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VarGoats international initiative, a 1000 goat genomes project

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VarGoats international initiative, a 1000 goat genomes project

Licia Colli^{1,2}, Paola Crepaldi³, Paolo Ajmone-Marsan^{1,2}, Alessandra Stella⁴, Gwenola Tossier-Klopp⁵, The VarGoats Consortium⁶

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licia.colli@unicatt.it

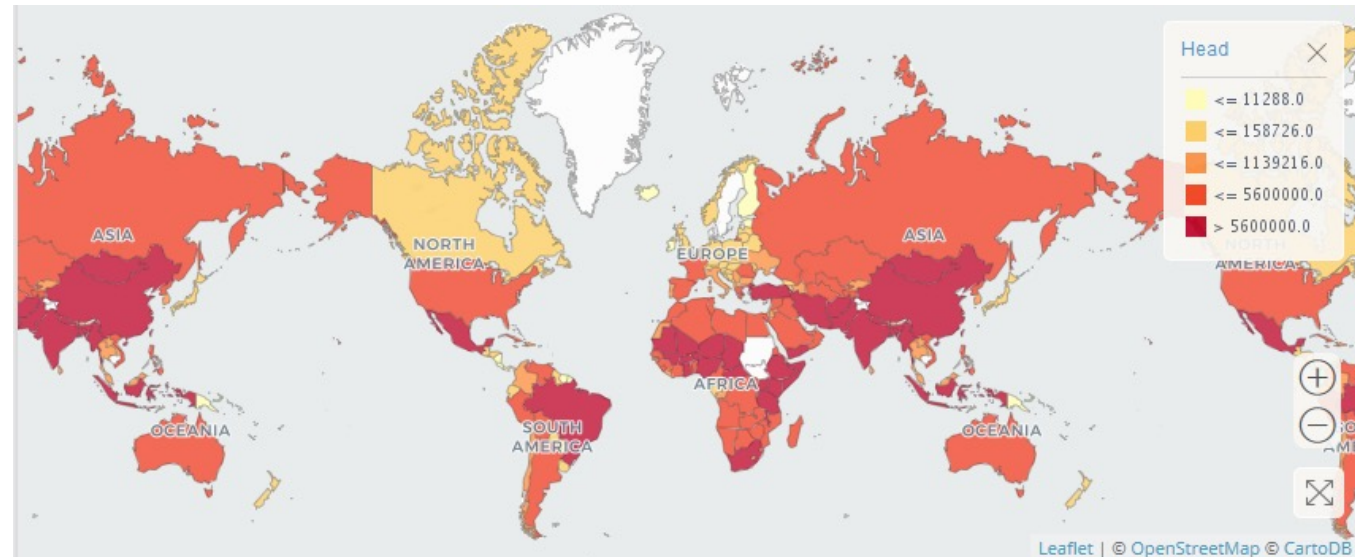


Domestic goats:

- ❖ Goat was domesticated from bezoar (*Capra aegagrus*) ca. 10,000-15,000 years ago.
- ❖ Goats are adapted to various (sometimes harsh) environments.
- ❖ Breed concept is ca. 200 years old.
- ❖ Milk, meat and fiber breeds.
- ❖ Nowadays a few breeds represent most of the animals, particularly in developed countries. Ex: in France Alpine & Saanen ca. 80% animals.



1 billion goats in the world, 18% endangered.





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VARGOATS project:

France Genomique Project launched in 2016



Gwenola Tosser-Klopp, Université de
Toulouse, INRA
VarGoats coordinator



VarGoats

Identification of Variations in Goat genomes related to domestication and adaptation

VarGoats is the first step of a 1000 goat genomes project and is lead by [Gwenola Tosser-Klopp](#) (INRA, France).

It is supported by [FRANCE GENOMIQUE](#) through a call for Large Scale DNA Sequencing projects. This means the scientific Consortium provides DNA and gets back genome sequences, generated at Genoscope (Evry, France). TGCC (Très Grand Centre de calcul du CEA) is the bioinformatic infrastructure where sequences will be stored and available for the Consortium. The data will be made available to VarGoats participants and data analysis will be performed in working groups already created in [ADAPTMAP](#) program or if needed in new working groups. Data will be used only for academic purposes, specifically for performing population genetics studies, for the investigation of diversity, domestication and adaptation traits, the discovery of variants (SNPs, CNVs, structural variants, causal mutations), the detection of selective sweeps, with the final goal to develop breeding solutions. Hybridization between species will also be studied, thanks to the availability of sequences from various capra species. At the end of the project, data will be released in a public database for research purpose only, even in case of no publication.



<http://www.goatgenome.org/vargoaats.html> 3



VARGOATS aims:

- ❖ Use of **whole genome sequences**:
 - ❖ to investigate **domestication**, human-mediated **selection** and **adaptation** at the genomic level.
 - ❖ to study **genetic diversity**.
 - ❖ to **detect variants** (SNPs, CNVs, structural variants, causal mutations) and identify **Loss of Function** mutations.
 - ❖ To detect **selective sweeps**.

**Final goal:
to develop
breeding
solutions.**



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VARGOATS working context:

❖ International Goat Consortium (<2011)

❖ Core working group (INRA/USDA-
AGIN/LECA/PTP later joined by Roslin)

❖ Bioinformatics skills

❖ Genomic tools

❖ high quality assembly (ARS1 = golden goat genome)

❖ MD 50K chip

❖ Data availability from previous studies:

- ❖ ADAPTmap project = >4,000 50K SNP chip genotypes.
- ❖ NextGen project = ca. 190 WG sequences from Iran and Morocco.
- ❖ ClimGen project = 50K SNP chip genotypes and methylation studies.
- ❖ Publicly available data.





VarGoats sampling strategy:



Detailed description of sampling

Gene pools

Inbred breeds

Other Capra species

Relevant gene pools

Determined by Working Groups from ADAPTmap project (lead by Licia Colli and Paola Crepaldi)

- | | | |
|------------------------|-------------------|------------------------------|
| 1. Pakistan | 6. Madagascar | 11. Mediterranean |
| 2. Northern Africa | 7. Boer | 12. Northern Europe |
| 3. Western Africa | 8. Spain & France | 13. America |
| 4. Eastern Africa | 9. Saanen | 14. Australia |
| 5. Southeastern Africa | 10. Alpine | 15. Wild goats, Turkey, Iran |

Global diversity, post-domestication history, and selection signatures.

Aims:

- **to evaluate diversity, gene flow, population structure and migrations.**

- **to identify signatures of natural or human-mediated selection to the environmental or productive conditions.**

Relevant gene pools

Gene pools

Inbred breeds

Other Capra species

Inbred breeds

To explore deleterious mutations

1. Icelandic
2. Palmera

Detailed description of sampling

Gene pools

Inbred breeds

Other Capra species

Other Capra species

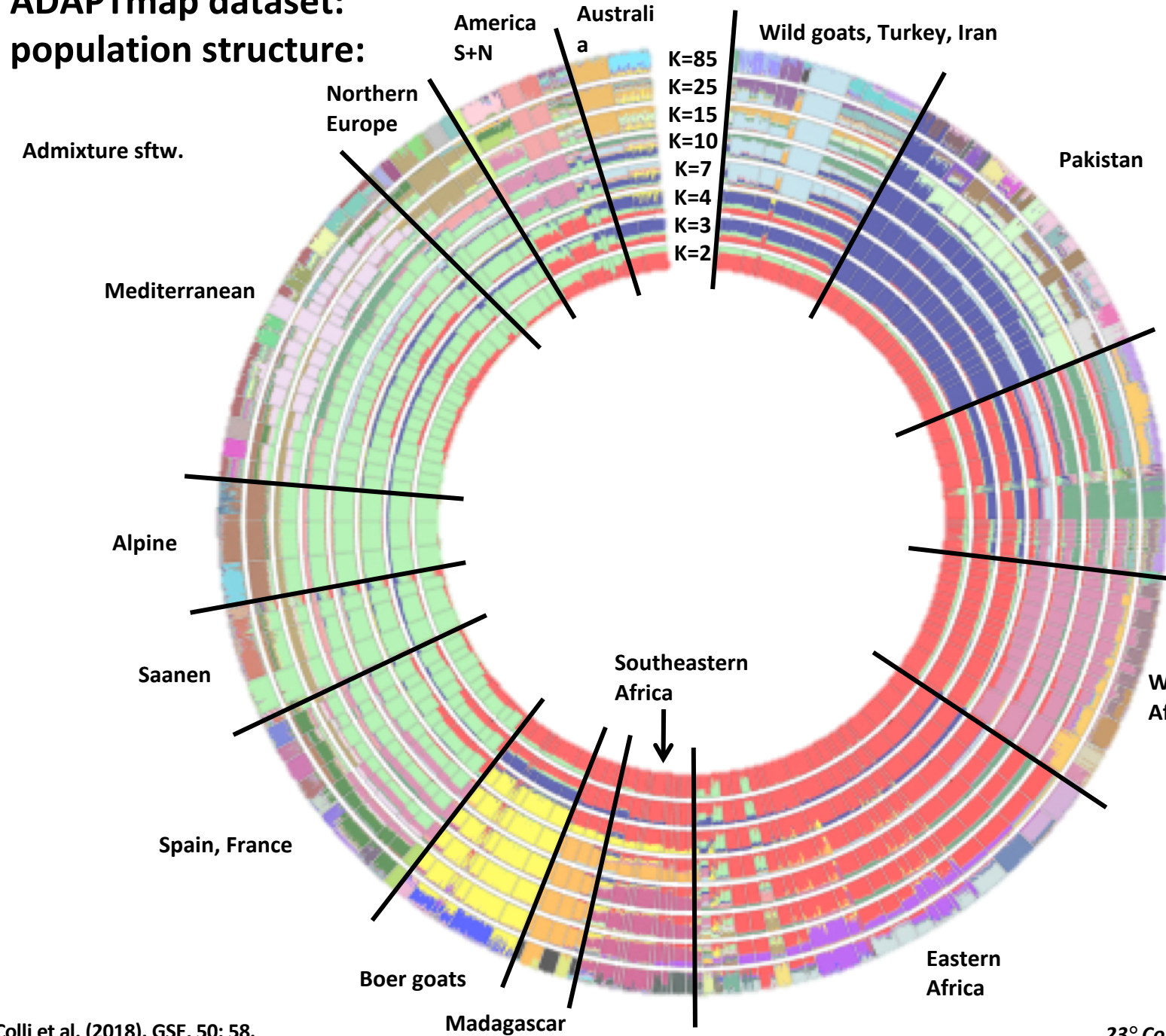
1. Capra falconeri
2. Capra ibex
3. Capra falconeri

ADAPTmap dataset: population structure:



Admixture sftw.

