The Korean Genome Project Using NGS and Genome Engine Informatics Pipeline

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TheragenEtex

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KPGP KOREAN PERSONAL GENOME PROJECT

TBI Theragen Bio Institute

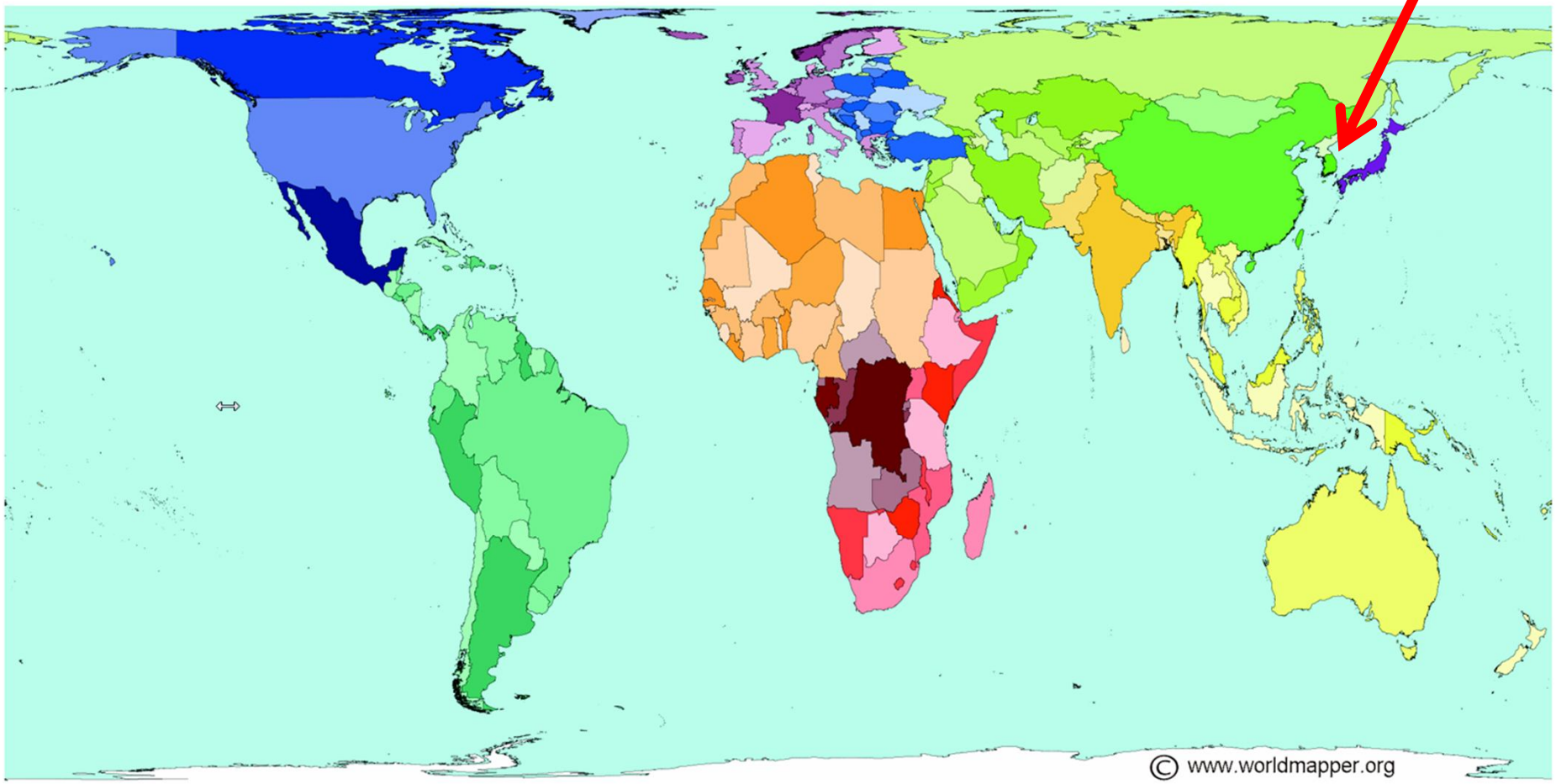
Cambridge Healthtech Institute's Inaugural Bio-IT World ASIA CONFERENCE 2012

Acknowledgement

- Scientists
- Tax payers
- BioIT Asia
- Ming Guo
- Kevin Davies
- TheragenEtex (http://therabio.org)

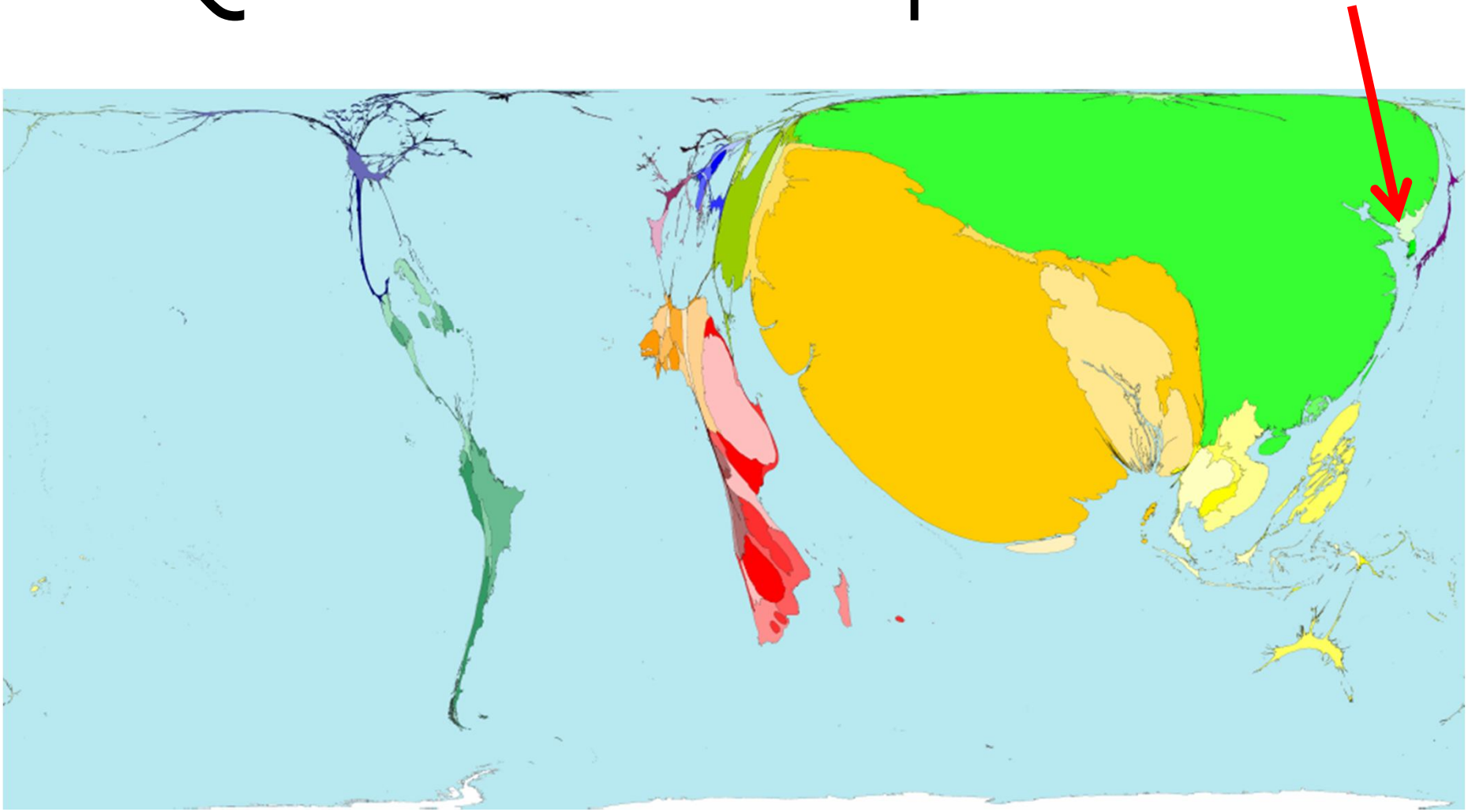
- Industrial Strategic technology development program, 10040231, "Bioinformatics platform development for next generation bioinformation analysis" by the Ministry of Knowledge Economy (MKE, Korea).

World Land **Area** Map



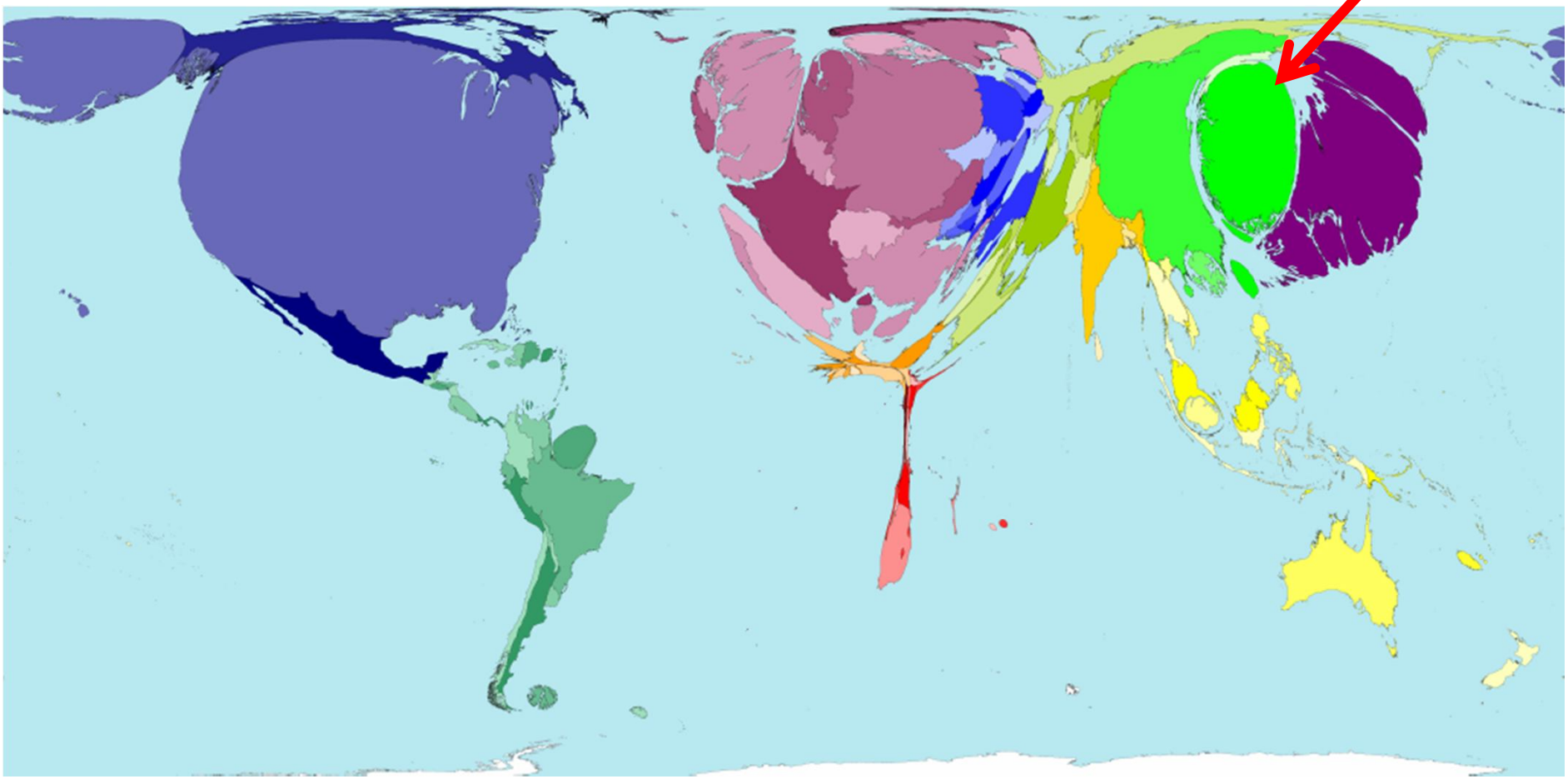
육지면적

Quiz: What map is this?



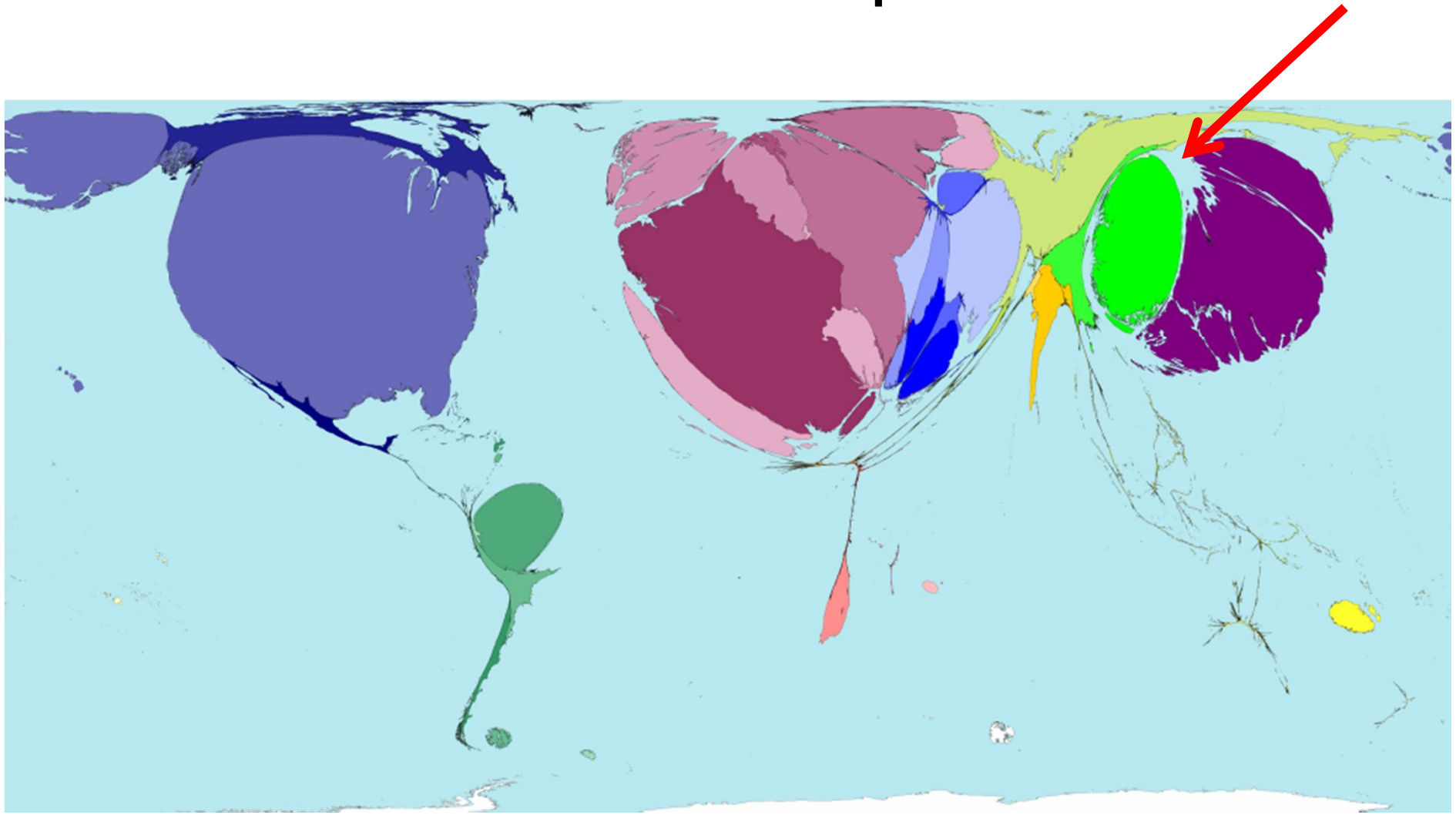
재앙으로 죽는사람

Quiz: What map is this?



