Human Genomics Analysis Interface

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University of Pittsburgh
Center for Craniofacial and Dental Genetics

FaceBase Annual Meeting
May 2-3, 2016

GOALS

- Develop software interface for Human Genomics Results
  - No access to individual level data
  - Secure hardware
- Identify appropriate craniofacial genomics projects
  - From craniofacial research community, dbGaP, publications
- Create and display results from genomics projects
  - E.g. Manhattan plots, LocusZoom

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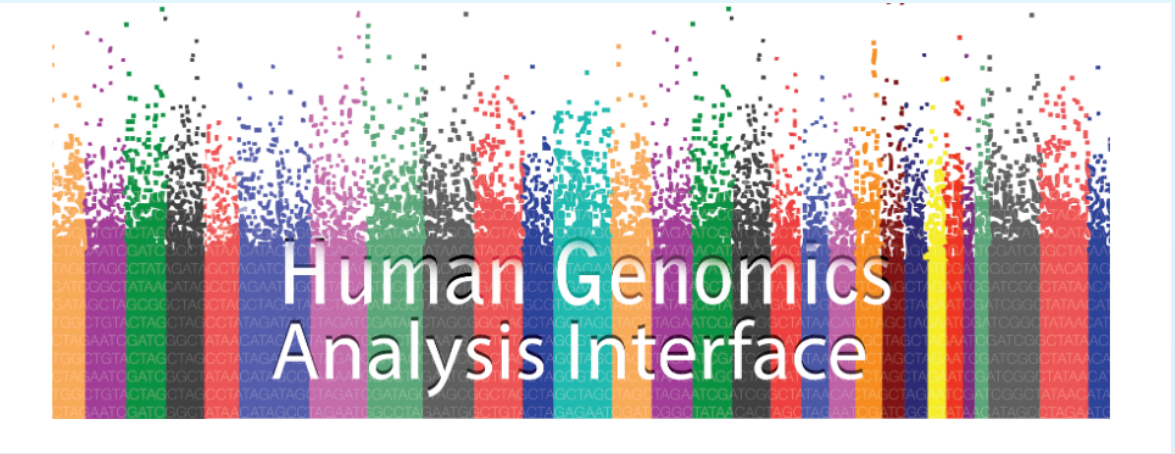
UPDATES



- Hardware established
- Basic software created
- WebSite created and updated
- Multiple projects identified
  - Orofacial Clefting, Facial Variation, Dental
- Project pages created
- Results databases and interface created

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APPROACH

- User friendly, save user time
- Pre-calculate results databases (e.g. p-values at SNPs)
  - For all relevant subsets: by ethnicity, by genotyped versus imputed panels, by phenotype, by environmental factors
  - Customized: with PIs (e.g. published results)
- Prepare Manhattan plot files
- Pre-run typical LocusZoom requests

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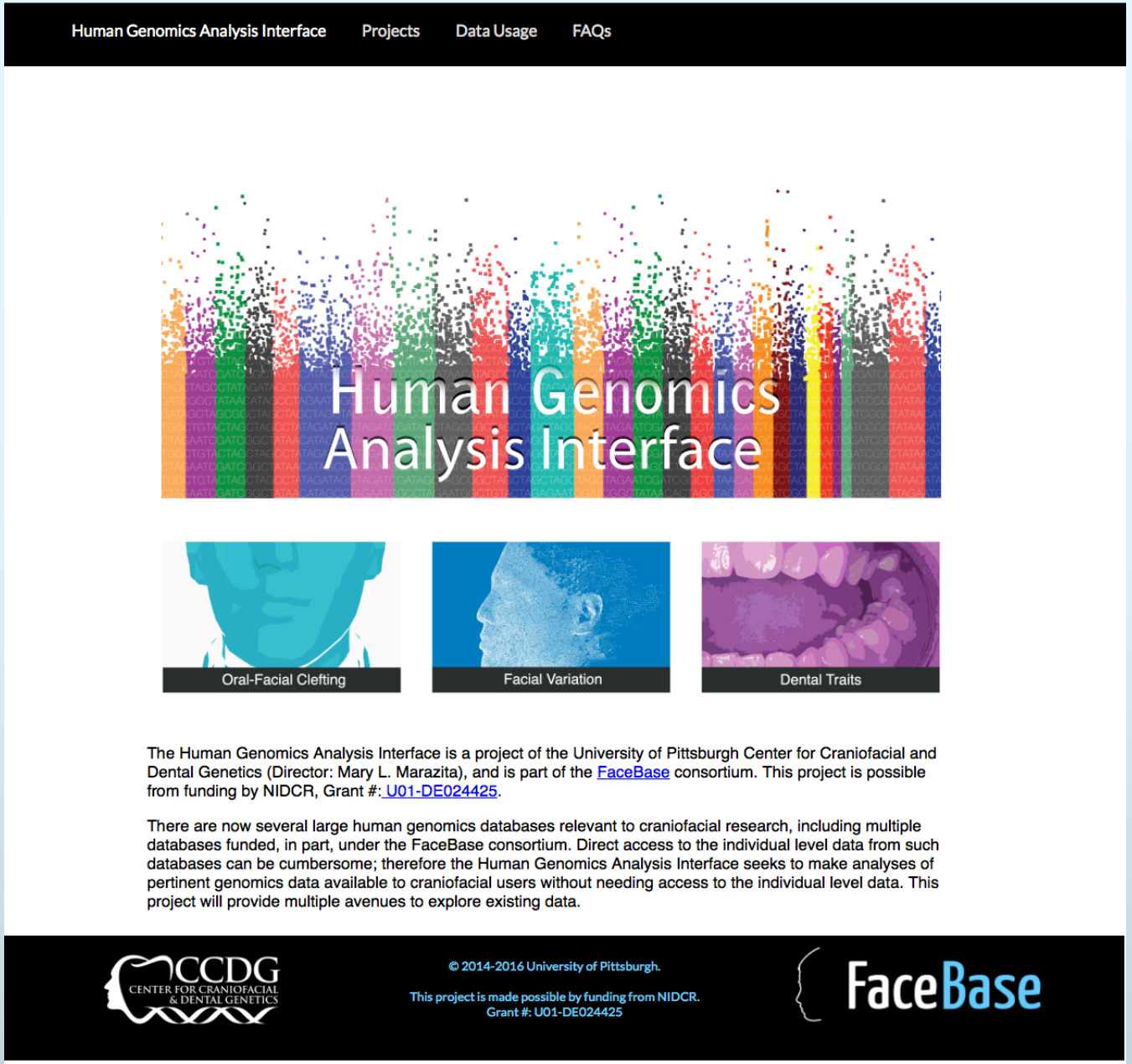
WEBSITE

FaceBase.sdmgenetics.pitt.edu

- Link also available on the FaceBase.org Home page, and our Project page


Human Genomics Analysis Interface
Projects
Data Usage
FAQs
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Oral-Facial Clefting
Facial Variation
Dental Traits
The Human Genomics Analysis Interface is a project of the University of Pittsburgh Center for Craniofacial and Dental Genetics (Director: Mary L. Marazita), and is part of the FaceBase consortium. This project is possible from funding by NIDCR, Grant #: U01-DE024425.
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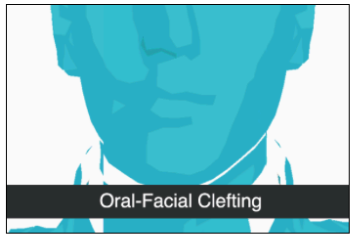
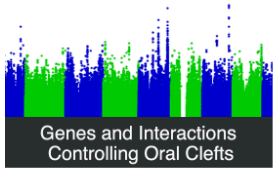
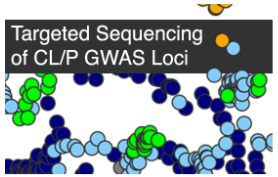
Human Genomics Analysis Interface | Projects | Data Usage | FAQs





International Consortium to Identify Genes and Interactions Controlling Oral Clefts- Genome Wide Association Study
dbGaP Study Accession: phs000094.v1.p1
Principal Investigator: Terri H. Beaty. Johns Hopkins School of Public Health, Baltimore, MD, USA



Targeted Sequencing of CL/P GWAS Loci
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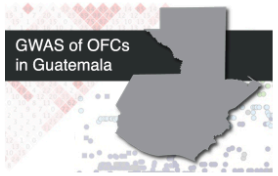
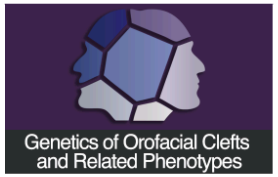
Principal Investigators: Jeffrey C. Murray, University of Iowa, Iowa City, IA, USA
Mary L. Marazita, University of Pittsburgh, Pittsburgh, PA, USA
Richard K. Wilson, Washington University School of Medicine, St. Louis, MO, USA
George Weinstock, Jackson Laboratory for Genomic Medicine, Farmington, CT, USA



GWAS of OFCs in Guatemala
dbGaP Study Accession: phs000440.v1.p1
Principal Investigator: Mary Marazita, University of Pittsburgh School of Dental Medicine, Pittsburgh, PA, USA



Genetics of Orofacial Clefts and Related Phenotypes
dbGaP Study Accession: phs000774.v1.p1
Principal Investigator: Mary Marazita, University of Pittsburgh School of Dental Medicine, Pittsburgh, PA, USA

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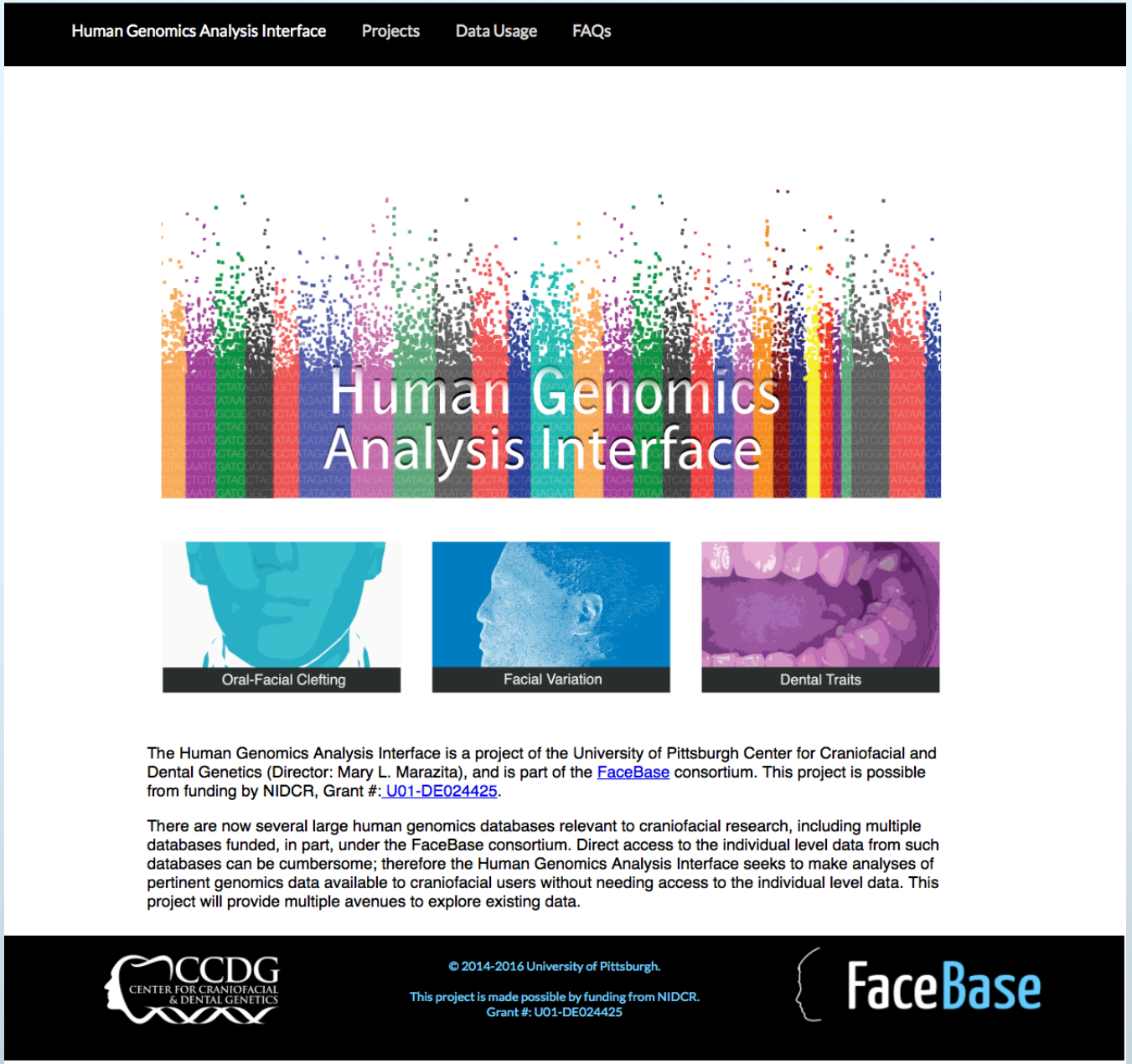
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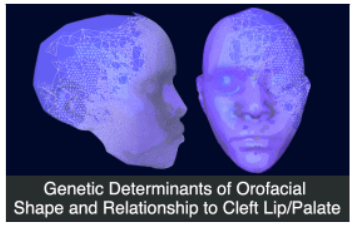
[3D Facial Norms]
dbGaP Study Accession:
Principal Investigator: Seth Weinberg. University of Pittsburgh School of Dental Medicine, Pittsburgh, PA, USA



