

Table SI. GEO microarray chip information.

Item	GSE30528	GSE30529	GSE30122	GSE96804
Platform	GPL571	GPL571	GPL571	GPL17586
Species	<i>Homo sapiens</i>	<i>Homo sapiens</i>	<i>Homo sapiens</i>	<i>Homo sapiens</i>
Tissue	Kidney	Kidney	Kidney	Kidney
Samples in DKD group	9	10	0	41
Samples in control group	13	12	25	20
References	PMID: 21752957	PMID: 21752957	PMID: 21752957 PMID: 26190114	PMID: 29242313 PMID: 30511699

DKD, diabetic kidney disease; GEO, Gene Expression Omnibus.

ID	Set size	Enrichment score	NES	P-value	P.adjust	Q-value
WP_TYROBP_CAUSAL_NETWORK_IN_MICROGLIA	50	8.12x10 ⁻¹	2.58	1.00x10 ⁻¹⁰	4.70x10 ⁻⁸	3.90x10 ⁻⁸
WP_EXTRAFOLLICULAR_B_CELL_ACTIVATION_BY_SARSCOV2	65	7.63x10 ⁻¹	2.53	1.00x10 ⁻¹⁰	4.70x10 ⁻⁸	3.90x10 ⁻⁸
WP_ALLOGRAFT_REJECTION	81	7.36x10 ⁻¹	2.52	1.00x10 ⁻¹⁰	4.70x10 ⁻⁸	3.90x10 ⁻⁸
KEGG_LEISHMANIA_INFECTION	67	7.24x10 ⁻¹	2.41	1.18x10 ⁻¹⁰	4.70x10 ⁻⁸	3.90x10 ⁻⁸
KEGG_ALLOGRAFT_REJECTION	33	8.22x10 ⁻¹	2.39	1.88x10 ⁻⁹	4.51x10 ⁻⁷	3.74x10 ⁻⁷
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	49	7.51x10 ⁻¹	2.38	2.30x10 ⁻⁹	4.74x10 ⁻⁷	3.93x10 ⁻⁷
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	106	6.62x10 ⁻¹	2.38	1.00x10 ⁻¹⁰	4.70x10 ⁻⁸	3.90x10 ⁻⁸
REACTOME_INTERLEUKIN_10_SIGNALING	43	7.48x10 ⁻¹	2.32	2.31x10 ⁻⁸	3.51x10 ⁻⁶	2.92x10 ⁻⁶
REACTOME_INTERFERON_GAMMA_SIGNALING	77	6.79x10 ⁻¹	2.32	1.36x10 ⁻⁹	4.07x10 ⁻⁷	3.38x10 ⁻⁷
KEGG_TYPE_I_DIABETES_MELLITUS	39	7.65x10 ⁻¹	2.31	1.52x10 ⁻⁸	2.60x10 ⁻⁶	2.16x10 ⁻⁶
KEGG_AUTOIMMUNE_THYROID_DISEASE	46	7.31x10 ⁻¹	2.31	2.44x10 ⁻⁸	3.51x10 ⁻⁶	2.92x10 ⁻⁶
WP_MICROGLIA_PATHOGEN_PHAGOCYTOSIS_PATHWAY	38	7.66x10 ⁻¹	2.30	2.64x10 ⁻⁸	3.51x10 ⁻⁶	2.92x10 ⁻⁶
KEGG_GRAFT_VERSUS_HOST_DISEASE	35	7.76x10 ⁻¹	2.29	8.20x10 ⁻⁸	8.29x10 ⁻⁶	6.88x10 ⁻⁶
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	70	6.73x10 ⁻¹	2.28	1.41x10 ⁻⁸	2.60x10 ⁻⁶	2.16x10 ⁻⁶
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	41	7.41x10 ⁻¹	2.28	1.81x10 ⁻⁷	1.50x10 ⁻⁵	1.24x10 ⁻⁵
WP_TYPE_II_INTERFERON_SIGNALING	36	7.61x10 ⁻¹	2.26	1.61x10 ⁻⁷	1.43x10 ⁻⁵	1.19x10 ⁻⁵
WP_INFLAMMATORY_RESPONSE_PATHWAY	29	7.41x10 ⁻¹	2.13	1.08x10 ⁻⁵	3.88x10 ⁻⁴	3.22x10 ⁻⁴
WP_IL18_SIGNALING_PATHWAY	244	4.59x10 ⁻¹	1.82	1.79x10 ⁻⁷	1.50x10 ⁻⁵	1.24x10 ⁻⁵
PID_IL12_PATHWAY	58	5.44x10 ⁻¹	1.79	1.07x10 ⁻³	1.89x10 ⁻²	1.57x10 ⁻²
WP_APOPTOSIS	81	5.02x10 ⁻¹	1.72	6.72x10 ⁻⁴	1.27x10 ⁻²	1.05x10 ⁻²

P.adjust, adjusted P-value; NES, normalized enrichment score.

Table SV. Results of Gene Set Variation Analysis for combined datasets.

