

Table 1 GEO Microarray Chip Information

	GSE33774	GSE57631	GSE106090
Platform	GPL6244	GPL15034	GPL10558
Species	Homo sapiens	Homo sapiens	Homo sapiens
Tissue	Peri-Implant Tissue	Peri-Implant Tissue	Peri-Implant Tissue
Samples in PI Group	7	6	6
Samples in Control Group	8	2	6
Reference	PMID: 22967131	PMID: 25406169	PMID: 31853997

PI, Peri-Implantitis; GEO, Gene Expression Omnibus

Table 2 Results of GO and KEGG Enrichment Analysis for FRDEGs

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue
BP	GO:0048660	regulation of smooth muscle cell proliferation	7/32	170/18800	1.22E-08	1.24E-05	6.50E-06
BP	GO:0048659	smooth muscle cell proliferation	7/32	173/18800	1.37E-08	1.24E-05	6.50E-06
BP	GO:0070169	positive regulation of biomineral tissue development	5/32	52/18800	2.53E-08	1.26E-05	6.61E-06
BP	GO:0110151	positive regulation of biomineralization	5/32	53/18800	2.79E-08	1.26E-05	6.61E-06
BP	GO:0033002	muscle cell proliferation	7/32	233/18800	1.06E-07	3.84E-05	2.01E-05
CC	GO:0044754	autolysosome	3/32	11/19594	6.47E-07	7.96E-05	5.59E-05
CC	GO:0005767	secondary lysosome	3/32	17/19594	2.65E-06	1.63E-04	1.14E-04
CC	GO:0101002	ficolin-1-rich granule	4/32	185/19594	2.25E-04	9.22E-03	6.47E-03
CC	GO:0042470	melanosome	3/32	109/19594	7.39E-04	1.64E-02	1.15E-02
CC	GO:0048770	pigment granule	3/32	109/19594	7.39E-04	1.64E-02	1.15E-02
MF	GO:0005506	iron ion binding	4/32	151/18410	1.31E-04	1.47E-02	8.39E-03
MF	GO:0008199	ferric iron binding	2/32	11/18410	1.59E-04	1.47E-02	8.39E-03
MF	GO:0003756	protein disulfide isomerase activity	2/32	18/18410	4.40E-04	2.04E-02	1.16E-02
MF	GO:0016864	intramolecular oxidoreductase activity, transposing S-S bonds	2/32	18/18410	4.40E-04	2.04E-02	1.16E-02
MF	GO:0015106	bicarbonate transmembrane transporter activity	2/32	22/18410	6.62E-04	2.14E-02	1.22E-02
KEGG	hsa04216	Ferroptosis	5/28	41/8164	2.24E-07	3.88E-05	2.45E-05
KEGG	hsa04621	NOD-like receptor signaling pathway	6/28	184/8164	3.01E-05	1.74E-03	1.10E-03
KEGG	hsa04217	Necroptosis	5/28	159/8164	1.80E-04	6.80E-03	4.30E-03
KEGG	hsa04657	IL-17 signaling pathway	4/28	94/8164	2.73E-04	7.73E-03	4.89E-03
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	4/28	100/8164	3.46E-04	7.73E-03	4.89E-03

GO, Gene Ontology; BP, Biological Process; CC, Cellular Component; MF, Molecular Function; KEGG, Kyoto Encyclopedia of Genes and Genomes; FRDEGs, Ferroptosis-Related Differentially Expressed Genes

