:2:2664:25147:4210	CTCCAAAGCTAACTTCAGATAGTGTCAGAATAGGATTGAGTTGTTGTACACCCAGTTGGTGTCCTAAGAAAGGGTACCCCACATTTGGTGTTAGAAGTAACGTCAGAAAGCATCACACAATTGTATG
25H	A00583:504:HM2HWDSXY:2:2660:32199:32581	CAGGGTTTGTTAAGATGGCAGAGCCCGGTAATCGCATAAAACTTAAAACTTTACAGTCAGAGGTTCAATTCCTCTTCTTAACAACATAACCATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGG
6M	A00583:504:HM2HWDSXY:2:2651:30309:23422	ACACACACACACACACAGAAGGGTAGAGCCCCAGGTGACCATGGTCTTCTCAGTTCACATGAAAGAGAATTAGAGAGAGCGGGAGGGGGGGAAGCAAAATATGGACCCATTGTGGAGTAAAGTTTTACAAACATGGACTGGATTCAAATAGAATGCAATAAGAGGAGAAATGAAAGAAATAATAGAAAAAACCTAAAAAATAAACTAAAAAATAAATTTGAATTTCTACCATTTATAGGCCAATTTATACTTC
5T	A00583:504:HM2HWDSXY:2:2645:31747:28354	GGGGCGGTTTCCCCCATGCTATTCTCATGATAGTGAGTGAGTTCTCACGAGAGCTGATGGTTTTAAAGTGTTGTACTTTCTGGTGCTCTATCTCTCTCTCTTGCCTGCCCCATGTAAGAATTGCCTTGCTTCCCCTTCACCTTCCACAATGATTGTAAGTTTCCTGATGACTCCCCAGCCAT
6T	A00583:504:HM2HWDSXY:2:2643:12174:30718	TTATGTTTAACTGATATTTGGGGATGATTAAAATACAAAGCAATACGTTTAAAAGTTTTATCTGTATTTAAAAGTCTTAGTATTTAGAATAAATGTATTCTGTGTGTTGCCTAAAGGCATAAATCAAACTGTACATGTGTATATAGATACATAGATATTTTCAAGCGACAACTTGATTGATTTGTTACAGTTGCCTACAATGATGTATAT

7T	A00583:504:HM2HWDSXY: 2:2641:19678:29496	AAGGGGTGCTGGAAACAAAGCAAACCATTTTCTCATTCTTATACAGAGGTACAAATGGGAGGGACATGTGGACTGCTGCCTGCATCACTAGTCACTGTGCCATG GAGTAGGCCCACAGGAGTAGGAGGGGTCCTGAGATGGGAAATCAACATGACCATGAAGAAGGAAGGCTTTGGAGTGATGTCATCCAACTTGGTTCTCA
21P	A00583:504:HM2HWDSXY: 2:2638:18023:8218	CCACCCACTCACGCATCCACCATTATCTACCGTCCAGATACCCAGTGTTTCGCAGTGATTAATATACATAT
8G	A00583:504:HM2HWDSXY: 2:2631:1931:27477	TTATTTTACCAGAAGGTTTTGAATTAGCTCCTTCTGATCGAATTCCTCCTGAAATGAAAGAAAAAATTGGTAATCTTTTTTTTCAACCTTATAGTAATGATAAAAAAA ATATTTTAGTAATATGTCCAGTTCCAGGAAAAAAATATAGTGAAATG
8T	A00583:504:HM2HWDSXY: 2:2628:3296:25488	TCTCGTTTATTAGTTCTAGTAGTTTTTTTTTTTGTAGATTATTTGGACTATTTTTTAGAGATCATCTCATTGTGTGGTAAAGACAGTTTTACCTACAACAAACCCCCAT GACACAAGTTTACCTATGTAATAAACCTGCACATGT
9T	A00583:504:HM2HWDSXY: 2:2627:10113:1344	GTCTGGTTGTGTACTCTGGTGTACATGTAATGTTTGGTGGAAATTGTATTGTTTATATTCTAGGACATGTTTCTCTACTCACCTCTCTCATCCCACAAATTGCCTTT CCAGTGATTAGCATGTAATAAAGGATTTATTCATTTGACATGTATTTGTTGAGTGTT
11T	A00583:504:HM2HWDSXY: 2:2625:28302:10488	AACACACACTCACATTCACACACACCACACACATTCACACACCACACATTCACACACCACACATTCACACACACCAACACACTCACACACACACCACACACATTC ACACACACACCCCACCTGCTTAAAATCCTCCAAAGGCTTCTCATTATGCAAAAACCTTCTG
12T	A00583:504:HM2HWDSXY: 2:2622:15456:1548	TGTTCCACTAATTCTATTATTTTGGCAACGATCTCTGACACAATAAAAAAATGAACAGAAAGATCAAATTTGTGATCTTTAACATT
13T	A00583:504:HM2HWDSXY: 2:2621:4752:20337	GACCTGCCTGGGCTCAGGTGATCCTCCCACCTCAGCCTCCTGAATAGTTGGGACTACAGGTGTGCACCACCACACCTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTT TAGAGATGAGTTTTAACCGTGTTGCCCAGGCTGGTCTTGAACTCCT
14T	A00583:504:HM2HWDSXY: 2:2614:18855:35556	TGTCCCCAGCCAGGTTGCAGGTGTGACCAGGCCTGGCCAGACTCTTGGGTTTTGCCCCTTGGACCAATCAATCCTGGAGGTCAATTTGAAGGGGGTAGCAGCC ATGTAAGGGAAAATACCCTGGTAAAGCTACACTCTCTATGAAATGGC
15T	A00583:504:HM2HWDSXY: 2:2608:23050:6621	ATGTGCAAAGACTTGGCAGACACAGCCATTGAGCCAAAGGCTATTTTCCCCAAAGATGAATTCTTGTACTGAAAGCCCTTCATAAGGCAAGGAATAGCAGCAGG CATTTACATAAAGCGAATAAACTGGCACTGTTAAGTTCCAGGACACGTCC
9A	A00583:504:HM2HWDSXY: 2:2605:23863:4836	TGTATAGCAGAATCTGTAGCCATAGACTGCTGCTAGCTGCCATATCTGCAATAAACAAACTGACACACATAACTCCTTCCATTAAGACAGATTTGAATGTCCATAG ATTAAACCTGCAAAAATTTGAGGGGCATGGGTGAATTTTACATCC
17T	A00583:504:HM2HWDSXY: 2:2603:3748:18004	GTAATGTTCCCCAAAACAAAGAAAAATGTTTCAAATAGTGGATATCCCAATAACCCTGATTTGATCATTGTACATTGTATACATGTATCAAAATATCACAAATGCCC CAAAATACATACAACTATAATAAATTGATTTCAAAATCT
18T	A00583:504:HM2HWDSXY: 2:2602:21070:36166	TTCTAACATGAGAGTCATAATATCTGTTCTCTGTTTCCCATTGAATCCAGAAACTGCACATTAAATTCCACAAAAATTTGTATTAAAGATCTCTCACAATTTTGAGGT AAAGCAACGACATCTCTCATCACTCTATCCCAGTATCCCAGTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGACAGAGTCTCGCTCTGTCGCCCAGGCTA GGGTACAGTGGCGCAATCTTGAGTCACTGC
32H	A00583:504:HM2HWDSXY: 2:2577:21504:30060	AGCCAACCCCTTAAACACCCCTCCCCACATCAATCCCGAATGAAATTTCCTATTCGCCTACACAATTCTCCGATCCGTCCCTAACAAACTAGGAGGCGTCCTTGC CCTATTACTATCCATCCTCATCCTAGCAATAATCCCCATCCTCCATATATCCAAACAACAAAGCATAATATTTCGCCCACTAAGCCAATCACTT

2A	A00583:504:HM2HWDSXY:2:2575:12310:12007	CAAGGCAGTGATGGCGCCCTTGTCTTGGGGCTGGGGTCCTCGATTTTCTCTTGAAACCCAGTGCCATCTGCGAGTCCCTAGACGCAGCACTCATACAACCACGAATGGCATGCATGCGTTGTCCAGGCTTGTCGCCAAGAACGACACGG
19T	A00583:504:HM2HWDSXY:2:2573:9724:28667	TCCCTTCCCCTCTCCAGGGACACAATCAGCCTCTGGCTTCAGTCTTGCTACTTCCTTCGCTTGGAAAGTTCTTACCCAAGAGGGCTCCATTCTACCTTTTTTTTTTTTTTTTTTTTTTTAGACAAGGTCTTACTCTGTCACCCAGGCATG
20T	A00583:504:HM2HWDSXY:2:2570:32497:34256	ACTTGGCAGACACAGCCATTGAGCCAAAGGCTATTTTCCCCAAAGATGAATTCTTGTACTGAAAGCCCTTCATAAGGCAAGGAATAGCAGCAGGCATTTACATAAAGCGAATAAACTGGCACTGTTAAGTTCCAGGACACGTCCTGGGGCTTAGCCTCCTTTCATTTATTCAGCCTAATTCCCACCGGTGACAGCTACCACCATGTTTAGGGCTGTGATGCCAGC
21T	A00583:504:HM2HWDSXY:2:2567:27760:22608	CCAAGAAGGAGCCACATTTTGCTCCTAAGTATTGTGATTCCCAGTGAATCCTGCCCACACACCTAGGCGTGGCATGGCCCAGAGGCTGCGTGTCTCCATGCCTGTGCAGATCAAGGCTATCTGGCCAGGTCCAGCTCAAAGGCCTTCTTGGTTGATTCTTTGTTTGAGTTTTTGTTGTTCTCGGATTTTTTTTTCAGACGGAGTCTCCTTCTGTTCCCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACCACAACCTCTGCTTCCCGGGTTCAAGTGATTCTC
35H	A00583:504:HM2HWDSXY:2:2566:7428:29575	GGTATGAAGTTAAGAAGAGGAATTGAACCTCTGACTGTAAAGTTTTAAGTTTTATGCGATTACCGGGCTCTGCCATCTTAACAAACCCTGTTATTGGGTGGGTGTGGGTATAATACTAAGTTGAGATGATATCATTTACGGGGGAAGGCGCTTTGTGAAGTAGGCCTTATTTC
22T	A00583:504:HM2HWDSXY:2:2562:15537:19695	GATAACCAGCTTTAGGCTTTGTTCATTGTTTTAAATTTATCTTTATTTTCTATTTCATTAATATCTGATATCATACTTATAGCTTCTATCT
23T	A00583:504:HM2HWDSXY:2:2561:30337:4993	GCCTGGAACAGAACCCACTCCCCCAGGTGAGCATCTGACAGTCTGGAACAGCACTCTGCACCCACATGTGAGCATCTGATAGCCTGGAACAGACCCCACACCCCCAGGTGAGCATCTGAC
10T	A00583:504:HM2HWDSXY:2:2561:17761:20134	CTCACCTCTCTCATCCCACAAATTGCCTTTCCAGTGATTAGCATGTAATAAAGGATTTATTCATTTGACATGTATTTGTTGAGTGTTTCCTATAAATCTGGTACTGAAAAGTACAGAGAGAATGGTATTAGCTGCCATTTATCAGT
22P	A00583:504:HM2HWDSXY:2:2559:31702:35383	TTAGTTTAATCTACTGAAAGAATAAAATGAAATTCTATGAAAATAATATAACAAATACTGAGAGAAAGTAATTTGTCTGTAACCCACTTACCACTCTTCAGAGTCCTTGATTCTGTGCCACCAGAAAGCCTCAGGAGTATTCAGGG
24T	A00583:504:HM2HWDSXY:2:2559:11758:24267	TAAACCCTCAAAGCCTCAGTTTCCTCATCTGAACAAAAAAAAAAAGGATGGTATTCTGTACAACACATGTTTGTGGTAATGACTGAGTGGTATAGTGTGTCAACAGGTTCTGGAACATGGTTAGTGATCAATA
23P	A00583:504:HM2HWDSXY:2:2556:7102:8594	TATTCTTAAGGAAAAAAACCACACTTATGAACTATGATGAAATCTGTTGTTTTGTCTGTGTAAGTTTCATCCACGCTTCCAGTAACACCAAGTAAACTTTTTTTGAGGAAACATCCTTCTCCCACTCACAGTCCTTGTGAT
33H	A00583:504:HM2HWDSXY:2:2553:5710:31140	GTAAGGGCGCAGACTGCTGCGAACATAGTGGTGATAGCGCCTAAGCATAGTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG
25T	A00583:504:HM2HWDSXY:2:2552:16179:26694	TCTTTTAACAGTTCTACAATGCTGAAACTGAGGAACAGCAAGGTTATGTCACCCAAAGACATACAGGACAGGGAAGGGGCAAACTCAACTTGACCTGTCTCCAAAATCTATGTTTTTTAAACTCAGCCACGCTTCTGCCCTCCTTTGAAAGGAGTTTCTTTTACTTGATGAATTTTCTAACTTACTGTTTAACCATATTTCTCTGTATTATAAAAAT

26T	A00583:504:HM2HWDSXY:2:2549:32172:6355	GAAACCTCTTTGCTCCTCTGGTAGGCATTTGTAAAGGTGGCTTGGGTCAGGCACAGGCGGCCCCCAACCCCGCGGATCCCTTGTGTTCTTAGTTTTAACATGGCGTTGATGGAAAGGTCACCCGTCTCCCCTTCCACCGGCACATGCCTGGACCCC
28T	A00583:504:HM2HWDSXY:2:2545:18285:23077	TGAGCCAAGATTGTGCCACTGCACTCCAGCCTGGGCAACAGGGCGAGACTCTGTCTCAAATAATAATAATAATAATAATAATAATAATTTTTTTCAGAGCTTACCATCTATTCATCCTCTCTGTTTGTTATTATTTATATAAATTATCTTTTGCAAACTTAATATTTGAGT
29T	A00583:504:HM2HWDSXY:2:2540:7455:31626	AAACCTCTCTTTTGGCACTTAACTATGAAAAGAAAAGACATAGGAATCAAGAATAATTTATAAACTTTTGATCTATTTATAACATCCAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGATGGAGTTTCACTCTTGTTGTTGCCCAGGCTGGAGTGCAATGGTGCGATCTTGGCTCACTGCAACCTCTGCC
30T	A00583:504:HM2HWDSXY:2:2537:13006:21261	ACAGATATACACACAGCCTGTGGATCAAGAGATGGGGTATAGGGGCTGCACTGTACCTAGAGGGACCAATTCTTTGTCTTTTCATGAGGAAAAAAAAGAAGAAAAATAAGAAAGAAAGAGAAGGAGGGAGGAAAGGGAGGAAAAGAGGGAGGGAGGAAAAGAGGGAGGAAGGAAAGAAGGAAGGAAGGAAC
26H	A00583:504:HM2HWDSXY:2:2536:18918:31594	GAGTCATGTAGTTAGTATTAGGAGGGGGGTTGTTAGGGGGTCGGAGGAAAAGGTTGGGGAACAGCTAAATAGGTTGTTGTTGATTTGGTTAAAAAATAGTAGGGGGATGATGCTAATAATTAGGCTGT
5M	A00583:504:HM2HWDSXY:2:2534:32624:28401	GATAGCACGTCTTACAGACGCTTTGCCACTGGCAGCATCGGTAAATGACGAAACACATATTCAATCTGGCCGATCAATGGTCGAATATCAAAATCAAGCCAAACAACTATTTAAGAAAATGAACCAGAATTCGCCGATTAGAGGCACTCTCGAAACCGGACCATATCTGTTCCAGTAATACACT
6P	A00583:504:HM2HWDSXY:2:2534:26422:1658	AGACACTCCAAGGCACTTCCCAAAGCCAAACTTGCACCATTATAGGTCATGGTCACTGTTTGATTGTCTGCTGCCGGTCTGATTCACTACAGCTTTCTGAATCCCAGTAAAACCATTACTTCTGAGAAGTACACTCAGCGCATCAATGAGATGCACCAAAAACTGC
31T	A00583:504:HM2HWDSXY:2:2533:27389:23563	GGGAAGAGCCAGAGGAGGAACCCAGCTCTTCTGAGCCAAATGGCAGCAGTCTCAGTCCTGGGTATATTGAGGGTGTGACCAGTGGCACTGTGGCCATTTCCAAGTGGA
32T	A00583:504:HM2HWDSXY:2:2527:26051:8813	TTAAAATATATGTAAATATAGAAGATGGTTTTAAAGAGCTTTTTGTTGTTGTTTTGAGACGGAGTCTCGCTCTGTCGCCCAAGCTGGAGTGCAGTGGCACAATCTCAGCTCACTGCAACCTCTGCCTCCTGGGTTCAATAAGTTCTCTGC
33T	A00583:504:HM2HWDSXY:2:2524:3079:29622	TCAGATCCTCTGGCGCCCGGGCGCCCCCTCCCGGCGACACCTCCCGGCTGTGAGCGCGCGGGAAGAGGCCAGAGGCAGGGCCTCTCACCTGCTCGGACTGCAAACCACAAAGCGTCTCTTTTTTTTTTTTTTTTGAGGGGCGGAGGTGGTCATTTTTATGTTCCCTGGGCAAAGCGAGCAGCCGTTTGGCTTATAAAATA
36T	A00583:504:HM2HWDSXY:2:2524:23457:33692	TCCAGCCTGGGCAACAGAGCGAGACTCTATCTCACACACACACACACACACACACACACACAATTTTGGTAAATATACATAAATAAAATGTACTATGTTAACC
37T	A00583:504:HM2HWDSXY:2:2523:19054:3114	ACTGCACTCCAGCCTGGGTGACAGAGTGAGACTTCGTCTCAAAAAAAAAAAAAAAAGATACAGGTTCTCGGTTATACTTTGCAGATTTCAGTTGTTCCTAATCTCTCTAACTTCATGTCAATCTTTCCTTATCCATCTCCTGCACTC
39T	A00583:504:HM2HWDSXY:2:2522:8431:15562	TTGAGGCTACAGTGAGCTATGATCATGCTACTACCTGGGTGACAGAGCAAGACCCGGTCTCAAAAAAAAAAAAAAAAAAAAGAGCAGAGCCAGGCGTGGTGGCTCGTGCTTATAATCCTGGCACTTTGGGACACCAAGGTGGGTGGAATGCTTGAGCTCAGGCGTTCAAGACCAGCCTAGGCAATATAGCGAAAC