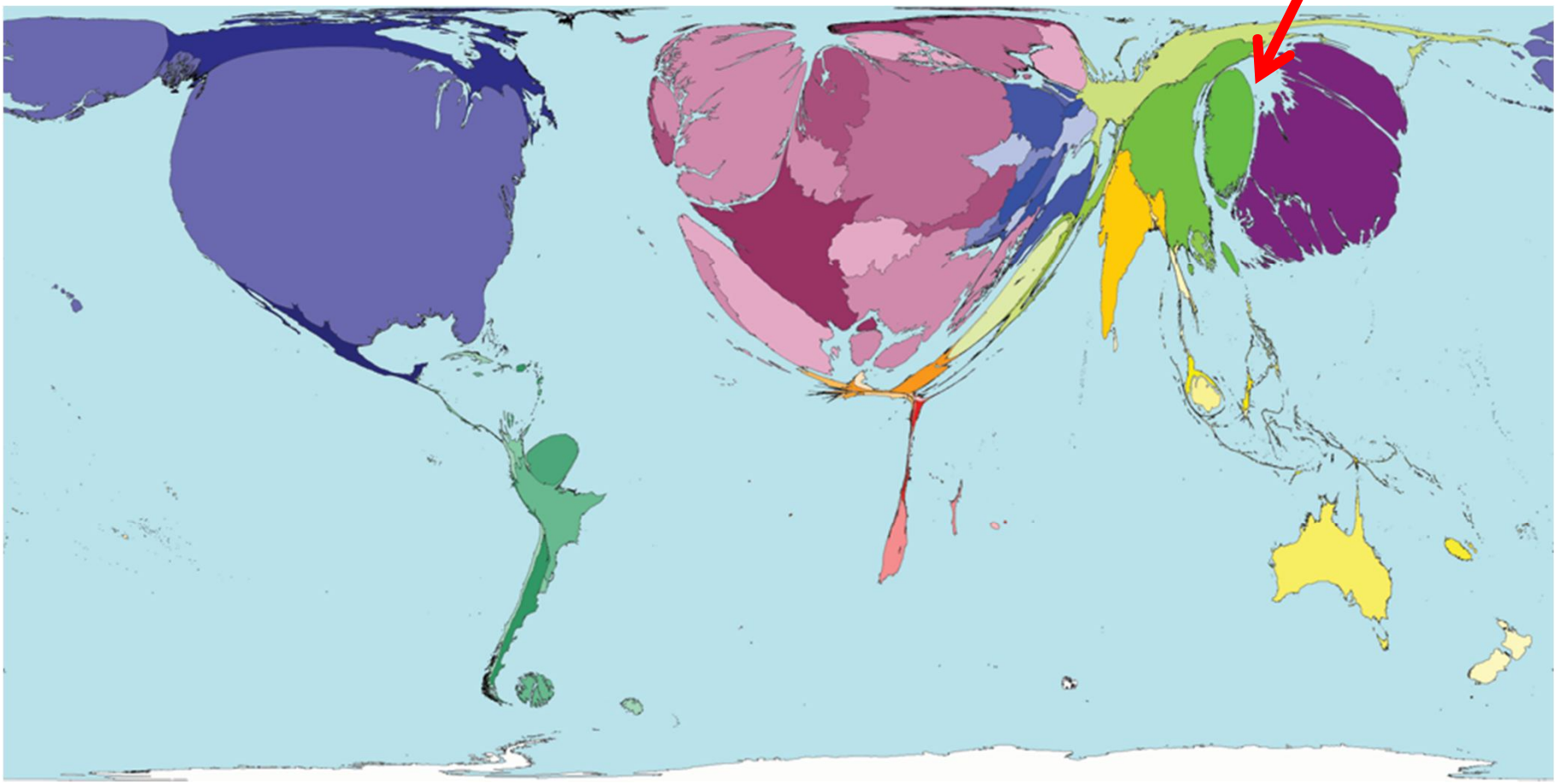
개인용 컴퓨터 숫자

What map?



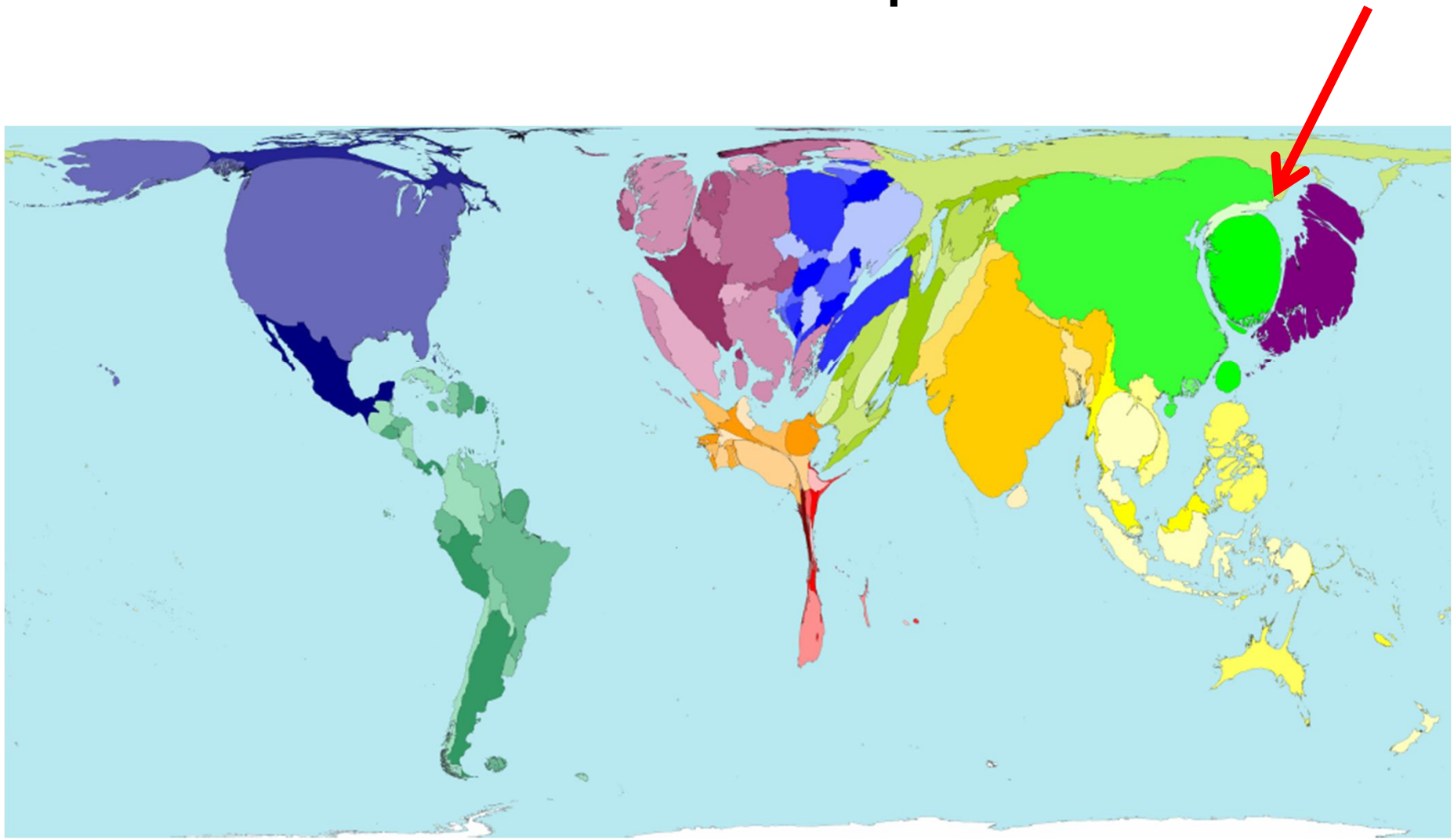
핵연료 사용

What map?

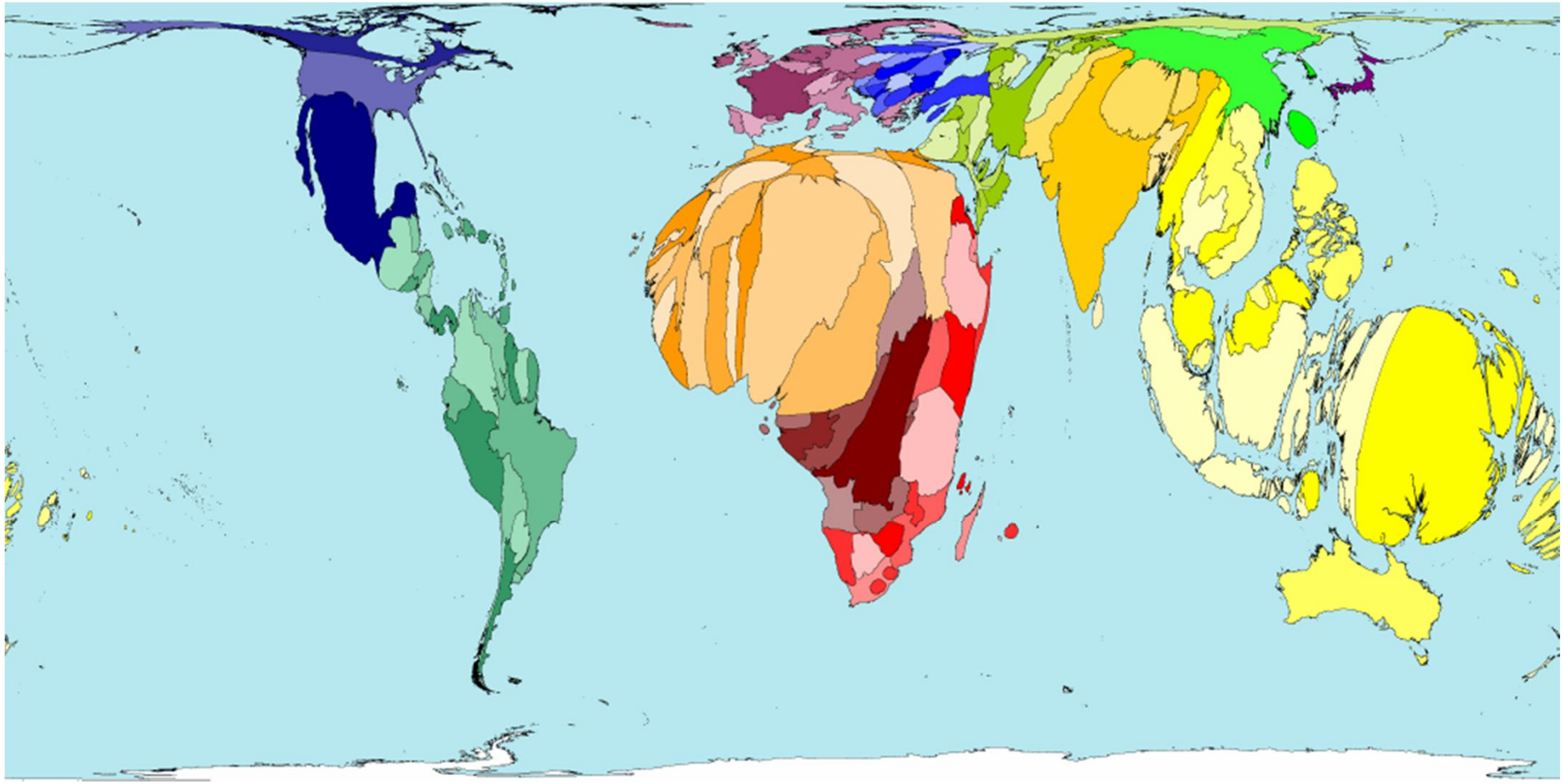


과학연구

What map?



고급(대학)교육



고유 원주민 언어의 수

Contents

Conclusion

Let’s do more sequencing

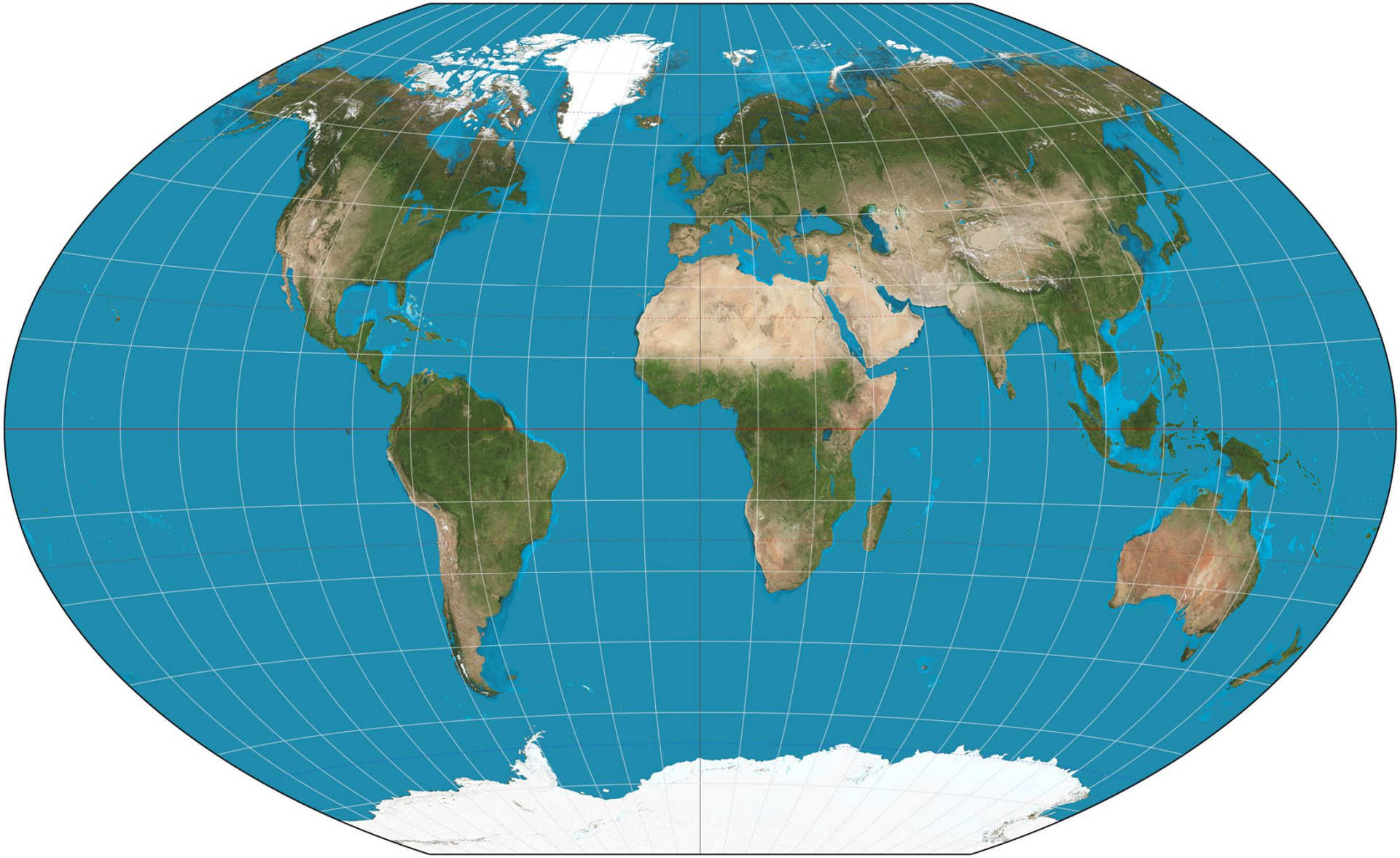
Conclusion

Let’s sequence 7 billion human genome

7 billion genome project (7BGP)

The End

BIM: Biological Information Mapping



Bioinformatics Is about Mapping

X is IEP
Y is Size

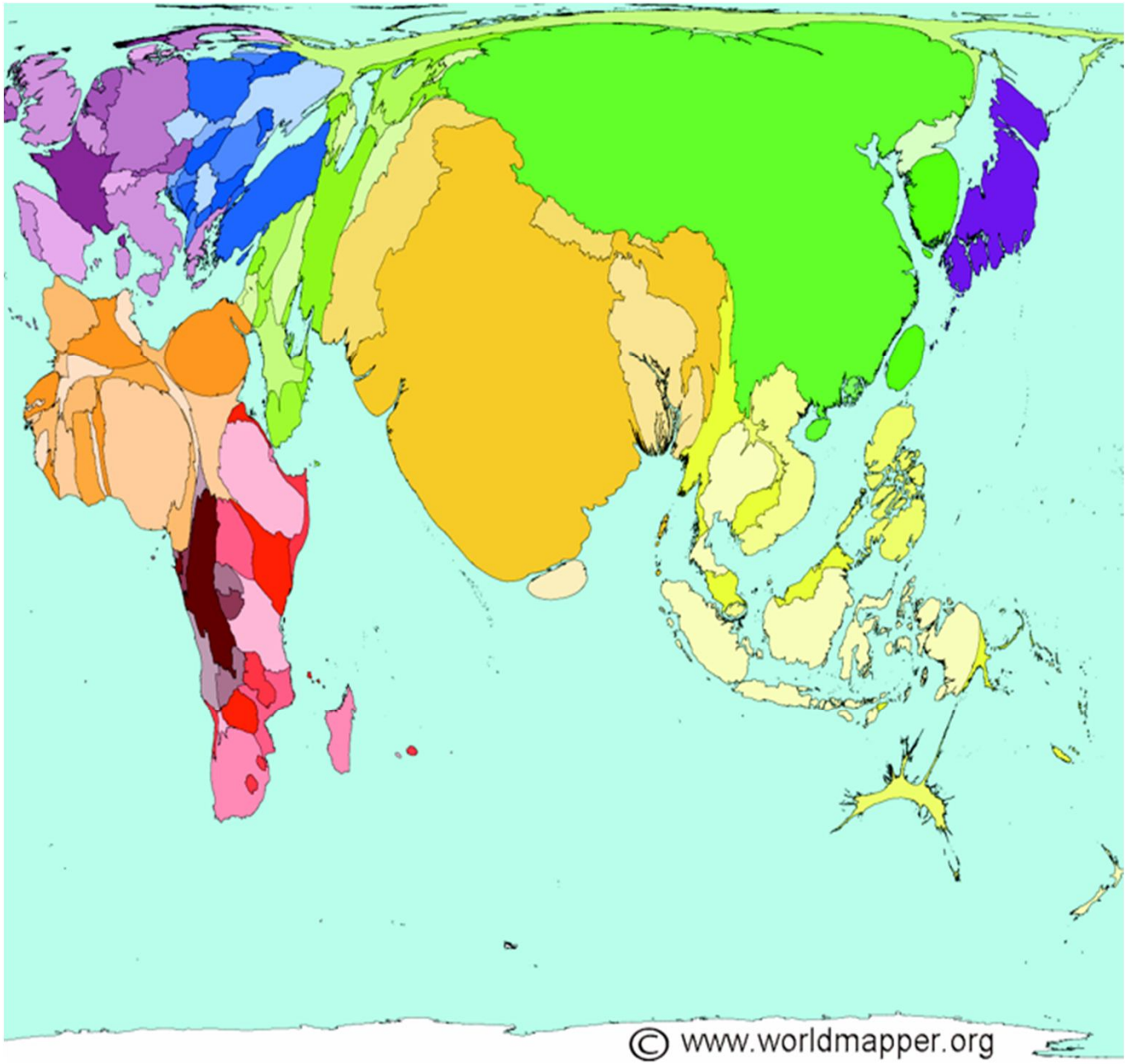
Old map
Is not
Accurate.

