

# **Allogenic faecal microbiota transfer induces immune-related gene sets in the colon mucosa of patients with irritable bowel syndrome**

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**Table S1: Differentially expressed genes two weeks after allogenic FMT compared to baseline.** Genes with a fold change >1.5 and < -1.5 and p<0.005 are shown.

Upregulated				Downregulated			
Gene name	Fold change	p-value	FDR	Gene name	Fold change	p-value	FDR
MFAP5	1.5	0.0021	0.509	SNORA3B	-2.3	0.0007	0.465
PIM2	1.5	0.0000	0.054	ZNF695	-1.7	0.0004	0.435
IGHV3-73	1.5	0.0034	0.542	LOC107984255	-1.6	0.0004	0.435
IGLV9-49	1.5	0.0034	0.542	SNORD65	-1.6	0.0014	0.484
LOC107986494	1.5	0.0015	0.484	MIR2276	-1.6	0.0009	0.467
LINC02499	1.5	0.0011	0.484	SNORA75	-1.6	0.0033	0.542
TPSB2	1.5	0.0000	0.410	SCARNA16	-1.6	0.0038	0.547
IGHV5-51	1.6	0.0030	0.542	OR5L2	-1.5	0.0006	0.465
SNHG28	1.6	0.0017	0.484	SNORD15A	-1.5	0.0003	0.435
IGLV3-1	1.6	0.0023	0.527	SCARNA8	-1.5	0.0005	0.465
NA	1.6	0.0029	0.542	LOC105378235	-1.5	0.0011	0.484
TRGV10	1.7	0.0005	0.436	LOC105378177	-1.5	0.0034	0.542
ZIM2	1.7	0.0003	0.435	LINC01811	-1.5	0.0004	0.435
LOC105372651	1.7	0.0043	0.560				
IGLV1-44	1.7	0.0044	0.560				
LOC107985535	1.7	0.0011	0.484				
IGHV1-18	1.9	0.0021	0.511				

*No individual genes were significantly differentially expressed (FDR<0.05). FDR- False discovery rate.*

**Table S2: Differentially expressed genes eight weeks after allogenic FMT compared to baseline.**  
Genes with a fold change >1.5 and < -1.5 and p<0.005 are shown.

Upregulated				Downregulated			
Gene name	Fold changes	p-value	FDR	Gene name	Fold changes	p-value	FDR
LINC00537	1.5	0.0019	0.976	LOC105369187	-2.2	0.0003	0.696
LINC01563	1.6	0.0000	0.293	LOC107985377	-2.1	0.0002	0.631
CST9LP1	1.6	0.0029	0.976	KRT8	-2.0	0.0017	0.976
ALG10B	1.7	0.0014	0.976	RPL39L	-1.9	0.0001	0.480
LOC105372255	1.7	0.0029	0.976	C9orf106	-1.7	0.0024	0.976
SPAG5-AS1	1.8	0.0016	0.976	ZNF695	-1.7	0.0004	0.840
LY6G6F	1.8	0.0011	0.976	LOC101927960	-1.7	0.0048	0.976
				LAGE3	-1.7	0.0017	0.976
				SCARNA11	-1.6	0.0026	0.976
				SCNM1	-1.5	0.0046	0.976
				TUBA4A	-1.5	0.0033	0.976
				CHRNA5	-1.5	0.0006	0.915

*No individual genes were significantly differentially expressed (FDR<0.05). FDR- False discovery rate.*

**Table S3: Differentially expressed genes two weeks after autologous FMT compared to baseline.**  
Genes with a fold change >1.5 and < -1.5 and p<0.005 are shown.

Upregulated				Downregulated			
Gene name	Fold changes	p-value	FDR	Gene name	Fold changes	p-value	FDR
CYP2C18	1.5	0.0048	0.395	RNA5SP99	-3.1	0.0011	0.310
LOC112268420	1.5	0.0011	0.310	LOC105369864	-2.1	0.0022	0.345
ANKRD34C-AS1	1.5	0.0036	0.364	SNORA35B	-2.0	0.0043	0.371
LINC02525	1.5	0.0006	0.310	MIR4774	-1.9	0.0006	0.310
CEACAM6	1.5	0.0000	0.273	HPF1	-1.9	0.0001	0.273
LOC105378093	1.6	0.0036	0.364	SNORA31	-1.9	0.0009	0.310
LGALS9C	1.6	0.0001	0.273	LINC02384	-1.8	0.0039	0.369
LOC105375896	1.6	0.0026	0.353	CLEC17A	-1.8	0.0028	0.353
TFF1	1.6	0.0002	0.298	RNU6-431P	-1.8	0.0003	0.301
ABHD17A	1.6	0.0010	0.310	BTLA	-1.8	0.0001	0.291
MIR1237	1.7	0.0007	0.310	TRBV20-1	-1.8	0.0045	0.380
MIR516A2	1.7	0.0023	0.345	SNORA18	-1.7	0.0002	0.298
CLEC18C	1.7	0.0022	0.345	LINC02211	-1.7	0.0027	0.353
LOC107984574	1.7	0.0005	0.310	PPP1R16B	-1.7	0.0002	0.298
MIR4427	1.9	0.0013	0.314	KIF5C	-1.7	0.0023	0.350
ZNF705G	2.0	0.0006	0.310	LOC105374318	-1.7	0.0001	0.273
				KRTAP9-4	-1.7	0.0016	0.330
				TAS2R20	-1.6	0.0012	0.310
				SLAMF1	-1.6	0.0006	0.310
				TRAJ27	-1.6	0.0018	0.343
				MIR2276	-1.6	0.0018	0.343
				SNORA50A	-1.6	0.0009	0.310
				SNORD90	-1.6	0.0004	0.310
				C7	-1.6	0.0018	0.343
				SNORA26	-1.6	0.0032	0.357
				LOC107984034	-1.6	0.0022	0.345
				MIR3145	-1.6	0.0029	0.353
				SNORD102	-1.6	0.0006	0.310
				SCARNA18	-1.5	0.0037	0.364
				SNORD19C	-1.5	0.0010	0.310
				SNORD31	-1.5	0.0003	0.301
				SNORA79	-1.5	0.0003	0.301
				SNORD9	-1.5	0.0023	0.345
				SNORD3K	-1.5	0.0042	0.371
				LOC105372733	-1.5	0.0015	0.317
				LOC105377901	-1.5	0.0014	0.317

*No individual genes were significantly differentially expressed (FDR<0.05). FDR- False discovery rate.*

**Table S4: Differentially expressed genes eight weeks after autologous FMT compared to baseline.**  
Genes with a fold change >1.5 and < -1.5 and p<0.005 are shown.

