Geneticist Assistant – Change Log

Version 1.8.0

Added and Updated the Following Features

Subject	Date	Algorithm Change	Risk
Report Designer – Redesign	10/31/18	No	Low
Quality Metrics for CAP/AMP	10/31/18	No	Low
Custom patient attributes	10/31/18	No	Low
Search for variants by custom patient attributes	10/31/18	No	Low
Variant interpretation field	10/31/18	No	Low
Mark variants for reporting	10/31/18	No	Low
Variant counts for any group of samples	10/31/18	No	Low
Variant search by HGVS	10/31/18	No	Low
Human Phenotype Ontology support	10/31/18	No	Low

Version 1.4.15

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Miscellaneous	IGV option to automatically search for BAM file (on by default)	07/16/18	No	Low
Panel	Add command line option for panel preferred transcripts	06/18/18	No	Low
Variant	Setting to show warning when a variant isn’t submitted due to missing AF (on by default)	04/25/18	No	Low
Variant	Add setting to derive AF from GT if AF missing from VCF	04/23/18	No	Low
Run	Remember last used chemistry and instrument	04/20/18	No	Low
Miscellaneous	Setting to load sample’s variant in IGV (on by default)	04/20/18	No	Low

Version 1.4.15

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Filtering	Save filters work on hidden columns	08/01/18	No	Low
Miscellaneous	Make all instances of “N/A” consistent	07/05/18	No	Low
External Data	Show all fields even for ones without a value	06/20/18	No	Low
Miscellaneous	Fix OMIM for their new API	06/04/18	No	Low
Miscellaneous	Fix variant’s comments not changing row height	04/23/18	No	Low

Version 1.4.14

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Miscellaneous	Add setting to clear samples in IGV	04/04/18	No	Low

Version 1.4.14

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Panel	Fix submitting panel regions and preferred transcripts at the same time	04/09/18	No	Low

Version 1.4.13

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Report	Prevent hang if report cannot open output file	03/23/18	No	Low

Version 1.4.12

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Reference	Fix reference download quitting	02/13/18	No	Low

Version 1.4.11

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Variant	Add setting for default artifact type	01/24/18	No	Low

Version 1.4.11

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Variant	Fix default transcript when gene only has one	01/22/18	No	Low
VCF	Fix submission when file extension is upper case	01/17/18	No	Low
BAM	Support BAM filenames with unicode characters	01/11/18	No	Low
BAM	Fix crash when BAM file is unsorted	01/11/18	No	Low

Version 1.4.10

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Variant	Apply global preferred transcript to search results	01/02/18	No	Low

Version 1.4.9

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Variants	Zygosity lower bound setting not saved	12/27/17	No	Low

Version 1.4.8

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Logging	Add sub-tab "Change Log" to "Database Log"	10/13/17	No	Low

Version 1.4.8

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Variants	Fix variant type for dup frame-shifts	11/29/17	Yes	Medium
Reports	Support UTF-8 for PDF reports	11/17/17	No	Low
Miscellaneous	IGV interface fix	11/03/17	No	Low
Patients	Patient samples not shown when patient is not owned by current user	10/31/17	No	Low
Miscellaneous	Fix saved custom column configuration corruption	10/30/17	No	Low
Reports	Patient Report not exported	10/23/17	No	Low

Version 1.4.6

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Panels	Keep stats for the same panel regions between panel revisions	07/25/17	Yes	Medium
Filtering	Setting to disable remembering applied filters	07/21/17	No	Low

Version 1.4.6

Corrected the Following Bugs

Category	Subject	Due date	Algorithm Change	Risk
VCF	VCF export chromosome position off by 1	09/12/17	Yes	High
External Data	Fix find Rs number from dbSNP	08/14/17	No	Low
Reports	Fix wrong number of rows not exported	08/08/17	No	Medium
Filtering	Fix new filters not saved	08/01/17	No	Low
Reports	Csv reports contain NA for filtered values	07/18/17	No	Low

Version 1.4.5

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
User Interface	Allow users to change fonts	05/12/17	No	Low
Logging	Show changes to all variants, runs, samples, and patients in one place - Change Log	05/04/17	No	Low

