

Kidney Outcomes R01 data schema

1. The main table should include the Histocompatibility ID, the donor ID, and the high resolution HLA typing results from the NGS method

histocompatibility_ID	donor_ID	typing.recipient	typing.donor
integer	character	HLA typing data	HLA typing data

The typing data can be in various formats. Examples include:

- A. A column for HLA-A-allele 1, HLA-A-allele2, etc.
- B. A column with the full type at the A locus (HLA-A*02:01+HLA-A*68:01).
- C. One column each for recipient and donor, with a GL string for the full genotype.

2. If NGS is not available for each recipient and donor, then the full ambiguity strings from the intermediate resolution assay used. Examples:

- A. If LinkSeq RT-PCR data is available, I have provided code that will find the xml files created by the software and add the results to a table:

histocompatibility_ID	donor_ID	sample_type	ambiguities
integer	character	RT-PCR	A* 01:01:01:01, 01:02:01, 01:03:01:01;A* 01:01:01:03e-01:01:55e, 01:01:57e-01:01:121e, 01:02:02e, 01:03:01:02e-01:03:02e, 01:08e+A* 01:04:01:01Nd;A* 01:01:01:02Ne, 01:04:01:02Ne, 01:11Ne, 01:15Ne-01:16Ne, 01:18Ne, 01:22Ne, 01:27Ne+A* 01:06d, 01:09:01:01d

- B. If SSO data is available, I have provided code that will extract the ambiguity strings from Fusion.

study_ID	donor_ID	ReportableCommentsTxt	IMGT_version_A	IMGT_version_B	genotypes_A	genotypes_B
integer	character	"A*PYC:=:02:01/02:01L"	3.17.0	3.17.0	A*02:01/A*02:01L/A*02:01Q	B*35:01/B*35:07/B*35:30

3. Single antigen bead antibody data from One Lambda will be compiled from Fusion. I have provided code for this.

study_ID	days_post_Tx	SpecificityTxt	ModerateRiskAntibodyTxt	LowRiskAntibodyTxt	BeadID	RawData	NormalValue	Description	SpecAbbr	Specificity
integer	character	B:37 47	NA	NA	3	225.91	41.52	LABScreen Single Antigen Class I Lot 013	A1,-,-,-,- ,-,-	A*01:01,- ,-,-,-

4. Crossmatch data should include the raw values as reported by your lab.

study_ID	donor_ID	days_post_Tx	StatusCd.test	CellCd	RatioTxt	ResultCd
integer	character	-72	PRE	T	0.6	Negative