40T	A00583:504:HM2HWDSXY:2:2520:4182:13620	CATCTATACAGGGGGCATGTGGGGCAGGGCTGCTTTGGGGTCAAGGGGTCAGATGTAGAGTTGTTTTGTTGTTGTTGTTTTTTGAGACGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACTGCAAACTCTGCCTCCCGGGTT
7P	A00583:504:HM2HWDSXY:2:2517:9742:6433	GAAAAAACTGTCCATGGTTAAAAGCTGTTCTGTTACGTTGGATCTTCCATGTTGCTGATGCATACCAACATTTACTTAGTAAACAGGTATTGAATACCTACTCTGTGCCAGGCACTGTGCCAGGCAGAGGACCTATAAGATAGTTCCCAGCTCTCAAGGTGTTCATGGTCTGAAGGGTTTAGACACA
8P	A00583:504:HM2HWDSXY:2:13448	TGTCTATGATTTATAATGCCTCATGAAATCAAAATTTTTGGGAAAAGTGTTTTACCTTAGAAATTTCTGAAAAGTCAGGCTTAGTTAATTTAT
41T	A00583:504:HM2HWDSXY:2:2512:18412:16877	TTATTGTCATTACAATAATTAAAAGTATCTCTTCTCTGTCTATCAAGTGTTATTTTCTTCATTTATTTTCCAATACATTTTCATTAGCCTGAAATTATTTGTGTATCTGTTTTTGGCAACTCATCATAAATAAGAAAAAAAAAATCATTCTCAATGTTTCTCCATAGATAATACATTTTATTC
19H	A00583:504:HM2HWDSXY:2:2505:28592:5603	ACCATAGCCGCCTAGTTTTAAGAGTACTGCGGCATGTACTATTGACCCAGCGTTGGGGGCTTCTACATGGGTTTTTGGGAGTCATAAGTGGAGTCTGTAAAGTGGTATTTTTACTATAAATGCTATTGTGTATGTTAGTCATATTAAGTTGTTGGCTCTGGTTTTTTATTTTTTTTG
3A	A00583:504:HM2HWDSXY:2:2478:25563:24064	GTGGATTAAGGGCTGAGACTGGGGTGGAAGTGAGCTTGGTGGGGATGCAGCGCAGTCACATGTGTACAAGGCTGTGACGCCCAGGGGGATTGTATCCACAGCTGGTCCTGCGGGTGCTGCCTTCTAAATATGTAGAATCCACGG
42T	A00583:504:HM2HWDSXY:2:2477:12020:3427	TACCAATGAAGCTAGCTAGCAGTCAGTGAGTCAGAGTTGCATGACATTGGCAATGGGTAAGAAACAATTCATAAAATAGTTTGAGCACATTACAAGGAGTT
4G	A00583:504:HM2HWDSXY:2:2475:24605:28228	GATTTCGACTTCCATGACCACCGTCCTGCTGTTTATATGAATCAACACCCTTTGTGGGATCTAGGTTAGTGCGTAGTTGGGCG
43T	A00583:504:HM2HWDSXY:2:2474:15293:12790	TTATGACATCTCTTTATGCTCCTCTTGGATGAGACATTTTCTTAGACATTCCTTGTTTTTGATGATCTTGACAGTATTGAAGACACTTGGCAAGTATTTTCTAGGATATCCCTCAGTTAGGATCTGTCATTTTTTTTTTTTTTTTTTTTTTCATGATCAGACTGGGCTTACAGGTTTTGATGAGGAA
9P	A00583:504:HM2HWDSXY:2:2473:22752:35947	TACCAGGAGCCAATCCAGGAGCTGATGTCGTAGCGTGGACTTCACACTGACATCCAGGCTTACTCCACGTTCTTTTTAAAGCATTCTTCAACCCTGTCTTCTGACTACTCATTTCTTAAAATGAAAAAGAAACATTTTACTTGTTAAATAAAGCCTTGCTTTTTTTGGTGCTATAGTA
44T	A00583:504:HM2HWDSXY:2:2472:3938:28228	GATAACACCGATGGGAAAAGAAAAAACGAAACAGTGTCCTTCTAAGCAAAATTTCCTTCCTATGAAATTGAATCTACATGCTCAAGTACAGTGAAGTG
45T	A00583:504:HM2HWDSXY:2:2471:32497:16188	CCTGTTCTTGGGGAGGAAAAAAAAGGCCCATCAGTGAAAGAGCCAAAGGCATGCCTCCTCCAGTGTGTCAGCACAGTTGGCCACGGTCAGCCACTCTTACCACATGGCCTATTGGTGGAAACAGTTCCCTCTTGTCTCTCTCCTTCCCTCCTACCTTTCTCTTACTGGGAATATTGCGTTCATAGACTACACAGTC
47T	A00583:504:HM2HWDSXY:2:2471:16116:4570	ACGCCGACGGCACCACACTCAGCTAATTTTTTAAATTTTTTTGTAGACATGGTCTCACTTTGCTGCCCAGGTTGGTCTAAAACTCCTGGCTTCAAGTGA

10P	A00583:504:HM2HWDSXY:2:2471:14380:24392	CATGCCCAGCTAATTTTTGTATTTTTATTAGAGAGGGTTTCACCATATTGGCCAGGCTGGTTTCAAACTCCTAACGTCAAGTGATCCGCCTGCCTCAGCCTCCCAAGTGTTGGGATTACAG
48T	A00583:504:HM2HWDSXY:2:2471:13422:1658	GCCTGGAAACAGCTATACATCCACTTGTATAGTAAGGGTCTTTTGGTTGAAAGTGACAGAAACAAACCCAACTCAAAGTGACTTAAAAAAAATAGTGTGTTTTTCTGTGAATGTTTTGGTTTATGTAAATGAAAAGTCCAGATGGTTTCAACTTCAGGAATGGCTGGATTCAGGTGTGCACGTGTTGTTTAGGAATAATGTTGTTTCCACT
2M	A00583:504:HM2HWDSXY:2:2468:13304:35869	GGAGAGTAATTATGTGGCTAGAGGGACAATAGGTAACTGTTCTTTCTCTTTGATGTCATTCATTCCGTAATGCTTTTATG
12A	A00583:504:HM2HWDSXY:2:2463:32461:35509	TGTTTTTCATACAATACAATTAAAATCCTGATTAGCAAACCTGACCACAGTTCCTCTTCCATGTACTTTATGGAGGCAGCCTCCAAGCAGGACTGCATTTTAAATAATAAACAGTAACTTTCCACTCCACTAGCTAGAGCACATTAATTTTTACATTATCTATTTTAAGCAAGTGGGCATATGCAATTCACACTTTTCTTAATAGCTTTGGATTTTCTCTAGGAAGTGTTATGCAAAGATTGCTCTGTGACAGATCAGCTGTGTTTATGGTATAAATTAGTGTGAATG
24H	A00583:504:HM2HWDSXY:2:2463:1172:21809	CGTGAGGAAATACTTGATGGCAGCTTCTGTGGAACGAGGGTTTATTTTTTTGGTTAGAACTGGAATAAAAGCTAGCATGTTTATTTCTAGGCCTACTCAGGTAAAAAATCAGTGCGAGCTTAGCGCTGTGATGAGTGTGCATGCAAAGATGGTAGAGTAGATGACGGGTTGGGCC
49T	A00583:504:HM2HWDSXY:2:2461:7527:17002	GAGCCGAGATCATGCCACTGCACGCCAGCCTGGACGACAGAGTGAGACTCCATCTCAATAAAATAAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAGCATCACAGGTCAATCTTACC
50T	A00583:504:HM2HWDSXY:2:2461:17833:14497	GTAGCATGGTTACTTGCTTGTTAGGAGACCCTTAGAAAATAGCTAAGTTTTTGTTTGTTTGTTTGTTTTGTTTTGATTTTTTTGAGACGGAGCCTCGCTCTGTCCCCCAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAA
51T	A00583:504:HM2HWDSXY:2:2459:11351:22936	TTCACCATGTTGGTCAGGCTGGTCTCGAATACCTCAGGTGATCTGCTCATCTTGTCCTCCCAAAGTGCTGGGATTACAGGCGTGAACCACCGTACCTGGCTGCTATTGGAGTTTTAAGCAGGGAGTGGCATAATCAATTCTGAGAAATCTTAGAGGTAACATTCTCAGAATTAGGTAATTTCTAAAAATACATTTAAAGG
52T	A00583:504:HM2HWDSXY:2:2458:15573:35446	AGTGGTGTGCTGGTAAATGCTTAACCCACCCCTAAAAAAAAGAATATAAATATATATATACATATTTATGATTGTTATAAATTTTACTGCTATAAAGGATGTGTAATGAACACTTTACAAATAATAATAATAAAACAGGCAATACTCTATGTTGTAAATTCCTTATAGTTGATTGATTCTAACAGAATGCTTTCACTGATTTTTGCCA
53T	A00583:504:HM2HWDSXY:2:2455:2727:22060	TTCTGAACTTGGTTTTCTCATTTGTAAAATAAAAGAAGTTGAACTATGATCCCCAAGGCCCCATTTGCTTATCAACAGTGCTGATTCTTAACTACAGTAGCAATAAGATCATCAAAAAAATTCACTT
54T	A00583:504:HM2HWDSXY:2:2452:29695:33129	GTTTTTTAAAAATTTATTTGTTTGTTGTTGTTGCATTTTGTTTGTTTTGAGACAGATGCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCACATTCTTGGCTCACTGCAATCTCTCCCTCCCAGGTTCAAGCAATTCTCCCACCTCAGC
55T	A00583:504:HM2HWDSXY:2:2448:25292:11725	CTCCATTTTATTTATTTTCTTTCTAATCTTTATTATTTTCTTCCTGATGCTTATTTTTGGGTTTAGTTTGTTTTTCTTTTTCTAATTTCTGAGGATGGAATGTTAGATTATTAATATGAG
56T	A00583:504:HM2HWDSXY:2:2447:32244:28964	TCCCACAGAGGATCGCTGAGAAAGACAGAGAGTAACTGCCCGCAGGGTCACAGAGAGGGGATGAAGTTCTTTTTAAAAAACACTATTTTTTATTGTGGTGA

33P	A00583:504:HM2HWDSXY:2:2445:12536:27618	AGCTCCACCTGCAGCCCCGGTGTGGGATCCTCTAGGTGAAGCGAGCTGGGCTCCTGAGTCTGCTGGTGACTTGGAGAATCTTTATGTCTAGCTAGGGGATTGTAAATACACCAATCAGCACTCTGTGTCTAGCTCAAGGTTTGTAAACACTCTAATCAGCACCCTGTGTCTAGCTCAAGGTTTGTAAATGCACCATTCAGTGCTCTGTG
57T	A00583:504:HM2HWDSXY:2:2442:21314:16172	GGCGTCCAGCCTATCCGCGGGGACTCCACGTGCACCCCTTCCTCATTGTCCTTGTCTAGGGCCGCGGCAAGGTCCTCGCTCCCATGGCGCGACTCCGGGGGTGTAGGAGCCTGGGCTGAGCAGGTGGAGTAGGGT
58T	A00583:504:HM2HWDSXY:2:2442:19235:1767	ACCTCATTTAACCTTGATCACTTCCTTACTCCAAATCCAGCCACACTGGGCACTAGGACTTCAACACATGAACTGGAGAGCACAGTTCAGTCCATAGCATTCCGGCTTTTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGAAAGGGTCTTGTTCTGTTGCCCAATGTGGAGTGCAGTGGTACAAT
31P	A00583:504:HM2HWDSXY:2:2438:9372:15718	ATCTATACATGTATATGTGTGTGTATATATATGTGTGTATATATATAAAAAACACACATGCACGGATTCACCACCACCAACTCAGAAATTACCGTCTCCCTCTATTCTAAGGAATCATTTTTCATTTTGCCATCT
11P	A00583:504:HM2HWDSXY:2:2438:30843:15076	TGAACAGCTGTAGAATTATGTCATTGATAGATAAAAAGAATAAGCCCCAGAAATAGATGAATGCTCCCATTCATGTAAACAAACAAGTAAAAATTTGTCTGCATACAAAGACCTCTCAACGAGTAGAAGATGGCCTGGGAGTCTTGCGGG
5N	A00583:504:HM2HWDSXY:2:2429:32262:27774	GGGCCATTTGGCTTTATTGTTTTGCTTTCCTTAACCACCCTTTACGCCGTGGTGTTATCAACTGGGGCCTCTCGTTTAACCGCGGTGGCTGGCACGAGTTTTACCGGCCCTCT
38H	A00583:504:HM2HWDSXY:2:2426:1280:22748	CACTCGAATAATTCTTCTCACCCTAACAGGTCAACCTCGCTTCCCCACCCTTACTAACATTAACGAAAATAACCCCACCCTACTAAACCCCATTAAACGCCTGGCAGCCGGAAGCCTATTCGCAGGATTTCTCATTACTAAAA
59T	A00583:504:HM2HWDSXY:2:2424:3857:19225	TTTAGAAAGTAAGTATAGATGGAATAAGTATGCCTAGTTTTTGGCAACTTTCTCCTAATCATGAATTTATCTTTAAGCTTTTTTTTTTTTCCTTCCAGAGGTGATTCCTATGCACATGCTCTAATTTCCTTTTAATTATTAG
60T	A00583:504:HM2HWDSXY:2:2422:14769:3427	AGTGTGATCATGGCTCACTGCAGCCTTGACCACTGGGGCTCAAGCATTCCTCTTGCCTCAGCCTCCCCAGTAGTTGGGACCACAGGCCGGCACCTCCATGCTTTTTTTTTTTTTTTTTTTTTTTTGTGATATGATGTGTCAATGTGTTGCCCAGGCTGGTCTTGAACTCCTGGGTTCAAATGATCCTCC
61T	A00583:504:HM2HWDSXY:2:2422:10800:19977	CTACTCTCTCCTTCTATGAGATCAGGTTTTTTTTTTTTTTAGCTTCCAACATGTGAGAACATGTGTATTTGTCTCTCTGTGCATGGCTTATTTCACTTAACATAATGT
62T	A00583:504:HM2HWDSXY:2:2421:2826:27993	CATTCCATTCCATTTCATTCCATTCCATTCCATTCCATTTCATTCCATTGCATTGCGTTGCATTCCATTCCATTCCATTGCATTCCATTCCAGTACATTGCATTACTCTCGGGGTGATTCCTTTCCATTCCACTCCATTCCATTCCACTGG
63T	A00583:504:HM2HWDSXY:2:2416:4128:15812	CCTTTGGCCTCCACCTGTTCTTCTGGGTGTTGACTATTGTCCCTTTTCCTTAATCACCACTTTTGTGGTAAGGTGCCCCCCTCTAAGAGACTTC
67T	A00583:504:HM2HWDSXY:2:2416:13648:23970	TAAGATACTACTACACACCTATTAGAATCTAGCCTGAAATTAAAAAGACTGACCATTCCGAAGTGTTGGCAAGGGTGTGGAGCAACTGAAACCTTCATACATTGTTGCCAGGAATGTAAAATGGTACAGCCACTTCGAAAAACACTATGACAGTTTCTTAAAATTTAAGCAGACACCTACCTTATGACCCAGCCATTCTACCCCTAGAAGTTTACCTAAGAAAACAGGAAAATGTATG

68T	A00583:504:HM2HWDSXY:2:2415:5475:2049	GGGTGGCCTGGCAGAGGGGCTCCTCACATCCCAGACAATGGGCAGCCAGGCAGAGACACTCCTCACATCCTAGACGGGATGACGGCTGGGAAGAGGCGCTCCTCACTTCCCAGACTGGGTGGCCGGGCAGAGGGGCTCCTCACATCCCAGACGGGGTGGCGGCCGGGCAGAGGCTGCAATCTCAGCACTTTGGGAGGCCAAGGCAGGCGGCTGGGAGGTGGAGGTTGTAGCGAGCCGAGATCACGCCACTGCACTCCAGCCTGGGCA
5G	A00583:504:HM2HWDSXY:2:2413:25572:3756	TCTCCTGGTATCTCGAGCTTGGTTTTCTTCCACAATCCTTCGGTACTGGCGAATACAAGAGGTAGGCAGAGACCACTTGCGGCACCAAAACATAGCAACC
30P	A00583:504:HM2HWDSXY:2:2412:28619:3865	TGGGTGACAGAGCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAAGAGTAGAAAAAGGAGTTTGATCTGTAACTGACTATGAACAATCAACTGAGATA
29P	A00583:504:HM2HWDSXY:2:2412:27453:4288	TGGGTGACAGAGCAATACTCTGTCTCAAAAAAAAAAAAAAAAAAGAGTAGAAAAAGGAGTTTGATCTGTAACTGACTATGAACAATCAACTGAGATA
69T	A00583:504:HM2HWDSXY:2:2410:6325:10755	AGATCTGATTGGATGGGTTAAGTAATATCTATCTATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGTCTCTCTGCTCTCCCCCTCT
1M	A00583:504:HM2HWDSXY:2:2408:26250:30608	GCTCAGTCTGGCGGCGCGTCTACGACCGCGCGCCCCTGCAGCGGGGATGAAGCGGGGATGAAGCGGGCCTGAAGCGAG
6H	A00583:504:HM2HWDSXY:2:2405:2917:2253	TAGATGGAGACATACAGAAATAGTCAAACCACATCTACAAAATGCCAGTATCAGGCGGCGGCTTCGAAGCCAAAGTGATGTTTGGATGTAAAGTGAAATATTAGTTGGCGGATGAAGCAGATAGTGAGGAAAGTTGAGCCAATAATGACGTGTAGTCCGTGGAAGCCTTTGGCTACAAAAAATGTTGAGCCGTA
2H	A00583:504:HM2HWDSXY:2:2404:22426:21762	AACACCTCTTTACAGTGAAATGCCCCAACTAAATACTACCGTATGGCCCACCATAATTACCCCCATATTCCTTACACTATTCCTCATCACCCAACTAAAAATATTAAACACAAACTACCACCTACCTCCCTCACCAAAGCCCATAAAAATAAAAAATTATAACAAACCCTGAGAACCAAAATGAACGAAAATCTGTTCGCTTCATTCATTGCCCCCACAATCCTAGGCCGACCCGCCG
70T	A00583:504:HM2HWDSXY:2:2403:7600:2566	CTCACTGCATTCTCCACCACCACCCAGGCTCAAGTGAGCCTCTTGAGTAGCTGAGATGTCCAGTTAATTTTTATTTTTTATTTTATTATTATTATTATTATTATTTGGTAGAGACAGGGTTTTGCCATGTTGGCCAGGCTGGTCTTCAATTGAA
27H	A00583:504:HM2HWDSXY:2:2378:15501:31469	ACAGCCTAATTATTAGCATCATCCCCCTACTATTTTTTAACCAAATCAACAACAACCTATTTAGCTGTTCCCCAACCTTTTCCTCCGACCCCCTAACAACCCCCCTCCGAATACTAACTACCTGACTC
71T	A00583:504:HM2HWDSXY:2:2377:12689:7560	CACAATAGCTGCCGAGAGAAGGAAGGGAAGGGAAGAGAAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCCTAGGAATACATCTAACCAAGGAGATGAACTACAAGTTCTACAAGGAGATCTACAAAACACTGCTGGAAGAATCA
1A	A00583:504:HM2HWDSXY:2:2376:16694:28933	AAAAATATTGGGTTTTGACAACATGGAAGGCAATAGTGACTTTGGCAAGAAAAATGTGGATGGGATTCTAGTGTCTGGAGTCAAATTAAGAGTCCGAAGAGTGGGTGGAAGCTGAGG
72T	A00583:504:HM2HWDSXY:2:2375:26151:29465	AAATATAGAGAAATAATGGCAGAGACAAAATATTTATCAGGATACAGAAAGAGCGAAAGTATTACTTTCCCCACACCTTCCAAGACTGGAATAGTCTCCTTCATACTTGAGAGAGTGAAGACATCAGTTGGGAAAGTAGCATCTGCAGACACG