However
It helps
People to
Explore.

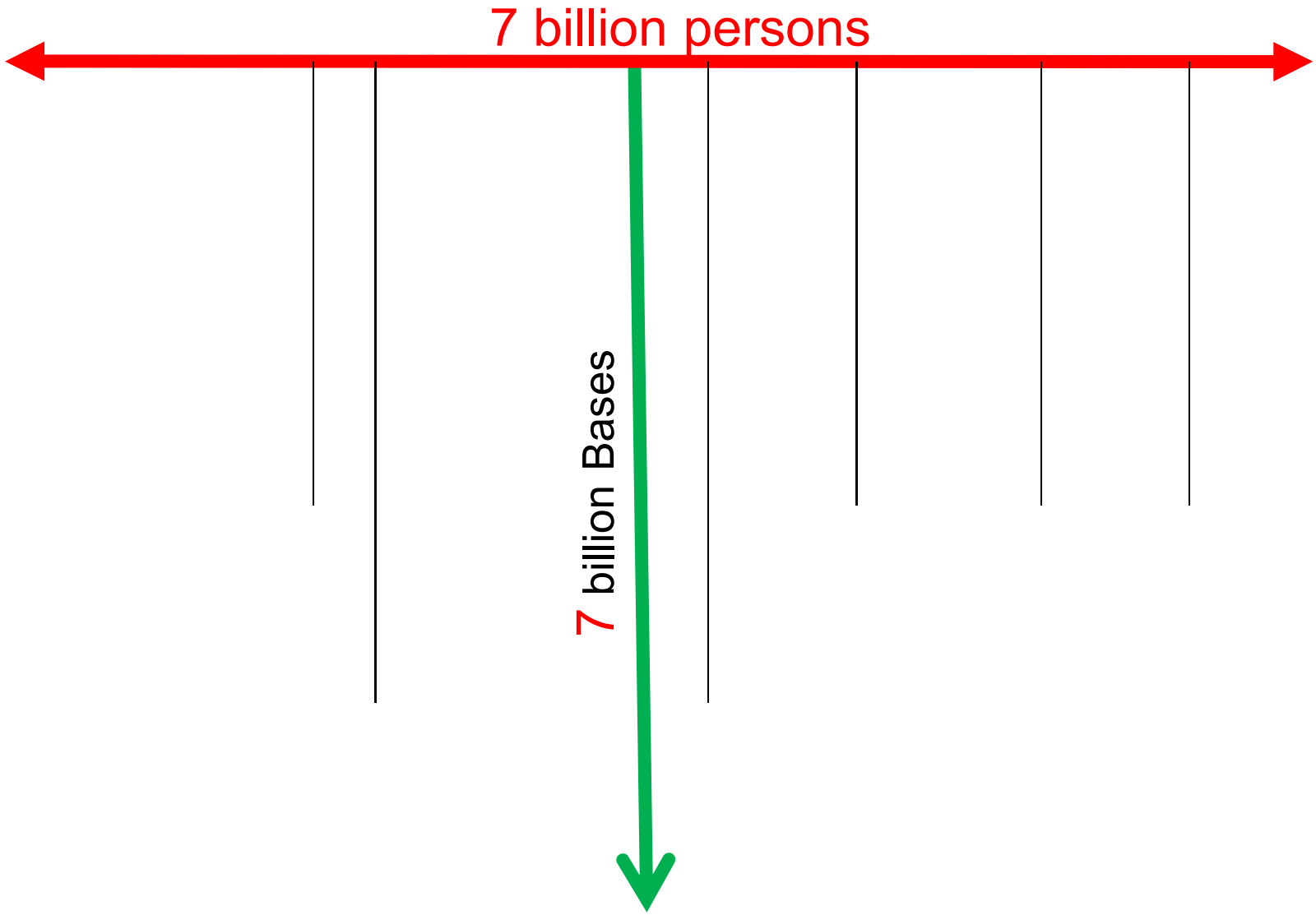
Data
Information
Knowledge

Gangnido 1402

World Population map (2002)

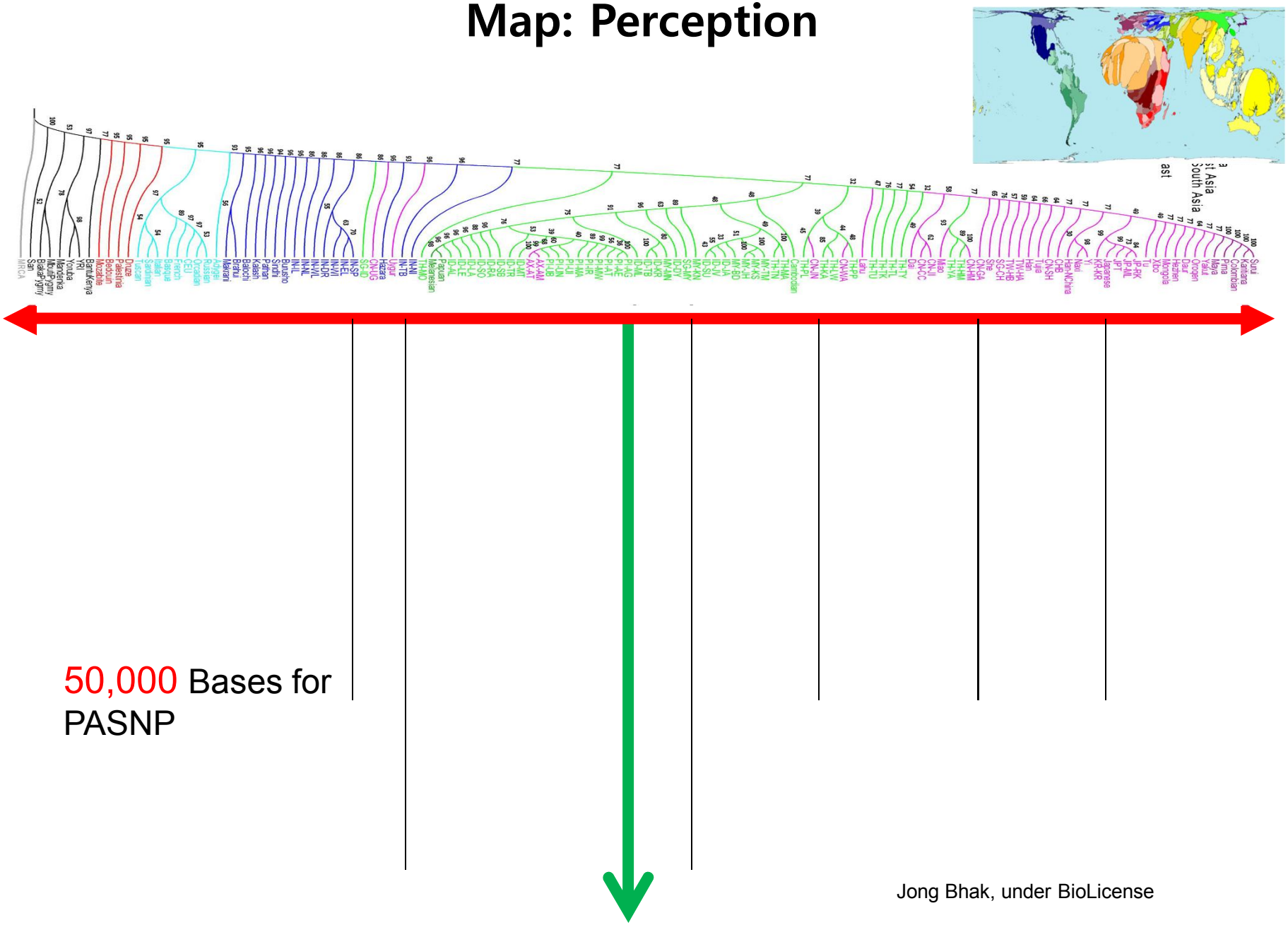


Genomic T map

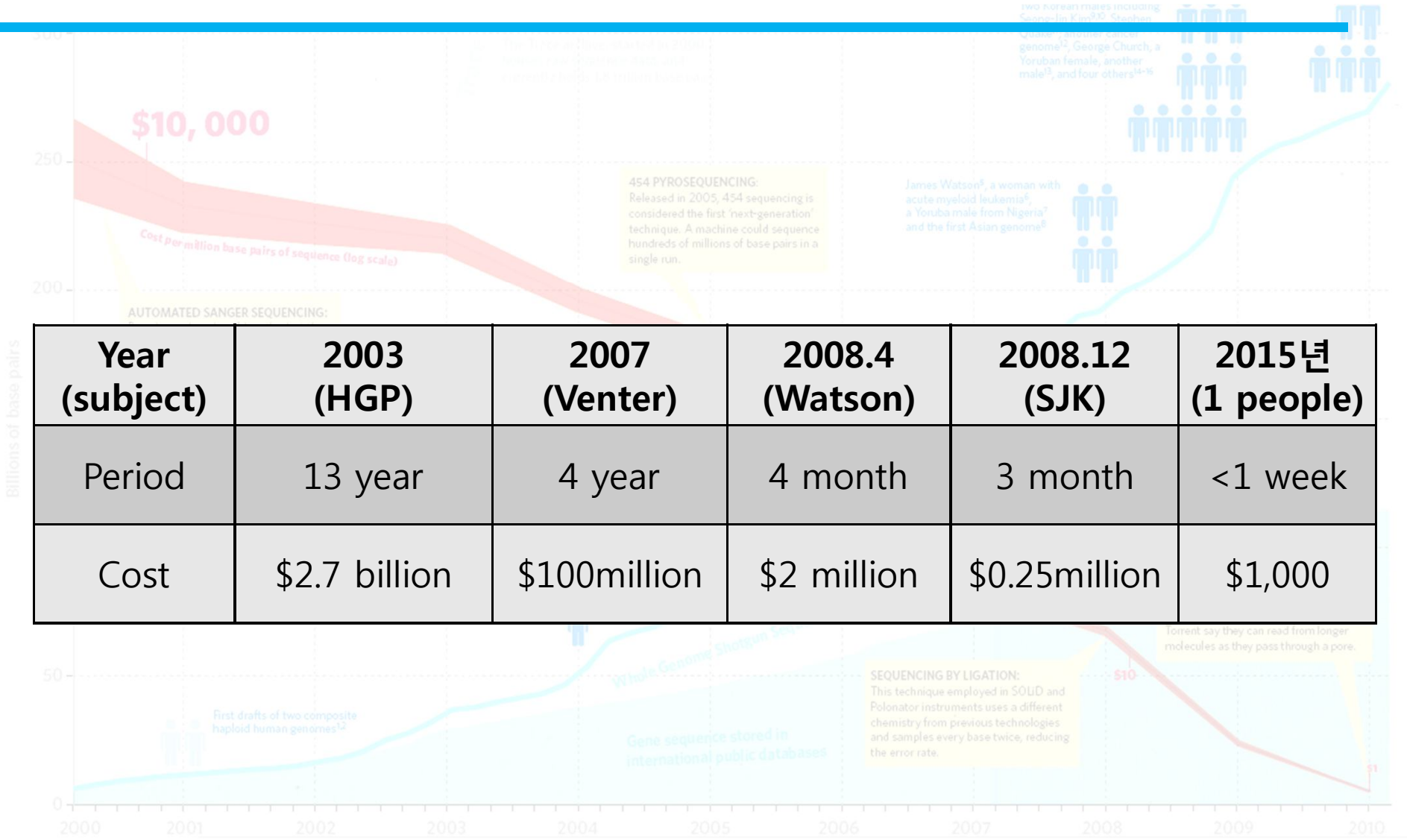


Genome Diversity and Genome Variation

Map: Perception



Background – Cost & Period

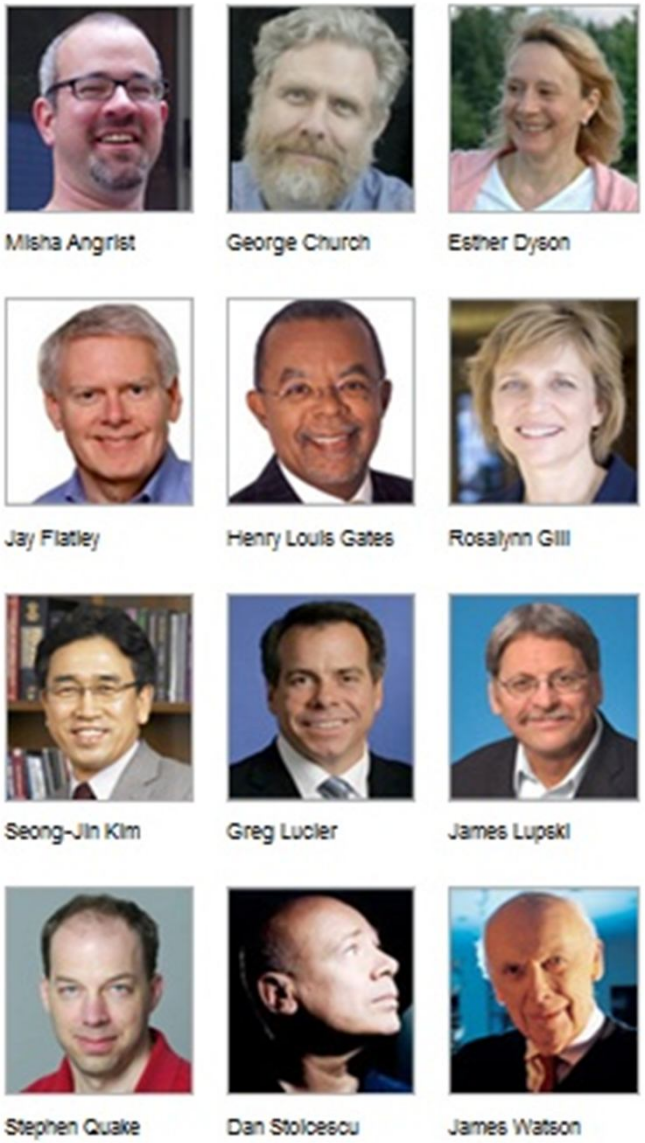


Year (subject)	2003 (HGP)	2007 (Venter)	2008.4 (Watson)	2008.12 (SJK)	2015년 (1 people)
Period	13 year	4 year	4 month	3 month	<1 week
Cost	$2.7 billion	$100million	$2 million	$0.25million	$1,000

Sequence explosion, *Nature*, **46**(1), 670-671

Personal Genome analysis

- 2008.12 SJK personal genome
- 2008.11 Chinese Personal genome
- 2008.4 J. Watson Personal genome
- 2007 C. Venter Personal genome
- 2006 PGP(Pesrsonal Genome Project)
- 2003 Human Reference Genome



Personal Genome Data

2011 year

Whole Genome Sequencing Analysis and Publically Available :

about 300 people

The first Korean Genome Sequence

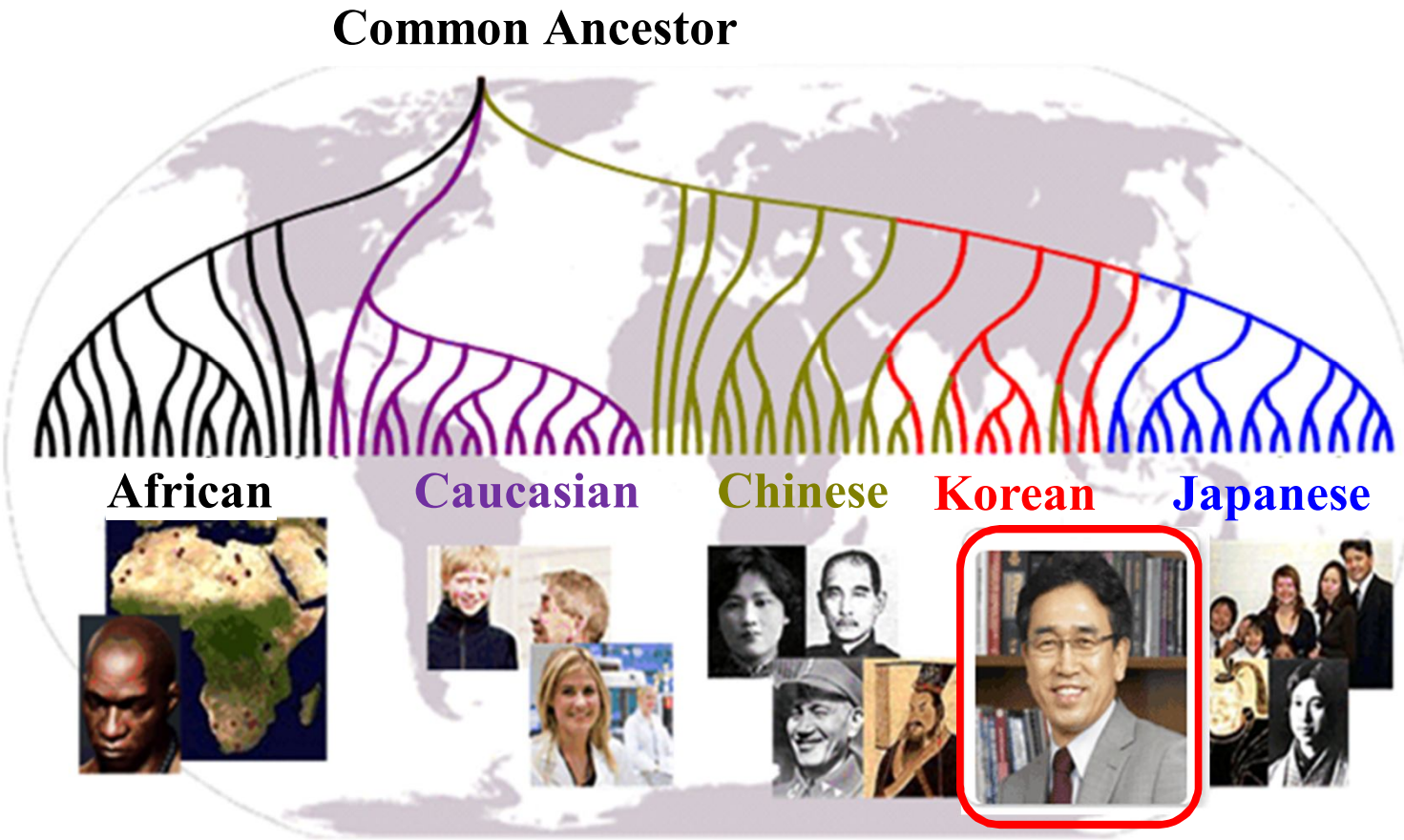
The first Korean genome sequence and analysis: Full genome sequencing for a socio-ethnic group

Sung-Min Ahn, Tae-Hyung Kim, Sunghoon Lee, et al.