Version 1.4.5

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Reports	Specify sample name in batch variant reports	06/26/17	No	Low
Permissions	Fix edit user	06/07/17	No	Low
Miscellaneous	Submit certificate to server only when changed	05/31/17	No	Low
Patients	Fix edit patient birthday	05/19/17	No	Low
Patients	Correctly decrypt patient detail information in search results tab	05/19/17	No	Low
Comparison	Copy paste for sample comparison limited	05/16/17	No	Low
Variants	Variant normalizer fix for hotspots	05/09/17	Yes	Medium
Reports	Encoding error in xml reports	04/24/17	No	Low

Version 1.4.4

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
User Interface	New HGVS rename interface	04/21/17	No	Low
Variants	Reset HGVS changes to default	04/19/17	No	Low

Version 1.4.4

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Permissions	NextGENe create and edit user compatibility	04/21/17	No	Low
User Interface	IGV and NextGENe interface missing from some tabs	04/19/17	No	Low

Version 1.4.3

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
User Interface	Select and copy functionality update	04/06/17	No	Low
User Interface	Shortcut keys for NextGENe and IGV	04/05/17	No	Low

Version 1.4.3

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
VCF	Multiple samples in single VCF	04/10/17	No	Low
User Interface	Current jobs shows same samples for multiple runs	04/10/17	No	Low
Filtering	Genes filter crashes on coverage regions tab	04/07/17	No	Low
Panels	Panel statistics can't find reference	04/06/17	No	Low

Version 1.4.2

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Command Line	Reports not generated from command line	03/22/17	No	Low
Command Line	Update statistics when submitting from command line	03/21/17	No	Low
Miscellaneous	Open 64bit NextGENe Viewer instead of 32bit	03/17/17	No	Low
Miscellaneous	NextGENe Viewer interface – Search for VCF file in parent directory too	03/17/17	No	Low
Miscellaneous	IGV interface without BAM file	03/15/17	No	Low

Category	Subject	Date	Algorithm Change	Risk
Command Line	Patient id from command line	03/08/17	No	Low
Reports	Loading PDF report templates	03/07/17	No	Low

Version 1.4.1

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Reports	Extra blank rows added in custom report	02/23/17	No	Low
User Interface	Comment box not resize-able	02/20/17	No	Low
Miscellaneous	Find samples with variants broken	02/17/17	No	Low

Version 1.4.0

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Samples	Select multiple panels when viewing a sample by panel	12/12/16	No	Low
Command Line	VCF filter column on command line option	12/08/16	No	Low
Miscellaneous	Don't show Explorer on save	11/14/16	No	Low
Reports	Digitally sign (encrypt) PDF files	10/13/16	No	Low
Cases	Add/Edit Objects - Priorities	10/05/16	No	Low
Reports	Report Designer - PDF Reports	09/07/16	No	Low
Miscellaneous	NextGENe Viewer interface	05/05/16	No	Low
Miscellaneous	IGV - Load Samples and Variants	05/05/16	No	Low
Miscellaneous	IGV interface	05/05/16	No	Low
VCF	Export annotations to VCF files	05/05/16	No	Low
External Data	Reference Downloader	01/27/16	No	Low

Version 1.2.1.0

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Variants	CDS number column	11/28/16	No	Low
Samples	Samples with multiple BAM files	10/06/16	No	Low

Category	Subject	Date	Algorithm Change	Risk
Patients	Patient batch import for extended data	10/06/16	No	Low
Variants	Delete supporting info	10/05/16	No	Low
Patients	Barcode verification	09/28/16	No	Low
User Interface	Filter right click menus	09/16/16	No	Low
Patients	Auto create patient ID based on sample name	07/29/16	No	Low
Patients	Blank default values for patients	07/29/16	No	Low
Filtering	Save samples applied filters	07/29/16	No	Low
Variants	Multiple Variant Interpretation	07/29/16	No	Low
Patients	Patient Encryption	07/29/16	No	Low

Version 1.2.0.4

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Reports	Custom report crashing on save	12/28/16	No	Low

Version 1.2.0.3

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
VCF	Filtering vcf files based on bed files	11/15/16	Yes	Medium

