

Release Notes

You can find more detailed information at [GitHub Issues](#).

2.0.0-RC1 (June 2020)

Catalog

- [FEATURE] Improve audit ([#1322](#), [#1483](#))
- [FEATURE] Allow queries based on permissions ([#1486](#))
- [FEATURE] Enable possibility of creating asynchronous tasks support ([#1408](#), [#1509](#))
- [FEATURE] Support ACID transactions in Catalog !! ([#1338](#))
- [FEATURE] Implement an automatic client generator valid for R, Java, Python and JS OpenCGA libraries ([#1464](#))
- [FEATURE] Add new permission to execute jobs ([#1445](#))
- [FEATURE] Improve job data model ([#1447](#))
- [FEATURE] Enable job dependencies ([#1475](#))
- [FEATURE] Support multistudy jobs ([#1549](#))
- [FEATURE] Add webhooks ([#1448](#))
- [FEATURE] Create jobs top webservice and command line ([#1460](#))
- [FEATURE] Create new **opencga** administrator user with a default project and study ([#1425](#), [#1491](#))
- [FEATURE] Improve count functionality ([#1448](#))
- [FEATURE] Add a new webservice to download files from external sources ([#1453](#))
- [FEATURE] Add dynamic parameter types in VariableSets ([#1478](#))
- [FEATURE] Add new *allowedKey* field to VariableSet ([#1554](#))
- [FEATURE] Add new /head and /tail web services in file ([#1497](#))
- [FEATURE] Add new jobs/log/head and job/logs/tail web services to see job logs ([#1495](#))
- [FEATURE] Load annotations from TSV files ([#1488](#))
- [FEATURE] Allow passing a map of sample ids when linking VCF files ([#1527](#))
- [FEATURE] Give users the option to set their own statuses ([#1545](#))
- [FEATURE] Add new permission to view variants ([#1559](#))
- [FEATURE] Assign implicit permissions automatically ([#1561](#))
- [FEATURE] Remove base64 codification from UUIDs ([#1569](#))
- [FEATURE] Improve Solr queries by annotation ([#1484](#))
- [FEATURE] Add new webservice to fetch individual relatives ([#1552](#))
- [FEATURE] Add new webservice to fetch base64 content of images ([#1584](#))
- [FEATURE] Keep individual references in samples ([#1346](#))
- [CHANGE-FEATURE] Improve panel operations ([#1577](#))
- [CHANGE] Configuration file changes ([#1415](#))
- [CHANGE] DataResponse data model changes ([#1424](#))
- [CHANGE] Rename variable type in VariableSet ([#1479](#))
- [CHANGE] Remove group name ([#1513](#))
- [CHANGE] Rename a few ACLs ([#1601](#))
- [CHANGE] Data model changes ([#1538](#))
- [CHANGE] Main login endpoint changes ([#1568](#))
- [CHANGE] Change webservice to change user password ([#1586](#))
- [CHANGE] Ensure all REST webservices return on OpenCGAResult ([#1569](#))
- [BUGFIX] Sync users CLI didn't work for AD ([#1297](#))
- [BUGFIX] Unable to update "relatedFiles" list ([#1451](#))
- [PERFORMANCE] Move deleted documents to different collection ([#1369](#))

Analysis

- [CLINICAL] Tiering interpretation analysis for cancer ([#1300](#))
- [VARIANT] Implement Fisher Test Analysis MapReduce ([#1361](#))
- [VARIANT] Implement VariantStats OpenCGA Analysis ([#1376](#))
- [VARIANT] Implement Gwas OpenCGA Analysis ([#1386](#))
- [VARIANT] Complex sample query by variant to enable cohort creation for clinical trials ([#1474](#))
- [CLINICAL] Implement mutational signature analysis ([#1490](#))
- [CORE] Create a Dockerfile with the R packages used by OpenCGA analysis ([#1493](#))
- [CLINICAL] Implement the inferred sex analysis ([#1544](#))
- [ALIGNMENT] Implement statistics analysis for alignment coverage ([#1588](#))
- [CLINICAL] Implement the relatedness analysis based on IBD/IBS ([#1521](#))
- [CLINICAL] Implement genetic checks to compare with the reported results ([#1522](#))