[Genetic Determinants of Orofacial Shape and Relationship to Cleft Lip/Palate]
dbGaP Study Accession: phs000622.v1.p1
Principal Investigator: Richard Spritz, MD. University of Colorado School of Medicine, Aurora, CO USA

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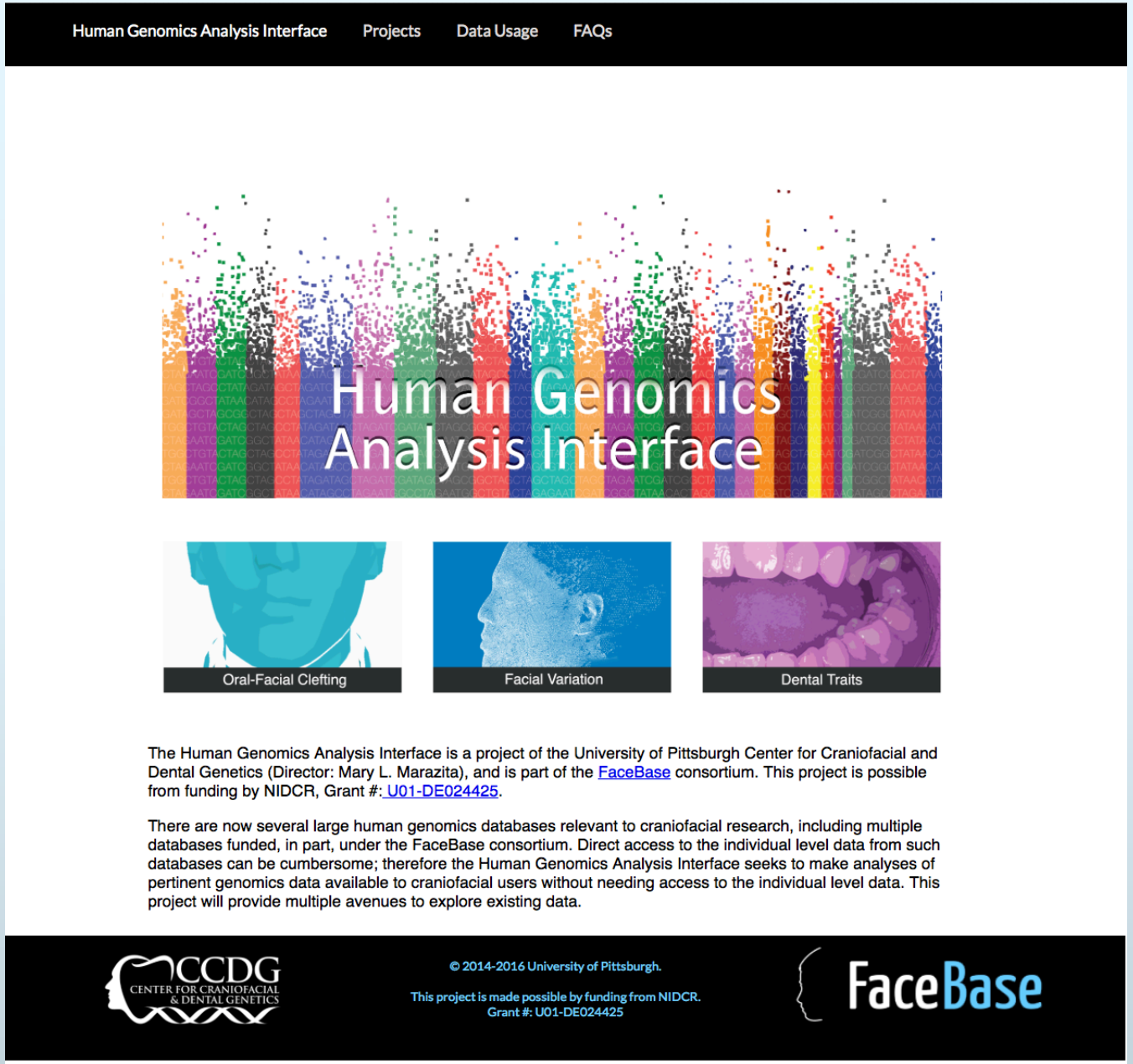
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Childhood Caries
dbGap Study Accession: phs000095.v3.p1
Principal Investigator: Mary Marazita, University of Pittsburgh School of Dental Medicine, Pittsburgh, PA, USA

Caries in Permanent Dentition
dbGap Study Accession: phs000095.v3.p1
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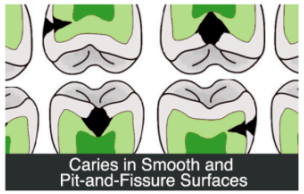

Caries in Smooth and Pit-and-Fissure Surfaces
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Principal Investigator: Mary Marazita, University of Pittsburgh School of Dental Medicine, Pittsburgh, PA, USA

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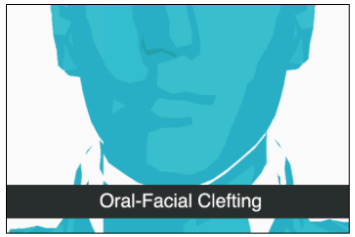

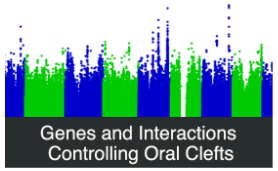

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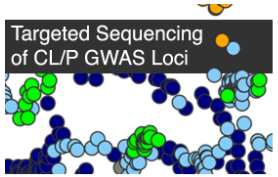

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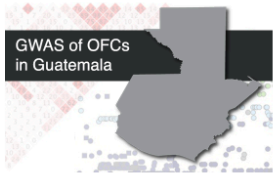

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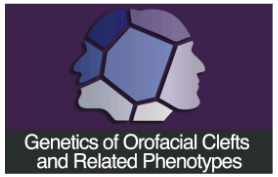

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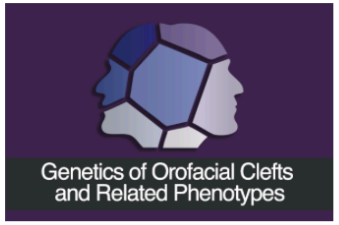

dbGaP Study Accession: phs000774.v1.p1.
Principal Investigator: Mary L. Marazita, University of Pittsburgh, Pittsburgh, PA, USA
Funding Sources:

X01-HG00784 Genetics of Orofacial Clefts and Related Phenotypes. National Human Genome Research Institute, CIDR Genotyping, National Institutes of Health, Bethesda, MD, USA

R01-DE-016148, Extending the Phenotype of Nonsyndromic Orofacial Clefts. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DE-012472, HOMOZYGOSITY MAPPING OF ORAL-FACIAL CLEFTS IN TURKEY. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DE-009886, GENE MAPPING STUDIES OF ORAL/FACIAL CLEFTS - CHINA/INDIA. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

P50-DE-016215, CRANIOFACIAL ANOMALIES RESEARCH CENTER. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

K99-DE-022378, GENETIC STUDIES OF NONSYNDROMIC CLEFTS IN POPULATIONS OF AFRICAN DESCENT. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R37-DE-008559, MOLECULAR GENETIC EPIDEMIOLOGY OF CLEFT LIP AND PALATE. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DE-014667, CLEFT LIP GENETICS: A MULTI CENTER INTERNATIONAL CONSORTIUM. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DD-000295, HEALTH OUTCOMES AND IMPROVED PHENOTYPIC CHARACTERIZATION OF CLEFT LIP AND PALATE. National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA

R21-DE-016930, PLANNING INTERNATIONAL OROFACIAL CLEFT GENETIC STUDIES. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

The current study is the culmination of many years of ongoing collaborations among the study investigators (for complete list of investigators, see dbGaP). Molecular genetic studies of orofacial clefts (OFC) by members of this research consortium began in the 1980's, followed by genome-wide linkage studies in the 1990's-early 2000's, and then genome-wide association studies in the 2010's. A rich phenotyping approach was first added to the consortium in 1999 as a project led by Dr. Mary Marazita under a center grant headed by Dr. Jeff Murray. Additional sites were added throughout the 2000's, until multiple populations and a large number of individuals (~12,000) comprise the current study population for genetic studies of OFCs and related subclinical phenotypes—subtle features believed to represent mild manifestations of the same underlying genetic susceptibility responsible for OFCs. As such, their inclusion in case-control and family-based genetic studies can help to clarify and refine the relationship between genotype and phenotype. Information on how to obtain individual level data is available on dbGaP.