Version 1.2.0.2

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Miscellaneous	View in UCSC	10/18/16	No	Low
Patients	Add Patient Dialog - Relationship selection	10/06/16	No	Low
Runs	Cannot add comment to run	10/05/16	No	Low
Patients	Patient batch import large files	10/05/16	No	Low
Miscellaneous	Read balance statistics	09/19/16	No	Low

Version 1.2.0.1

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Filtering	Gene filter list	09/12/16	No	Low
Miscellaneous	Delete Multiple Runs / Samples	08/31/16	No	Low
Variants	Genotype Column	08/12/16	No	Low
Samples	Directory select for batch samples	07/29/16	No	Low
Patients	Barcode generation for patients	07/26/16	No	Low
Patients	Patient submission web form	07/22/16	No	Low

Version 1.2.0.1

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Patients	Batch patient import fails	09/09/16	No	Low
Coverage Regions	Coverage region change - crashes if cancelled	09/08/16	No	Low
VCF	Indel allele frequency calculations for VCF files from IsaacVariantCaller	09/07/16	No	Low
User Interface	New run dialog resizing	09/06/16	No	Low
Miscellaneous	Gene search doesn't finish loading	08/26/16	No	Low
Miscellaneous	Missed clinical variants support removed	08/24/16	No	Low
VCF	GZ not recreated when VCF modified	08/23/16	No	Low
Classifications	Import variant pathogenicity tool	08/20/16	No	Low
Coverage Regions	GC Content no longer supported	08/12/16	No	Low
Coverage Regions	Coverage region comment - disable edit	08/12/16	No	Low
Reports	Batch variant report applies column configration templates inncorrectly	07/21/16	No	Low
User Interface	Column configuration templates broken after using create batch variant report	07/21/16	No	Low
Variants	Variant tab crash	06/09/16	No	Low
Variants	Gene column sorting	06/08/16	No	Low

Version 1.2.0.0

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Samples	Change Run	04/18/16	Low	No
VCF	VCF filter column support	04/11/16	Medium	Yes
User Interface	Context menu rearrangements	03/29/16	Low	No
External Data	Always show track fields on Variant Tab	03/23/16	Low	No
Reports	Export Filtered Samples	03/18/16	Low	No
Comparison	Sample Comparison	03/15/16	Low	No
Patients	Family Comparison	03/15/16	Low	No
Coverage Regions	Batch Coverage Region report	03/03/16	Low	No
Variants	Sample table includes Variant Frequency and Coverage	02/22/16	Low	No
Panels	Save panels directly from Bed Builder	02/18/16	Low	No
Panels	Bed builder button in new panel dialog	02/05/16	Low	No
User Interface	New button for panels in new run dialog	02/04/16	Low	No
User Interface	Reorder columns dialog	02/01/16	Low	No
Variants	Ref and Alt always shown relative to positive strand	02/01/16	High	Yes
User Interface	Permission Updates improve UI	01/27/16	Low	No

Version 1.2.0.0

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
VCF	GZ not recreated after VCF file changed	04/18/16	Low	No
Permissions	User's first and last name not displayed	03/18/16	Low	No
Filtering	Filter templates per user	11/02/15	Low	No

Version 1.1.8.1

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Coverage Regions	QC report output on command line	03/17/16	No	Low
Reports	JSON output	03/17/16	No	Low
VCF	Allele Frequency calculation for VCF files produced with Atlas2	02/22/16	No	Low
Coverage Regions	Coverage Regions Standard Deviation	02/18/16	No	Low
Coverage Regions	Panel Statistics for run or selected samples	02/18/16	No	Low
Filtering	Highlight filters	01/27/16	No	Low
Filtering	Filter date-time by +/- time period	01/18/16	No	Low
Reports	Remember last report settings	01/15/16	No	Low
HGVS	HGVS short form nomenclature for frame shifts	01/11/16	No	Low
Comments	Comment time stamp column	01/07/16	No	Low
User Interface	Proxy settings during login	01/07/16	No	Low

Version 1.1.8.1

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Bam Viewer	Coverage QC progress bar doesn't finish	04/18/16	No	Low
Permissions	Disable users instead of deleting them	03/18/16	No	Low
Genes	Genes across contigs	03/01/16	Yes	High
Variants	Mitochondrian Ammo Acids	02/25/16	Yes	High
External Data	Add fields from external database crash	02/09/16	No	Low
Genes	Gene search returns results from alternate assembly for some genes	01/27/16	No	Low
VCF	NextGENe's allele score not read properly from VCF	01/25/16	No	Low
Miscellaneous	Proxy support	01/07/16	No	Low

