Name: N/A
Date: 13/07/2025

SECOND PARENT ANCESTRY ESTIMATION REPORT

The Second Parent ancient break down is :

Population	Percentage
Han :	56.53 %
Gambian :	18.54 %
Jarawa :	10.05 %
TUR_Barcin_N :	6.14 %
Yamnaya_RUS_Samara :	5.17 %
Levant_PPNB :	2.45 %
BRA_LapaDoSanto_9600BP :	0.86 %
MAR_Taforalt :	0.15 %
WHG :	0.07 %
ETH_4500BP :	0.05 %

The Second Parent Neolithic Breakdown Interpretation (by OpenAI) :

Your Neolithic breakdown shows the estimated proportions of your ancestry linked to various ancient populations, based on genetic analysis. Here’s how to interpret your results:

- **Han (56.53%)**: The majority of your ancestry is related to the ancient Han Chinese, indicating strong East Asian roots. - **Gambian (18.54%)**: A significant portion of your ancestry is connected to populations from West Africa, specifically the Gambia region. - **Jarawa (10.05%)**: This suggests a notable link to the indigenous peoples of the Andaman Islands, reflecting ancient South or Southeast Asian ancestry. - **TUR_Barcin_N (6.14%)**: This refers to Neolithic farmers from Barcın, Turkey, representing early Anatolian agricultural populations that contributed to the spread of farming in Europe and Asia. - **Yamnaya_RUS_Samara (5.17%)**: This ancestry is linked to the Yamnaya culture from the Pontic-Caspian steppe in Russia, known for their role in spreading Indo-European languages. - **Levant_PPNB (2.45%)**: This points to ancestry from Pre-Pottery Neolithic B populations in the Levant (Eastern Mediterranean), early agriculturalists of the Middle East. - **BRA_LapaDoSanto_9600BP (0.86%)**: This reflects a small connection to ancient populations from Brazil, likely representing ancient Native South American ancestry. - **MAR_Taforalt (0.15%)**: This shows a minor link to the ancient Taforalt population from Morocco, North Africa. - **WHG (0.07%)**: Western Hunter-Gatherers, ancient populations of prehistoric Europe, are a very small part of your background. - **ETH_4500BP (0.05%)**: A minimal trace from ancient Ethiopian populations, representing Northeast African ancestry.

Overall, your genetic heritage is predominantly East Asian, with substantial West African and minor contributions from South Asian, Middle Eastern, European, and Native American-related ancient populations. This mix reflects the complex migrations and interactions of ancient peoples across Eurasia, Africa, and the Americas.

All the reports below are based on Euclidean distance. Please refer to the legend below to help you evaluate whether your genetic distance result is a good match. Keep in mind that most ethnicity reports are based on **genetic similarity** rather than **direct ancestry**

GREAT	GOOD	AVERAGE	DISTANT		VERY DISTANT				

The Second Parent modern break down is :

How to interpret ? This report estimates the ancestry using modern reference populations. If you have mixed ancestry, you may see different ancestral backgrounds reflected in the results. If the ancestry is less mixed, the report may highlight older or more ancient genetic connections.

Population	Percentage
Fit :	0.0097123154681704
Han_Fujian :	23.49 %
Li :	16.55 %
Gambian :	7.28 %
Igbo :	7.15 %
Mari :	6.96 %
Igorot :	6.59 %
She :	6.46 %
Ho :	5.11 %
Sardinian :	4.63 %
Saudi_Mecca :	2.94 %
Ket :	2.38 %
Cameroon_Bangwa :	2.31 %
Moroccan_South :	1.83 %
Surui :	1.61 %
Agta :	1.56 %
Dusun :	1.35 %

The Second Parent modern Breakdown Interpretation (by OpenAI) :

Your modern breakdown reflects the estimated genetic contributions from various contemporary populations. Here’s how to interpret each component:

- **Han_Fujian (23.49%)**: A significant portion of your ancestry is linked to the Han Chinese population from Fujian province in China, suggesting strong East Asian roots. - **Li (16.55%)**: This refers to the Li people, an ethnic group primarily found on Hainan Island, China, indicating additional Southern Chinese or Southeast Asian ancestry. - **Gambian (7.28%)** and **Igbo (7.15%)**: These are West African populations (from The Gambia and Nigeria, respectively), showing notable West African heritage. - **Mari (6.96%)**: The Mari are a Finno-Ugric ethnic group from Russia, pointing to some Northern Eurasian or Uralic ancestry. - **Igorot (6.59%)** and **Agta (1.56%)**: Both are indigenous groups from the Philippines, suggesting Southeast Asian or Austronesian roots. - **She (6.46%)**: The She are an ethnic minority in China, further supporting East Asian ancestry. - **Ho (5.11%)**: An indigenous group from India, indicating South Asian influence. - **Sardinian (4.63%)**: This reflects Mediterranean European ancestry, specifically from the island of Sardinia, Italy. - **Saudi_Mecca (2.94%)** and **Moroccan_South (1.83%)**: These indicate Middle Eastern and North African ancestry. - **Ket (2.38%)**: The Ket are a small indigenous group from Siberia, Russia, suggesting some Siberian or Central Asian heritage. - **Cameroon_Bangwa (2.31%)**: This is another West African group, reinforcing your West African links. - **Surui (1.61%)**: The Surui are an indigenous group from the Amazon in Brazil, pointing to a small amount of Native American ancestry. - **Dusun (1.35%)**: An indigenous group from Borneo, Malaysia, reflecting additional Southeast Asian heritage.

Overall, your breakdown shows a highly diverse ancestry with strong East Asian (especially Southern Chinese), West African, Southeast Asian, and smaller contributions from European, Middle Eastern, Siberian, and Native American populations. This suggests a rich and complex genetic background, with connections spanning multiple continents and ethnic groups.

The Second Parent ancient break down is :

How should this breakdown be interpreted? This analysis aims to trace your ancestry by referencing ancient populations.

Population	Distance
Fit :	0.008662550359719575
Hmong-Mien*(AD*1400-1500) :	28.68 %
Southeast*Asian*(2000*BC-AD*1800) :	18.74 %
Sub-Saharan*African :	11.87 %
Magyar :	8.89 %
Jomon*(6900-800*BC) :	6.90 %
West*African :	5.18 %
Greek*(770-400*BC) :	3.20 %
Sinitic*(1230*BC-AD*1670) :	3.13 %
Sinitic*(1230*BC-AD*200) :	3.13 %
Roman*Sardinia*(AD*400-500) :	2.52 %
Ancient*Ancestral*South*Indian :	1.71 %
Cushitic*(2000*BC-AD*600) :	1.18 %
South*Amerindian*(9000*BC-AD*1500) :	1.17 %

Your Ancient Breakdown Interpretation (by OpenAI) :

Your ancient breakdown shows the estimated proportions of your genetic ancestry as connected to specific ancient populations or regions and their approximate time periods. Here’s how to interpret each component:

- **Hmong-Mien (AD 1400-1500, 28.68%)**: A significant part of your ancestry is linked to ancient Hmong-Mien-speaking peoples of Southeast Asia, particularly from the late medieval period. - **Southeast Asian (2000 BC-AD 1800, 18.74%)**: A large portion connects you to broader Southeast Asian populations over a long period, indicating deep regional roots. - **Sub-Saharan African (11.87%)**: You have a notable proportion of ancestry from populations south of the Sahara, showing African heritage. - **Magyar (8.89%)**: This reflects ancestry from the ancient Magyar people, ancestors of modern Hungarians, suggesting a Central/Eastern European link. - **Jomon (6900-800 BC, 6.90%)**: This part connects you to the ancient Jomon people of Japan, indicating a deep East Asian lineage. - **West African (5.18%)**: A specific subset of your African ancestry comes from West Africa, further detailing your African roots. - **Greek (770-400 BC, 3.20%)**: This shows a connection to populations from ancient Greece during the classical period. - **Sinitic (1230 BC-AD 1670, 3.13%)** and **Sinitic (1230 BC-AD 200, 3.13%)**: These indicate links to ancient Chinese (Sinitic) populations, spanning both early and later historical periods. - **Roman Sardinia (AD 400-500, 2.52%)**: A smaller part of your ancestry traces to Roman-era Sardinia, an island in the Mediterranean. - **Ancient Ancestral South Indian (1.71%)**: This points to ancient populations from South India, showing a South Asian influence. - **Cushitic (2000 BC-AD 600, 1.18%)**: This reflects ancestry from Cushitic-speaking peoples of Northeast Africa. - **South Amerindian (9000 BC-AD 1500, 1.17%)**: A small part comes from ancient indigenous peoples of South America.