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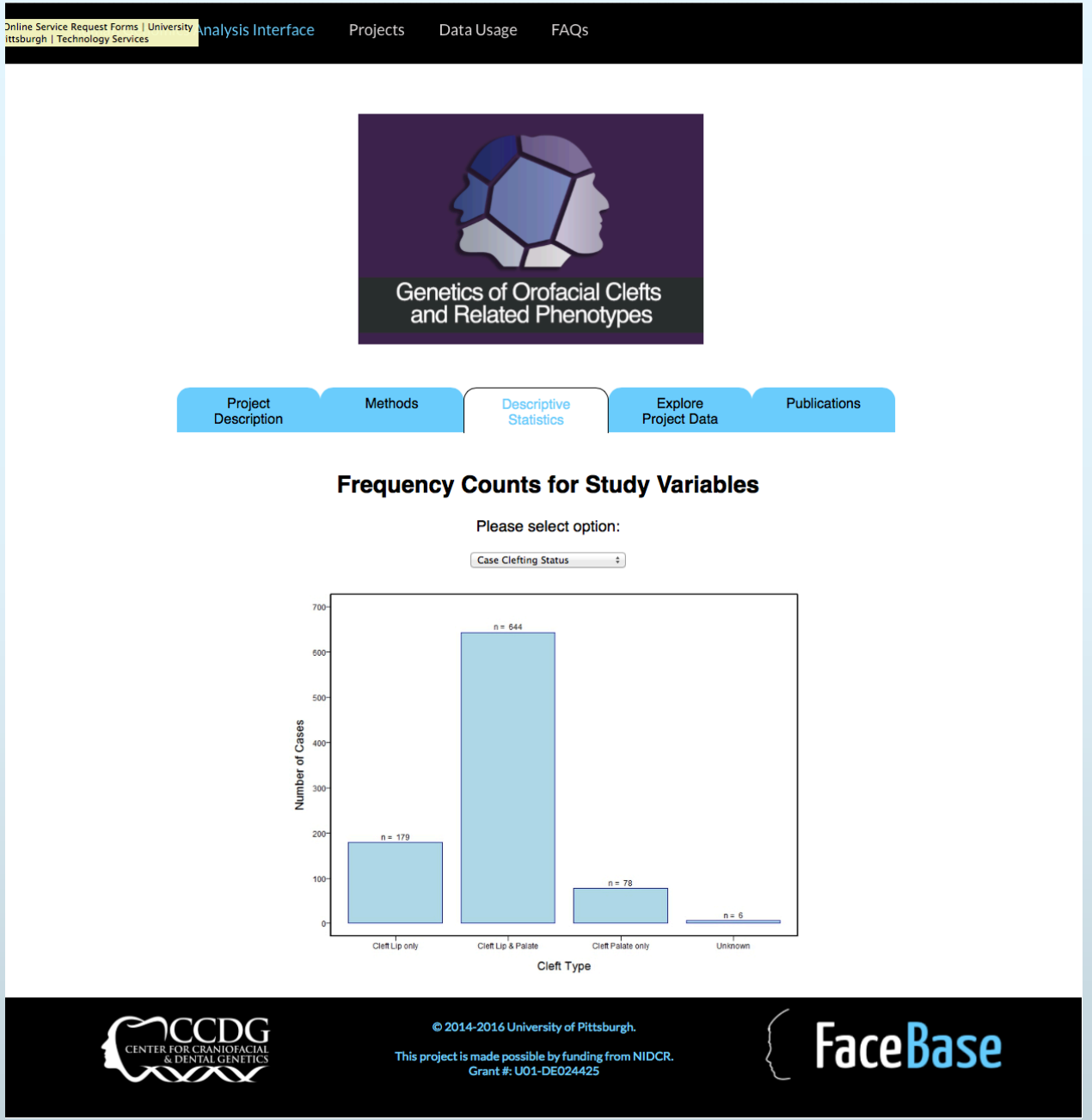
Online Service Request Forms | University of Pittsburgh | Technology Services
Analysis Interface
Projects
Data Usage
FAQs
Genetics of Orofacial Clefts and Related Phenotypes
Project Description
Methods
Descriptive Statistics
Explore Project Data
Publications
Frequency Counts for Study Variables
Please select option:
Case Clefting Status
Number of Cases
n = 179
n = 644
n = 78
n = 6
Cleft Lip only
Cleft Lip & Palate
Cleft Palate only
Unknown
Cleft Type
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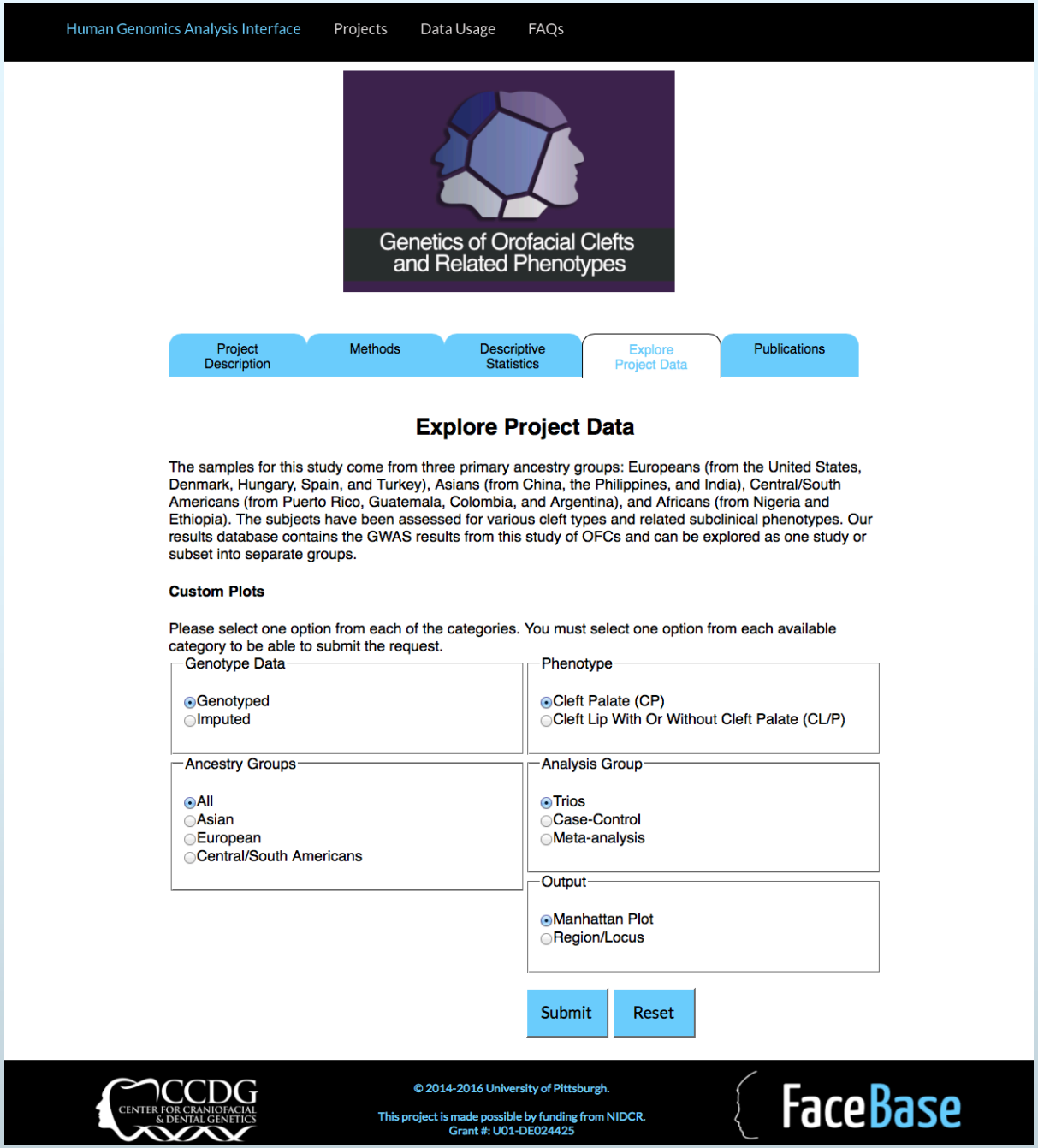
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Data Usage
FAQs
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The samples for this study come from three primary ancestry groups: Europeans (from the United States, Denmark, Hungary, Spain, and Turkey), Asians (from China, the Philippines, and India), Central/South Americans (from Puerto Rico, Guatemala, Colombia, and Argentina), and Africans (from Nigeria and Ethiopia). The subjects have been assessed for various cleft types and related subclinical phenotypes. Our results database contains the GWAS results from this study of OFCs and can be explored as one study or subset into separate groups.
Custom Plots
Please select one option from each of the categories. You must select one option from each available category to be able to submit the request.
Genotype Data
Genotyped
Imputed
Phenotype
Cleft Palate (CP)
Cleft Lip With Or Without Cleft Palate (CL/P)
Ancestry Groups
All
Asian
European
Central/South Americans
Analysis Group
Trios
Case-Control
Meta-analysis
Output
Manhattan Plot
Region/Locus
Submit
Reset
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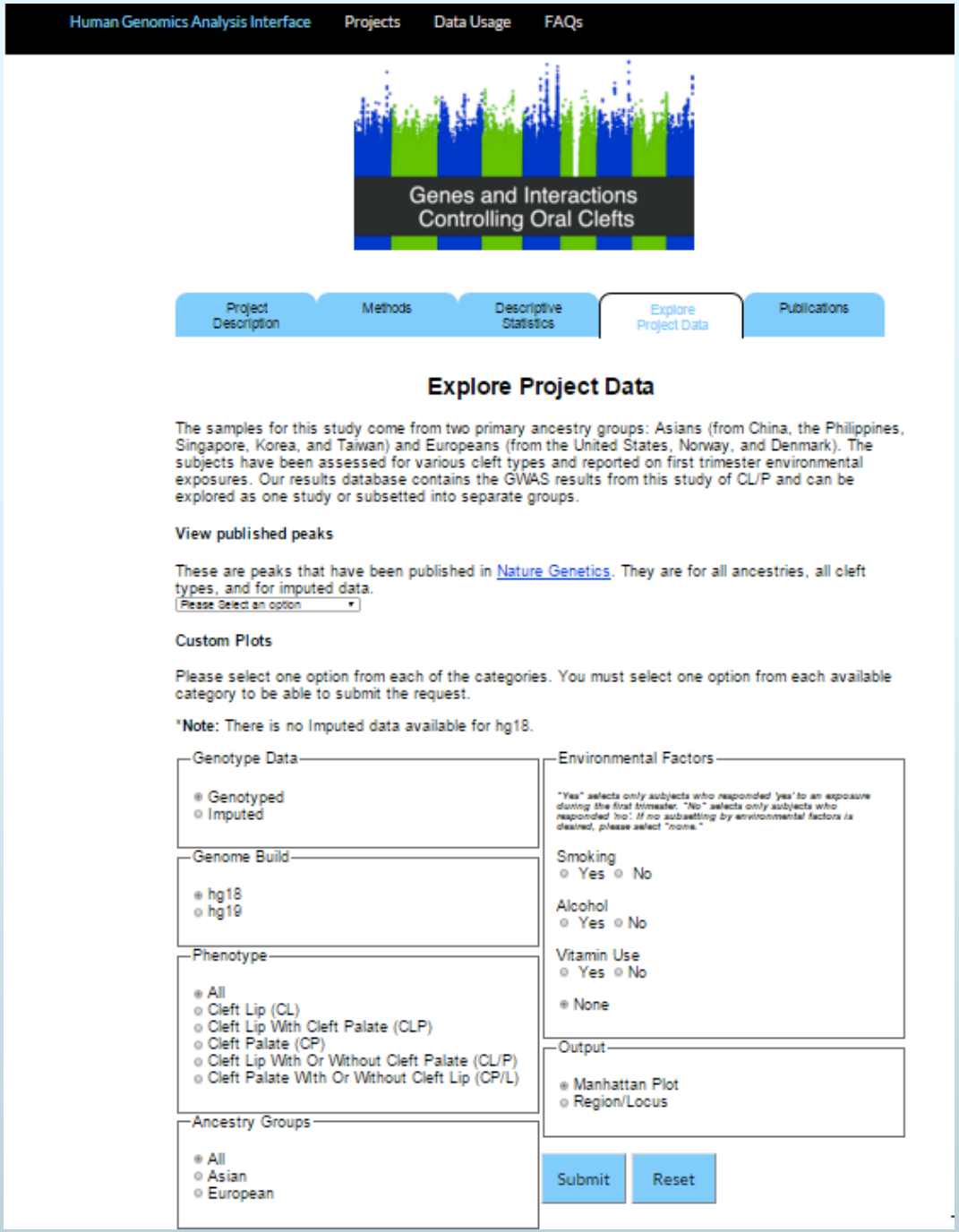
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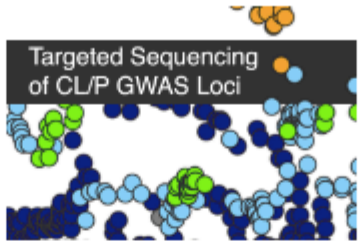
The samples for this study come from two primary ancestry groups: Asians (from China, the Philippines, Singapore, Korea, and Taiwan) and Europeans (from the United States, Norway, and Denmark). The subjects have been assessed for various cleft types and reported on first trimester environmental exposures. Our results database contains the GWAS results from this study of CL/P and can be explored as one study or subsetted into separate groups.
View published peaks
These are peaks that have been published in Nature Genetics. They are for all ancestries, all cleft types, and for imputed data.
Please Select an option
Custom Plots
Please select one option from each of the categories. You must select one option from each available category to be able to submit the request.
*Note: There is no Imputed data available for hg18.
Genotype Data
Genotyped
Imputed
Genome Build
hg18
hg19
Phenotype
All
Cleft Lip (CL)
Cleft Lip With Cleft Palate (CLP)
Cleft Palate (CP)
Cleft Lip With Or Without Cleft Palate (CL/P)
Cleft Palate With Or Without Cleft Lip (CP/L)
Ancestry Groups
All
Asian
European
Environmental Factors
"Yes" selects only subjects who responded 'yes' to an exposure during the first trimester. "No" selects only subjects who responded 'no'. If no subsetting by environmental factors is desired, please select "none."
Smoking
Yes
No
Alcohol
Yes
No
Vitamin Use
Yes
No
None
Output
Manhattan Plot
Region/Locus
Submit
Reset

Human Genomics Analysis Interface | Projects | Data Usage | FAQs



Project Description | Methods | Descriptive Statistics | Explore Project Data | Publications

Explore Project Data

This project involved targeted sequencing of GWAS loci for CL/P. Thirteen regions were sequenced. The samples for this study come from two primary ancestry groups: Asians (from China and the Philippines) and Europeans (from several sites in the United States. Our results database contains the association results for each of the thirteen sequenced regions and can be explored in the combined sample or in each ancestry group separately.

Custom Plots

Please select one option from each of the categories. You must select one option from each available category to be able to submit the request.

Ancestry Groups
- All
- Asian
- European

Locus
- 1p36 (PAX7)
- 1p22 (ARHGAP29)
- 1q32 (IRF6)
- 4p16 (MSX1)
- 8q24
- 9q22 (FOXE1)
- 9q22 (PTCH1)
- 10q25 (VAX1)
- 10q26 (FGFR2)
- 14q22 (BMP4)
- 17p13 (NTN1)
- 17q22 (NOG)
- 20q12 (MAFB)

Submit | Reset

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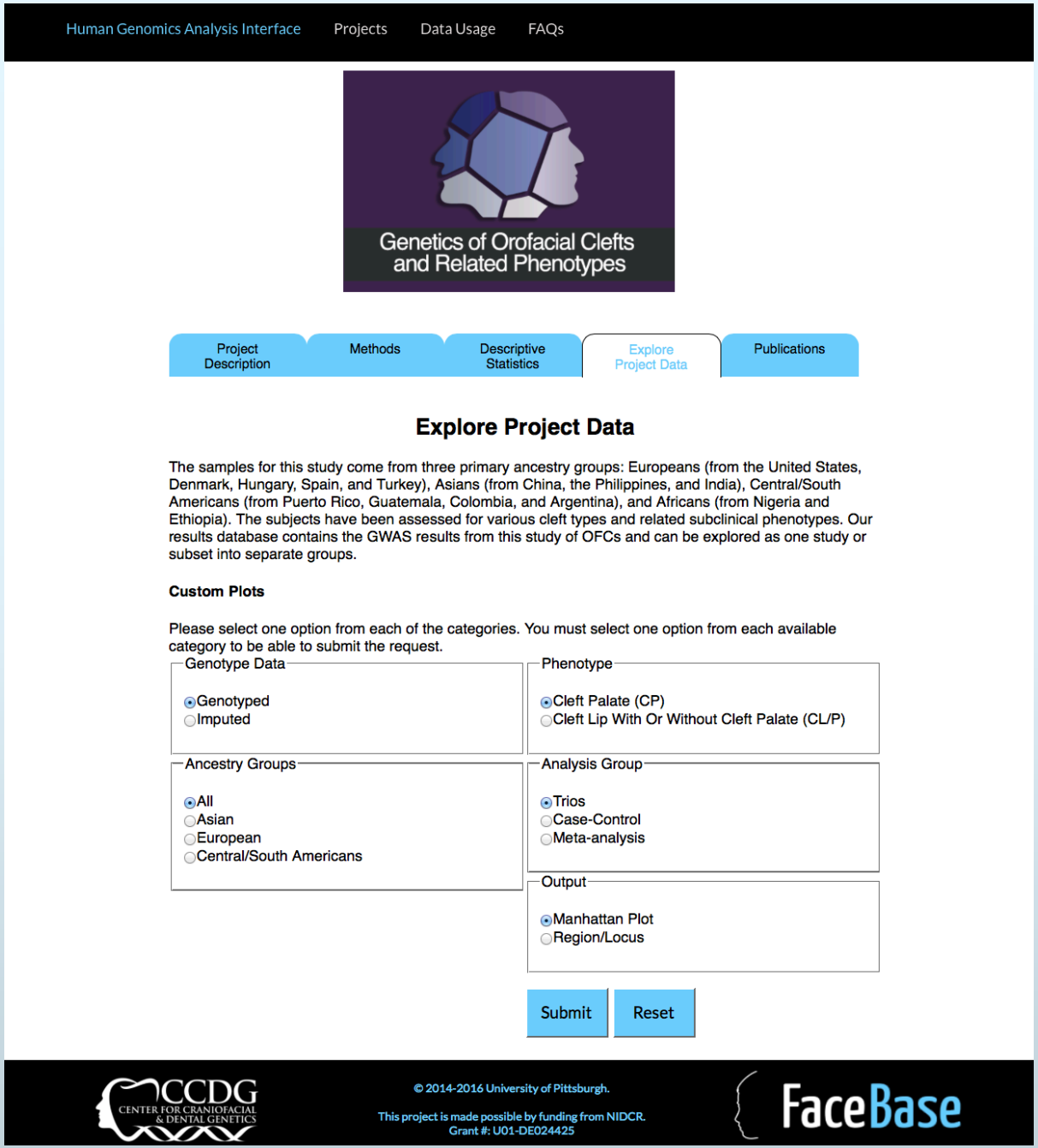
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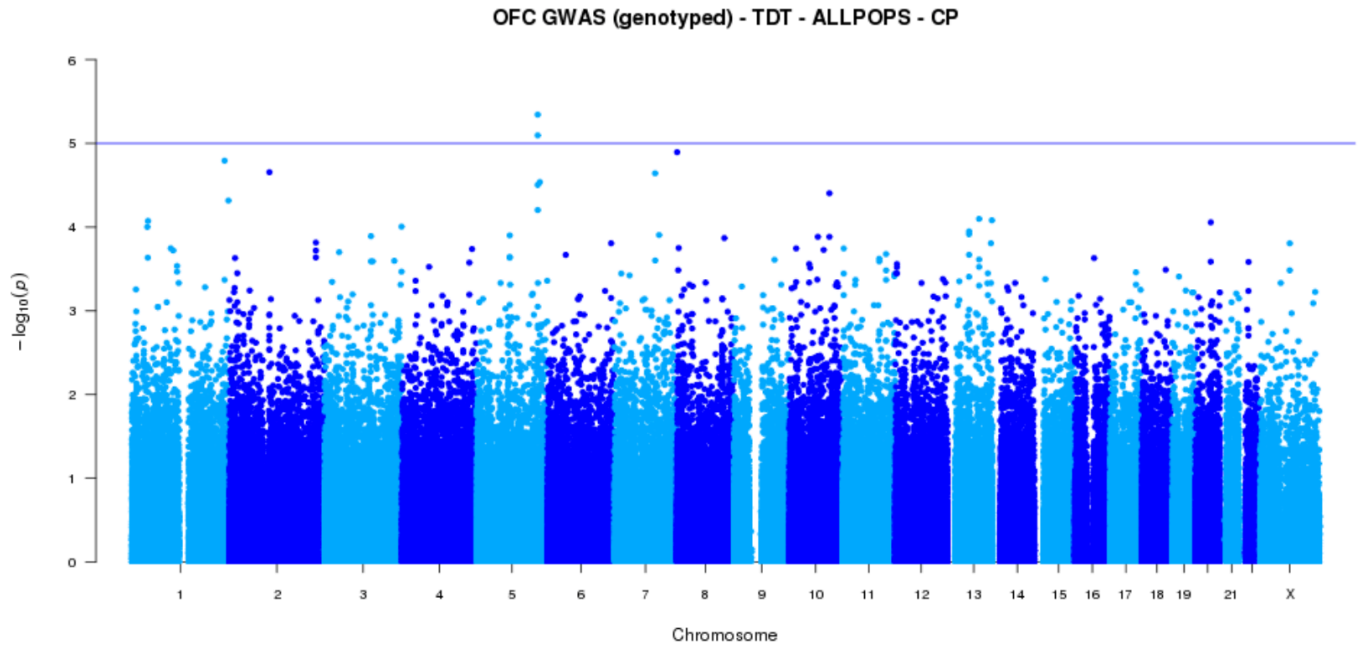

