

From: [Richard Chen](#)
To: [John West](#); [Carol Tillis](#); [Christian Haudenschild](#); [Eliane Sousa](#); [Richard Chen](#)
Subject: Final Board Slides
Date: Tuesday, September 4, 2012 4:32:56 PM
Attachments: [board.09.05.12.v9.roc.ppt](#)

Ready for Printing....

Product Development

Personalis, Inc.

09.05.2012

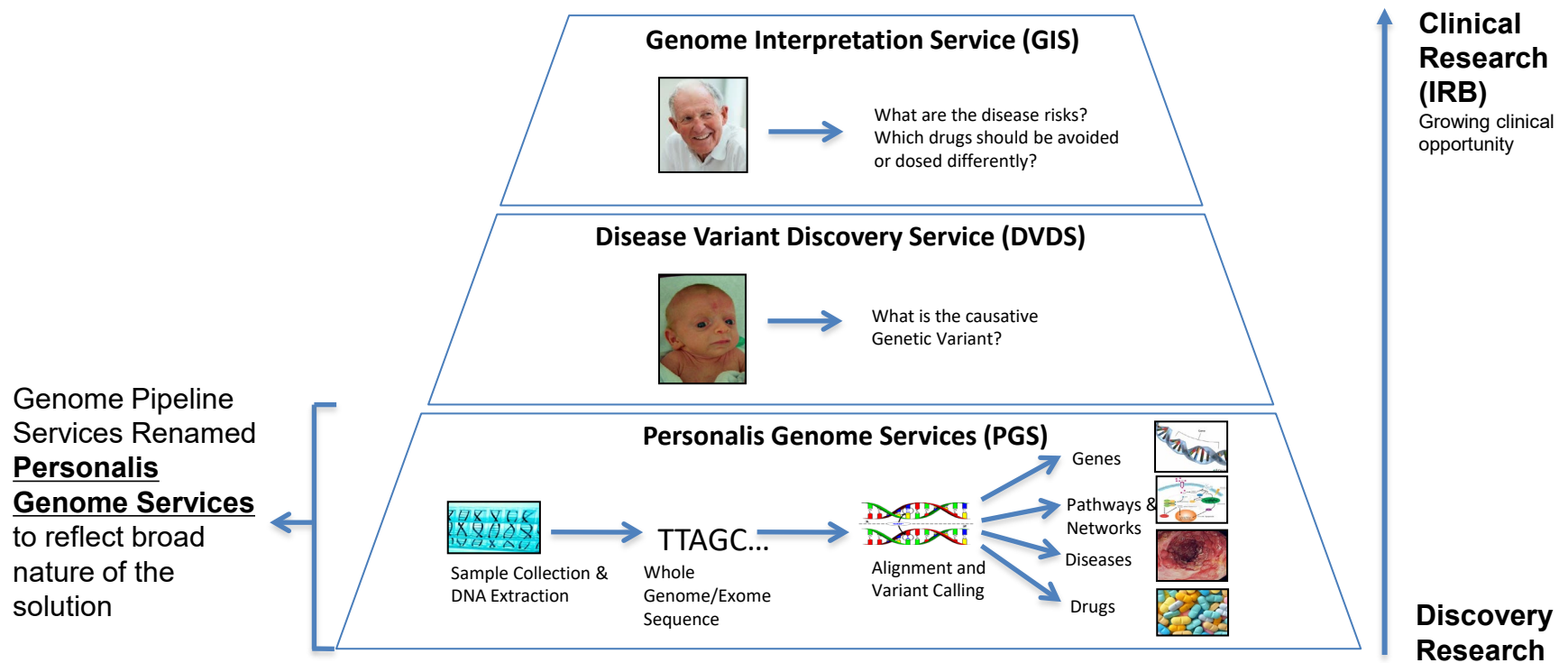
Richard Chen, CSO

Personalis EX2083

Product Development Overview

- Product
 - Prototype
 - Early Customers/Collaborations
 - Product Features, Deliverables, and Differentiation
- Content Development
- Computing Infrastructure
- Hiring

Product Roadmap



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Personalis Genome Services: Prototype

Prototype Ready for Testing with Customers

- Achieved August delivery Milestone for Prototype Service.
 - In past 3-4 months of development. Four sprints, 545 tasks/features completed
 - Moved and set up infrastructure for Confluence, Jira, Git, went from 80 to over 350 cores, more than doubled storage capacity to >300 TB of storage
 - Tested internally: 25 genomes in 25 days
 - All prototype components functional & developer tested
 - Able deliver prototype despite hiring challenges
- Prototype goal: Do enough product development to:
 - Evaluate overall value proposition
 - Test our process for delivering the service
 - Provide early feedback for v1 product, Generate some early revenue
 - Prototype type is not yet optimized for performance, scalability, usability, visualization
- Planning process for v1 of PGS includes balancing multiple new priorities:
 - New laboratory efforts including building Exome+ offering are critical for product differentiation but resource intensive
 - Working with early customers/collaborations such as the Moyamoya
 - Key differentiators for v1 also include improved SV detection, Improved graphics/visualization, new analytics

Personalis Genome Services

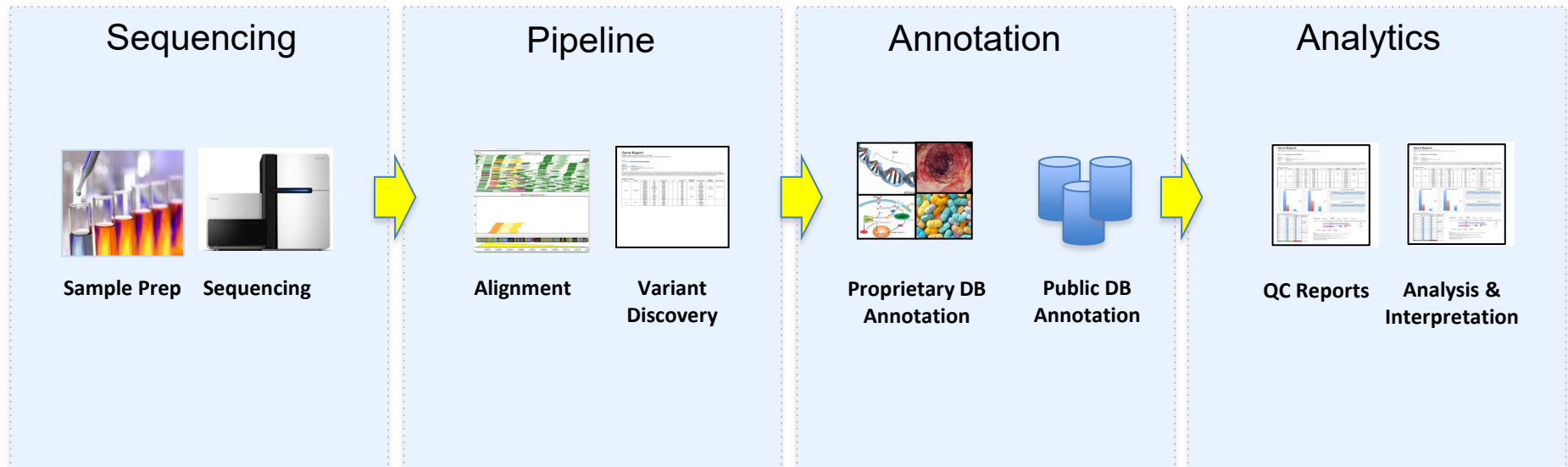
Moyamoya project: Typical Case-Control Study

- First customer: Moyamoya study with Dr. Gary Steinberg @ Stanford
 - Genetic disease of unknown cause resulting in early onset strokes and seizures
 - Caused by blockage of key vessels in the brain resulting in collateral development
 - Phenotypically heterogeneous: Can be isolated or seen in conjunction with neurocutaneous syndromes, Down's syndrome, etc.
- Typical case-control customer:
 - 130 cases of Moyamoya, would like to understand genetic cause
 - clinical expert with patient samples
 - limited bioinformatics capability
 - no controls
- R&D involved in designing & executing these early projects, enabling rapid feedback loop into development for v1
 - We will provide an end-to-end solution consisting of exome sequencing, alignment, variant calling, annotation, case-control analysis
 - Use gender and ethnicity matched controls from 1000 genomes
 - Will do subgrouped analysis based on different phenotypes