31H	A00583:504:HM2HWDSXY:2:2374:32316:21668	CCGACCACACCGCTAACAATCAATACTAAACCCCCATAAATTGGAGAAGGCTTAGAAGAAAACCCCACAAACCCCATTACTAAACCCACACTCAACAGAAACAAAG
73T	A00583:504:HM2HWDSXY:2:2373:3323:23406	AAAGGCTAAAAGAAAGTGTCATATTACACATGTAGATTTTGAGAAATATTTGTTATTTTTCTTATGATAAAGGTTATGCATACACACTCACACACACACACACACACACACACACACACAACTAGAAATTACAGACAAGAAAAAAGATTAGCCAGAATGT
74T	A00583:504:HM2HWDSXY:2:2373:12038:29324	CTGCTATAACAAACTACCCTGGACTACATGGCTTATAAACAACAGAAATTGATTTCTTTTATTTTTTTTTTTGAGACAGAGTCTCGCTCTATCGCCCATGCTGGAGT
75T	A00583:504:HM2HWDSXY:2:2369:5032:3975	GAAATTATCAGAGACTGGGTCACAAATTTATATAAAAGTTCAGTGCTGCATTATTAAGAATAGTACCAAAAATGAAAACCTAAGCGTT
76T	A00583:504:HM2HWDSXY:2:2368:32660:15718	TTTTCTGGTCTCCTACTATTTATCATTTACTTTCCACCTTGTCTTAAGTGGTAATCAAGAAAGGTTTGATTTATTTTTAATTTAATTTAATTTAATTTAATTAATTAATTTTTTTTTTGCT
77T	A00583:504:HM2HWDSXY:2:2364:3748:24737	GTGCGTTGCCTGCTGTCCCTGCTGCCCAGGCCCTCCCCAACATGTCAGGACTTCTGGCTGATTCCTGCAGGGCAGACTGTCTGTTCATCCTCAGGGGGCGTTTGTTGAGTGA
78T	A00583:504:HM2HWDSXY:2:2361:21739:4914	ACAAAGAAGAGAAGAAAACTTCTGGGATTTAAGCTTGAAGGGTGAAATGAGACAACTCTAAAGTTCTGTTTCAGTTAGAGTCTACTCTGCAAATTTAATCAAGGTCTTCCGCAGGCATCAGCTTGACATTAAATTTAAGTGCCCCTTAAAGTGAGAGTT
64T	A00583:504:HM2HWDSXY:2:2354:8748:9846	AAGGTTATCTCCCCTCCTACCTGCCTCCTGTCCCTTCTTTTACCATAAACTTCCGTCATCAAATTTACATCCCAATAACTGCCTTAGAATGGCTGCCAGACTCTCTCATTCCATGTGGTATGCCAGTGTAAATTTGCACAGTCTACACACAGTGTTGCCTCCCACTGTCATCTTCCAGAAACTCCTTTTCATCTTCAACATCCAGTCCTGCATGCCCTGCCACCTCCAAGTCAATCCACAGACTCAGGAATCTTT
12P	A00583:504:HM2HWDSXY:2:2354:14299:19617	TTGAAAATTCTTTAGCCTAAACTAATTATTCTCAATCCTGGCCAAACATTAGAACCACTTGGGGTACTTTTAAAAATTGCTGATGTCCAAGCCCCATTCCTGAATCAGAATCCTTGGGCTTGGGACCCTAGCATCAATATTTTCTATTCTATTCTATTCTATTCTACTCTATTTTATTTTATTTTATTTTATTTTTTTTGAGACAGAGTTTCACTGTCATTGCCCAGGCTGGAGTGCAATGGTGCAATCTCGGCTCACTGCAGC
80T	A00583:504:HM2HWDSXY:2:2354:10086:23500	AACTGTAATCTGTCACAATACTCTTTTGTGCCATCTGTATCTGTTTGGATGTTTTGTTATTGCAGGATATTTTGATATTGAGAGTTTGTCCTTGCAATATCATACTAGATCATAATACCATCATGTTGATATCTAGGTA
81T	A00583:504:HM2HWDSXY:2:2353:29541:24565	AATACAAGGTTAATGTAAAAAACATTATATATACACATATTCATATATGCACATATACATATATATATATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGACAGAGAGAGGGAGAGAGACACTAGCAGCAAACCATTGGAAAATAAAATAATTTTTTACAAT
13P	A00583:504:HM2HWDSXY:2:2352:18584:31266	CAACTGCCAATTAGAAAAATCTTTAAATCCACCTATACCCTGTAAGCCACCCACTTCAAGATATCTCACCTTTTCAGATGGAACCAATGGTCACTTTCCATATTTCGATTTATGATGT
82T	A00583:504:HM2HWDSXY:2:2352:11885:21104	AATACAAAAAAAAAATTAGCCAGGCGTGGTGGCGGGCACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCAGGAGGCAGAACTTATAGTGAGCCGAGATCACGCCACTGTACTCCAGCCTGGTGACAGAGCAAGACTCTGTCTCAAAAAATAAAAAAATTAAAAAAAAATTTTCAGTTGGCAGAACTTTGCACTACGCACCTTGTCATTCACTTTGCATGGA

11H	A00583:504:HM2HWDSXY:2:2350:13250:20462	GGTCTTTGGAGTAGAAACCTGTGAGGAAAGGTATTCCTGCTAATGCTAGGCTGCCAATGGTGTGGGAGGTTGAAGTGAGAGGTATGGTTTTGAGTAGTCCTCCTATTTTTC
83T	A00583:504:HM2HWDSXY:2:2347:14055:11146	TATCAATCATGGGATTTGCAGTTGGTTCGTGGGGCACATGCATAGTGTATGTGCAGCATAATTATTTTTATTGCATAAACAGAATGACCATATGTGTATATCTCACCACTAACTAACACAACTTAGCATGGTGCTTGGCACACAGTTGGTAATCAATAAAATTATATTTACTAAGTAAATAGAATACTGAAGATGTTAACTCTGATTTAACTATACTGAAAAATACATCACTCATGTA
84T	A00583:504:HM2HWDSXY:2:2347:11867:15781	TACACAGAAGCATTCTGAGAAACTACTTTGTGATGTGTCCATTGAACTTACAGTGTTGAACCTATCTTTTGCAGAATCTGCAAGTGGATATTTGGAGCACTTTGAGGACTACT
85T	A00583:504:HM2HWDSXY:2:2343:4173:28260	TGCGCATTGTTCACCTGCGTGGGGGCTTGTGGGGGCTGAGGGGGGCTTGCTGTCATTTTTGTTACACGAGAAGCCCCAGTGCAGTGGGCACGGCCAGTGAGAATGAGTGGAAACGTGCGAGGACCCTGCACATGAGCTTCTATCAGGTCAGCAAACGGCCGCTCGCTTGGGGCTGGGTAAC
86T	A00583:504:HM2HWDSXY:2:2339:4535:9283	GACAGTTCCGTGCTGTCCCCTGTTTCCCTCGGGGTCTTCCCTTCGGAGGCTGCAGCTCGTCTGAGCATCCAGCCTTGAAGGCACCAAGCAGGCAAGGAGGTAGGGCTTTTCTCTGGGGAGGCCTGCGTTGCAGTACGGCTTCCTCATCCCCACCAAGGGCAGGGAAGGGCAGGAGTCTAGGACTTACCTGAATACAGAACACCTGGG
7M	A00583:504:HM2HWDSXY:2:2337:13404:11898	CGTTAATTCCCATATATTCCCGTTAATTCCCATGGAAAGTTTCCAGCTTTGAAAATTCCCGGAATTTTGCAACCCTAGGAACAATACATTCACAATGCAAATCATGTTTTATTCATAACTGTAAAATTACTATTGTTACGATTATAAGTTACTCTGTTGTACCTTTCAGTTGTTGGTGTTGTTTTGTGTTTGACACACTGTTA
5A	A00583:504:HM2HWDSXY:2:2335:3206:35884	TTCTGCCTTCCCCGGAACAGCCCTGGCCCCTGTGCATCTAGGCTGAGATAAAAGGAGAAGCCAGAGAATTCTTTAAATCCTCTTCCCCAGGATGAGCCTTTAGAAGTCCCCGCAAAGGCTGTGTGTGTATTGGGGTGAGTCAGTCTGGGAAGACTGGACAGT
87T	A00583:504:HM2HWDSXY:2:2333:25762:19899	ACCATACACTTTATCTTTGAATTACCACAAATATTTGTAGAATTTTTTTTAATGTCTTTGCCCTTTTAGTTTTTGGATATTCATTAAATTGAGTTTCTAAGTCTGTGTGTGTGTATGTGTATGTGTGTGTGTTTGTGTTTTTTGAGATGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGT
89T	A00583:504:HM2HWDSXY:2:2332:2709:15953	ATGGCGCGTGCCTGTAATCCCAGCTATCCAGGAGGCTGAAGCAGTGAACCTGGGAGGCGATGGTTGTAGTGAGCCGAGATCGCACCATTGCACTCCAGCCTGGGTGACGACTGCGATACTCTGTCTAAAAAAAAAAAAAAATAAAAAAAAAAAAAAAGCATGCAGTAGATGCTTGAATGAATGGTTGAAGAAGCACAGGAT
90T	A00583:504:HM2HWDSXY:2:2331:12355:7513	GCCCCCAGTCTCATTGCTTGCCTACCAAACTGATTGTAGGAGCCGCATGATGCACATGACCTTGCTTCTAACCTACCTGGATGTTTTCACGCTCTGCTGTCTCTTTGAAGTGACTTCCTCTTCTTTCTTCCCTCTTCTTCCTTGCAGTGGCTGTTATGATCTTTAAAGATCTGGTTCAAACA
29H	A00583:504:HM2HWDSXY:2:2327:31729:8563	GGTGAGCATCAAACACAAACTACGCCCTGATCGGCGCACTGCGAGCAGTAGCCCAAACAATCTCATATGAAGTCACCCTAGCCATCATTCTACTATCAACATTACTAATAAGTGGCTCCTTTA
91T	A00583:504:HM2HWDSXY:2:2327:16062:35446	ACAATGAAGATGCTTCCTTATCTACCACAGGCTGTGAACCGCTCTAACTATCCACTTCAAATTCTCCAAAAAGAGTATTTCAATACTGTTCTATCGAAAGGAAAGTTCAACTCTGTGAGTGGAATGCACATATCACAAAGAAGATCCTGT

34P	A00583:504:HM2HWDSXY:2:2325:15772:27430	TGCATGTAAATGTTTTAAATGGCTGATACAACCTTGGTTATCTTCCCTGCTGTTTCAATCTCTTATGAAAGTTTCTTTACTTCCTCTACCAATTCACTTGTGCTCCAAATGTGCTAAAATCATTCTTGCCACAGCCACCACTGTGCCTTTACTCTTTACTGCA
92T	A00583:504:HM2HWDSXY:2:2320:14443:36213	GGCCAGGACTGAGGTCCGTGAGGTTGGAGGCTCTCTTCTACTTTCCTTCTGGCCGGGACTGAGGTCCGTGGGGTTGGAGGCTCTCTCTTCTACTTTCCTTCTGGCCG
2C	A00583:504:HM2HWDSXY:2:2314:11035:19257	GGACACCATTGAGATAAATGGAACTTTTAAACACCGCAAAATGACCCTGGTGGAGGAGGGCTTTAACCCTGCTGTCATCAAAGATGACTTGTATTTCTTGGATGACACAGCAAAAATGTATTTGCCTATGACTGATGACATCTATAATGCCATACGTGCTAAAACCCT
15H	A00583:504:HM2HWDSXY:2:2313:7600:17566	TGACGTTGACAATCGAGTAGTACTCCCAATTGAAGCCCCCAGTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGAGCTGTCCCCACATGAGGCTTAAAAACAGATGCAATTCCCGGACTTCTAAACCAAACCACTTTCACCGCTACACGACCGGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCA
93T	A00583:504:HM2HWDSXY:2:2311:5810:10050	GCTTTTCCATTTTTTTTTTTGTCTCCAACTGCCAGAACCTGGCTAAATTAGACACACCTAAATTATAATCCAAGATCAGCCATTTAGTAATTGTGAAATCT
94T	A00583:504:HM2HWDSXY:2:2309:21432:10989	AAAATGTGCAAAAGATATGAACAGACATTTTACTAAAGTAAAAAGCCAGATGGCAAGCACATGAAAAGACGTTCTTGTATCACTAAATCAGCAGTGAACTGAAAATTAGAACTACAGTGAGATAGCAATGTTCTCTGATCAGAACGGCTACAATAAAAAAATAGTGTCAACACGGAATGCTGCTGAGGGTGAGCAGAGGCTTGATCATTCACATATTGC
1C	A00583:504:HM2HWDSXY:2:2307:5981:28667	CGATTTTTGAGTGGTAGGAGGGGTGATGGGTTCTGGGCTTAGTGGGGGGGGGGGGTCCCGGGCGACTGGGGGTGAGGCCTCACCTCAAACACGTGCAGCTCCTCCAGGAGCAGCC
38T	A00583:504:HM2HWDSXY:2:2306:12436:11537	ACTGCACTCCAGCCTGGGTGACAGAGTGAGACTTCGTCTCAAAAAAAAAAAAAAAAAAAGATACAGGTTCTCGGTTATACTTTGCAGATTTCAGTTGTTCCTAATCTCTCTAACTTCATGTCAATCTTTCCTTATCCATCTCCTGCACTC
8A	A00583:504:HM2HWDSXY:2:2303:8187:26005	AGCTTGAATTAAAAGGAATTCACTTCAGAGTCTATTTTGGTTTGTTAGGGCAGATCGTTGGTGTGCTGGGGGCGCAAACTGATGCACTTGAGGTATGCATTAGCTGGTCCTGCCATATGGCCTGTCACGTCTTACTGGTTAATGTAACCATCTGTCACCTCTTGACAATTTGCATTCACTTTCAGCACTTGGGTTAGAGACATTTTCTTTGGTATTTTGCTGT
14P	A00583:504:HM2HWDSXY:2:2277:29505:8656	ATGAGGTGGATGGATCACGGGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCATCTCTAAAAAAATACAAAAAAAAAAAAAAAAAAAAAAATTAGCCGGGCATGATGGTGGTGCCTGTAATCCCAGCT
95T	A00583:504:HM2HWDSXY:2:2277:16206:31876	AATTGTCCCTGGCTTGTATGCAGTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGCAGGTGGAGTGGGGAGAGGTGCATGAGGTGTCTGTAAAGGGGTGTTCTGGGGCCTGGGCTCACCAAACA
96T	A00583:504:HM2HWDSXY:2:2275:7636:8484	TGATGTGTATTAGAATGGGTTTCTTATTCGTCCTGTTTGAGATTCATTAAGATTTCTCAGTCTGATAATTGACATGTTTTATAAATTCTAAAAAAAAAAAAACCAAGCTACTATGTTTTTTGAATATTGCTTTCTCTCATTCGAATCT
98T	A00583:504:HM2HWDSXY:2:2272:9462:17628	GGATGGGTGGGTGGATGAGTGAATGGATGGAGGAAGGGTGGATGGGTGAATGGATGGAGGAAGGGTGGATGGGTGGTGGGTGGGTGGATGGGTGGGTGTGTGAGTGGATGAATGGATGGGTGGGTGGGTGGGTGAGTGGATGGATGAGTGAATAGATGGATAGATGAGTGAACATGTGAATGAATGGGCGAGTAGGTGGATAAGTGGATGGATGGATG

99T	A00583:504:HM2HWDSXY:2:2262:21522:10394	TAATGTAACAGAATGAAAAGTATATTGTATGGTTTTAGATTCTACTCAATGACTTAACCTACCACATGTCAAGTTTTGGTATAGCATAAAAGAACATCCACAGTTATCGG
100T	A00583:504:HM2HWDSXY:2:2258:23068:11318	GGTGATTGTGATGGAGGTGGTGACAGTGGTGGAGGTGGTCTTGGTTGTGTTGGAATTGGGGAGCTGATGGAGCTGGTGGTG
101T	A00583:504:HM2HWDSXY:2:2257:16586:15687	GGAGGGCTAGACAGGTTTAAATTTTTTTTTTTTTTTTTTTTTTTGGAGATGGATAAGCAATATGTTGCCCAGGCTGGAGTGAAATGGGGCAATAAAGGCTCACTACAACCACCGCCGCAAGGGTTAAAGCGATTATCATGTAACAGCCG
102T	A00583:504:HM2HWDSXY:2:2257:11505:6073	CTCCAGCCTGGGTGACAGAGTGAGACCCTGTCTCAAAAAAAAAAAAAAAAAAGAAAATGAAAATGGAAAAAATTTGTTTGTGAAGAAAGACCCCTGAAAAGAAAGTCAACTGCCAGTATTAATTATGAAAGCAAAAAAAGAAAAGTCTATAAAAGTAATGGAATGTGAATAAAGGTAGAAGGGATGGACACACTTTTGCATATATTAGGTGGAACGTTAGCCTCAGTAATGAAGAGCCAGGACACAT
36H	A00583:504:HM2HWDSXY:2:2256:3106:5087	GACTGATAATAAAGGTGGATGCGACAATGGATTTTACATAATTGGGGTATGAGTTTTTTTTGTTAGGGTTAACGAGGGTGGTAAGGATGGGGGGAATTAGGGAAGTCAGGGTTAGGGTGGATATAGTAGTGTGCATGGTTATTAATTTTATTTGGAGTTGAACCAAAATTTTTGGGGCCTAAGACCAATGGATAGCTGTT
103T	A00583:504:HM2HWDSXY:2:2250:10809:5431	CAGAGCCTGGAAAACAGTGAGCACTGAATAAGCATTATCTATTGTTATTTGATCATCTTCAGATGTAATTAAAAGCTTACGATGAAACATTTGTCAATTTCATGCTAACTAGAGAAATCTTTGTAATTTCATGTGTAAAATGTGCTAGTGTTTTCAC
104T	A00583:504:HM2HWDSXY:2:2246:3450:9032	GTGAAAACACTAGCACATTTTACACATGAAATTACAAAGATTTCTCTAGTTAGCATGAAATTGACAAATGTTTCATCGTAAGCTTTTAATTACATCTGAAGATGATCAAATAACAATAGATAATGCTTATTCAGTGCTCACTGTTTTCCAGGCTCTG
27T	A00583:504:HM2HWDSXY:2:2244:9263:26490	GCCGGTGGAAGGGGAGATGGGTGACCTTTCCATCAATGCCAAGTTAAAACAAAGAACACCAGGGACCCGCGGCGTGGGGGGCCGCCTGTGCCTGACCCAAGCCACCTTTTCAAATGCCTACCAGAGGAGCAAAGAGGTTTCTGCAAAATTCGCAACACCCCCA
106T	A00583:504:HM2HWDSXY:2:2244:11116:17926	TTATCCAAATAATTAGGTATAAATATTGCTTTTTAAAAAATATTTGTCTCTATAGGTTTTTGGGTTTTTTTCCATTCTTCCTGTTCTCCTTTTAGATTTATTAAATATTTTAGGGTCTCATTTTTCTCTCATTGACT
107T	A00583:504:HM2HWDSXY:2:2243:27362:35352	CGTGGTGGCATGCCTTTAATCTCAACTTACTCGGGAAGCTGATGCAGGAGAATCACTTGAACCAGGAGGTGGAGGTTGCAGT
109T	A00583:504:HM2HWDSXY:2:2233:9263:32127	AGAGCAAGACTCCGTCTCAAAAAATAAAATAAAATATTAGTTTTGGCTGGCTGGGCTCAGTGGCTCAGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGACCAGGAGTTTGAGACCAGCCTGGGCAACATAGCAAG
110T	A00583:504:HM2HWDSXY:2:2233:29089:24659	AGGGTATTATATTATAATTGAGGCACTTTATGAATATATAAATAATATTATGTTTTCATGCTAGAGATCATGCCAATGAAGATATTTACTTTGAAAAGGGGAAGATTAGAAGTTTAAAAGCATTTCCATATTGAAGTAAATATTCATTTCCATATCTTCACAGTTATCTTTCTCTGAGTTCTCTGACTCATTGTGAAAAAAAATTCCAACCTTCTTCACAGCTCTACCATCTTCG
111T	A00583:504:HM2HWDSXY:2:2229:30752:12633	TGCTAACTTTGGTTGTTATGCCATGCCTCTTTTAATCTAAACTGGCCTCTCCTTACTATTTTTATTTCCCATTTCATGAATTCTTTGTGGAAAGTTATTTCTTTTAAAATAGCATGCTCATGAGGTTGAAGGGGTAAAGAACATTGATCTCGTGGTTGCAGTGTGGATGAAAATTCAGCCTGAAATGTGCC

