

v124 released!

November 3, 2021 —  

Announcing v124 release of the ENCODE portal, highlighted by the following updates:

- Schema changes
 - Removed control_type property of Series
 - Removed columns from Dataset schema
 - Added “NcoI,” “MseI,” and “MboI and MseI” enums to File restriction_enzymes
 - Upgraded “CRISPRi-FlowFISH” enum of Functional Characterization Experiment expression_measurement_method to “PrimeFlow”
 - Added dependency to Functional Characterization Experiments in which expression_measurement_method must be specified if examined_loci is specified
 - Added datapoint property to Transgenic Enhancer Experiments
 - Added “released,” “revoked,” “listed,” and “unlisted” enums to Cart status
 - Upgraded both “disabled” and “current” enums of Cart status to “unlisted”
 - Added description property to Carts
 - Added carts property to Publications
 - Added scATAC Counts Summary Quality Metric schema
 - Renamed the following properties of HiC Quality metric:


Original property name	New property name
alignable_normal_and_chimeric_paired	2_alignments
chimeric_ambiguous	3_or_more_alignments indices
chimeric_paired	2_alignments_a1_a2b_a1b2_b1a2
duplicates	total_duplicates
normal_paired	2_alignments_a_b

pct_alignable_duplicates	pct_2_alignment_duplicates
pct_alignable_normal_and_chimeric_paired	pct_2_alignments
pct_alignable_unique_reads	pct_2_alignment_unique
pct_chimeric_ambiguous	pct_3_or_more_alignments
pct_chimeric_paired	pct_2_alignments_a1_a2b_a1b2_b1a2
pct_normal_paired	pct_2_alignments_a_b
pct_sequenced_total_duplicates	pct_sequenced_total_duplicates
pct_sequenced_unique_reads	pct_sequenced_total_unique
pct_single_alignment	pct_1_alignment
pct_unmapped_reads	pct_one_or_both_reads_unmapped
single_alignment	1_alignment
unique_reads	total_unique
unmapped_reads	one_or_both_reads_unmapped

- Added the following properties to HiC Quality Metric:
 - Read_type, 2_alignment_duplicates, 2_alignment_unique, no_chimera_found, pct_no_chimera_found, 0_alignments, pct_0_alignments, pct_1_alignment_unique, pct_1_alignment_duplicates, pct_sequenced_1_alignment_unique, pct_sequenced_1_alignment_duplicates, pct_sequenced_2_alignment_unique, pct_unique_total_duplicates, pct_sequenced_total_unique, library_complexity_estimate_1_alignment, library_complexity_estimate_2_alignment, library_complexity_estimate_1_and_2_alignments, pct_sequenced_2_alignment_duplicates
- Renamed pct_properly_paired_reads, pct_mapped_reads, and pct_singletons properties of scATAC Alignment Quality Metric to frac_properly_paired_reads, frac_mapped_reads, and frac_singletons respectively
- Renamed pct_duplicate_reads of scATAC Library Complexity Quality Metric to frac_duplicate_reads
- Added “inclusion list,” “sparse gene count matrix of all reads,” “sparse gene count matrix of unique reads,” “unfiltered sparse gene count matrix of all reads,” “unfiltered sparse gene count matrix of unique reads,” and “unfiltered sparse splice junction count matrix of unique reads” enums to File output_type
- Added “capped RNA enrichment,” “uncapped RNA enrichment,” and “PCR-free” enums to Library construction_method
- Added “Streptavidin magnetic beads” enum to Library library_size_selection_method

- Adjusted Functional Characterization Series assay_title to exclude mentions of control datasets
- Upgraded “Caucasian” enum of Human Donor ethnicity to “European”
- Added processed property to Files
- UI updates
 - Added matrix page for Deeply Profiled data collection
 - Fixed bug on Deeply Profiled Matrix page in which some links returned unexpected queries
 - Added facet groupings to the following search pages:
 - Aggregate Series, Annotation, Biosample, Collection Series, Differentiation Series, Disease Series, Experiment, Experiment Series, File, Fly Donor, Gene Silencing Series, Human Donor, Matched Set, Mouse Donor, Multiomics Series, Organism Development Series, Pulse Chase Time Series, Reference Epigenome, Replication Timing Series, Single Cell RNA Series, Treatment Concentration Series, Treatment Time Series, Worm Donor
 - Adjusted search result titles of Functional Characterization Series
 - Fixed bug on Region Search genome browser in which tracks were not filtered when selections were made in Experiment facets
 - Added purpose to both Treatment and Biosample pages
 - Added Purpose facet on Treatment search page
 - Fixed bug on Biosample pages in which “Biosamples that part of this biosample” tables would cause page crashes
 - Added experimental input links on Annotation pages
 - Fixed legend of genome browser for cCREs
 - Added library construction method to Experiment pages and Experiment search pages
 - Allowed addition of datasets from Collection Series to Carts
 - Added drop-down menu to select a specific object type when navigating to a Report view from a search that includes multiple object types
 - Fixed bug in which some Analyses with mixed assemblies did not display the correct title in file tables
 - Adjusted queries for processed files for Carts and batch downloading to utilize the processed property of Files and not the assembly property
 - Adjusted queries on Body Map and Reference Epigenome pages to exclude controls by default
 - Updated graph drawing software, allowing graph collapsing on SESCC page
- Other updates
 - Excluded long read scRNA-seq from “unreplicated experiment” audit

v124 software version: <https://github.com/ENCODE-DCC/encoded/releases/tag/v124.0> 

All of the source code used for the portal website is open source and available through our repository hosted at GitHub ([www.github.com/ENCODE-DCC/](https://github.com/ENCODE-DCC/) )

v124.0

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