Overall, your genetic profile is highly diverse, with strong Southeast Asian, African, and East Asian components, alongside influences from Europe, South Asia, and the Americas. Each percentage reflects the estimated proportion of your DNA that matches ancient samples from those regions and time periods. This breakdown highlights the complex and interconnected nature of your ancestry.

The Second Parent 50 closest modern populations are :

How to interpret? If the closest population result shows a low genetic distance (for example, highlighted in bright green), you are very likely from that ethnicity or a closely related group. If you do not obtain a good distance with any population, it may indicate that you are of mixed ancestry, or that the specific ethnicity is not included in the Davidski reference datasheet.

Population	Distance
Maori_(European-Mixed)	0.147025698802964
Chamorro_(European-Mixed)	0.14897772638888
Tibetan_Muslim_Srinagar	0.160820562896222
Rakhine_Myanmar	0.173619923000731
Manipuri_Brahmin	0.175357990334123
Brahmin_Manipuri	0.175358153571484
Bamar	0.175376390078069
Nepali_(Tamang_Profile)	0.175796260617227
Tripuri_Jamatia	0.177319094365273
Jamatia	0.177319710277792
Aeta	0.178391613936866
Nepali_(Mixed_Himalayan_Profile)	0.178915870958951
Tripuri	0.179427133265847
Nepali_(Newar_Profile)	0.179854659461501
Nepali_(Tharu_Profile)	0.179979634956986
Mon	0.18104681763566
Mon_Thailand	0.181046905836554
Nyishi	0.18171088264328
Burmese	0.182142109074206
Kusunda	0.182273393604223
Agta	0.182323196796239
Tharu	0.182894767902201
Dongxiang	0.183260458978471
Jehai	0.183529737655782
Thai	0.183729910847418
Maniq	0.184397331810957
Nepali_Tamang_Simigaon	0.184497528566103
Tamang_Simigaon	0.184497724821629

Riang	0.184755099978323
Tripuri_Reang	0.184755219166523
Newar	0.186842889672045
Magar	0.186971136296488
Salar	0.187914692312762
Tamang	0.188263699050029
Dungan	0.189492419935469
Uyghur_(Dungan_Profile)	0.191958915223414
Mamanwa	0.19437213014473
Baoan	0.195003570931406
Batak_Palawan	0.196479388495969
Batak	0.196479637008521
Hui_Gansu	0.19678535929399
Kazakh_China	0.1980153576443
Kazakh_Gansu	0.198015568064696
Kyrgyz_China	0.198208485118911
Kirghiz_China	0.198208814685422
Yuku	0.198734386984236
Kyrgyz	0.200328323201047
Hui	0.200379800591277
Kirghiz_Tajikistan_Pamir	0.200522634206216
Kyrgyz_Bishkek	0.200586093287959

Closests modern populations (by OpenAI) :

Your list shows the closest modern populations to your genetic profile, ranked by genetic distance (the number in parentheses; lower values mean closer similarity). Here's how to interpret the results:

1. **Top matches:** - Your closest matches are "Maori_(European-Mixed)" and "Chamorro_(European-Mixed)," both with distances around 0.147–0.149. This suggests your genetics are most similar to modern individuals from these populations, which are Oceanic groups with significant European admixture. 2. **South and Southeast Asian populations:** - Many of your matches are from Himalayan, Northeast Indian, Burmese, and Southeast Asian groups (e.g., Tibetan_Muslim_Srinagar, Rakhine_Myanmar, Manipuri_Brahmin, Bamar, Tripuri, Mon, Thai, etc.), with distances around 0.16–0.19. This indicates a strong affinity with populations from this geographic region, including both Indo-Aryan and Tibeto-Burman speakers. 3. **Austronesian and indigenous Southeast Asian groups:** - Groups like Aeta, Agta, Jehai, Maniq, Mamanwa, Batak, and others are indigenous to the Philippines, Malaysia, and Indonesia. Their presence on your list suggests you have some genetic similarity to these Austronesian or "Negrito" populations. 4. **Central and East Asian influences:** - Populations like Dongxiang, Salar, Dungan, Uyghur, Kazakh, Kyrgyz, Hui, and Kirghiz show up with slightly higher distances (0.18–0.20), pointing to some Central or East Asian genetic components. 5. **Interpretation summary:** - Your genetic profile is closest to populations from Oceania with European admixture, followed by Himalayan, Northeast Indian, Burmese, and Southeast Asian groups, as well as indigenous and Central Asian populations. This pattern may reflect a combination of South/Southeast Asian ancestry, with possible minor Oceanic, European, or Central Asian influences.