Variant Storage

- [FEATURE] Support Hadoop3.x and HBase2.x ([#925](#))
- [FEATURE] Divide opencga-storage-hadoop-deps in submodules ([#1333](#))
- [FEATURE] Store custom variant scores ([#708](#))
- [FEATURE] Allow load VCFs split by region in Hadoop ([#1471](#))
- [FEATURE] Copy MapReduce jobs result submitted through an ssh connection ([#1432](#))
- [FEATURE] Add FilterCount and MeanQuality to VariantStats ([#1502](#))

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- [FEATURE] Allow to configure the variant storage from REST ([#1518](#))
- [FEATURE] Allow skip sample index when loading variant files ([#1530](#))
- [FEATURE] Allow indexing multiple files per sample in StorageHadoop ([#1542](#))
- [FEATURE] Return MendelianError code as an IssueEntry ([#1547](#))
- [FEATURE] Extend sample filter functionality ([#1567](#))
- [CHANGE] Add specific permissions to view variants ([#1559](#))
- [CHANGE] Rename VariantQueryParams 'format', 'includeFormat' and 'info' ([#1556](#))
- [CHANGE] Remove SAMPLE_ID and FILE_IDX from Format. Add INCLUDE_SAMPLE_ID ([#1555](#))
- [CHANGE] Transform endpoint analysis/variants/sample/query into an Analysis ([#1435](#))
- [CHANGE] Improve variant storage functionality for returning samples ([#1353](#))
- [CHANGE] Change variant.id and variant.names content ([#1514](#))
- [CHANGE] Make gene/id/xref query params more strict ([#1515](#))
- [PERFORMANCE] Add extended clinical index to SampleIndex ([#1454](#))
- [PERFORMANCE] Add Biotype+Ct combination to SampleIndex ([#1364](#))
- [PERFORMANCE] Count numTotalResults from covered SampleIndex queries asynchronously. ([#1352](#))
- [PERFORMANCE] Improve SampleIndex File ([#1343](#))
- [BUGFIX] Remove Jetty9.4 from Hadoop MapReduce classpath ([#1504](#))

1.4.2 (June 2019)

Catalog

- [CHANGE] Rename web services from `/stats` to `/aggregationStats` ([#1253](#))
- [BUGFIX] Index fails when passing "." instead of "/" ([#1241](#))
- [BUGFIX] Alignment index daemon fails ([#1232](#))
- [BUGFIX] Migration script issue ([#1226](#))
- [BUGFIX] `Upload` web service fails when uploading to root folder ([#1276](#))
- [BUGFIX] Missing `id` query parameter in `studies/{studies}/groups` web service ([#1275](#))
- [BUGFIX] Versioning issues ([#1270](#))
- [BUGFIX] Web service `studies/{studies}/groups/create` not working ([#1250](#))
- [BUGFIX] Order not respected when querying lists of ids ([#1246](#))
- [FEATURE] Support passing relatedFiles object to File during `link` ([#1295](#))
- [FEATURE] Support `htsget` protocol for data streaming ([#1277](#))
- [FEATURE] Add new user category "`application`" ([#1268](#))
- [PERFORMANCE] Analysis queries take too much time ([#1245](#))

Migration required

 1.4.2. contains a small series of internal changes requiring running a small migration. To do so, please head to the main OpenCGA source folder and run the following:

```
mongo {mongo_ip}:{mongo_port}/{database_name} opencga-app/app/migration
/utis/migrateCollection.js opencga-app/app/migration/v1.4.2/catalog
/migration.js
```