Table 3 Results of GSEA for Combined Datasets

ID	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues
WP_TYROBP_CAUSAL_NETWORK_IN_MICROGLIA	57	7.63E-01	2.58E+00	1.00E-10	1.43E-08	1.10E-08
WP_EXTRAFOLLICULAR_B_CELL_ACTIVATION_BY_SARSCOV2	65	7.47E-01	2.55E+00	1.00E-10	1.43E-08	1.10E-08
WP_COMPLEMENT_SYSTEM	91	6.86E-01	2.53E+00	1.00E-10	1.43E-08	1.10E-08
KEGG_LEISHMANIA_INFECTION	61	7.40E-01	2.51E+00	1.00E-10	1.43E-08	1.10E-08
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	125	6.46E-01	2.49E+00	1.00E-10	1.43E-08	1.10E-08
WP_COMPLEMENT_AND_COAGULATION_CASCADES	56	7.32E-01	2.47E+00	1.00E-10	1.43E-08	1.10E-08
REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	109	6.54E-01	2.46E+00	1.00E-10	1.43E-08	1.10E-08
REACTOME_INTERLEUKIN_10_SIGNALING	43	7.69E-01	2.45E+00	1.30E-10	1.76E-08	1.35E-08
WP_PHOTODYNAMIC_THERAPYINDUCED_NFKB_SURVIVAL_SIGNALING	32	8.11E-01	2.43E+00	2.70E-10	3.12E-08	2.39E-08
REACTOME_NEUTROPHIL_DEGRANULATION	421	5.59E-01	2.42E+00	1.00E-10	1.43E-08	1.10E-08
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	40	7.65E-01	2.40E+00	5.71E-10	6.03E-08	4.63E-08
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	65	6.99E-01	2.39E+00	1.78E-10	2.28E-08	1.75E-08
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	45	7.37E-01	2.37E+00	1.73E-08	1.24E-06	9.51E-07
WP_MICROGLIA_PATHOGEN_PHAGOCYTOSIS_PATHWAY	37	7.66E-01	2.37E+00	2.37E-09	2.05E-07	1.58E-07
PID_INTEGRIN2_PATHWAY	26	8.24E-01	2.36E+00	2.72E-08	1.83E-06	1.41E-06
KEGG_CELL_ADHESION_MOLECULES_CAMS	112	6.20E-01	2.35E+00	1.95E-10	2.36E-08	1.82E-08

WP_ALLOGRAFT_REJECTION	74	6.68E-01	2.35E+00	6.34E-10	6.41E-08	4.93E-08
PID_IL8_CXCR2_PATHWAY	33	7.13E-01	2.15E+00	9.67E-06	2.30E-04	1.77E-04
WP_CYTOKINES_AND_INFLAMMATORY_RESPONSE	24	7.63E-01	2.15E+00	5.99E-06	1.51E-04	1.16E-04
WP_IL1_AND_MEGAKARYOCYTES_IN_OBESITY	23	7.69E-01	2.14E+00	3.16E-06	8.81E-05	6.76E-05

GSEA, Gene Set Enrichment Analysis

Table 4 Results of GSVA for Combined Datasets

ID	logFC	AveExpr	p value	adj.p value
RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_UP	8.43E-01	-2.39E-02	5.01E-07	3.19E-03
WORSCHER_TUMOR_EVASION_AND_TOLEROGENICITY_DN	7.01E-01	-4.17E-02	1.52E-06	4.85E-03
BIOCARTA_D4GDI_PATHWAY	7.32E-01	5.16E-02	1.34E-05	2.42E-02
REACTOME_TRIF_MEDIATED_PROGRAMMED_CELL_DEATH	6.62E-01	-9.78E-02	2.67E-05	2.49E-02
REACTOME_FCGR_ACTIVATION	6.65E-01	-8.74E-02	3.22E-05	2.49E-02
PARK_OSTEOBLAST_DIFFERENTIATION_BY_PHENYLAMIL_DN	7.69E-01	1.67E-02	3.82E-05	2.49E-02
KUMAMOTO_RESPONSE_TO_NUTLIN_3A_UP	6.51E-01	2.58E-02	5.99E-05	2.92E-02
BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS	-6.63E-01	-2.12E-02	6.96E-05	2.92E-02
ZHAN_EARLY_DIFFERENTIATION_GENES_UP	8.79E-01	-7.44E-03	8.33E-05	3.04E-02
REACTOME_NEF_AND_SIGNAL_TRANSDUCTION	7.17E-01	8.37E-03	1.69E-04	3.20E-02
BIOCARTA_BBCELL_PATHWAY	6.92E-01	-2.78E-02	1.80E-04	3.20E-02
WP_PLATELETMEDIATED_INTERACTIONS	6.75E-01	-2.53E-02	1.88E-04	3.20E-02
FIGUEROA_AML_METHYLATION_CLUSTER_2_DN	6.55E-01	-1.08E-01	2.26E-04	3.42E-02
FINETTI_BREAST_CANCER_KINOME_GREEN	6.70E-01	-8.82E-02	3.00E-04	4.00E-02
GALI_TP53_TARGETS_APOPTOTIC_UP	6.57E-01	-1.31E-02	3.52E-04	4.14E-02
REACTOME_TRAIL_SIGNALING	6.62E-01	4.98E-02	3.87E-04	4.32E-02
BIOCARTA_NEUTROPHIL_PATHWAY	6.94E-01	-2.19E-02	4.74E-04	4.94E-02

GSVA, Gene Set Variation Analysis