ID	logFC	AveExpr	P-value	P.adjust
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP	5.24x10 ⁻¹	-1.13x10 ⁻¹	1.10x10 ⁻¹²	7.02x10 ⁻⁹
CHEOK_RESPONSE_TO_HD_MTX_UP	5.01 x10 ⁻¹	-8.70x10 ⁻²	7.56x10 ⁻¹⁰	1.20x10 ⁻⁶
SALVADOR_MARTIN_PEDIATRIC_TBD_ANTI_TNF_THERAPY_NONRESPOND ER_POST_TREATMENT_DN	5.32 x10 ⁻¹	-4.12x10 ⁻¹	4.15x10 ⁻⁹	2.40x10 ⁻⁶
FIGUEROA_AML_METHYLATION_CLUSTER_2_DN	6.19 x10 ⁻¹	-5.04x10 ⁻²	1.45x10 ⁻⁷	2.37x10 ⁻⁵
WP_LIPID_PARTICLES_COMPOSITION	-5.04x10 ⁻¹	2.83x10 ⁻²	2.96x10 ⁻⁷	3.85x10 ⁻⁵
BIOCARTA_SET_PATHWAY	5.24x10 ⁻¹	-2.19x10 ⁻²	3.41x10 ⁻⁷	4.18x10 ⁻⁵
VERRECCHIA_RESPONSE_TO_TGFB1_C4	5.14x10 ⁻¹	-5.64x10 ⁻²	8.65x10 ⁻⁷	7.56x10 ⁻⁵
REACTOME_BETA_DEFENSINS	5.33x10 ⁻¹	-1.48x10 ⁻¹	8.87x10 ⁻⁷	7.56x10 ⁻⁵
REACTOME_RUNX3_REGULATES_IMMUNE_RESPONSE_AND_CELL_MIGRAT ION	5.68x10 ⁻¹	-2.30x10 ⁻²	1.87x10 ⁻⁶	1.20x10 ⁻⁴
WP_ROBO4_AND_VEGF_SIGNALING_PATHWAYS_CROSSTALK	-5.03x10 ⁻¹	2.13x10 ⁻³	2.03x10 ⁻⁶	1.27x10 ⁻⁴
BIOCARTA_THelper_PATHWAY	5.27x10 ⁻¹	-9.78x10 ⁻²	2.08x10 ⁻⁶	1.28x10 ⁻⁴
BIOCARTA_TCYTOTOXIC_PATHWAY	5.39x10 ⁻¹	-9.25x10 ⁻²	2.17x10 ⁻⁶	1.33x10 ⁻⁴
BIOCARTA_MONOCYTE_PATHWAY	5.74x10 ⁻¹	-2.34x10 ⁻²	2.55x10 ⁻⁶	1.49x10 ⁻⁴
REACTOME_PHOSPHORYLATION_OF_EMI1	5.10x10 ⁻¹	-5.73x10 ⁻²	3.14x10 ⁻⁶	1.74x10 ⁻⁴
IM_SREBF1A_TARGETS	-5.71x10 ⁻¹	3.17 x10 ⁻³	3.93x10 ⁻⁶	1.99x10 ⁻⁴
BIOCARTA_LYMPHOCYTE_PATHWAY	5.72x10 ⁻¹	-1.61x10 ⁻²	4.17x10 ⁻⁶	2.03x10 ⁻⁴
FARMER_BREAST_CANCER_CLUSTER_4	5.01x10 ⁻¹	-3.80x10 ⁻²	5.96x10 ⁻⁶	2.60x10 ⁻⁴
ROETH_TERT_TARGETS_DN	5.62x10 ⁻¹	3.25x10 ⁻²	6.54x10 ⁻⁶	2.80x10 ⁻⁴
BIOCARTA_NEUTROPHIL_PATHWAY	5.86x10 ⁻¹	-2.70x10 ⁻²	6.59x10 ⁻⁶	2.80x10 ⁻⁴
FINETTI_BREAST_CANCER_KINOME_GREEN	5.11x10 ⁻¹	-5.14x10 ⁻²	6.69x10 ⁻⁶	2.82x10 ⁻⁴
BIOCARTA_TCAPOPTOSIS_PATHWAY	5.38x10 ⁻¹	-6.17x10 ⁻²	8.93x10 ⁻⁶	3.32x10 ⁻⁴
KASLER_HDAC7_TARGETS_2_UP	5.31x10 ⁻¹	-2.38x10 ⁻³	1.80x10 ⁻⁵	5.41x10 ⁻⁴
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_GRANUL OCYTE_DN	5.11x10 ⁻¹	5.09x10 ⁻³	5.95x10 ⁻⁵	1.31x10 ⁻³
TERAMOTO_OPN_TARGETS_CLUSTER_5	5.29x10 ⁻¹	4.58x10 ⁻³	4.82x10 ⁻⁴	5.82x10 ⁻³

P.adjust, adjusted P-value; FC, fold change; AveExpr, average expression.