112T	A00583:504:HM2HWDSXY:2:2229:23484:4429	AGAAGAATTGAATTTAAGAACTGATTGCCAGTAAGCAAAAATAATGATTAATTTGTTTTGTTTTTAATCTTCACCCACTTTTCTGTATACTTTTTTTTATTAGATGTCC
113T	A00583:504:HM2HWDSXY:2:2227:26919:24314	GGCTGCAGTAAGCCGAGATTGTGCCACTGCACTCCGGCCTCGGCGAAACATAGAGACTGTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAAGAAAAA
114T	A00583:504:HM2HWDSXY:2:2225:13503:21778	GTGCCACTGCACTCCAGCCTTGGTGACACAGTGATATCCTGTTGAAAGAAAGGAATGGAATGCAATTGAGTGAAATGGAATGGAATGGAGTGGAGTGGAGTGG AGTGGAATGGAATGGAATGGAATCGAATCAAATCAAATTGAATGGAATGGAATCGAATCAAATTGAATGGAATGGAATTGAATGGGAGCTGAGATTTTGCCACTG CGCTTCAGTCTGTGT
15P	A00583:504:HM2HWDSXY:2:2222:13910:25050	AAAGTTTTTATAATTTTAGTTGCTATCGATTTAAAGATTACAGAATTCTTTTGTAATCATATGTTCTCACCTATTCTTAATATAATATACATTTATGATCAAATAACATC TATAATATGATATTCATTTTACAATCAAATAAATTGAAA
116T	A00583:504:HM2HWDSXY:2:2219:22155:13620	TCTGTGCTTAGAGAATTATTTTCTGGCAACTCTCTTTCTGCAGCTCAGTAAGTGTCTCTTGAGCAATTCTATAATTTCAAGAACGATACATGTGCCA
117T	A00583:504:HM2HWDSXY:2:2215:25084:33285	GGAACATTGTGAATATACTAAAAGCAAGTGCATTGTATGCTTTAAAATGGTTGTTATTAATTTTATATTATGTGATTTTTACCTTAAAAAACAAAAAAGAGAAAATAG CCTTACTCTATATACAATAAATTCAAGATGTGTTACAAATTTATATGTGAAATCCAAAATAGTATAATATTTAAGGAATAGC
118T	A00583:504:HM2HWDSXY:2:2211:23249:11945	TCTGGCCCAAGTCCCCGGCACCCAGAAGGAGGCCCATAAAAACTTCCCAGACTGAAGGGACCATGAGCTAAAGTCAGCAGGGGAAAAGGTGGCTCCAAGCAA GGAGAGGAAAACCCACAGACAGCAGCCTGTGGGGCCGTCACCGCCACCACACCCTGGAGCCCCGAGAACCATCACTTCTGCTCCCTG
119T	A00583:504:HM2HWDSXY:2:2209:7889:10050	ATAGGGAGCCAGTGAAGGGTATTGAGCTGGGGAGGTCAGATTTGCATTTTGGAAAGATCTCTCTTGCAACTTTTTTTTTTTTTTTTTTTTTTTTTTTTAATGGGTCTCC TATCACCCAGGCTGGAGTGTAGTGGTACAATTATGGCTCACTGCAGCCTCTACCTCTTGGGCTCAAGTGATCCTCCCACCTCAGCCTCCCAAGTAGCTGGCCAC TACTACACACAGGTGCATACAACCATGTCCAGCTAGTT
120T	A00583:504:HM2HWDSXY:2:2209:23249:27320	CCCCACTCCTTCCTGAGCGTCTCCCTCCACAGACATCCGTGACTGTACCGCTACTCCCACCCCCGATTCCTT
20H	A00583:504:HM2HWDSXY:2:2203:3314:31219	ACCGCAAACATATCATACACAAACGCCTGAGCCCTATCTATTACTCTCATCGCTACCTCCCTGACAAGCGCCTATAGCACTCGAATAATTCTTCTCACCCTAACAG GTCAACCTCGCTTCCCCACCCTTACTAACATTAACGAAAATAACCCCACCCTACTACACCCCATTAAACGCCTGGCAGCCGGAAGCCTATTCG
17H	A00583:504:HM2HWDSXY:2:2203:1271:29966	ACCGCAAACATATCATACACAAACGCCTGAGACCTATCTATTAATCTCATCGCTACCTCCCTTACAAGAGCCTATAGCACTCGAATAATTCTTCTCACCCTAACAG GTCAACCTCGCTTACCCACCCTTACTAACATTAACGAAAATAACCCCTCCCTACTAAACCCCATTAAACGCCTTGCAGCCGGAAGCCTATTCG
4A	A00583:504:HM2HWDSXY:2:2202:28754:29622	TGATGCCCCGATCGGGTGTTTTTGTTCACAGACTAGTTCAGGGTTCAGGTTGCTCTCTGATCAGAGGTGAGGAACTGGTAGCCCCCGCTGTCTGTTT

121T	A00583:504:HM2HWDSXY:2:2177:22227:1125	CTGACCTTGTGATCCACCCACCTCTGCCTCCCAAAGTGTTGGGACTACAGGCATGAGCCACCATGCCTGGCCTTCTTATTTTTTTTATAGGTGTGATTACAAAGCAAAGAAAGAGTAGTGACAGAGAAATTGATGAAAAGAGATGAAAATTC
122T	A00583:504:HM2HWDSXY:2:2171:8910:36119	CCTCCCGGGCGGGGCAGCTGGCCGGGCGGGGGCTGACCCCCCCACTTCCCTCCCGGACGGGGCGGCTGGCTGGGCGGGGGGCTGGCCCCACCACCTCCCTCCCAGATGGGGCGGCTGGCCTGGCGGGGGCTGACCCCC
123T	A00583:504:HM2HWDSXY:2:2171:28917:13182	CTCTGGGCCTACAACACTGTAAATTATCTCAGCCTCTAGCATGAAATTCGTATTTCATATCTTGTTCTAACTCTCTTTCCCTCTCCTGTATGCACGCGGCATGCACACCAAGCCGTACCGGAG
79T	A00583:504:HM2HWDSXY:2:2170:25174:6511	GTTGTGTGAAGGAGGTGAAACATTACTGAGGTGGGTGGCTTAAGGTAGTATATACCAAGTTATGTTTCTTAATTTGAAGATAATCATGCAGGAAAATTTATTATAGGGAAAAGGATGATATGGTGCAGTGAAAAAATGGGGAATTAGGAATCAAAAGGTTTGAGTTCCCACTG
124T	A00583:504:HM2HWDSXY:2:2169:13313:24956	GGCAAGAGAATGGCGTGAACCCAGGAGGCACAGCTTGCAGTGAGCTGAGATTGCGCCACTGCACTCCAGGCTGGGCAACAGAGCGAGACACCGTCTCTAAAATAACATAACATAACATAACATAACATAAACTAAACTAAACTAAACTAAAATAATAAATCATGATAGGTAAGTCCAGATATTCAAACCTCTCAAGTAACAGAATTATTGTTAGAGCTATCTACAGGCCAACCCAAGTTTGGCAAATCCATATTCTAG
16P	A00583:504:HM2HWDSXY:2:2166:18032:15593	GGCACTGTTGGCAGTGACCTTGTCATTGAGCTCCTGGCCAGTTGGGACCAGTCAGTGGTTTGGATCAGTGGGGCCTGGTCGGTGGGGCTGTGGTACTGCAGGCCTGGTCTGTGGGGCC
88T	A00583:504:HM2HWDSXY:2:2163:19072:24220	GCCGGGTGCAGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGGTGGATCACTTAAGGTCAGGAGTTCAAGGCCAGCCTGGTCAGCATGGTGAAACCCCATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTGGTGG
125T	A00583:504:HM2HWDSXY:2:2162:16957:17581	CACCATCGGCACTCTGAGTCCTTCCCAGGTTCCCTAAAGGGGGAGGAGGGGACACCGTTTTAGATTTAATTTGTACTGTACCTGATATGATTGTGATAATTTTCCAATGAATAATTGTTAATCTTACCTAATTAAAATAATTATATGTTAAATAAAATATGCAGATGTTAAA
40H	A00583:504:HM2HWDSXY:2:2158:3604:34726	TGCCCCAACTAAATACTACCGTATGTCCCACCCTAATTAACCCCATATTCCGTACACTAGTACTCATCACCCAACTAAAAATATTAAACACAAACTACAACCTAACTCAATCACCAAAGACCATAAAAATAAAAAATTATAACAAACCCTGAGAACAAAAATGAACGAAAATCTGTTCGCTTAATTCATTGCACCAACAATCCTAGTACTAACAGCCGCAGTAAT
126T	A00583:504:HM2HWDSXY:2:2154:14642:28510	TACTTTTCATACGATGGAATTATAATGTGAAATCATGTTTTATTAAAATCATGTTTTAGAAGAATATTTTACAATGTTATTGGGAAACAATCTTGAAATATGAC
21H	A00583:504:HM2HWDSXY:2:2152:29812:33426	CAATTAGGGAGATAGTTGGTATTAGGATTAGGATTGTTGTGAAGTATAGTACGAATGCTACTTGTCCAATGATGGTAAAAGGGTAGCTTACTGGTTGTCCTCCGATTCAGGTTAGAATGAGGAGGTCTGCGGCTAGGAGTCAATAAAGTGATTGGCTTAGTGGGCGAAATATTATGCTTTGTTGTTTGG
128T	A00583:504:HM2HWDSXY:2:2149:1244:13667	ATTTTATTATTATTATTATTATTATTATTTTGAGATGGAGTCTTGCTCTTTTTCCCAGTCTGGAGTGCAGTGGCGAGATATCGGCTCACTGCATGCTCCTCTTCCTGTGTTCGCACCGTTATCCTGCCTCAGCATCCGGAGTAGCTGGGA
129T	A00583:504:HM2HWDSXY:2:2145:15971:3912	TATTTATAGGATAAAGTGATTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGAGGGAGGCTCGCTCTGTCGTCCAGGCTGGAGTGCAATGGCGAGATCTCGGCTCACTGCAAGCTC

131T	A00583:504:HM2HWDSXY:2:2144:4499:27289	ACTACTGGTAGAAGAAAGTGAAAACACAAAGGACAAAAGATGCAAACACATGTGGTTCCTTATTTAGATTGCGACAGGCATTTTGCTACAGTAAGAGTTAAGAAAAATCGGTGTCAGGGAAATTTTAAATGAAGAATTTACTAATTCCAAGATATCCAGACAGCATTACTGACTCAGTTTGGCCTTCAGTTTGACTCACAACTATCTGAATACTTAGAAGTAGCATATTTTTGAGAGAAAGAAGTAGATGAAG
132T	A00583:504:HM2HWDSXY:2:2141:30617:34100	AAAATATAATCTGCCAAAGATGTTTTGGACAAATTACCGAAAACTATGGAAGAAGCATGACTCAGGGATGAAATGGCTACAAAACCACAGTTCAGTGAAATCCTGTCCCACAGCTTAACTGTGATCAGAGTGATTTCTGTCTAATTTTCTGC
30H	A00583:504:HM2HWDSXY:2:2140:6533:1094	GTTGTAGGCCCCTACGGGCTACTACAACCCTTCGCTTACGCCATAAAACTCTTCACCAAAGAGCCCCTAAAACCCGCCACATCTACCATCACCCTCTACATCACCGCCCCGACCTTAG
134T	A00583:504:HM2HWDSXY:2:2132:32407:29653	AGATACTTAATCTCTCTCAGACTCATTTTTACTATCTTTACTCATCTTTTTTTTTTTTTTTTTTTTTTTACCACTCCTAAACTAGGAGTACTAATCATTTAGAATTCAAAAAGTTTTAAATTGG
1H	A00583:504:HM2HWDSXY:2:2124:2528:23500	TCAACTACCTAACCAACAAACTTAAAATAAAATCCCCACTATGCACATTTTATTTCTCCAACATACTCGGATTCTACCCTAGCATCACACACCGCACAATCCCCTATCTAGGCCTTCTTACGAGCCAAAACCTGCCCCTACTCCTCCTAGACCTAACCTGACTAGAAAAGCTAGTACCTAAAACAATTTCACAGCACCAAATCTCCACCTCCATCATCACCTCAACCCAAAAAGGCATAATTAAACTTT
135T	A00583:504:HM2HWDSXY:2:2123:26476:31031	CAGTGCACTTGCTGGCAGATTTTGAATGTGCATAGCAACTCTGTTCCTGGAATTTTAAAATGTGGAATCTGTGACAGACTCTTACCATTTTATAATCAGTTTCAGTACTTTTTTTTTTTTTAACTTTTGACTTGTTTTGTGTCTTGTAGCTCAGATAAGTGATTGCAATAATTTATCCAAATTTATCTTTTAAAACTCTGCAGAGAATAGTCTTTCTCCGGGATTATTAACATACCT
136T	A00583:504:HM2HWDSXY:2:2123:24198:6950	TTTGAAAGCTAGATAACAGTAAAACAATGTCTTTAAAATTCTGAGAGACGTAATATTCAGCTTACAAATTTTTACCCAAACTATCAATCAAATATGAAGGTAGAATAAGGGCATTTTCAGACAATTAAATGTCACAGTAAATTGGCTTGTCTCATCCCCATTCTTAAAATGCTATTGAAATATGTGCTCTTTCAACAGAAAG
24P	A00583:504:HM2HWDSXY:2:2123:16866:11005	CACCACCACGGAGACCACCTCACACAGTCCTCCCAGGTTCACTTCTTCAATCACCACCACCAAGACCACCTCAGACAGTACTCCCGTCTTCACTCCTTCTATCGCCACGTCCGAGACAAGCTCACACAGTACTCCCGGCTACACTTCTTCAACTGCCACCACC
137T	A00583:504:HM2HWDSXY:2:2121:20582:2096	CACTGAGACCACCTCACACAATACTCCCAGCTTCACTTCTTCGATCACCACCACCGAGACCACATCCCACAGTACTCCCAGCTTCACTTCTTTGATCACCACCACGGAGACCACCTCACAAAGTACTCCCAGCTTCATTTCTTTGATAAACACGTCTGAGACCCCCTCACA
97T	A00583:504:HM2HWDSXY:2:2119:9200:9502	TGGCTACATTTTTTTGTTGTTGTTTCTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCGTGATCCGTCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGCCCG
138T	A00583:504:HM2HWDSXY:2:2118:9598:20995	ACGAAAACAACACTAATGAATGTTAATGAAAGCAATGAAGAGAATCTCCAGATCTTTCACATTCATCTTTGACATCTTTGACATAGGCTGTGAACATATGTCAAGGAGATTGAATTTCCAGGTGATAAAATATTGGTAATGTGGAAACAA
139T	A00583:504:HM2HWDSXY:2:2117:15076:18490	CAAGATTGCGCCACTGTACTCCAGCCTGGGCAACAAGAGTGAAACTCCATCTCAAAAAAAAAAAAAAAAAATACAGAATTAGCCAGGCATGGTGGCGTGTGCCTGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGAGGTTGC
140T	A00583:504:HM2HWDSXY:2:2116:5990:31344	CTGTGCCTCACTAAAATTCAGAGACTTGTGGGTCAGTTTAGTTGGGGTAACCCTGTACACACACACACACACACACACACACACACACACACACACACACACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAGGTAGGGCAACACTTTAAACACACTCTCTTTCTCTTTTTCTCTCTCTCTCTCTCTCTCTCTCAGGTGGGGCAACCC

37H	A00583:504:HM2HWDSXY:2:2116:32072:6527	CCCACTCATCCTAACCCTACTCCTAATCACATAACCTATTACCCCGAGCAAGCTAAATTACAATATATACACCAACAAACAATGTTCAACCAGTAACTACTACTAATCAACGCCCATAATCATACAAAGCCCCCGCACCAATAGGATCCTCCCGAATCAACCCTGACCCCTTTCCTTCATATATTATTCAGCTTCCTACACTATTAAAGTTTACCACAACCACCCACCCATCATACTCTTTCACCCACAGCACCAATCC
141T	A00583:504:HM2HWDSXY:2:2115:14534:4116	GCAAGACTTCCTGACAGTCACATCTGTCCTGTCCTTGTGTTGGTTGGTCTTGTTGCTCTGGTCACTTCCTCTGTCTGGCTTTCTGAGTTCAAGTAAAACATACTGAGCAAGTCTCAACACACACACACACACACACACACACACAACACACATAAAAAAA
142T	A00583:504:HM2HWDSXY:2:2114:3766:32377	GCAGAGGTTGCAGTGAGCCGAGATCCCGCCACTGTACTTCAGCCTGGCGACAGAGTGAGAGACTCCGTCTCAGAAAAAAGAAAAAAGAAAAGAAAAGCCCCACAGACCCAGCGTGA
143T	A00583:504:HM2HWDSXY:2:2110:5376:14372	TTATTGCCATAACTTTTTCTCTTTATACCACTTTAGCTGTGTCCTGCAACTTCTGGTATGTTGTTCTTGTATTTTCATTCAGTTCAAAATATTTTTATAACTTCGTTATGATTTCTTCTTTCACCTATGGGTCATTTAAAAGTGTGTGTGTGTGTGTGTTTGAATCCCGATGTTTCCTTTTTTCTTGATATCTTTCTATTACGTATTTCTCGTTCAATTTCTTTTTGGCCAGAGAA
144T	A00583:504:HM2HWDSXY:2:2101:21721:3693	ACTATAGCTTTGTAATACAATTTTAAATCAAGAGGTGTGATGCCTCCAACTTTTTCTTTCACAGTAATCTGTTGGCTGTTTGGGGTTTTTTGTGGTTCCATACGAGTTTCAGGATTGTTTTTTCTGTTTTTGTTTTTTTTTTTTTTTCTTGAGATGAAGTCTCACTCTGTTGCCCAAGTTGGAGTGCAGTGGCACAACCTTGGCTC
145T	A00583:504:HM2HWDSXY:2:1676:1922:15749	TCAGCAGTTTTCACAATTTAATTATTTTATTATTATTATTATTATTATTATAGTAGAGACAGGGTCTTGCCATGTTGCTAGGCAAGTGTCAAACTCCTGGGCTCAAGTGACCCTCCCACTTCAGCCTCCCAAAGTGCCAGGGT
8M	A00583:504:HM2HWDSXY:2:1676:18548:15640	AAATCAACGAGGGGGGCAAACCATTGGAACCACTTGTTAATATAATGCACCCAAGTATGACCACCCACTGAGACATCAATAATAGACACATACTAGGCATATAATTTTTCCTGACAATTAAAACCTTGTAGAAGTATAATTTGTCAGAGCTGCTGTATTGGATTGCATTAACTTGTATGGGTGTGCC
146T	A00583:504:HM2HWDSXY:2:1676:15935:12806	GCAGACTGACACCTCACACGGCCGGGTACTCCTCTGAGACAAAACTTCCAGAGGAACGATCGCGGTTCACGAAAAACCACTGTTCGGCAGACACTGCTGCTGATACCCAGGCAAACAGGGTCTTGAGTGGACCTCTAG
147T	A00583:504:HM2HWDSXY:2:1675:3432:28322	AGTTGCCATCTGTGGCTAAGAGCACCGCAGACTGCAGGCCCCGAGGCGGAGCAAAGGTGGGTGTTCAAGCGAGAGGCTGGCATGCAGGTCTGG
148T	A00583:504:HM2HWDSXY:2:1675:15338:16752	AATATAGATCATATGATACATCACAAAACAAATCTCAATTTTTTTTTTCATATTCAGGCACCTCAAAACATATTTTCTTTATTTCCTCCAGAGAACTGGCTTTAGTTCTGTGGTCTTTGTAAACATTTAACACAAAATAACAAACTGAAGAATTTATATCTTTGCCCTGTGTTGGTGGGTTGTGTTTACTTATGTTTAAGTTG
149T	A00583:504:HM2HWDSXY:2:1669:7970:9064	GCACTTGCGGTTGCCAGCTTCTCCTGGATCTTTCCCCCACAGGTTTAAAATGAAAAAAAAAAAAAAAAAAAGAAAGAGAACAAGATCCTAAATGTAACATATTTTTCCCCACTATTTTCTAAGCTTCCTTATTTG
150T	A00583:504:HM2HWDSXY:2:1668:8603:12007	AGCTTTTGGATTTGATTCTTATTGGAAACAAAGTCATTTATACACAATCATGTTATTTTTCCCTTCCATTAGCCAAAATAGCCAACAACAACAACAACAACAACAACAACAACAAAACAAAACCAACAGTAATAACAAGAATTGAGTGGACATAAATAATGACAAATATATGTAGGCTAGACATATCTATATGTACGTACATGGGCTAGTTGAATTCTAAAACAGAGGTAAAATCTGTTCTTCAACTAATATTAACATCTATTGCTAATCTTCCATGTGCTTTGAAAG