Upregulated				Downregulated			
Gene name	Fold changes	p-value	FDR	Gene name	Fold changes	p-value	FDR
ABHD17A	1.5	0.0046	0.198	LOC105369151	-2.4	0.0002	0.064
LRRC26	1.5	0.0014	0.123	TRAJ16	-2.4	0.0009	0.112
LOC339260	1.5	0.0003	0.080	IGLV1-47	-2.4	0.0024	0.155
ZNF443	1.5	0.0011	0.116	TRAJ19	-2.2	0.0004	0.088
PRSS53	1.5	0.0016	0.132	RNY1P11	-2.2	0.0000	0.039
FAM21EP	1.5	0.0036	0.179	IGLV3-21	-2.1	0.0000	0.039
RAB6C	1.5	0.0047	0.199	LOC107986275	-2.1	0.0000	0.026
LOC101929976	1.5	0.0018	0.139	DEFB108B	-2.0	0.0024	0.155
LOC100996643	1.5	0.0031	0.170	POU2AF1	-1.9	0.0001	0.050
PCAT6	1.5	0.0015	0.130	TRGV2	-1.9	0.0002	0.064
ANKRD34C-AS1	1.5	0.0027	0.164	SNORA3A	-1.9	0.0045	0.196
TMEM150B	1.5	0.0004	0.085	IGKV6-21	-1.9	0.0035	0.179
MIR25	1.5	0.0013	0.123	TRAJ14	-1.9	0.0035	0.178
TPSG1	1.5	0.0000	0.039	TRAT1	-1.9	0.0002	0.064
LOC105371044	1.6	0.0040	0.185	FAM30A	-1.9	0.0001	0.050
MIR3190	1.6	0.0012	0.120	ITK	-1.9	0.0000	0.037
HAVCR1	1.6	0.0010	0.113	TRAJ10	-1.9	0.0002	0.064
OR6B1	1.6	0.0017	0.137	TRAJ38	-1.8	0.0014	0.124
CLEC18C	1.6	0.0046	0.198	LOC105371932	-1.8	0.0000	0.039
CYP2C18	1.6	0.0009	0.112	IGLV3-25	-1.8	0.0003	0.080
LOC101927093	1.7	0.0022	0.151	LINC02211	-1.8	0.0005	0.094
LOC105370700	1.7	0.0014	0.125	BTLA	-1.8	0.0001	0.045
ACY3	1.7	0.0000	0.012	MIR4774	-1.8	0.0013	0.123
MIR4746	1.7	0.0034	0.177	IGKV3-11	-1.8	0.0001	0.050
OVCA2	1.8	0.0044	0.196	STAP1	-1.8	0.0014	0.124
LOC105378835	1.8	0.0009	0.112	TRAJ27	-1.8	0.0002	0.064
TRIM29	1.8	0.0001	0.053	SNORA23	-1.8	0.0038	0.185
GOLGA6L17P	1.8	0.0018	0.139	SLAMF1	-1.8	0.0001	0.045
LOC107983959	1.9	0.0009	0.112	PPP1R16B	-1.8	0.0000	0.039
LOC644277	1.9	0.0034	0.177	GPR15	-1.8	0.0000	0.012
LOC107985377	1.9	0.0009	0.112	IGKV4-1	-1.8	0.0000	0.012
LOC105374334	1.9	0.0020	0.145	IGLV1-40	-1.7	0.0002	0.068
LINC01080	1.9	0.0005	0.092	CHIT1	-1.7	0.0030	0.169
TFF1	2.0	0.0000	0.012	IGLV6-57	-1.7	0.0004	0.085
REG4	2.7	0.0000	0.039	GPR171	-1.7	0.0001	0.054
SPINK4	3.3	0.0002	0.071	LOC400464	-1.7	0.0002	0.072
OLFM4	3.5	0.0003	0.080	FCRL5	-1.7	0.0024	0.155
				SCARNA18	-1.7	0.0003	0.080
				SNORA31	-1.7	0.0024	0.155
				TRAV8-4	-1.7	0.0005	0.090
				TRAJ34	-1.7	0.0036	0.179
				TRBV30	-1.7	0.0032	0.172
				PTPRC	-1.7	0.0002	0.064
				IGHV3-72	-1.7	0.0000	0.043
				TRAJ36	-1.7	0.0011	0.116
				TRAJ35	-1.7	0.0008	0.110
				CD38	-1.7	0.0002	0.072
				IGKV1-5	-1.7	0.0003	0.084
				CD96	-1.7	0.0001	0.050
				TRAJ21	-1.7	0.0010	0.116