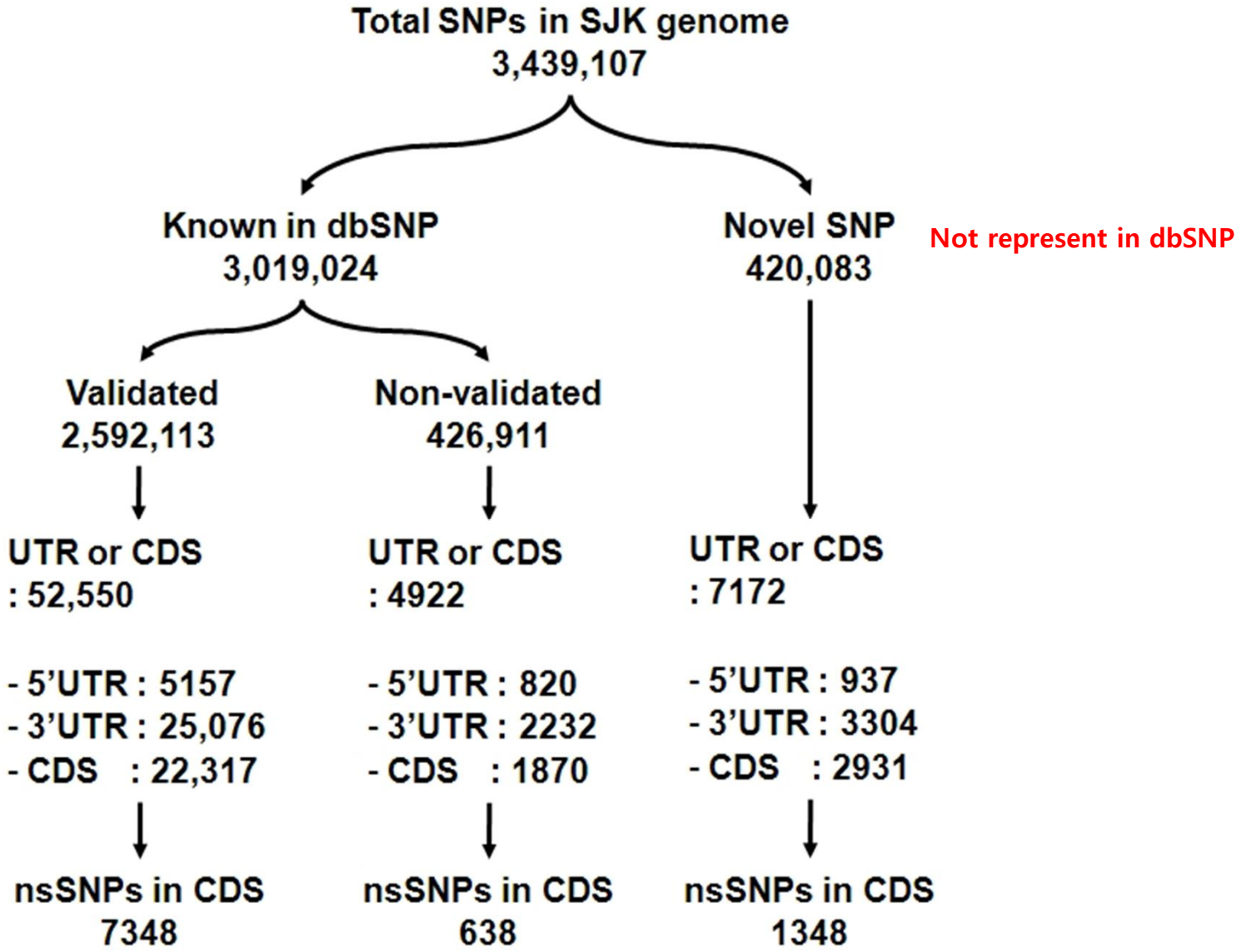
Genome Res. published online May 26, 2009
Access the most recent version at doi:10.1101/gr.092197.109

Data publicized: 2008. Dec. ftp://bioftp.org

The first Korean Genome analysis



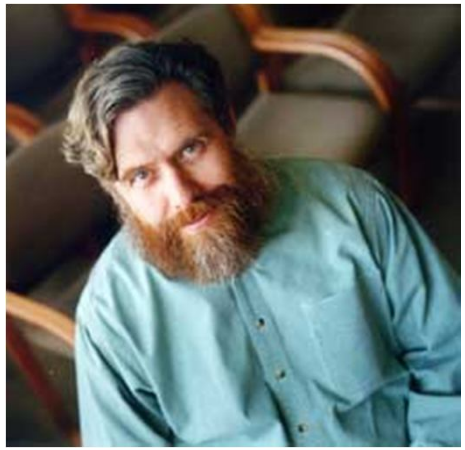
Classification and number of intra-genic SNPs



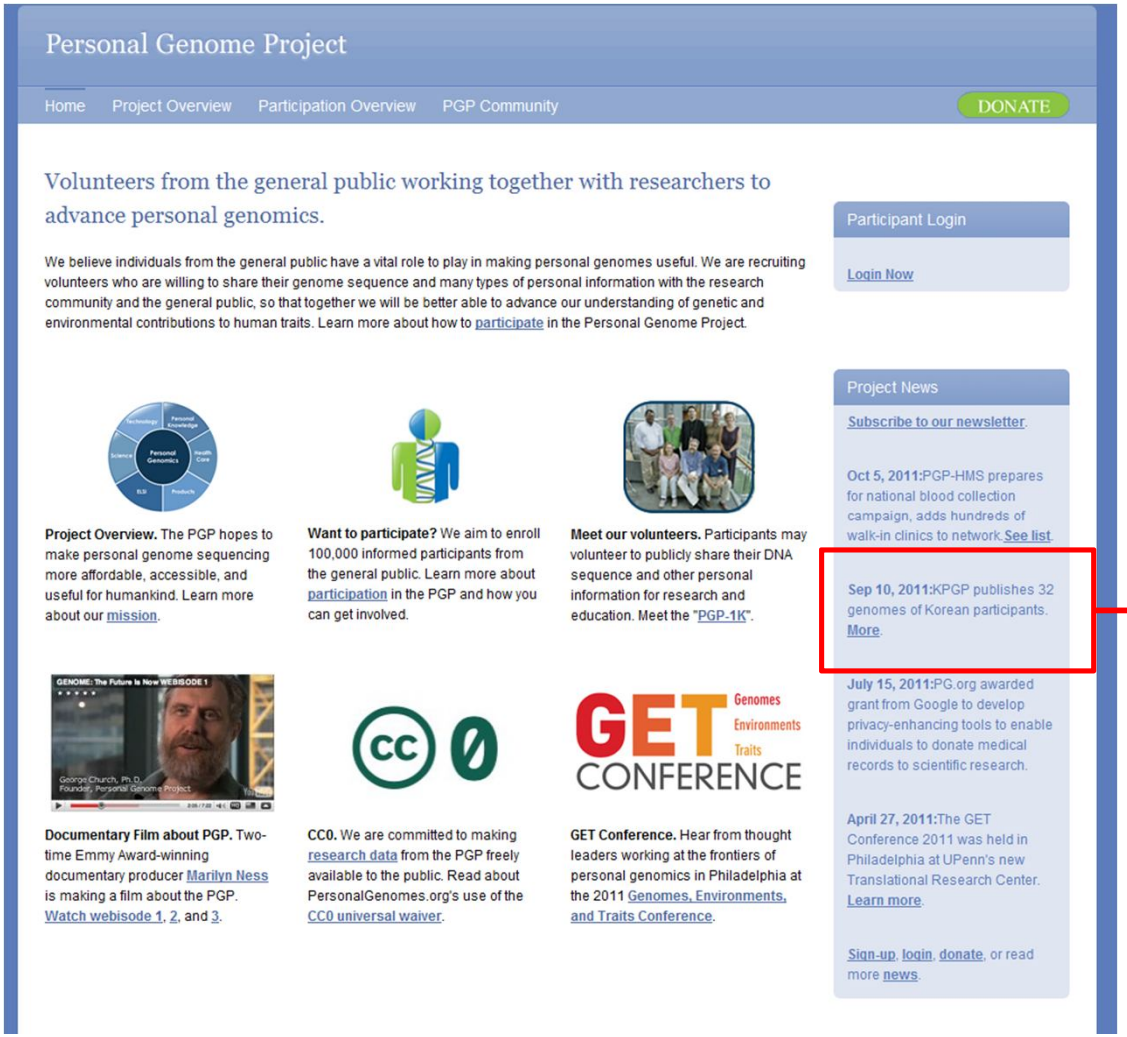
KOREAN PERSONAL GENOME PROJECT

Personal Genome Data

- Public Open Source Genome Project
- Volunteers from the general public working together with researchers to advance personal genomics
- Led by Prof. George Church in Harvard Medical School
- 100,000 informed participants from the general public (US Citizen)
- Research Data freely available to the public



Personal Genome Project



KPGP Mission

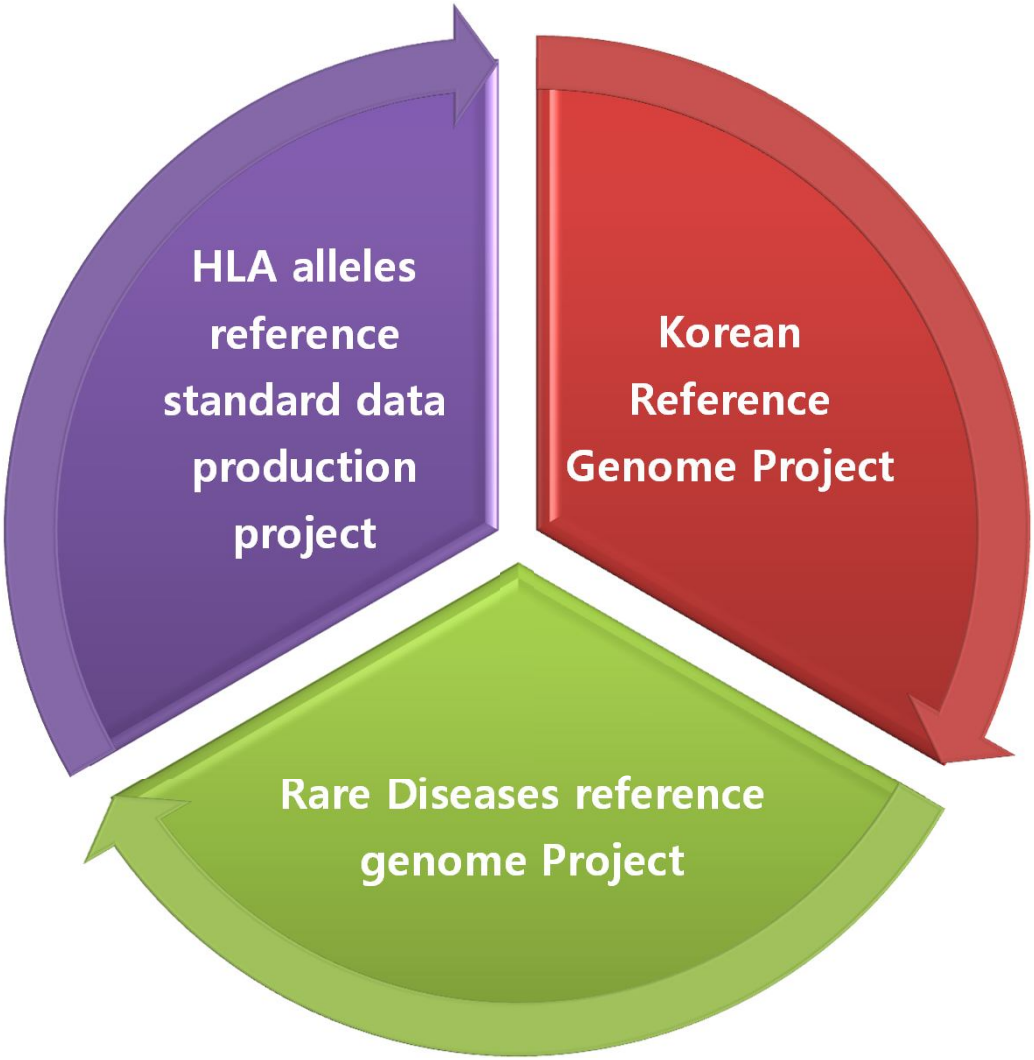
To build a **standard Korean genetic information** database

To promote **personalized** and **personal genome** research and commercialization

To develop **genome sequencing and analysis technologies** in the age of personal genetic information services

To help **community be aware of ethical, social, and legal issues** in regard to genetic information

Research field



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KPGP-20

Thanks to KT (Korea Telecom)

Population Genomics Project

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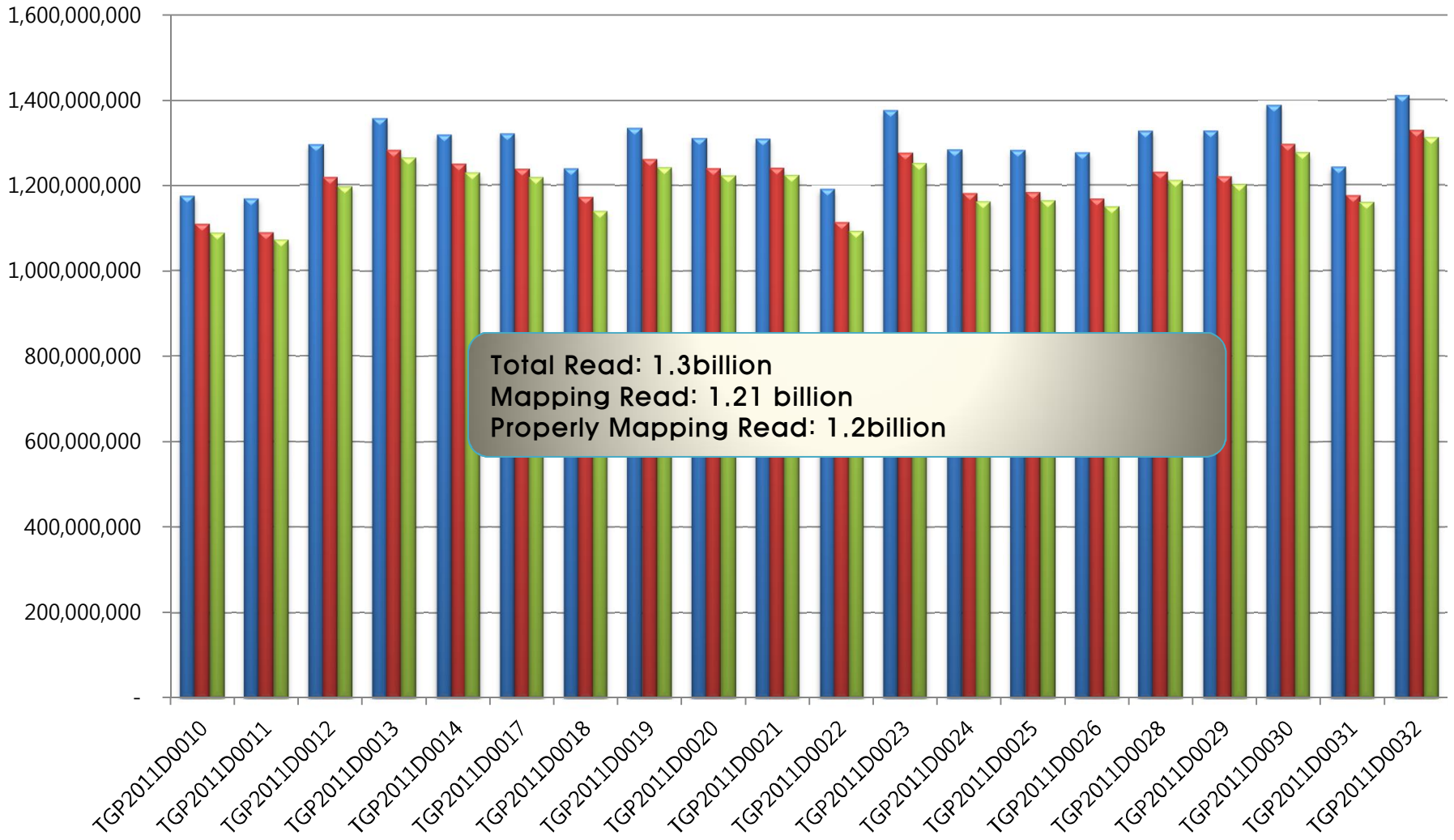
KPGP-20 Result 1

