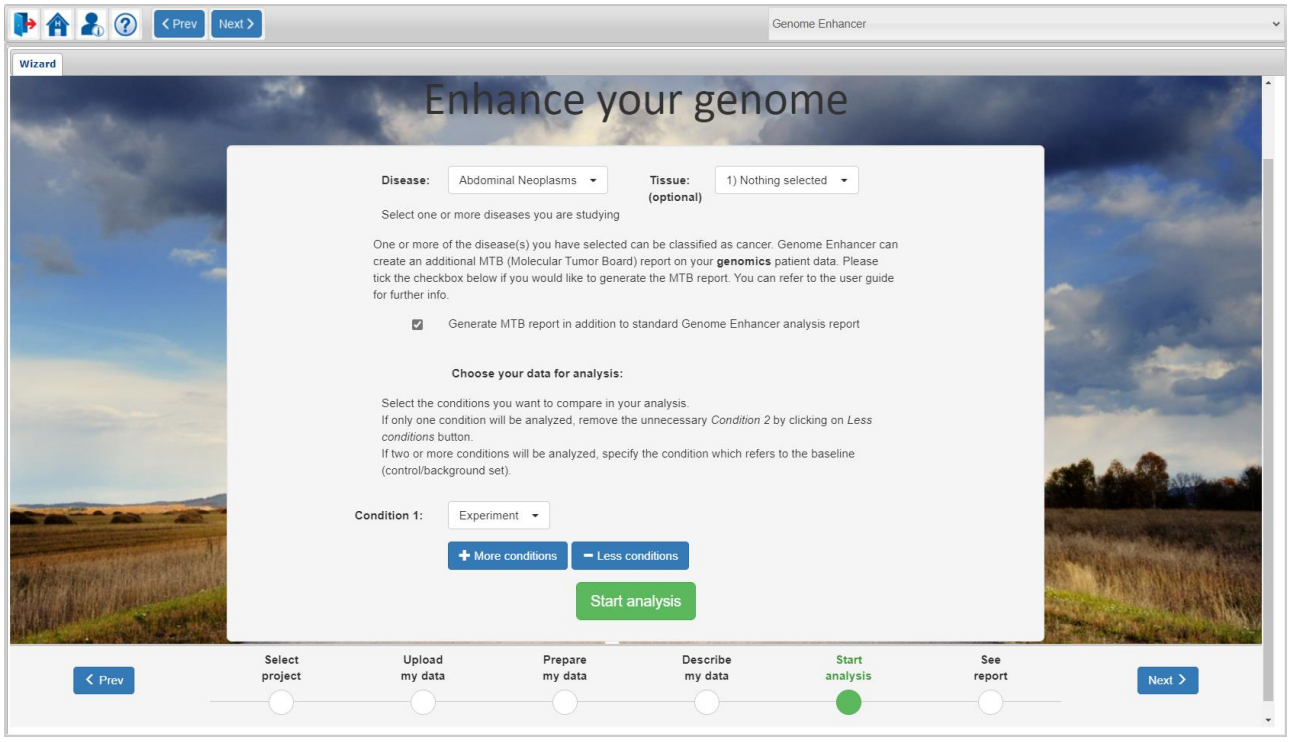
Genome Enhancer release 2.2

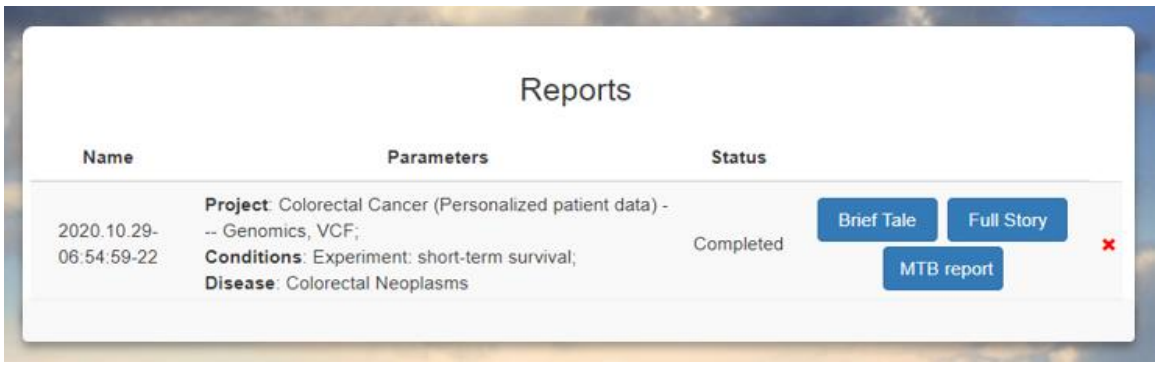
New features

The 2.2 release of Genome Enhancer comes with the following new features:

Integrated MTB report generation option: now MTB (Molecular Tumor Board) report can be automatically generated by Genome Enhancer for cases when genomics data is studied for a certain list of cancer-related pathologies if up to 2 conditions were selected during the analysis launch. The *Generate MTB Report* option will automatically appear on the analysis launching form once those requirements were fulfilled:



If the *Generate MTB Report* option was selected during the analysis launch, the generated MTB report will appear on the *See Report* step of Genome Enhancer wizard together with the standard *Brief Tale* and *Full Story* reports:



The MTB report is based on the *gene-drug predictive associations method*: somatic variants of one patient (mutations, amplifications, deletions, rearrangements) are searched in curated databases of predictive biomarkers (GKDB, CIViC) and are reported according to their clinical evidence. The MTB report is constructed inside Genome Enhancer pipeline on the basis of the results of MTB method.

The report summarizes all predictive associations in a detailed table. The results are sorted by level of evidence (A1-B1-A2-B2-A3-B3). To allow a quick interpretation, the type of the association (response, resistance) is colored (green, red) and new variants are displayed in gray color.

Gene	Variant	Disease	Known Variant	Association	Drugs	Evidence	PMID	Level
PML	F645L F597L	Acute Promyelocytic Leukemia	pml-rara	sensitivity/response	All-trans Retinoic Acid,Arsenic Trioxide	approved	11704842	B1
BRCA1	S408I S408I S370I S370I S1512I S1512I S1533I S1533I S3I S3I F304L F304L S1465I S1465I S362I S362I F1...	Estrogen-receptor-Positive-Breast-Cancer	any mut.	sensitivity/response	Olaparib	approved	19553641	B1
BRCA2	V2466A V2466A	Estrogen-receptor-Positive-Breast-Cancer	any mut.	sensitivity/response	Olaparib	approved	19553641	B1
ERBB2	I655V I640V I24V I379V I625V I95V	Gastric Adenocarcinoma	ampl.	sensitivity/response	Trastuzumab	approved	20728210	B1
ERBB2	I655V I640V I24V I379V I625V I95V	Her2 receptor Positive Breast Cancer	ampl.	sensitivity/response	Trastuzumab	approved	16236737	B1
POLE	V384L V411L	Colorectal Adenocarcinoma	any variant (LoF)	response	PD1 blockade	case report	28188185	A2
RNF43	L291M L418M R343H R216H L377M R302H P231L P104L P190L I47V	Colorectal Adenocarcinoma	any variant (GoF)	response	porcupine inhibitors	case report	ENA 2015 (abstract C45)	A2
ALCAM	T301M N258S T250M N207S	Colorectal Cancer	expression	resistance	5-fluorouracil	clin. trials	24708484	A2
PPP1R15A	K277E A316P R31H V199A	Colorectal Cancer	RS557806	sensitivity/response	Bevacizumab,FOLFIRI Regimen	clin. trials	27177629	A2
ERBB2	I655V I640V I24V I379V I625V I95V	Colorectal Cancer	ampl.	resistance	Cetuximab	clin. trials	22586653, 28223103	A2
PTEN	R130Q	Colorectal Cancer	loss	resistance	Cetuximab	clin. trials	21163703	A2
NT5E	A230T T141A T72A T376A	Colorectal Cancer	overexpression	sensitivity/response	Cetuximab	clin. trials	25520391	A2

Level of Evidence: findings are classified into six levels of evidence combining the axis A-B and the axis 1-2-3. Level A means evidence was found in the same cancer type as the one which is being studied. Level B means evidence was found in any other cancer type. On the 1-2-3 axis, level 1 means the evidence is supported by drug approval organizations or clinical guidelines, level 2 contains a clinical evidence (clinical trials, case reports) and level 3 consists of a preclinical evidence.

An example of MTB report, generated for the Genome Enhancer demo project 'Colorectal Cancer (Personalized patient data) --- Genomics, VCF' can be found here.