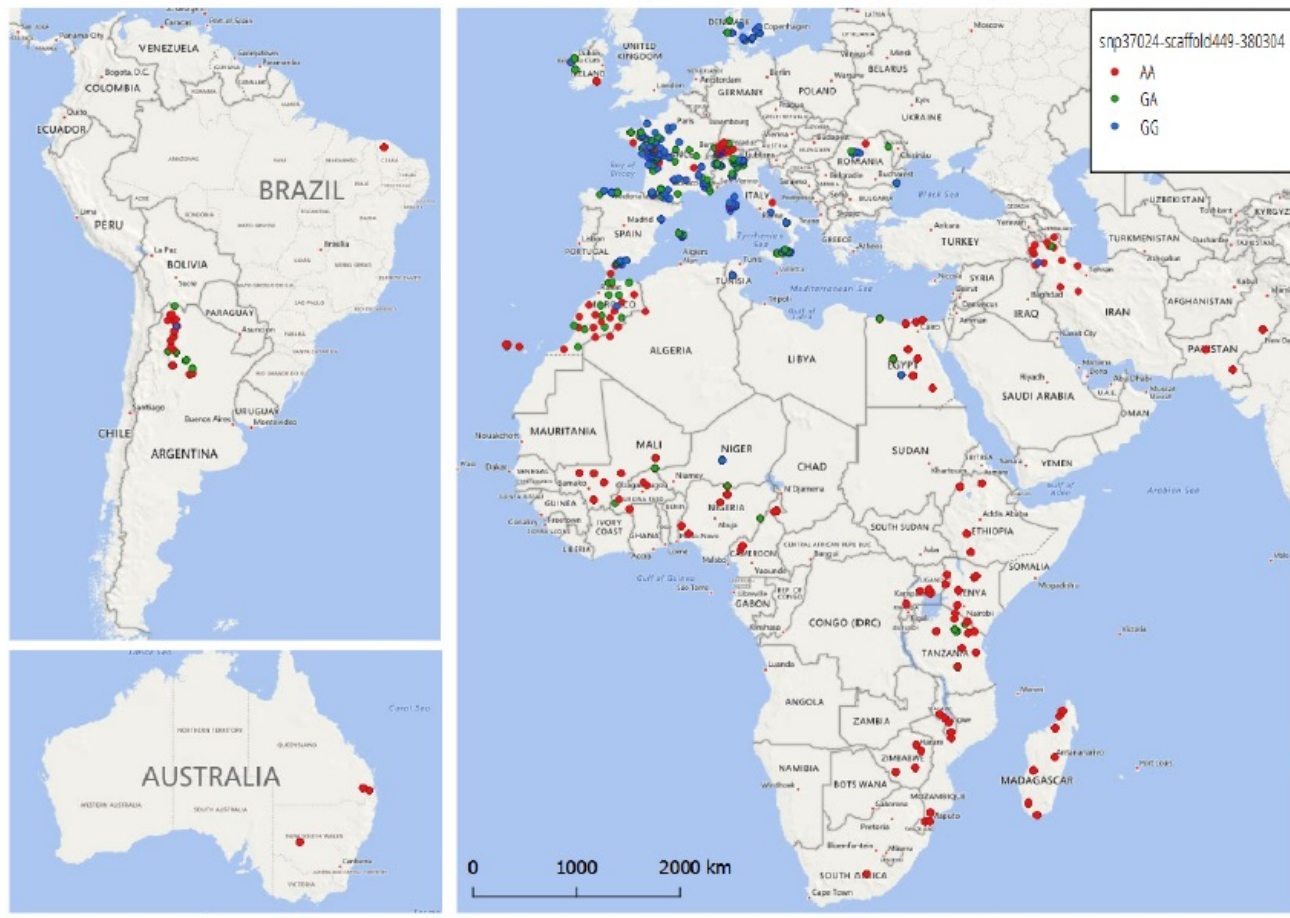
K=85
K=25
K=15
K=10
K=7
K=4
K=3
K=2





ADAPTmap dataset: Selection signatures

Chr 14, snp37024-scaffold449-380304, Temperature (tmax2)



Annotated gene: LYPLA1 (feed intake).



VarGoats sampling strategy:



Detailed description of sampling

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Gene pools

Inbred breeds

Other Capra species

Inbred breeds

To explore deleterious mutations

1. Icelandic
2. Palmera

Aim: to study ROHs and deleterious mutations.

Inbred breeds

Detailed description of sampling

Gene pools

Inbred breeds

Other Capra species

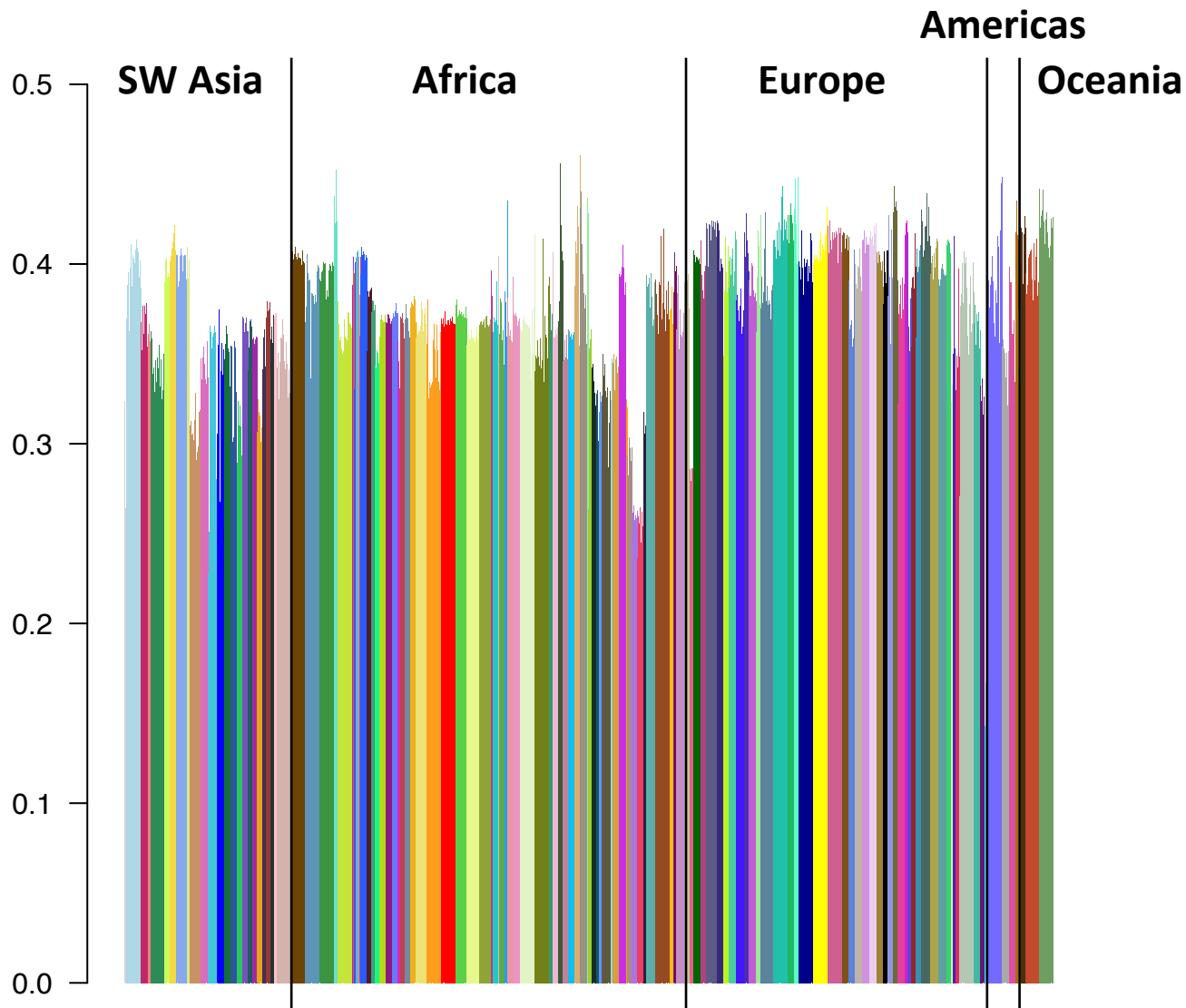
Other Capra species

1. Capra falconeri
2. Capra ibex
3. Capra falconeri



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ADAPTmap dataset: Observed Heterozygosity

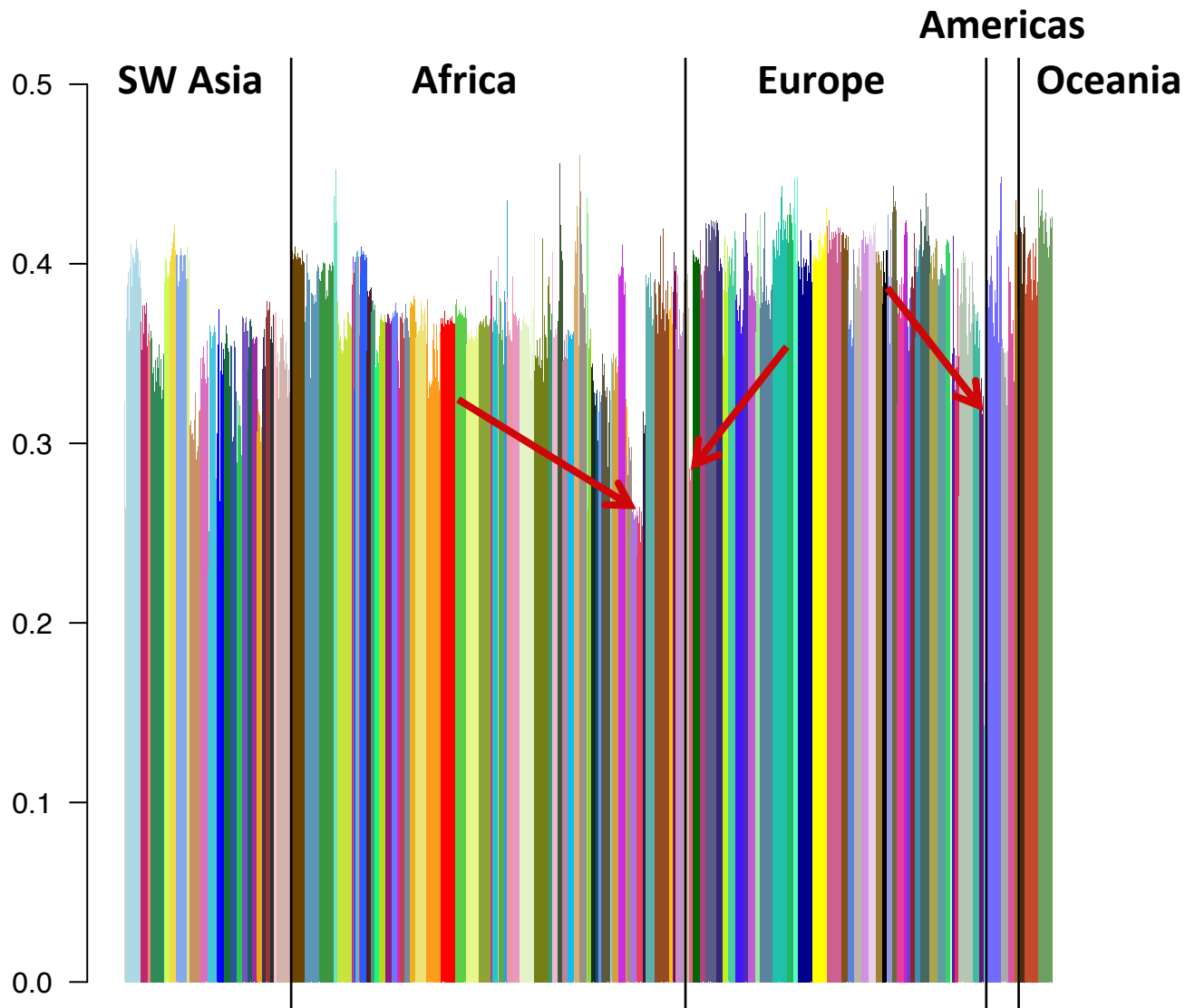


Analysis performed
by M. Milanesi & E. Vajana.