				IGHG4	-1.7	0.0010	0.114
				FCRL4	-1.7	0.0035	0.178
				IKZF3	-1.7	0.0012	0.119
				SCARNA1	-1.6	0.0029	0.166
				RHOH	-1.6	0.0009	0.112
				TRAJ30	-1.6	0.0025	0.160
				SNORA50A	-1.6	0.0004	0.088
				TNFRSF17	-1.6	0.0001	0.050
				IGKV3-7	-1.6	0.0001	0.061
				EVI2A	-1.6	0.0001	0.050
				TRAJ20	-1.6	0.0015	0.130
				SNORD3K	-1.6	0.0010	0.114
				CGB8	-1.6	0.0049	0.203
				LRRC37B	-1.6	0.0013	0.122
				IGKV1-17	-1.6	0.0000	0.037
				CD69	-1.6	0.0021	0.147
				SNORD115-32	-1.6	0.0021	0.147
				RNY1P13	-1.6	0.0036	0.179
				GCSAM	-1.6	0.0009	0.112
				TRAJ41	-1.6	0.0015	0.130
				IGHV3-15	-1.6	0.0000	0.039
				LOC101928354	-1.6	0.0039	0.185
				RNU4ATAC	-1.6	0.0024	0.155
				KHDRBS2	-1.6	0.0000	0.039
				RUNX1-IT1	-1.6	0.0019	0.141
				KLRB1	-1.6	0.0011	0.116
				LAX1	-1.6	0.0002	0.064
				SNORA18	-1.6	0.0009	0.112
				IKZF1	-1.6	0.0016	0.133
				TRBC2	-1.6	0.0027	0.164
				IGKV3-15	-1.6	0.0034	0.176
				TIFAB	-1.6	0.0006	0.101
				LOC101929272	-1.6	0.0002	0.072
				CD48	-1.6	0.0012	0.122
				CD180	-1.6	0.0038	0.185
				TRAJ47	-1.6	0.0040	0.185
				IGKV1-27	-1.5	0.0028	0.164
				TAS2R19	-1.5	0.0012	0.119
				LOC107985224	-1.5	0.0016	0.132
				LOC105378235	-1.5	0.0016	0.134
				CCDC69	-1.5	0.0000	0.038
				MIR4742	-1.5	0.0004	0.087
				IGLV8-61	-1.5	0.0016	0.133
				MIR4755	-1.5	0.0040	0.185
				TRAJ6	-1.5	0.0044	0.196
				GPR65	-1.5	0.0003	0.084
				SNORD111	-1.5	0.0001	0.061
				LRRN3	-1.5	0.0004	0.087
				ST8SIA4	-1.5	0.0001	0.050
				IGKJ3	-1.5	0.0001	0.064
				ITGB7	-1.5	0.0001	0.061
				RASSF2	-1.5	0.0002	0.064
				LILRB4	-1.5	0.0018	0.139
				ARHGAP15	-1.5	0.0001	0.061
				EMB	-1.5	0.0002	0.064

				CD53	-1.5	0.0011	0.116
				ZMAT1	-1.5	0.0018	0.138
				CD226	-1.5	0.0002	0.064
				MRPL42P5	-1.5	0.0031	0.170
				LOC374443	-1.5	0.0010	0.113
				SNRPA1	-1.5	0.0031	0.170

*No individual genes were significantly differentially expressed (FDR<0.05). FDR- False discovery rate.*

**Table S5: Significantly differentially expressed genes after multiple testing eight weeks after autologous FMT compared to baseline.** Genes with a fold change >1.5 and < -1.5 and FDR<0.05 are shown.

Upregulated				Downregulated			
Gene name	Fold changes	p-value	FDR	Gene name	Fold change	p-value	FDR
TPSG1	1.5	0.0000	0.039	RNY1P11	-2.2	0.0000	0.039
ACY3	1.7	0.0000	0.012	IGLV3-21	-2.1	0.0000	0.039
TFF1	2.0	0.0000	0.012	LOC107986275	-2.1	0.0000	0.026
REG4	2.7	0.0000	0.039	POU2AF1	-1.9	0.0001	0.050
				FAM30A	-1.9	0.0001	0.050
				ITK	-1.9	0.0000	0.037
				LOC105371932	-1.8	0.0000	0.039
				BTLA	-1.8	0.0001	0.045
				IGKV3-11	-1.8	0.0001	0.050
				SLAMF1	-1.8	0.0001	0.045
				PPP1R16B	-1.8	0.0000	0.039
				GPR15	-1.8	0.0000	0.012
				IGKV4-1	-1.8	0.0000	0.012
				IGHV3-72	-1.7	0.0000	0.043
				CD96	-1.7	0.0001	0.050
				TNFRSF17	-1.6	0.0001	0.050
				EVI2A	-1.6	0.0001	0.050
				IGKV1-17	-1.6	0.0000	0.037
				IGHV3-15	-1.6	0.0000	0.039
				KHDRBS2	-1.6	0.0000	0.039
				CCDC69	-1.5	0.0000	0.038
				ST8SIA4	-1.5	0.0001	0.050

*Genes with an FDR<0.05 were considered to be significantly differentially expressed. FDR – False Discovery Rate*



**Table S6: Differentially expressed genes when comparing the allogenic group to the autologous group two weeks after FMT (baseline-corrected).** Genes with a fold change >1.5 and < -1.5 and p<0.005 are shown.