- **mongo_port**: Typically 27017
- **database_name**: Typically opencga_catalog

Variant Storage

- [CHANGE] Rename filter "`transcriptionFlag`" to "`transcriptFlag`" ([#1256](#))
- [BUGFIX] `HashMap$Node` cannot be cast to `java.util.HashMap$TreeNode` ([#1323](#))
- [BUGFIX] Wrong usage of `SampleIndex` on invalid queries ([#1274](#))
- [BUGFIX] Fix RowKey generation for non symbolic structural variants [#1259](#)
- [FEATURE] Add chromDensity query filtering by sample genotype ([#1249](#))
- [FEATURE] Accept nested fields in chromDensity by sample genotype ([#1263](#))
- [FEATURE] Use SamplingSize field at SampleIndex query executor ([#1339](#))
- [FEATURE] Add new variant filters: "`cohortStatsAlt`", "`cohortStatsRef`" ([#1239](#))
- [FEATURE] Query by compound heterozygous ([#1247](#))
- [FEATURE] Export variants given a file of variant ids ([#1254](#))
- [FEATURE] Accept keyword "`LoF`" in consequence type filter ([#1262](#))
- [FEATURE] Implement a MR to extract number of variants per file [#1287](#)
- [PERFORMANCE] Remove unneeded FileMetadata reads from HBaseToStudyEntryConverter ([#1350](#))
- [PERFORMANCE] Improve SampleIndex read performance ([#1319](#))
- [PERFORMANCE] Add annotation counters to SampleIndex ([#1258](#))
- [PERFORMANCE] Reduce size of SampleIndex table ([#1252](#))
- [PERFORMANCE] Include parents genotype in the SampleIndex ([#1244](#))
- [PERFORMANCE] Skip join SampleIndex with Variants table when possible [#1242](#)
- [IMPROVEMENT] Improve approximate count of CompoundHeterozygous in StorageHadoop [#1299](#)

- [IMPROVEMENT] Improve DeNovo variants definition ([#1340](#))
- [IMPROVEMENT] Improve Genotype filter to include by default phased genotypes ([#1273](#))
- [IMPROVEMENT] Make /sampleData support somatic studies ([#1329](#))
- [IMPROVEMENT] Add VarinatStats to SampleData result ([#1286](#))
- [IMPROVEMENT] Native implementation of sampleData endpoint in storage-hadoop ([#1285](#))
- [IMPROVEMENT] Extend panel filter to include regions and single variants [#1272](#)
- [IMPROVEMENT] Extract variant query executor from VariantStorageEngine [#1240](#)
- [COMMAND LINE] Add missing SampleIndex command line operations ([#1282](#))

1.4.0-rc1 (August 2018)

Catalog

- [IMPROVEMENT] Recognise bigwig files automatically. ([#283](#))
- [IMPROVEMENT] **Major improvements in annotationSets** ([#635](#), [#772](#), [#849](#)):
 - Queries can be performed by any of the fields. ([#772](#))
 - All the fields are indexed in the database, supporting really fast queries. ([#772](#))
 - Projections can be added so only specific fields of an annotationSet are included. ([#635](#), [#772](#))
 - Annotation set web services have been changed. ([#849](#))
 - See [AnnotationSets 1.4.0](#) section from the OpenCGA documentation for the whole description of features.
- [FEATURE] Implement new "Permission rules" feature ([#745](#))
- [FEATURE] Add new /admin web services to be able to perform administrative operations through REST ([#759](#))
- [IMPROVEMENT] Improve /user web services. Remove duplicated *configs* web services ([#661](#))
- [FEATURE] Implement *delete* operations for most of the entries ([#792](#))
- [IMPROVEMENT] Store *creationDate* field as an actual date object to improve queries ([#752](#))
- [CHANGE] Important *id* changes ([#819](#)):
 - Data model *ids* have been redefined to contain any user-defined *id* for every entry. Migrations produced in every entity are described in the ticket.
 - Old numeric *ids* are now lost and only used for internal purposes. Users cannot query by those fields anymore.
 - Update REST web services to support *id* changes ([#834](#))
- [IMPROVEMENT] Stop creating empty directories when linking *Files* ([#865](#))
- [FEATURE] Add new *{entry}Action* field to some update web services to support adding, setting or removing single entries to arrays of them. (Example: *samplesAction* to add, set or remove samples from an individual, file or cohort) ([#850](#))
- [IMPROVEMENT] Deprecate *VariableSet* web services and move them to *Study* web services. Improve and clean old *Study* web services ([#846](#))
- [IMPROVEMENT] General data model improvements described in [#823](#):
 - Add new immutable ***uuid*** field to all entries.
- [FEATURE] Create catalog solr sync mechanism and enable facet queries [#875](#)

