

eTable 17. Significantly Enriched GO and KEGG Pathways in MAGMA gene-set analysis					
Pathway	BETA	BETA STD	SE	P. value	P. adjusted
KEGG_GRAFT_VERSUS_HOST_DISEASE	0.80421	0.03620	0.18227	5.15E-06	5.34E-04
KEGG_ALLOGRAFT_REJECTION	0.87341	0.03769	0.19902	5.74E-06	5.34E-04
KEGG_ASTHMA	0.79213	0.03046	0.19299	2.04E-05	1.06E-03
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.29747	0.03460	0.07293	2.27E-05	1.06E-03
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT	0.58064	0.02881	0.15609	1.00E-04	3.21E-03
KEGG_AUTOIMMUNE_THYROID_DISEASE	0.65235	0.03378	0.17578	1.04E-04	3.21E-03
KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.40452	0.02707	0.11551	2.32E-04	6.11E-03
KEGG_JAK_STAT_SIGNALING_PATHWAY	0.30169	0.02698	0.08725	2.73E-04	6.11E-03
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.32799	0.02482	0.09550	2.98E-04	6.11E-03
KEGG_CELL_ADHESION_MOLECULES_CAMS	0.32685	0.02697	0.09592	3.28E-04	6.11E-03
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.41921	0.02771	0.12764	5.12E-04	8.66E-03
KEGG_VIRAL_MYOCARDITIS	0.43679	0.02624	0.13510	6.14E-04	9.51E-03
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.27640	0.02326	0.09094	1.19E-03	1.70E-02
KEGG_PATHWAYS_IN_CANCER	0.16279	0.02125	0.05630	1.92E-03	2.55E-02
KEGG_TYPE_I_DIABETES_MELLITUS	0.47645	0.02257	0.17217	2.83E-03	3.51E-02
GOBP_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_I_MMUNOGLOBULIN_SUPERFAMILY_DOMAINS	0.25068	0.02863	0.06494	5.69E-05	9.51E-03
GOBP_ADAPTIVE_IMMUNE_RESPONSE	0.26839	0.03908	0.05294	2.01E-07	1.57E-04
GOBP_ADRENAL_GLAND_DEVELOPMENT	0.90934	0.03010	0.22835	3.43E-05	6.98E-03
GOBP_ALPHA_BETA_T_CELL_ACTIVATION	0.45471	0.03970	0.08783	1.14E-07	9.68E-05
GOBP_ALPHA_BETA_T_CELL_DIFFERENTIATION	0.58094	0.04312	0.10614	2.24E-08	3.26E-05
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	0.79750	0.02951	0.22606	2.10E-04	2.64E-02
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_PEPTIDE_ANTIGEN	0.97561	0.03064	0.25190	5.40E-05	9.33E-03
GOBP_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I_VIA_ER_PATHWAY	1.43680	0.02815	0.42177	3.30E-04	3.50E-02
GOBP_B_CELL_ACTIVATION	0.22397	0.02548	0.06528	3.02E-04	3.27E-02
GOBP_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	0.45331	0.03230	0.11058	2.08E-05	4.71E-03
GOBP_CD4_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	0.63943	0.04120	0.12319	1.06E-07	9.68E-05
GOBP_CD8_POSITIVE_ALPHA_BETA_T_CELL_DIFFERENTIATION	1.18740	0.03289	0.27949	1.08E-05	3.06E-03
GOBP_CELL_ACTIVATION	0.10000	0.02592	0.02873	2.50E-04	2.90E-02
GOBP_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN	1.07900	0.03294	0.28132	6.29E-05	1.00E-02
GOBP_CELL_FATE_COMMITMENT	0.28034	0.03189	0.06713	1.49E-05	3.73E-03
GOBP_CELL_FATE_SPECIFICATION	0.37314	0.02542	0.11129	4.01E-04	4.08E-02
GOBP_CELLULAR_RESPONSE_TO_X_RAY	1.00220	0.02571	0.28718	2.42E-04	2.87E-02
GOBP_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	0.17903	0.03554	0.03816	1.37E-06	6.80E-04