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Inaccuracies in current sequencing solutions lead to incorrect conclusions/false leads that result in increased cost and time for researchers and clinicians, poor outcomes for patients

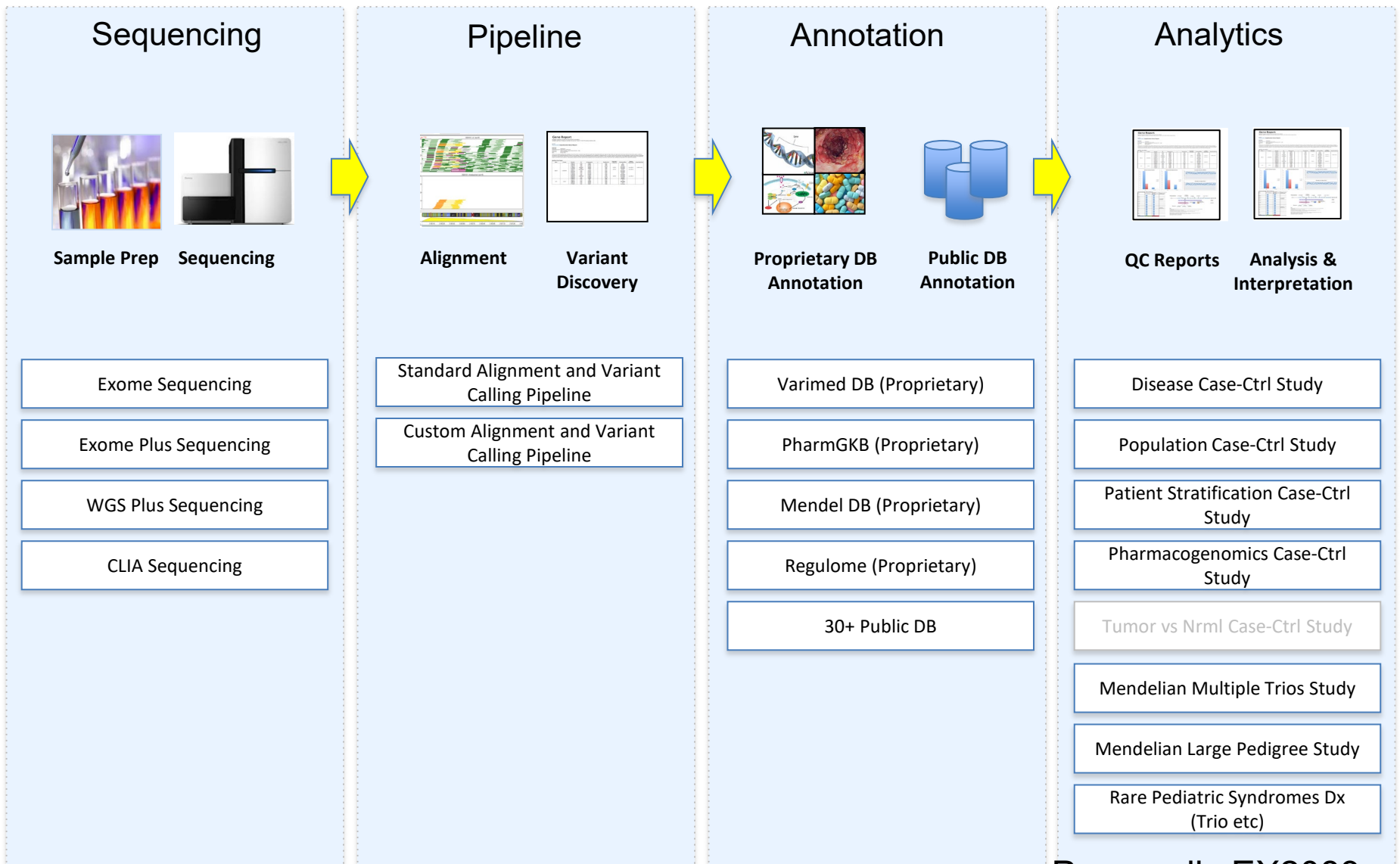
Personalis Aims to Provide the Most Comprehensive, Accurate, End-to-End Genome Service Available Today



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Personalis Genome Services

Components of our Service Planned for Version 1.0

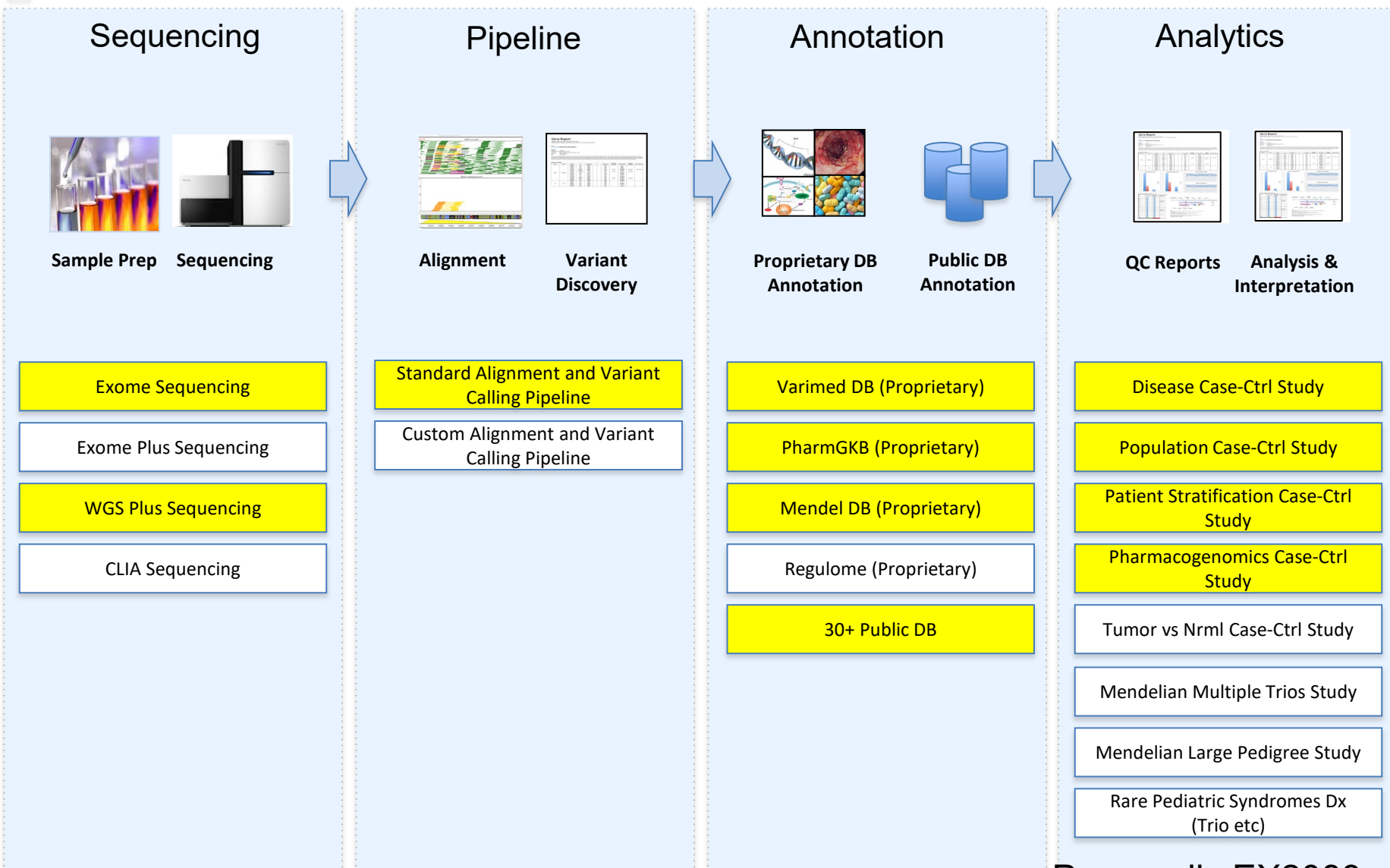


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Prototype vs Version 1.0 Features