Variant Storage

- [FEATURE] Aggregate operation for all samples from a study in the Variant ([#757](#))
 - [IMPROVEMENT] Move HBase write step to a separated MR for fill-missing operation ([#815](#))
 - [IMPROVEMENT] Mark already processed variants in fill missing operation ([#803](#))
 - [IMPROVEMENT] Do not iterate over all VcfRecords when filling gaps or missing variants ([#794](#))
 - [IMPROVEMENT] Fill missing prepare step: copy variants to fill into archive table ([#793](#))
 - [IMPROVEMENT] Split VcfSlice from archive table in REF and NON_REF columns ([#778](#))
 - [IMPROVEMENT] Split archive table in file batches ([#777](#))
 - [CHANGE] Remove merge=advanced from storage-hadoop ([#796](#))
- [FEATURE] Index Sample Genotypes in HBase ([#838](#))
 - [FEATURE] Genotype index intersect in HBase ([#862](#))
 - [FEATURE] Integrate Variants export using MapReduce ([#867](#))
 - [FEATURE] Support enriched genotypes when querying to SampleIndex ([#870](#))
 - [IMPROVEMENT] Use variants SampleIndex when reading from MapReduce ([#868](#))
- [FEATURE] New Variant query filter "clinicalSignificance" ([#872](#))
- [FEATURE] Add new filters for INFO and FORMAT fields other than GT ([#863](#))
- [FEATURE] Add filter by QUAL in Storage Variants ([#809](#))
- [FEATURE] Accept enriched genotypes at GENOTYPE filter ([#750](#))
- [FEATURE] Variant filtering in a samples group ([#578](#))
- [CHANGE] Automatic INCLUDE_STUDY if possible ([#878](#))
- [CHANGE] Automatic INCLUDE_SAMPLE if GENOTYPE VariantQueryParam is present ([#814](#))
- [IMPROVEMENT] Match Consequence type with the specified Gene filter (if any) for Storage Hadoop ([#874](#))
- [CHANGE] Untie internal Catalog and Storage IDs ([#859](#))

- [FIX] Synchronize Catalog ID to UID changes in Storage Managers catalog (#861)
- [FEATURE] Create a ProjectMetadata object for Variant Storage (#832)
- [IMPROVEMENT] Move storage-hadoop metadata to a separated table (#781)
- [FEATURE] Support and load BREAKENDS in Variant Storage (#760)
- [FEATURE] Support of Symbolic and Structural variants in Hadoop Variant Storage (#857)
- [IMPROVEMENT] Add direct loader for the first file in a chromosome to load directly to the variants collection (#354)
- [FEATURE] Move removed variants into a trash bin (#831)
- [CHANGE] By default, load all FORMAT fields in Variant Storage MongoDB (#824)
- [CHANGE] Change storage-hadoop table naming policy (#782)
- [IMPROVEMENT] Review and improve Variant Annotation in OpenCGA Storage (#805)
- [IMPROVEMENT] Create one Stage Collection per study in Variants Storage MongoDB (#801)
- [IMPROVEMENT] Filter out overlapping files in variants in storage-hadoop (#779)
- [IMPROVEMENT] Improve remove file in variant-storage-hadoop (#776)
- [IMPROVEMENT] Load annotation using BufferedMutator (#775)
- [FIX] Do not store phoenix primary key columns in HBase as separated columns (#802)
- [FIX] Adapt remove file to new archive schema (#800)
- [FIX] Do not map namespace for VIEW tables under phoenix 4.12.0 (#799)
- [FIX] Avoid PhoenixIOException timeout when dropping columns from phoenix (#795)

1.3.11 (August 2019)

Catalog

- [FEATURE] Support "application users" (#1268) (**migration required**) <https://github.com/opencb/opencga/blob/develop/opencga-app/app/migration/v1.4.2/catalog/migration.js#L24>
- [FEATURE] Add CRAM support (#1301)
- [IMPROVEMENT] Change long fileid to File file in RelatedFile data model (#1294) (**migration required**) https://github.com/opencb/opencga/blob/v1.3.11/opencga-app/app/migration/v1.3.0/catalog/11_related_files.js
- [IMPROVEMENT] RelatedFiles can be passed during file link (#1295)
- [FIX] Fix --sync-all option from opencga-admin.sh users sync command line (#1297)

1.3.10 (February 2019)

Catalog

- [FIX] Remove base64 conversion of the secret key.
- [FIX] Update pom dependencies to avoid conflicts.