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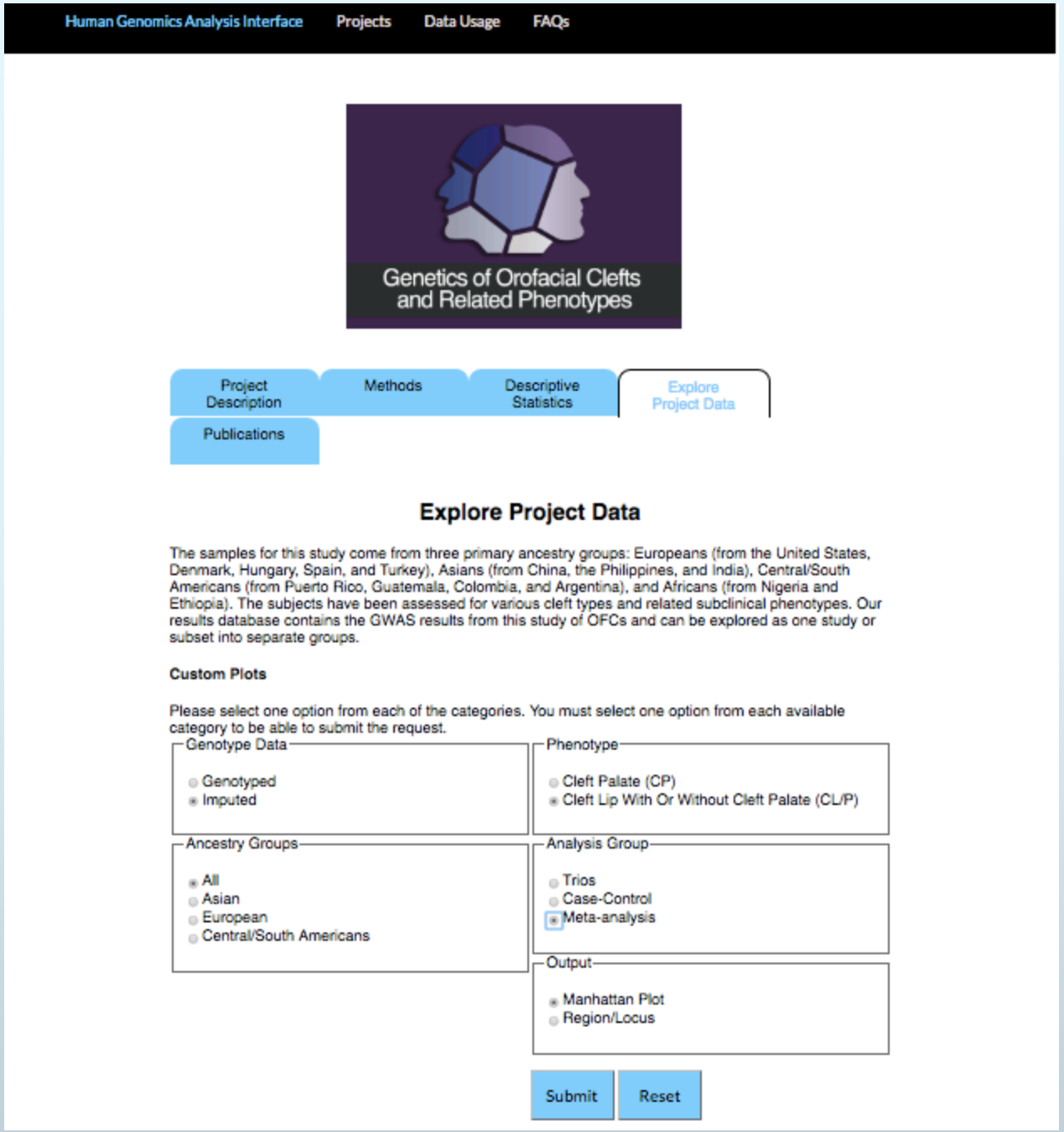
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Projects
Data Usage
FAQs
Genetics of Orofacial Clefts and Related Phenotypes
Project Description
Methods
Descriptive Statistics
Explore Project Data
Publications
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Cleft Lip With Or Without Cleft Palate (CL/P)
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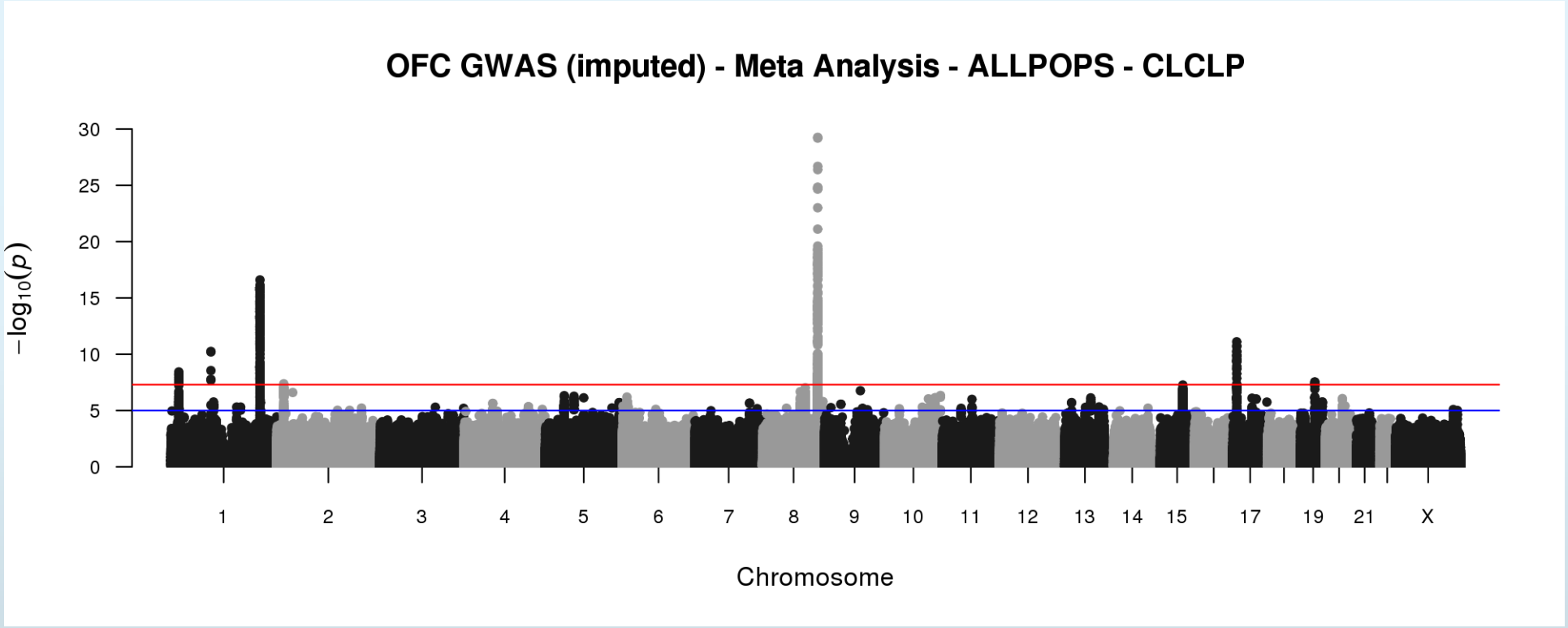
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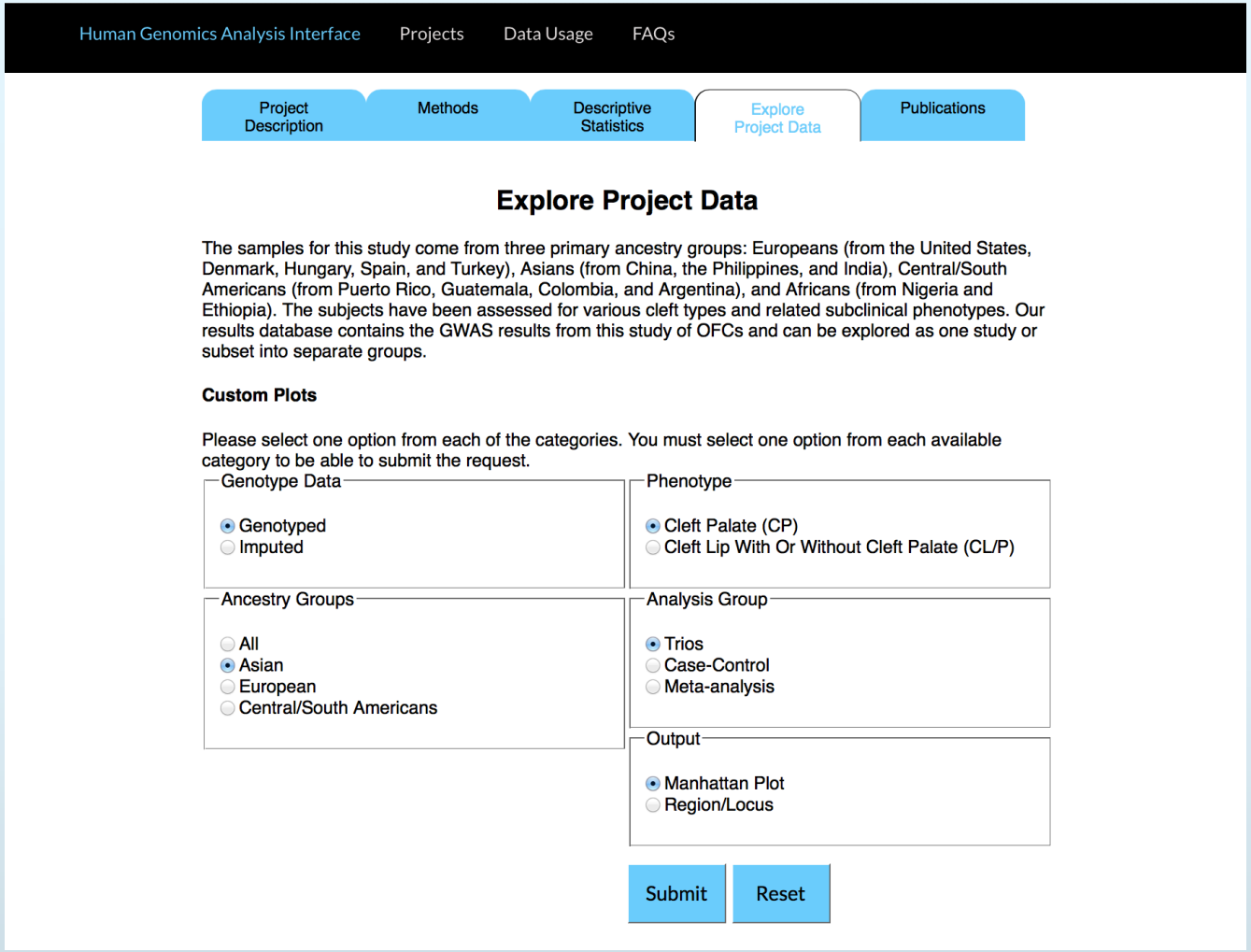