The MTB method and the corresponding report structure were developed by Julia Perera-Bel in the research group of Prof. Dr. Tim Beißbarth at the University Medical Center Göttingen (UMG). Perera-Bel J, Hutter B, Heining C, et al. From somatic variants towards precision oncology: Evidence-driven reporting of treatment options in molecular tumor boards. Genome Med. 2018;10(1):18. Published 2018 Mar 15. doi:10.1186/s13073-018-0529-2).

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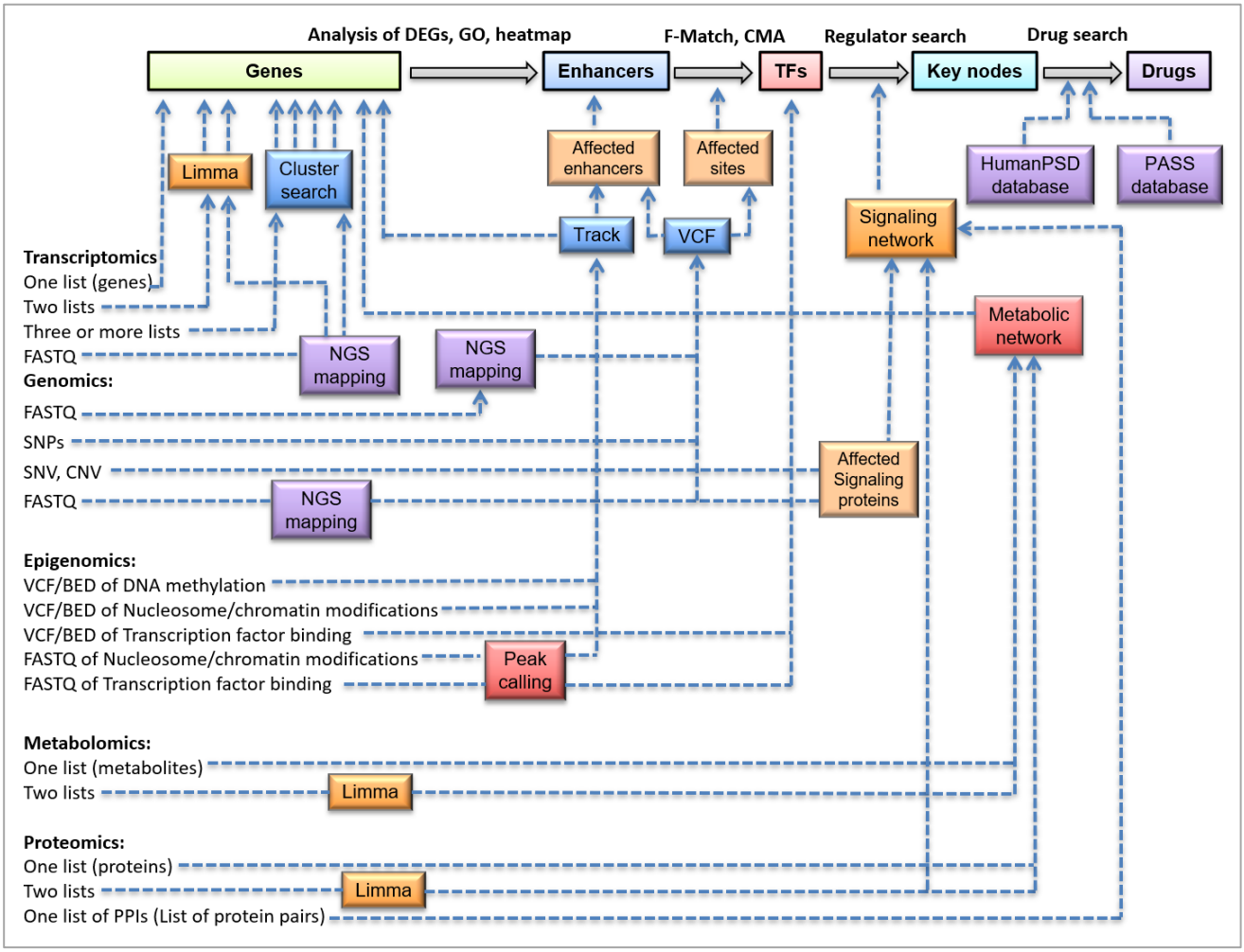
Databases update: TRANSFAC®, TRANSPATH® and HumanPSD™ databases used in the Genome Enhancer analysis were updated to the release 2020.3. The Ensembl database was updated to Ensembl release 100.