1.3.9 (January 2019)

Catalog

- [FEATURE] Support Azure AD authentication.
- [CHANGE] Add id to Group data model (**migration required**) https://github.com/opencb/opencga/blob/v1.3.9/opencga-app/app/migration/v1.3.0/catalog/10_add_group-id.js

1.3.8 (August 2018)

Catalog

- [FIX] Fix permission issue affecting users and groups with the "_" symbol (#881)

1.3.7 (July 2018)

Catalog

- [ENHANCEMENT] Add new tags field to the File data model (#855)
- [CHANGE] Configuration change. Add hooks to configuration file (#856)

1.3.6 (May 2018)

Catalog

- [FIX] Improve performance of sample queries filtering by individual ([#843](#))

1.3.5 (May 2018)

Catalog

- [FIX] Fix issue when assigning permissions given the id(s) of different entities ([#836](#))

1.3.4 (April 2018)

Catalog

- [ENHANCEMENT] Performance improvement when assigning permissions ([#829](#))

1.3.3 (March 2018)

Catalog

- [ENHANCEMENT] Remove old deprecated fields from Family data model ([#810](#))
- [ENHANCEMENT] Allow looking for Individuals and Families by a new sample field ([#811](#))
- [FIX] Fix command line to support non-expiring tokens
- [FIX] Support SKIP_COUNT parameter
- [CHANGE] Remove family completeness check

1.3.2 (February 2018)

Catalog

- [FIX] Add missing individual-sample indexes ([#790](#))
- [FIX] Fix smart name resolution ([#791](#))

1.3.1 (February 2018)

Catalog

- [FIX] Propagation of permissions sample-individual not working ([#780](#))
- [ENHANCEMENT] Ask for admin password automatically when using admin command line ([#785](#))
- [FIX] Filtering by file size not working ([#786](#))

1.3.0 (January 2018)

General

- [FEATURE] Admin migration command line ([#690](#))
- [FEATURE] Implement AutoComplete for CLI ([#714](#))

Catalog

- [REMOVE] Remove ACL from data models. ([#666](#))
- [ENHANCEMENT] Clean old code and refactoring. ([#667](#), [#668](#), [#669](#), [#670](#))
- [ENHANCEMENT] Remove some hidden and deprecated methods from webservises and command line ([#672](#))
- [CHANGE] Changes to family data model ([#677](#))
- [FEATURE] Add new analysis tool webservises ([#679](#))

- **[FEATURE]** Add version support for *Sample*, *Individual* and *Family* (#684)
- **[ENHANCEMENT]** Clean and remove unnecessary dependencies for the client module (#687)
- **[ENHANCEMENT]** Change some fields from *Clinical Analysis* (BETA) data model (#688, #702)
- **[ENHANCEMENT]** Remove unnecessary *Relatives* data model (#693)
- **[ENHANCEMENT]** Improve some individual webservices to better support the *Individual-Sample* relation (#701)
- **[CHANGE]** Change *individual* parameter in the sample/create webservice (#703)
- **[CHANGE]** Internal modification regarding the way the *Sample-Individual* relation was stored (#706)
- **[ENHANCEMENT]** Add new *admins* group in studies (#711)
- **[ENHANCEMENT]** Add new *stats* field to *Sample* data model (#717)
- **[CHANGE]** Rename *ontologyTerms* field in *Sample*, *Individual* and *diseases* field in *Family* for *phenotypes* (#718)
- **[FEATURE]** Add new option to export and import data from/to catalog (#720)
- **[ENHANCEMENT]** Improve *groupby* webservices (#721)
- **[ENHANCEMENT]** Support a list of ids in all GET webservices (#727)
- **[CHANGE]** Internal modification: Change ACL delimiter used (#740)