The distances are all relatively low (below 0.2), indicating broad regional affinities. Your genetic background appears to be a mix of South, Southeast, and East Asian components, with some Oceanic-European admixture. The exact proportions would depend on your full admixture breakdown.

The Second Parent 50 closest modern 2-Ways are :

About 2Ways Analysis

The 2Ways feature compares the coordinates to those of all referenced populations in the modern Davidski datasheet. It measures how closely the admixture percentages align with each population. Please note that 2Ways does not measure shared DNA between the kit and the reference samples—it is a statistical comparison based on admixture profiles.

- If you come from a single ethnicity, focus on the populations closest to you, as these will be the most relevant.
- If you are of mixed ancestry (for example, if the parents come from different ethnic backgrounds), the closest 2Ways result will likely reflect a combination close to '50% Parent 1 Ethnicity / 50% Parent 2 Ethnicity.'
- For people with complex or multiple recent admixtures (such as many from Latin America), the 2Ways analysis may not provide highly accurate results, as it is less effective for individuals with highly mixed heritage.

Population	Distance
64% Dong_Guizhou + 36% Berber_Algeria	0.0433558499666807
64% Han_Guangdong + 36% Berber_Algeria	0.0435232514471165
65% Kinh_Vietnam + 35% Berber_Algeria	0.0436261062078851
64% Dong_Hunan + 36% Berber_Algeria	0.0440800082573124
64% Mulam + 36% Berber_Algeria	0.0460278424313578
64% Miao + 36% Berber_Algeria	0.0465739867004538
64% Hmong + 36% Berber_Algeria	0.0466544223430492
64% Han_Fujian + 36% Berber_Algeria	0.0476896817354308
64% Tujia + 36% Berber_Algeria	0.0488353891461332
64% Gelao + 36% Berber_Algeria	0.0488627704995345
64% Han_Chongqing + 36% Berber_Algeria	0.048929271417746
64% She + 36% Berber_Algeria	0.0500813543644457
65% Lahu + 35% Berber_Algeria	0.0501861282908491
66% Akha + 34% Berber_Algeria	0.0504765978530245
64% Han_Hubei + 36% Berber_Algeria	0.0507065891453845
64% Han_Sichuan + 36% Berber_Algeria	0.0510161627364012
64% Maonan + 36% Berber_Algeria	0.051129279983264
64% Li + 36% Berber_Algeria	0.0512962344819193
65% Tai_Lue + 35% Berber_Algeria	0.0517617084818945
65% Dai + 35% Berber_Algeria	0.0518329151457799
71% Mon + 29% Berber_Algeria	0.0524521774506241
64% Han_Zhejiang + 36% Berber_Algeria	0.0566398010335776