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ADAPTmap dataset: Observed Heterozygosity

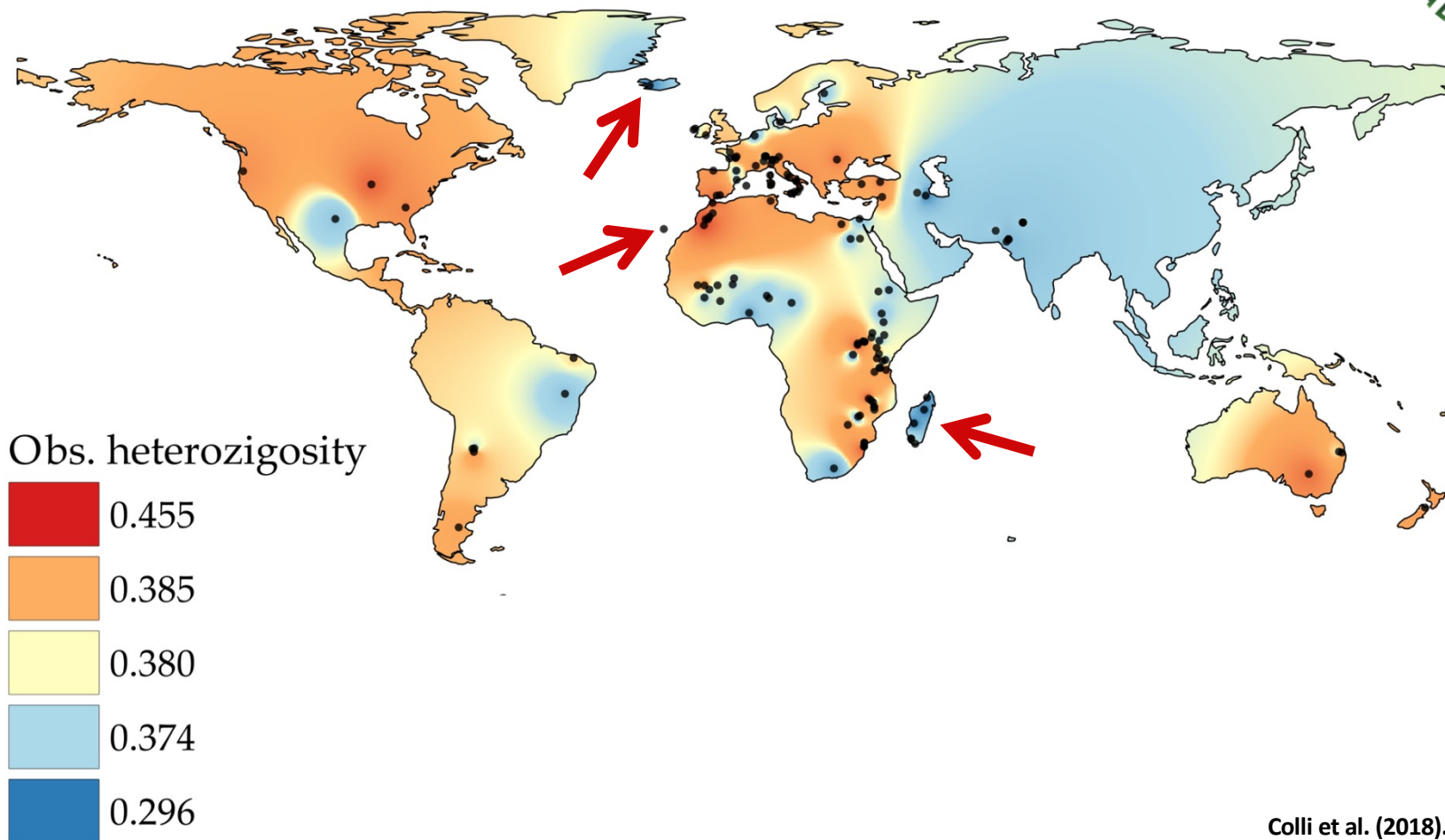


Analysis performed
by M. Milanesi & E. Vajana.



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ADAPTmap dataset: Observed Heterozygosity map



Colli et al. (2018). GSE, 50: 58.



VarGoats sampling strategy:



Detailed description of sampling

Gene pools

Inbred breeds

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Relevant gene pools

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Gene pools

Inbred breeds

Other Capra species

Inbred breeds

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1. Icelandic
2. Palmera

Detailed description of sampling

Gene pools

Inbred breeds

Other Capra species

Other Capra species

1. Capra falconeri
2. Capra ibex
3. Capra falconeri

Other Capra species

Aim: to study wild x domestic hybridization and adaptive introgression.



VarGoats WGs:

4 WGs follow up from ADAPTmap + 4 new WGs

VarGoats WG11 – “SNP calling and CNV detection”: B. Rosen & T. Faraut.

VarGoats WG12 – “Methods (demographic models, imputation)”: not started.

VarGoats WG13 – “Extent of loss of function alleles”: M.Amills & G. Tosser-Klopp.

VarGoats WG14 – “Hybridization between species”: L. Colli & P.Crepaldi.

ADAPTmap WG1 – “Improvement of genome assembly” & ADAPTmap GROUP 2 – “Genome annotation” now called “Genome annotation/Pan Genome Analysis” & **ADAPTmap WG6** – “Integration, standardization and visualization of genomic data”: not started.

ADAPTmap WG3 – “Comparative genomics (with other ruminants)”: Clet Wandui Masiga & E.Clark.

ADAPTmap WG7 – “Population genetics analyses and population history domestication reconstruction”: L. Colli & P. Crepaldi & F.Pompanon.

ADAPTmap WG8 – “Selection signatures (landscape genomics, iHS, CLL, EHH, XPEHH, Fst, Visible genetic profile)”: L. Colli & P. Crepaldi & F.Pompanon.



VarGoats workflow:

- ❖ Sequencing started in Jul. 2016.
- ❖ **Several sequence data sources** (Genoscope / CEA / Roslin / Public data).
- ❖ Data are being produced in several steps:
 - ❖ 248 animals in Dec. 2017 → 830 animals in Nov. 2018 → **ca. 1000 animals in Dec. 2019.**



VarGoats dataset:



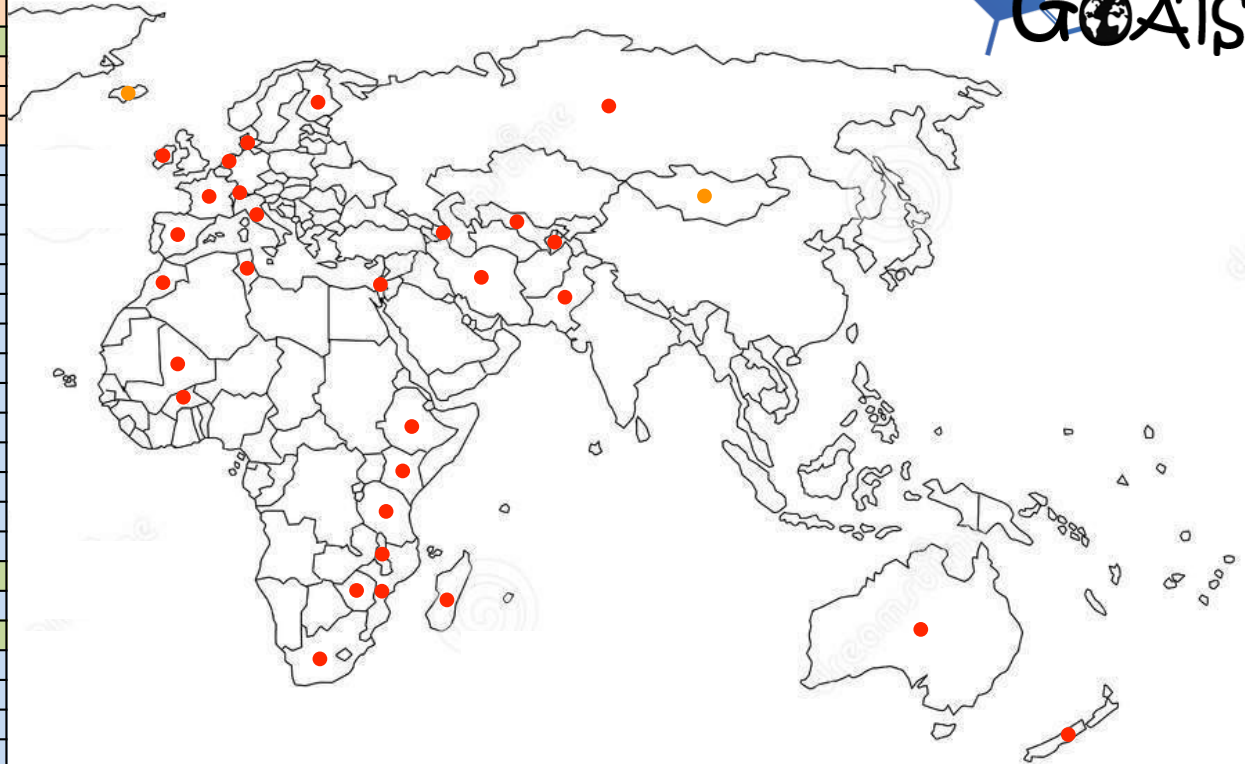
To date: 829 individuals representing 8 species, 84 populations, 30 countries and 4 continents.



VarGoats dataset:



| continent | country | populations | animals |
|-------------|--------------------|-------------|---------|
| Asia | Azerbaijan | 1 | 1 |
| | Iran | 1 | 20 |
| | Israel | 1 | 1 |
| | Pakistan | 7 | 31 |
| | Russian Federation | 1 | 1 |
| | Tajikistan | 1 | 1 |
| | Uzbekistan | 1 | 1 |
| Africa | Burkina Faso | 1 | 1 |
| | Ethiopia | 4 | 28 |
| | Kenya | 3 | 16 |
| | Madagascar | 6 | 43 |
| | Malawi | 5 | 25 |
| | Mali | 6 | 36 |
| | Morocco | 1 | 163 |
| | Mozambique | 1 | 163 |
| | South Africa | 1 | 3 |
| | Tanzania | 9 | 66 |
| | Tunisia | 1 | 5 |
| | Zimbabwe | 3 | 28 |
| | Europe | Denmark | 1 |
| Finland | | 1 | 1 |
| France | | 18 | 222 |
| Ireland | | 1 | 5 |
| Italy | | 10 | 39 |
| Netherlands | | 1 | 5 |
| Spain | | 4 | 22 |
| Switzerland | | 3 | 13 |
| Oceania | Australia | 3 | 5 |
| | New Zealand | 1 | 8 |



815 sequences from 84 local and transboundary domestic populations, and 14 sequences from 7 wild goat species.



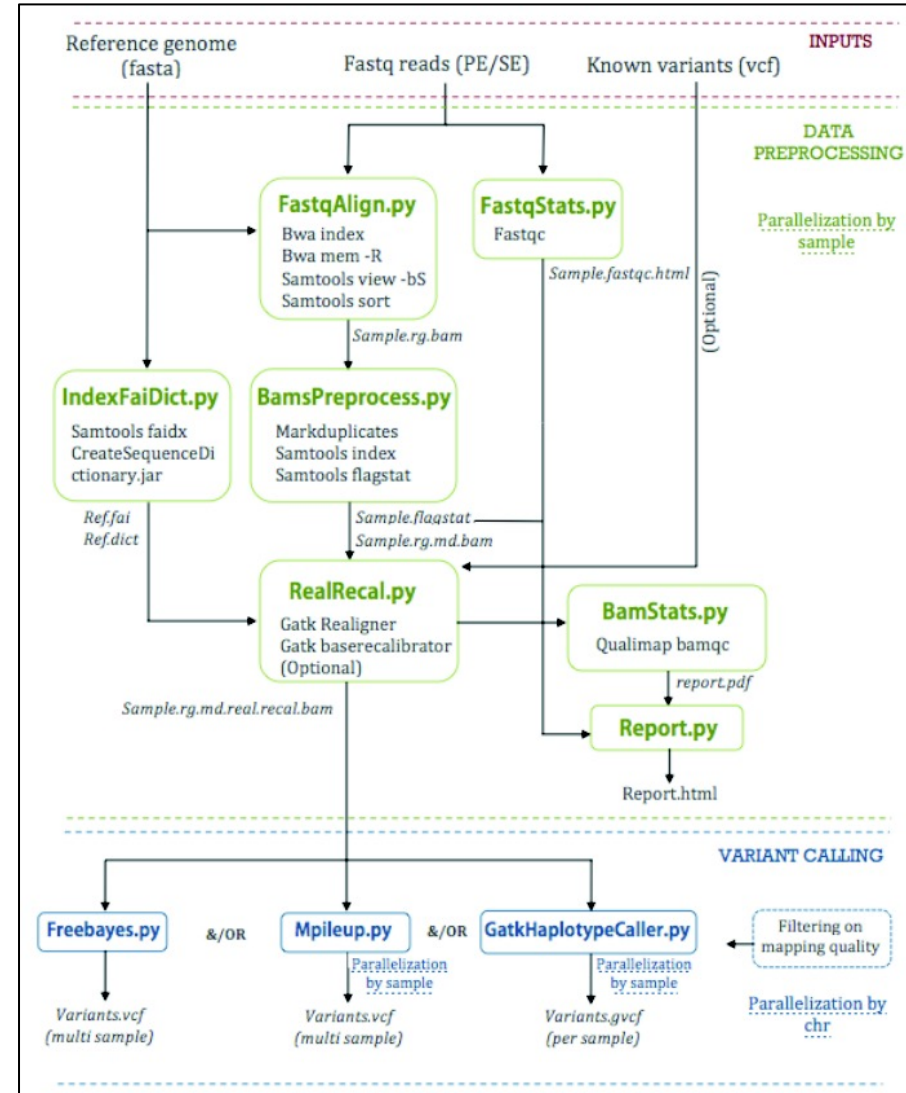
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- ❖ **One single bioinformatics pipeline** for SNP calling at TGCC run by Philippe Bardou (INRA-Toulouse, Sigenae team)
- ❖ **Filtering criteria and analyses pipelines are being optimized on intermediate datasets.**