Version 1.1.8

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
User Interface	Keyboard shortcuts for saving sample reports, switching tabs, etc	11/18/15	No	Low

Version 1.1.8

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
VCF	Check that reference allele matches reference	12/04/15	No	Low
HGVS	HGVS repeat regions adjusted wrong	11/22/15	Yes	High
Patients	Wrong ID opened for sorted tables	11/09/15	No	Low
Comments	Editing comment causes table view not aligning to top	10/29/15	No	Low
Patients	SampleVariantTab patient text browser not aligning to top after "set patient"	10/29/15	No	Low

Version 1.1.7

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Patients	Add ethnicity in add patient dialog	09/29/15	No	Low
Coverage Regions	Coverage region statistics cache	09/28/15	No	Low
Reports	Set default report type to CSV	09/25/15	No	Low
Filtering	Apply filter after loading	09/01/15	No	Low
Samples	Select multiple samples to view variants	08/31/15	No	Low
Patients	Patient phenotypes	08/05/15	No	Low
Permissions	Transcript permissions	08/04/15	No	Low
Variants	Custom column formulas	07/30/15	No	Low
User Interface	Link out to UCSC browser	07/30/15	No	Low
Database Design	Database design change for speed improvements	07/30/15	Yes	High
Miscellaneous	Move settings from registry to appdata	07/22/15	No	Low
Miscellaneous	Fix reference directory location automatically	07/22/15	No	Low
Reports	Add applied filters section to reports	07/21/15	No	Low
External Data	Load OMIM independently	07/20/15	No	Low
Permissions	Set multiple Sample's/Run's/Patient's permissions at once	07/14/15	No	Low
Genes	Bed builder warning messages improvement	07/08/15	No	Low

Category	Subject	Date	Algorithm Change	Risk
Variants	Variant statistics cache	06/30/15	Yes	High
Genes	Gene info loading speed improvement	06/25/15	Yes	Medium
User Interface	Show variants filtered by panel from samples tab	06/12/15	No	Low
Permissions	New run's group permission	06/10/15	No	Low
Coverage Regions	Sub panels for coverage calculations	06/09/15	Yes	Medium
Reports	Add supporting Information to reports	06/05/15	No	Low
Comments	Submit multiple variant comments at once	06/05/15	No	Low
Miscellaneous	Proxy Support	06/04/15	No	Low
External Data	ExAC link	06/01/15	No	Low
Genes	Load gene info into memory when program starts	05/27/15	No	Low
User Interface	Indicator external data has finished loading	05/22/15	No	Low
Panels	Bed file builder – Include UTR option for all exon mode	05/01/15	No	Low
Variants	Variant submit – Hotspot option	04/13/15	Yes	Medium

Version 1.1.7

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Database Design	All tables converted to UTF8	10/02/15	No	Low
Objects	Pathogenicity and Artifact objects can't be added.	09/28/15	No	Low
User Interface	Column configuration deletes wrong configuration	09/28/15	No	Low
Classifications	Pathogenicity sort	09/24/15	No	Low
Patients	Patient's samples list	09/23/15	No	Low
External Data	HGMD id missing	09/14/15	No	Low
Genes	Bed builder shows no transcripts for some genes	08/10/15	No	Low
Coverage Regions	Coverage region status change	07/23/15	No	Low
VCF	MT and M submit	07/22/15	Yes	Medium
Samples	Samples tab takes too long to load	07/17/15	No	Low
Genes	Bed file build rejects valid gene names	07/16/15	No	Low
Patients	Patient tab doesn't finish loading	07/16/15	No	Low
Samples	Sample group submit	07/09/15	No	Low
Samples	Sample request	07/09/15	No	Low
VCF	Export to variants to vcf file doesn't show existing vcf files in directory	06/04/15	No	Low
Licensing	Licesning - Don't convert hostname to IP	05/22/15	No	Low
User Interface	Main window progress bar	05/22/15	No	Low
Variants	Server memory overflow	05/13/15	No	Low