 PGS Prototype
 PGS Version 1.0

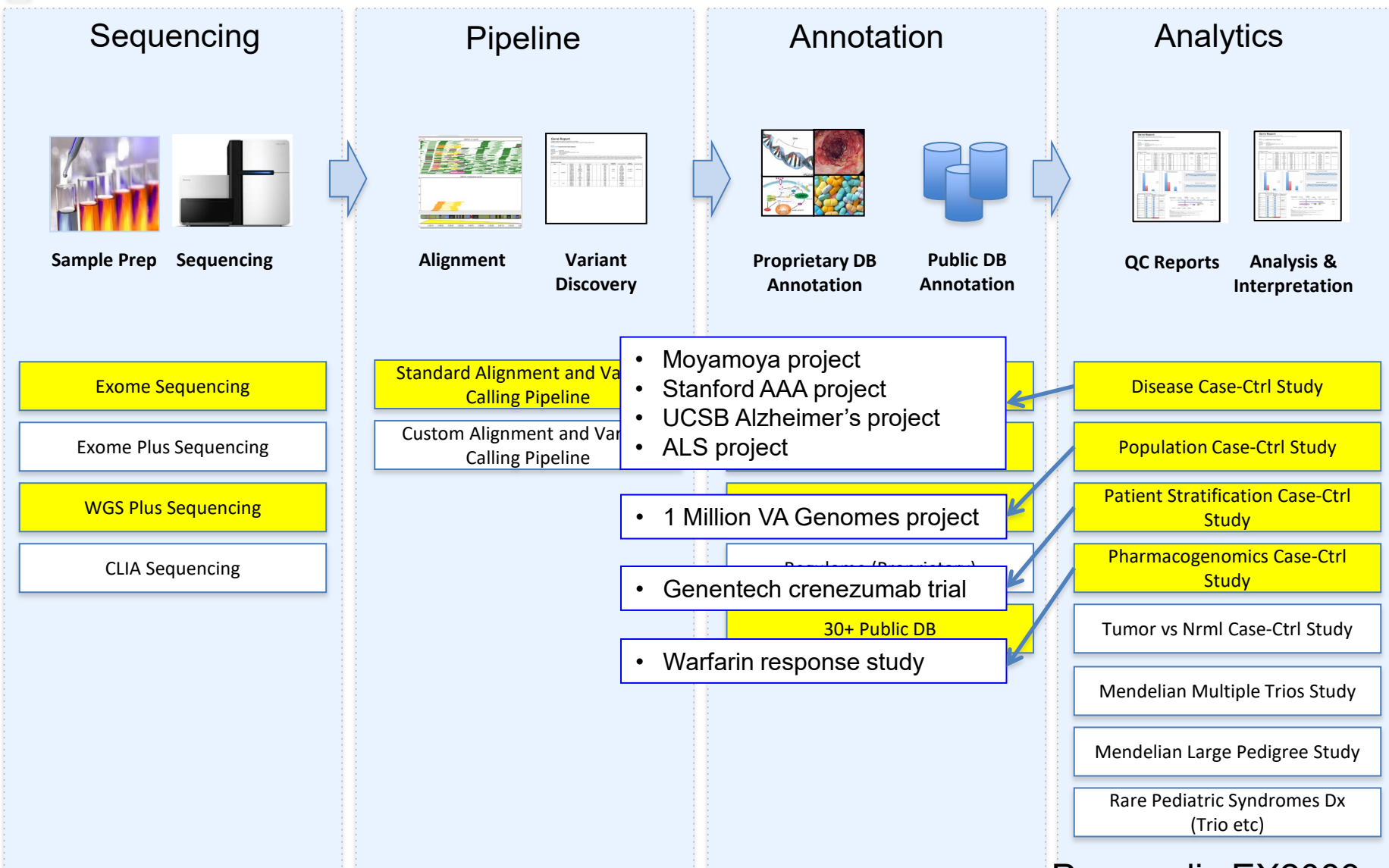


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Prototype vs Version 1.0 Features

 PGS Prototype
 PGS Version 1.0



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Personalis Genome Services

Significantly Differentiated at Each Step

Sequencing



Sample Prep Sequencing

- Exome and WGS with optimized sample prep for improve performance over problematic regions of the genome
- Exome Plus capability improves accuracy and extends exomes to biomedically important non-coding regions
- CLIA sequencing capability for clinical grade exomes or whole genomes

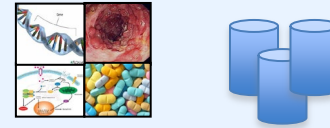
Pipeline



Alignment Variant Discovery

- State of the art alignment pipeline implementing best of breed algorithms resulting in better alignments, tested and optimized for accuracy and performance
- Personalis enhanced and corrected reference genome for improved alignment and accuracy
- Improved variant (SNP/Indel/SV) calling through integration of orthogonal methods to improve accuracy

Annotation



Proprietary DB Annotation Public DB Annotation

- Four high-quality, detailed, manually curated proprietary databases that enable genome annotation and analysis of complex disease, Mendelian disease, pharmacogenomics, and regulatory regions
- Comprehensive genome annotation integrating and managing data from over 30 public databases

Analytics



QC Reports Analysis & Interpretation

- Cutting edge proprietary analytics engine for case control analysis reveals statistically significant enrichment of genes, pathways, and diseases
- Analytics powered by proprietary databases
- Proprietary family/pedigree analysis and filtering methods
- Comprehensive QC reporting for better accuracy assessment

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Personalis Genome Services: Sequencing

Personalis Sequencing Improves Problematic Regions and Medically Interpretable Regions of the Genome

Problem: Segmental Duplications

- 7% of exome is in segmental duplications leading to ambiguous alignments, phantom variants and missed calls

Personalis solution:

- Supplement exome with long paired reads (2x250) in regions having high identity segmental duplications.
- Longer reads improve alignment and subsequent sequence determination

Problem: Repeat Expansion Disorders

- Repeat Expansion Disorders (e.g. Huntington's) are problematic for short read sequencing. Clinical interpretation requires accurate repeat length determination

Personalis solution:

- Supplement exome with long paired reads (2x250) anchored to interpretable expanding repeat region flanks
- Use high coverage spanning reads to correctly genotype region

Personalis
Exome

Personalis
Exome +

Personalis
WGS

Personalis
CLIA Seq

Problem: Low Coverage Regions

- Some areas of the genome (or exome) are underrepresented in NGS because of process biases, e.g. high GC content
- Low coverage tends to drive genotyping errors

Personalis solution:

- Supplement genome (or exome) with targeted libraries supplementing systematically low coverage in areas of medical interest
- Enriching weak spots is more effective (and economical) than just pushing up average coverage

Problem: HLA

- HLA is poorly addressed with NGS and standard analysis
- Complex repeat structure
- Typing requires phasing / haplotyping

Personalis solution:

- Develop targeted longer read library linking critical variant loci
- Develop or acquire haplotype-based typing analysis pipeline

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Personalis Genome Services: Pipeline

Personalis Pipeline Solves Critical Problems that Hinder Other Approaches

Problem:

Over 15 public and proprietary algorithms to integrate, keep up to date, test and maintain. E.g. GATK 2.0 bug with recalibration detected by Personalis

Personalis Solution:

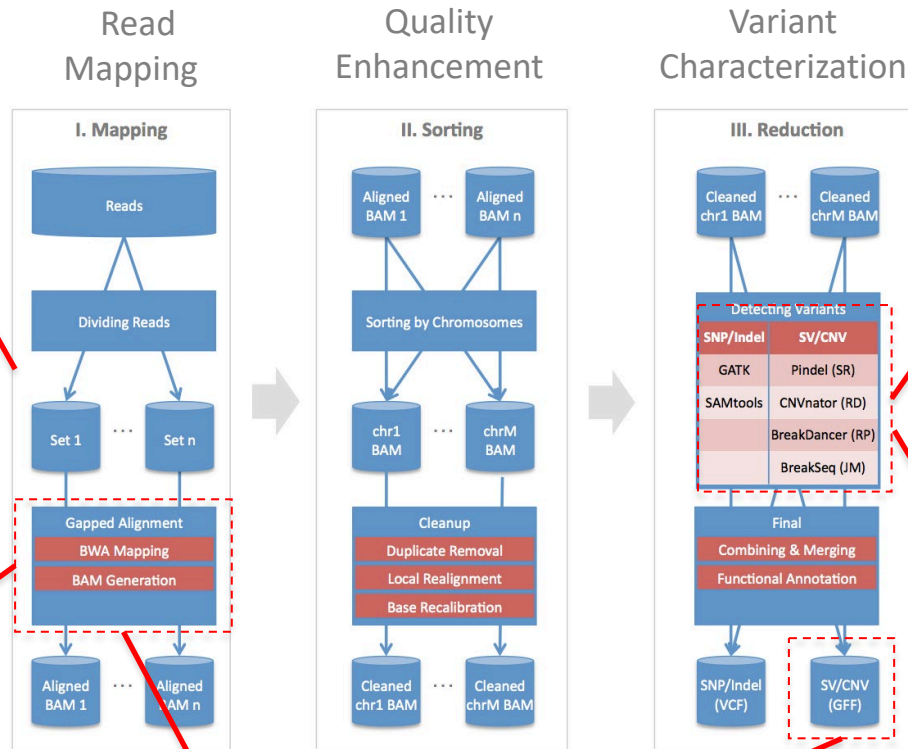
Systematic update, testing procedures and dedicated accuracy team to ensure integrity of various components

Problem:

Minor alleles in the public reference result in medically interpretable variants being missed. E.g. Factor V Leiden would be missed using current reference

Personalis Solution:

Corrections to public reference enabling better alignments and variant calls



Problem:

Ethnicity differences not accounted for in aligning to public reference

Personalis Solution:

Personalis corrections to public reference enabling better alignments

Problem:

Zygosity of SV's not reported by conventional pipelines resulting in poor interpretability for clinical impact

Personalis solution:

Personalis pipeline proprietary algorithm for detecting SV with reference calls, breakpoints and zygosity.

ANALYSIS

Performance comparison of whole-genome sequencing platforms

Problem:

Lam et. al. Nature Biotech
12% discordance for SNPs
73% discordance for indel's between platforms

Personalis solution:

Combining results of orthogonal SNP and SV detection algorithms to improve accuracy
One of the algorithms invented by Personalis scientist

Problem:

SV's such as Indels, Long Indels, STRs, CNV's poorly detected using conventional methods

Personalis solution:

New algorithms for improving detection
Laboratory optimization to enhance ability to detect

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Personalis Genome Services: Annotation

Problems with Existing Databases as a Primary Source of Annotations

Problem: Accuracy Of Existing Databases

- Estimated 25% of variants in HGMD are not pathogenic
- Personalis analysis suggests many of the variations in OMIM are present at high MAF (>35%) bringing into question their validity (ex MSUD, Sandhoff, etc)

Personalis solution:

- Personalis has a high quality, manually curated proprietary variant, Mendelian, and PGx database
- Automated cross checking between proprietary and public DB sources enables error correction

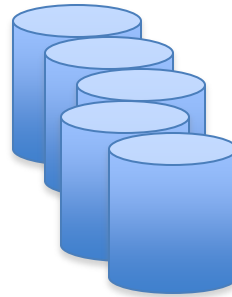


Problem: Public DB's have Large Gaps in Coverage

- As a matter of practice, many public DB's such as OMIM don't attempt to systematically curate disease causing variants
- Many causative variants are missing from OMIM
- HGMD has no pathogenicity scores

Personalis solution:

- Personalis is systematically cataloguing variants for the most common Mendelian phenotypes



Problem: Primary Source Errors

- Even published literature can harbor errors
- E.g. Original reports on causative alleles for multiple Mendelian disorders were incorrectly assigned because of the presence of the minor allele in the public reference.
- E.g. *COMP* and *MMAB*: discrepancy between tables within GeneReviews (pathogenic) and descriptive text and/or allele freq. (polymorphic)

Personalis solution:

- Personalis' Mendel DB uses manual QC to catch and correct errors in primary sources



Problem: Public DB's have variants incorrectly mapped to reference genome

- E.g. *CFTR* deltaF508 is incorrectly converted from protein change to DNA sequence in dbSNP

Personalis solution:

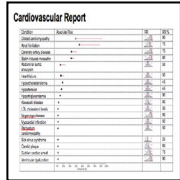
- Personalis' QC process developing methods to accurately map published variants to the reference genome



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Personalis Genome Services: Annotation

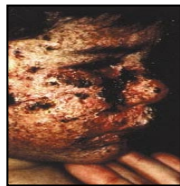
Personalis Proprietary DBs Provide Unique, Accurate, Comprehensive Content



Cardiovascular Report	
Cholesterol	180 mg/dL
Triglycerides	150 mg/dL
HDL Cholesterol	40 mg/dL
LDL Cholesterol	120 mg/dL
Non-HDL Cholesterol	80 mg/dL
Apolipoprotein B	120 mg/dL
Apolipoprotein A	150 mg/dL
LDL Particle Number	120 x10 ⁹ /L
LDL Particle Size	250 nm
LDL Particle Concentration	120 x10 ⁹ /L
LDL Particle Mass	120 x10 ⁹ /L
LDL Particle Volume	120 x10 ⁹ /L
LDL Particle Surface Area	120 x10 ⁹ /L
LDL Particle Permeability	120 x10 ⁹ /L
LDL Particle Oxidizability	120 x10 ⁹ /L
LDL Particle Aggregability	120 x10 ⁹ /L
LDL Particle Stability	120 x10 ⁹ /L
LDL Particle Functionality	120 x10 ⁹ /L
LDL Particle Viability	120 x10 ⁹ /L
LDL Particle Proliferation	120 x10 ⁹ /L
LDL Particle Differentiation	120 x10 ⁹ /L
LDL Particle Apoptosis	120 x10 ⁹ /L
LDL Particle Necrosis	120 x10 ⁹ /L
LDL Particle Inflammation	120 x10 ⁹ /L
LDL Particle Fibrosis	120 x10 ⁹ /L
LDL Particle Calcification	120 x10 ⁹ /L
LDL Protein	120 mg/dL
LDL Lipid	120 mg/dL
LDL Carbohydrate	120 mg/dL
LDL Nucleic Acid	120 mg/dL
LDL Metal	120 mg/dL
LDL Other	120 mg/dL

Varimed

- Comprehensive, detailed, high quality curated Variant to phenotype DB
- 12,000+ papers manually curated, QC checked for quality
- ~500,000 variant to phenotype relationships
- ~200,000 variants described
- ~5000 phenotypes described
- Large number of variants outside of exomes
- Updated weekly with >200 new papers



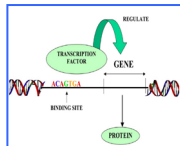
MendeIDB

- Personalis curated database of Mendelian phenotypes
- Manually QC'd for quality
- Most common 300+ Mendelian phenotypes represented and thousands of pathogenic variants



PharmGKB

- World's leading curated PGx database
- Manually QC'd for quality
- 12 years, \$30M NIH funding
- Exclusive commercial license
- 376 drugs, >4000 variant annotations



