

Supplemental Table 1. A description of the published experimental data sets used in each figure, as well as the PRESTO settings used and the number of genes or proteins passing the pre-processing filters.

name	data type	platform	PRESTO settings	description	source
Human PBMCs after flu vaccination	Transcriptomics n = 20,898 genes	Affymetrix Human U133 Plus 2.0 Array	CoV ≥ 2 (=1298 genes; 1,875 for combined) perp = 50	PBMCs isolate from 33 patients at day 0, 3, and 7 after flu vaccination with the 2011 vaccine.	GSE74816
Peritoneal macrophages of 75 mouse strains	transcriptomics n = 13,699 genes	Affymetrix HT Mouse Genome 430A Array	CoV ≥ 1.5 (= 2,423 genes) perp = 50 (100 for combined analysis)	Peritoneal macrophages of 75 commercially available strains of the hybrid mouse diversity panel were elicited using thioglycollate for 4 days, harvested, and activated with 2ng/ml LPS or 50ug/ml oxPAPC in vitro for 4h or before sequencing.	GSE38705
Activated human macrophages	transcriptome 15798 genes	Illumina HumanHT-12 V4.0	CoV factor ≥ 1.8 (= 2083 genes) perp. = 50	Human monocyte-derived macrophages from one single donor (ficoll-concentrated PBMCs 10 days in culture) were activated in vitro using 33 different stimuli combinations.	GSE68854
Kidney transplant rejection, training set	transcriptomics n = 20,872 genes	Affymetrix Human Gene 1.0 ST Array	CoV ≥ 2.1 (= 1549 genes) perp = 30	Kidney transplant biopsies of patients with a healthy transplant (n=20) or with antibody-mediated rejection (n=28) as assessed by histology. The latter had a positive titer of donor-specific antibodies.	GSE50084
Kidney transplant rejection, test set	transcriptomics n = 20,647 genes	Affymetrix Human Genome U133 Plus 2.0 Array		Large dataset of kidney biopsy transcriptomes of patients with antibody-mediated rejection (n=65) or healthy status (n=281) confirmed by histology. Healthy nephrectomy samples (not transplanted) were used as controls (n=8).	GSE36059
Acute myeloid leukemia, training set	transcriptomics n = 18,308 genes	Illumina HumanHT-12 V4.0 expression beadchip	CoV ≥ 2.25 (= 1,474 genes) perp = 50	Bone marrow cells from 83 patients were sorted based on CD34/CD38 expression in fractions (n=227) and tested for leukemia stem cell (LSC) activity.	GSE76008
Acute myeloid leukemia, test set	transcriptomics n = 13,480 genes	Affymetrix Human Genome U133A Array		Peripheral blood mononuclear cells of untreated patients with cytogenetically normal acute myeloid leukemia were sequenced (n=163).	GSE12417
Clear cell renal carcinoma	proteomics n = 783 proteins	LTQ Orbitrap XL	CoV ≥ 1.03 (= 209 proteins) perp = 20	Tumor biopsies and adjacent normal tissue were taken from patients undergoing nephrectomy. Each sample was classified by histology. Stage 1 (n=17), stage 2 (n=20), stage 3 (n=21), stage 4 (n=26)	PMID 27128972