Version 1.1.6.1

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Genes	Transcript filtering options	07/20/15	No	Low
User Interface	Remove .dat from new run dialog	07/16/15	No	Low
Reports	Multiple rows per transcript	07/16/15	No	Low
Filtering	Delete filter templates	07/09/15	No	Low
Filtering	Blank filter support	05/18/15	Yes	High

Version 1.1.6.1

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
HGVS	incorrect HGVS for indels	09/29/15	Yes	High
Coverage Regions	Chromosome Mt coverage	08/20/15	No	Low
Miscellaneous	Variant search for variants not in the database	07/20/15	No	Low
External Data	Alamut - don't send transcript	07/17/15	No	Low
User Interface	Current jobs shows progress bar of previous tab	07/16/15	No	Low
User Interface	Change reference dir crashes	07/16/15	No	Low
Panels	Filter by panel	07/15/15	Yes	Medium
Permissions	Group permissions broken	07/14/15	No	Low
Permissions	Add users to existing group	07/09/15	No	Low
Audit	Logger doesn't accept unicode	07/09/15	No	Low
Filtering	Coverage Regions Filters by Percent	06/25/15	No	Low

Version 1.1.6

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
HGVS	Show all unique protein changes for each variant	06/24/15	Yes	Yes

Version 1.1.6

Corrected the Following Bugs

Category	Subject	Date	Algorithm Change	Risk
Miscellaneous	SGCOV file not closed after creation	05/26/15	No	Low
HGVS	Insertion's p. translation caused crash	05/12/15	Yes	Medium

Version 1.1.5

Added and Updated the Following Features

Category	Subject	Date	Algorithm Change	Risk
Filtering	Update number of rows	04/08/15	No	Low
Permissions	Read/write user permissions for runs and samples	04/08/15	No	Low
Artifacts	Artifacts – Add/Edit objects	04/06/15	No	Low
Objects	Soft delete objects	04/06/15	No	Low
User Interface	Pathogenicity and pathogenicity status “New” buttons	03/30/15	No	Low
External Data	VCF – Support for fields with multiple values	03/26/15	No	Low
User Interface	ExAC link for rs numbers	03/26/15	No	Low
Variants	Variant Tab – Panel group specific info only	03/20/15	No	Low
Runs	Add run status to Add/Edit Object dialog	03/20/15	No	Low
VCF	Support additional NextGENe data	03/20/15	No	Low
Objects	Allow user to rename existing object in Add/Edit Object dialog	03/17/15	No	Low
User Interface	Move progress bar to status bar	03/17/15	No	Low
User Interface	Load saved column configurations via right click	03/17/15	No	Low
Runs	Set run status like sample status	03/11/15	No	Low
Classifications	Default variant classifications updated to new ACMG recommendations.	03/09/15	No	Low

Category	Subject	Date	Algorithm Change	Risk
Coverage Regions	Times observed in passed regions added	02/25/15	Yes	Medium
Reports	Ability to associate custom reports with samples and patients	02/20/15	No	Low
User Interface	Show number of records in status bar	02/20/15	No	Low
User Interface	Show version, build, revision and license info in status bar	02/20/15	No	Low
User Interface	Column preferences – new implementation	02/16/15	No	Low
User Interface	OMIM – Show error message for incorrect API key	02/05/15	No	Low
Filtering	Filter variants by BED file	01/21/15	No	Low
Permissions	Default user permissions when creating a new user	01/16/15	No	Low
VCF	Export comments to VCF files	01/14/15	No	Low
Audit	Login tracker support for multiple sessions.	01/13/15	No	Low
External Data	HGMD – match observed alleles	01/13/15	No	Low
Command Line	Gene info request from the command line	01/08/15	No	Low
Variants	New variant statistics for times observed	12/18/14	No	Low
VCF	Calculate allele frequency from allele depth and allele observed	12/04/14	Yes	Medium
Patients	Add patients to search bar	12/01/14	No	Low
Coverage Regions	Add comment column to coverage regions	11/25/14	No	Low
User Interface	Update search bar list immediately when new items are added to database	11/19/14	No	Low
VCF	Support VCF files with multiple samples	11/18/14	Yes	Medium
VCF	Export VCF – Multiple samples selected via multiple runs	10/30/14	No	Low
Filtering	Filter tree	10/30/14	No	Low
HGVS	HGVS upstream and downstream of CDS	10/29/14	No	Low
Objects	Don't delete associated samples/variants when deleting object types	10/29/14	No	Low
Patients	Auto detect date format and internationalization	10/29/14	No	Low
User Interface	Sub tabs	10/29/14	No	Low
Variants	Do not display preceding nucleotide in Ref and Alt columns when the variant is an indel	10/29/14	Yes	Medium
Genes	Ensembl gene info – GTF support	10/29/14	Yes	Medium
Samples	Multiple samples' variants in one table	10/29/14	No	Low
User Interface	Sample tab layout	10/27/14	No	Low
User Interface	Tab IDs	10/27/14	No	Low
Samples	Sample comparison	10/27/14	No	Low