Regulome

- Hundreds of thousands of putative transcription factor binding sites
- Multiple levels of evidence, with ~40,000 in Tier 1
- Enables annotation outside of exome

High Quality, Reliable, Comprehensive Genome scale Variant to Disease Annotations

High Quality Variant to Drug Phenotype Annotations

Enables Interpretation of Intergenic regions outside of Exomes

Proprietary content powers Personalis Analytics enabling novel biomedical insights

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Personalis Genome Services: Annotation

Personalis Public DB Annotation Engine is Comprehensive and Current

- Complement to our high quality proprietary databases
- > 30 public databases integrated in to our variant annotation output, useful as filtering criteria. This is significantly more than our competitors
- Cross referencing with our proprietary databases reveal significant errors in public DB's such as dbSNP, OMIM, etc
- Maintained, integrated, and updated as new versions are released
- General framework for integrating new databases as they appear

Gene Annotations	RefSeq, Entrez, AILUN, Ensembl, UCSC KnownGene
Region Annotations	Cytoband, TFBS, miRNAs, TargetScan (miRNA Targets), Segmental Duplications
Population Frequencies	1000 Genomes, ESP 5400 Exomes, CG Genome Diversity Panel, HapMap
Mutational Impact	dbNSFP, SIFT, Polyphen2, PhyloP, GERP++, Mutation Taster
Conservation	PhastCons, Evofold
Known Variants	dbSNP 130,131,132,135
Structural Variations	DGV
Variant to Disease Relationships	OMIM, ClinVar, Genetic Associations Database (GAD), GWAS Catalog, HGMD
Networks, Interactions, Pathways	Reactome, HPRD, BioCyc, WikiPathways, KEGG, PID
Functional Annotations	GeneOntology
Drug Targets	DrugBank
Genetic Tests	Genetic Testing Registry

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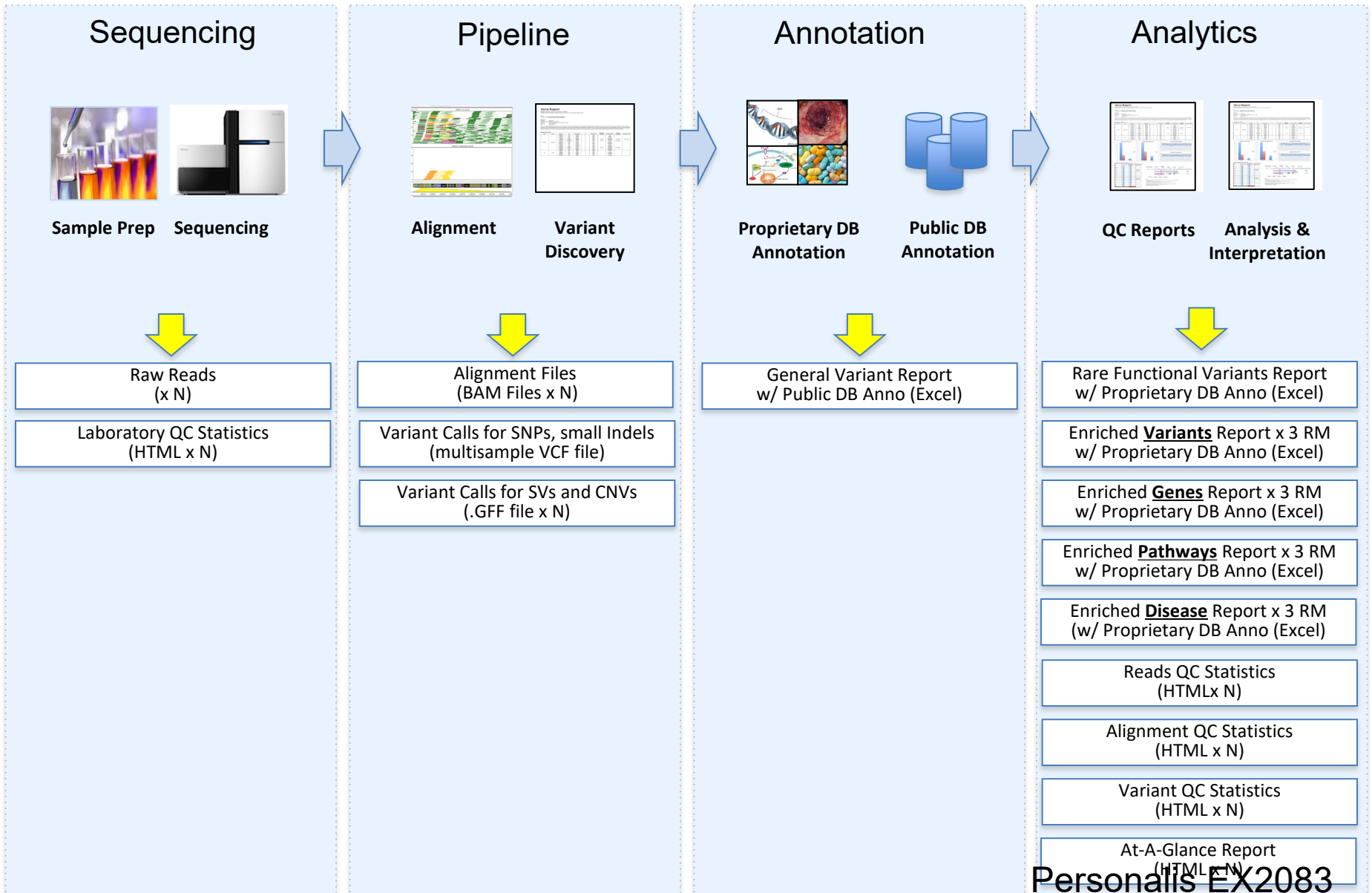
Personalis Genome Services: Analytics

Leading-edge Analytics for Case-Control and Familial Studies

- Leading-edge analytical methods focused on Case Control Studies where typically scientist are analyzing 10's to 1000's of genomes
 - Disease Case-Control, Population, Patient Stratification, and PGx Studies
 - Exome >> Whole Genome
- Critical for helping scientists distill sequence data into actionable science
- Personalis analytics calculate statistically significant differences between cases and controls for:
 - Variants, Genes, GeneSets, Pathways, PharmGKB pathways, Varimed Disease Risk
 - Each enrichment is calculated assuming a recessive, dominant or additive risk model
 - The result is 15 different reports
 - Computationally intensive, requires >80 million Fisher's exact tests
 - Use of Madsen-Browning collapsing method which is best of breed
- Analytics utilize proprietary databases comprehensiveness and depth to provide differentiated analysis results for disease and PGx associations
- For Version 1, we will be developing new analytics modules for enabling analysis of family trios and larger pedigrees