	1 person (First Korean genome)	20 people	Percentage change
Announcement	12 /2008	9 /2011	-
Genome Analysis Duration	3 month	1 month	3-fold decrease
Genome Analysis Cost (per person)	$0.25million	$0.6million ($30,000)	8-fold decrease
Detected Variation (Removed duplication)	3.43M	71.32M (8.76M)	20-fold increase
Novel Variation (Removed duplication)	420K	4.24M (1.84M)	10-fold increase
Read Length	36bp, 75bp	90 bp	2-fold increase
Depth	28.73	37.11	0.3-fold increase

KPGP-20 Result 2

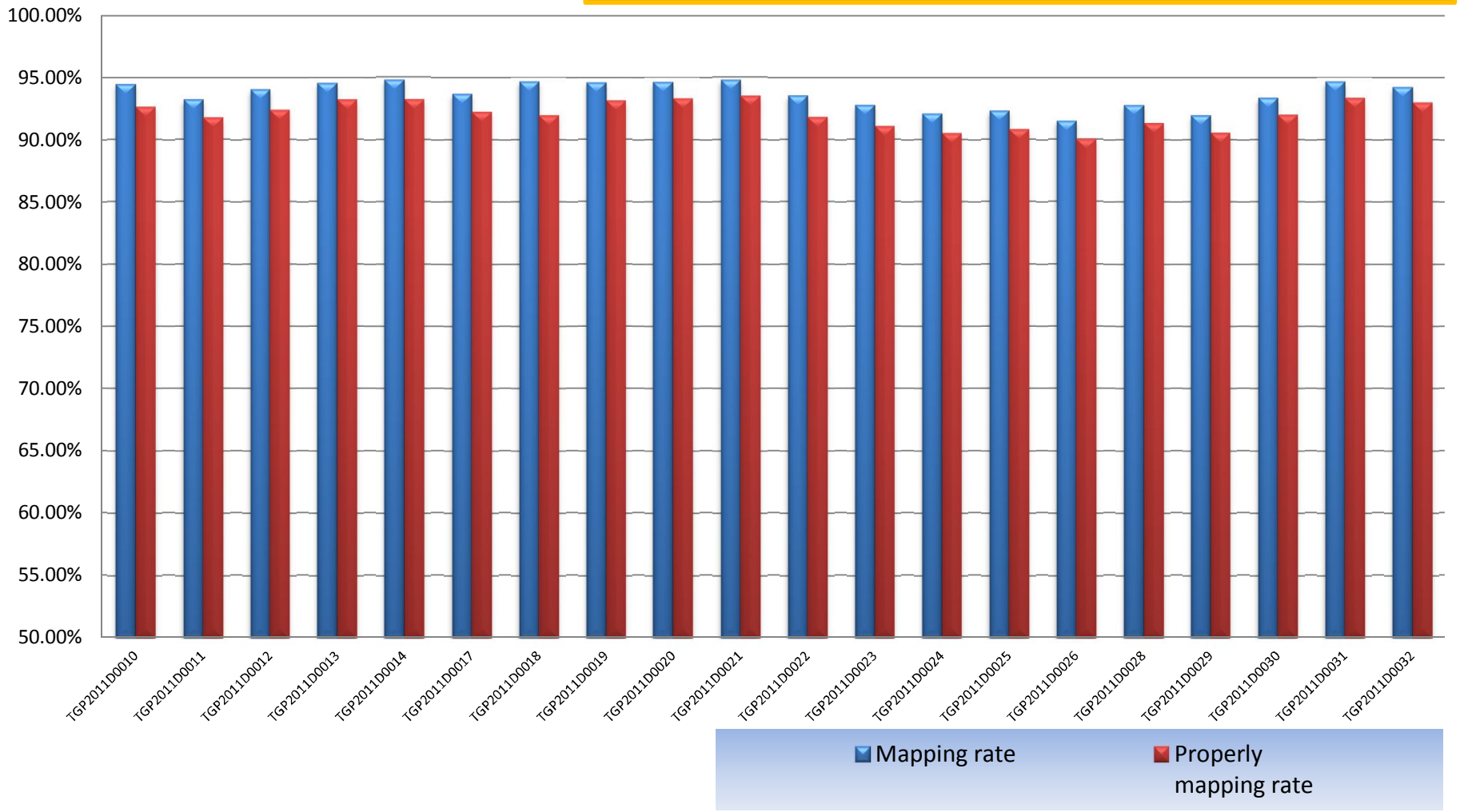
Sample	Raw data Size	Total_reads	Mapped_reads	Mapping_rate	Properly mapped_reads	Properly mapping rate	Depth	Coverage
TGP2011D0010	85Gb	1,174,786,230	1,109,519,944	94.44%	1,088,051,304	92.62%	33.97	98.67%
TGP2011D0011	86Gb	1,167,798,192	1,088,172,839	93.18%	1,071,377,522	91.74%	33.23	98.67%
TGP2011D0012	94Gb	1,295,848,662	1,218,097,132	94.00%	1,197,064,878	92.38%	37.13	99.41%
TGP2011D0013	101Gb	1,358,192,924	1,283,956,209	94.53%	1,265,733,484	93.19%	39.66	98.67%
TGP2011D0014	98Gb	1,318,559,622	1,250,065,225	94.81%	1,229,266,548	93.23%	38.43	99.33%
TGP2011D0017	97Gb	1,320,926,164	1,237,634,224	93.69%	1,218,621,568	92.26%	37.75	99.23%
TGP2011D0018	90Gb	1,238,984,198	1,173,023,066	94.68%	1,139,456,378	91.97%	36.25	98.66%
TGP2011D0019	99Gb	1,334,920,326	1,262,381,805	94.57%	1,242,631,260	93.09%	38.56	99.36%
TGP2011D0020	97Gb	1,311,413,946	1,241,084,671	94.64%	1,223,679,352	93.31%	38.26	98.69%
TGP2011D0021	96Gb	1,309,436,430	1,241,318,554	94.80%	1,224,736,606	93.53%	38.42	98.67%
TGP2011D0022	86Gb	1,190,268,342	1,113,253,155	93.53%	1,092,477,330	91.78%	34.00	99.39%
TGP2011D0023	101Gb	1,376,317,182	1,276,555,687	92.75%	1,252,845,038	91.03%	38.97	98.68%
TGP2011D0024	94Gb	1,282,791,040	1,181,054,915	92.07%	1,161,234,780	90.52%	35.58	99.33%
TGP2011D0025	93Gb	1,281,863,526	1,182,955,980	92.28%	1,163,771,886	90.79%	35.75	99.39%
TGP2011D0026	94Gb	1,277,607,666	1,168,806,522	91.48%	1,149,977,950	90.01%	35.28	99.44%
TGP2011D0028	97Gb	1,327,623,402	1,232,059,676	92.80%	1,212,545,772	91.33%	37.69	98.82%
TGP2011D0029	97Gb	1,328,229,348	1,221,368,842	91.95%	1,202,909,240	90.56%	37.35	98.83%
TGP2011D0030	103Gb	1,389,159,180	1,297,117,533	93.37%	1,277,997,460	92.00%	39.42	99.44%
TGP2011D0031	89Gb	1,242,908,982	1,176,511,586	94.66%	1,160,494,548	93.37%	35.89	99.42%
TGP2011D0032	105Gb	1,411,123,640	1,329,762,106	94.23%	1,312,030,388	92.98%	40.51	99.39%

KPGP-20 Result 3



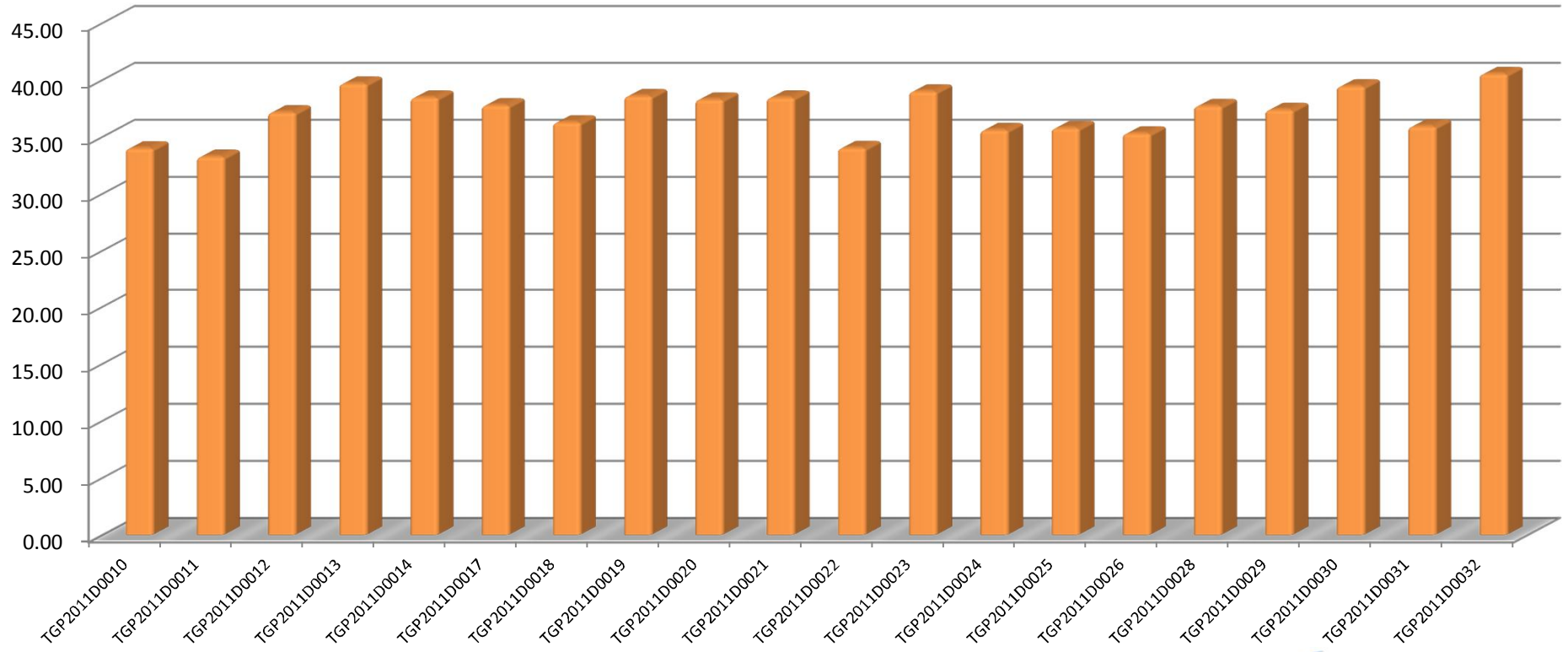
KPGP-20 Result 4

Average Mapping Rate: 93.62%
Average Properly Mapping Rate:92.08%



KPGP-20 Result 5

Average Depth: 37.11X



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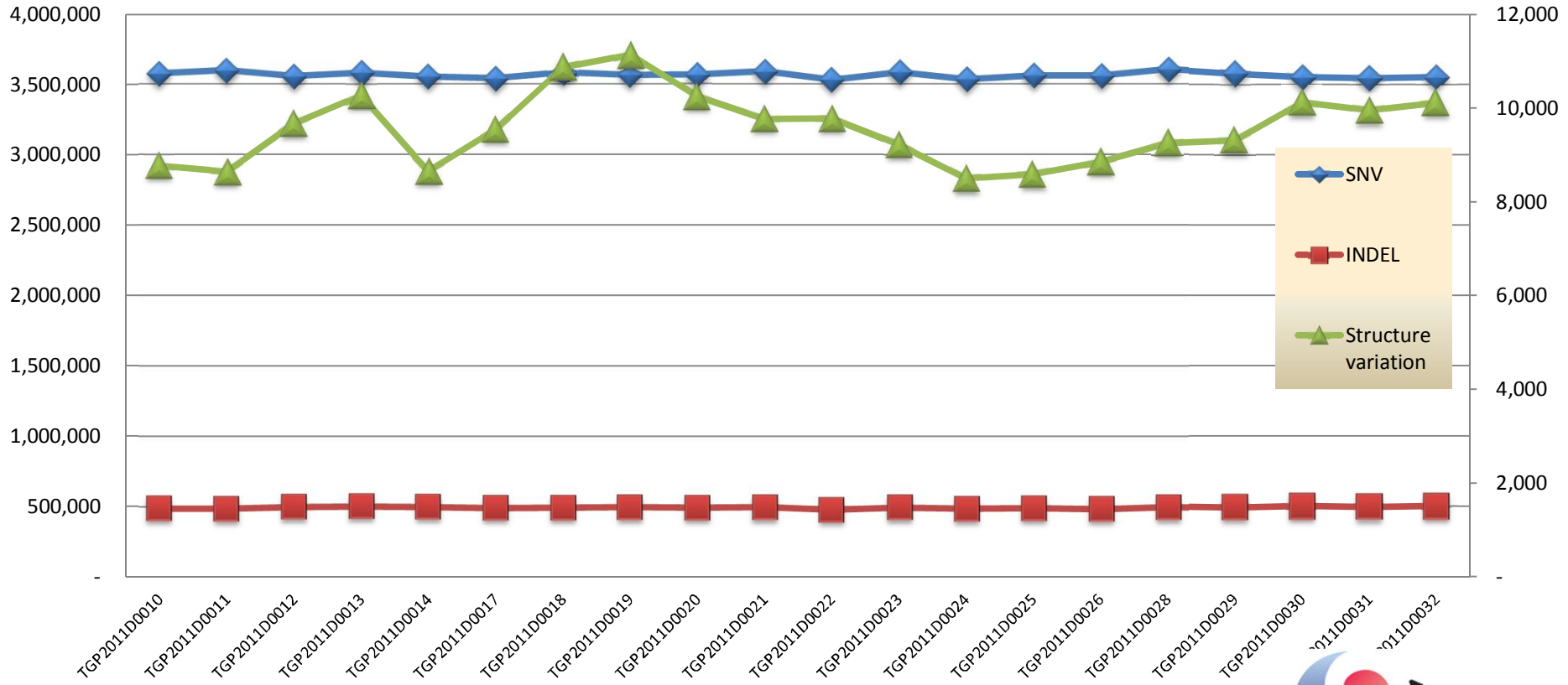
KPGP-20 Result 6

