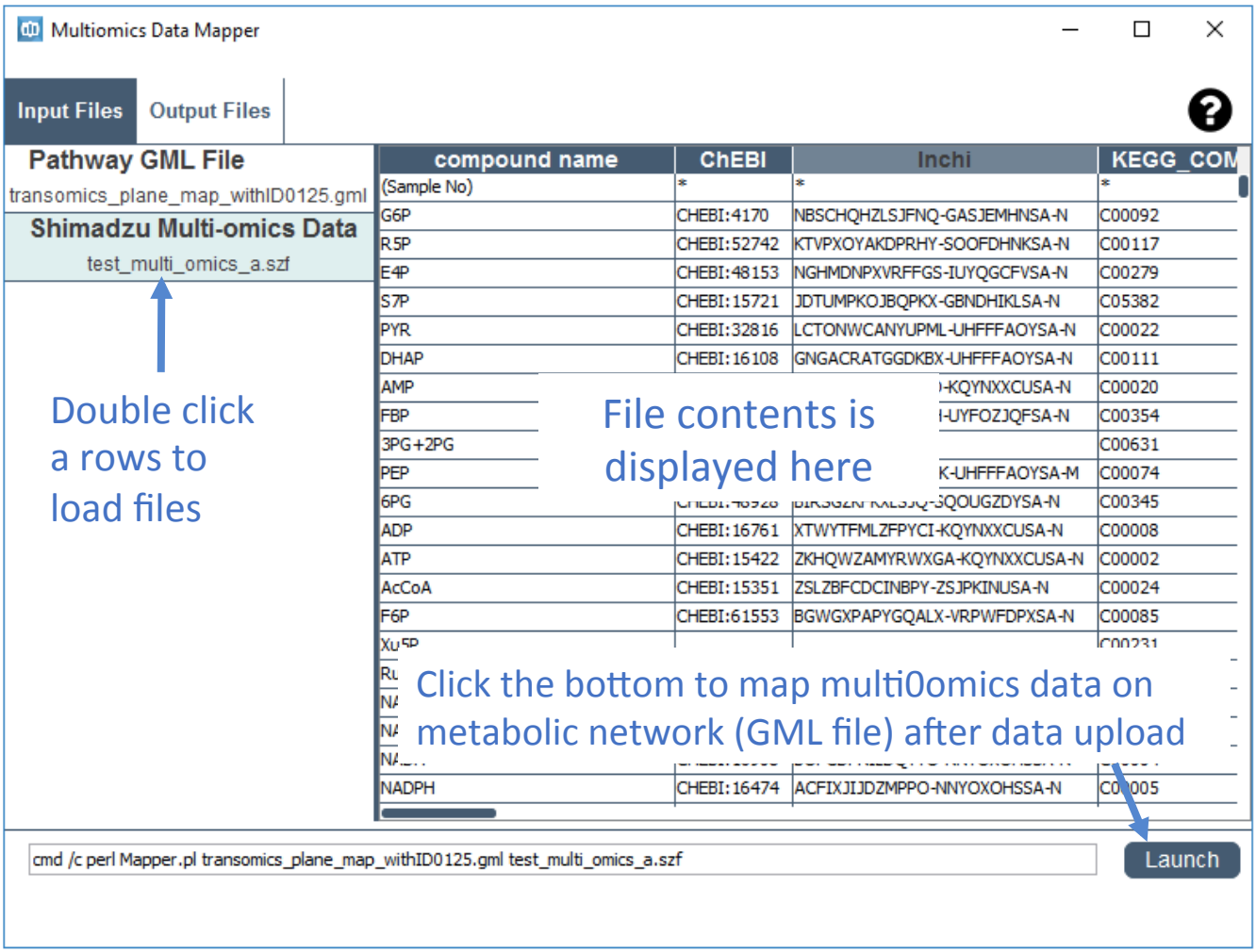
Multiomics Data Mapper (Input files)

This gadget merges Shimadzu multi-omics data with gml file of blank molecular pathway. The integrated gml file is used as input to VANTED gadget to visualize the multi-omics data on the molecular pathway map.



compound name	ChEBI	Inchi	KEGG_COM
(Sample No)	*	*	*
G6P	CHEBI:4170	NBSCHQHZLSJFNQ-GASJEMHNSA-N	C00092
R5P	CHEBI:52742	KTVPXOYAKDPRHY-SOOFDHNKSA-N	C00117
E4P	CHEBI:48153	NGHMDNPXVRFFGS-IUYQGCFVSA-N	C00279
S7P	CHEBI:15721	JDTUMPKOJBQPKX-GBNDHIKLSA-N	C05382
PYR	CHEBI:32816	LCTONWCANYUPML-UHFFFAOYSA-N	C00022
DHAP	CHEBI:16108	GNGACRATGGDKBX-UHFFFAOYSA-N	C00111
AMP		-KQYNXXCUSA-N	C00020
FBP		-UYFOZJQFSA-N	C00354
3PG+2PG			C00631
PEP		K-UHFFFAOYSA-M	C00074
6PG		-3QOUGZDYSA-N	C00345
ADP	CHEBI:16761	XTWYTFMLZFPYCI-KQYNXXCUSA-N	C00008
ATP	CHEBI:15422	ZKHQWZAMYRWXGA-KQYNXXCUSA-N	C00002
AcCoA	CHEBI:15351	ZSLZBFCDCINBPY-ZSJPKINUSA-N	C00024
F6P	CHEBI:61553	BGWGXPAPYGQALX-VRPWFDPXSA-N	C00085
NADPH	CHEBI:16474	ACFIXJIJDZMPPO-NNYOXOHSSA-N	C00005