Category	Subject	Date	Algorithm Change	Risk
User Interface	Rename "Create Variants Report"	10/24/14	No	Low
External Data	BED files as external databases	10/16/14	No	Low
External Data	External database naming	10/14/14	No	Low
Patients	Patient import – Date internationalization	10/01/14	No	Low
Comments	Arbitrary length comments	09/22/14	No	Low
Genes	Preferred transcript rules	09/16/14	Yes	Medium
Patients	Patient batch import – Allow missing columns from end of row	09/08/14	No	Low
External Data	LOVD – world-wide query service	09/08/14	No	Low
Variants	Search for variants by chrom,pos,ref,alt	09/08/14	No	Low
Classifications	Import pathogenicity with samples	08/12/14	No	Low
Patients	Patient tab	08/08/14	No	Low
VCF	Include coverage and allele frequency in VCF export	08/08/14	No	Low
VCF	Ion Torrent VCF files – FAO and FDP	08/06/14	No	Low
Patients	Open variant from patient tab	08/01/14	No	Low
Objects	Sample groups – Add/Edit Objects	07/31/14	No	Low
External Data	OMIM – Inheritance column	07/31/14	No	Low
VCF	Ion file format – Don't submit variants when AO = 0	07/29/14	Yes	Medium
User Interface	Highlighted row color	07/28/14	No	Low
User Interface	Search bar support expanded	07/28/14	No	Low
User Interface	ClinVar link	07/25/14	No	Low
External Data	OMIM Support	07/24/14	No	Low
Permissions	Permission denied dialog	07/21/14	No	Low
Comments	Delete and edit comments	07/21/14	No	Low
User Interface	Indexing notification dialog	07/18/14	No	Low
User Interface	Indicate owner of saved column configurations	07/14/14	No	Low
Permissions	Password requirements	07/14/14	No	Low
External Data	Supporting info hyperlink – UI change	07/11/14	No	Low
External Data	LOVD interface	07/11/14	No	Low
User Interface	Column widths	07/09/14	No	Low
Coverage Regions	Expand statistics for coverage regions	07/09/14	No	Low
Samples	Sample groups for statistics	07/09/14	No	Low
External Data	CAF – display only observed allele's value	06/26/14	No	Low
User Interface	Report dialog title changes	06/23/14	No	Low
Reports	Batch report – remove CSS option	06/19/14	No	Low
External Data	Show all available columns from VCF file	06/18/14	No	Low

Category	Subject	Date	Algorithm Change	Risk
User Interface	Column formatting – Zygosity and Chr:Chr Pos	06/18/14	No	Low
Samples	VCF and BAM files – change file location	06/16/14	No	Low
Variants	Splice site type (simple)	06/16/14	No	Low
Genes	Gene name translations	06/13/14	No	Low
Permissions	Permission management of users	06/13/14	No	Low
Genes	BED builder – Replace old gene names with new	06/13/14	No	Low
Variants	Missed ClinVar variants	06/05/14	No	Low
Audit	Audit log	06/05/14	No	Low
Audit	Login and Logout times	06/05/14	No	Low
User Interface	Display "No data" – when a table is empty	06/04/14	No	Low
Permissions	Grey out all other permissions if user is Administrator	06/03/14	No	Low
External Data	HGMD cache	06/02/14	No	Low
User Interface	Sort arrows on column headers	06/02/14	No	Low
Panels	Panel statistics	06/02/14	No	Low
User Interface	HGMD HGVS column name	05/29/14	No	Low
BAM	BAM merge tool	05/29/14	No	Low
User Interface	Patient tab – Hide "Times observed per Run"	05/21/14	No	Low
Objects	Add panel region status to Add/Edit Objects	05/16/14	No	Low
Audit	Audit log of database changes	05/16/14	No	Low
Licensing	License address – only support ipv4	05/15/14	No	Low
User Interface	Columns preferences that all users can use	05/14/14	No	Low
User Interface	Variant tab – remove group boxes	05/01/14	No	Low