Pipeline - alignment and variant calling:

- ❖ Based on Jflow workflow manager
- ❖ <http://jflow.toulouse.inra.fr>
- ❖ Main steps :
 - ❖ **Mapping fastq file on the reference genome ARS1 (BWA)**
 - ❖ Mapping post-processing (Picard tools, GATK): **bam file**
 - ❖ Variant discovery (GATK HaplotypeCaller, ...): **VCF/gVCF file**
 - ❖ Generate a vcf file by chr.
 - ❖ Generate a multiple-sample gVCF file (GATK CombineGVCF)
 - ❖ Perform “genotyping” and generate **30 vcf files** (GATK GenotypeGVCF)
 - ❖ Filter and annotate (snpeff) vcf files and generate **30 vcf annotated files**
 - ❖ Data release.





VarGoats workflow:

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- ❖ **One single bioinformatics pipeline** for SNP calling at TGCC run by Philippe Bardou (INRA-Toulouse, Sigenae team)
- ❖ **Filtering criteria and analyses pipelines are being optimized on intermediate datasets.**
- ❖ **Data will be released in the public domain** (expected at the end of 2019).



VarGoats searchable database:

Data access

Last update: 829 goats available - December 05th 2018.

Data access (authentication required): [Shared Data](#).

Remarks:

The Vargoaets_829_20181205 directory contains "raw data" VCF files (HardFiltering).

The Vargoaets_829_20190220 directory contains filtered VCF files (VQSR + GATK QUAL>100 + countVariant())>=2 + biallelic).

Short informations on available data (based on FASTQ, BAM files and "raw data" VCF)

- ID: Internal animal name
- PPaired: % reads mapped in a proper pair (from BAM file)
- MeanDP1: Mean depth of coverage (from VCF file)
- Ts/Tv: Ratio of transitions to transversions (from SnpSift TsTv)
- OneAlt: Hom/Het stats One ALT (from SnpSift TsTv)
- Missing: Hom/Het stats Missing (from SnpSift TsTv)
- Multiall: Variant type Multiallelic (from SnpSift TsTv)
- X: Depth of coverage (from FASTQ file)
- X_BAM: Depth of coverage (from BAM file)
- MeanGQ1: Mean genotype quality (from VCF file)
- HomoRef: Hom/Het stats Homozygous ref. (from SnpSift TsTv)
- TwoAlt: Hom/Het stats Two ALTs (from SnpSift TsTv)
- SNP: Variant type SNP (from SnpSift TsTv)

Show 10 entries

Search all columns:

| ID | X | PPaired | X_BAM | MeanDP1 | MeanGQ1 | Ts/Tv | HomoRef | OneAlt | TwoAlt | Missing | SNP |
|---------------|-------|---------|-------|---------|---------|-------|----------|---------|---------|----------|--------|
| ITCH-VAL-0013 | 3.22 | 69.39 | 2.14 | 1.74 | 8.31 | 2.166 | 56155081 | 816906 | 1484700 | 46539036 | 230160 |
| FRCH-SAA-0001 | 2.99 | 83.67 | 2.65 | 2.10 | 7.14 | 2.337 | 77751465 | 1124931 | 2551275 | 23568052 | 367620 |
| FRCH-CRE-0002 | 6.39 | 9.37 | 2.97 | 2.27 | 7.95 | 2.259 | 72448692 | 942786 | 2196123 | 29408122 | 313890 |
| FRCH-ALP-0006 | 3.83 | 79.83 | 3.35 | 2.73 | 9.69 | 2.270 | 81452555 | 1583973 | 2870546 | 19088649 | 445451 |
| ITCH-VAL-0003 | 5.63 | 89.30 | 3.89 | 3.57 | 13.07 | 2.330 | 74281708 | 1784150 | 2646024 | 26283841 | 443017 |
| FRCH-CRE-0001 | 9.57 | 41.46 | 4.34 | 3.79 | 11.05 | 2.254 | 84930925 | 1444332 | 2644116 | 15976350 | 408844 |
| FRCH-SAA-0006 | 5.32 | 88.22 | 4.72 | 3.88 | 11.24 | 2.327 | 89279621 | 2505009 | 3318028 | 9893065 | 582303 |
| FRCH-ALP-0002 | 5.13 | 93.17 | 4.66 | 4.39 | 13.93 | 2.391 | 90248705 | 2729143 | 3323053 | 8694822 | 605219 |
| ITCH-ALP-0009 | 14.24 | 86.39 | 6.04 | 4.42 | 16.86 | 2.246 | 69132089 | 2249216 | 2552400 | 31062018 | 480161 |
| FRRR-BAU-0028 | 15.38 | 92.34 | 5.16 | 4.56 | 13.40 | 2.539 | 74873800 | 12986 | 2599846 | 27509091 | 261283 |

Showing 1 to 10 of 829 entries

First Previous 1 2 3 4 5 ... 83 Next Last



VarGoats preliminary results:

- ❖ **829 genomes** to date.
- ❖ **Sequencing depth** between **1.74x** and **35.38x**.
- ❖ 16 WGS < 5x depth → 9 sequences with <4.5x depth will be discarded.
- ❖ Avg. Number of SNPs:
 - ❖ **SNPs overall**: **domestic goats 2.3M-9.6M**; **wild goats 2.6M-21.7M**.



Variant selection:

Biallelic SNPs



Multiallelic SNPs



- Number?
- Species-specific differences?
- Distribution along the genome?
- Distribution with respect to geographical origin?



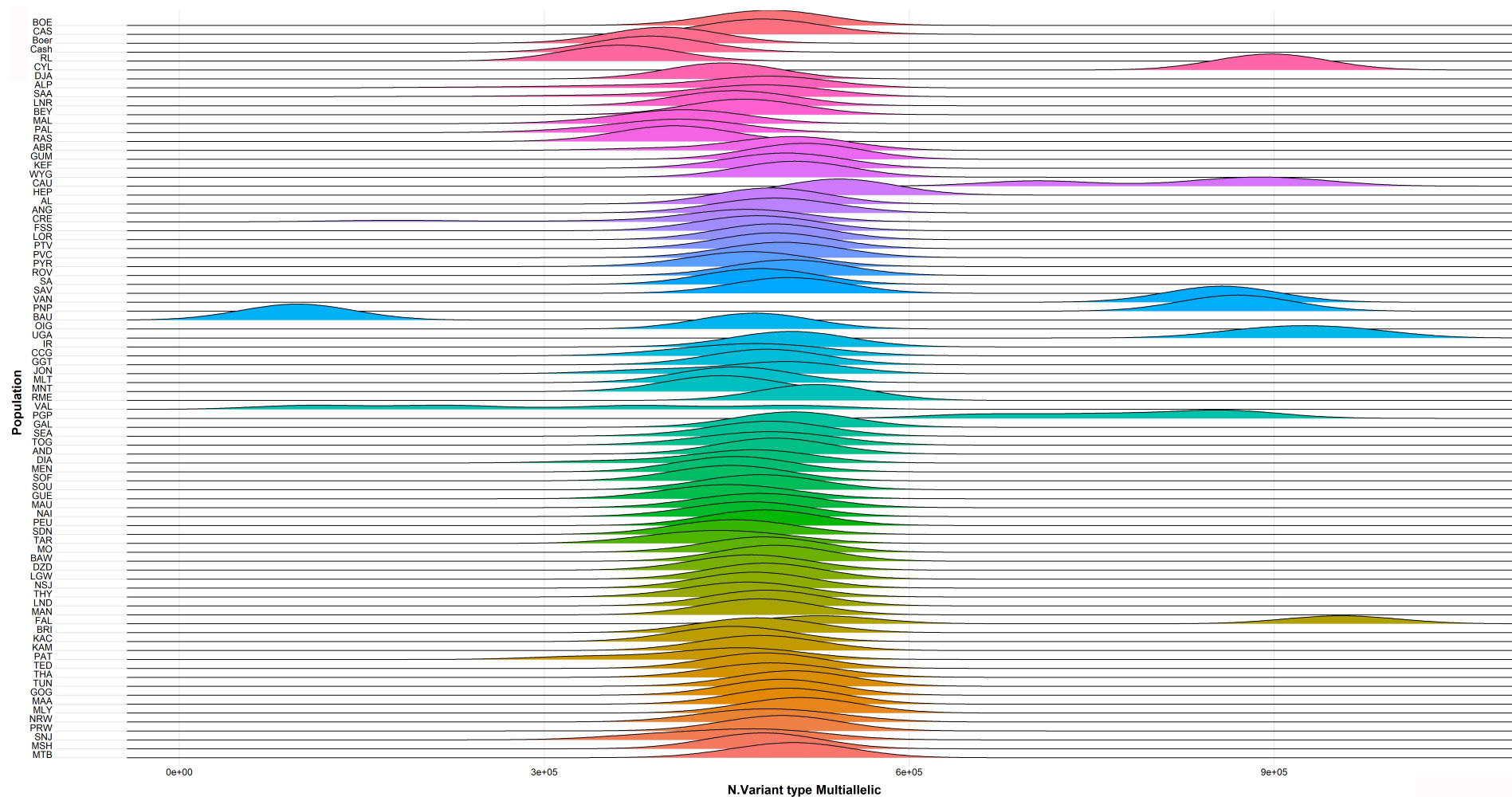
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- ❖ Avg. Number of SNPs:
 - ❖ **SNPs overall**: domestic goats 2.3M-9.6M; wild goats 2.6M-21.7M.
 - ❖ **Multiallelic SNPs**: domestic goats 0.12M-0.57M; wild goats 0.09M-1.04M.