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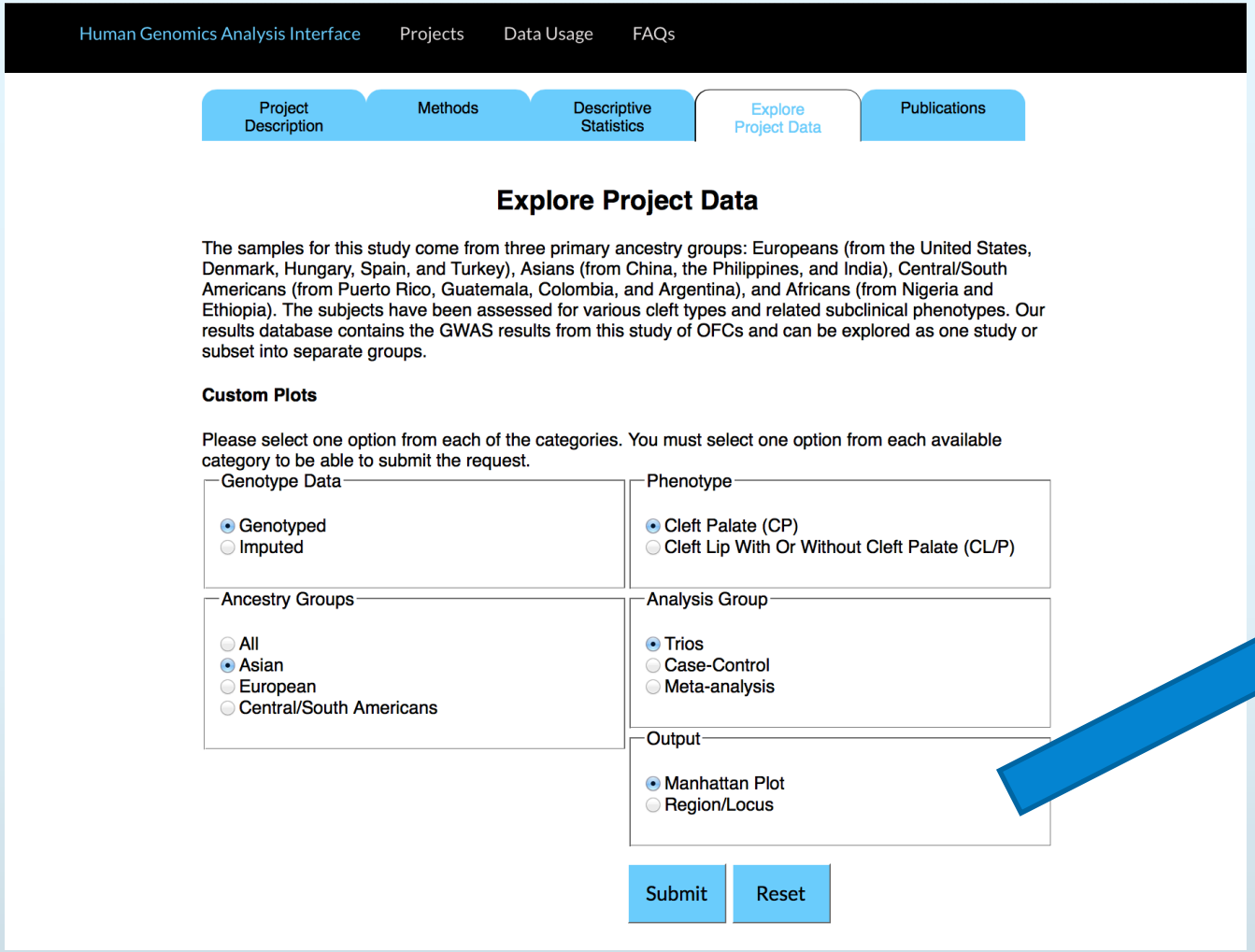
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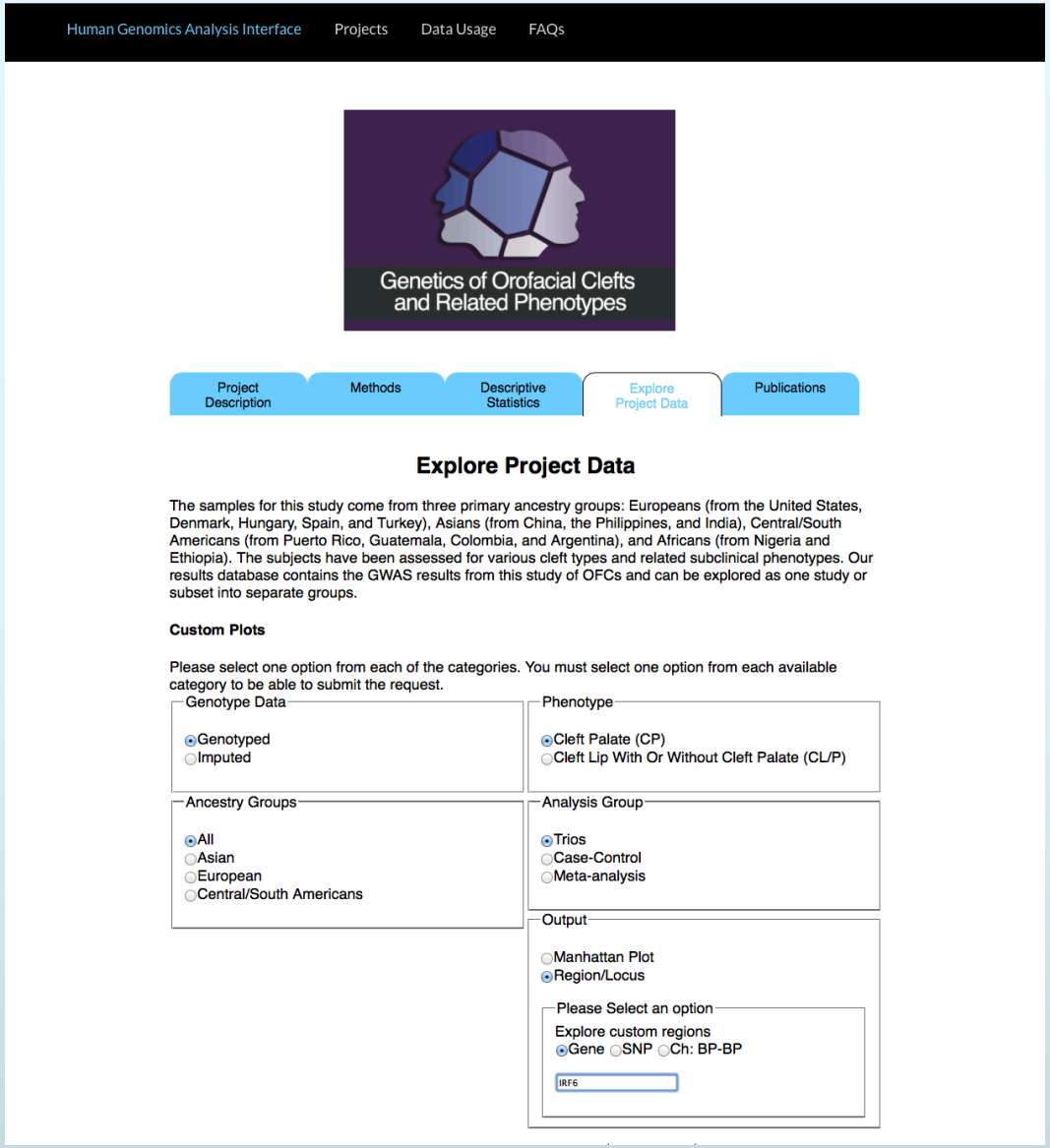
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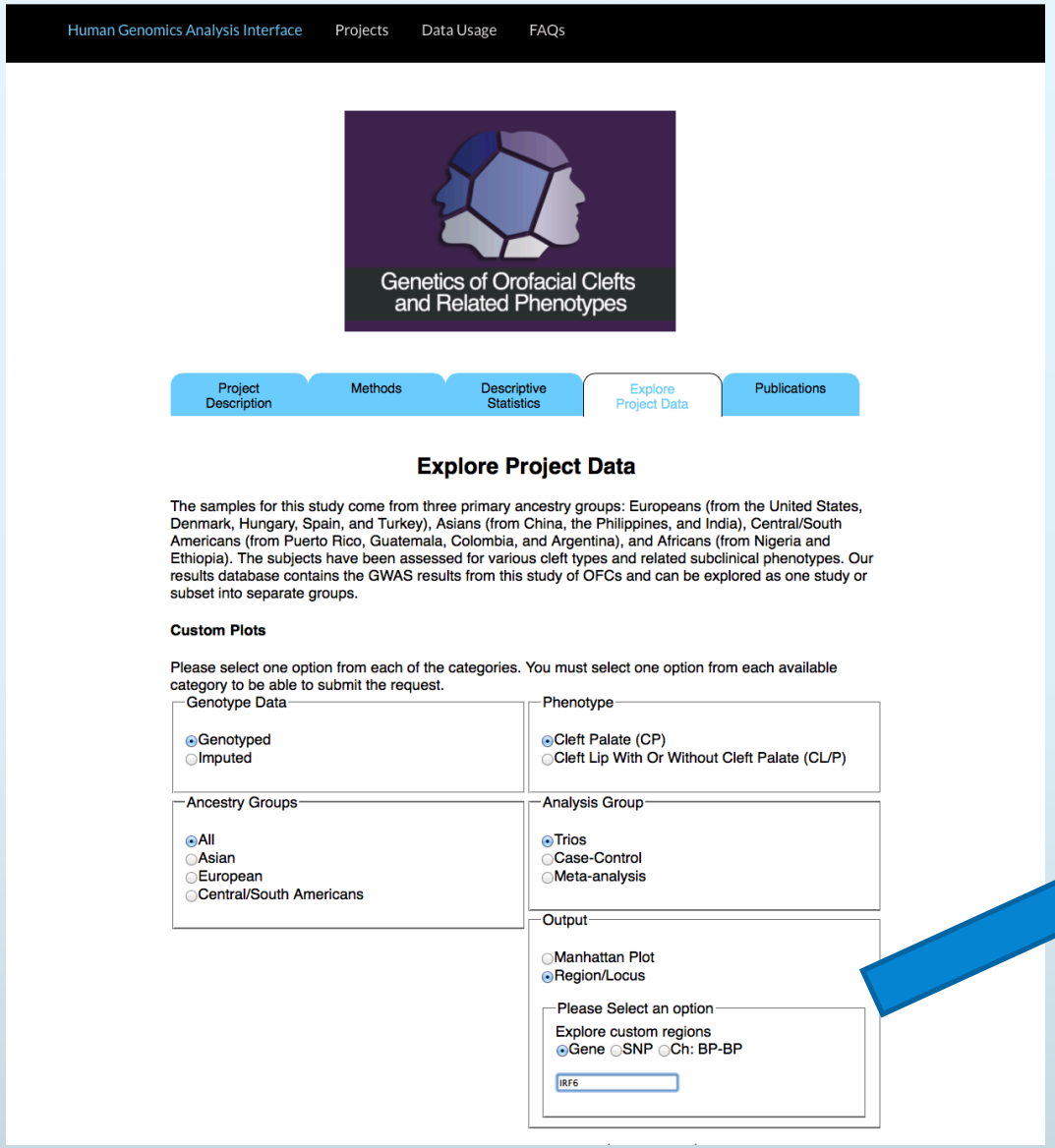
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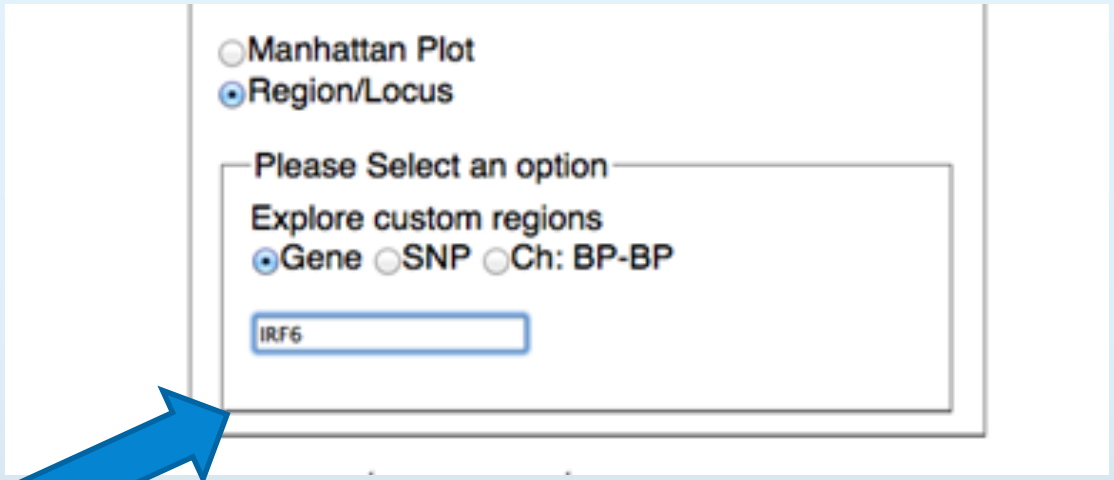
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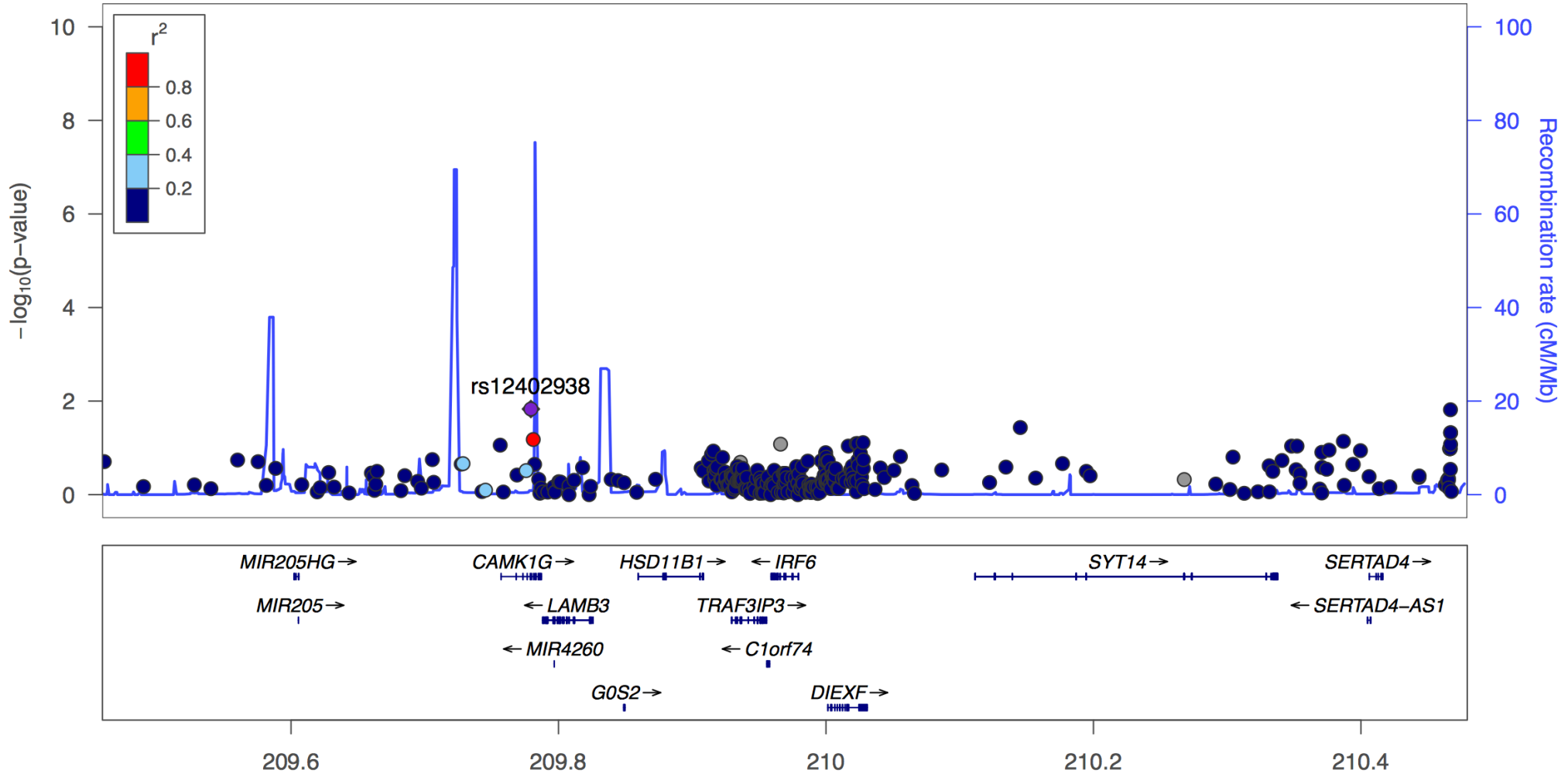
Geno HG19,All Ancestry, CP, Trios, Gene:IRF6