Corrected the Following Bugs

Category	Subject	Change Date	Algorithm Change	Risk
Variants	Allele frequency calculations and hotspots	06/24/15	Yes	High
HGVS	Mitochondrial HGVS nomenclature	06/04/15	Yes	Medium
HGVS	HGVS protein call wrong for some indels	05/28/15	Yes	High
Patients	Remove patient of a sample	04/06/15	No	Low
Patients	Sample tab – Patient info empty	04/06/15	No	Low
User Interface	Panes in variant tab hidden when they should be shown or vice versa	04/06/15	No	Low

Category	Subject	Change Date	Algorithm Change	Risk
Variants	Reverse complement of ref and alt was applied twice for variant on minus strand	04/06/15	Yes	Medium
Runs	Run renaming	04/03/15	No	Low
Action List	Action list crashes	04/02/15	No	Low
External Data	Multiple sections for same external database	04/02/15	No	Low
User Interface	Single click links in tables / don't change font	03/26/15	No	Low
Artifacts	Artifact change pane	03/23/15	No	Low
User Interface	Panel statistics – default tab	03/23/15	No	Low
User Interface	Variant table links broken	03/20/15	No	Low
User Interface	"My Documents" opens when paths have spaces	03/09/15	No	Low
VCF	Multiple samples' variants crash	03/06/15	Yes	Medium
Licensing	License checking timeout	02/24/15	No	Low
User Interface	Configure reference directory – opens wrong dialog	02/20/15	No	Low
HGVS	Translation error on exon end	02/13/15	Yes	High
External Data	External databases not loading	02/03/15	No	Low
User Interface	Audit log – sorting	01/28/15	No	Low
User Interface	BED file builder – missing names	01/28/15	No	Low
User Interface	Blank Search – Show All Variants	01/21/15	No	Low
User Interface	Variant Table Crash	01/16/15	No	Low
Bam Viewer	Pileups not loaded after jumping to X chromosome	01/15/15	No	Low
User Interface	CAF – renaming column broken	01/15/15	No	Low
Variants	Zygosity – X Chromosome	01/07/15	Yes	High
Variants	Mutation Type – Stop Codons	01/05/15	Yes	High
Miscellaneous	File path max length	12/23/14	No	Low
External Data	CAF stopped using observed allele	12/08/14	No	Low
Coverage Regions	Panel region status update bug	12/03/14	No	Low
Variants	Variant Submit – Ref or Alt too large for database	12/01/14	Yes	High
User Interface	Runs tab – "No Data" centered instead of aligned top	11/24/14	No	Low
User Interface	Variant table – frequent crashes	11/23/14	No	Low
HGVS	HGVS protein – deletions wrong	11/20/14	Yes	High
VCF	INDEL of same length – Extra Padding Removed	11/20/14	Yes	High
External Data	HGMD loading issue	11/13/14	No	Low
Filtering	Filtering doesn't always apply	11/13/14	No	Low
Variants	Patient variant frequency – Zygosity	11/13/14	Yes	Medium
User Interface	Indexing notification dialog – Always shows up	10/29/14	No	Low
Command Line	Command line parsing errors	10/24/14	No	Low