Variant Storage

- **[FEATURE]** Make use of the new VariantMetadata model from Biodata (#673)
- **[FEATURE]** Major support of Symbolic variants in Variants Storage (#695)
- **[FEATURE]** Create profiles to select hadoop flavour (#707)
- **[FEATURE]** Store info fields on storage-hadoop improvement storage (#704)
- **[FEATURE]** Allow loading multiple variant files from the same sample with non overlapping variants (#696)
- **[FEATURE]** New optional pipeline step "fill-gaps" (#713)
- **[CHANGE]** Rename some Variant REST query parameters (#751)
- **[CHANGE]** GO and EXPRESSION filter must be combined as an AND with other region (#694)
- **[CHANGE]** Update CellBase to v4.5.3 improvement (#770)
- **[ENHANCEMENT]** Speed up GENOTYPE filter with FILES filter, when possible (#675)
- **[ENHANCEMENT]** Add field "source" to VariantQueryResult (#758)
- **[ENHANCEMENT]** Indicate if "numTotalResults" is an approximated count in VariantQueryResult (#749)
- **[FIX]** Inconsistent configuration param to select variant annotator (#747)
- **[FIX]** Duplicate Key Warn/Error in Stage Collection (#766)
- **[FIX]** IllegalArgumentException when CellBaseRestVariantAnnotator skips a variant (#746)
- **[FIX]** Concurrent table modification error when loading in Hadoop with merge=basic (#709)

1.2.0 (September 2017)

Catalog

- **[FIX]** Fix job search by input and output files. (#533)
- **[ENHANCEMENT]** Hide deprecated webservices. (#599)
- **[ENHANCEMENT]** Set *ontologyTerms* array during *Sample/Individual /create* and */update* webservices. (#613)
- **[FEATURE]** Add the concept of release in OpenCGA. (#616)
- **[FIX]** Fix behaviour where individual ids are not recognized when creating new family. (#617)
- **[FEATURE]** Implement JWT based session management (#618)
- **[ENHANCEMENT]** Change List<Long> for List<Object> in corresponding data models (#621)
- **[ENHANCEMENT]** Make ACL permissions part of the query (#628)
- **[FIX]** Fix count parameter not working in search webservices and command line (#629)
- **[CHANGE]** Change annotationsets REST webservices. (#631)
- **[FEATURE]** Support multigroups (#633)
- **[ENHANCEMENT]** Return HTTP 403 error code when user tries to access not granted data (#636)
- **[FEATURE]** Add a new members group for every study (#642)
- **[FEATURE]** Automatically sync OpenCGA groups with external LDAP groups during login (#647)
- **[FEATURE]** Add new projects/search webservice (#651)
- **[FEATURE]** Add new *confidential* parameter to VariableSet data model. It allows defining confidential variable sets and corresponding annotation sets, so a new special permission will be needed to access them. (#653)
- **[FEATURE]** Propagate permissions from samples to individuals. (#657)
- **[ENHANCEMENT]** Return HTTP 401 error code when user is not successfully logged in or the token is invalid. (#658)

Variant Storage

- **[FEATURE]** Improve Solr integration with VariantStorage when querying (#638)
- **[ENHANCEMENT]** Improve Solr variant iterator by using Solr cursors (#640)
- **[ENHANCEMENT]** Variant Solr Search manager improvements (#639)
- **[ENHANCEMENT]** Configure VariantMerger and VariantNormalizer with VCFHeader (#630)
- **[ENHANCEMENT]** Store DisplayConsequenceType from VariantAnnotation at MongoDB (#659)

- [ENHANCEMENT] Return VariantTraitAssociation as TraitAssociation (EvidenceEntry) (#692)
- [FEATURE] Remove files from variants storage (#192)
- [FEATURE] Command line and rest endpoints for remove operations on variant storage (#623)
- [FEATURE] Simple merge mode for loading variants in opencga-storage-hadoop (#609)
- [FEATURE] VariantQueryParam INCLUDE_FORMATS. Select format fields to return (#608)
- [FEATURE] Store other genotype fields on storage-hadoop (#602)
- [FEATURE] Export variant statistics (#309)
- [FIX] Sample filter not working when the sample is in multiple files (#641)
- [FIX] Possible error loading overlapping multiallelic variants (#626)
- [FIX] Do not delete files (or related entries) from catalog if still loaded in variants storage (#625)
- [FIX] Avoid OutOfMemoryError updating storage metadata from catalog (#645)
- [FIX] Error indexing vcf files containing "variants" in the file name (#691)

