

WAGER 2.0.4 Release

Release notes

Study Manager

JIRA Issue Tracking Key	Release Comment
WAG-262	The ability to add multiple notes for a field is now supported
WAG-422	An issue associated with the selection of new genes that have been added to WAGER has been resolved
WAG-425	Uploading files that contain erroneous genotype data no longer continue loading while dropping off the rows for SUBJECTIDs that aren't in the database
WAG-447	The genotype marker definition uploading process has been refined
WAG-461	The ability to automatically add a subject to a subject group when bulk loading or typing in new subjects has been added
WAG-477	Include ASRB number and Fam ID as searchable options in subject search window
WAG-479	Pedigree tab showing when editing study details
WAG-480	Consent no longer fails when importing Subjects with only SUBJECTIDs
WAG-481	Subject Import not displaying correct DUPLICATE SUBJECTID in error report
WAG-483	Creating a new fieldset using a name that already exists no longer causes an error
WAG-489	Adding New Subject whose UMRN is already in the system no longer causes an error
WAG-686	A report to determine duplicate error rates & % call rates for genotypic data has been added to the system
WAG-881	Added a calculated, read only field on the Subject Demographic Data screen

	showing a subjects current age in years
WAG-903	Format of UMRN has been broadened to accommodate differences in other states.
WAG-432	Study Manager and the LIMS have been enhanced to allow patients that have not had their consent paperwork completed to be identified when selecting biospecimens so that they can be excluded

Data Analysis

JIRA Issue Tracking Key	Release Comment
WAG-449	The format for displaying genes on the genotype page in Data Analysis has been standardised
WAG-472	The column shifting error that was occurring when a variable was in more than one collection being extracted has been resolved
WAG-475	WAGER Data Analysis User Staistics Screen shows counts for all extracts for all studies, not just those that a user is allowed to see
WAG-484	X' as been added as an option for missing genotypes in the Data Analysis files
WAG-848	Handle for >2000 items selected in selection screens (mod_plsql restriction)
WAG-856	Data Analysis now clears the collections list cache between data sets for different extractions
WAG-857	"Collection does not exist error" that occurred under certain conditions when selecting collections for extraction in Data Analysis has been resolved
WAG-862	Phenotype page "Add all phenotypes in study" data restrictions updated to reflect the users true full access
WAG-876	Data dictionary no longer prints multiple lines for phenotypes that are in multiple collections

WAG-890	List of Studies no longer disappears after pressing 'Previous' in Data Analysis
WAG-703	Modify the data dictionary to identify values for a data element that are not to be exported

LIMS

JIRA Issue Tracking Key	Release Comment
WAG-442	Require a barcode suitable to fit on label of 50.8mmH x 6.35mmW for use on 96 & 384 well plates
WAG-451	The error with the nanodrop upload functionality has been resolved
WAG-507	The existing 2D barcode has been elongated to fit on the narrower 50.8mm x 6.35mm labels
WAG-847	"Lithium Heparin Blood" biospecimens will now be processed properly in the LIMS
WAG-888	"Print all barcodes" now prints more than one style of label.
WAG-917	Searching for Frozen Lymphocytes fails in the Biospecimen Search window.
WAG-921	Added ability for RNA/Plasma/Serum samples to be counted into the "BIOSPECIMEN REPORT" function in LIMS
WAG-922	The Biospecimen Report has been modified to separate out "H" only, "J" only, "H&J" (already available) and "W" only
WAG-894	Able to process blood into more than one biospecimen type
WAG-907	Site based barcode selection is now supported.
WAG-935	Biospecimen OD 260/280 field is now available to search.