GOBP_CYTOKINE_PRODUCTION	0.17265	0.03322	0.03892	4.60E-06	1.80E-03
GOBP_DEFENSE_RESPONSE	0.10370	0.02903	0.02730	7.31E-05	1.10E-02
GOBP_DEMETHYLATION	0.49701	0.02985	0.12979	6.45E-05	1.01E-02
GOBP_DNA_METABOLIC_PROCESS	0.13184	0.02844	0.03389	5.04E-05	9.01E-03
GOBP_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	0.24864	0.02647	0.06963	1.78E-04	2.33E-02
GOBP_FOCAL_ADHESION_ASSEMBLY	0.36902	0.02484	0.11306	5.51E-04	4.92E-02
GOBP_GENE_SILENCING	0.22116	0.02597	0.06412	2.82E-04	3.16E-02
GOBP_IMMUNE_SYSTEM_DEVELOPMENT	0.13964	0.03098	0.03326	1.35E-05	3.62E-03
GOBP_INTERLEUKIN_10_PRODUCTION	0.48983	0.02662	0.14613	4.02E-04	4.08E-02
GOBP_INTERLEUKIN_21_PRODUCTION	4.54330	0.04759	0.84863	4.37E-08	5.57E-05
GOBP_ISOTYPE_SWITCHING_TO_IGG_ISOTYPES	1.27300	0.03398	0.31140	2.19E-05	4.85E-03
GOBP_LEUKOCYTE_DIFFERENTIATION	0.22122	0.03606	0.04602	7.74E-07	4.64E-04
GOBP_LUNG_EPITHELIUM_DEVELOPMENT	0.61704	0.02662	0.16942	1.36E-04	1.82E-02
GOBP_LUNG_SACCULE_DEVELOPMENT	1.27630	0.02673	0.32901	5.26E-05	9.24E-03
GOBP_LYMPHOCYTE_ACTIVATION	0.17335	0.03198	0.04037	8.82E-06	2.64E-03
GOBP_MACROPHAGE_ACTIVATION	0.36991	0.02650	0.10546	2.27E-04	2.73E-02
GOBP_MACROPHAGE_COLONY_STIMULATING_FACTOR_PRODUCTION	1.72440	0.02856	0.47290	1.33E-04	1.81E-02
GOBP_MONONUCLEAR_CELL_DIFFERENTIATION	0.22998	0.03324	0.05199	4.89E-06	1.81E-03
GOBP_MYELOID_CELL_DIFFERENTIATION	0.17211	0.02512	0.05015	3.00E-04	3.27E-02
GOBP_MYELOID_LEUKOCYTE_DIFFERENTIATION	0.24746	0.02539	0.07304	3.53E-04	3.71E-02
GOBP_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	0.11904	0.02440	0.03641	5.41E-04	4.92E-02
GOBP_NEGATIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.16060	0.04271	0.02774	3.59E-09	1.22E-05
GOBP_NEGATIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	0.15944	0.04367	0.02691	1.58E-09	8.05E-06
GOBP_NEGATIVE_REGULATION_OF_POSTTRANSCRIPTIONAL_GENE_SILENCING	0.72823	0.02411	0.20769	2.28E-04	2.73E-02
GOBP_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MIRNAS_INVOLVED_IN_GENE_SILENCING_BY_MIRNAS	0.89838	0.02576	0.25242	1.87E-04	2.39E-02
GOBP_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	0.17528	0.03644	0.03540	3.71E-07	2.52E-04
GOBP_PEPTIDYL_SERINE_MODIFICATION	0.19471	0.02537	0.05626	2.70E-04	3.09E-02

GOBP_PHENYLPROPANOID_METABOLIC_PROCESS	1.10870	0.02322	0.32127	2.80E-04	3.16E-02
GOBP_POSITIVE_REGULATION_OF_CELL_ACTIVATION	0.22929	0.03007	0.05716	3.03E-05	6.30E-03
GOBP_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	0.24329	0.02901	0.06376	6.82E-05	1.05E-02
GOBP_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	0.34826	0.02534	0.10471	4.41E-04	4.33E-02
GOBP_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	0.20760	0.03078	0.04988	1.58E-05	3.77E-03
GOBP_POSITIVE_REGULATION_OF_GENE_EXPRESSION	0.11043	0.02496	0.03264	3.58E-04	3.73E-02
GOBP_POSITIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	0.11589	0.02499	0.03480	4.35E-04	4.30E-02
