# 20151105_data_release_notes

## Overview of changes in the release of November 5, 2015

Please also see our RSS feed for information about accessing the data.

## Overview of submissions:  2015

| Date | Total Submissions |
|---|---|
| Jan 01, 2015 | 149013 |
| Feb 01, 2015 | 156999 |
| Mar 01, 2015 | 162455 |
| Apr 01, 2015 | 171408 |
| May 01, 2015 | 172044 |
| Jun 01, 2015 | 173236 |
| Jul 01, 2015 | 184506 |
| Aug 01, 2015 | 154686 |
| Sep 01, 2015 | 158580 |
| Oct 01, 2015 | 160538 |
| Nov 01, 2015 | 170931 |

## Content

| Brief | Explanation |
|---|---|
| ENIGMA expert panel submission | An initial submission of 1030 interpretations of BRCA1 and BRCA2 variants was provided by ENIGMA (Evidence-based Network for the Interpretation of Germline Mutant Alleles). |
| CFTR2 expert panel submission | 142 interpretations of CFTR variants were submitted by the expert panel CFTR2. |
| Invitae submission | Invitae submitted 4380 interpreted variants, including novel and updated submissions. |
| GeneDx submission | GeneDx provided several new datasets, inlcuding 76 updated interpretations of cancer variants,  2210 variants in nuclear genes for mitochondrial proteins (both novel and updates),  and 1636 variants in cardiomyopathy genes (both novel and updates). |
| Genetic Services Laboratory; University of Chicago | The Genetic Services Laboratory at the University of Chicago submitted 3437 interpretations, including both novel and updated submissions. |
| Baylor Miraca Genetics Laboratories | Baylor Miraca Genetics Laboratories submitted 119 interpretations of variants from patients undergoing exome sequencing. |
| HudsonAlpha Institute for Biotechnology | An initial submission of 7 variants was provided by HudsonAlpha Institute for Biotechnology. |

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|---|---|
| Coming soon - change in variant types for duplications | Coming soon - ClinVar will use the more specific variant type "tandem duplication" (SO:1000173), rather than "duplication", for duplications defined at the level of sequence. This includes short variants that are typically described as "dup" in HGVS as well as large structural variants that are known to be tandem duplications, not copy number gains. |
| date last evaluated for OMIM's interpretations | In this release, the last date an interpretation of clinical significance was evaluated was changed for most of the records from OMIM. The date used to be calculated based on the last date the gene-specific record in OMIM was modified; it is now calculated based on the publication date of the latest publication cited in an Allelic variant record. |

## Overview of submissions: 2014

| Date | Total Submissions |
|---|---|
| Jan 01, 2014 | 68204 |
| Feb 01, 2014 | 73492 |
| Mar 01, 2014 | 83343 |
| Apr 01, 2014 | 111501 |
| May 01, 2014 | 112349 |
| Jun 01, 2014 | 117209 |
| Jul 01, 2014 | 127132 |
| Aug 01, 2014 | 127557 |
| Sep 1, 2014 | 143114 |
| Oct 1, 2014 | 143601 |
| Nov 1, 2014 | 144117 |
| Dec 1, 2014 | 148008 |

## Overview of Submissions: 2013

| Date | Total Submissions |
|---|---|
| Apr 05, 2013 | 30333 |
| May 01, 2013 | 30386 |
| Jun 01, 2013 | 39047 |
| Jul 01, 2013 | 39170 |
| Aug 01, 2013 | 45901 |
| Sep 01, 2013 | 50263 |
| Oct 01, 2013 | 52047 |
| Nov 01, 2013 | 64750 |
| Dec 01, 2013 | 64881 |