Structural variation

Average SNV: 3.5M
Average Indel: 490K
Average SV: 9,500



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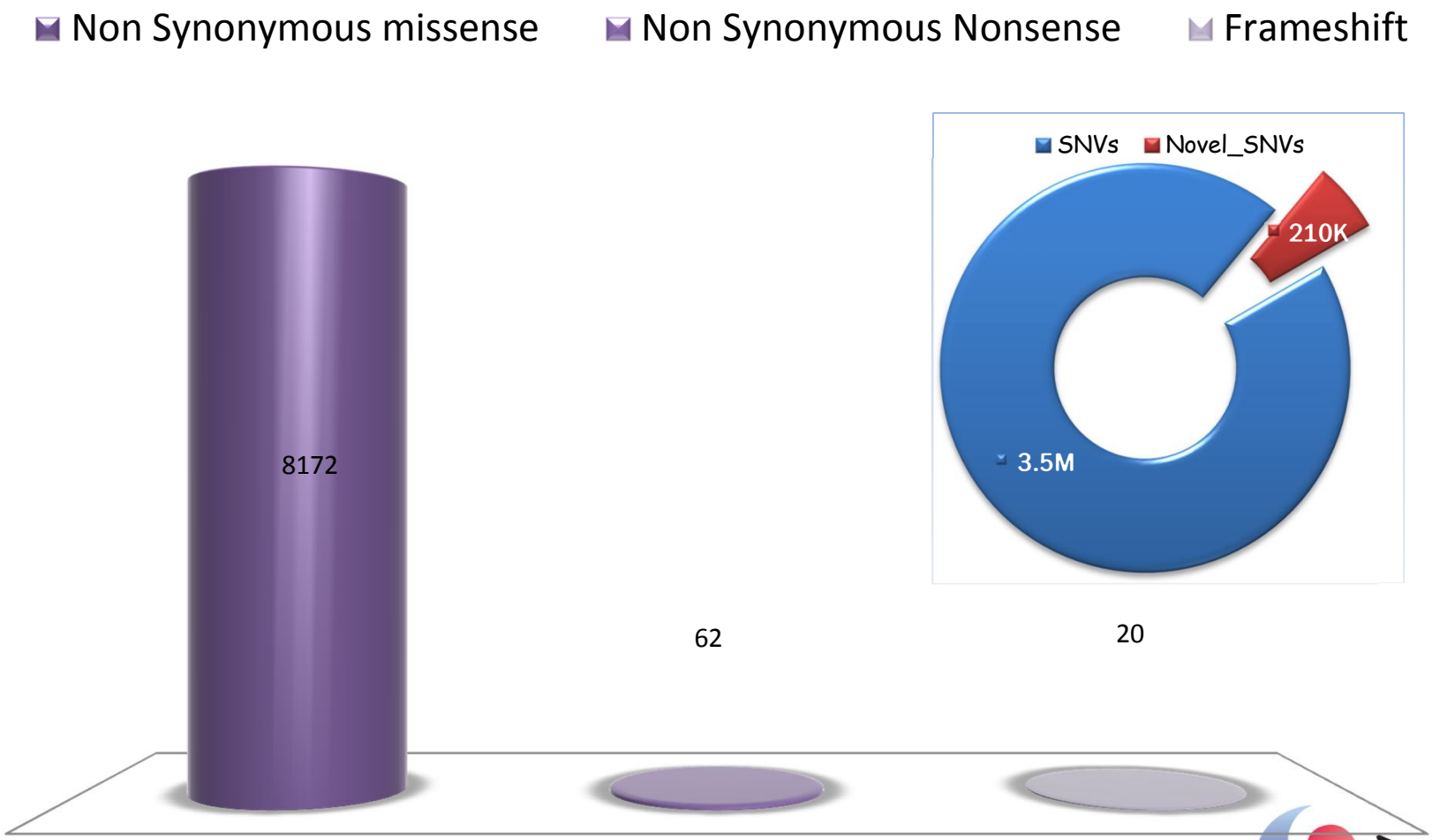
KPGP-20 Result 7

Individual Average SNVs



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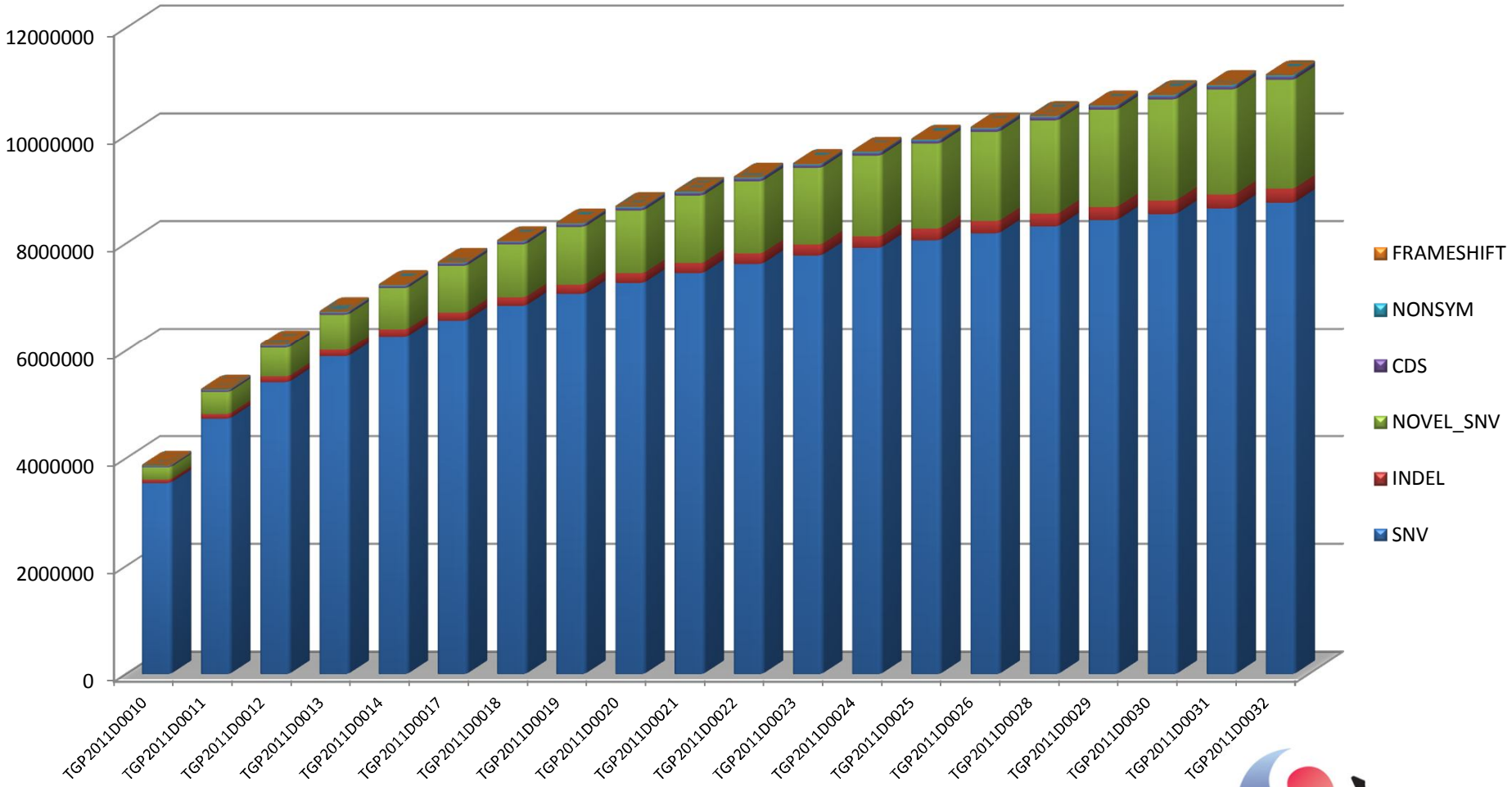
KPGP-20 Result 8 / 10

Cumulative of Genetic Variant



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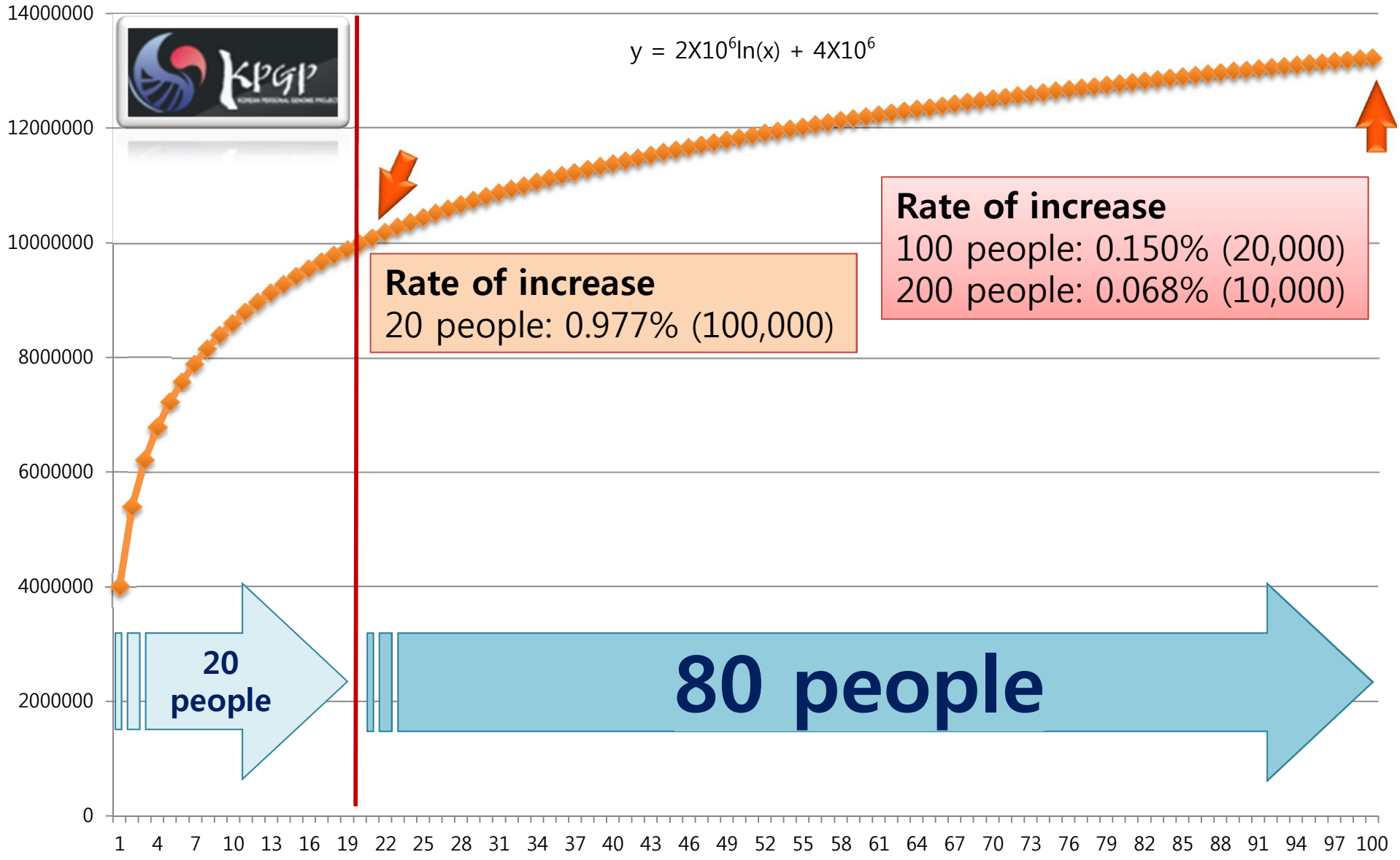
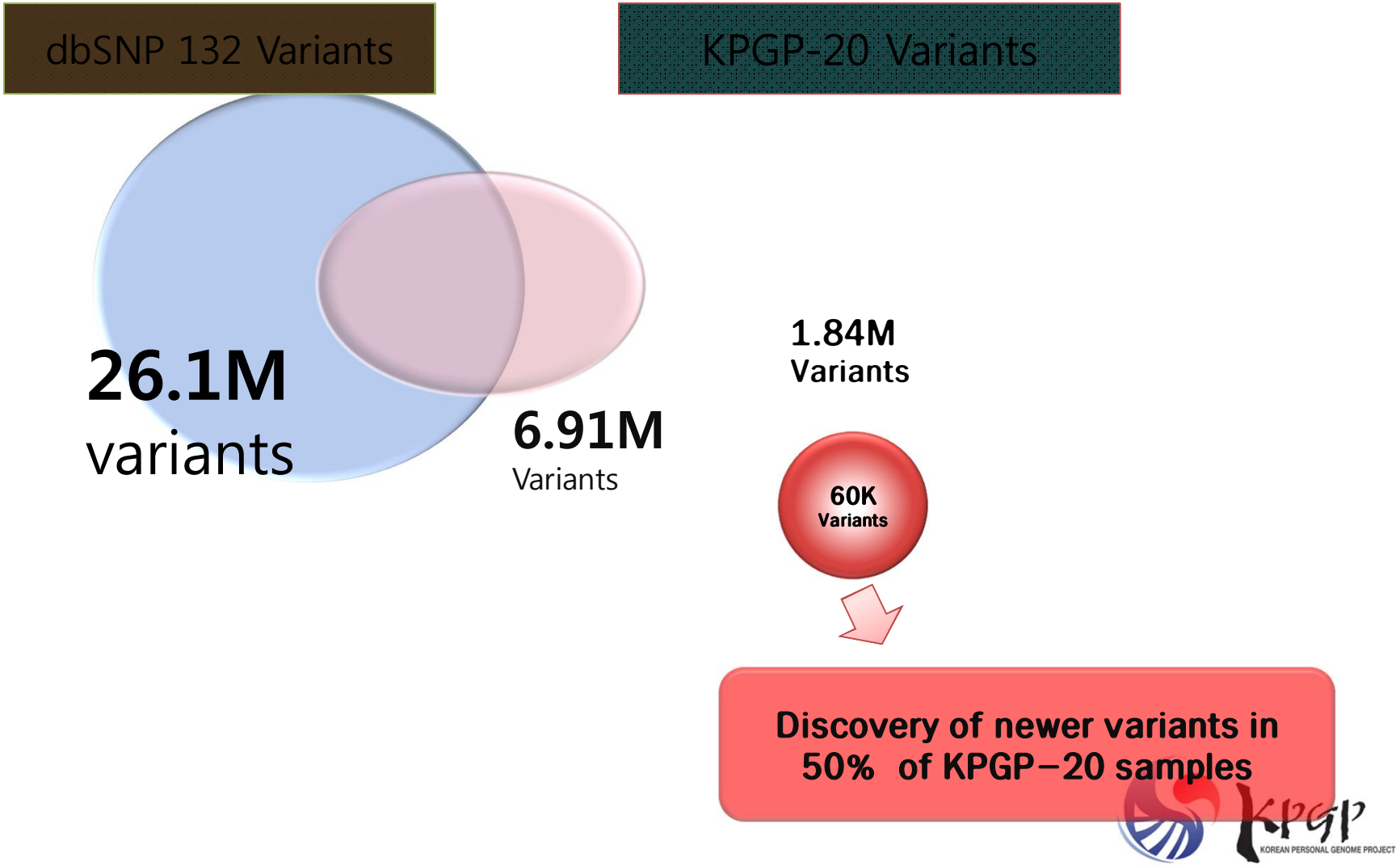
KPGP-20 Result 9 / 10



KPGP-20 Result 10

Representative genetic variants of Korean



OPEN KPGP

OPEN KPGP

OPEN KPGP

Korean Participation of PGP
'OPEN KPGP' Launched by Genome Research Foundation(GRF)
Providing Genome Data to Researchers without Restrictions

Korean Personal Genome Project (KPGP) is a participative research project established by Genome Research Foundation(GRF).
The international Personal Genome Project (PGP), led by U.S. none-profit research group, is founded in 2006 and seeking a diverse range of volunteers with the purpose of improving human health.
In concordance with the international PGP, KPGP has started to improve Korean people's health and medical welfare. > more about us

KPGP Public Data


Korean


Other


Rare Disease Patients


Miltiracial(people)


Monozygotic Twin

olleh ucloud
KTuCloud+PGI


Dizygotic Twin

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OPEN KPGP - Data

KPGP 00001

- Public Profile ID : KPGP_00001
- Gender : F
- Nationality : Korea
- Ethnic Group : East Asian
- Platform : Illumina,HiSeq2000

BioFTP Download | Torrent Download

Genetic data Download

- Raw Data Raw Data
- Aligned Data Mapping
- Nonsynonymous SNVs Nonsynonymous SNVs
- Read me Read me
- Genome Variation SNVs CNVs INDELs SVs

Torrent Download

```
# Ome Data File Format (ODFF) Readme recommended by Genome Research Foundation
File name : KPGP1_G_110915_HiSeq_EastAsian_Kor_F

Sample ID : KPGP_00001
Other IDs : TGP2010D0010
Sample type : Genomic DNA
Tissue type : Blood
Data Publication Date: 2011.9.15
Sequencing platform : Illumina, HiSeq2000
Ethnic Group : East Asian
Nationality : Korea
Gender : F
Brith Date : N/A
Dieases : N/A
Name : N/A
Data depository: ftp://bioftp.org/Bi0/Distribute/Open-KPGP/TGP2010D0010/
Project name: KPGP
Reference: UCSC, HG19
Contact email: jongbhak@yahoo.com
-----------------------------------------------
Data analysis tool information
- Rawdata          fastq
- mapping result   bwa(0.5.9)
- SNV              samtools(0.1.16)
- INDEL            samtools(0.1.16)
- SV               breakdancer (1.1)
- NSSNV            GRF's pipeline
- CNV              N/A
- STATISTICS       GRF's pipeline
```