Increased				Decreased			
Gene name	Fold changes	p-value	FDR	Gene name	Fold changes	p-value	FDR
LOC105369623	1.5	0.005	0.484	ADAMTS7P1	-2.3	0.004	0.476
PIM2	1.5	0.001	0.437	CCL27	-2.2	0.003	0.458
MAGEH1	1.5	0.003	0.463	ANKRD34C-AS1	-2.1	0.000	0.430
LOC100507557	1.5	0.003	0.463	LOC105375368	-2.0	0.002	0.437
BRD3OS	1.5	0.002	0.437	LOC105378093	-2.0	0.002	0.437
ZKSCAN3	1.5	0.002	0.437	HSFX4	-2.0	0.004	0.463
RPS15AP10	1.5	0.001	0.437	LINC01811	-1.9	0.000	0.430
IGKV1-17	1.5	0.002	0.437	LOC105369199	-1.9	0.001	0.437
LOC105375079	1.5	0.004	0.463	TFF1	-1.9	0.000	0.430
ST8SIA4	1.5	0.003	0.443	LOC107984574	-1.8	0.004	0.463
EAF2	1.5	0.004	0.463	C8orf76	-1.8	0.004	0.476
MS4A7	1.5	0.001	0.437	LGALS9C	-1.8	0.000	0.430
CD27	1.5	0.003	0.463	DHRS9	-1.8	0.002	0.437
PDE1B	1.5	0.003	0.456	LINC02073	-1.8	0.002	0.437
GPR15	1.5	0.003	0.451	LOC105375577	-1.7	0.001	0.437
NYX	1.5	0.004	0.463	OR2G6	-1.7	0.000	0.430
AFF3	1.5	0.004	0.463	ERVH48-1	-1.7	0.004	0.463
DDX28	1.5	0.000	0.430	PRODH	-1.7	0.001	0.437
SORCS1	1.5	0.002	0.437	LOC105378662	-1.7	0.001	0.436
MANEA	1.5	0.000	0.430	CYP1B1-AS1	-1.7	0.004	0.463
LYPD3	1.5	0.002	0.437	FRG2DP	-1.7	0.001	0.437
ALDH1A3	1.5	0.002	0.437	LINC02393	-1.7	0.001	0.437
OR4B1	1.6	0.001	0.437	PROB1	-1.7	0.002	0.437
CDK14	1.6	0.003	0.463	PEBP4	-1.7	0.001	0.437
C11orf53	1.6	0.001	0.437	MIR200A	-1.7	0.001	0.437
LOC101927516	1.6	0.003	0.443	LOC102723548	-1.7	0.000	0.430
MIR577	1.6	0.003	0.442	ESPNP	-1.7	0.001	0.437
SERPINI1	1.6	0.003	0.442	CEACAM6	-1.7	0.000	0.430
NCKAP1L	1.6	0.002	0.437	LINC01143	-1.6	0.001	0.437
TPSB2	1.6	0.002	0.437	CBY3	-1.6	0.001	0.437
RASGRP1	1.6	0.002	0.437	MTCL1	-1.6	0.003	0.443
EMB	1.6	0.002	0.437	LINC00029	-1.6	0.004	0.470
IPCEF1	1.6	0.003	0.442	HPCAL4	-1.6	0.002	0.437
RASSF2	1.6	0.002	0.437	HBE1	-1.6	0.005	0.484
KLRD1	1.6	0.001	0.437	PCAT29	-1.6	0.002	0.437
LAPTM5	1.6	0.002	0.437	YY2	-1.6	0.004	0.463
GPR65	1.6	0.003	0.451	LOC105376433	-1.6	0.003	0.442
RRP7BP	1.6	0.003	0.463	TRIM9	-1.6	0.002	0.437
CD226	1.6	0.001	0.437	TMEM150B	-1.6	0.004	0.463
GNB4	1.6	0.002	0.437	LINC02369	-1.6	0.005	0.484
GLIPR1	1.6	0.001	0.437	MIR520F	-1.6	0.003	0.442
MS4A4A	1.6	0.002	0.437	LINC02304	-1.6	0.000	0.430
PLEKHF1	1.6	0.002	0.437	GAS1RR	-1.6	0.001	0.437
LOC105370765	1.6	0.001	0.437	PLA2G2C	-1.6	0.000	0.430
P2RY12	1.7	0.001	0.437	PABPC1L2A	-1.6	0.004	0.463
NLRC4	1.7	0.000	0.430	FTH1	-1.6	0.001	0.437
CD96	1.7	0.002	0.442	TRAV8-7	-1.5	0.002	0.437
IGKV4-1	1.7	0.000	0.430	LOC107985285	-1.5	0.001	0.437
LCP1	1.7	0.005	0.482	LINC01664	-1.5	0.002	0.437

LINC01948	1.7	0.002	0.437	LOC105376395	-1.5	0.005	0.482
P2RY13	1.7	0.003	0.451	C11orf87	-1.5	0.004	0.463
FABP3	1.7	0.001	0.437	MIR3178	-1.5	0.001	0.437
GFRA2	1.7	0.001	0.437	VCX3B	-1.5	0.003	0.463
LOC441239	1.7	0.004	0.463	PHACTR3	-1.5	0.002	0.437
ITGB7	1.7	0.000	0.430	LOC102724589	-1.5	0.001	0.437
RHEX	1.7	0.002	0.437	C17orf98	-1.5	0.002	0.437
TRAJ4	1.8	0.004	0.463	KLC3	-1.5	0.001	0.436
LOC105376287	1.8	0.001	0.437	LINC01395	-1.5	0.002	0.437
SCN1A-AS1	1.8	0.001	0.437	LOC105379010	-1.5	0.004	0.463
LRRN3	1.8	0.001	0.437	LOC107984414	-1.5	0.000	0.430
TRBJ2-3	1.8	0.002	0.437				
SLAMF1	1.8	0.002	0.437				
GPR155	1.8	0.000	0.430				
ITK	1.8	0.001	0.437				
ANKRD30B	1.8	0.004	0.463				
IGKV1-5	1.8	0.002	0.437				
BTLA	1.8	0.002	0.437				
KIRREL1-IT1	1.8	0.000	0.430				
FAM30A	1.8	0.003	0.463				
GPR171	1.8	0.001	0.437				
LOC107986412	1.9	0.000	0.430				
IGKV3-11	1.9	0.001	0.437				
LILRB4	1.9	0.001	0.437				
LRRC37B	1.9	0.002	0.437				
MIR3161	1.9	0.001	0.437				
LOC105372733	2.0	0.000	0.430				
PPP1R16B	2.0	0.000	0.430				
RNY1P11	2.0	0.004	0.463				
IGLV9-49	2.0	0.002	0.437				
MIR181A1HG	2.0	0.004	0.464				
TRAT1	2.0	0.002	0.437				
MIR4774	2.0	0.004	0.463				
ZNF382	2.1	0.003	0.463				
TRGV10	2.1	0.001	0.437				
ZIM2	2.2	0.000	0.430				
TRBV20-1	2.3	0.002	0.437				
LINC02211	2.3	0.000	0.430				
TRAJ40	2.3	0.005	0.484				
IGHV1-18	2.4	0.005	0.484				

*No individual genes were significantly differentially expressed (FDR<0.05). FDR- False discovery rate.*

**Table S7: Differentially expressed genes when comparing the allogenic group to the autologous group eight weeks after FMT (baseline-corrected).** Genes with a fold change >1.5 and < -1.5 and p<0.005 are shown.

