

Latest updates

Date	Update																		
UPCOMING mid May 2024 ?	Goal: Manuscript draft complete.																		
UPCOMING early May, 2024 ?	Goal: submission to GenBank complete.																		
UPCOMING May 15, 2024	Next status check conference call																		
May 1, 2024	<div>Apollo manual review stats (as of today)</div> <table><tr><th>Type</th><th>Number</th></tr><tr><td>under primary review</td><td>0</td></tr><tr><td>under secondary review</td><td>0</td></tr><tr><td>unable to update</td><td>14</td></tr><tr><td>updated, secondary review requested</td><td>0</td></tr><tr><td>for discussion</td><td>49</td></tr><tr><td>updated, no secondary review needed</td><td>2504</td></tr><tr><td>secondary review completed, accepted</td><td>979</td></tr><tr><td>no update needed</td><td>68</td></tr></table>	Type	Number	under primary review	0	under secondary review	0	unable to update	14	updated, secondary review requested	0	for discussion	49	updated, no secondary review needed	2504	secondary review completed, accepted	979	no update needed	68
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April 3, 2024	Poll sent out for next status update call																		
March 22, 2024	Extended deadline: Final GFF2 data files from all external annotation groups to TAIR.																		

March 21, 2024	Apollo manual review stats (as of today) <table> <tr> <th>Type</th><th>Number</th></tr> <tr> <td>under primary review</td><td>1</td></tr> <tr> <td>under secondary review</td><td>0</td></tr> <tr> <td>unable to update</td><td>14</td></tr> <tr> <td>updated, secondary review requested</td><td>55</td></tr> <tr> <td>for discussion</td><td>54</td></tr> <tr> <td>updated, no secondary review needed</td><td>2156</td></tr> <tr> <td>secondary review completed, accepted</td><td>883</td></tr> <tr> <td>no update needed</td><td>68</td></tr> </table>	Type	Number	under primary review	1	under secondary review	0	unable to update	14	updated, secondary review requested	55	for discussion	54	updated, no secondary review needed	2156	secondary review completed, accepted	883	no update needed	68
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March 8, 2024	Status check conference call																		
March 4, 2024	Doodle poll sent out for March status conference call.																		
March 1, 2024	Goal: Manuscript writing begins in earnest. Done: Google Drive for shared documents created.																		
February 29, 2024	Goals: All review, quality control, nomenclature resolution, rule-creation for annotation retention, coordinate updates for V12 should be completed by this date. Final GFF2 data files from external annotation groups to TAIR. Files expected: TEs, 5sRNAs, NOR2/NOR4, lncRNAs, TRASH pipeline results																		
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February 6, 2024	<p>Status check conference call</p> <p>Most of the review, quality control, nomenclature resolution, rule-creation for annotation retention, coordinate updates for V12 should be completed by this date.</p>
January 15, 2024	<p>PAG 2024 Arabidopsis Informatics session 12:50 - 13:00 Pacific time (some slide presentations available here)</p> <p>DEADLINE: sample GFF3 data files from external annotation groups to TAIR</p>
December 13, 2023	Conference call: status update, remaining tasks, manuscript planning
November 28, 2023	Ongoing quality control of manual review, various groups finishing up their sets of annotations (TEs, lncRNAs, repeats, rDNAs).
November 3, 2023	195/620 of secondary review left. Lots of progress made! Only 2 of 'under primary review' left.
November 1, 2023	Pikaard team paper on the sequences and functional organizations of the A. thaliana Col-0 NORs published https://www.science.org/doi/full/10.1126/sciadv.adj4509
October 31, 2023	Deadline secondary review.
October 30, 2023	Zoom call of secondary review participants to touch on some complicated cases, decision making.
October 17, 2023	Secondary manual review begins.
September 30, 2023	Deadline for primary manual review of genes. (620 total marked for review)
September 21, 2023	Filtered long read coverage and read tracks finally available. These have replaced the older tracks that were cluttered with overly long introns (>12kbp). The capped and merged RNAseq read track has also been filtered and replaced. This will now be converted to bw for an even better coverage track. Track Metadata is in the Apollo Tips .
August 29, 2023	<p>Summary of other annotation-related activities and groups:</p> <ol style="list-style-type: none"> Transposable element reannotation (in progress) <ol style="list-style-type: none"> Alex Bousios (University of Sussex) Shujun Ou (Ohio State University) Zhigui Bao (Max Planck Tübingen) integration of NOR2 and NOR4 into Col-CC (in progress) <ol style="list-style-type: none"> Craig Pikaard, Ramya Enganti, Dalen Fultz, Anastasia McKinlay (Indiana University) Korbinian Schneeberger, Xiao Dong, Raul Wijfjes (MPIPZ, Uni München) rDNA reannotation (in progress) <ol style="list-style-type: none"> Craig Pikaard, Ramya Enganti, Dalen Fultz, Anastasia McKinlay (Indiana University) Ian Henderson, Piotr Włodzimierz (University of Cambridge) Tandem repeat reannotation (complete) <ol style="list-style-type: none"> Ian Henderson, Piotr Włodzimierz (University of Cambridge) lncRNA reannotation (in progress) <ol style="list-style-type: none"> Andrew Nelson, Caylyn Bailey, Kyle Palos (Cornell University) Michael Schon (Wageningen University & Research) Thomas Blein (Centre national de la recherche scientifique, CNRS) Aleksandra Kornienko (Gregor Mendel Institute) Selene Fernandez Valverde (UNSW Sydney)
August 28, 2023	<p>NEW TRACK:</p> <p>RNAseq combined and recapped, coverage view - an even more reduced combined coverage view of ALL the 62 RNAseq tracks that resulted from sequential rounds of capping and merging instead of individual capping and then final merging (the scale bars will be different and more lowly expressed RNAseq reads will be more visible)</p>
August 11, 2023	<p>NEW TRACKS:</p> <ol style="list-style-type: none"> RNAseq combined, coverage view - combined coverage view of ALL the 62 RNAseq tracks, partially filtered to remove alignments with extra long introns and with excessive coverage in certain regions capped to 200. RNAseq capped and merged, reads - individual reads of all files that were not able to be filtered but were individually capped at 200 and then merged. RNAseq filtered capped and merged, reads - individual reads of all files that were individually filtered, then capped at 200, and then merged.
August 6, 2023	<p>Plant Biology 2023 in Savannah, GA: Plant Bioinformatics Resources for FAIR Agricultural Data Discovery and Reuse workshop (10:30 am - 12:30 pm)</p> <p>Update on the reannotation effort included in the TAIR presentation</p>