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	0.63172	0.02766	0.17925	2.13E-04	2.65E-02
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_13_PRODUCTION	1.50500	0.03696	0.34996	8.58E-06	2.64E-03
GOBP_POSITIVE_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	1.63800	0.03639	0.37063	4.98E-06	1.81E-03
GOBP_POSITIVE_REGULATION_OF_ISOTYPE_SWITCHING_TO_IGG_ISOTYPES	1.50570	0.03345	0.40609	1.05E-04	1.49E-02
GOBP_POSITIVE_REGULATION_OF_LEUKOCYTE_CELL_CELL_ADHESION	0.28638	0.03134	0.06843	1.44E-05	3.73E-03
GOBP_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION	1.04280	0.03183	0.26475	4.11E-05	7.62E-03
GOBP_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	0.12376	0.03167	0.02939	1.28E-05	3.53E-03
GOBP_POSITIVE_REGULATION_OF_NUCLEOBASE_CONTAINING_COMPOUND_METABOLIC_PROCESS	0.12834	0.03802	0.02451	8.34E-08	8.50E-05
GOBP_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	0.10770	0.03248	0.02400	3.64E-06	1.48E-03
GOBP_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	0.30179	0.03041	0.07588	3.50E-05	6.98E-03
GOBP_POSITIVE_REGULATION_OF_PRI_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_II	0.56860	0.02627	0.16174	2.20E-04	2.70E-02
GOBP_POSITIVE_REGULATION_OF_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	0.56704	0.02845	0.15551	1.33E-04	1.81E-02
GOBP_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	0.13147	0.03162	0.03056	8.53E-06	2.64E-03
GOBP_POSITIVE_T_CELL_SELECTION	0.78411	0.03433	0.18781	1.50E-05	3.73E-03
GOBP_PRI_MIRNA_TRANSCRIPTION_BY_RNA_POLYMERASE_I	0.50530	0.02669	0.14203	1.88E-04	2.39E-02
GOBP_PRIMARY_MIRNA_PROCESSING	0.98200	0.02622	0.29885	5.09E-04	4.76E-02
GOBP_PROTEIN_PHOSPHORYLATION	0.10307	0.02854	0.02667	5.60E-05	9.51E-03
GOBP_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	0.27073	0.02541	0.08304	5.58E-04	4.95E-02
GOBP_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	0.52023	0.02373	0.15788	4.93E-04	4.67E-02
GOBP_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	0.34529	0.02486	0.10569	5.45E-04	4.92E-02
GOBP_REGULATION_OF_CD40_SIGNALING_PATHWAY	1.95860	0.03553	0.51884	8.03E-05	1.19E-02
GOBP_REGULATION_OF_CELL_CELL_ADHESION_MEDIATED_BY_INTEGRIN	1.39610	0.03429	0.36701	7.15E-05	1.09E-02
GOBP_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	0.11119	0.02954	0.02798	3.56E-05	6.98E-03
GOBP_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	0.42513	0.02475	0.12368	2.95E-04	3.26E-02
GOBP_REGULATION_OF_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY	1.44410	0.03025	0.36794	4.36E-05	7.94E-03
GOBP_REGULATION_OF_MULTICELLULAR_ORGANISMAL_DEVELOPMENT	0.09804	0.02484	0.02961	4.66E-04	4.48E-02
GOBP_REGULATION_OF_PRODUCTION_OF_SMALL_RNA_INVOLVED_IN_GENE_SILENCING_BY_RNA	0.72307	0.02676	0.20747	2.47E-04	2.89E-02
GOBP_REGULATION_OF_RESPONSE_TO_STRESS	0.09564	0.02450	0.02866	4.24E-04	4.24E-02
GOBP_REGULATORY_T_CELL_DIFFERENTIATION	0.75850	0.03175	0.19679	5.82E-05	9.57E-03