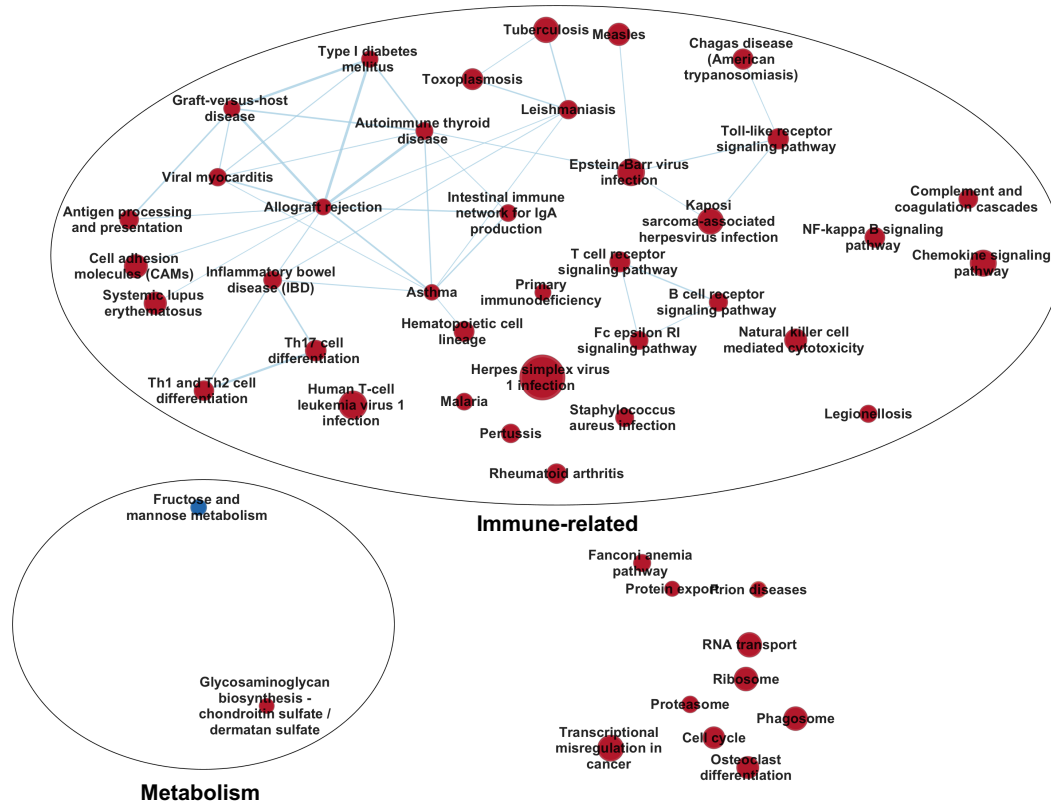
Increased				Decreased			
Gene name	Fold changes	p-value	FDR	Gene name	Fold changes	p-value	FDR
ARHGAP15	1.5	0.0044	0.406	OLFM4	-5.0	0.0008	0.300
GMFG	1.5	0.0038	0.395	LOC107985377	-4.0	0.0000	0.062
MXRA5	1.5	0.0001	0.182	SPINK4	-3.6	0.0027	0.372
TRAM1L1	1.5	0.0013	0.324	REG4	-3.3	0.0001	0.183
KHDRBS2	1.5	0.0040	0.396	LOC105374334	-3.1	0.0002	0.215
GIMAP7	1.5	0.0037	0.395	LOC644277	-2.6	0.0016	0.324
LOC112268039	1.5	0.0032	0.386	MIR4746	-2.5	0.0006	0.281
FAM126A	1.5	0.0011	0.320	C9orf106	-2.4	0.0009	0.300
ADPGK-AS1	1.5	0.0010	0.306	LOC105369187	-2.4	0.0031	0.386
LOC284581	1.5	0.0044	0.406	LOC101927960	-2.3	0.0026	0.364
MZB1	1.5	0.0024	0.346	LOC101927851	-2.2	0.0024	0.347
P2RY12	1.5	0.0045	0.412	TFF1	-2.1	0.0001	0.182
ZNF431	1.5	0.0010	0.306	LAGE3	-2.1	0.0018	0.333
NOX4	1.5	0.0020	0.337	RPL39L	-2.0	0.0024	0.346
TXK	1.5	0.0043	0.406	GSDME	-1.9	0.0021	0.337
NA	1.5	0.0043	0.406	LOC101929976	-1.9	0.0011	0.320
JAML	1.5	0.0004	0.230	ARHGEF39	-1.8	0.0005	0.264
SLC14A2	1.5	0.0028	0.376	GNMT	-1.8	0.0015	0.324
RNU6-744P	1.5	0.0048	0.416	LOC107984461	-1.8	0.0008	0.300
LRRK2	1.5	0.0014	0.324	MIR3190	-1.8	0.0031	0.386
C14orf132	1.5	0.0009	0.300	FNDC10	-1.8	0.0002	0.196
LAPTM5	1.5	0.0035	0.390	IQGAP3	-1.7	0.0040	0.396
SORCS1	1.5	0.0020	0.337	TPSG1	-1.7	0.0001	0.196
CCDC69	1.5	0.0007	0.300	ITLN1	-1.7	0.0023	0.346
PIP4K2A	1.5	0.0002	0.196	LOC107986870	-1.7	0.0019	0.337
TMEM183A	1.6	0.0020	0.337	PDGFRL	-1.7	0.0016	0.324
KCNQ5-IT1	1.6	0.0016	0.325	EP300-AS1	-1.7	0.0027	0.372
INHBE	1.6	0.0013	0.324	KIF18B	-1.7	0.0032	0.386
RPS15AP10	1.6	0.0005	0.264	PCAT29	-1.7	0.0008	0.300
ARHGAP25	1.6	0.0046	0.414	LOC105370772	-1.7	0.0000	0.088
TM6SF1	1.6	0.0031	0.386	SLPI	-1.7	0.0000	0.158
ATP6V1C2	1.6	0.0008	0.300	TMEM125	-1.7	0.0001	0.183
NCKAP1L	1.6	0.0019	0.337	LINC02089	-1.6	0.0021	0.337
ZNF571-AS1	1.6	0.0048	0.416	LOC105373728	-1.6	0.0049	0.420
CD226	1.6	0.0021	0.337	ALDH1L1	-1.6	0.0015	0.324
ST8SIA4	1.6	0.0014	0.324	ACY3	-1.6	0.0003	0.229
ZNF197-AS1	1.6	0.0009	0.300	LINC02408	-1.6	0.0039	0.395
IGKJ3	1.6	0.0021	0.337	LOC105375172	-1.6	0.0028	0.378
NFYC-AS1	1.6	0.0045	0.411	LOC105376433	-1.6	0.0018	0.333
IGHM	1.6	0.0005	0.264	FAHD2A	-1.6	0.0037	0.395
KANSL1-AS1	1.6	0.0002	0.196	CEACAM16	-1.6	0.0004	0.230
LOC105379012	1.6	0.0003	0.229	VPREB1	-1.6	0.0035	0.390
PLCG2	1.6	0.0022	0.343	LOC105376434	-1.6	0.0024	0.347
LOC105369759	1.6	0.0009	0.300	LINC00159	-1.6	0.0022	0.343
CST7	1.6	0.0014	0.324	LOC105372330	-1.6	0.0016	0.325
OR52W1	1.6	0.0023	0.346	LOC102723539	-1.6	0.0038	0.395
LOC101928202	1.6	0.0015	0.324	CRIM1-DT	-1.6	0.0013	0.324
LINC01563	1.6	0.0031	0.386	KLK1	-1.6	0.0003	0.229
DTHD1	1.6	0.0006	0.281	ASRGL1	-1.5	0.0015	0.324
ANKRD36BP2	1.6	0.0003	0.229	LOC401040	-1.5	0.0017	0.327