66% Salar + 34% Madagascar_Vezo	0.0566659959809907
67% Salar + 33% Madagascar_Mikea	0.057899375516743
66% Dongxiang + 34% Madagascar_Vezo	0.0579289675697697
71% Thai + 29% Berber_Algeria	0.0580507764087043
67% Salar + 33% Madagascar_Temoro	0.0581418903991056
67% Dongxiang + 33% Madagascar_Mikea	0.0590355970034968
66% Dongxiang + 34% Madagascar_Temoro	0.0593596068242918
65% Dungan + 35% Madagascar_Vezo	0.0596857104440223
63% Han_Jiangsu + 37% Berber_Algeria	0.0603487833048018
67% Karen_Sgaw + 33% Berber_Algeria	0.0603917832059518
66% Dungan + 34% Madagascar_Mikea	0.06070092270865
66% Dungan + 34% Madagascar_Temoro	0.061048905183222
76% Mon + 24% Kikuyu	0.061446836397
71% Burmese + 29% Berber_Algeria	0.061460411363493
64% Han_Shanghai + 36% Berber_Algeria	0.0636144641928628
67% Lawa + 33% Berber_Algeria	0.0639797331860313
63% Dong_Hunan + 37% Moroccan_South	0.0640598133974698
64% Han_Shandong + 36% Berber_Algeria	0.0640649829513854
63% Han_Guangdong + 37% Moroccan_South	0.0642909644574035
76% Mon + 24% Bulala	0.0643295660995198
74% Mon + 26% Elmolo	0.0643549484361276
75% Mon + 25% Sandawe	0.0643636310367394
63% Dong_Guizhou + 37% Moroccan_South	0.0646771435591091
65% Yi + 35% Berber_Algeria	0.0647232447732475
76% Thai + 24% Kikuyu	0.0651548617565933
65% Kinh_Vietnam + 35% Moroccan_South	0.065274172948572
63% Mulam + 37% Moroccan_South	0.0654609216389606
75% Mon + 25% Ogiek	0.0657501983196189
65% Tibetan_Xinlong + 35% Berber_Algeria	0.0666692468288618

The Second Parent closest 2Ways interpretation (by OpenAI) :

Your "closest 2Ways" results show the two populations that best model your genetic ancestry, along with the proportion from each and a distance value in parentheses. Here’s how to interpret your results:

1. Populations and Proportions: Each line shows a mix between two reference populations. For example, "64% Dong_Guizhou + 36% Berber_Algeria" means your DNA is best modeled as 64% similar to the Dong people from Guizhou, China, and 36% similar to Berber people from Algeria.

2. Distance Value: The number in parentheses (e.g., 0.0433) is a statistical distance. Lower values mean a better fit between your DNA and the two populations. Values below 0.05 are considered very close matches.

3. Main Patterns in Your Results: - Most of your top results are a mix of East or Southeast Asian populations (such as Dong, Han, Kinh, Miao, Hmong, etc.) and Berber_Algeria. - The proportions are consistently around 64–66% East/Southeast Asian and 34–36% Berber_Algeria. - Some less frequent models include Malagasy (from Madagascar), North African, or East African populations as the secondary component.

4. What This Suggests: - Your genetic profile is best explained as a mix between East/Southeast Asian ancestry and North African Berber ancestry. - The high percentage of East/Southeast Asian populations indicates a strong genetic connection to this region. - The consistent presence of Berber_Algeria (and occasionally Moroccan_South or Madagascar) suggests a significant North African or possibly ancient Eurasian-African admixture component.

5. Summary: Your DNA is most similar to people from East/Southeast Asia, but with a notable North African (Berber) component. The distance values are low, supporting the accuracy of this model. The results do not imply direct, recent ancestry from these specific modern populations, but rather that your genetic makeup is best explained as a combination of groups most genetically similar to these references.

The Second Parent ancient map :

How to interpret? This map aims to illustrate your ancient ancestry by displaying your genetic similarities to historical populations across different regions.

GREAT	GOOD	AVERAGE	DISTANT	VERY DISTANT

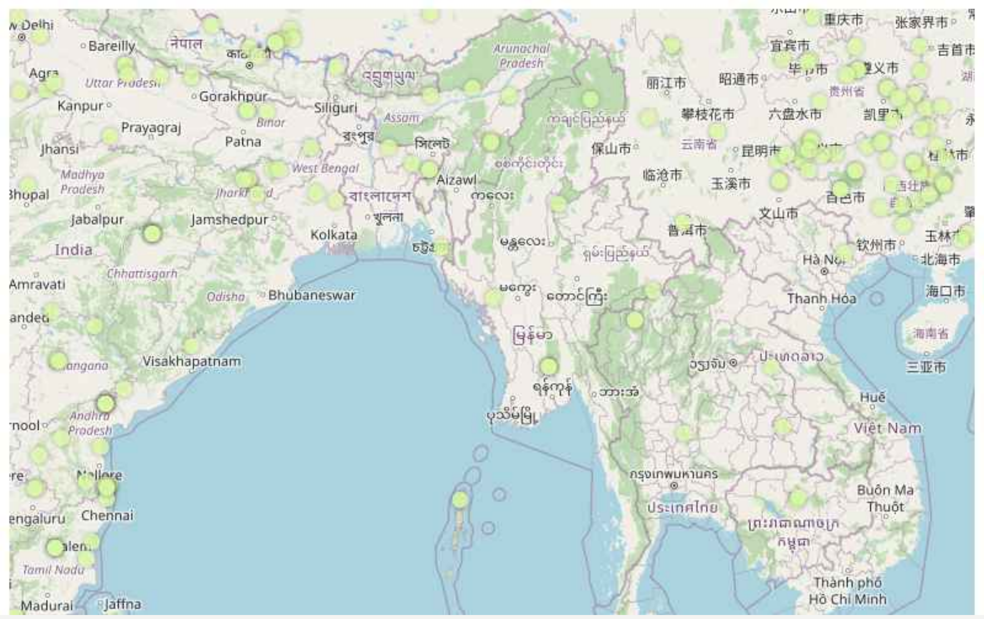
The Second Parent modern similitude map :