151T	A00583:504:HM2HWDSXY:2:1659:27172:5556	GAGTTTGACCTCTGACGGCCAGTTGTAATAGCATTAAGTCTTTGAAATTTTGTAGCGGGGTAGAAGGGGCTAGGAAAGGAAGAAAACATCTTTTTAAAAATATAAGCGATCGGCCGGGCGCGGT
115T	A00583:504:HM2HWDSXY:2:1639:3974:9627	GTGCAATTGAAAGTTGACATGTAATGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTTGGTGACACAGTGATATCCTGTTGAAAGAAAGGAATGG
155T	A00583:504:HM2HWDSXY:2:1638:29604:35853	TGGAGATGATAGATAACAGATACATAGAGATGATAGGTAGATTAGATAATAGATAGATGAAAGATCAATAGATAGATAGATAGATAGATAGATAGATAGATATGATAAGTAGATAGGGAGAGAGATAGAGAGATGATAGGCAGACAGATGATAGATAATCACACACACATACATCCTATTGGTTCTGTTTCTCTGGTCTCAGGCTGAACC
156T	A00583:504:HM2HWDSXY:2:1637:8232:10300	GATTGAAGTTCTATTTACTGCTGGCAAAAAGCAACTTCATGGTTTGAAAAAAAAAAAAAAAGACATACAAAATACTCATACC
157T	A00583:504:HM2HWDSXY:2:1636:2889:8938	TCATGCCTGTAATCCCAGCTACTCGGGAGGCTGAGTCAGGAGAATTGCTTGATCACAGGAGGCAGTGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGACTGGGTGACAGAGCAAGATTC
35P	A00583:504:HM2HWDSXY:2:1635:16333:1564	CGGGGGGCCGTGGCCGGGTGCTGCGGCGGGCGAATTGGGGGCGCGGGCCGCGTGCAGCGGGAGGGGGAGGGGCTGGCCGGGTCCCCTCGGGTGTGGCGGAGTCCTGGCTTCCGCGCTGTGGACCATCGCAACTCCCAGCACACCTGCGGG
25P	A00583:504:HM2HWDSXY:2:1629:26169:26772	CAGCTGATAGTGAAAGAGACATCAACAGACATGTGGTCAATACCAGTAGATTTTTAGAAGATAGATTTCTCCAAGGTGTACTTTTTATTTTCATATCATTTCAAAAATTAACTCTAGATTCAATTTGCTATTTCTACAGAAGTGCTAC
158T	A00583:504:HM2HWDSXY:2:1625:28537:28369	TGGTATTTATTCTATTGATATGCTATAATATATTAATTAATTTTTGGCTGTTAAACAAAATTTGCCTCCTAGGATGAATCCCACTTGGCCAAGATATATAATTATTTCAACATGCTGATCAATTAG
3G	A00583:504:HM2HWDSXY:2:1624:32687:9157	GTGATCTATAATGATACTCAAAAAGAACATTGTGATGCAGTTCTCAGGATCATCCGTAAGCTTGCTAACGCAGGGCTTCAACTTGATTTTGATAAGAGCGAGTTTGAAGCAGGCACTATTAAGTATCTTGGATATTTGGTGAAGACCGGTTGGGGTTTGCAGGCTGATCGCACAAAACT
17P	A00583:504:HM2HWDSXY:2:1621:14886:29246	TAGTGTCTTAATTATGTCATAAAGTTACCTAGTAACAGAATCCAATAAAATATCAATGTACATTCTAGTATCTTTGCTTTTTGGGATATATATATGTATGTATATATATTATATATATATTATAAATATATTTTATAATATATATTTTTTGGAAACAGGATCTTCCACTGTCACCCAGGCTGGAGTGCAGTGGCAT
6C	A00583:504:HM2HWDSXY:2:1617:30273:9768	CGGCCCCTGAGACAGCGGGTTCCGCCGAAGCTCCGCTGCAGTACAGCCTGCTCCTGCAGGACCTGGTGGGTGTCAACCGTCAGCCCCGGCTCCCGGAGCCTGGGAGCCTGGGCGGGATCCCAAGTCCAGCCTATAGTGAGGTGCAGATGATGTTCTAGTAGGGGTAGGAAAGCTGCGCCTTCAAGGCTGCGCTGGCCTGCGTGGGAG
159T	A00583:504:HM2HWDSXY:2:1617:19877:35540	GTGTCTCCACCCGAATCTCATCTTGAACTGTAGCTCCCACAATTCCCACATGTCCTAGGAAGGACCTGGTGGGAGGCAGTTGA
9M	A00583:504:HM2HWDSXY:2:1617:18873:15734	GCTTGTGTTCCATCACCTGGACAACAACAAACAGACTGAGTCAAGTACAAGTCCCAGAGTGCACTGCTGTCAGTGCTGTCACT

160T	A00583:504:HM2HWDSXY:2:1613:11822:29356	GACAATTACTGGCCAGGCGCGGTGGCCAGAGCGAGACTCCATCTCAAAAAAGAAAAGAAAAGAAAAGAAAATTACTGGCGGCAAGCAGGAACATTGTAGATTTTGAAACTGTCTTGTTTTACAAGATACTGAAGCAAGGTGGTGCAATTATTACGTCCTTCTAAAGCTGATCGGATAAAGGCTTTAATTTTGTAATTTTCAGAGAATATTACCAATGTAGC
16T	A00583:504:HM2HWDSXY:2:1612:9362:11412	GCTGGCATCACAGCCCTAAACATGGTGGTAGCTGTCACCGGTGGGAATTAGGCTGAATAAATGAAAGGAGGCTAAGCCCCAGGACGTGTCCTGGAACTTAACAGTGCCAGTTTATTCGCTTTATGTAAATGCCTGCTGCTATTCCTTGCCTTATGAAGGGCTTTCAGTACAAGAATTCATCTTTGGGGAAAATAGCCTTTGGCTCAATGGCTGTGTCTGCCAAGT
161T	A00583:504:HM2HWDSXY:2:1612:31385:6057	TGGCTGGGCCTCACGATCTGGCCGGGTGCCCGTGAGGGCTGGCCCGCTGGCACCCTTGGTAACAAAGGCCAATCATGGACCCTCCGCCTGGTCAGGAACATAAGGAGCCGGTCCTGGGCTGGGCCCTGGGGGTGAGGGACGTCTGACACCCAGAACCAGAGTGCAGGACAGAGGCCGTGGCTGTGGCTGGGCTCTGGGTGCTGAGTGGGACA
26P	A00583:504:HM2HWDSXY:2:1611:4878:6057	TACTAGTTTACCTTTCAGATTTGTGATTAAGGGCTGGGTGTGTGTGTGTGTGTGTGTGTGTAAGTGTGTTGGGGGAGGGAGGAGTCTGAGAAAGTGAGCAAGTACGTAGAAACTTTTTTTTAAAAAGTCCAGATTAAGTGATTGAAATCGACT
162T	A00583:504:HM2HWDSXY:2:1609:6686:31892	GGACAAGTAGAATTGTACAATATGTGATCTTTTGTGGCTTTTTTTTCCCTCTTAGCACAATGTTTTCAAAGTTCCTTTATGTCATAGTGTGTATCAGTATTTCATTTCTTCTGTGGCTGAATAATATTCCATGGTAGAGACACACT
163T	A00583:504:HM2HWDSXY:2:1609:3052:5212	ATCCTAAAATTCCCTACTGTGTCCCATTACAAACACTACTCAAGCTGCCTTTTAATGCCACAGATAGTATTGCCTGACTCTGAACTGTGTATACAAGGAATTATATGGTAATTCCACATCTGACTTCTTCCACTTAGTATTATGTTTGATTCAGCAATGCTGTTGGTACTAACAGTTAGTACATATTTTAAAGTAAAAAGTAGTCTTGGATGTGTAATATGCAAGTATGTCTGTCAAAAAAGACTAAGATGCTGTTAAGAACAA
165T	A00583:504:HM2HWDSXY:2:1608:19144:11224	AGGAGTATGATGATGCCTCTGGCTTTATTATTTTGCTTGGGATTGGTTTGGCTGCTTGGGCTTTTTTTT

170T	A00583:504:HM2HWDSXY:2:1574:29668:34710	CCCAAGATCATGCCATTGTACTCCAGCCTGGGTTACAGAGTGAGACTTTGTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATATATATATATATATATGTAAATAATAATGGCTGAAATTTGATAGATGTTTTTTACCCTCTTAATTTCTTAGT
2L	A00583:504:HM2HWDSXY:2:1572:3568:4601	AAGAAGGAAGCTCTATCTGCAAGCCAAGAAGAGAGCCCTTAGAAGAAACAAACTTGCCAATACCTTAATCTTAGACTTCTAGCCTCCAGAACTGTGATAAAATAAATTTCTGTTGTTTAAGCCTCATTGCTTGTGTCTTTTTGTTATAGCAGCCCTAGCAAACTAATACAGAGGTCATAGTGATCATTAATGGGTATATACCACACAATAGATCTTCTAAACACAGGAAAGAATAAAAGAGTTAGAAGGA
3M	A00583:504:HM2HWDSXY:2:1570:3884:16297	AATGAAAGAATATAATGTCCCTGTCGGGATTCGAACCCACAGCGGTGAGGGGCAAGTGGTTTGAAGTCAACGACCTTAACCTCTCGGCCACG
10M	A00583:504:HM2HWDSXY:2:1568:15257:11068	GGGATTTAAAAAATCAACTTAGGATTTTCATAAATTTATTCATTTTAGGGTTAGGGTTAGGGTTAGGGTTAATATTAGGATTAGGTTTCTAAATCCCAAGTTACGGCAAAAAAATCTCGAGATACGGCAAA
5H	A00583:504:HM2HWDSXY:2:1565:24469:28087	TGAGTGGTTAATAGGGTGATAGACCTGTGATCCATCGTGATGTCTTATTTAAGGGGAACGTGTGGGCTATTTAGGCTTTATGGCCCTGAAGTAGGAACCAGATGTCGGATACAGTTCACTTTAGCTACCCCCAAGTGTTATGTGCCCGGAGCGAGGAGAGTAGCACTCTTGTGCGGGATATTGATTTCACGGAGGATGGTGGTCAAGGGACC
171T	A00583:504:HM2HWDSXY:2:1559:25943:11005	CCTAAAACCTCATGGCTTGCCTGCCTCCACAGTCTTTTTCCTTTTCAATAGCCTATCCATCACCTGGTCCTGGCGAACCCACCTCAGAAATGTTTCCCAGATAGGTCCAGACCTAAAGAGCCAAC
9C	A00583:504:HM2HWDSXY:2:1551:14922:6230	GTTGCGTGTCCTGTGGATATTGAGGTAACGTTGGTGAGAGGAAGAGGGGTAGCGTGACCTGTGGACTCTGAGTAAGCGGCGGTGACAGGAAGAGTGGTGGCGTGACCTGTGGACTCTGAGGAAGCGTCGGTGACAGGAATAGGGG
127T	A00583:504:HM2HWDSXY:2:1549:27579:26428	AAGGTTGCATGGTCAACCTGTTGACCACGGCTGGTGCTGCCATGGGAGAAATGGTGATAATGGT GGTGGTGATGGTGATGGTGATATGATGTTGATGGTGATGTGATGATGATATAATGGTGATGGTAATGGTGATGGTGATGTTGGTGATGGTGGTTATGTGATGGTGATAGTGATGGTGATGTA
172T	A00583:504:HM2HWDSXY:2:1548:31611:9518	TGGCCTCTCAAAGTGCTGGGATTACAGTCATGAGCCACTCTGCCCGGCTGATAATTTCTAATCTTTTAGACTACTATATCCCAGGGAAAAACCTCTCATCCAGCCTTCCTTGTTTTAAAACAGTTTCCTGAGCCTATTTCATCACACACACACACACACACACACACACACACACACACTTCTCTTTACTCATGCTTTTCCATTGTTAATAAACATGCTTATTAAAAAAC
173T	A00583:504:HM2HWDSXY:2:1541:18665:31062	AAATCCCAAGGGAAAATTAAAACTCAAGTGGACCACTCAGATATCTGTCTTATAAATTGACTTCTCATCTCATCACTACTTTGCCTGACGAAGTCTCAATTTTCGAACAAATTGTAATATATTCTCCATGGGAAAAAGCTACAAAC
174T	A00583:504:HM2HWDSXY:2:1538:23185:33849	CCAAGCCGAGCATCAGCCCGTCGTGGCCCATGGACTCTGGGTTCCCCAGGCAGGGGAAATGTGCCAGAGCCACGGGGAAAGCTGAGCTCTGCGGCCCTGCGAGCGCGTTCACAAAGGTTTATCAGTTTGTAAAACTTGCAGAAAACTCAGCCATCCGTGTTTGGGACAGGCGGCCCCTTCCACTCAGGGTTCATCCGTCACGCTCCTTTCGCCT
4N	A00583:504:HM2HWDSXY:2:1536:9851:21684	ATGTTAAAAGTACTAATTCCTACCATTATATTATTCCCAACAATCTGATTAACTTCCCCCAAATGACTATGAACAACCACAACCACACATAGCCTCCTAATTGCCCTTATTAGCCTCACATGATTAAAATGAACATCAGAAACCGGATGGACTATATCCAATTCATATTTAGCCACAGATCCACTATCAACCCCTCTCTTAGT

175T	A00583:504:HM2HWDSXY:2:1536:25554:21887	TATTTTTAACTTTTAAAGTAACTTTCATACTGGCTACACCAACTTACATTCCCACCAAGAGTGTTCAAATTTTCCACTTTCCTTTACTCCACATCCTTGCCAACAAATCTATCTATCTACCTATTATATATCTATTTATCTCTCTCTCTCTCTCTCTCTCTACTTATCTAATAGCCAACCTAACAGGTGTGAGGTGATATGTTATTGTGTTACAGTAAGGACTTTTTGCTTGAAAAT
176T	A00583:504:HM2HWDSXY:2:1535:23475:13119	CCTTGCAAGAGTTTCTCTTGTTTATTTGTTTGTTTGCATTTTTATTTATTTAAATAGTCAAATCTGTGACTGAGATAGTTTTTTATGCTTTTTTACCC
177T	A00583:504:HM2HWDSXY:2:1533:8287:28964	CCTCTCACCATTTCCCAGTGTCCCTCACCATTCCCTAGTGCTCTTCACCATTTCCCAGTGCCTCTCACCATTCCTCAGTGCCTGATGCCCTCTCTTCCCTGGACATGCACACATATTGTTATCTTGGATGGCCACCCTTC
178T	A00583:504:HM2HWDSXY:2:1533:25075:8907	GTTGCACAAGTCCATAAATTTACTAAGAATCATTAAATTGTATGCTTACAATGAGTGAATTTTGTAAAATGTAAATCATATCTCAATGAAATTGTTAAGAGAAGAAGCTGGGGACATTTCGACTCTGATTAGTCACCCACCTGACTAGTCATAG
179T	A00583:504:HM2HWDSXY:2:1530:31114:23437	GTGAACCCAGGAGGCGGAGCTTGCAGTGAGCTGAGATCGCACCACTGCACTCCAGCCTGGGCAACAGAGCGAGACACTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAGGAGTCTTTAGGGTAAGGAATATTAACAAGGATAAAGTCAGACATTCCATCATGATAAACAGTCAATTCATCAAGAAGATATGCAACAATCCTAAATCTGATGGACTAAATAA
180T	A00583:504:HM2HWDSXY:2:1525:15167:18897	GGAATGGAGTGGAATAGAGTGGAGTGGAATGGAGTGGAATAGAATGGAATGGAATGGAATGGTGAAATGAAATGTGAGCTGAGATTGTGCCACTGTATTCCAGCCATTTTTGACACTGTGAGATCTTGTCAAAAGAAAGGAATGGAATCGATTGGGATGGAATAGAATGGAGTGGAATGGAATGTTGTGGAGTGGAGTGGAGTGGTGTCGAGTGGAACGGAGTGGAATGGAATGGGATG
181T	A00583:504:HM2HWDSXY:2:1522:22752:32033	GCAGACTTAAAAGTTATGAATAAAAATACCTTCTGTGATGAACAGAAGTTTCTCATTGATCACACTGACAAGAAACCTTTCGATGAACAGTCCGGGTAGAAGACATGTCACTCTAAACAGTGTCTGTCTTCTTTCCTGGGCCTAACTGAACTTTGCAGAGTTCATTTGGGACATAAGGAAACAGAAGGTGTCAACTTGGCCCTTGTGCTCACTGGGAAAATGGGGAGAGACAGAACTCATTCAGGAGACCT
182T	A00583:504:HM2HWDSXY:2:1520:24578:20134	GAGAATGGCGTGAACCCAGGAGGCGGAGCTTTCAGTTATCTTTTATCGGGCCACTGCACTCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAGTACAGGGCCAGGGTCCTTTTCCATGAATCTCCT
183T	A00583:504:HM2HWDSXY:2:1519:18123:21512	GTGAGAGTTACCTAAAGCTCAGCGTCCATGATGGTCTACGGGGCTTCTGAGGTGATCGGGCAGCATAAGTCTTCAGCCGCTAAGCTGAGAAGATCTGGGAAGGAGTCAGTCAGAGAGCCTTGGGGCAGAGTTCCAGGGGCTCTGGGAGTG
184T	A00583:504:HM2HWDSXY:2:1515:29866:35744	CGGGAGGTGGAGGTTGTAGTGCCTAGATTGTGCCATTGCACTCCAGCCTGGGTGACAGAGTGACAGAGTGAGAC
23H	A00583:504:HM2HWDSXY:2:1515:29731:25207	CCTCAAGATACTCCTCAATAGCCATCGCTGTAGTATATCCAAAGACAACCATCATTCCCCCTAAATAAATTAAAAAAACTATTAAACCCATATAACCTCCCCCAAAATTCAGAATAATAACACACCCGACCACACCGCTAACAATCAATACTAAACCCCCATAAATAGGAGAAGGCTTA
186T	A00583:504:HM2HWDSXY:2:1514:2772:15781	GATCACGCCATTGCACTCCAGCCTGGGAGACAGGGCAAGAGTCTGTCTCAAAACAAACAAACAAACAAACAAACCCAATGGTGGTTTTTGAAATACAGAAAAATTCATTCTCATATTCAGATGGAATCTCAAGGAACCCTTAATAGCTGAAACAAACTTGA
187T	A00583:504:HM2HWDSXY:2:1513:4101:26537	TGTTTACGATATGACTTTCAGCTATTGAATTTTCCCCCACAGATGTGAAGGGATTAAATAAATCAGACAAGACATTATTAATGTCAATGCAGTTGGCCTTGTAGAATGACATTTGTCCAGAAGGCCTCCAAAGTTATCCTCAGTCACAGC