OPEN KPGP – Available Data

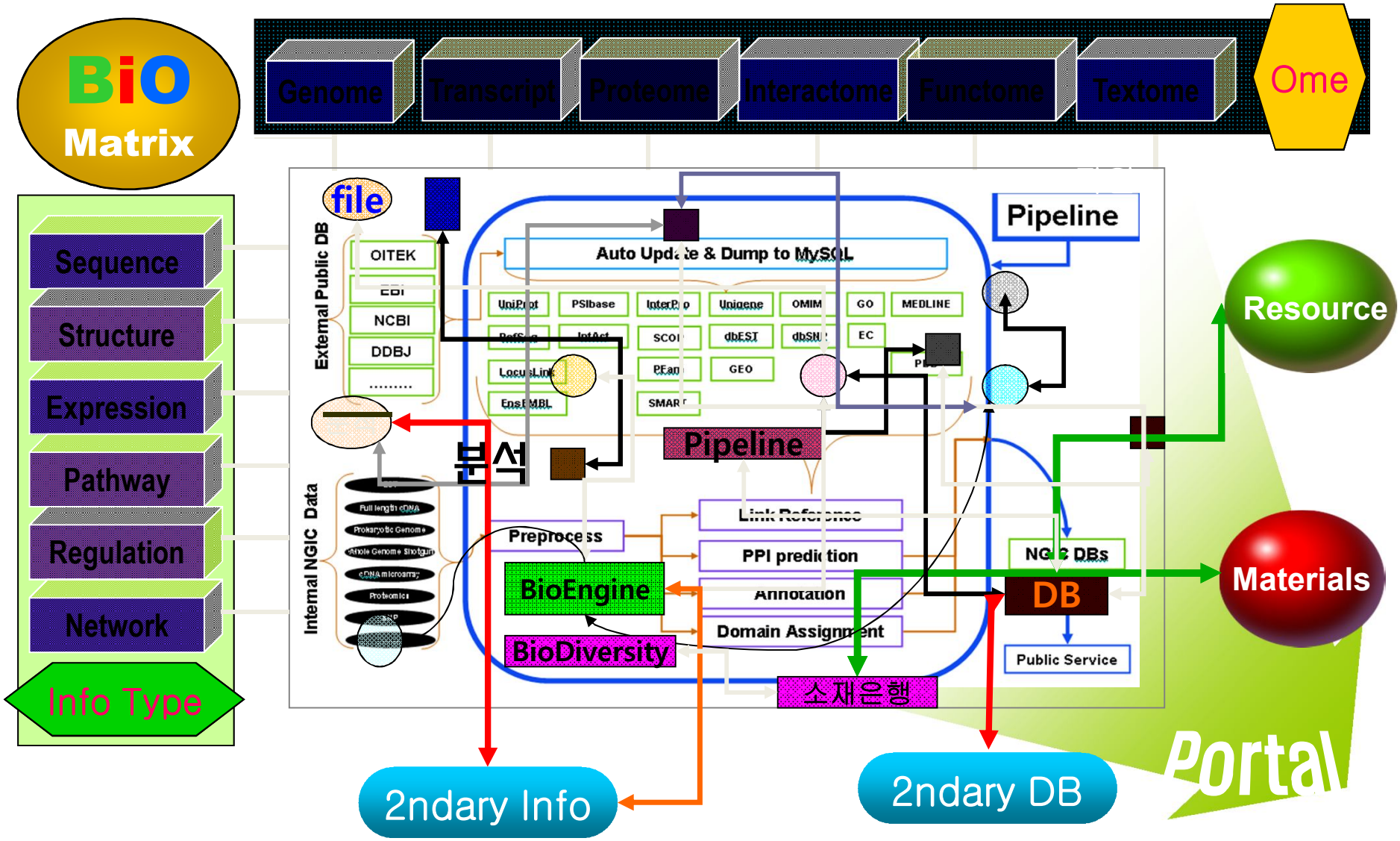
Korean		35 people
Multiracial		2 people
Caucasian		1 person
Monozygotic twin		2 people
Dizygotic twin		2 people
Publically available samples		38 people

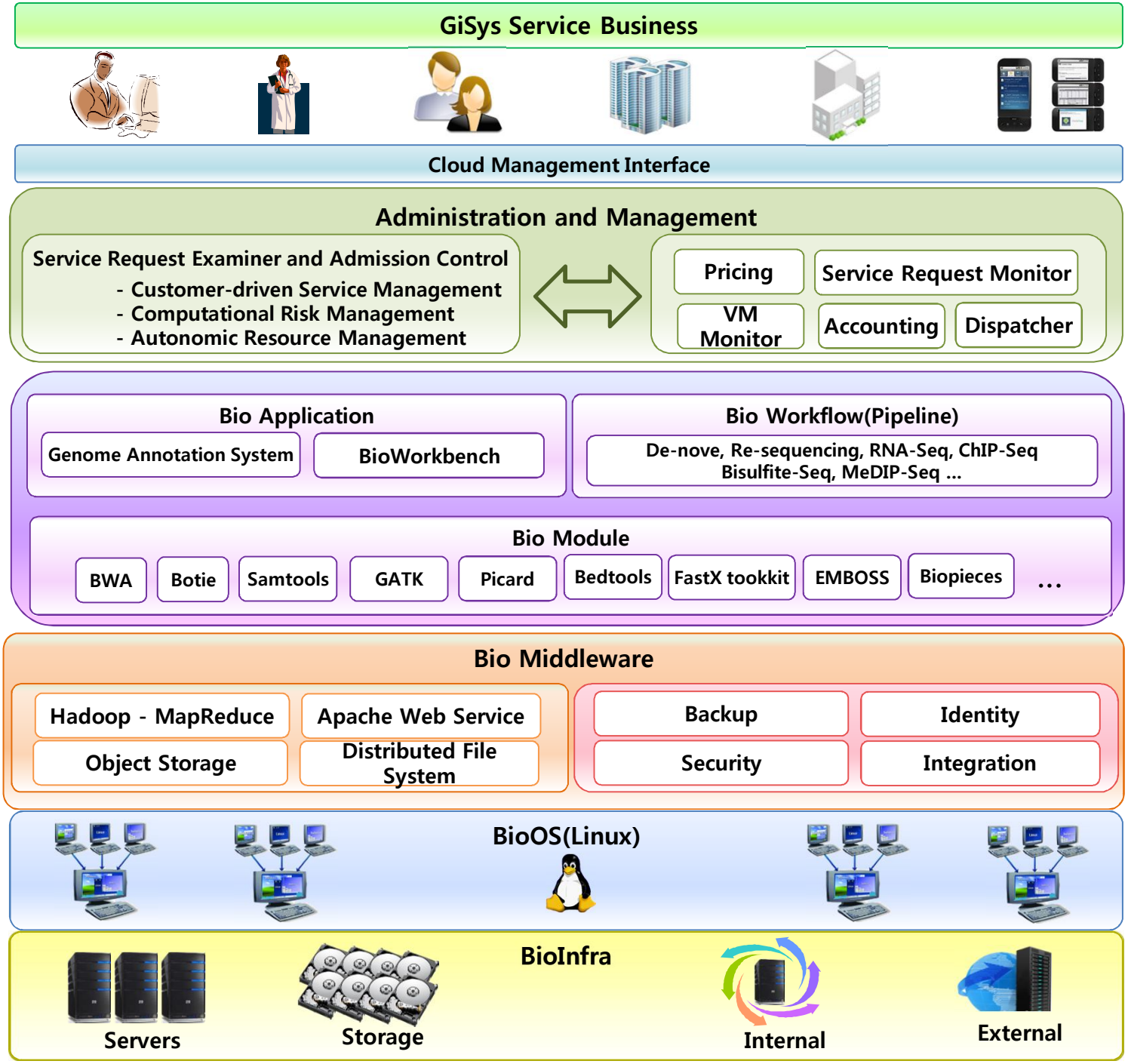
Genome Engine (GiSys)

Korean National NGS software project

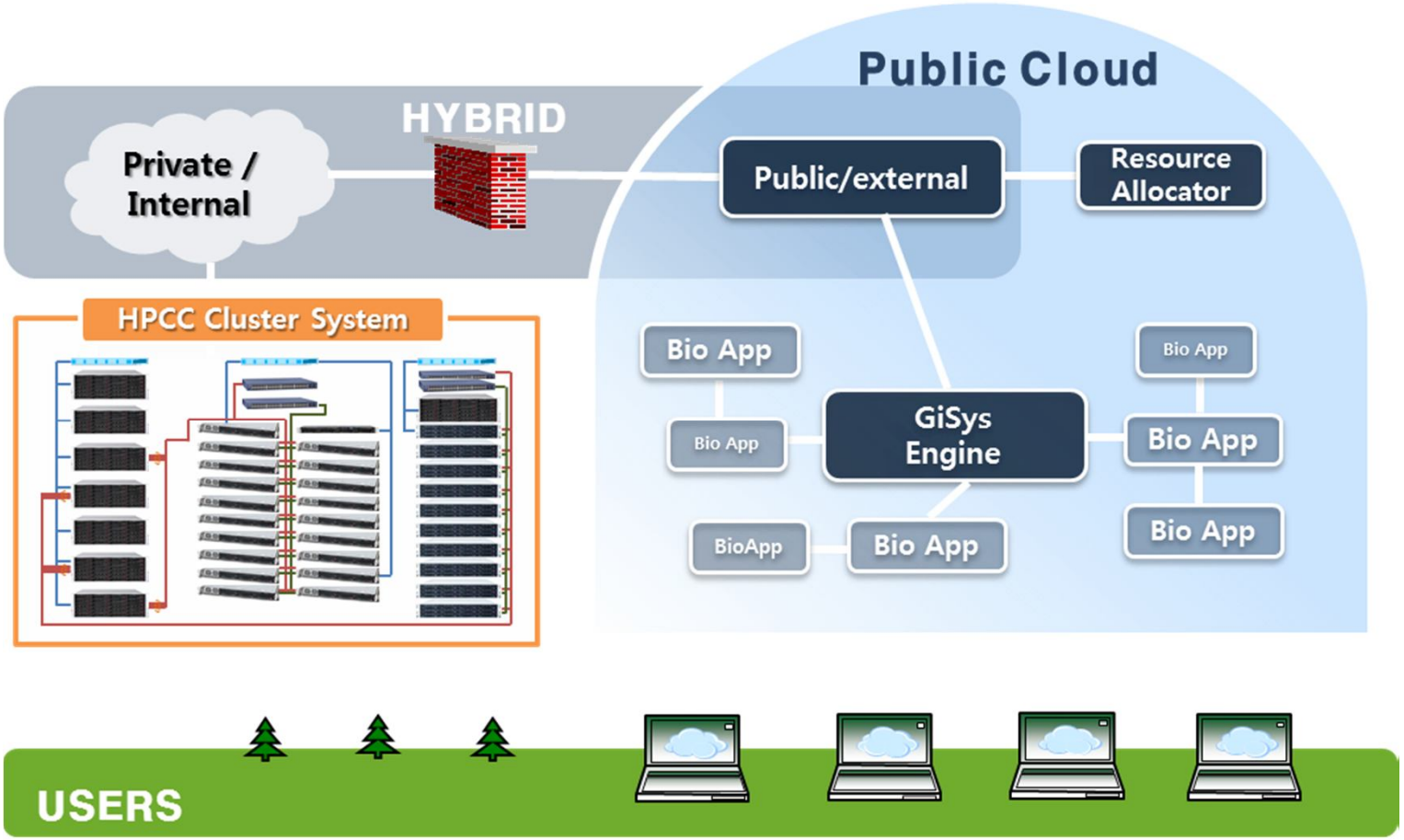
Ministry of Economy and Knowledge

BioEngine: Putting structure in omics

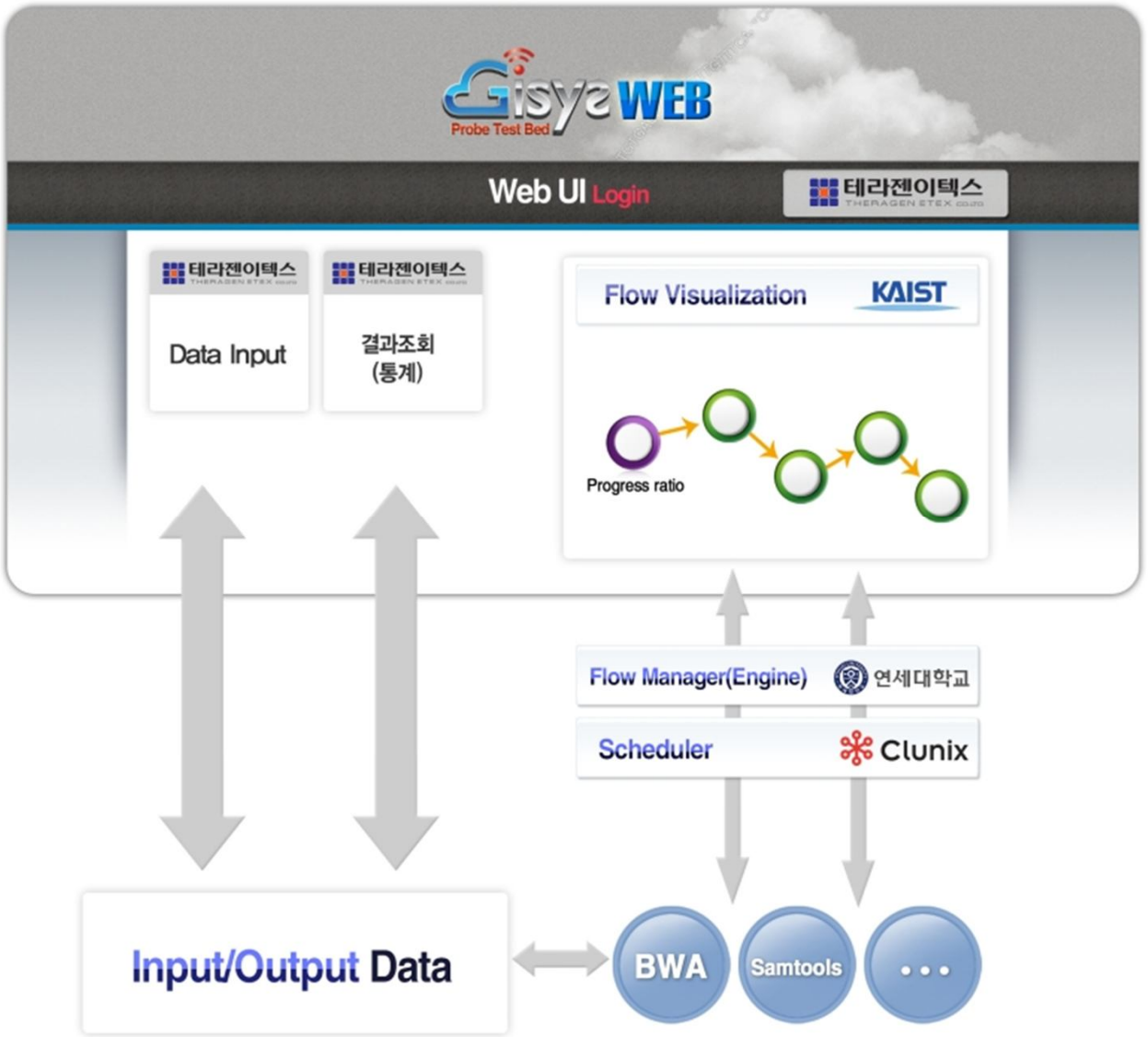



GiSys Service Business
Cloud Management Interface
Administration and Management
Service Request Examiner and Admission Control
- Customer-driven Service Management
- Computational Risk Management
- Autonomic Resource Management
Pricing
Service Request Monitor
VM Monitor
Accounting
Dispatcher
Bio Application
Genome Annotation System
BioWorkbench
Bio Workflow(Pipeline)
De-nove, Re-sequencing, RNA-Seq, ChIP-Seq
Bisulfite-Seq, MeDIP-Seq ...
Bio Module
BWA
Botie
Samtools
GATK
Picard
Bedtools
FastX tookkit
EMBOSS
Biopieces
...
Bio Middleware
Hadoop - MapReduce
Apache Web Service
Object Storage
Distributed File System
Backup
Identity
Security
Integration
BioOS(Linux)
BioInfra
Servers
Storage
Internal
External

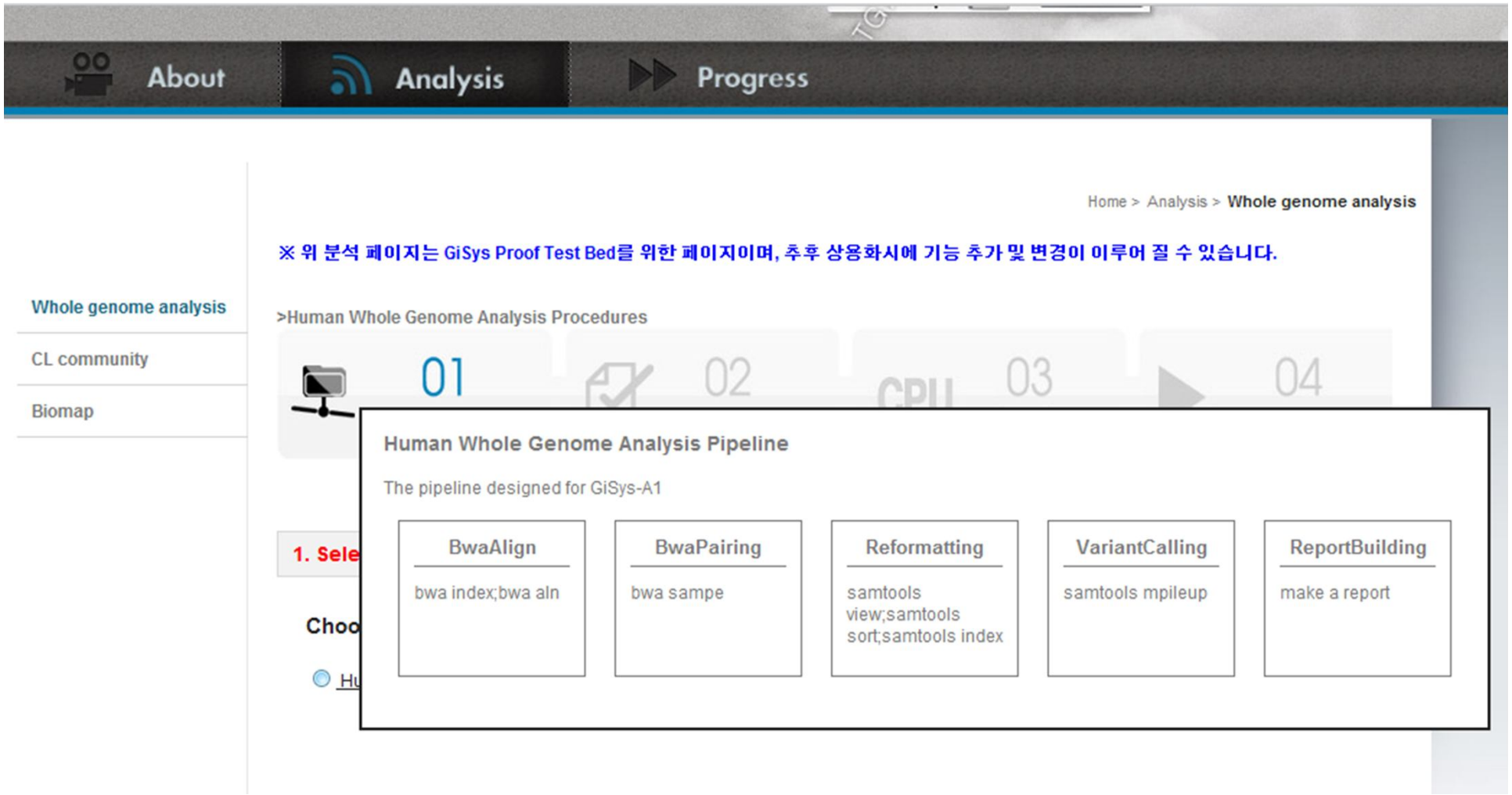
GiSys (Genome Informatics System)