MIAT	1.6	0.0035	0.390	MRAP2	-1.5	0.0032	0.386
COLQ	1.6	0.0042	0.401	GDPD3	-1.5	0.0012	0.323
MIR1231	1.6	0.0009	0.300	LOC105374454	-1.5	0.0042	0.401
LYPD3	1.6	0.0009	0.300	LOC105375074	-1.5	0.0046	0.413
PAN3-AS1	1.6	0.0003	0.230	GSTM2P1	-1.5	0.0041	0.397
APBB1IP	1.6	0.0047	0.416	THEM6	-1.5	0.0018	0.333
LOC374443	1.6	0.0039	0.395	ENTPD3-AS1	-1.5	0.0021	0.337
IGHG2	1.6	0.0033	0.388	IL9R	-1.5	0.0032	0.386
IGHJ2	1.6	0.0000	0.158				
IGHV3-23	1.6	0.0021	0.337				
RNU6-1048P	1.6	0.0015	0.324				
LINC02531	1.6	0.0047	0.416				
LDOC1	1.6	0.0022	0.339				
LAX1	1.6	0.0020	0.337				
MIR514B	1.6	0.0017	0.333				
IGKV1-17	1.6	0.0004	0.235				
LINC01948	1.6	0.0039	0.395				
IL10	1.6	0.0003	0.229				
IGKV2D-24	1.7	0.0017	0.333				
ZNF300P1	1.7	0.0015	0.324				
LOC101928721	1.7	0.0004	0.230				
RASGRP1	1.7	0.0005	0.264				
ACTR3-AS1	1.7	0.0013	0.324				
SCN1A-AS1	1.7	0.0021	0.337				
GFRA2	1.7	0.0009	0.300				
ST3GAL6	1.7	0.0012	0.322				
CCDC141	1.7	0.0038	0.395				
LOC105372733	1.7	0.0020	0.337				
GPR15	1.7	0.0003	0.224				
LCP1	1.7	0.0034	0.388				
CD38	1.7	0.0037	0.395				
STK33	1.7	0.0033	0.388				
LINC02189	1.7	0.0009	0.300				
EMB	1.7	0.0003	0.224				
LOC100507599	1.7	0.0005	0.264				
CD96	1.7	0.0012	0.323				
CD27	1.8	0.0002	0.197				
THEMIS	1.8	0.0045	0.411				
MEOX2	1.8	0.0011	0.317				
DISC1	1.8	0.0015	0.324				
CCL18	1.8	0.0033	0.388				
IGHV3-72	1.8	0.0007	0.300				
IGKV1-5	1.8	0.0024	0.346				
TRBC2	1.8	0.0040	0.396				
PTPRC	1.8	0.0016	0.324				
RASSF2	1.8	0.0001	0.183				
IGKV4-1	1.8	0.0001	0.182				
GPR171	1.8	0.0011	0.317				
TIFAB	1.8	0.0006	0.281				
IGLV1-40	1.9	0.0022	0.339				
TRAJ35	1.9	0.0035	0.390				
TRAJ47	1.9	0.0032	0.386				
LOC105375724	1.9	0.0049	0.420				
ITGB7	1.9	0.0000	0.169				
BTLA	1.9	0.0011	0.317				
TRAJ6	1.9	0.0021	0.337				

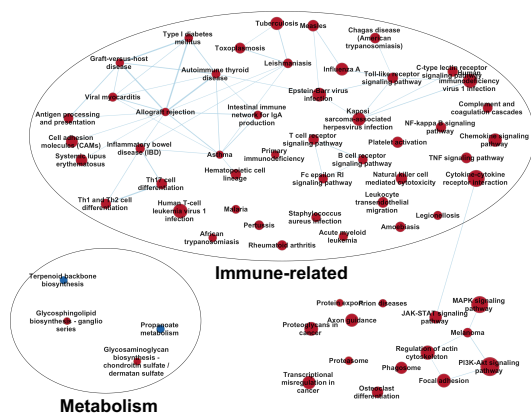
IKZF3	1.9	0.0023	0.346				
TRAV8-4	1.9	0.0018	0.333				
MIR3115	2.0	0.0017	0.333				
LILRB4	2.0	0.0003	0.230				
IGKV3-7	2.0	0.0001	0.183				
PPP1R16B	2.0	0.0002	0.197				
IGKV3-11	2.0	0.0004	0.232				
TRAJ10	2.0	0.0015	0.324				
LRRC37B	2.0	0.0006	0.281				
POU2AF1	2.0	0.0014	0.324				
TNXB	2.0	0.0006	0.264				
LOC105371264	2.0	0.0031	0.386				
LINC02211	2.1	0.0019	0.337				
TRAJ38	2.1	0.0048	0.416				
ALG10B	2.1	0.0014	0.324				
ITK	2.2	0.0000	0.158				
IGLV3-21	2.2	0.0005	0.264				
LOC105371932	2.2	0.0001	0.182				
RHOQ	2.2	0.0037	0.395				
SPAG5-AS1	2.3	0.0015	0.324				
TRAV29DV5	2.3	0.0010	0.306				
CGB8	2.3	0.0005	0.264				
LOC107986275	2.3	0.0001	0.182				
TRAT1	2.4	0.0002	0.197				
FAM209A	2.5	0.0035	0.390				
RNY1P11	2.7	0.0001	0.183				
LOC105369151	3.7	0.0001	0.183				