Personalis Genome Services

Key Deliverables to the Customer



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Personalis Genome Services

Competitive Analysis of Key Features

	Personalis		Informatics Companies				Genome Center	Platform Companies	
	PGS (Prototype)	PGS (Version 1)	Knome	DNANexus	Omicia	Ingenuity	BGI	Complete Genomics	Illumina
Platform									
Platforms supported	Illumina	Illumina,, CG	Illumina	Illumina, CG,ABI	Illumina	Illumina, CG	Illumina	CG	Illumina
Results delivery format	Reports, Excel, Datafiles	Reports, Excel, Datafiles	Report, DB, Datafiles	Web Portal/Cloud	Reports, Datafiles	Web Portal	Reports, Excel, Datafiles,Cloud	Reports, Excel, Datafiles, Cloud	Reports, Excel, Datafiles,Cloud
Sequencing									
Exome	●	●	●	○	○	○	●	○	○
Exome Plus	○	●	○	○	○	○	○	○	○
WGS Plus	●	●	●	○	○	○	●	●	●
CLIA	○	●	○	○	○	○	○	●	●
Pipeline									
Mapping	●	●	●	●	○	○	●	●	●
Enhanced Public Reference	●	●	○	○	○	○	○	●	○
SNP/Short Indel Detection	●	●	●	●	○	○	●	●	●
SV Detection	●	●	●	●	○	○	●	●	●
Zygosity, breakpoints for SV's	●	●	○	○	○	○	○	●	○
Phasing	○	●	○	○	○	○	○	●	○
MEI's	○	●	○	○	○	○	○	●	○
Annotations/Content									
Public DB Anno	30+	30+	10+	<5	10+	20+	<5	<5	<5
Proprietary DB: Variants to Dz	●	●	●	○	○	●	○	○	○
Proprietary DB: Variants to Drug	●	●	○	○	○	●	○	○	○
Proprietary DB: Variants to Mend Dz	●	●	○	○	○	●	○	○	○
Proprietary DB: Variants to TFBS	●	●	○	○	○	●	○	○	○
Proprietary DB: Pathways/Networks	○	○	○	○	○	●	○	○	○
Analytics									
Case-Control Analytics	●	●	●	○	●	●	○	●	○
Family Pedigree Analytics	○	●	●	○	●	●	○	○	○
QC Analytics/Reports	●	●	●	●	○	○	○	●	●
Normal Range Reporting	●	●	○	○	○	○	○	○	○
Propagation of Error/Quality	●	●	●	●	○	○	●	●	●
Exploration Capability									
Public Genome Visual/Explor Tools	○	●	●	●	●	●	●	○	○
Proprietary Visual/Explor Tools	○	○	●	●	○	●	○	○	○
Publication Ready Graphics	○	●	○	○	○	●	○	○	○

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Personalis Genome Services

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Platform									
Platforms supported	Illumina	Illumina,, CG	Illumina	Illumina, CG, ABI	Illumina	Illumina, CG	Illumina	CG	Illumina
Results delivery format	Reports, Excel, Datafiles	Reports, Excel, Datafiles	Report, DB, Datafiles	Web Portal/Cloud	Reports, Datafiles	Web Portal	Reports, Excel, Datafiles, Cloud	Reports, Excel, Datafiles, Cloud	Reports, Excel, Datafiles, Cloud
Sequencing									
Exome	●	●	●	No Sequencing Option			●	No Exomes	
Exome Plus	○	●	○				○		
WGS Plus	●	●	●				●		
CLIA	○	●	○				○		
Pipeline									
Mapping	●	●	●	●	Limited Pipeline		●	●	●
Enhanced Public Reference	●	●	○	○			○	●	○
SNP/Short Indel Detection	●	●	●	●			●	●	●
SV Detection	●	●	●	●			●	●	●
Zygosity, breakpoints for SV's	●	●	○	○			○	●	○
Phasing	○	●	○	○			○	●	○
MEI's	○	●	○	○	○	○	○	●	○
Annotations/Content									
Public DB Anno	30+	30+	10+	<5	10+	20+	<5	<5	<5
Proprietary DB: Variants to Dz	●	●	Lack of Proprietary Content			●	Lack of Proprietary and Limited Public Content		
Proprietary DB: Variants to Drug	●	●				●			
Proprietary DB: Variants to Mend Dz	●	●				●			
Proprietary DB: Variants to TFBS	●	●				●			
Proprietary DB: Pathways/Networks	○	○	○	○	○	●	○	○	○
Analytics									
Case-Control Analytics	●	●	Analytics Limited By Content			●	Limited Analytics		
Family Pedigree Analytics	○	●				○			
QC Analytics/Reports	●	●				○			
Normal Range Reporting	●	●				○			
Propagation of Error/Quality	●	●	○	○	○	○	○	○	○
Exploration Capability									
Public Genome Visual/Explor Tools	○	●	●	●	●	●	●	●	●
Proprietary Visual/Explor Tools	○	○	○	○	○	○	○	○	○
Publication Ready Graphics	○	●	○	○	○	○	○	○	○

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Personalis Genome Services

Personalis IP

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Sequencing				No Sequencing Option				No Exomes					
Exome	●	●	●				○			○	○	●	○
Exome Plus	○	●	○				○	○	○	○	○	○	
WGS Plus	●	●	●				○	○	○	●	●	●	
CLIA	○	●	○	○	○	○	○	●	●				
Pipeline					Limited Pipeline								
Mapping	●	●	●	●			○	○	●	●	●		
Enhanced Public Reference	●	●	○	○			○	○	○	●	○		
SNP/Short Indel Detection	●	●	●	●			○	○	●	●	●		
SV Detection	●	●	●	●			○	○	○	○	○		
Zygosity, breakpoints for SV's	●	●	○	○			○	○	○	●	○		
Phasing	●	○	○	○			○	○	○	○	○		
MEI's	○	●	○	○	○	○	○	●	○				
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Proprietary DB: Variants to Mend Dz	●	●	○				○			○	○	○	○
Proprietary DB: Variants to TFBS	●	●	○	○	○	○	○	○	○				
Proprietary DB: Pathways/Networks	○	○	○	○	○	○	○	○	○				
Analytics				Analytics Limited By Content				Limited Analytics					
Case-Control Analytics	●	●	○				○			○	○	○	○
Family Pedigree Analytics	○	●	○				○			○	○	○	○
QC Analytics/Reports	●	●	○				○			○	○	○	○
Normal Range Reporting	●	●	○	○	○	○	○	○	○				
Propagation of Error/Quality	●	●	○	○	○	○	○	○	○				
Exploration Capability													
Public Genome Visual/Explor Tools	○	●	●	●	●	●	●	○	○				
Proprietary Visual/Explor Tools	○	○	○	○	○	○	○	○	○				
Publication Ready Graphics	○	○	○	○	○	○	○	○	○				

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Personalis IP

Lack of Proprietary Content

Lack of Proprietary and Limited Public Content

Analytics Limited By Content

Limited Analytics

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MendelDB Dashboard

- High quality curated DB of Mendelian phenotypes and their variants
 - Managed by Sarah Garcia and Gemma Chandratillake, both Genetics Ph.D. & Genetic Counselors
- Critical content to support Disease Variant Discovery Service and Genome Interpretation Service
- On track to finish all (~560) GeneReviews by Oct 2012, corresponding to >300 common Mendelian disease phenotypes
- Will then continue phenotype curation and variant curation from other sources
- Flexible workforce for other curation tasks in the future



phenotypes



genes (blue)
variants (red)



productivity
(rows/hr)

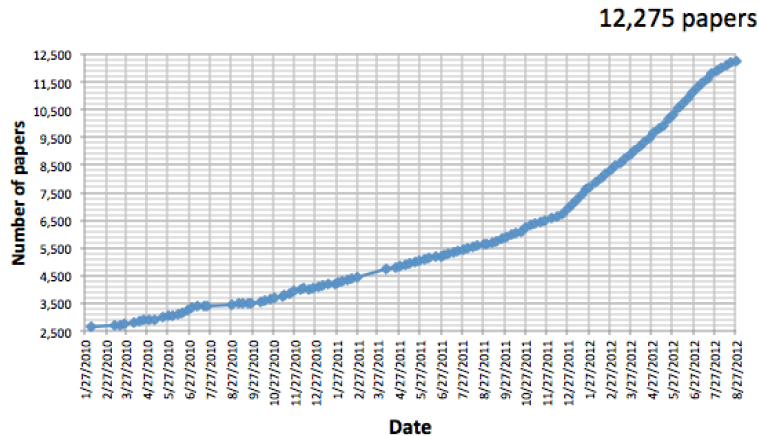


Raw error rate
(# errors/row)
(prior to QC)

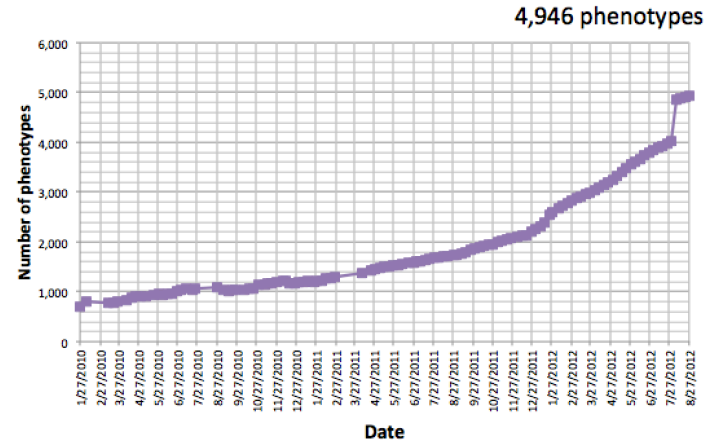
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VarimedDB Dashboard