Results – Multiallelic variants:

Multiallelic variants per population

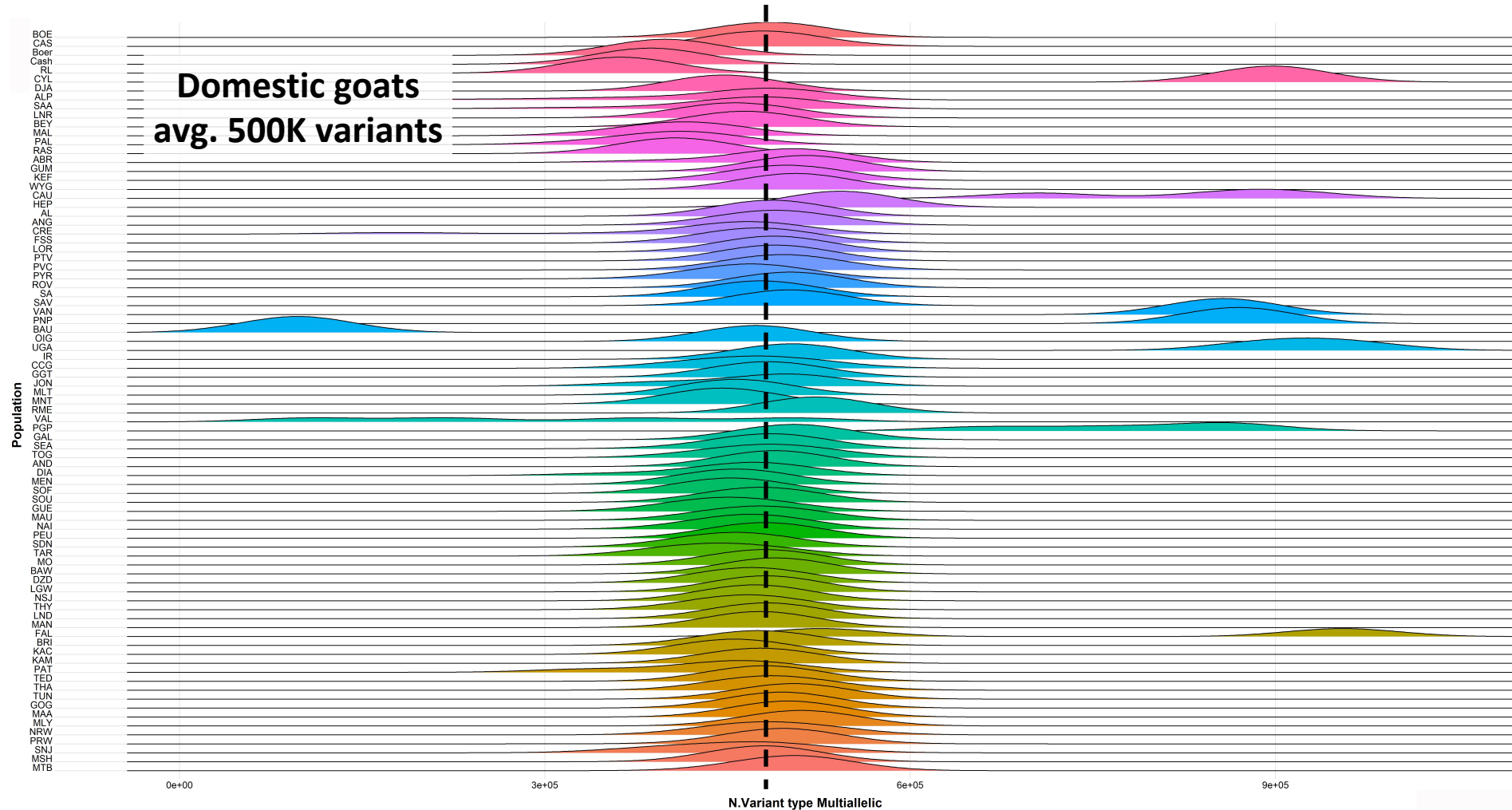




Results – Multiallelic variants:

Multiallelic variants per population

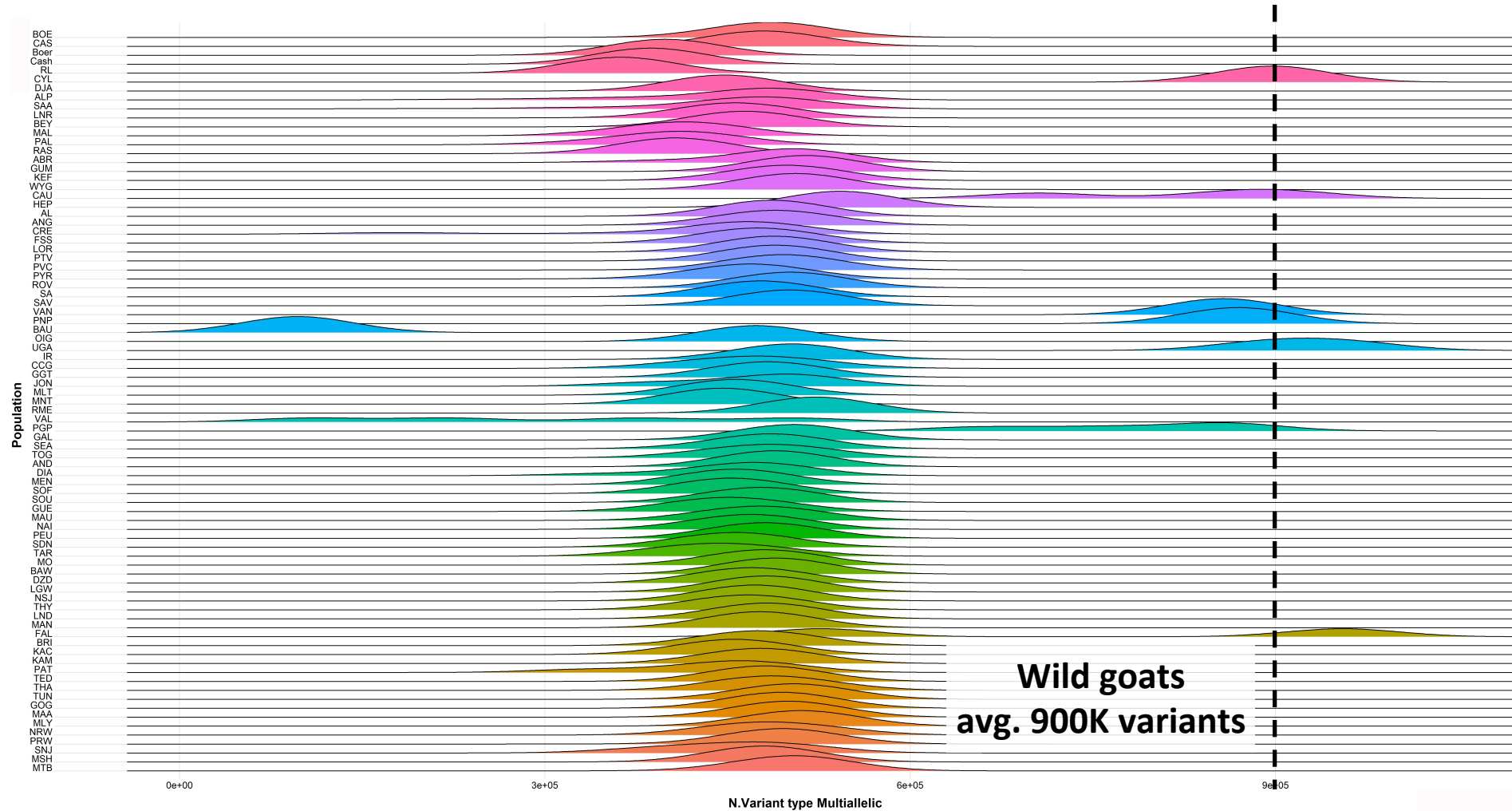
Domestic goats
avg. 500K variants





Results – Multiallelic variants:

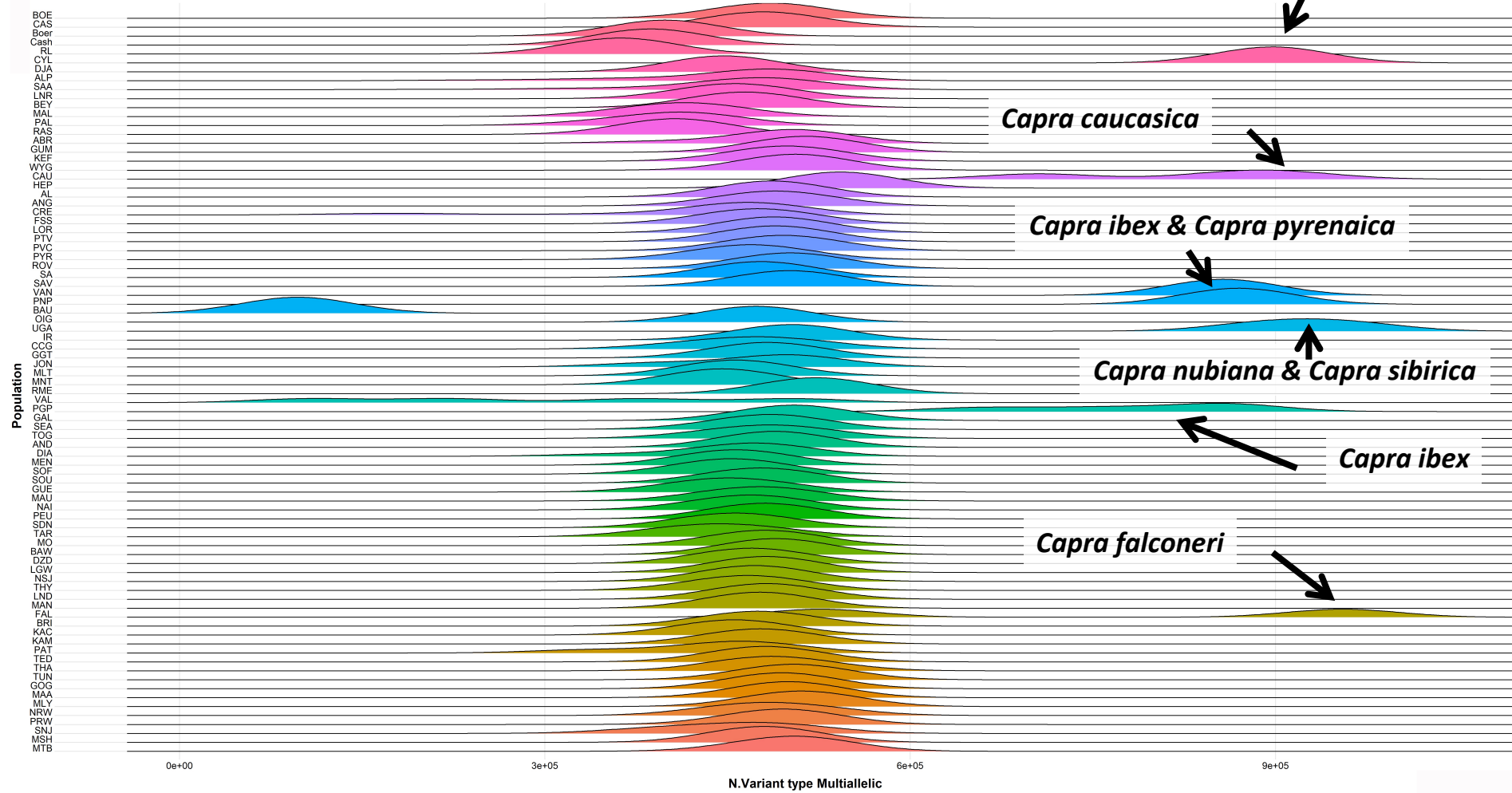
Multiallelic variants per population





Results – Multiallelic variants:

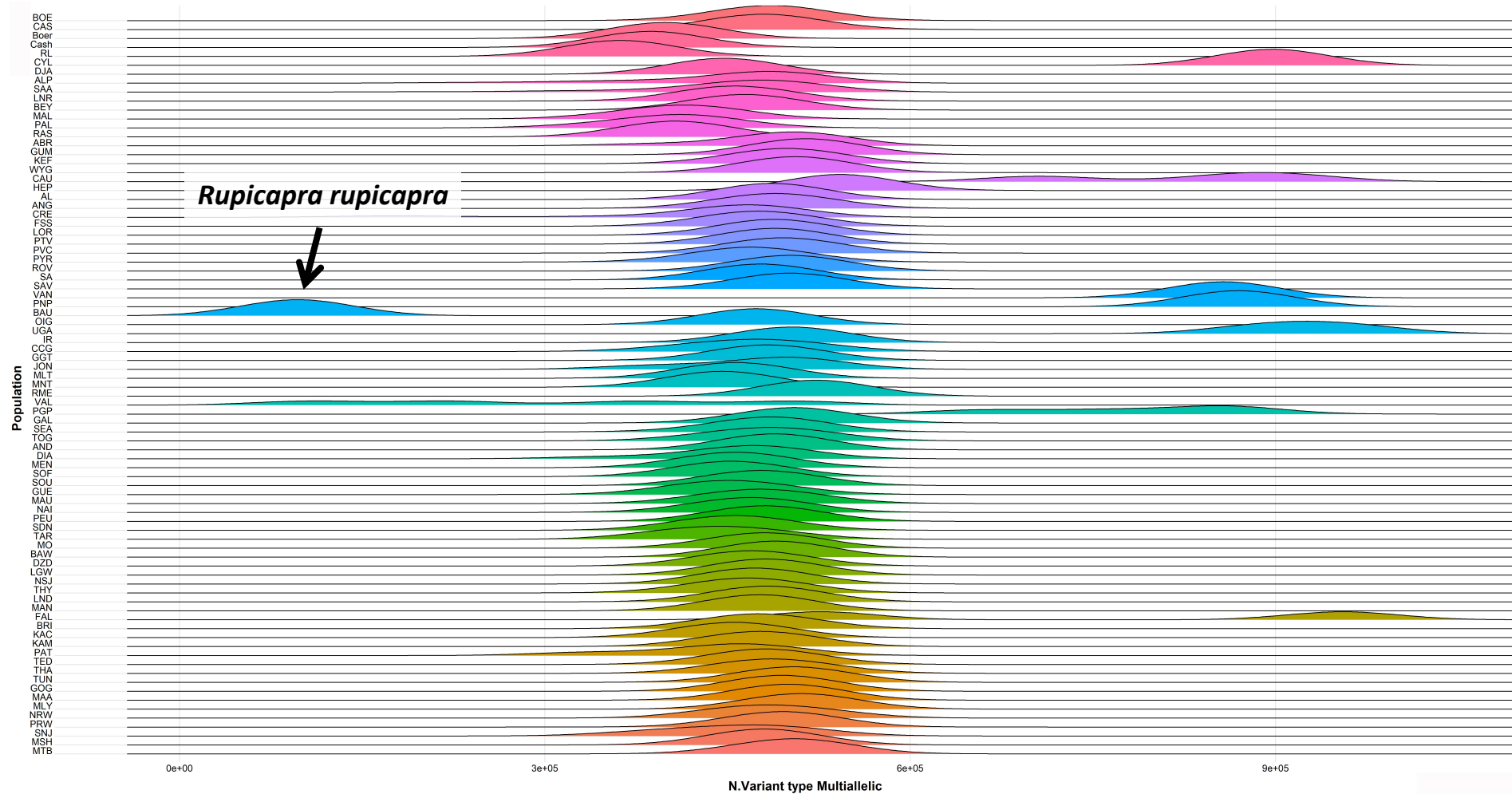
Multiallelic variants per population





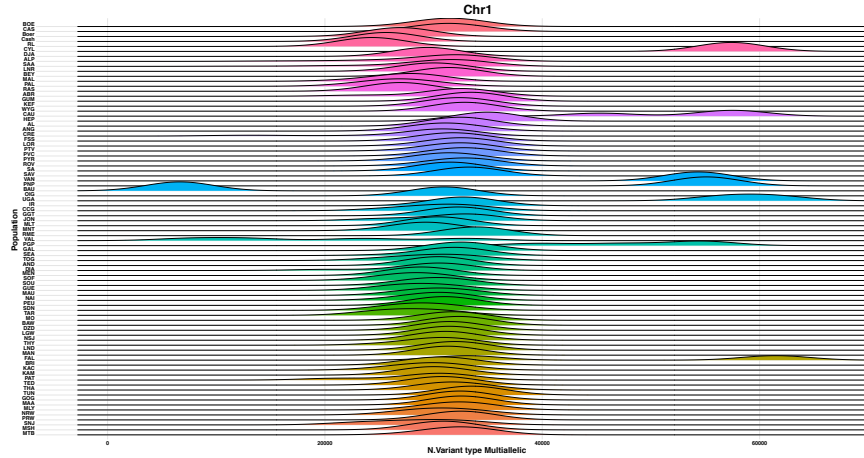
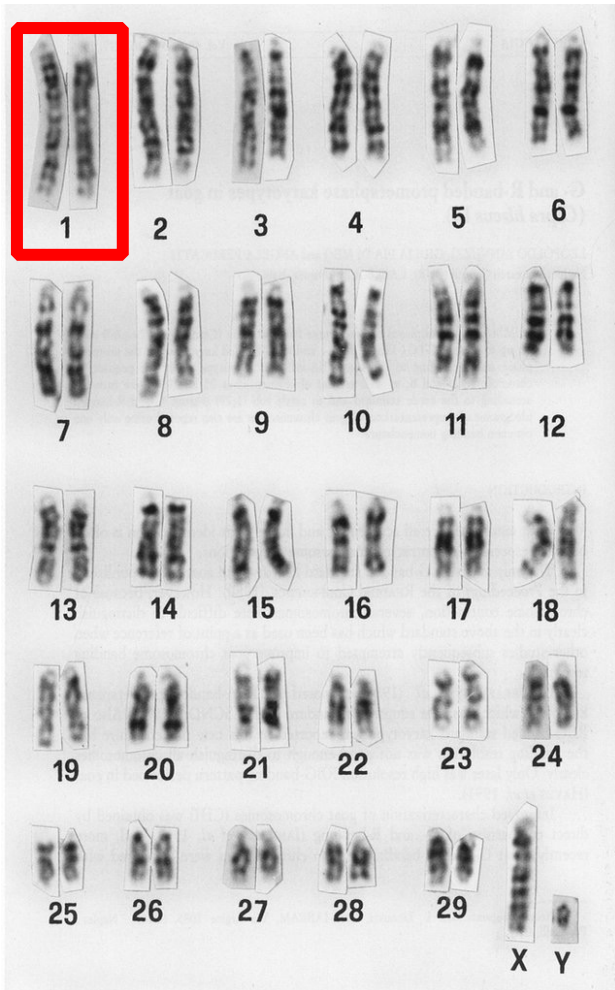
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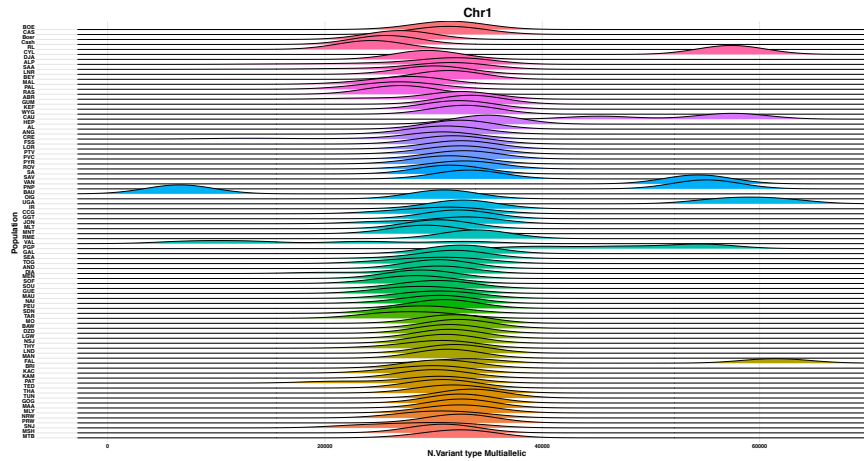
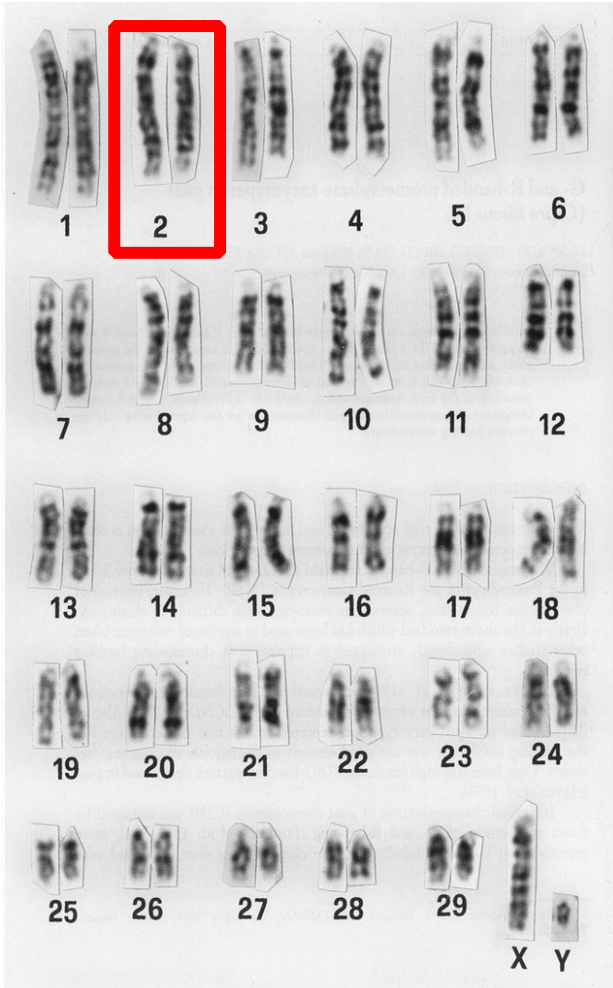
Multiallelic variants per chromosome:



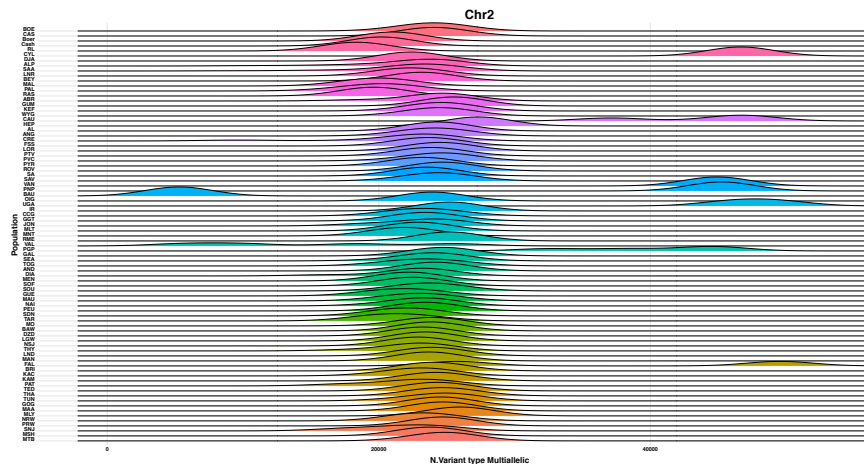
CHR1 = 32K
multiallelic
SNPs on avg.