Email notification when analysis is ready: now you do not need to manually check whether your Genome Enhancer analysis has finished or not – an automatic email notification will be sent to you once the results will be ready. You can close the Genome Enhancer tab in your browser, once the analysis was launched, and enjoy the time you have saved for yourself by using our automatized bioinformatics pipeline. Once your analysis will be finished, you will receive an email notification from us.

Extended user guide with data annotation examples and analysis schema description: the Genome Enhancer user guide was extended with examples on how the data annotation diagram could look like for various analysis scenarios. This information is available at the help section of the *Describe my data* step of Genome Enhancer wizard.

A detailed description of how the analysis inside the Genome Enhancer pipeline is performed was also added. This description can be found in the help section of the very first step of Genome Enhancer wizard – *Select Project* or on a dedicated page of our web site. The overall analysis schema can be summarized as follows:

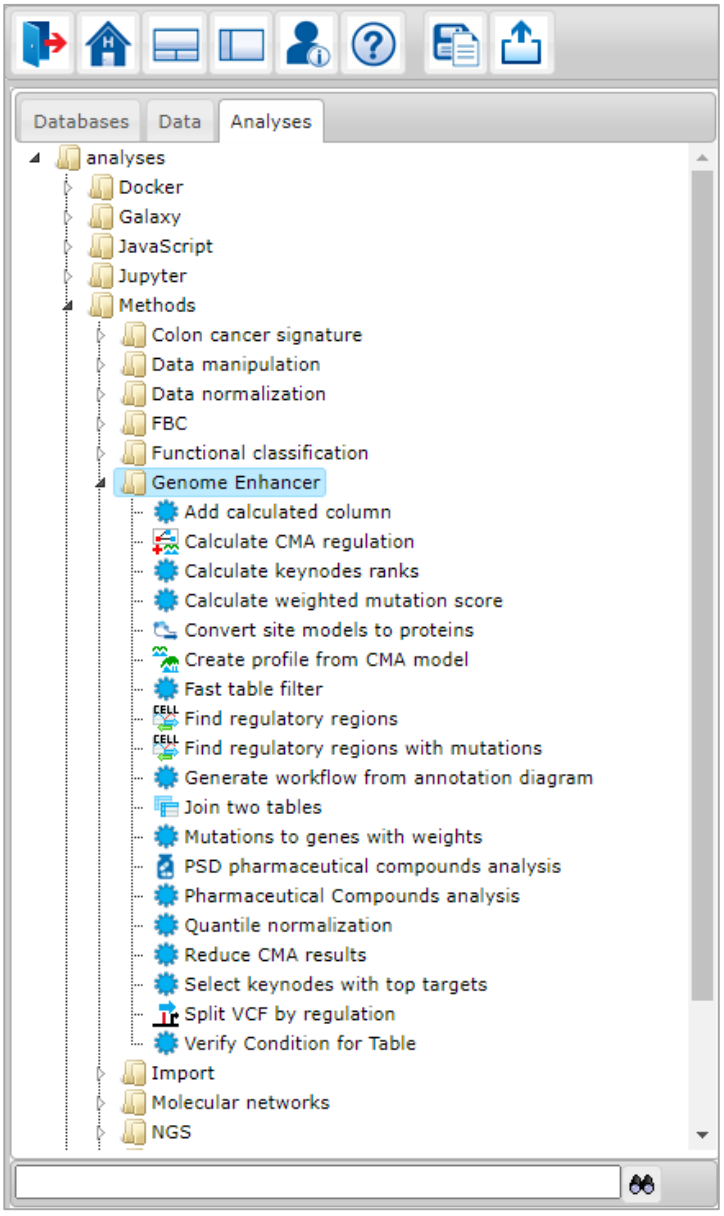


Demo reports update: all demo reports of Genome Enhancer pipeline were updated to the analysis results provided by Genome Enhancer version 2.2. The demo reports can be freely accessed with a demo account at https://ge.genexplain.com or at Genome Enhancer product page on our web site.