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Genotype Data

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- ( ) Imputed

Phenotype

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- ( ) Cleft Lip With Or Without Cleft Palate (CL/P)

Ancestry Groups

- (•) All
- ( ) Asian
- ( ) European
- ( ) Central/South Americans

Analysis Group

- (•) Trios
- ( ) Case-Control
- ( ) Meta-analysis

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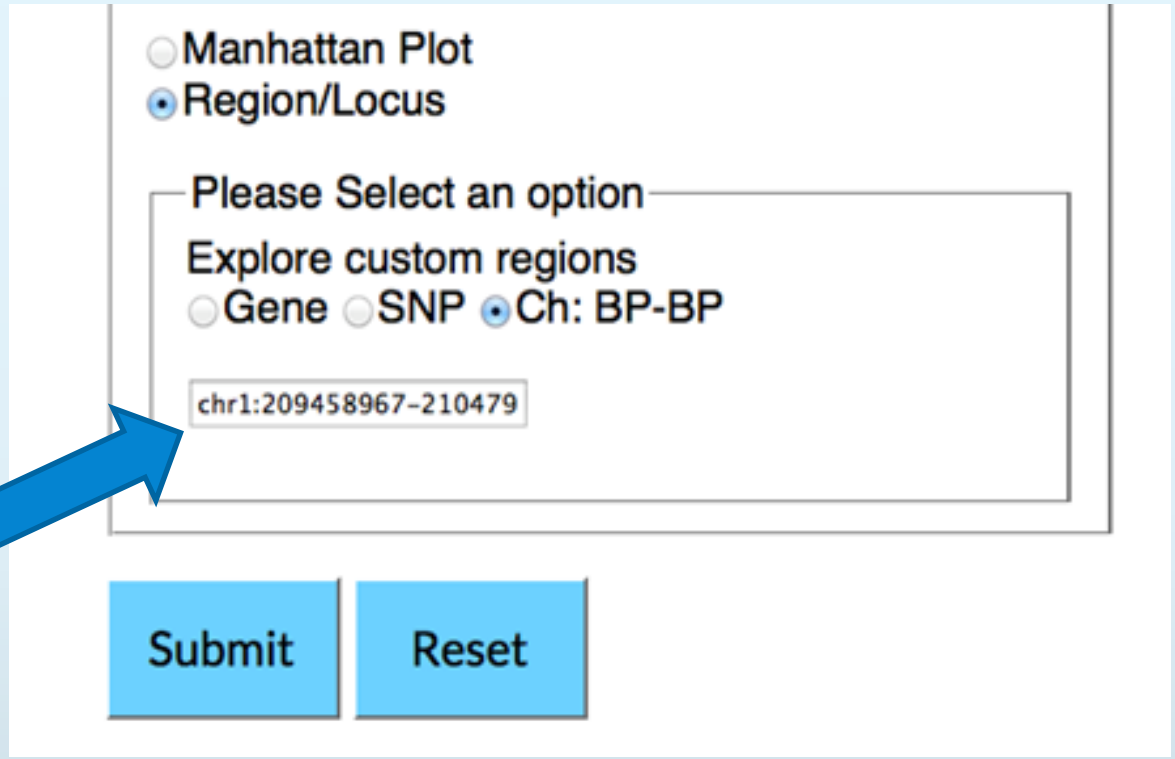

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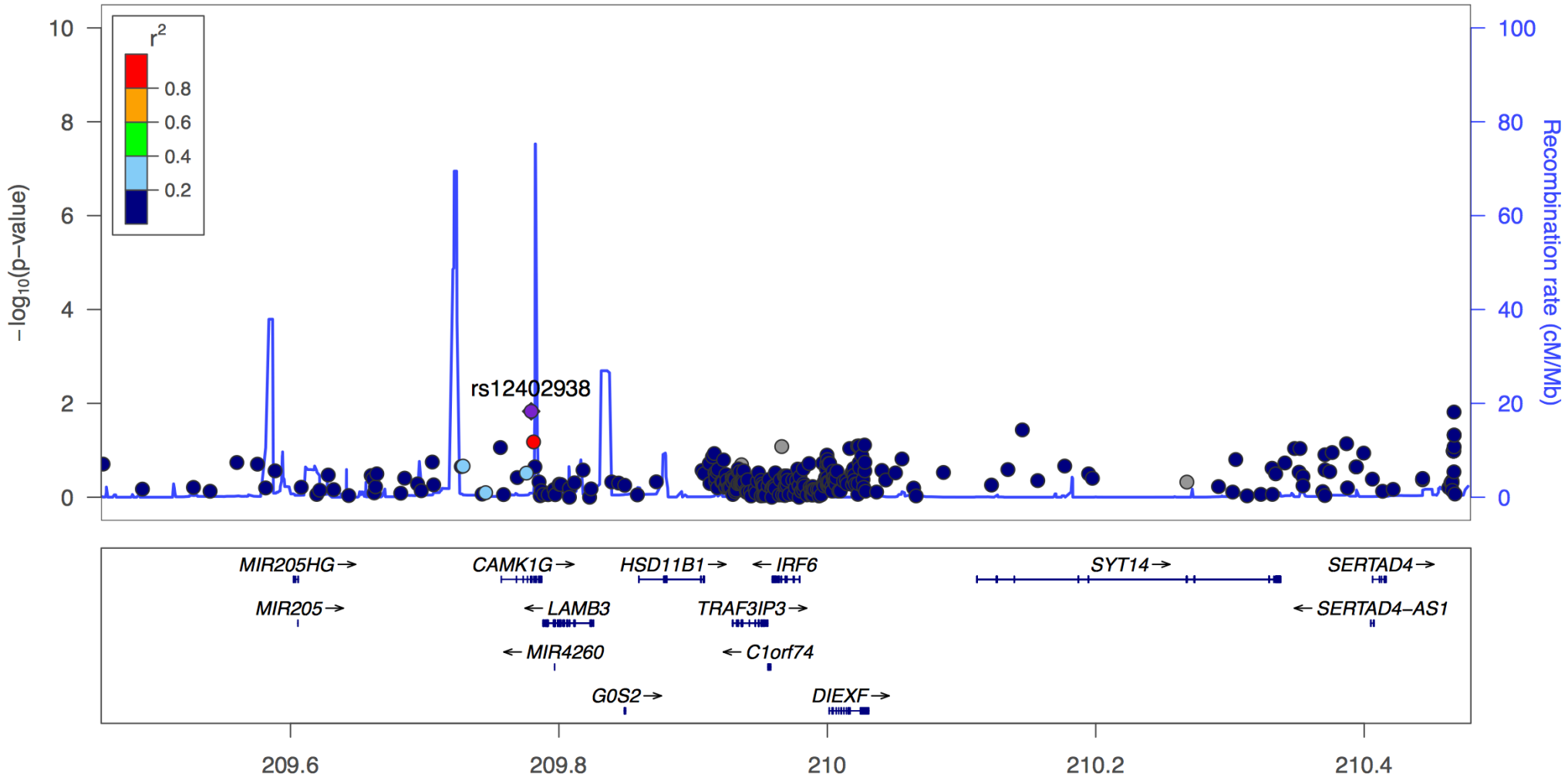

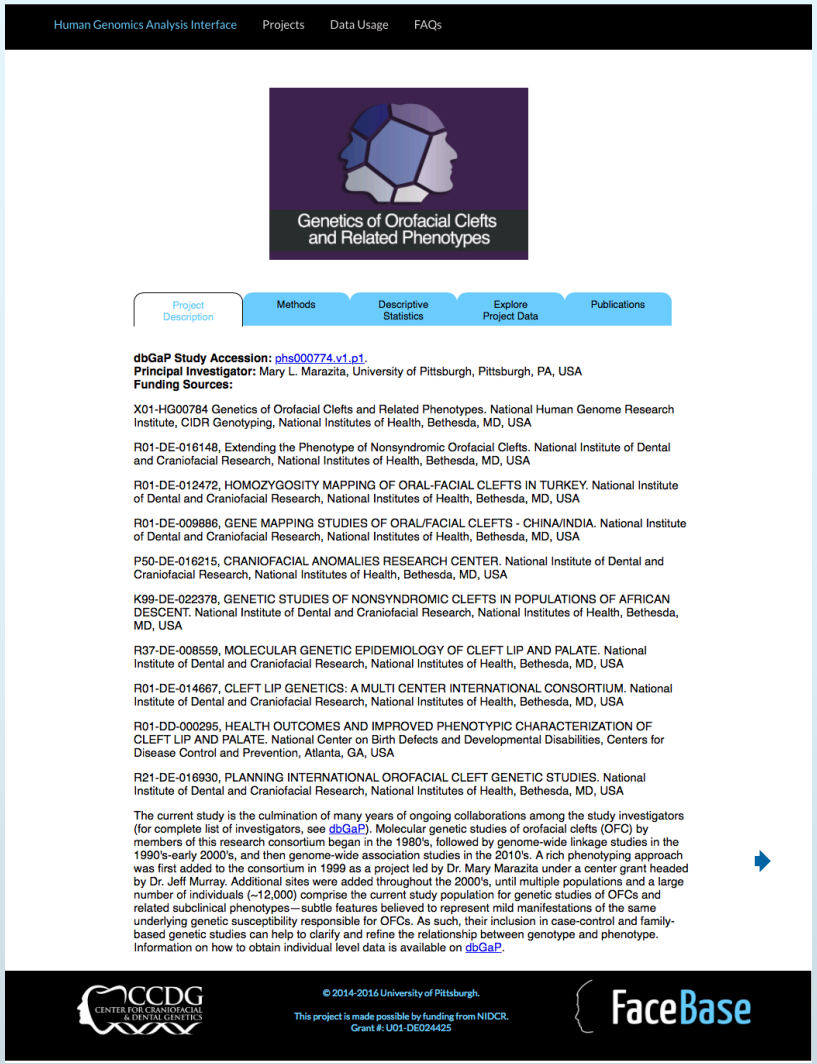

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The current study is the culmination of many years of ongoing collaborations among the study investigators (for complete list of investigators, see dbGaP). Molecular genetic studies of orofacial clefts (OFC) by members of this research consortium began in the 1980's, followed by genome-wide linkage studies in the 1990's-early 2000's, and then genome-wide association studies in the 2010's. A rich phenotyping approach was first added to the consortium in 1999 as a project led by Dr. Mary Marazita under a center grant headed by Dr. Jeff Murray. Additional sites were added throughout the 2000's, until multiple populations and a large number of individuals (~12,000) comprise the current study population for genetic studies of OFCs and related subclinical phenotypes—subtle features believed to represent mild manifestations of the same underlying genetic susceptibility responsible for OFCs. As such, their inclusion in case-control and family-based genetic studies can help to clarify and refine the relationship between genotype and phenotype. Information on how to obtain individual level data is available on dbGaP.