*No individual genes were significantly differentially expressed (FDR<0.05). FDR- False discovery rate.*

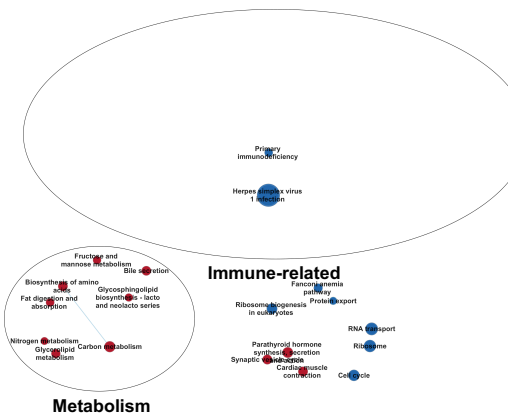
## A. Allogenic versus autologous FMT (two weeks after)



## B. Allogenic FMT (two weeks after vs baseline)

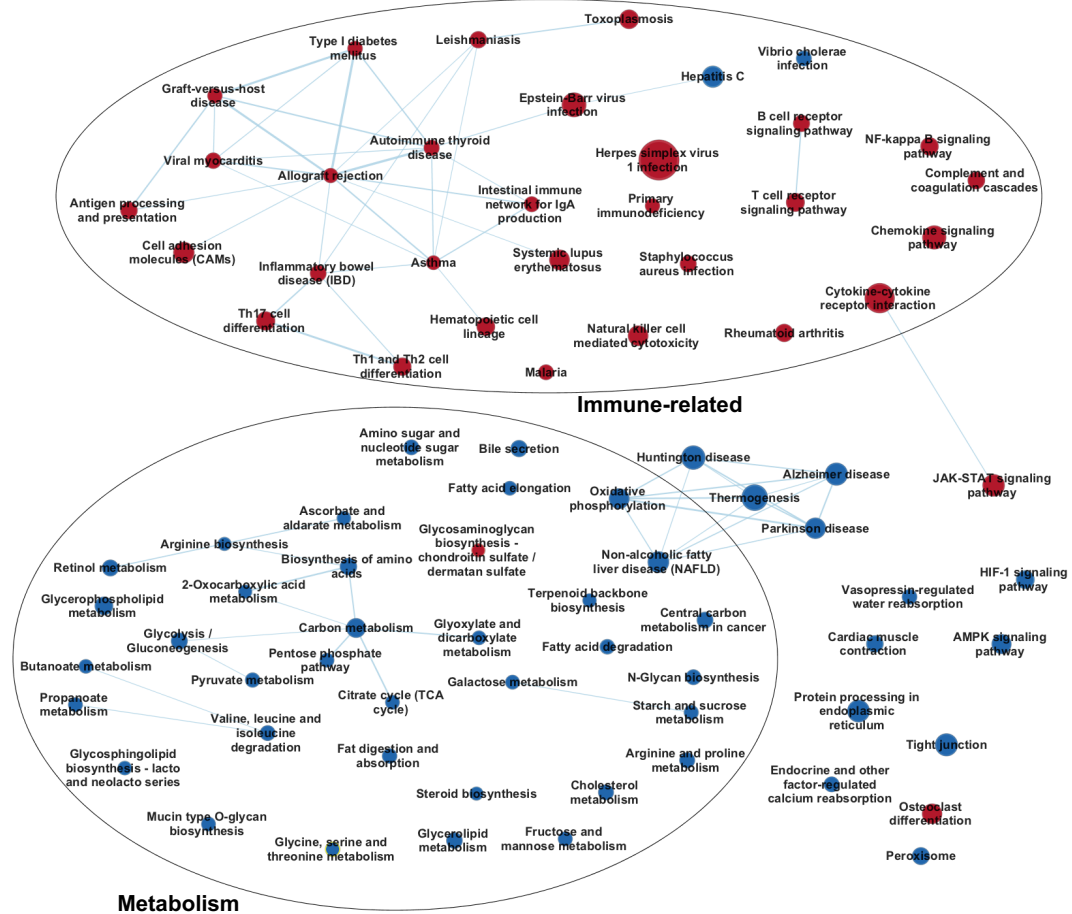


## C. Autologous FMT (two weeks after vs baseline)

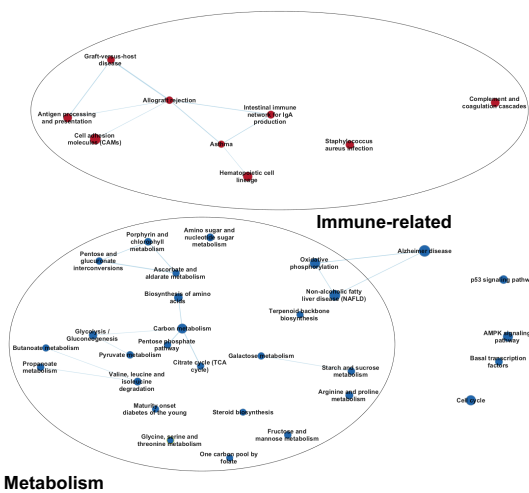


**Figure S1: Enrichment maps (including gene set names) of gene sets changed two weeks after FMT.** A. Allogenic versus autologous FMT (baseline-corrected). B. Allogenic FMT (within-group comparison). C. Autologous FMT (within-group comparison). Nodes represent KEGG gene sets and the edges between the nodes represent their similarity. Red nodes indicate enriched (increased expression of) gene sets and blue nodes indicate suppressed (decreased expression of) gene sets. Node size represents the number of genes in the gene set, and the thickness of the edges indicates the degree of overlap between the two connected gene sets (nodes). The gene sets are manually grouped according to their biological functions among these gene sets.