Category	Subject	Change Date	Algorithm Change	Risk
User Interface	"Filters Applied" label disappears after refresh	10/15/14	No	Low
Filtering	Filter data type for external columns wrong	10/10/14	No	Low
Genes	BED file builder crashes on some gene names	10/01/14	No	Low
Patients	Patient import – Date not imported	10/01/14	Yes	Medium
Genes	BED file builder doesn't work with dashes in gene names	09/22/14	No	Low
External Data	CAF empty	09/09/14	No	Low
External Data	CAF – separate out correct alt allele – code was reverted	09/08/14	No	Low
User Interface	New run date time wrong	09/02/14	No	Low
External Data	OMIM – unnecessary variant table search	08/29/14	No	Low
External Data	Add values to variant table – dbNSFP	08/27/14	No	Low
External Data	HGMD username and password settings – ignore extra spaces	08/19/14	No	Low
VCF	Export VCF – Extra variants being exported	08/19/14	Yes	Medium
Genes	Some genes missing info	08/01/14	Yes	Medium
VCF	Variant not imported	08/01/14	Yes	High
External Data	OMIM – crashes patient tab	07/31/14	No	Low
Reports	Batch report – Missing data in report	07/28/14	No	Low
Licensing	Configure license – opens wrong tab of settings	07/25/14	No	Low
User Interface	Recent runs hidden	07/15/14	No	Low
Coverage Regions	Panel region status reasoning – defaults	07/14/14	No	Low
Reports	Add/Remove sections to custom report	07/14/14	No	Low
User Interface	Add comment to sample doesn't refresh display properly	07/14/14	No	Low
User Interface	Select column saving – change saved settings	07/14/14	No	Low
Filtering	Save/Load filters	07/09/14	No	Low
Reports	Patient tab – Add all variants to custom report duplicates section	07/09/14	No	Low
User Interface	Pathogenicity coloring not showing	07/07/14	No	Low
Filtering	Load filters not applied	07/01/14	No	Low
User Interface	Blank search doesn't query	06/25/14	No	Low
Coverage Regions	Loading saved filter does not work for coverage regions	06/24/14	No	Low
Samples	Add comment to sample broken	06/24/14	No	Low
VCF	Prepopulate pathogenicity doesn't submit	06/24/14	No	Low
Panels	BED file crashes	06/23/14	No	Low
User Interface	Shared tab preferences aren't applied	06/23/14	No	Low
User Interface	Password doesn't match warning shown too soon	06/20/14	No	Low

Category	Subject	Change Date	Algorithm Change	Risk
User Interface	Coverage regions – title changes	06/19/14	No	Low
Coverage Regions	Coverage information fails to load.	06/18/14	No	Low
HGVS	HGVS – palindromic sequences	06/18/14	Yes	High
Variants	Variants of type "delins" cannot be imported	06/18/14	Yes	High
Genes	Gene search crash	06/13/14	No	Low
User Interface	"Remove this custom column" crashes	06/13/14	No	Low
Genes	BED builder – gene names with dashes fail	06/10/14	No	Low
BAM	BAM coverage wrong	06/09/14	Yes	High
Genes	Gene info missing	06/04/14	Yes	Medium
User Interface	Column order issues	05/30/14	No	Low
Patients	Batch patient import from new run dialog	05/29/14	No	Low
User Interface	"Remove this sample" context menu does not work	05/29/14	No	Low
User Interface	Open coverage regions for sample right click broken	05/28/14	No	Low
Variants	Variant search results don't show pathogenicity	05/27/14	No	Low
Genes	Gene info missing	05/23/14	No	Low
Genes	Genes on alternative assemblies	05/22/14	No	Low
External Data	External columns with same header name not displayed	05/21/14	No	Low
Reports	Patient's variants – Add select to custom report	05/21/14	No	Low
User Interface	Delete variant dialog missing variant description	05/21/14	No	Low
User Interface	Patient variant table in patient tab is duplicated every time "Refresh" is clicked	05/21/14	No	Low
VCF	VCF Parsing info field bug	05/21/14	Yes	Medium
Filtering	Clear all filters broken	05/20/14	No	Low
User Interface	Supporting information display format wrong	05/20/14	No	Low
External Data	HGMD still says “loading...” after failure	05/14/14	No	Low
User Interface	Patient tab name missing	05/14/14	No	Low
User Interface	Quality thresholds not refreshed after change	05/14/14	No	Low
Patients	Delete patient	05/08/14	No	Low
Classifications	Prepopulate pathogenicity	05/07/14	No	Low
Reports	CSV export – comma bug	05/06/14	No	Low