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dbGaP Study Accession: phs000774.v1.p1

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Study Description

The purpose of this study is to investigate the genetics of orofacial clefts (OFCs) in a large study population, and importantly, to incorporate subclinical phenotypic features into these studies.

Orofacial clefts (OFCs) comprise a significant fraction of human birth defects (about 1/700 live births (Rahimov et al. 2012) and represent a major public health challenge, as individuals with these anomalies require surgical, nutritional, dental, speech, medical and behavioral interventions, thus imposing a substantial economic and personal burden (Berk and Marazita 2002*). The most common forms include OFCs of the lip alone (CL, Figure 1A), CL plus cleft palate (CL+CP, Figure 1B) or of the palate only (CP, Figure 1C). Individuals born with OFC may have their first surgical repair at age 3 months, but this initial surgery is just the beginning of a lifetime of health burdens. An individual born with an OFC has a hospital use rate increased for most ages (up to 233% increase for children ages 0-10 years and 16% for middle aged adults (Wehby et al. 2012). Healthcare costs for children with OFCs are estimated to be 800% greater compared with their unaffected peers (Boulet et al. 2009). Data from Denmark show that people born with CL with or without CP (CL/P) have an increased mortality up to age 55, which may be attributed to an increased risk of suicide and/or certain cancers (Christensen et al. 2004). The focus of most OFC genetic research has been CL and/or CP. Furthermore, the majority of OFC, i.e. about 70% of CL/P and 50% of CP is considered "nonsyndromic" (Jones 1988), i.e. isolated anomalies with no other apparent cognitive or structural abnormalities.

Important Links and Information

- Request access via Authorized Access
  - Instructions for requestors
  - Data Use Certification (DUC) Agreement
- Talking Glossary of Genetic Terms

Figure 1 Sample OFC Types

A: Bilateral Cleft Lip; **B**=Cleft Lip plus Cleft Palate; **C**:Cleft Palate Alone

The factors leading to the majority of nonsyndromic OFCs are still unclear, particularly at an individual family level. As is true for many complex traits, substantial progress in gene identification has occurred in the OFC field in the last two years (Dixon et al. 2011; Marazita 2012). Genome Wide Association Studies (GWAS) and sequencing studies to date by our research team and others have focused on genetic risk factors for overt CL/P and CPO-and have been very successful. A major finding from this work is that OFCs exhibit significant genetic heterogeneity, i.e., multiple genetic regions have been implicated (Beaty et al. 2010; Ludwig et al. 2012). Thus, approaches are needed to understand this genetic heterogeneity. Are there GxG interactions at work? Are there subsets of families, each due to a different gene? Our research group has shown that a promising approach to dissect the etiology of OFC is to focus on subclinical phenotypic features within entire cleft families (not just in affected cases, but also in their non-cleft relatives). These subtle features are believed to represent mild manifestations of the same underlying genetic susceptibility responsible for OFCs; as such, their inclusion in case-control and family-based genetic studies can help to clarify and refine the relationship between genotype and phenotype.

The study population comprises a large number of families and individuals (~12,000 individuals) from multiple populations worldwide (Caucasians from the US and Europe, Asians from China and the Philippines, Mixed Native American/Caucasians from South America, and Africans from Nigeria and Ethiopia). There are cases, case families (nuclear families and extended kindreds), as well as controls with no history of OFC nor other developmental defects.

*Berk NW, Marazita ML (2002) Costs of Cleft lip and Palate: Personal and Societal Implications. In: Wyszynski DF (ed) Cleft Lip and Palate: From Origin to Treatment. Oxford University Press, Inc., New York, pp 458-467.

- Study Types: Parent-Offspring, Nuclear Families, Extended Pedigrees
- Number of study subjects that have individual level data available through Authorized Access: 11925
  - 11925 phenotyped subjects

Authorized Access

- **Data access provided by:** dbGaP Authorized Access
- **Release Date:** November 02, 2015
- **Embargo Release Date:** November 02, 2015
- Data Use Certification Requirements (DUC)
- **Use Restrictions**

Consent group	Is IRB required?	Data Access Committee	Number of participants
Disease-Specific (Craniofacial Research)	No	Joint NIAMS-NIDCR Data Access Committee (jardedac@mail.nih.gov)	11925

- List of components downloadable from Authorized Access

Publicly Available Data (Public ftp)

Connect to the public download site. The site contains release notes and manifests. If available, the site also contains data dictionaries, variable summaries, documents, and truncated analyses.

Study Inclusion/Exclusion Criteria

Inclusion criteria for Families with OFCs:

- Case diagnosed with nonsyndromic OFC (CL/P or CPO).
- At least 2 additional family members' participation.
- Male or female, aged 1 month to 110 years.
- Provide signed and dated informed consent form.
- Willing to comply with all study procedures and be available for the duration of the study.

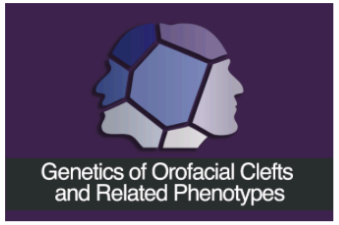
Inclusion criteria for Controls:

- Male or female, aged 1 month to 110 years.
- No known personal or family history of OFCs, genetic conditions, or birth defects.
- No personal history of facial surgery.
- In good general health.
- Provide signed and dated informed consent form.
- Willing to comply with all study procedures and be available for the duration of the study.

Exclusion criteria - individuals who met any of the following criteria were excluded from participation in this study:

- An affected case with a genetic syndrome or multiple congenital anomalies.
- An affected case without participation of other family members.
- Persons who were adopted and cannot report family history.
- For controls, a positive history of OFC, genetic syndrome/defects in themselves or family.
- For controls, a previous facial surgery.
- Male controls may be excluded from certain phenotypes if it is determined that their facial hair hinders the ability to collect accurate facial measurements.

Molecular Data



dbGaP Study Accession: phs000774.v1.p1.
Principal Investigator: Mary L. Marazita, University of Pittsburgh, Pittsburgh, PA, USA
Funding Sources:

X01-HG00784 Genetics of Orofacial Clefts and Related Phenotypes. National Human Genome Research Institute, CIDR Genotyping, National Institutes of Health, Bethesda, MD, USA

R01-DE-016148, Extending the Phenotype of Nonsyndromic Orofacial Clefts. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DE-012472, HOMOZYGOSITY MAPPING OF ORAL-FACIAL CLEFTS IN TURKEY. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DE-009886, GENE MAPPING STUDIES OF ORAL/FACIAL CLEFTS - CHINA/INDIA. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

P50-DE-016215, CRANIOFACIAL ANOMALIES RESEARCH CENTER. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

K99-DE-022378, GENETIC STUDIES OF NONSYNDROMIC CLEFTS IN POPULATIONS OF AFRICAN DESCENT. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R37-DE-008559, MOLECULAR GENETIC EPIDEMIOLOGY OF CLEFT LIP AND PALATE. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

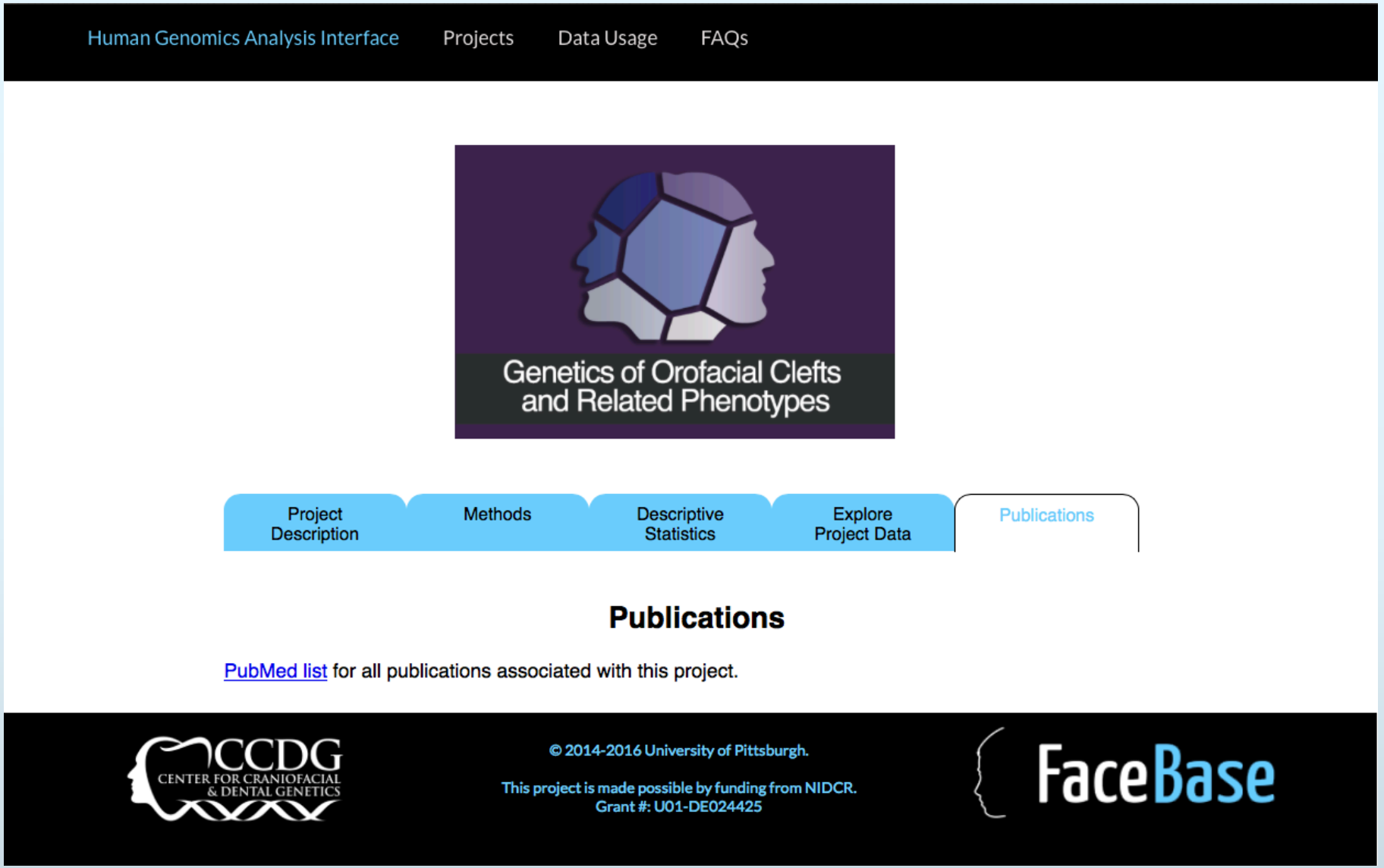
R01-DE-014667, CLEFT LIP GENETICS: A MULTI CENTER INTERNATIONAL CONSORTIUM. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

R01-DD-000295, HEALTH OUTCOMES AND IMPROVED PHENOTYPIC CHARACTERIZATION OF CLEFT LIP AND PALATE. National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA

R21-DE-016930, PLANNING INTERNATIONAL OROFACIAL CLEFT GENETIC STUDIES. National Institute of Dental and Craniofacial Research, National Institutes of Health, Bethesda, MD, USA

The current study is the culmination of many years of ongoing collaborations among the study investigators (for complete list of investigators, see dbGaP). Molecular genetic studies of orofacial clefts (OFC) by members of this research consortium began in the 1980's, followed by genome-wide linkage studies in the 1990's-early 2000's, and then genome-wide association studies in the 2010's. A rich phenotyping approach was first added to the consortium in 1999 as a project led by Dr. Mary Marazita under a center grant headed by Dr. Jeff Murray. Additional sites were added throughout the 2000's, until multiple populations and a large number of individuals (~12,000) comprise the current study population for genetic studies of OFCs and related subclinical phenotypes—subtle features believed to represent mild manifestations of the same underlying genetic susceptibility responsible for OFCs. As such, their inclusion in case-control and family-based genetic studies can help to clarify and refine the relationship between genotype and phenotype. Information on how to obtain individual level data is available on dbGaP.

This project is made possible by funding from NIDCR.
Grant #: U01-DE024425


Human Genomics Analysis Interface
Projects
Data Usage
FAQs
Genetics of Orofacial Clefts and Related Phenotypes
Project Description
Methods
Descriptive Statistics
Explore Project Data
Publications
Publications
PubMed list for all publications associated with this project.
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This project is made possible by funding from NIDCR.
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Abstract Send to:

Am J Hum Genet. 2016 Apr 7;98(4):744-54. doi: 10.1016/j.ajhg.2016.02.014. Epub 2016 Mar 24.