GOBP_RESPONSE_TO_CYTOKINE	0.12921	0.03087	0.03136	1.90E-05	4.40E-03
GOBP_RESPONSE_TO_INTERLEUKIN_2	1.23910	0.03178	0.33791	1.23E-04	1.72E-02
GOBP_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	0.41190	0.02436	0.12293	4.04E-04	4.08E-02
GOBP_T_CELL_ACTIVATION	0.20634	0.03212	0.04831	9.77E-06	2.85E-03
GOBP_T_CELL_DIFFERENTIATION	0.31408	0.03558	0.06687	1.33E-06	6.80E-04
GOBP_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	0.55191	0.03414	0.12660	6.56E-06	2.21E-03
GOBP_T_CELL_SELECTION	0.77151	0.03913	0.15964	6.80E-07	4.33E-04
GOBP_T_HELPER_17_TYPE_IMMUNE_RESPONSE	0.72671	0.02994	0.19516	9.85E-05	1.43E-02
GOBP_TRANSFORMING_GROWTH_FACTOR_BETA3_PRODUCT	2.05580	0.02637	0.52173	4.09E-05	7.62E-03
GOBP_TRANSFORMING_GROWTH_FACTOR_BETA_ACTIVATION	1.01810	0.02500	0.29833	3.22E-04	3.46E-02
GOBP_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCT	0.57390	0.02618	0.15913	1.56E-04	2.06E-02
GOCC_CHROMATIN	0.17923	0.04333	0.03216	1.27E-08	2.16E-05
GOCC_CHROMOSOME	0.12032	0.03467	0.02607	1.97E-06	8.37E-04
GOCC_LUMENAL_SIDE_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	1.38980	0.05144	0.23130	9.56E-10	8.05E-06
GOCC_LUMENAL_SIDE_OF_MEMBRANE	1.16940	0.04895	0.20939	1.19E-08	2.16E-05
GOCC_MHC_CLASS_II_PROTEIN_COMPLEX	1.66870	0.04623	0.35184	1.06E-06	6.00E-04
GOCC_MHC_PROTEIN_COMPLEX	1.36080	0.04725	0.26914	2.16E-07	1.57E-04
GOCC_SMAD_PROTEIN_COMPLEX	1.18730	0.02638	0.30848	5.96E-05	9.64E-03

GOMF_CHROMATIN_BINDING	0.14575	0.02406	0.04425	4.95E-04	4.67E-02
GOMF_CIS_REGULATORY_REGION_SEQUENCE_SPECIFIC_DNA_BINDING	0.12877	0.03124	0.03269	4.10E-05	7.62E-03
GOMF_CYTOKINE_RECEPTOR_BINDING	0.28993	0.03392	0.06967	1.59E-05	3.77E-03
GOMF_DEMETHYLASE_ACTIVITY	0.56374	0.02432	0.17023	4.65E-04	4.48E-02
GOMF_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	0.14712	0.03841	0.03140	1.40E-06	6.80E-04
GOMF_ENZYME_BINDING	0.09838	0.02975	0.02451	3.01E-05	6.30E-03
GOMF_INTERLEUKIN_1_RECEPTOR_ACTIVITY	2.06840	0.03752	0.44690	1.86E-06	8.24E-04
GOMF_INTERLEUKIN_2_RECEPTOR_BINDING	2.31340	0.03831	0.53129	6.72E-06	2.21E-03
GOMF_KINASE_ACTIVITY	0.12658	0.02407	0.03873	5.42E-04	4.92E-02
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	2.06980	0.04598	0.38876	5.14E-08	5.82E-05
GOMF_NADPLUS_NUCLEOSIDASE_ACTIVITY	1.50280	0.04163	0.34152	5.44E-06	1.91E-03
GOMF_SEQUENCE_SPECIFIC_DNA_BINDING	0.13196	0.03704	0.02844	1.76E-06	8.16E-04
GOMF_TAU_PROTEIN_KINASE_ACTIVITY	0.91823	0.03188	0.22846	2.93E-05	6.30E-03
GOMF_TRANSCRIPTION_FACTOR_BINDING	0.15474	0.02754	0.04159	9.95E-05	1.43E-02
GOMF_TRANSCRIPTION_REGULATOR_ACTIVITY	0.14704	0.04375	0.02638	1.27E-08	2.16E-05
GOMF_TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	0.11548	0.02396	0.03536	5.46E-04	4.92E-02
GOBP, Gene Ontology biological process; GOCC, Gene Ontology cellular component; GOMF, Gene Ontology molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes; SE, standard error;					
P.adjusted represents the FDR-corrected P value.					