How to Interpret This Map?

This similarity map is based on the modern Davidski G25 dataset and the French averages from the Explore Your DNA Project. The map is most accurate for individuals who belong to a single ethnicity. For people with mixed ancestry, it will show midpoint populations closest to the overall genetic composition.

Keep in mind, this map represents the genetic similarity compared to pre-colonial populations. For example, individuals from Latin America may see results reflecting ancestry in both the Americas and Europe. Similarly, North Americans, Australians, and South Africans may have mixed regional results.

Nomadic tribes and diasporic populations (such as Ashkenazi Jews, Roma, etc.) may not appear directly on the map. Instead, their results may indicate ancient ancestral locations (e.g., Ashkenazi Jews may appear in both the Levant and Europe).



Conclusion (by OpenAI):

Based on the genetic breakdowns and population matches you provided, your ancestry appears to be a highly mixed profile with strong East and Southeast Asian roots, notable African admixture, and minor West Eurasian and Amerindian influences.

Neolithic and Ancient Components: - The majority of your ancient ancestry is East Asian, particularly Han-related (over 56%), with substantial Southeast Asian (Hmong-Mien, Southeast Asian, Jomon), and a clear but smaller West Eurasian (Yamnaya, Barcin, Levant) and African (Gambian, Jarawa, Sub-Saharan, West African) signal. - There are minor traces of South Asian (Ancient Ancestral South Indian), Mediterranean (Greek, Roman Sardinia), and Amerindian (BRA_LapaDoSanto, South Amerindian) ancestry.

Modern Components: - Your closest modern populations are predominantly East and Southeast Asian (Han_Fujian, Li, She, Ho, Igorot, Agta, Dusun, Thai, etc.), with significant African (Gambian, Igbo, Cameroon_Bangwa, Moroccan_South) and some Central Asian/Siberian (Mari, Ket) and Mediterranean (Sardinian, Saudi_Mecca) input. - The admixture models consistently show a blend of East/Southeast Asian and North/West African components, with the best fit being around 64–65% East Asian (Dong, Han, Kinh, etc.) and 35–36% North African (Berber_Algeria, Moroccan_South).

Population Proximity: - Your closest matches are admixed or transitional groups in Southeast Asia and the Himalayan region (Maori-European Mixed, Chamorro-European Mixed, Tibetan Muslim, Rakhine, Manipuri Brahmin, Bamar, Tripuri, Aeta, Mon, Thai, Burmese, etc.), along with some Philippine Negrito and Tibeto-Burman populations. - The two-way mixture models reinforce this, showing your genetic profile is best explained as a mix of East/Southeast Asian and North African, with a minor but consistent African (possibly Sub-Saharan) component.

Summary: Your ancestry is primarily East and Southeast Asian, with a strong Han/Southern Chinese and Hmong-Mien/Southeast Asian base, significant North and West African admixture, and minor Eurasian and Amerindian traces. The closest modern populations are found in Southern China, Mainland Southeast Asia, and among some admixed groups in the Himalayas and Island Southeast Asia, with clear signals of African and Mediterranean input. This points to a complex admixture history, likely involving multiple migration and admixture events between East/Southeast Asia and Africa, possibly via maritime or overland routes.