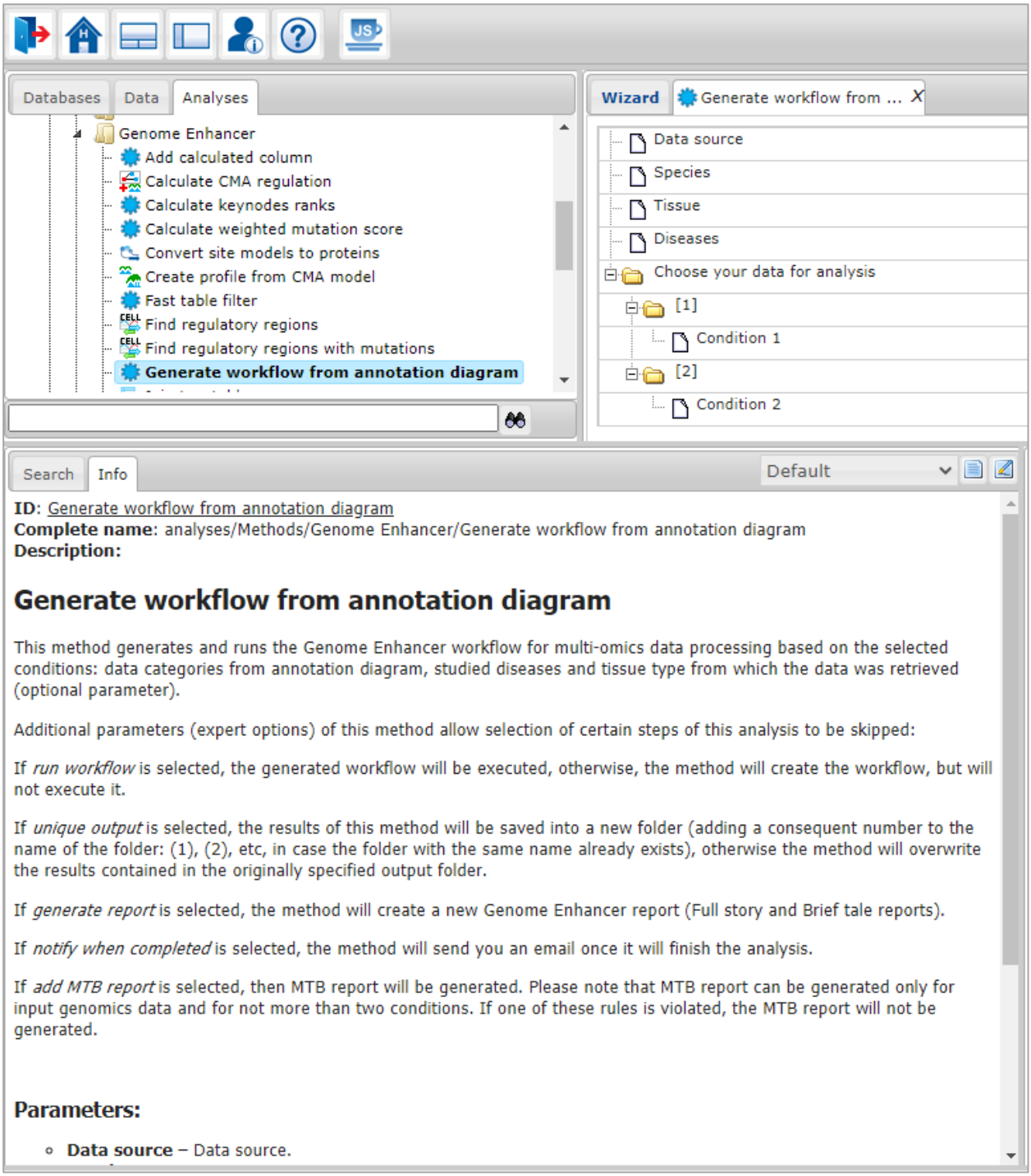
Genome Enhancer Expert

Starting from release 2.0 Genome Enhancer offers to its users a powerful synergism between the automatic pipeline for multi-omics data processing of Genome Enhancer and the comprehensive bioinformatics toolbox of the geneXplain® platform.

In the Genome Enhancer release 2.2 additional methods were added to the Genome Enhancer folder inside the Analysis → Methods folder of Genome Enhancer Expert solution under the geneXplain® platform view perspective:



Description of all methods and their parameters can be found in the info box field, which is located at the bottom panel of Genome Enhancer Expert in the geneXplain® platform view perspective:



The Genome Enhancer methods folder can be accessed only by Genome Enhancer Expert users (users holding the full geneXplain license, including geneXplain® platform, Genome Enhancer and TRANSFAC®, TRANSPATH® and HumanPSD™ databases).

You can contact us via info@genexplain.com to find out how to upgrade your current geneXplain license to the Genome Enhancer Expert solution.