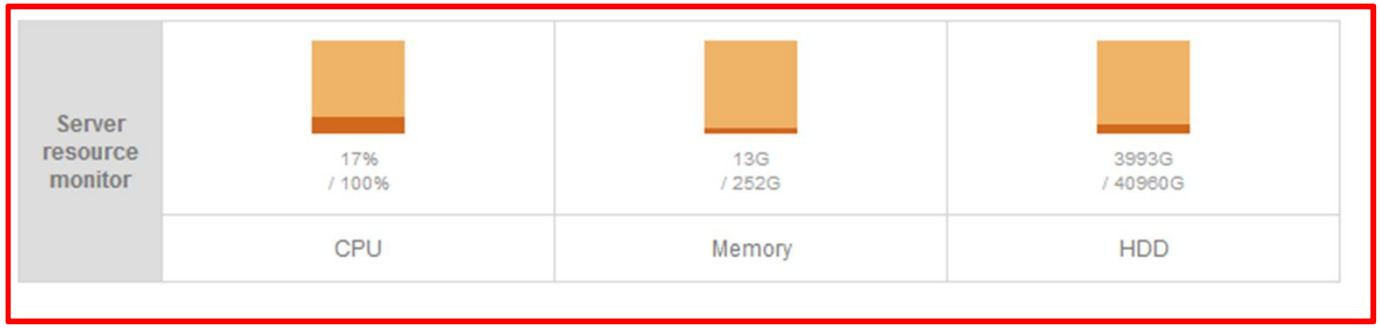
GiSys (Genome Informatics System)

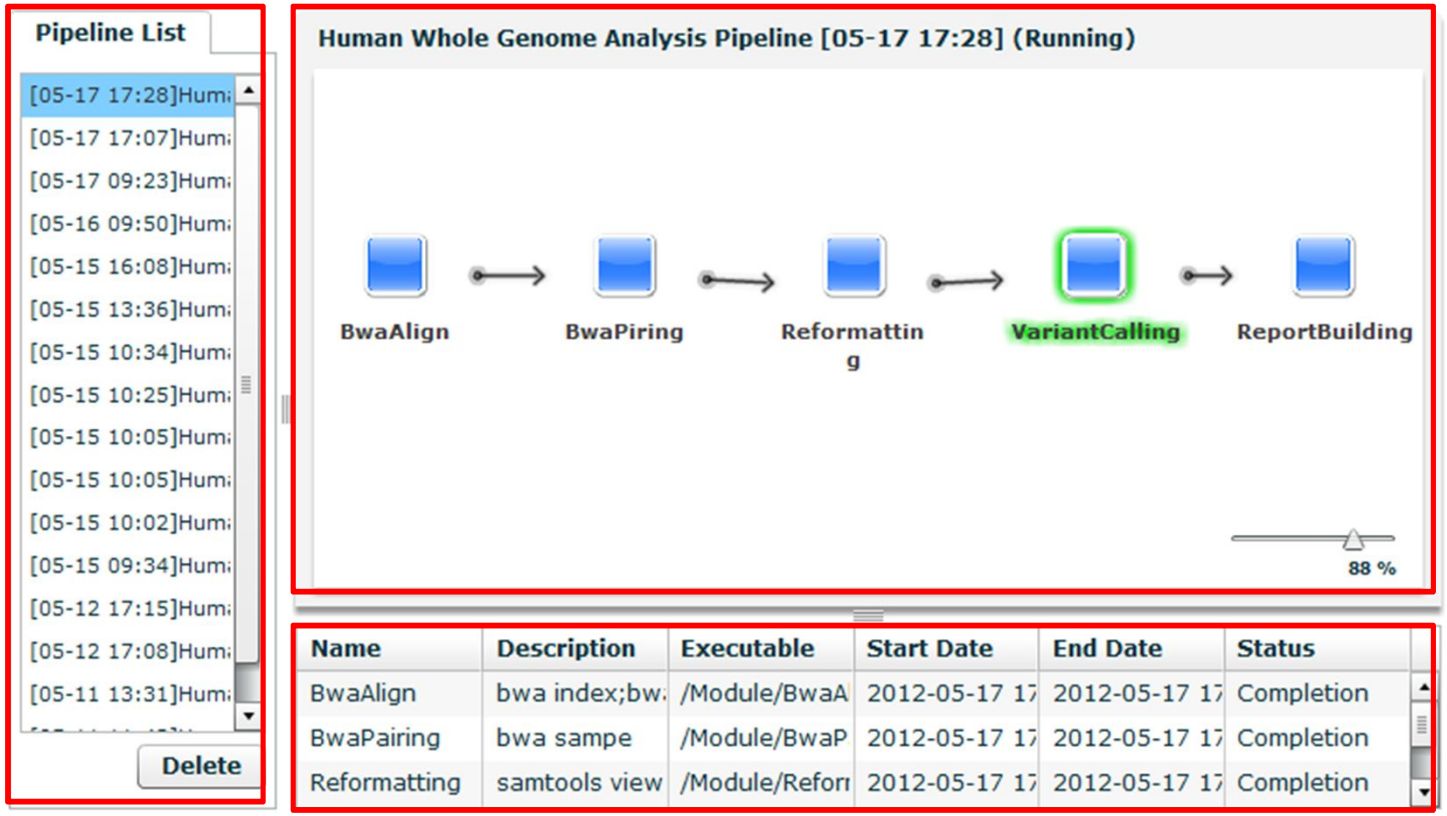


GiSys


About
Analysis
Progress
Home > Analysis > Whole genome analysis
※ 위 분석 페이지는 GiSys Proof Test Bed를 위한 페이지이며, 추후 상용화시에 기능 추가 및 변경이 이루어 질 수 있습니다.
Whole genome analysis
CL community
Biomap
>Human Whole Genome Analysis Procedures
01
02
03
04
Human Whole Genome Analysis Pipeline
The pipeline designed for GiSys-A1
BwaAlign
bwa index;bwa aln
BwaPairing
bwa sampe
Reformatting
samtools view;samtools sort;samtools index
VariantCalling
samtools mpileup
ReportBuilding
make a report

GiSys (Genome Informatics System)





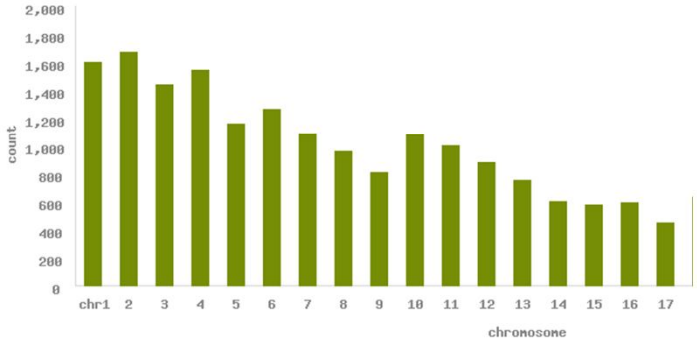
GiSys (Genome Informatics System)

> SNV (Single Nucleotide Variation)

- 단기염기서열변이 : 하나의 서열 또는 종내 소수의 집단에서 나타나는 단일염기의 차이로, 시퀀싱 데이터에서 나타나는 표준 염기서열과의 차이.

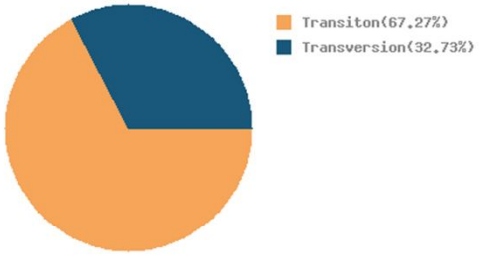
1. SNV count

- 단일염기서열변이(SNV)의 개수
- 정렬된 read 서열을 이용하여, reference 서열과 샘플 염기서열의 비교를 통해 샘플 특이적인 다형적 유전자형을 확인한다. 다형적 유전자형은 높은 신뢰도의 SNV 데
를 생성하기 위해 필터링 과정을 거친다. 게놈의 coding 지역의 SNV의 발생에 의해 아미노산이 치환 및 단백질의 구조 및 기능의 변화를 일으킬 수 있다.



2. Transition / Transversion

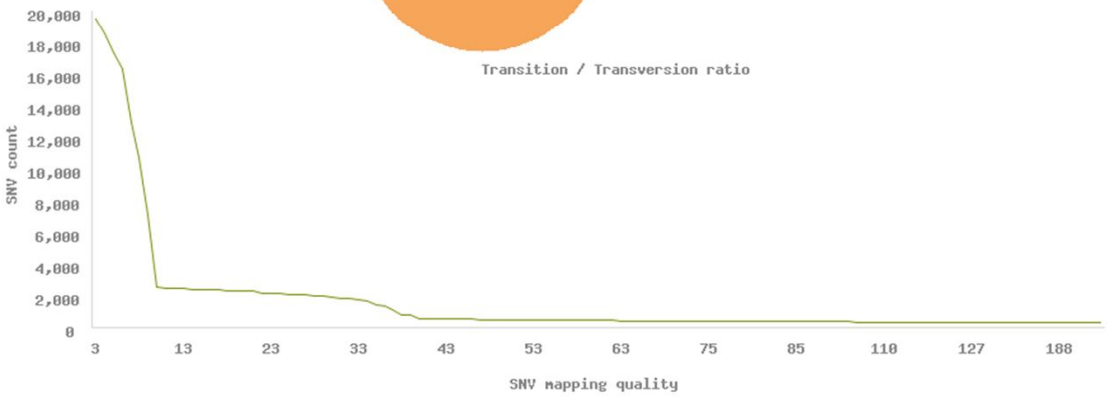
- 유사성 염기치환 (Transition) : 퓨린이 다른 퓨린에 의해 또는 피리미딘이 다른 피리미딘에 의해 교체된 염기치환
- 교차형 염기치환 (Transversion) : 퓨린에서 피리미딘으로 대체되고, 피리미딘이 퓨린으로 대체되는 염기 치환
- 일반적으로 모든 게놈상의 모든 DNA 서열에 있어 Transition(T<->C, A<->G)의 빈도가 Transversion (T<->A, T<->G, C<->A, C<->G)의 빈도보다 높다 (Brown et al. 1982; Gojobori et al. 1982;Curtis and Clegg 1984; Wakeley 1994, 1996). Transition / Transversion 비율은 DNA 서열 진화의 일반적 특성이라고 알려져 있다 (Wakeley 1996). 또한, Transition / Transversion 비율은 normal 샘플과 cancer 샘플에서 차이를 보이는 특징이 있다.



Transition count	Transversion count	Transiton / Transversion ratio
13,270	6,456	2.055

3. SNV mapping quality

- 정렬된 read 서열 정보를 이용하여 측정된 SN
SNV mapping quality의 누적 그래프로, 특정 m



Transition / Transversion ratio

SUMMARY

- 2006, PGP
- 2008, Korean Genome Project
- 2010, KPGP
- 2011, KPGP-20
- 2012, OPENKPGP – TOTAL 38 genomes
- **GiSys** **(Genome Informatics System)**

TBI and **PGI**

- **TBI** (Theragen BiO Institute) of **TheragenEtex**
  - For profit commercial entity

- **PGI** (Personal Genomics Institute) of **GRF** (Genome Research Foundation)
  - Non-profit, Government managed org.

Theragen (주)테라젠

GRF Genome Research Foundation
Personal Genomics Institute
재단법인 게놈연구재단 / 게놈연구소

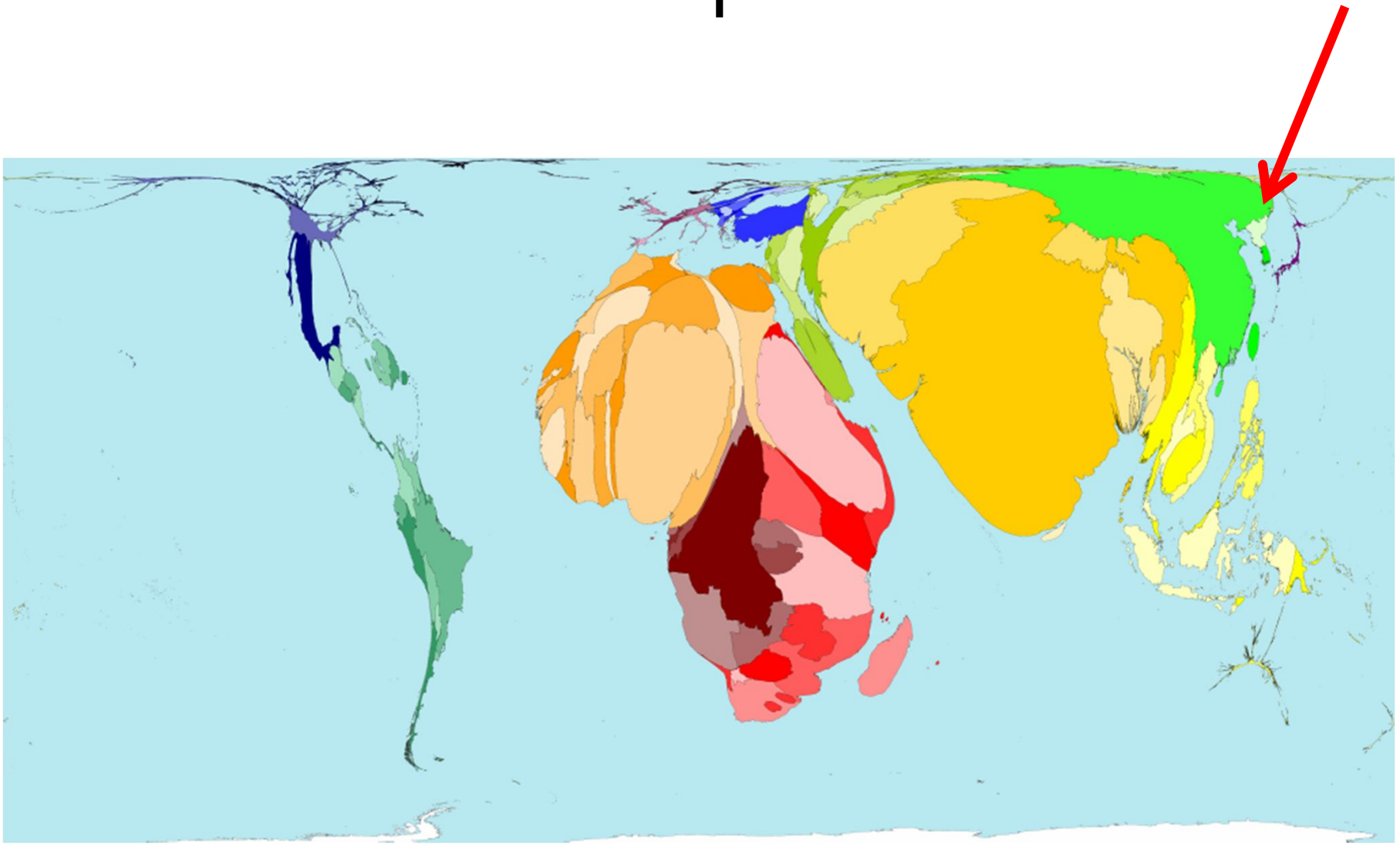
TBI Projects

- HelloGene/ HelloGenome ➔ Personal gene information service
- Tiger (Theragen)
- Whale (with KORDI)
- Gastric Cancer (NCI, Korea)
- Lung Cancer
- Spleen Cancer
- Pancreatic Cancer
- Bladder Cancer
- Korean Horse, Korean Cow, Dog, Monkey, Birds,
- Soybean

Totalomics

- Totalomics: Sequencing and Bioinformatics service by TheragenEtex.
- http://totalomics.com
- http://totalomics.kr

What map is this?



유아사망률