Relevant changes

- CLI install changed and need two additional parameters 1: secretKey, algorithm
- Configuration file has changed and need to be adopted on all opencga installation
- No logout
- Changes on #616, #618, #621, #628 and #633 require several migration scripts to be run over the Catalog database: <https://gist.github.com/pfurio/2ca0cb2da46eac9e309101066f8758f5>
- Changes on #192 and #626 require to execute a migration script on all Variants databases in MongoDB: <https://gist.github.com/j-coll/3dec01abc70644943d33de78105c633e>
- Changes in VariantAnnotation model. See [variantAnnotation.avdl](#)
 - Field "exonNumber" replaced with "exonOverlap".
 - Added field "traitAssociation" that will replace "variantTraitAssociation" in next releases.

1.1.0 (June 2017)

Catalog

- [ENHANCEMENT] Support integers and floats type for variables. (#545)
- [BUG] Fix link race condition. (#551)
- [FEATURE] Add new parameter *propagate* to Individual web service when setting permissions to propagate permissions to the related samples. (#558)
- [FEATURE] Add support to give permissions using queries in sample, individual and file web services. (#560)
- [CHANGE] Change Acl REST web services. (#561)
- [FIX] Not return fields that are of no interest (using include/exclude). (#569)
- [FEATURE] Add new admin command line to synchronise and add users from LDAP groups. (#573)
- [FEATURE] Added new Family data model. (#582)
- ~~[FEATURE] Add list<Sample> to individual/create web service. (#582)~~
- [FEATURE] Add new /meta/status, /meta/ping and /meta/about web services. (#572)
- [ENHANCEMENT] Support creating an Individual when calling to the Sample create web service. (#586)
- [DEPRECATE] Deprecate *species* field of Individual data model. (#588)
- [ENHANCEMENT] Deprecate usage of *variableSetId*. Add field *variableSet* to corresponding web services that accepts an id or a name. (#589)
- [ENHANCEMENT] Support passing an array of *annotationSets* when creating an Annotable entry (Sample, Cohort, Individual and Family). (#590)
- [ENHANCEMENT] Add new *type* field to Sample model. (#591)
- [FEATURE] Add *father* and *mother* information in *attributes* field of Individual. (#592)
- [ENHANCEMENT] Add support to change *public/private* User registration (#594)
- [DEPRECATE] Deprecate all *xx/create* and *xx/update* GET webservices. (#598)

Variant Storage

- [FEATURE] Make optional to merge non same overlapping variants in MongoDB (#574)
- [FEATURE] Implement a benchmark framework for OpenCGA Storage (#248)
- [ENHANCEMENT] Filter VcfRecord before converting into Variant object when possible (#577)
- [BUGFIX] Not loading new overlapping variants in HBase (#581)
- [ENHANCEMENT] Increment variant size threshold for CellBase annotation (#596)
- [BUGFIX] Fix ArrayIndexOutOfBoundsException when loading variants data (#597)
- [FEATURE] Add VCF export to gRPC command line (#606)

Relevant changes - migration

- Add new permissions to admin user in the general configuration file. To add: VIEW_STUDY, UPDATE_STUDY and SHARE_STUDY
- ~~Added sampleIds parameter in each individual entry.~~
- Catalog changes require this migration script: [opencga-1.1.0-migration.js](#)
- Changes of #574 require to execute a migration script on all Variants databases in MongoDB: [opencga_574_add_studies_field_to_stage.js](#)

1.0.2

General

- [BUGFIX] Fix VCF output format ([#584](#))

Catalog

- [ENHANCEMENT] New *dateOfBirth* field added to Individual ([#580](#)) and *somatic* field to Sample ([#576](#))
- [ENHANCEMENT] Performance improvement when annotating new variants ([#575](#))