Multiallelic variants per chromosome:



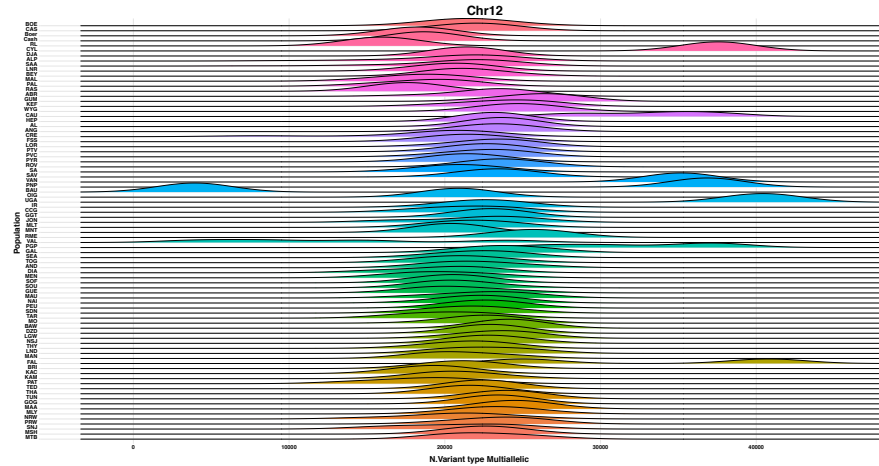
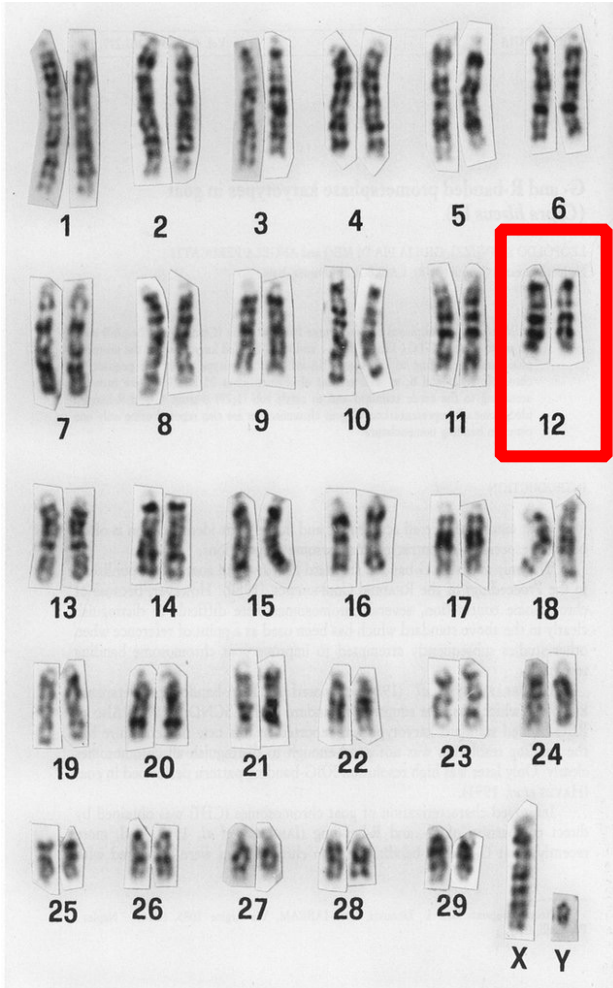
CHR1 = 32K
multiallelic
SNPs on avg.



CHR2 = 25K
multiallelic
SNPs on avg.



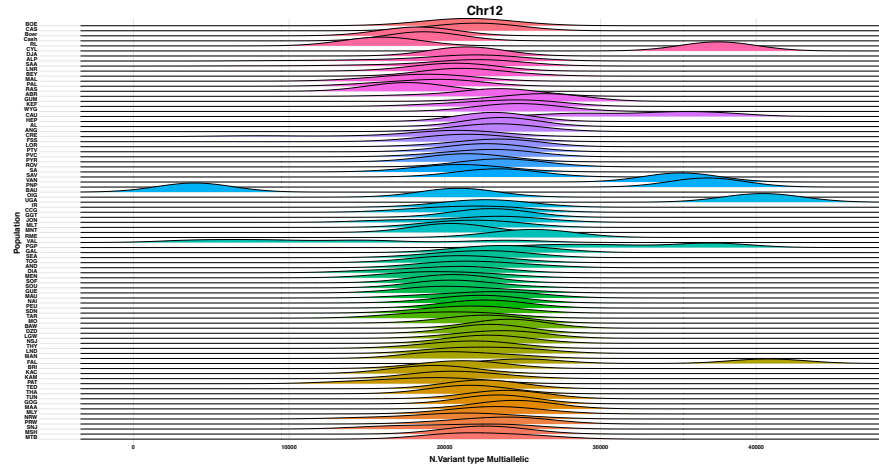
Multiallelic variants per chromosome:



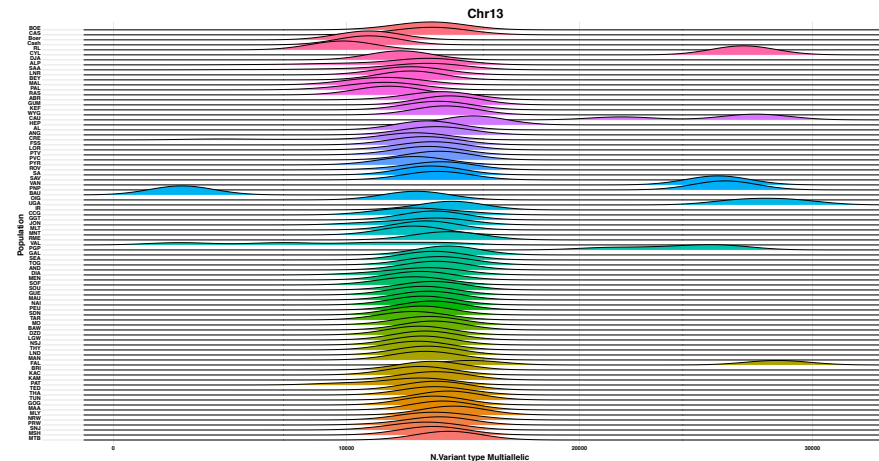
CHR12 = 22K
multiallelic
SNPs on avg.



Multiallelic variants per chromosome:



CHR12 = 22K
multiallelic
SNPs on avg.



CHR13 = 14K
multiallelic
SNPs on avg.



Conclusions:

- The **preliminary evaluation of diversity** suggests that **wild goat species** have a **higher variation** (10-20M SNPs) compared to domestic goats (<10M SNPs).
- **Multiallelic SNPs** show a **similar trend** and represent **ca. 1/20 of the total variants**.
- **Multiallelic SNPs number** is generally **proportional to chromosome size** (some exceptions → further investigation).

Next steps → evaluate their genomic and within-chromosome distribution, and their functional role.



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We want you(r samples):

**60 WG sequencing slots are still available
(sequencing completion deadline Dec. 2019).**

We'd like to improve the number of Asian goats

→ Samples?

Deadline for providing DNA: Sept. 2019.



Acknowledgements:

- ❖ Institutions: INRA, USDA, PTP, CNRS, UGA
- ❖ Platforms: Adriana Alberti, Patrick Wincker (Génoscope),
- ❖ Bioinformaticians: Philippe Bardou (INRA), S.Engelen (Génoscope)
- ❖ Scientists (non exhaustive):
 - ❖ Jim Reecy and Muhammad Moeen-ud-Din, Pakistan
 - ❖ Marcel Amills, Spain
 - ❖ Alessandra Stella, Paola Crepaldi, Italy
 - ❖ Thomas Faraut, François Pompanon, Gwenola Tosser-Klopp, France
 - ❖ Ben Rosen, Curt Van Tassell, USDA, AGIN
 - ❖ Emily Clark, Clet Wandui Masiga
- ❖ Technicians: Julien Sarry (INRA), Céline Orvain (Génoscope)
- ❖ Animal selection: Isabelle Palhière (French goats), Licia Colli (International goats)
- ❖ Sample providers (non exhaustive):
 - ❖ Jim Reecy and Muhammad Moeen-ud-Din, Pakistan
 - ❖ Marcel Amills, Amparo Martinez, Vincenzo Landi, Felix Goyache and Isabelle Alvarez & Armand Sanchez, Spain
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 - ❖ James Kijas, Australia
 - ❖ Christine Flury, Cord Droegemueller, Switzerland
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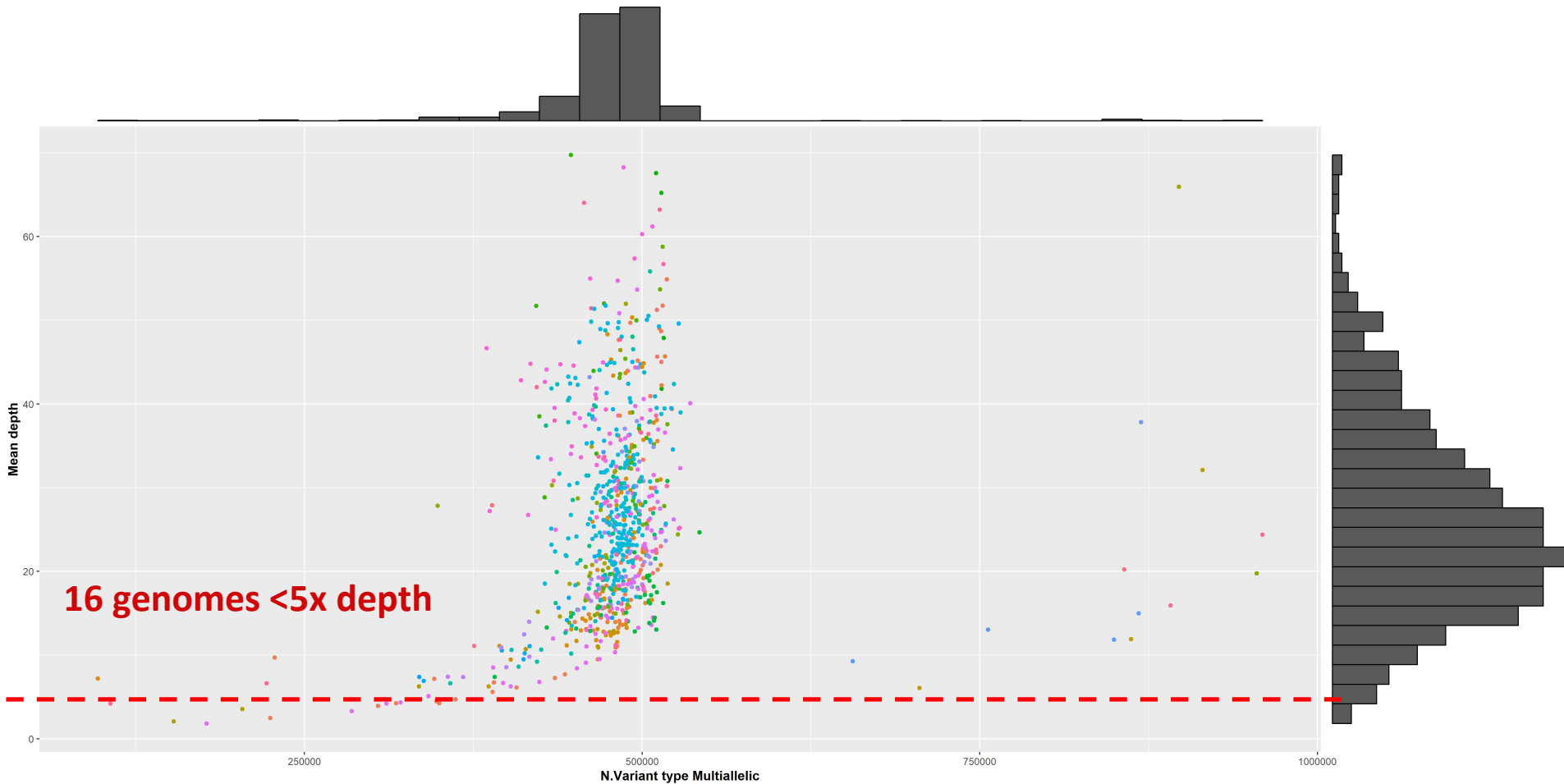


**Thank you for your
attention.**



Results – Multiallelic variants:

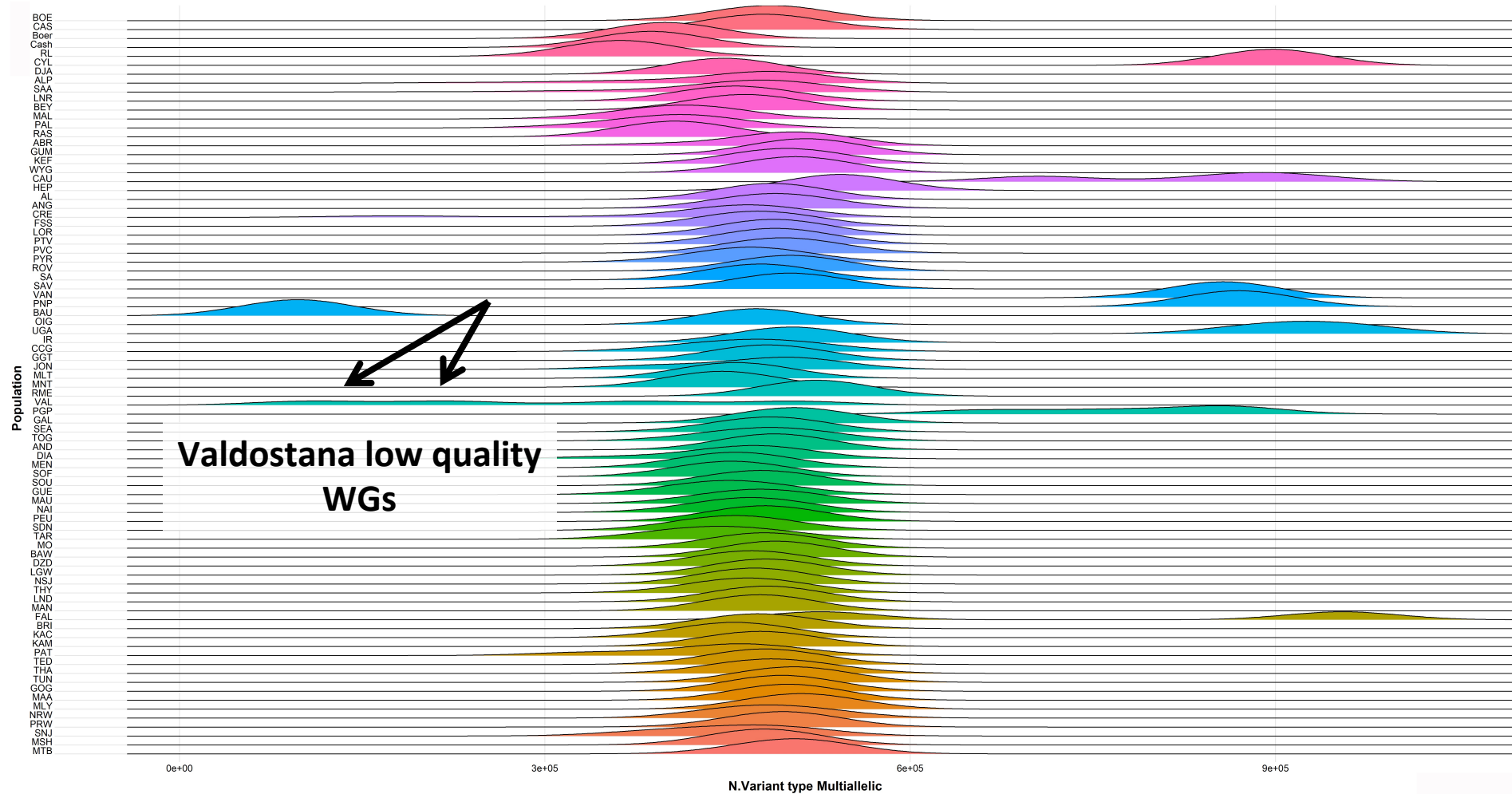
Mean depth vs. number of multiallelic variants





Results – Multiallelic variants:

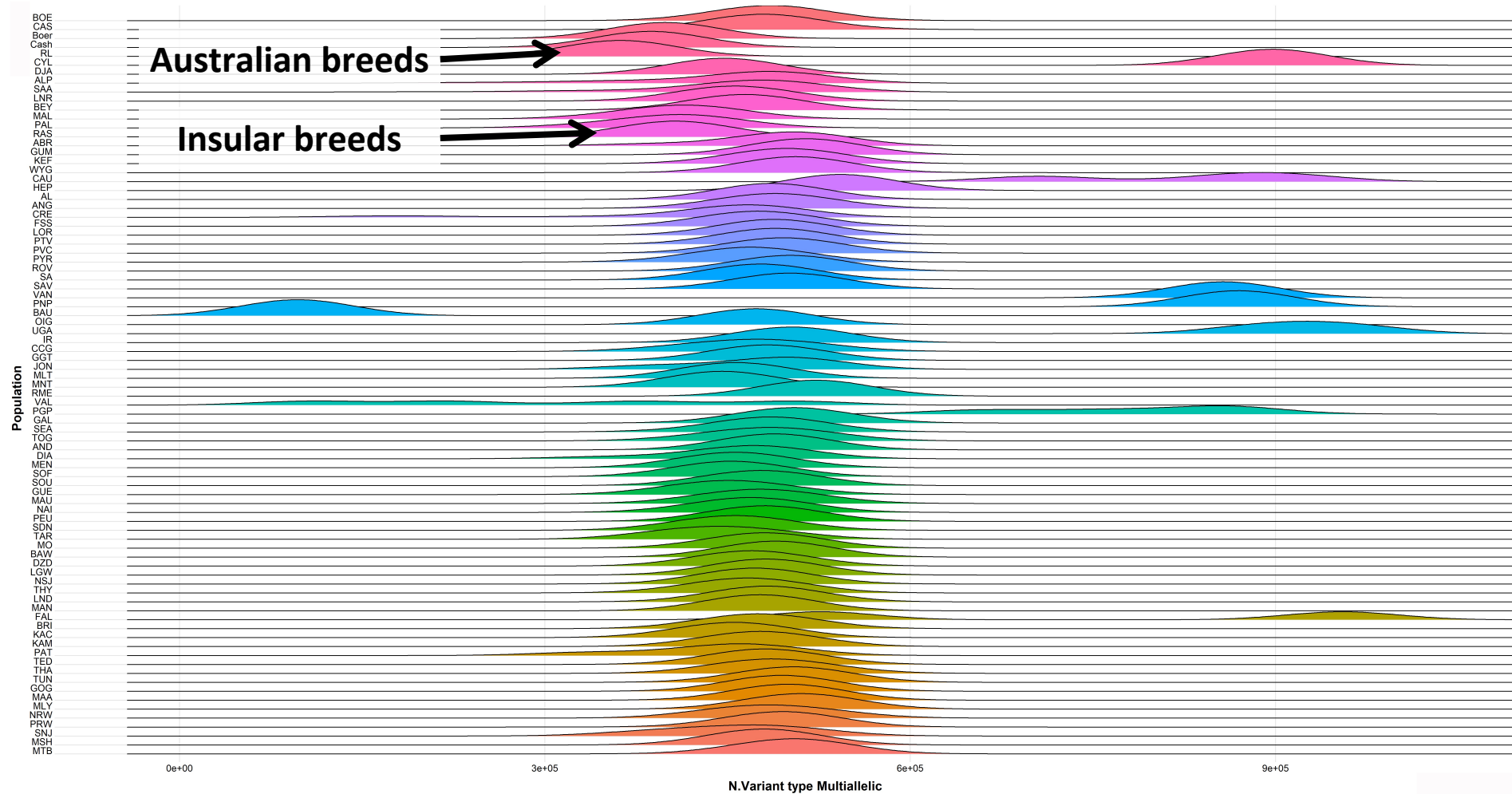
Multiallelic variants per population





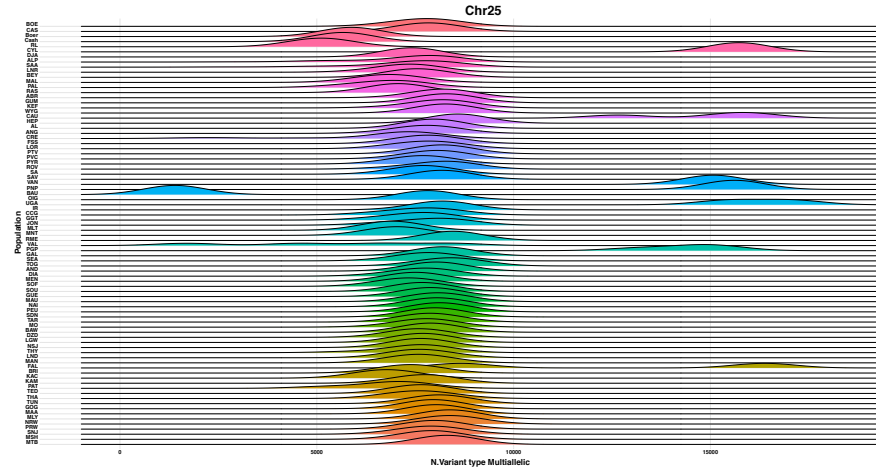
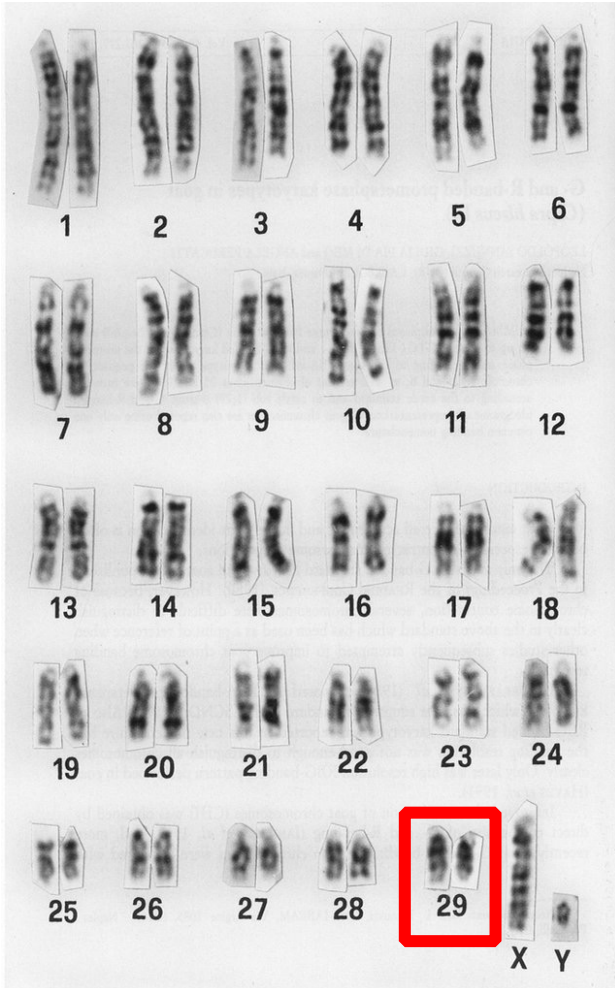
Results – Multiallelic variants:

Multiallelic variants per population

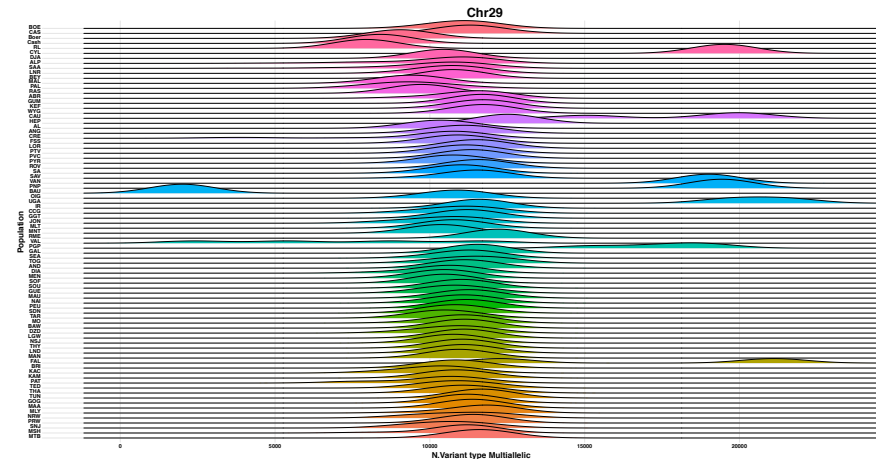




Multiallelic variants per chromosome:



CHR25 = 8K
multiallelic
SNPs on avg.



CHR29 = 12K
multiallelic
SNPs on avg.