August 3, 2023	IMPROVED TRACK: Protein alignments chained : We have now connected the Protein Alignments track elements so that pieces of the same protein are seen together. This is a great improvement over the isolated boxes view (which is now gone).
July 27, 2023	NEW TRACK: TranscriptomeReconstructoR models (from Sebastian Marquardt's group at U of Copenhagen)
July 24, 2023	<ol style="list-style-type: none"> over 300 genes have been started, about 70 are done 4 office hours held (Wednesdays by Slack) discussions going on in Slack <ol style="list-style-type: none"> what to do with insertion of mt sequence in chr2 - annotate genes or not? should we have a scoring system for genes? new track suggestions <ol style="list-style-type: none"> PFAM domains - community suggested, created, and loaded PANTHER families - community suggested, created, and loaded track metadata table available in Apollo Tips
July 7, 2023	Gene list assignments (over 2000 genes) distributed (email and Slack)
June 29, 2023	Apollo editing training session 3: 14 participants
June 28, 2023	Apollo basics training session 3: 10 participants
June 8, 2023	Arabidopsis Bioinformatics workshop at ICAR2023 in Chiba: Update on reannotation effort.
June 1, 2023	Apollo editing training session 2: 18 participants.
May 31, 2023	Apollo editing training session 1: 28 participants.
May 26, 2023	Apollo basics training session 2: 25 participants from 6 countries. Now 10 countries total!
May 23, 2023	Apollo basics training session 1: 35 participants from 8 countries.
May 12, 2023	Apollo training dates set: May 23 (T) and May 25 (F), 7 - 8:30 am US Pacific time (UTC -7)
Apr. 27, 2023	Call for community volunteers for manual review phase goes out.
Apr. 17, 2023	Initial assessment of automated annotation pipeline results begins.
Apr. 11, 2023	NCBI Eukaryotic Annotation automated pipeline complete.
Feb. 23, 2023	NCBI Eukaryotic Annotation team begins process of running the automated annotation pipeline with several datasets suggested by the community included
Jan. 26, 2023	TAIR puts out community call via social media for additional expression datasets that could be included in annotation run
Jan. 25, 2023	NCBI completes review of assembly and releases to public: https://www.ncbi.nlm.nih.gov/assembly/GCA_028009825.1
Jan. 16, 2023	Arabidopsis Informatics Workshop at PAG30 in San Diego: Two talks given that contained information relevant to the v12 project.
Dec. 23, 2022	Schneeberger lab submits Col-CC (community consensus) assembly to NCBI
Oct. 27, 2022	First community meeting