

tranSMART 16.2 Release (Feb 2017)

tranSMART 16.2

The tranSMART 16.2 was released in February 2017 for the postgres database. The Oracle version is expected in a few weeks.

Access to an [demo installation](#) or the 16.2 release can be found [HERE](#).

[Installation instructions](#) can be found [HERE](#).

The release can be found as [signed artifacts](#) (recommended) for download [HERE](#) and on the tranSMART-Foundation [Github](#) [HERE](#) in each repository as the branch 'release-16.2'.

Presentations at the tranSMART Foundation Annual Meeting Session A2 explored the release and details on the new capabilities that can be seen [HERE](#).

- Overview of the Release [SLIDES - RECORDING](#)
- SmartR (SLIDES coming soon) - [RECORDING](#)
- GWAS PLINK [SLIDES - RECORDING](#)
- GWAS Extensions (SLIDES coming soon) - [RECORDING](#)
- HiDome genomics extensions - See below
- XNAT plugins - See below
- ETL Enhancements - See below
- Bugfixes (plus HiDome, XNAT, ETL) - [SLIDES - RECORDING](#)

The goals of this release are:

Continuous process improvements

- Code management and bug tracking
- Automated regression testing
- Improved beta testing and bug fixing
- PMC processes

Technical improvements

- Outstanding JIRAs from 16.1
- GWAS enhancements from Pfizer
- ETL improvements

- Installation framework, improved modularity
- Cohort selection on -omics data from J&J

External interfaces & plugins from the Community

- [SmartR](#) (eTRIKS, ITTM)
- HiDome Subsetting on -omics data (J & J, eTRIKS, TraIT)
- GWAS Results Enhancements from Pfizer
- GWAS PLINK integration from Clarivate Analytics/U Liverpool (Formerly Thomson Reuters)
- XNAT imaging platform interfaces:
 - [TraIT/Erasmus MC](#) (video presentation [here](#))
 - eTRIKS/Imperial College

- [Ingenuity IPA pathway analysis](#) (ITTM)
- Return of Genome Browser and Metacore plugins
- ETL Improvements (tranSMART Foundation)

New and updated features

Link	Description
New features in 16.2	New features not described under the plugins below
Issues fixed in 16.2	This is the current list of JIRA issues being worked on for 16.2 (including those that have been completed). This includes JIRAs from 16.1 as well as new entries.
SmartR	Interactive analysis workflows to supersede selected advanced workflows
HiDome	Support for high-dimensional data in Comparison and Summary Statistics
Ingenuity IPA Connector	Ingenuity pathway analysis workflow under SmartR

XNAT import (TraIT /Erasmus)	Import of clinical variables from XNAT image systems
XNAT viewer (Imperial)	Links from grid view to images in XNAT systems.
GWAS enhancements (Pfizer)	Updates to GWAS analysis tab from Pfizer
GWAS PLINK (Clarivate)	Launch of PLINK to run new analyses
Dalliance genome browser	Genome browser fully supported from release 16.2
Metacore Plugin	Metacore plugin fully supported from release 16.2
ETL improvements	Improved scalability, updates to ICE tool , closer integration with tMDataLoader