188T	A00583:504:HM2HWDSXY:2:1510:3079:23359	GCCATGGTTTACCAGATGCACAAGGCACTGTTCTTGAAGTGCTTACCTTCCAGTTGGGGGATATAAAAAAGGCACAAACAAGAGAATGAGTTAGAGAAACAGACCATGTGAAATCACACAAACACATGGACAGCTGGATTGACCATTTGGTCCCATTTTTCACTGTCATTTAACTTCTTAGTCTTCCTCATCTGTGAAAGAGAAGAAGAAGATGTGACTTACCTGTTT
189T	A00583:504:HM2HWDSXY:2:1510:26485:13228	TGGAATTTCCCTAGTGATCAGGGTGAGAGGACTGTTTCTGTTATTCATAGTAAGCC
190T	A00583:504:HM2HWDSXY:2:1506:9290:15201	CCTCTGAGGAAGTCTTCAAAAAGATACATAAAATACCTGTGACTCTATTAAAGATTCCTCTTAAGGAGGCAAACCCTGACCTTCGAGTGACTGAGTCTGTGACAT
3H	A00583:504:HM2HWDSXY:2:1502:4598:29121	TATACTAAAAGAGTAAGACCCTCATCAATAGATGGAGACATACAGAAAAAGTCAAACCACATCTACAAAATGCCAGTATCAGGCGGCGGCTTCGAAGCCAAAGTGATGTTTGGATGTAAAGTGAAATATTAGTTGGCGGATGAAGCAGATAGTGAGGAAAGTTGAGCCAATAATGACGTGTAGTCCGTGGAAGCCTGTGGCTACAAAAAATGTTGA
1P	A00583:504:HM2HWDSXY:2:1473:5095:19398	CAATTTATGGTTGCCAGGAATATAATCACTAAAGACTTGCTTCAGACCAAAGTCTTGAGGTCTTTTTCTGATGAAGAAGGGAGTGCCGTTGATCTGCTGTTGCTGTCAGACGTTGACATTGATTCATCTGACATTAGGTTAATCATGCCC
191T	A00583:504:HM2HWDSXY:2:1471:6262:9862	CAAAAAAGTAAAATAAAATAAAAGAGAAAGAAGAAATGTGCTATTCAAGATGACAGCAGGTATTGAATTTAAAACTTTTTTTCAAATAAGTTTTGGAAACTATTTTTTTTGTGACAGCTACTTATAATGTCTTTC
192T	A00583:504:HM2HWDSXY:2:1471:30526:30405	GCCTGGGTGACAGAGCAAGGCTCTGTCTCAAAAAAAAAAAAAAAAAAAGGTATGATTTACTTTTCATTTAACTGGGTGTCTGGTGAGACATTTCTCACCTGAGGCATGGATAAATATC
1G	A00583:504:HM2HWDSXY:2:1469:20347:7670	ATTAAAAATAGATGTATTCTTACTGGTCGTACTCATTCAGTATTACGAATTTGTAAGAATACATCTATTTTTAAT
193T	A00583:504:HM2HWDSXY:2:1468:26883:16705	CGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCTTTTTTTTTTTTTTTTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCAGGCTGGAGAGTGCAGTGGTACGGTCTCAGCTCACTGCAACCTCCAC
194T	A00583:504:HM2HWDSXY:2:1467:11912:4805	AAAATCTATGCACACAAATCAGTAGCACTGCTATATACCAACAGTGACCAAGGTGAGAATCAAATCACGAACTCAACCCCTTTTACAATAGCTGCAAAAAATAAAATAAAATAAAATACATAGGGATATACCTACCAAGGAGGTGG
195T	A00583:504:HM2HWDSXY:2:1466:28971:22921	GGAGGCCTAGGAGGAAAAAATGGTTTTATGGGCCAGGCCCAGGGCCCCCTTGCTCTGTGCAGCCTAGGGACTTAGTGCCCTGCATCCCAGCCATTTCAGCCATGGCTAAAAGGAGCCAAGGTATAGCTTGGGCTTTTGCTTCAGAAGGAT
196T	A00583:504:HM2HWDSXY:2:1466:19904:19617	CGCCATCCTCACCATCCTCACTGTCCTCGCCATCCTCGCCATCCTCAGAGTCCTCGCCATCGTCGCCACCGCTTCGCCCTTCGTCGGCCTGTTCGGCACCGTCTGGGGCATC
197T	A00583:504:HM2HWDSXY:2:1465:23339:35806	AGGTTTACTGATTTGGCTTTGATGAGGACTCTGAGCTGTATAACATGTACATTCATTCATTTAAATTATACATATATATATATATATATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAATCTCACTGTCACCCAGGCAGGAGTGCAGTGGCACAATCCTGGCTCACTGCAACCTCTGCCTCCTGGGTTCGAGTGATTCTTGTACCTCAGCTGCTCAGCAGCTGGCATTACA

198T	A00583:504:HM2HWDSXY:2:1461:8938:13495	TGGACAAAAATGACCACAGATAACTAGCTCTTAATATACAAAATTTGCAAAAAAAAAAAAAACATTGTGA
199T	A00583:504:HM2HWDSXY:2:1461:22679:24549	GACAGAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGAAAAAGAAAAAGAAAAGAAAAAGAAAAGCCTAGGCCAAGTATTTGGTAGAATGTTCTTCAATTTAGGTGTGACTGATGTTTCCTCATGAGG
133T	A00583:504:HM2HWDSXY:2:1460:4707:5447	CGTGTGCCCAGGGGTCCTCTGTGTGCCCAGGAGTCCTCCCCTTGCTTCTGACATGATTATTTACGCCCATGGCCTGCATGCCCATGCATGAGACATCATGGTTTTCCCTGTAATCGTTATCTCAAAACCAGCTTTCCCCTGTGGCAACCCTCCCTCCTGAGGGCATTTTCAAT
200T	A00583:504:HM2HWDSXY:2:1457:13060:7889	GTTTTTATCTTCATGTTCTATGTTGTTTGTAAGTACAGTGACCTGGTCAGTGGGCTGAGGGAGTCTGAGAAGTTGCTGGGAACACTTTTTCTTGCCT
201T	A00583:504:HM2HWDSXY:2:1453:30463:3552	CATTCAACTCACAGAGTTGAACTTATCCTTTCATTGAGCGGTTTTGAATCTCTCTTTCTGAAGAATCTGCAAGTGGATATTTGGAGCCCTTTGCTCCGTATGGTGGAAAAAGAAATATCTTC
202T	A00583:504:HM2HWDSXY:2:1451:5773:30592	TTCTCATATAGATTTATTCTAGTTTTCATCCTGGGATATTAGCTTTTTCACCATAGGGTGCAATATACTCCCAAATATCCCTTCACCAATCGTACAAACACAGTGTTTCCAAAATGCTGAATGAAAAGAAAGGTTTAACTTTGTGAGGTGAATGCACACATGACAAAATGGTTTCTCAGATAGCTTCGTTGTAGTTTT
3N	A00583:504:HM2HWDSXY:2:1451:26033:17832	CCCGCAATAATTCACCGACTCCCCCCTAAACTTAACCTAACCTTAGGGCAATCAGTCGCCACCAAACTCGACCAAACATGA
203T	A00583:504:HM2HWDSXY:2:1448:4345:5948	GAATGGAATGAAATGGAATTGAATGGAATCAACGCGAGTGCAGGGGAATGTAATGGAAAGAAATGCAATTGAATGGAATCATGCTGAATGGAATGGAATGGAATGGAATGGAATGGAATCAACCCGAGTGCAATGGAATGGATTGGAATGGAATGGAATGGAATGGAACAACCCGAATGGAATGGAATGTAATGGAGAGT
2P	A00583:504:HM2HWDSXY:2:1447:4969:12508	TCTGTTTCTAGAGAACCCAGCCTGCAACACAGTCCTACGTGATCTAGCTCCCTGTAGCCTCTCTGAATTCCTGCTCACTCTGTGCCAAGCACACTGGCCTTTGATATTTCCAGAGGATTGGC
14H	A00583:504:HM2HWDSXY:2:1444:3468:32174	ACCCAACAATGACTAATCAAACTAACCTCAAAACAAATGATAGCCATACACAACACTAAAGGACGAACCTGATCTCTTATACTAGTATCCTTAATCATTTTTATTGCCACAACTAACCTCCTCGGACTCCTGCCTCACTCATTTACACCAATCACCCAACTATCTATAAACCTAGCCATGGCCTGCCCCTTATGAGCGGGCGCAGTGATTATAGGCTTTCGCTCTAAGATTAAAAATGCCCTAGC
164T	A00583:504:HM2HWDSXY:2:1439:8793:23735	GTAATAATAGTAGCTATCTTGTACTATGCATTTACAATGGTCCAGGCACTCTTCCAAACTCTAGATAGATAGATATATACATACATACATACATACATACATACATCATACATACATACATACATAGCTAGGTAGATAGATAGGCAGATGAAGTTC
204T	A00583:504:HM2HWDSXY:2:1439:19822:17879	CCAGCTTTCAGTCCTGGCTCTGTCTCATCCTAGCTGCCTGCCCTGGGGCCACTCTCTGCTTCCTCATCCATAAACCAGTGGCAGGAATGCCCACCCCATAGACTCGTGGTGAAGATGAAATGAGCCACATATGCGGAAGCAGATGGCACC
205T	A00583:504:HM2HWDSXY:2:1437:19931:30248	CAGCTCCTCCGGAGTTTGAGGCAGGTGTTTGTGGCTGCAGTGGGCCGTGATCATGCCACTGCACTGAAGCCTGGGTGACAAAGTGAGATCGTGTCTCTAAAACATTAAAAAAAAAAAAAAAAAAAAAGGAAAAATGAGAGTGAGAACTGAAACAGC

206T	A00583:504:HM2HWDSXY:2:1436:20446:28260	CAGCTGGTGGCTTTCAGGGCCAGGGCAGCACCACACAGCACACCTCAGATGCCCAAACACGCTAACCCTAGAAACAGAGCCTCAGACAACTTGGTGCCAGAACTGCTCCTTTGGGCTTTTGTTTTGCTGTATTTTATTTTATTTATTTATTTTTTTGAAACAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGTAG
10A	A00583:504:HM2HWDSXY:2:1434:13196:5901	AGGAAACAAAAATGTACAGTTTTTGTCGTGCTACACGCTTGAGTTCCTAGGACTGCAAACTATAGCTTTAGCAGTTCTGTTTCTTGTCAAATACAAGCTATGTCCAAATCTGCTGTG
207T	A00583:504:HM2HWDSXY:2:1430:32389:9612	GGTTGGAACTTGCAGTTTGAAGCATACACCTAAATCTAAGATAGTTTTTTCTTTCTTTGTTTTTCTTTGTTTTTGTTTCATTTTTTAAAAGTCTGAGCATAAATAAGAGAGGTGGAAGTAAAATTTATGTT
208T	A00583:504:HM2HWDSXY:2:1429:2121:25175	GACAAATTCCTTTGGCTTTTACTTGTCTGGGAATGTCTTTTTCTCTCCTTTATTTCTGAAGGATGGCTTTGCTGGATACAGTATTCTTGGTCAGCAGGGTTTTTTGTTTTTATTTTTTTCTTCTTCAACCCTCTGAATATATTTTCTAAATTCCTAGAAGCCTATAAAATTTCTGCTGAGAAATCTGCTGCCA
105T	A00583:504:HM2HWDSXY:2:1427:18041:17018	TCCACGGCTTCTTCAAGACTGTACCCCCATCCAAGGGCAGCCGCTTGTCTTTTTACAGCTCACCCCAGCCCACACACACATACAAGCACACATAAACACACAGGCACACAATTCTG
13H	A00583:504:HM2HWDSXY:2:1424:1967:34898	CTCAAGGACTTCAAACTCTACTCCCACTAATAGCTTTTTGATTACTTCTAGCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACTGGGAGAACTCTCTGTGCTAGTAACCACTTTCTCCTGATCAAATATCACTCTCCTACTTACAGGACTAAACATACTAGTCACAGCCCTATACTCCCTCTACATATTTACCACAACACAATGGGGCTCACTCACCCACCACATTAACAACATAAAACCCTCATTCACACGAGAAAACACCCTCATGTT
22H	A00583:504:HM2HWDSXY:2:1421:28565:10661	CTCTTCTTAACAACATACCCATGGCCAACCTCCTACTCCTCATTGTACCCATTCTAATCGCAATGGCATTCCTAATGCTTACCGAACGAAAAATTCTAGGCTATATACAACTACGCAAAGGCCCCAACGTTGTAGGCCCCTACGGGCTACTACAACCCTTCGCTGACGCCATAAAACTCGTCACCAAA
209T	A00583:504:HM2HWDSXY:2:1414:11984:36276	GAAGACTATGGGAAAAGCATAGTATCTGGGCCAGAGTGCACCATTCCTCACAGCACAGTCCCTCAGGGCTTCTCTTGGCTAGGGGAGGGAGTTCCCCG
210T	A00583:504:HM2HWDSXY:2:1411:7554:31234	CAGCAGGAGAATCGCTGCCACAGCGCGGCGGTGGCGATATTTAAAGGGGACGCAGCCTATCTGGCAGGAGCAGCGCGCCAGTCGGCTCAGCCAATGCGCATGCGCGAGGCGCGAGCGGTTTCTCCCATCACAGTGGTTCCCACGG
211T	A00583:504:HM2HWDSXY:2:1411:22083:36824	AAACTCAGACATGGTAGTGATCCCTGCTGCACCTGGCTTGATGAACTAATGCAATGTGGGCTATAAACAGTCTTTTAGATAATGTTTAAAGCTCTTCTTCTAAGGCTTATTTTTGGGACAACATGTGATTTTTTTTTAATCCGAAGACACCATCCCGAGTGCTACACTGAAATATATGTGCTTCTGTTCTCTTTATTTTCTAAATGTGCTCATTATATTGCTAAAACAAATGCGAGGAGATA
7H	A00583:504:HM2HWDSXY:2:1410:19045:31908	GCCTCACTCATTTACACCAACCACCCAACTATCTATAAACCTAGCCATGGCCATCCCCTTATGAGCGGGCGCAGTGATTATAGGCTTTCGCTCTAAGATTAAAAATGCCCTAGCCCACTTCGTACCACAAGGCACACCTACACCCCTTATCCCCATACTAGTTATTATCGAAACTATCAGCCTACT
212T	A00583:504:HM2HWDSXY:2:1410:18774:32878	CACGCCTGTAGTCCCAGCTCCTCAGGAGGCTGAGGCAGGAGAATTGCTTGAATCTGGGAGGCAGAGGTTGCAGTAAGCCGAGATTGTGCCATTGCACTGCAGCCTGAGCAACAGAGCAAGATACTGTCTAAAAAAAAAAAAAAAAAAAAAAAATTAATAAACTATTAGGACAGTCTTGGAGGAAAAAGTCTTGGAAGAAAAAGTCTCTTGGGTAAGGATTAATTAACTGGTACACAGGCTGGCAAGGTG

18P	A00583:504:HM2HWDSXY:2:1406:28556:9361	GCCTGTCTTTGTAAATAAAGTTTGATTGGAACAGAGTCATGCCCATGTATCTACACATTGTCTGTGGATGCCTTTCTGCTATAATGGCAGAGTTGCAGAGTTGCCAAAGAGGACATATGTCCCACGAAGCCTAAAATATT
213T	A00583:504:HM2HWDSXY:2:1404:14868:25081	AGCATCCCGCTTTCCATTGACAAGGAGGTCAGCAAAAAATCACTAGCTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTCTTGCTCTGTCCCCCAGGCTGGAGTGCAGTGGTGTGATCTCCACTCACTGCAACCTCCGCCTCCCTGGTTCAAGGGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGTG
214T	A00583:504:HM2HWDSXY:2:1375:18222:13698	AGTCTGGCCCCTCCCTTTCTCTCTCTCTTTTGCTCCCGCTCTCATCATGTGACATGCTGTCTCCCTGTCACCTTCCACCGTTATTGAAAACTTCCTGAAGCCTCACCAGAAGCCAGATGTTGGTGCCATGCTTCCTGTACAGCCTGCAGAACCCAGAGCCAATTAAACCTCTTTTCTTTGTAAGTTACCCAATTTCAGGTA
216T	A00583:504:HM2HWDSXY:2:1374:29903:9878	GAAAGAAAGAAAGAAAGAGAGAGAGAGAGCCAGGTGTGGTGGCTCACGCCTGTAATCCCAGCACTCTGGGAGGCCAAGGCGGGCGGATCACAAGG
217T	A00583:504:HM2HWDSXY:2:1373:25554:21104	TCAGGTGAGGGAGGCAGGAGGCAGGGTCTGGGGACTGGGGGCAGCGGCTCGACCTCCGCTTTGGAAGGGAGAAGGGTTAGCTGGGTCCCACCCTGCTCTCCCTTCCCTTTCCTC
218T	A00583:504:HM2HWDSXY:2:1372:28510:21872	ATATTTTTTACTATGAAAATCATTATAATGAAAAAAATCAAAATTTAGTAAGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAGGTGACTTCATGGCTATGAACAGAGTTAAAAGGCCAGCAGATAAAGAGAAATGTCAATCTCT
1L	A00583:504:HM2HWDSXY:2:1372:24957:21480	GTGGTTCTCACCACCACCACCACCACACCGACCCGGCTCTGCGTGCTGCTGACGGTCCGTACCTGCAGATCCTGGAACAGCCGAAACAGCGTGGTTTCCGTTTCCGTTACGTTTGCGAAGGTCCGTCTCACGGTGGTCTGCCGGGTGCTTCTTCTGAAAAAAACAAAAAATCTTACCCGCAGGTTAAAATCTGCAACT
219T	A00583:504:HM2HWDSXY:2:1368:27877:19460	TAAGCCTGGGAGTTTGAGACCAGCCTGGGCAACATAAGGAGACCTTGTCTTTACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAATTAGCCAGGTGTGATGGTG
220T	A00583:504:HM2HWDSXY:2:1368:17372:10786	TGACTCAGCTCCTGGGTGTGGGCCACGTATCCAGATGAGCCAGTTTATGGGTTTAGGTGGCACCCGCTGATCTGTCAGGATGCAAGTTATGAAAAATACCTCAAACACCAATCTTAG
221T	A00583:504:HM2HWDSXY:2:1366:7247:24283	AATGGTTCCTTCTGTACAAGTTTTTCTCAGCTCTCATAAATTGCACAAAACAAAGAAATGTGATTCCTTCTATTTCGGCATTTGGTAGACCAATTTATA
222T	A00583:504:HM2HWDSXY:2:1366:20175:34898	ATATGTTTTATAGTGATAAATATGTCTTGTTTTATTATTCTTTAGGCTCCATATTTCTGAGATGTGTGTTTTTCTTTTTCTTTTTTTTTTTTTTAACACTTCTATTCTCACATCTTAATACCTTCTTTCATCTTGGAGGTGGAGCTATGTATGTGACCATAGGAACGTGAAGATATCTTATGATTTGGTAGGGAGGGAATGAAATTTGGATGTGAATGTGAC
39H	A00583:504:HM2HWDSXY:2:1364:2736:22795	CACCAATGGTACTGAACCTACGAGTACACCGACTAAGGCGGACTAATCTTCAACTCCTACATACTTCCCCCATTATTCCTAGAACCAGGCGAACTTCGACTCCTTGAAGTTGACAATCGAGTAGTACTCCAAATTGAAGCCCCCATTCGTAT
15A	A00583:504:HM2HWDSXY:2:1362:11406:27132	CTTATTTATAGATGCGCTAGACTTCAACATCTGTTACGAGTGCTACTAACTAGTTAGAAGTTGTCCCATGCTTTCGCATTGAACTTACCCCACCAACCTACCG