1.0.0 (February 2017)

Catalog

- [FIX] Authenticated users can now see public data ([#501](#))
- Permissions assigned to *individuals* are directly propagated to *samples* ([#509](#))
- [CHANGED] *CREATE* and *UPDATE* permissions have been merged into *WRITE* ([#506](#))
- [CHANGED] Permissions given to folders are now propagated in the database ([#505](#)), this increase significantly the performance of the ACL resolution
- [CHANGED] Changes in session data model ([#479](#))

Storage

- Complete the implementation of *exclude* and *include* of fields for Variant queries ([#515](#))

Clients

- [Python] new Python client implemented following the same architecture than Java and Javascript clients (<https://github.com/opencb/opencga/pull/516>). This improves the quality significantly and add many new features, thanks [Antonio Rueda](#)!
- Java and Javascript client libs use always POST when available

Server

- [REST] Add new *files/create using* POST to create new folders and files with some content ([#514](#))
- [REST] Rename parameters from *acl/update* ([2617993](#))
- [REST] Hide from Swagger all *create* and *update* ACL web services using GET ([cbea817](#)), these should always use POST, this affects to *studies*, *samples*, *files*, ... (these will be removed in version 1.1)
- [REST] Complete the implementation of *exclude* and *include* of fields for Variant queries
- [REST] Remove from *users* the GET methods to *create* and *update* filters ([5125a22](#))
- [REST] Add a warning to Swagger to **all** *create* and *update* methods using GET ([ee6d66](#)). It is encourage that all *create* and *update* actions use always POST
- [GRPC] Complete the implementation of *exclude* and *include* of fields for Variant queries

1.0.0-rc3 (January 2017)

General

- Major changes in maven properties and configuration files. ([#480](#))
- *catalog-configuration.yml* and *configuration.yml* have been merged. ([#476](#))

Catalog

- Added support to fetch shared projects and studies.
- Added organism information to the project data model. ([#455](#))
- Renamed *diskUsage* and *diskQuota* for size and quota respectively in all data models were present.

- Closed sessions are now removed from the array of sessions (but they can still be found in the audit collection). ([#475](#))

Storage

- Improve error handling for storage operations ([#447](#), [#463](#), [#465](#))
- Add param --resume to opencga-analysis.sh and opencga-storage.sh command line ([#465](#))
- Import and export variants datasets ([#459](#), [#460](#))
- Enable gRPC as top level feature ([#492](#))
- New top layer StorageManager connecting catalog with storage ([#486](#))
- Shade proto and guava dependencies for Hadoop ([#440](#))

Server

- Create and update webservices have been all implemented via POST.

Known issues

- OpenCGA storage hadoop is not available in this version. To compile use this line:

```
mvn clean install -DskipTests -pl '!:opencga-storage-hadoop-core'
```

1.0.0-rc2 (November 2016)

1.0.0-rc1 (September 2016)

This release constitutes the first release candidate (RC1). This is the biggest release ever with more than **1,400 commits**, special mention to [j-coll](#) and [pfurio](#) for their contribution in Catalog, Storage and Server components.

General

- New command line interfaces (CLI) for users (*opencga.sh*), admins (*opencga-admin.sh*) and analysis (*opencga-analysis.sh*)

Catalog

- New catalog configuration file using YAML.
- New authorisation method. A big list of permission have been defined.
- New smart id resolver. Numerical ids are no longer mandatory and ids are now resolved internally given the alias.
- New and improved java and python command lines.
- New javascript, java and R client implementations.
- Support for annotations in cohorts.

Storage

- Many performance improvements and fixes in MongoDB storage engine, the most notable include a new load strategy to improve file merging scalability
- New storage engine based on **Apache HBase**, this is completely functional but is tagged as *beta* until more tests are done.
- New custom variant annotation implemented

Server

- An experimental gRPC server implemented

v0.7.0

Third Beta

v0.6.0

Second Beta

v0.5.0

First Beta

- [IMPROVEMENT] Add direct loader for the first file in a chromosome to load directly to the variants collection ([#354](#))