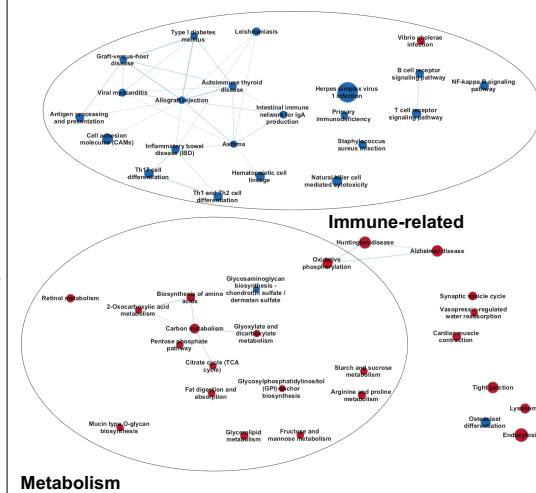
## A. Allogenic versus autologous FMT (eight weeks after)



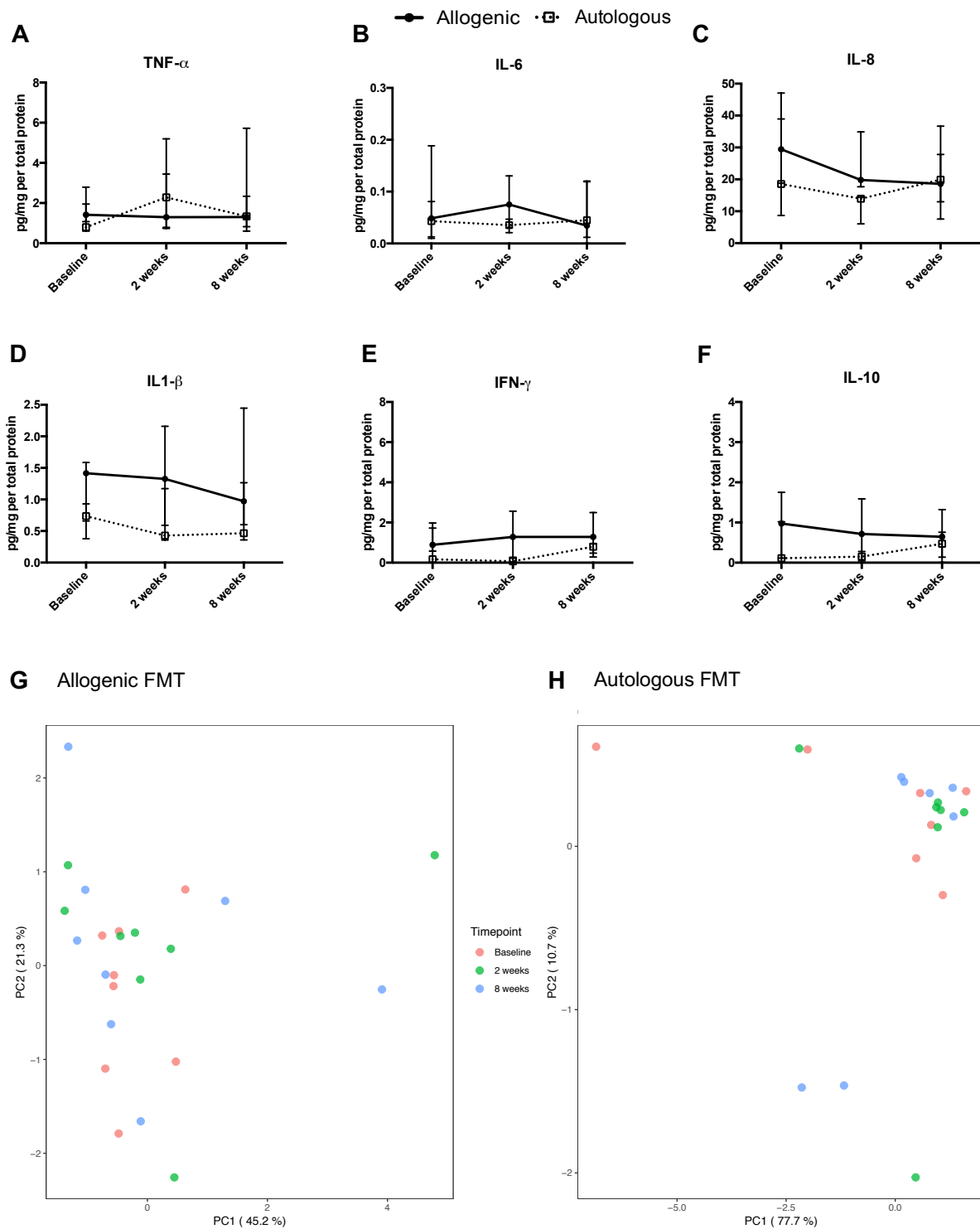
## B. Allogenic FMT (eight weeks after vs baseline)



## C. Autologous FMT (eight weeks after vs baseline)



**Figure S2: Enrichment maps (including gene set names) of gene sets changed eight weeks after FMT.** A. Allogenic versus autologous FMT (baseline-corrected). B. Allogenic FMT (within-group comparison). C. Autologous FMT (within-group comparison). Nodes represent KEGG gene sets and the edges between the nodes represent their similarity. Red nodes indicate enriched (increased expression of) gene sets and blue nodes indicate suppressed (decreased expression of) gene sets. Node size represents the number of genes in the gene set, and the thickness of the edges indicates the degree of overlap between the two connected gene sets (nodes). The gene sets are manually grouped according to their biological functions among these gene sets.



**Figure S3: Mucosal cytokine analysis.** A-F shows the univariate analysis, median with interquartile range are depicted. G, H shows the multivariate analysis (PCA, principal component analysis) in the allogenic FMT group (G) and the autologous FMT group (H).