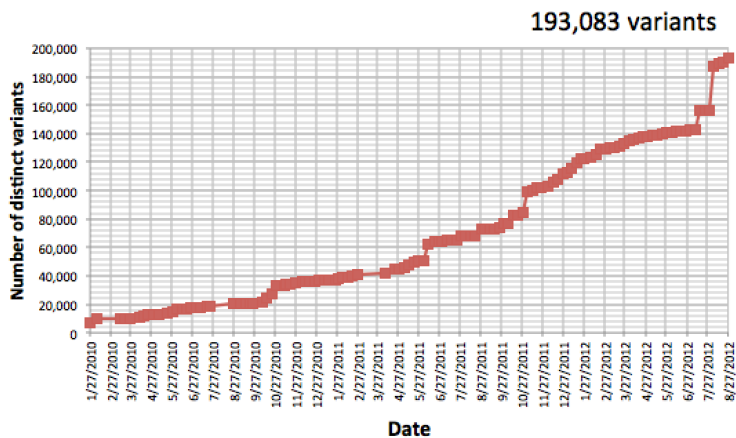
Number of papers



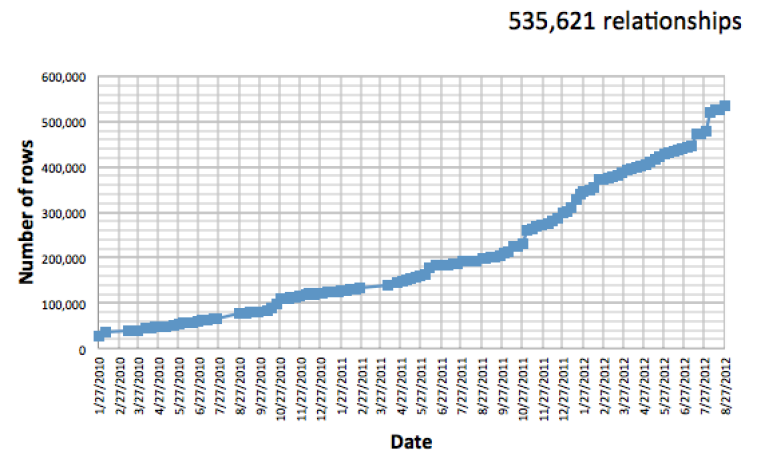
Number of broad phenotypes



Number of distinct variants



Number of variant-phenotype relationships (rows)



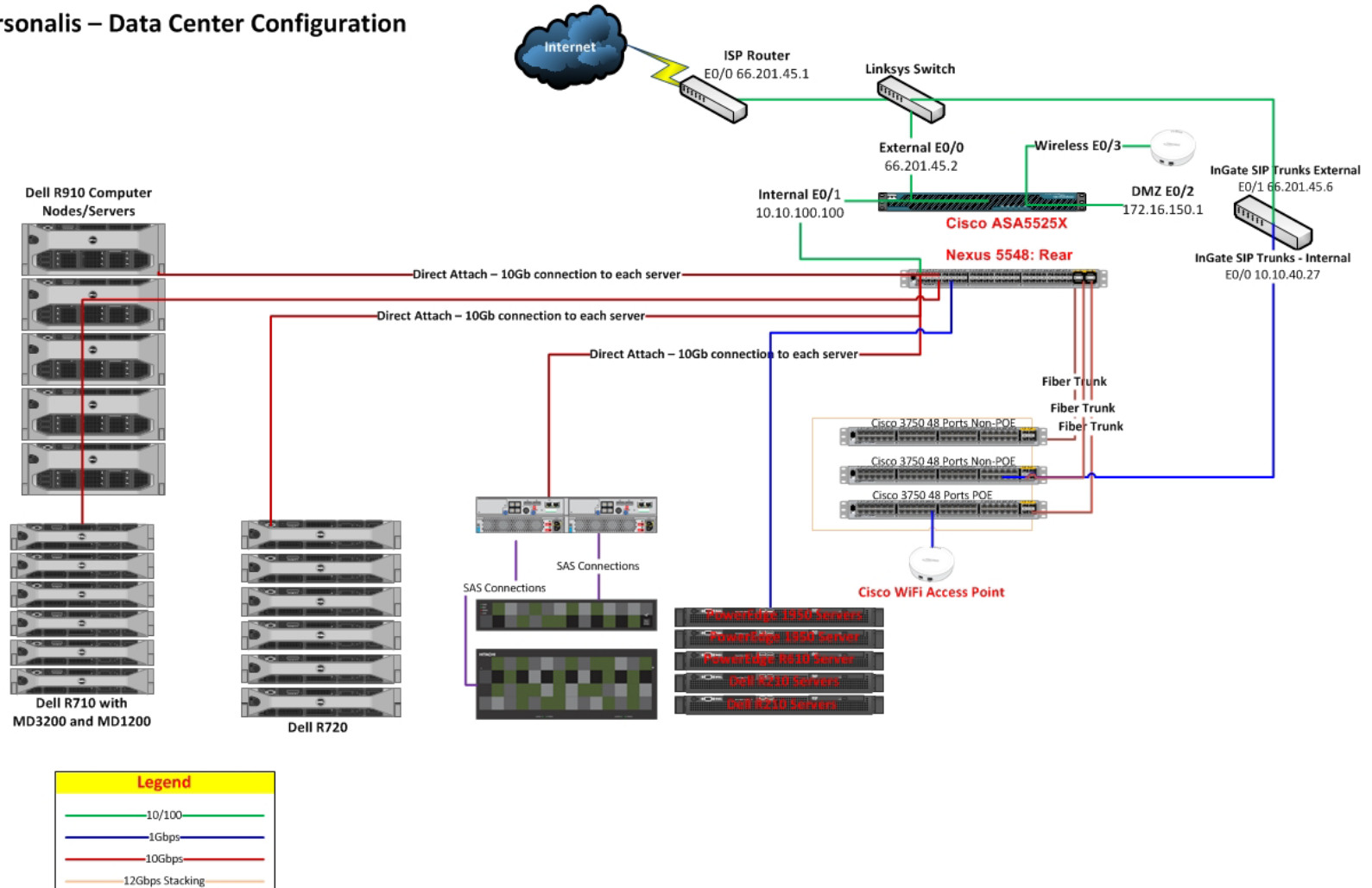
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Scientific Computing Infrastructure

- Genome processing capability increased from 80 to 350 cores
- Added ~120TB usable storage for R&D (Hitachi) for a total of >300 TB of storage
 - Bidding war between NetApp, Hitachi, Isilon, Dell
- Increased speed of internal network to 10G
- Server backup planning in progress
 - Disk to Disk to Cloud + Tape for most critical data
- Continuing search for Linus/Unix sys admin