273T	A00583:504:HM2HWDSXY:2:1359:11379:20823	GATCCACGGGGACGGGACCCAGGAGGTGAGGATCCACGGGGATGGGACCCAGGAGGTGAGGATCCACGGGGACGGGACCCAGGAGGTGAGGATCCACGGGGATGGGACTCAGGAGGTGAGGATCCACGGGGATGGGACTCAGGA
223T	A00583:504:HM2HWDSXY:2:1356:8883:18161	CCAGGCTGGCCATGCCACGTGGGAGATGGAGTTATTACTCAAATCAATCTCCCCCAAGAGACGGAGTTATTACTCAAATCAATCTCCTCCAAAATTCTCAGGCTCGGGTTTTTCAAGGATA
28H	A00583:504:HM2HWDSXY:2:1355:24442:1141	GCCACATATCCCTCGTAGTAACAGCCATTCTCATCCAAACCCCCTGAAGCTTCACCGGCGCAGTCATTCTCATAATCGCCCACGGACTTACATCCTCATTACTATTCTGCCTAGCAAACTCAAACTA
2N	A00583:504:HM2HWDSXY:2:1348:32488:25066	CCTTTAGCTGGAAACTTAGCCCATGCAGGAGCTTCAGTTGATCTAACAATTTTCTCCCTACACCTTGCAGGTGTATCATCAATCCTAGGGGCTATTAATTTCATTACCACAATTATTAACATAAAACCTCCCGCAATGTCTCAATACCAAACACCCCTGTTTGTCTGATCAGTACTAATCACAGCCATACTAC
224T	A00583:504:HM2HWDSXY:2:1348:20826:5368	TCAACAATCTCCTGGACAGTTTGAAGTTATTCTGCAGGCATAATTCCCTTTTCCTTGGGTAATGTCAGTCTTTTGTTTCTCTCTCTCCTTTTTTTTTTTTTTTTAGTCAGAATCTCGCTCTGTCACCCAGGCTGGAATTCAGTGGCATGA
16H	A00583:504:HM2HWDSXY:2:1346:2302:18630	GGGCCATACGGTAGTATTTAGTTGGGGCATTTCACTGTAAAGAGGTGTTGGTTCTCTTAATCTTTAACTTAAAAGGTTAATGCTAAGTTAGCTTTACAGGGGGCTCTAGAGGGGGTAGAGGGGGTGCTATAGGGTAAATACGGGCCCTATTTCAAAGATTTTTAGGTGAATTAATTCTAGGACTATGGG
18H	A00583:504:HM2HWDSXY:2:1343:6045:34475	AGTCAATACTTGGGTGGTACCCAAATCTGCTTCCCCATGAAAGAACAGAGAATAGTTTCATGTAGAATCTTAGCTTTTGGTGCTAATGGTGGAGTTAAAGTCTTTTTCTCTGATTTGTCCTTGGAAAAAGGTTTTCATCTCCGGTTTACAAGACTGGTGTTTTAGTTTTTACTTCATGGACAGGCCCATTTGAGTATTTTGTTTTCAATTAGGGAGATAGTTGGTATTAGGATTAGGATTGTTGTGAAGT
7A	A00583:504:HM2HWDSXY:2:1343:4878:18176	GCATGGAAGAGGCACACGCAAGAGGGTGCATGGCAAATGGGGAAGGTGTAGAGCCAAAGGAAGCAAGAGGTGGGAGTTAGCAGCAAACTGAACACATAGCTAAGACTTATTATTTTGCCAGATCTGAGGCTTAATCTGCT
9H	A00583:504:HM2HWDSXY:2:1342:30843:10473	ATTTACCGAGAAAGCTCACAAGAACTGCTAACTCATGCCCCCATGTCTAACAACATGGCTTTCTCAACTTTTAAAGGATAACAGCTATCCATTGGTCTTAGGCCCCAAAAATTTTGGTGCAACTCCAAATAAAAGTAATAACCATGCACACTACTATATCCACT
4C	A00583:504:HM2HWDSXY:2:1339:8621:32487	CGGGCGTAGTACATCTCCAGTCGTTCCATCTCCCGCGCAGTAACAGTGTCCGGATTTACTCGAGACTCAAGGGGGATGGCGTATGCTGTCACCACCAGAAGAATCCAACTCACCAGGAAAAACAGGGCGGAAACAAAGCAATAATCCACC
4H	A00583:504:HM2HWDSXY:2:1332:10447:13197	TATTGACTCACCCATCAACAACCGCTATGTATTTCGTACATTACTGCCAGCCACCATGAATATTGTACGGTACCATAAATACTTGACCACCTGTAGTACATAAAAACCCAATCCACATCAAAACCCCCTCCCCATGCTTACAAGCAAGTACAGCAATCAACCTTCAACTATCACACATCAACTGCAACTCCAAAGCCACCCCTCACCCACTTGGA
6A	A00583:504:HM2HWDSXY:2:1330:20112:31000	TGTGTCTCCTGCATTGCAGGTGGATTCTTTACCACCGAGCCACCACAGATAATTTGTGTAAAAGTTCTTTTAAGTTGTGGTGTGCTCAGCAAAGATGAACTCTTACTTCTGGCGATTCA
3P	A00583:504:HM2HWDSXY:2:1324:30626:15107	AGCAGTGTAGTGACTGTGTAGTATAAATATGGAAACCAGCATTTTGAGGCCTTTGGTCAATAT

225T	A00583:504:HM2HWDSXY:2:1322:13331:4570	GGAGGTTGCAGTGAGCCGAGATCACACCACTGTAATCCAGCCTGGGCAGCATAGTGAGACTCTGTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAGAGAAAGAAAGATTAAACTTTTGTCTTTACCTTTGTCTTTATTACAAATTATTTTCCTGACAATCATTTATCCTTTGACTATGTTTATGTCTTTTGCCATA
226T	A00583:504:HM2HWDSXY:2:1321:12852:25285	CCCTCCCTTTTGTGCCTGCTCCCTTCAAAACACACACACACACACACACACACACACACACAGCCTTAGCTTTTTTAAAACATAGGGGCTAGGGAGAAAAAAATAGAGAGCCAT
227T	A00583:504:HM2HWDSXY:2:1319:15076:23062	AACTATTGGGAGATTACGGCTCCATATGATAAAATAGCATGCCCTAACTTTCTTGGTAGGTTAAAGAATGTCCATTACCATCAAGAATTCA
152T	A00583:504:HM2HWDSXY:2:1314:4354:9345	TACAGGCATGAGCCACGGCGTTCGGCCAGCTGTTTCTAGATTCTGTCACTGCCCTGACAGTTTCTGCACTGAATACATATACGTACATACATGCGTACATACATACATAGATTTTTTCATTTAAAATGTTTAGGCCGGTTGCGGTCCTGTAATCGCAGCACTTTGGGAGGCAGAGGCAGGAGGATCACTTGAGCTCATGAGTTCGAGACCAGCCTGGGAAACATGGCAAGACCCTGTTGCTACAAAAAAAACT
66T	A00583:504:HM2HWDSXY:2:1311:24306:23140	GAATCTTTTTCCTCAATTTTTGGAAGATTTTCCTATTCAGAGCTCTCTTGGGCTTGCAGAATTCTATTTATGCTTAACAGTATCAAAGAAATAAGATCAAGAAACACTCAATAAAACAAGGGAGTTTATCTCCACTGAACATGGG
3C	A00583:504:HM2HWDSXY:2:1310:23357:5869	GTGTAATGAATGTGGGAAGACCTTTGGTCAAAATTCAGATCTTTTAATTCATAAGTCAATTCATACTGGGGAGCAACCTTACAAATGTGATGAATGTGAAAAGGTTTTCAGTCGTAAATCAAGCCTTGAGACACATAAGATAGGTCATACTGGAGAGAAACCATACAAATGTAAGGTTTGTGACTTGGTTTTTGCGTGTAATTCCTTTCTGGCAAAACATTCTAGATTTCTTAGTGTAGAGAAACCTTACTAGTTTAATG
228T	A00583:504:HM2HWDSXY:2:1310:13313:9361	CAGATGTGCAGAGAAACTGAGGTTTCTTTACTTCCTATGTATGACCTGACCTTCATGAGCTCACCCTGCTGGGTGATGGGGCAGTTTGTGTGTGTGTTTGTGTGTGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTAAGGGAGAGTGTATTAGTCTGTTCTCATGCTGCTAATAAATATATAGCTGACACTGGGTAATTTATA
230T	A00583:504:HM2HWDSXY:2:1308:29116:23422	CATGTGACAAACTATATTAGTCAGGGTTCTCTTAGAGGAACAGAACTATATATATATATATATGTACAGGAGTTTGGCCGGGCATGGTGGTCACACCTATAATCCCAGCATTTTGGGAGGCCAAG
231T	A00583:504:HM2HWDSXY:2:1307:16857:15029	CCGCGGGGTCAGGGTGGAAAAAGCCACAGCGGAGAAAAAGCCGCAGCGGCGGGGGGGCAAAAAGCCACGGCGGCGGGGGGGCAGAAAGCCACGGCGGCGGGGGCTAAAAAGCTGCTGCGGGCAAAAAGTCGCGGCGGCGGGATCGGTT
232T	A00583:504:HM2HWDSXY:2:1306:18367:29575	TGACGTGACATGATCAATAGTTATATAGTTATATATCCTTGATGTGCAGGTCAGGGTATAGACAGCACATAAGGAATAGCAAGGGCAGAATGTCTACCACATGTTTGACCACAAACCATTTTTTAATTCCTGGGCACACAAGAACGTGTACTACCTTTCCCAGTCTCTTATGACCAGTGGGAACTAGAACTGAGTTCTGGCCAATTGAATGTGGCAG
233T	A00583:504:HM2HWDSXY:2:1277:28158:13338	GGAGCTAAAAACATCACCTGTGCATTGGGGTTATATCTGTTTTACCATGTTTACGCTCATGAATGCCTTACAAATTCTGTGTTTGCAGTTTGGGTAAGAGTAATGCAGAGATGCTCAAGTTCAGATTCTTCTTGAGAACAATTACTAAAGTCAACAGAGTCTGGAGGAAAGCAATTGCTTAATT
234T	A00583:504:HM2HWDSXY:2:1277:23357:1924	GCTGGAAGCCATTATCCTCAGCAAACTAACGCAGGAACAGAAAACCAAACACCACATGATCTTATCATAAATGGGAGCTGAACAAGGAGAATGCATGGAAATGG

235T	A00583:504:HM2HWDSXY:2:1276:3812:3740	AGAGAAAAAAAAAAAAAACAGCAAGATACTATCTCACACCCATTAGGATGGCTACTATATATTTAAAAAATTGCACCTGTAGTCCTAGCTACTTGGAACACAGAGGCAGGATTGCTTGAGCTCAGGAGGTCAAGGCTGCAG
13A	A00583:504:HM2HWDSXY:2:1276:29487:24565	AGGTCTTTAGTGCTTGATATGACAAAAAATTACACTGCAGTCTTCCTTCAAGGAGCTATGAGTTGCATCTTTGCTCAACAGATACCTATTTC
236T	A00583:504:HM2HWDSXY:2:1273:4146:7012	GGCACTGCACCTGGCTGAAGAATCACAGCTTCTAAAGGCAGCAAAGATCTTTGCCGAATTGTATTTATTTAACTTCATTAATTGAAAAGAGGCATTGGTGGGTCAGTTCTCTTTCTTCTTTTTTCTTTTTTCCAGTCAGTGTATTCTATA
237T	A00583:504:HM2HWDSXY:2:1273:27905:33849	TGAAGGGGCCTCAGAGCAGAGAAACAGAAAGAGCTGAGAAGCAACGTTGCCCTCTTGAACATTTCTGCTCATGGCCGAAGCTGACTGAAGCGGTTTTTCAAAGAACATCTTCCCAGAAGGCTGGTGGACAACTTGGAGGTCTTTTATGAGTCAGAGACAGCTAGGCTTTCCTAAGGAGCTGGAAGTCAGGGCATGTCCACCCAGACAGAAGAACAGCTACCCTGGG
238T	A00583:504:HM2HWDSXY:2:1263:29839:26115	TGACTTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTGGGGTTAAAGGCATGAGACACTGCGTTCATCCACCTCCTATTTTACTTGGGAGAAATGCACAGATTCTGGGTGCCATGTGCATTTGTTTTGGGAGTGATAATTGATCTAACTTATGGAAATAATACTAAATAGTTAGCGGATGGATTCTGCATCTGATGAGAGTTTTGGGCAAAACGAATTCCTAGTTTCTGAGTCTTATTTTTCCCCTGATTCAAGAAAACTGTGAATTA
215T	A00583:504:HM2HWDSXY:2:1260:21531:31641	TGTGAATGTACTAAAAACCATTAAATTGTACACTATAAGTGGGTAAATTATGTAGTATGTAAATATATCTCAATGAATCTGTTATTTAAAAAAGATAATAGTAGCCTAAATATGAATGATATTCAGGTGTTTAACTATTCTCAAATATCATTTTGAATCTTCTGCTTTAAAATATCTTCACAGAATTTGGAAACTCTTCTC
19P	A00583:504:HM2HWDSXY:2:1254:15212:24048	AAAGGCAGCAACAGAATTCCTGGAGAAAGTAAGACATTGGAGAACTGCACAGCACCTCTTCTTGGGGTCTGGGGTTACCCAGACTTAGGGAGAGTTCACCTTCTGGGAAAAACTAAACTTCGGTTCTTGTCCTTTTTTGTTCTTATGGCAAGACCAAAATTTCAGAAAACCAAGATGAAGCACCAAGCTAAGGTGAAGTACTCTCTCTCTCTTTTCTTTTTAAGAATATCTAATACCAAGGATGATCCAT
10H	A00583:504:HM2HWDSXY:2:1253:1190:14575	TATGTCGCAGTATCTGTCTTTGATTCCTGCCTCATCCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACATATTTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAATAACAATTGAATGTATGCACAGCCGCTTT
239T	A00583:504:HM2HWDSXY:2:1250:11071:6825	ACAGGCAGGTCGTGTAGATAGAGTGGATCTGCTGGACAGGCAAGTAGTATAGATAGGGCGGGTCTGCTGGAGAGGCAGGTAGGGGAGATTGCGTGGAACTACTGCCCAGGCAGGTAGTGTAGACAGGGTGGATCTGCTGGCCAGGCAGGTAGTGTAGACATGGTGGACCTGCTGGACAAGCAGGTAGTGAAGAC
32P	A00583:504:HM2HWDSXY:2:1249:11831:15374	ATCCTGGAAATGATTATGTGGTTTTTGACCACAGGAAAAAAGGTGGTGATTGGGGATCTAACAATAGATTTATTAAGAAAAAATTGTGTCAAATAAACACAGA
240T	A00583:504:HM2HWDSXY:2:1248:31123:32002	GAAGTAACCCTTTCTACCCCATCCCATCTCCACCCACACGTCTACAAAAAGAATTTTATGCAAGACACAGATTTTGAAGCACATAGAGGAGGAGCTAACATGAGTTGCT
130T	A00583:504:HM2HWDSXY:2:1244:27868:13495	TCTCATATCCCTAGCTCTCAGTAGAGGTGGCATTATCTTCATATAATCCCTGTCCCTAGGTCACTATTTTATATGTCTACATT

27P	A00583:504:HM2HWDSXY:2:1244:15600:27978	AGAAAGTAGTACCTACCAATGCAAAACATTTCTGTGCTTGTGCCAGAGCAGACTCAGGTCTTAACCTAATACATTCATCAAAATCTGCCACTGCTTCTTCAACTTGATCAAGGAGTATTTTCAGCTAAGAAAAAAATACGTAAATAAATGTAATTCAACTAGGTGCACCAGTT
241T	A00583:504:HM2HWDSXY:2:1238:26069:32988	TGCAAGCTGGAGATAAACTTATTCTGAGGCATAGGCATGCTATGTAAGTATTTCATATTTGTTCAGAAGGCCTATGCTTTCATACAGGTATAGATACGTACATATCTATCAGCCATCTATCTATCTTTCTCTATTCTGAGTGAGAAATAGA
3L	A00583:504:HM2HWDSXY:2:1237:22064:30091	TTATTTTCATCGTAACATGAACAGTTACTCAATTTTCCAGTTGCAATTCCCATTTGGCTTGTGTTCCATGTTATCCTTCCTCCTTTCTAGACACTCTGCTTTTTTTTTTTTTGTAAAAAGGACAGCTCATATTCAGCCTTTTCACTTTTGTTATTTGCCTTGCAAGAACAAACTCAAAATTGCTTGATCCAATATGATTAACAACGTGCATCCCAAATAAAGCAAATTCCACTCTGTGGTGTGTGACAGAATGCAAAAACAGGTTAGCATCCT
34H	A00583:504:HM2HWDSXY:2:1236:31114:1830	GGTTAGCGAGGCTTGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTTGAGAGAGGATTATGATTCGA
7G	A00583:504:HM2HWDSXY:2:1235:5773:17002	TGAAGTAGTTCAACATATTGTTGTGCGAAAAGTAGATTGTGGTACTCTTTATGGTATAAATGTCAATAATTTATCAGAAAAAAAAAAAGAATTTTCAACAAAAATTAATTGGGCGGGTAATTGCAGAAAATATATATATAGATCATAGATGTA
242T	A00583:504:HM2HWDSXY:2:1232:14127:30405	AAGGGCGGTGCAAGATGTGCTTTGCTAAACAGATGCTTGAAGGCAGCATACTCGTTAAGAGTCATCACCACTCCCTAATCTCAAGTACCCAGGGACACAAGCACTGCAGAAGGCCGCAGGGCCCTCTGCCTAGGAAAACCAGAGACGTTTATTCACATGTT
8C	A00583:504:HM2HWDSXY:2:1230:3568:21543	GGCACCAGCTGCTGCCCAGGGTCCCTCACGCCGCCCCCTCCCCACTGTGCAGAGTCCCACACACCACACACACCACCAAGTGGGTGTCCAGGCTCTGGGCCTTCACGCCCCACCCCACCCCACGAGTAAGAGGCAGATGGTGTCACTGCAGGGCCCAGGG
4P	A00583:504:HM2HWDSXY:2:1230:3568:21543	AGGCACCAGCTGCTGCCCAGGGTCCCTCACGCCGCCCCCTCCCCACTGTGCAGAGTCCCACACACCACACACACCACCAAGTGGGTGTCCAGGCTCTGGGCCTTCACGCCCCACCCCACCCCACGAGTAAGAGGCAGATGGTGTCACTGCAGGGCCCAGGG
46T	A00583:504:HM2HWDSXY:2:1230:25943:33739	GATTGCTGAGAATAATTAATTGGTTAGTACTCGGATCCTTATGCATTTCTCCTGCCTCTTCCCCCTCACTTTCCTCAAATGCTATAGAGATATCATAAAAGTAAGTTACTGAAATAAAGGCCCTATTATGTCTGGGTATTTCCTTTTCAAAGCGCTGGTTAGTGCC
243T	A00583:504:HM2HWDSXY:2:1228:31412:6198	GAAGCTGAGGCAGTAGAATTGCTTAAACCCTGGAGGCGGAGGTTGCAGTGCACCAAGATTGTGCCACTGCACTGTAGCCTGGGCAAAAAAGAGCAAAACCCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAATTGAAGTAATAATAGC
185T	A00583:504:HM2HWDSXY:2:1226:19388:5415	TGGGATGCTCCTCTAGTACCAGGTACTCAGGAGGCTGAGGTGGGAGGATTGTTTGAGACTGGGAGGCTGAGGCTGCTGTTAGCCGTGATCACACCACTGCATTCCAG
244T	A00583:504:HM2HWDSXY:2:1223:3794:27070	GAGAAAAGTTTACTTTTCCCAACAAAGTTGAATAGCTTTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGCACCATCTCAGCTC
245T	A00583:504:HM2HWDSXY:2:1221:31159:15405	CAGAACAGTCACCAAAAATTATAATATATGAGGCTTTGACCCAATTACACTACCAAACATCCCCCATTAAATTTTTCCTGTGGATTTAAAACTCTTTATCTGTAGGAATCCTG
11A	A00583:504:HM2HWDSXY:2:1214:7392:4492	ATCTTAAAATATAAAAATGGGGATTTTTTTTCCCCCCAGCCACTAGGCACTTCTGGATACTTTCACTTCAGAGATGCTGTTTCAGTGTCAGTTGGATGTTTTGCCGACTTCATTATTTATCTGCATTAACGCTGTGCTTATCCTAAACAATCTCACGTCACTGCTCAGAAGCACGCCAGACTGAGCTGCCCTCCCCCT