A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3.

Leslie EJ[1], Liu H[2], Carlson JC[3], Shaffer JR[4], Feingold E[5], Wehby G[6], Laurie CA[7], Jain D[7], Laurie CC[7], Doheny KF[8], McHenry T[1], Resick J[1], Sanchez C[1], Jacobs J[1], Emanuele B[1], Vieira AR[4], Neiswanger K[1], Standley J[9], Czeizel AE[10], Deleyiannis F[11], Christensen K[12], Munger RG[13], Lie RT[14], Wilcox A[15], Romitti PA[16], Field LL[17], Padilla CD[18], Cutiongco-de la Paz EM[19], Lidral AC[20], Valencia-Ramirez LC[21], Lopez-Palacio AM[22], Valencia DR[23], Arcos-Burgos M[24], Castilla EE[25], Mereb JC[26], Poletta FA[25], Orioli IM[27], Carvalho FM[28], Hecht JT[29], Blanton SH[30], Buxó CJ[31], Butali A[32], Mossey PA[33], Adeyemo WL[34], James O[34], Braimah RO[35], Aregbesola BS[35], Eshete MA[36], Deribew M[36], Koruyucu M[37], Seymen F[37], Ma L[38], de Salamanca JE[39], Weinberg SM[1], Moreno L[20], Cornell RA[40], Murray JC[9], Marazita ML[41].

Author information

Abstract

Cleft palate (CP) is a common birth defect occurring in 1 in 2,500 live births. Approximately half of infants with CP have a syndromic form, exhibiting other physical and cognitive disabilities. The other half have nonsyndromic CP, and to date, few genes associated with risk for nonsyndromic CP have been characterized. To identify such risk factors, we performed a genome-wide association study of this disorder. We discovered a genome-wide significant association with a missense variant in GRHL3 (p.Thr454Met [c.1361C>T]; rs41268753; p = 4.08 × 10(-9)) and replicated the result in an independent sample of case and control subjects. In both the discovery and replication samples, rs41268753 conferred increased risk for CP (OR = 8.3, 95% CI 4.1-16.8; OR = 2.16, 95% CI 1.43-3.27, respectively). In luciferase transactivation assays, p.Thr454Met had about one-third of the activity of wild-type GRHL3, and in zebrafish embryos, perturbed periderm development. We conclude that this mutation is an etiologic variant for nonsyndromic CP and is one of few functional variants identified to date for nonsyndromic orofacial clefting. This finding advances our understanding of the genetic basis of craniofacial development and might ultimately lead to improvements in recurrence risk prediction, treatment, and prognosis.

PMID: 27018472 [PubMed - in process] PMCID: PMC4833215 [Available on 2016-10-07]

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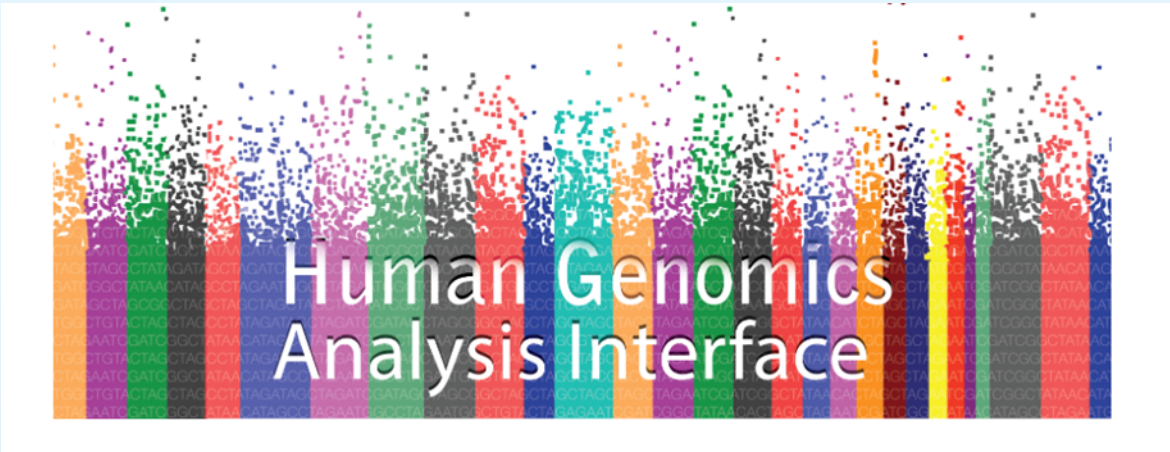

VISITS TO THE SITE

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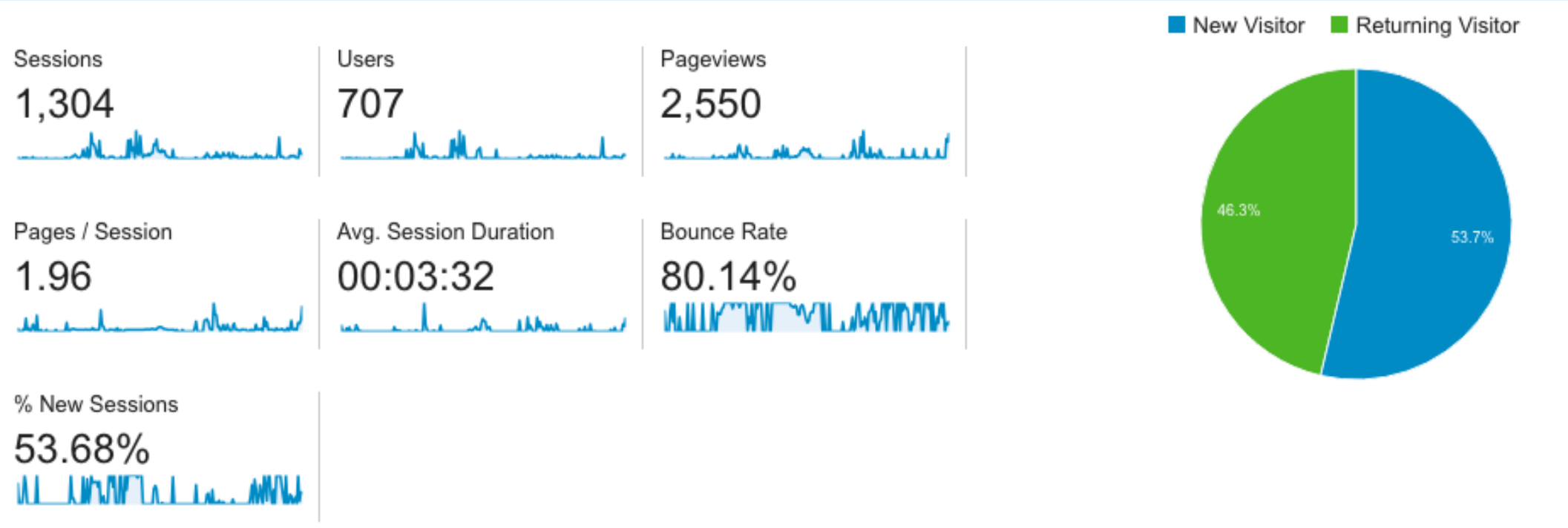

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	Country	Sessions	% Sessions
1.	United States	525	40.26%
2.	Russia	279	21.40%
3.	(not set)	195	14.95%
4.	China	41	3.14%
5.	United Kingdom	30	2.30%
6.	Japan	21	1.61%
7.	Netherlands	21	1.61%
8.	Germany	15	1.15%
9.	South Korea	14	1.07%
10.	Spain	11	0.84%

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FUTURE PLANS

- Complete existing projects
  - Other potential OFC GWAS: CHoP, Chinese, others
  - US Facial Variation, Dental
- Seek additional projects
  - UK Facial Variation
  - Other oral/dental
- Incorporate additional functionality
- Citing tool in papers
- Possible dbGaP link to tool

FUTURE PLANS: FaceBase HUB

- Add links from animal model pages to this human page and vice versa
  - E.g. for "look-up" of gene or region of interest
- FaceBase human data projects: any aspects that could be incorporated into this tool?
- Suggestions, requests?

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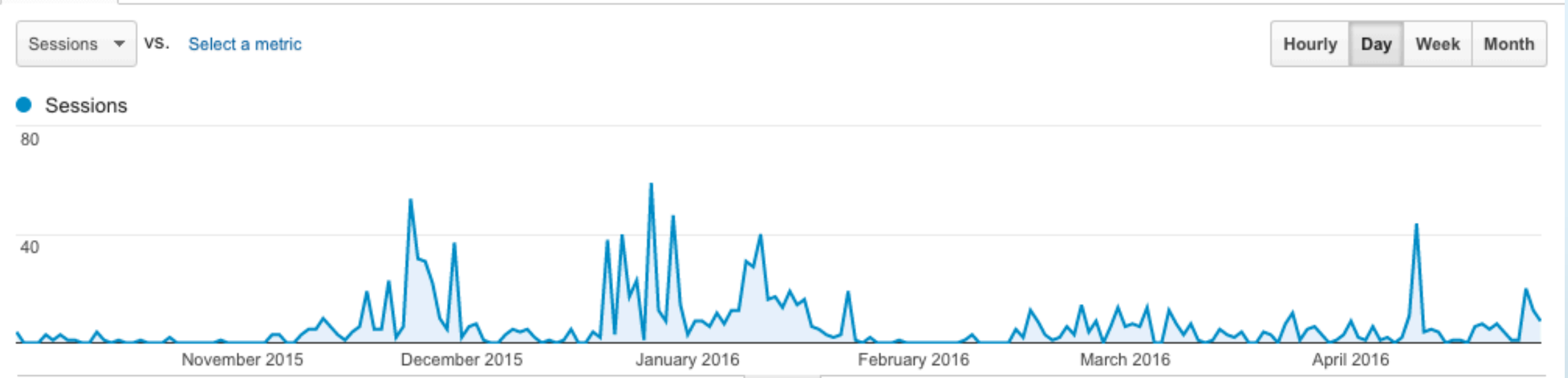

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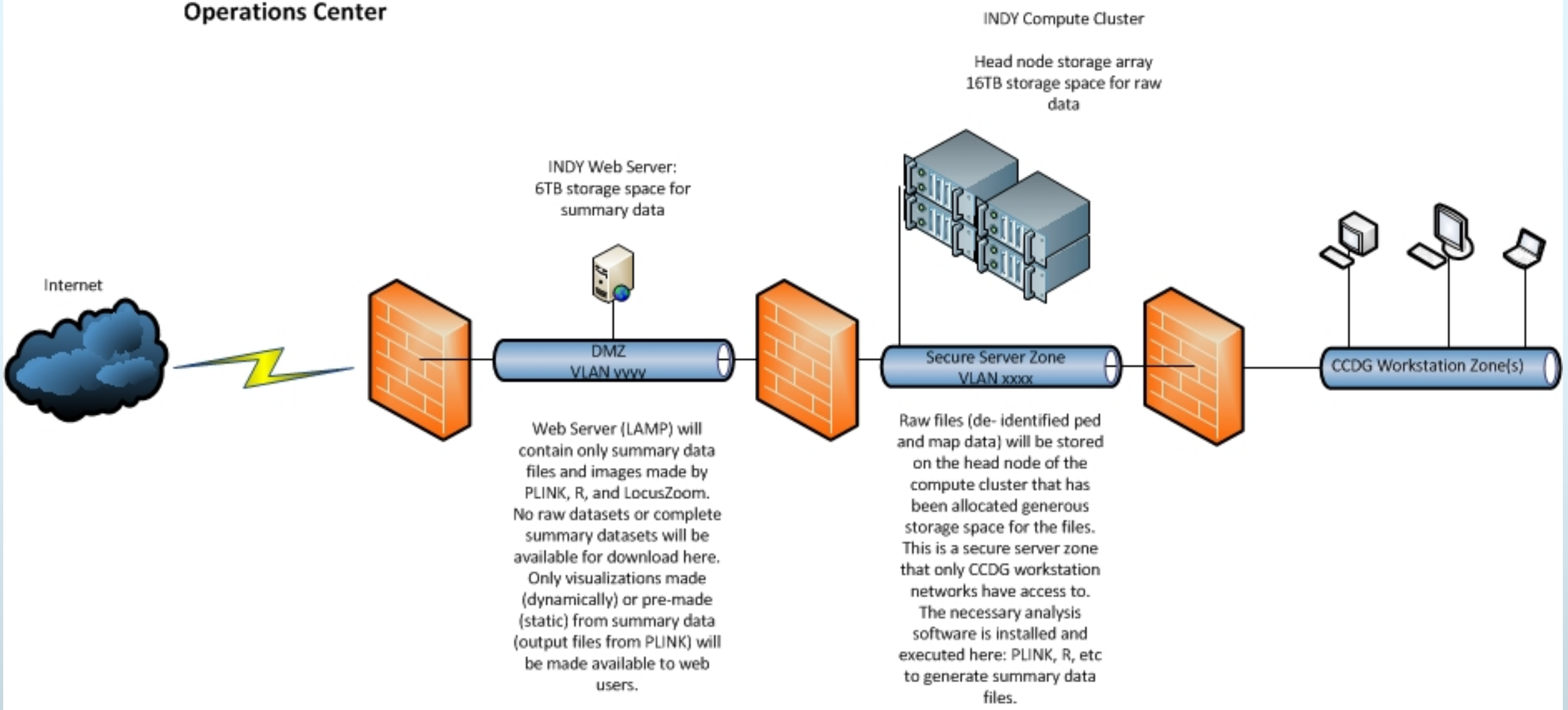
FaceBase2 Production cluster At University of Pittsburgh's Network Operations Center



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