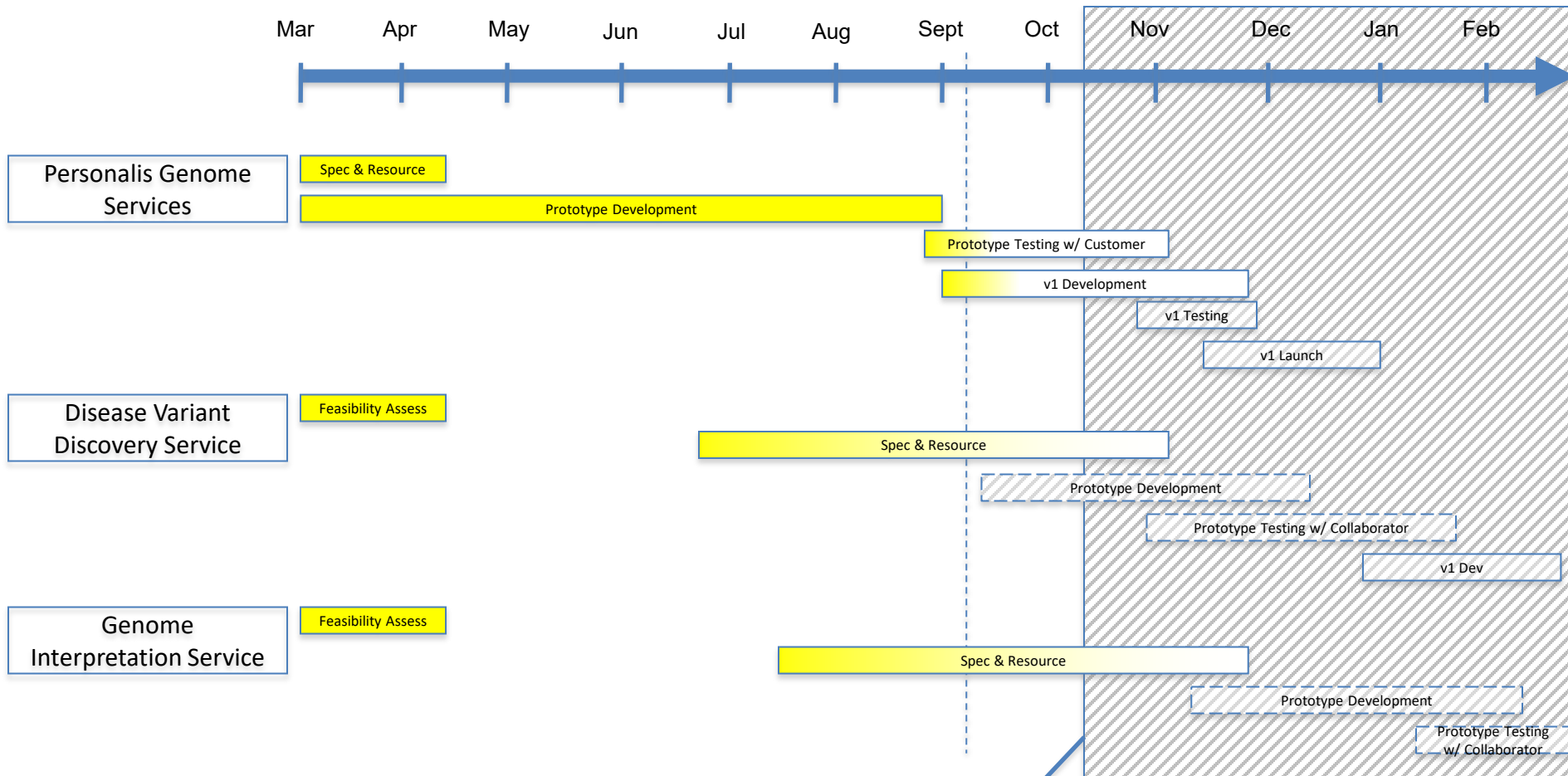
Scientific Computing Infrastructure

Personalis – Data Center Configuration



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Summary of Estimated Timelines



Now Revising Timelines & Reprioritizing accounting for:

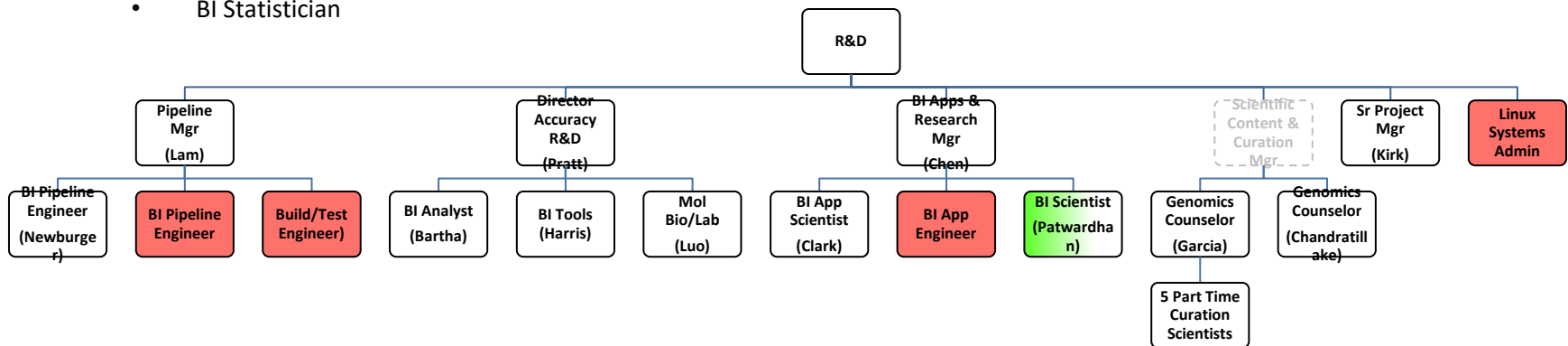
- New /Exome Plus initiative (Required for V1 Release?)
- Demands of Moyamoya project and other early customers
- DVDS and GIS
- Hiring Delays
- Early Feedback on Prototype

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R&D Hiring Update

- **New Hires**
 - Anil Patwardhan, Ph.D.: Senior Bioinformatics Scientist joining BI Apps & Research Team (Starting Sept 17th)
- **Slower hiring ramp than plan: ~ 2 months behind on Bioinformatics, Scientific computing hires**
 - Low volume of resumes through recruiters – has improved in past 2-3 weeks, starting to see steady flow of candidates, expanding number of recruiters involved
 - Looking for great hires, being very selective
 - Bioinformaticians and Unix Sys Admins are in high demand
- **Near Term Open Positions**
 - Linux systems admin – hired new recruiter, looking for consulting help
 - Test/Build Engineer
 - BI Applications Engineer
 - BI Pipeline Engineer
 - BI Statistician



-  Original Team
-  New hires (started)
-  New hires (not yet started)
-  Near Term Open Positions

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Summary of Resource Allocation

	Accuracy R&D Mark Pratt Gabor Barth Jason Harris Shujun Luo	Pipeline R&D Hugo Lam Daniel Newburger	Apps R&D Rong Chen Michael Clark	Content R&D Sarah Garcia Gemma Chandratillake PT Curators
Personalis Genome Services				
Disease Variant Discovery Service				
Genome Interpretation Service				
Research Collaborations				
Ethics Board				

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Overall R&D Risks and Mitigation

Risk	Mitigation
• R&D hiring delay of BI engineers and Unix sys admin. May impact schedule	• New IT recruiters now involved for Unix sys admin hire • Redoubled efforts on BI hires (new process, conferences, networking)
• Long lead time content curation and content quality items for GIS and DVDS	• Started dev on those items with long lead times to develop concurrently with Pipeline (MendelDB, etc)
• Licensing of applications and content for analysis	• Systematically reviewing and applying for licenses for key content and algorithms
• Ethical use of Genomes for R&D	• Ethics board approval for all Genomes used for R&D • Part of orientation training
• Product Differentiation	• Continuing to push differentiation in three key areas: Accuracy/Quality, Content, Features
• Identifying high quality collaborators for testing our services. Potentially long lead time.	• Have identified and started working with customers to test Prototype

Next Steps & Priorities

- Start planning, resourcing, prioritization, and development process for Version 1.
Will need to accommodate R&D resources required for:
 - Laboratory development (Exome Plus)
 - Collaboration/Customer projects
 - Hiring/Interviewing
 - Feedback from Prototype
- Continue Hiring for open positions
- Continue to Identify customers for testing Pipeline Service Prototype
- Continue to execute on content priorities, develop longer term content strategy
- Continue to execute on Accuracy objectives and integration with laboratory capabilities