153T	A00583:504:HM2HWDSXY:2:1212:10782:10895	ACTGGCCAGGAGAATAAGTTTCTGCCAAGTGAGTGGTTAAAAAAAGGCAGACTGGAAAAATAACTGTGGGATGGTAAGTATTTCTTTATTTACAAGGCTAACATAAGTTCTCTCCATGTGTTGGGTTTGGAAGAGGGGATGGATTGGTTA
246T	A00583:504:HM2HWDSXY:2:1208:31259:20682	GTGTGTCGTTTCTAGGCTTTTTCTTTTCTTTCTTTCTTTCTTTTGACAGGTTCTCACTCTGTCATCCAGGCTGGTGTGCAGTAGCACAATCACAGCTCACCTCAGCCTCGACCACCCAGGCTCAGGTGACCCTCCCACCTCAGCC
247T	A00583:504:HM2HWDSXY:2:1205:16107:32894	CTGGTATCTGCTTCTGGTGAGGCCTCAGGAAGCTTACAATCATGGCAGAAGGCCGCAGGGAGCCAGCATTTTACATAGGAAAAGCAGGAGCAAGAGAGAGAGTGGGGAGGTGCCACACACTTTTAAACAACTAGATCTCATGAGACCTCACTCAGTATCATGAGGACGGCACCAGGTCATTCATGAGGGATTCACTCTTATGACC
5P	A00583:504:HM2HWDSXY:2:1204:8540:20791	ACCCTCCGGCCAGGACGGAGGAGATGCGGCTGGAGCCGCCCCCGATGCCGCAGGAGCCCTTCATGGAGCTGGAGGAGGTGAACTGGCGGCTGCAGGTGCTCATGGTGCCGAGGAGGGAGGTGAGTGAGCGAGCAGTTGGCTGAGTGAAGAGAAGGTGCTCAGGT
248T	A00583:504:HM2HWDSXY:2:1202:28058:15295	GGTTTCAGGGAGATGATAATCCACACTTTGTAAAGCAAATGTCATATAAAATTGACAAAATAGAAATGAAAGCAAAAACAACCCTCAAGAGCAAAGCTGTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTTAATGAACATAGTAATTCAGGTCATTTTCTGGTGCCTAAAGAAAAATTGAGAACTTCAGATTAGGCTGGAGGGGGGAAGTTCATCACC
249T	A00583:504:HM2HWDSXY:2:1175:23827:11287	GCGGTATACAATATGTAAATGAATGAGTGTGGCTGTATTCCCATAAAAGTTTATCTTTGGATGCTGAGATTGGAATTTGATAGGTTTTTCATGAAATAGTCTTCTTTTTAATTTTTCTTCAACCATAAAAATGTAAAAAACATGATTAGCTCACAGGCAGTGCAAAACCAGTTTGTTAACACTTGCCCTAGGGCTTTGGAATCCTTACTTCCAGCCAGAGGCTGGAGAAAGGATCTTGCATGGGAA
250T	A00583:504:HM2HWDSXY:2:1171:7835:11365	TGCCTCAGCCTCCCGAGAAGCTGGGACTACAGGCGCACGCCACTGCACCTGGCTAATTTTTGTATTTTTAGTAAAGACGCGGTTTTGCCATGTTGGCCAGGCTG
251T	A00583:504:HM2HWDSXY:2:1169:10248:19774	CAGAGCAAGATTCTGTCAAAAAAAAAAAAAAAAAAAAAAAAAGAAGTTATAGCACCTCTGTATTTCTCAAAATTATTTTTGCCTTCTCAATAGCACTTGTGCCAACTTAGCTCTGATTTGGCCTATGAAACTCTCTTTTAATATAAATCTAAAAATATAATTTAGCCAGTACC
65T	A00583:504:HM2HWDSXY:2:1168:28628:25895	TAGGCACCTTCCCCCTACTTTCCTTTCCTAAGGATCCACTTCTGAAAAGCCTGGGATTTTGCCTCCCTACCGTAATCCTATGGGTTGGCCTTGATAAGAAGCATGATACCAACTTCCCTGAGATCTGATAAAACCCCATTTGGGGAACTCTGATTTCCTCCTTCCCCTTTTCTGCATCGGAC
1N	A00583:504:HM2HWDSXY:2:1166:28022:12759	ACCTAGAGGAGCCTGTTCTATAATCGATAATCCACGATTCACCCAACCACCCCTTGCCAGCATAGCCTACATACCGCCGTCGCCAGCCCACCTCTAATGAAAGAACAACAGTGAGCTCAATAGCCCCTCGCTAATAAGACAGGTCA
252T	A00583:504:HM2HWDSXY:2:1165:33003:5134	GTTGATATATATATATATATATATATATATATATATATATATCCCCTAGATAGTGTGTTATTGATTTTTTAACATATTCTGTTCATGTTTAGGTATGGAGGAAAGTTTTCAGTCCACAGCAGCTTTGCATTTGACAGATTTTCAAGTAACCATTATCTGAGCGAA
253T	A00583:504:HM2HWDSXY:2:1164:30798:29935	GAATAATATTCCTGATTTTTCTTTTCTATTAACTGTGGATTATCCACATTTTAGGAAAATCAAAGATTGAGTTTAAAGATTAAAAAAAGTTATTAGCAGAAACTTTGAATTTTTAAATTCATCAAATTCATAGATACACAAAACTGGTAATAATGCAGTAAAAACAAATTTTATTCAATAACTAATTTAGTATGGAAAGGAGCTGGGCTCAATTCCAATATGTTCAGAGGT
254T	A00583:504:HM2HWDSXY:2:1162:30861:1548	CAGCCTTTTCTTTTCTTTTCTTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCACTCTTGTTGCCCAGGCTGTAGTGCAATGGCAGGATCTCAGCTCACCGCAAACACTGCCTCCTGGGTTAAAGCGATTCTCCTGCCTCAGCCACCTGAGTAGCTGGGATTAGAGGCATGCACCAC

255T	A00583:504:HM2HWDSXY:2:1161:2148:6308	CGGGAGGGTGAGGCAGGAGAATCACTTGAGCCCATGAGTTGGAGGCTGAAGTGGGCTATTATGGAGCTACTGTATTTCATCCTTATTAACAGAGTGGTACCTTGTCTCCAAAAATTAAAAATGAAAAAAAAAAAAGAAATTACAAAATTTTTTAGTTATCAATATATATTTGGCAATAACAAATTTAAAAGCATTCG
256T	A00583:504:HM2HWDSXY:2:1158:8666:4570	AAATCACACACTCCAGGCTGGGGGTGAATGCACAGAGATCTGTCCACAATGAAATATTAAATAATTACTGTTAAATAGCTCATCAAAGCTTTGGGGGTGGGGGTAAAAAGTTAAGCTTCTTTAAGGAGAGTCCTGCTGCAAACAAGAAAT
257T	A00583:504:HM2HWDSXY:2:1154:7798:33379	GTGGCGGGCGCCTGTAATCCCAGCTACTGGGGAGGCTGAGGTGGGAGAATCGCTTGAACCCAGGAAGGCGGAGGTTGCAGTGAGCCGAAATTGCACCACTGCACTCCAGCCTGGGCAACAAGAGTGAAACTTGGTCTCCAGAAAAAAAAAAAAAAAAAAAAAAGAAGGCCAGGACTTGATCACACCATTCTTTGACTACTGTGTGGGTTCTAGGAGGGAAAGGAGA
258T	A00583:504:HM2HWDSXY:2:1154:16179:8688	GAGAAAGGCATGAACACAGGAGGCGGAGCTTGCAGTGAGCCGAGATGGCGTCACTGCACTCCAGCCTGGGGGACAGAGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAGCAGAAGGCAAGGCCCTATCCTGGTAGCTGGGGAGAGGAACCTGA
259T	A00583:504:HM2HWDSXY:2:1147:28420:27445	GTGCACGTGTAGTCCCAGCTACTCGGGAGGCTGAGGTGGGAGGATCCCTTGAGCCCTTGAGCCCAGGAGGTTGAGGCTGCAGTGTGCTATGATGGCAC
260T	A00583:504:HM2HWDSXY:2:1147:1108:34851	AATACAATCGAGGAGCAGAAAAATGCAATAAAGGTCATCAACAGTAGACCTGATAAGGCAGAAGAAAGAATCTGTGAACTTAAAGAAGAAATTATATAATTAGAACAGAAAAAAAGAAAGAAAGAATGAGAAAAT
261T	A00583:504:HM2HWDSXY:2:1140:9842:4977	TAGACCGAGACTCCGTCTAAGAAAGAAAGAGAGAAAGACAGCAAAGAAAGAAAGAGAAAGAGAGAAAGAGAGAGAGAAAGGGAGAAAGGGAAGGGAAAGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAACGGAGAAAGAAGGTGTTCTGCGAGAGGGAATAATAGCATAGTAAAATTTCAAGGAGTTTTGGG
154T	A00583:504:HM2HWDSXY:2:1139:21504:28651	GGCCACCATTTTATTTTCAACTCCCTTTCATGGAAGAACGTTTAGCCTTTGGTCTCTTTCTTGATTTATGACAGCTCGCGGCTTTCAAGAAAACTACCT
6G	A00583:504:HM2HWDSXY:2:1138:9932:3944	CCAAAAACCGATCAGGAGATAAGAGCACATGCCCACAAGTTCCCAGAACACGTATACTTGGACCAAATTAGGGCTAAGAACCAGACCTAGCATCGAGGCGGTAAACAAGCTAAGATAAACAAAAAAGCGGACGTATCCCTG
4L	A00583:504:HM2HWDSXY:2:1136:27082:4366	GCTCAAGTCATACTGGTCAACCCTGGACTACAAGATTGCCAGTCAGCAGAAAGAGGAAGACTCCACCAGATGAGTTGCAGGCCCCTGGTAAGCCCAATCTCTAACTCATATTCATAGATGGTCAAGTGACTGTCCATGTGTTTGTGGTCATCTGTACATTGTCCATACTTGCTATATTGTTCTTCATGAAGGATTGCCCATGAAAGAGGTTGC
20P	A00583:504:HM2HWDSXY:2:1133:3784:7138	TGTGCGTCCATTACTGCTACACTGACACCGGGTGAGTGCTCCTGGGCTGATGCTCCGGGTCCAGTGCTCCCAGGTGGTCATAGTACACGCCCCTGCCTCAGGCAGCAGGGCTGCAGGTGGC
262T	A00583:504:HM2HWDSXY:2:1129:2953:36198	GGTGAAGCAAACTTTGATTGTTAAATTATTATTGTTGTTGTTGCAGAGGTTCTTTTTAAAAACTTTGTTTGGTTTGGTTTATACACAGAAATATCTAGAAATGTTCTGGGACTAGTTGAGTTGTATCTTTAGTATTCAGGTTGTGAAAAATTAAGATGTTTGGCTATGCACAAAATAGTTTGTATGCTTTGAACTTTAGTTTACTTGGAGTTTGATATGGTTT

108T	A00583:504:HM2HWDSXY:2:1128:16052:24596	TAAAAAACTAAAAAAAAAAAAAAAAAATTCCAAACTCTCCACAATCTAATTGTAAATTGAAGAGTCTAAATTAAAATGCCGTTTATGAAGCTGGGTGAGATGGCACACACCTGTAATCCCAGCTACTTGGAAGGCTGAGGCAGGAGAATTGCTTGAGCCCAGGAATTTGAGGCTGCAATGAGCTATGATCATGCCACCACACTCCAGCCTGGGCAACATAGTGAG
263T	A00583:504:HM2HWDSXY:2:1125:25183:10723	AACCTTGGCAGAAGCCAAAACGGTCAGACAGTGTTGTGTAAAAATGATCACCCA
264T	A00583:504:HM2HWDSXY:2:1124:28339:10927	GGGAGGGGAGTGGGGGTTACCTGCTGGAGACTGTGTGCTATTTCACTAAAGGTGGTGTTGGCTTGGGGCAGGATACTGGCCAGTAAAGGTTTTGATGCCTTCTCTGTGCCCCCCAAGAAGGAATGATTGTTCAGAGTGTGGGAGGATACCCTGTTCTCCGCACAGTTTTACCACAAAGGCCAGGGTGGGGCTTTCTGGCTCTCTACCCACCAAAGCTTCATCTACAATGGCAATTGCTGGGAGTGGCAGGGGCATACTACATTTCCATTTGCTGGTGGGGCA
2G	A00583:504:HM2HWDSXY:2:1120:8386:24596	GAGGGTCAAGATTCCCTCACCCGGACAAGGCGTCAGACGGTGACGTGAGCGAGCCCGGAGACGCCGGCGTCGGCCCTGGGAAGAGTTTTCTTTTCTTCTTGAC
265T	A00583:504:HM2HWDSXY:2:1120:28682:27305	GCTCTTATTTTTGCAGCCTTTGTGGAAAAATCAAAACTCATTCATTTGCAAAGTTATTTCCATTGACTCCTTGCAATGTGCCTGGTACATTCTGCTCAATAAATGATGAGAGAATGAGTGAGTGAGTGCATGAATGACTGAATTAGTGAGTGAAGGAATGCGTGACCAAGTGAATGAATGAGTGAGTGAACAAGTGAATGGGTCAGTGAGTGAATGAGTGATTGAATGAGTGAGCAAGTAAGGGAATGAGTGAGT
274T	A00583:504:HM2HWDSXY:2:1120:19090:27665	CTTTTAGAGTGTCATGAATTAAACTAAAAATCTCAGGAACTATCTCTCTCTTTCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCACACACACACACACACACACACACACACACAACAAACAAATAAAAAACACACATTTTGACTTGAAGTTTTACTTTA
266T	A00583:504:HM2HWDSXY:2:1120:16721:21183	AGGTGGGTTTTACTCAGACTGCATACTGTGAAAAGGATAAATTAGTGTGGTTTGTGAACTAGATGTGGAAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGAGAGAGAGAGAGACCAATCCCACCATGAGGACCCGGAAATGGAGTTTGATTTGGG
8H	A00583:504:HM2HWDSXY:2:1118:21377:12618	GTAAGGTCAGCTAAATAAGCTATCGGGCCCATACCCCGAAAATGTTGGTTATACCCTTCCCGTACTAATTAATCCCCTGGCCCAACCCGTCATCTACTCTACCATCTTTGCAGGCACACTCATCACAGCGCTAAGCTCGCACTGATTTTTTACCTGAGTAGGCCTAGTAATAAACT
267T	A00583:504:HM2HWDSXY:2:1115:1452:29997	CCAACTGAAGCTGACCAGGCTGCCTCCCCTCCTCCACAGCGGATGAGACCACATGTATCCAGTGTCTCTCACATTCAGTATACACACACACACACACACACACACACACACACCCCTACCTTAGAGATTCGGCATTTATCATTGTGAAGAACTGTCCTACAAAATACAGAGGCTTTGAATACCTGTGGTCCACACTC
268T	A00583:504:HM2HWDSXY:2:1111:2682:12931	TGTAACTAACCTTCACAATGTGCACATGTACCCTAAAACTTAAAGTATAATAAAAAAAAAAAAAAAAAGAAAAGAGAAGAAACTCATCAGTGGGCTGCT
269T	A00583:504:HM2HWDSXY:2:1110:9715:22482	CTGATTTTGTTCTTTGGCCTTGAACTTGTTCAAGTTGAATTGTGTGTCCTGAACACTGATCTAGTTGTTCACAAACTAGGGTCAGCCAACTGTAGTGGTATGTTGATGTATTCTTGGGAATCGAGAGTTCTTTATTATAATCTTTTAATATTATGGCTAAAAAACCCAAAATATCTATGTGTAAATATATAATGTAAGCATGGATTCGTTCAT
270T	A00583:504:HM2HWDSXY:2:1110:32696:10269	AGTAACAAATATCATGGTAAAATGAAAGACCAGTAATCTGAAATACTTATATTCTAAGTGGTCATTTAATTGTCCCCCCAATTTTATTATAAAATTAAGAATTGACAGATGATAGATATTTTTTC

34T	A00583:504:HM2HWDSXY:2:1110:14335:5431	TCAGATCCTCTGGCGCCCGGGCGCCCCCTCCCGGCGACACCTCCCGGCTGGGAGCGCGCGGGAAGAGGCCAGAGGCAGGGCCTCTCACCTGCTCGGACTGCAAACCACAAAGCGTCTCTTTTTTTTTTTTTTTGAGGGGCGGAGGTGGTCATTTTTATGTTCCCTGGGCAAAGCGAGCAGCCGTTTGGCTTATAAAATA
36P	A00583:504:HM2HWDSXY:2:1110:12807:9330	TTTTTCTCCACAATCTTGCCAGCATCTATTATTGTTTTTTTTTTTTTTTTTTACTTTTAATAAATAGCCATTTGGACTGGTGTGAGATGGTATCTCATTGTGGTTTTGATTTGC
35T	A00583:504:HM2HWDSXY:2:1109:21884:24956	CAGAAGGAGTAGCCTTTTGATCTAGTGCACAGGTGTCCAGTCTTTTGGCTTCTCAGGGCCACATTGGAAGAAGAATGCTCCTGGGCCGCACATAAAATACACTAATGCTAACAACAGCTGATGAGGTTAAAAAAAAAAAAAAAACAAGGTTTGTGCATAATTTTCATGCTACCCACCACCACAGATAGGTGGAAAAGTCCTTGTAGTC
12H	A00583:504:HM2HWDSXY:2:1107:9480:32534	ACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGTCTGGGGGGTATGCACGCGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTCCTGCCTCATCATATTATTTATCGCACCTACGTTCAATATTATAGGCGAACATATTTACTAAAGTGTGTTAATTAATTAATGCTTGTA
5C	A00583:504:HM2HWDSXY:2:1106:5611:13839	CGCAAGGGCAACTAATCGGAGCGCGTGGGCGCCGGCGCCCCGGTCTATCTTGCCGCGGTGCTCGAGAACTTGACTTCCTAGATCCTGGAGAATGACGGCAACGCGGCGCGCGACAACAACAAGACGCGCATCATCACGCGCCACCTGCAG
229T	A00583:504:HM2HWDSXY:2:1104:23077:27211	ACCTCTTTTTCTTTATAAATTACCCAGTGTCAGCTATATATTTATTAGCAGCATGAGAACAGACTAATACACTCTCCCTTACATACATACATACATACATACATACATACATACATACACACACAAACACACACACAAACTGCCCC
271T	A00583:504:HM2HWDSXY:2:1103:31430:34882	GCGGCGGCAACGCCACCCTGCAGGTGGACAGCTGGCCGGTCCACGAGCGGTACCCGGCAGGTCGGCGGCGCGGGCCCGCGGAGGAGGCGCGGTGGCGGGGCGGGTGGCGGCCTCTGATAGGAGTGTGGCCGCACCGGGGCGGGGCTAAGCGAGAGACGAAGCTTGCGAGGCGGGACTAGGGCAGGGGCGTGGCTAGGAAAAGTCGGGATTTGTGGCGGCGGGGCGAGACCGTGGTGGTGCGAATGCGCCCCCTATGGGGGAGGGTGCAGGGCTGAGCTGGGAAGG
272T	A00583:504:HM2HWDSXY:2:1103:25229:7138	GTCCTTTCCTCTGTCGAACTCAATCCACCTGACCTTTCATCATCTCACCACACCCTTCATTGACACGTGGTCCCCTGTGTTTCCAAGGTAGCAGCACTTCTATGCCCTGCTTCTTCCTTGGCCTCCTCCCACCTCTCTTTCATTCCTTGCTTATCTTACCCACACTATGCTTTGTCATCCATGAACTGCGTCACACA
275T	A00583:504:HM2HWDSXY:2:1103:21224:1799	ACCACCGCTCTTCTGCCAGACAGCGGGCAAAGTGCTGGCCCATGTCGATGGGGTGAAGCTGGAGGGCAAGGAGCCCATGCACAAGCTGTTCTTGGAGATGCTCGAGGTCATGATGGACTGTGGCGAGGGGTGGGACTGGTGGGGGTTCTGGCAGGACCTGCCTAGCATGGGGTCAGCCCCAAGGGCTGGGGCGGAGCTGGGGTCTGGGCAGTGCCACAGCCTGCTGGCAGGGCCAGGGC