The gadget require two input files;

(1) glm file for blank metabolic pathway map
(e.g., transomics_plane_map_withID0125.gml)

(2) Shimazu multi-omics dataset (e.g., test_multi_omics_a.szf)

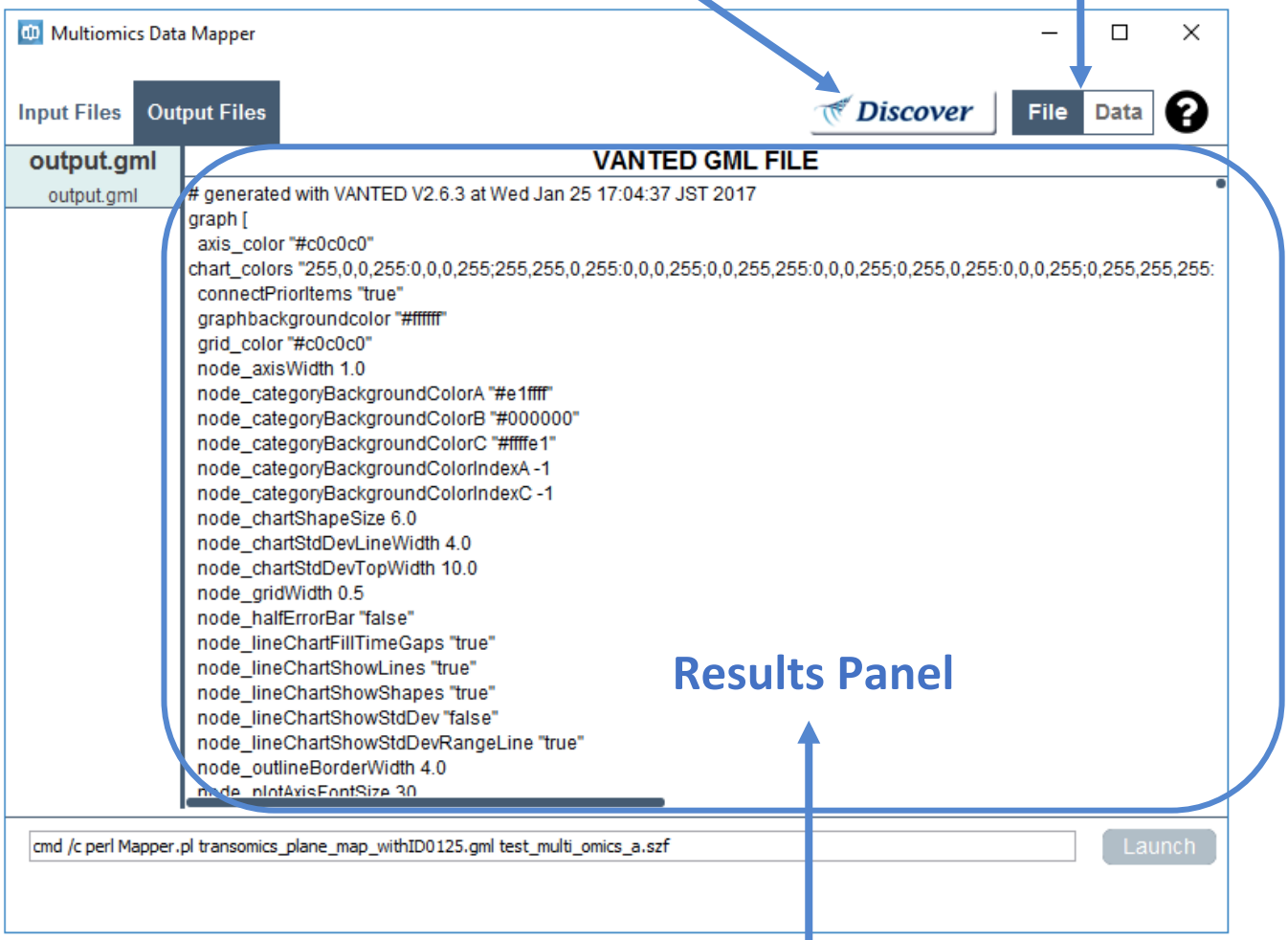
Sample File:
Sample file to test is available under **Samples > szf**

Requirement: The gadget requires, Anaconda > 2.5.0 (python > 3.5.1)

Multiomics Data Mapper (Output files)

1. Select whether you want to send the entire **File** or some **Data** to other gadgets

2. Click **Discover** to send data to other gadgets



Results Panel

Resultant merged gml is shown in the result panel