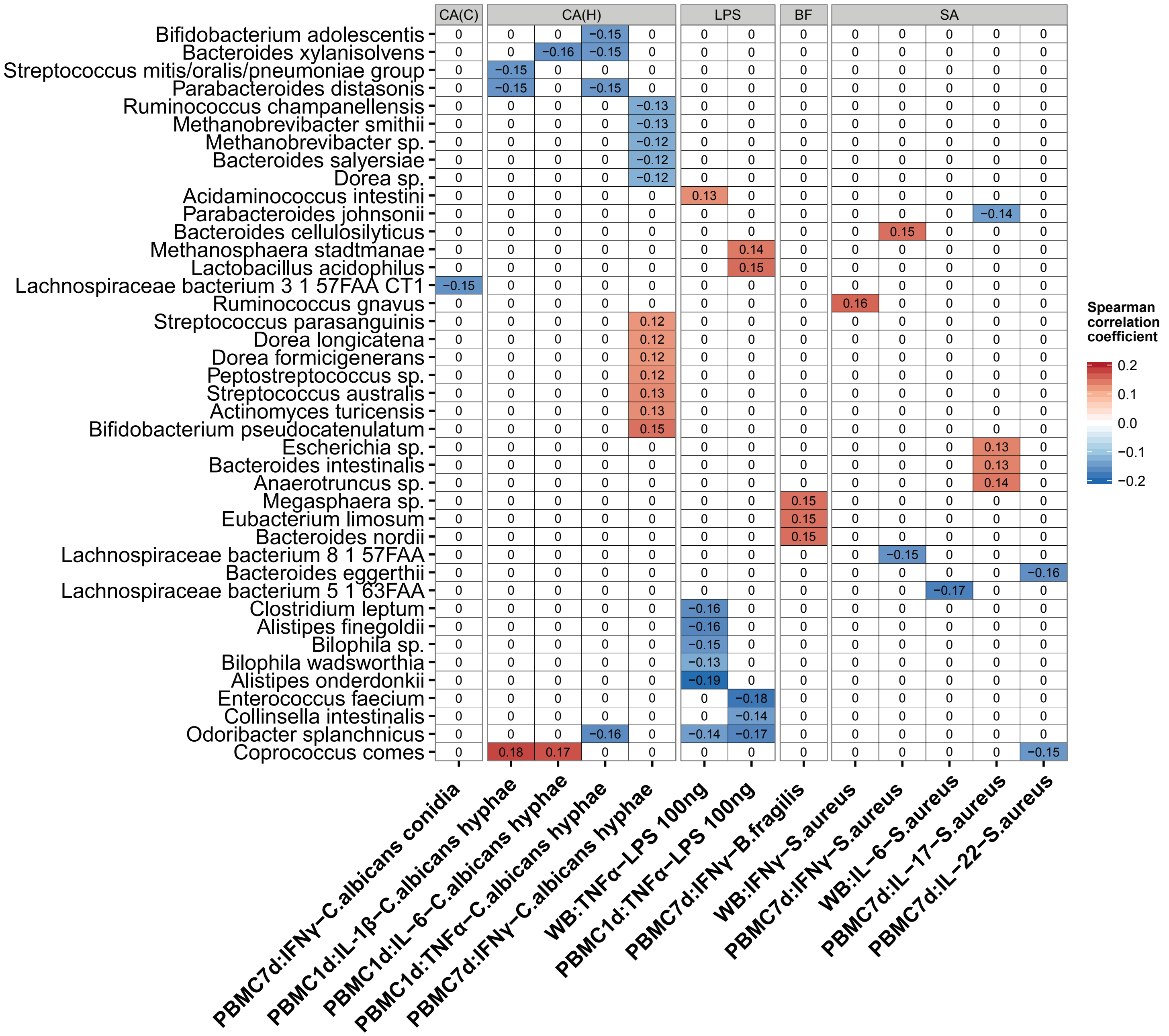
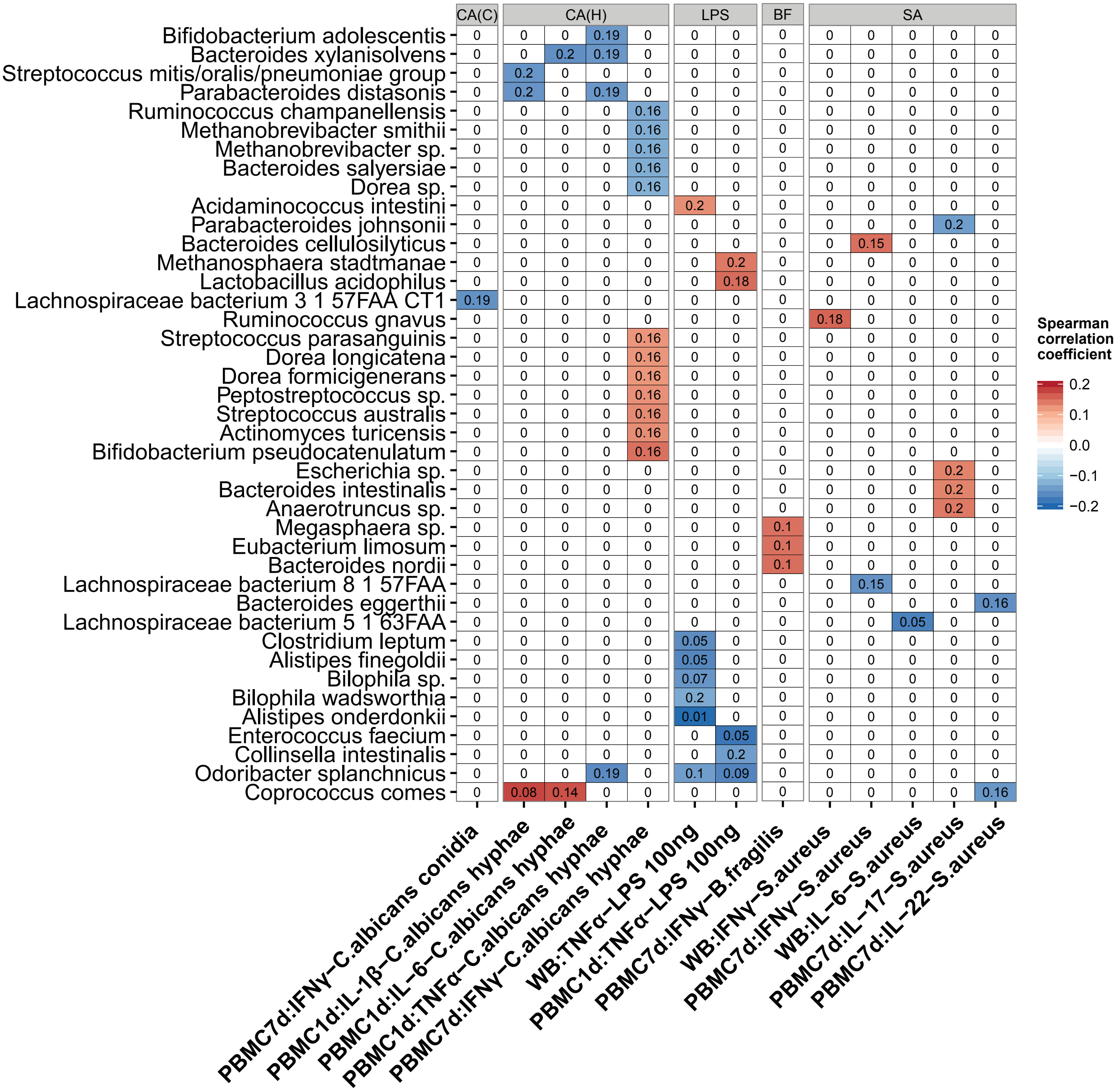
Table S1. Related to Figure 3. Correlation coefficients for all significant species associations



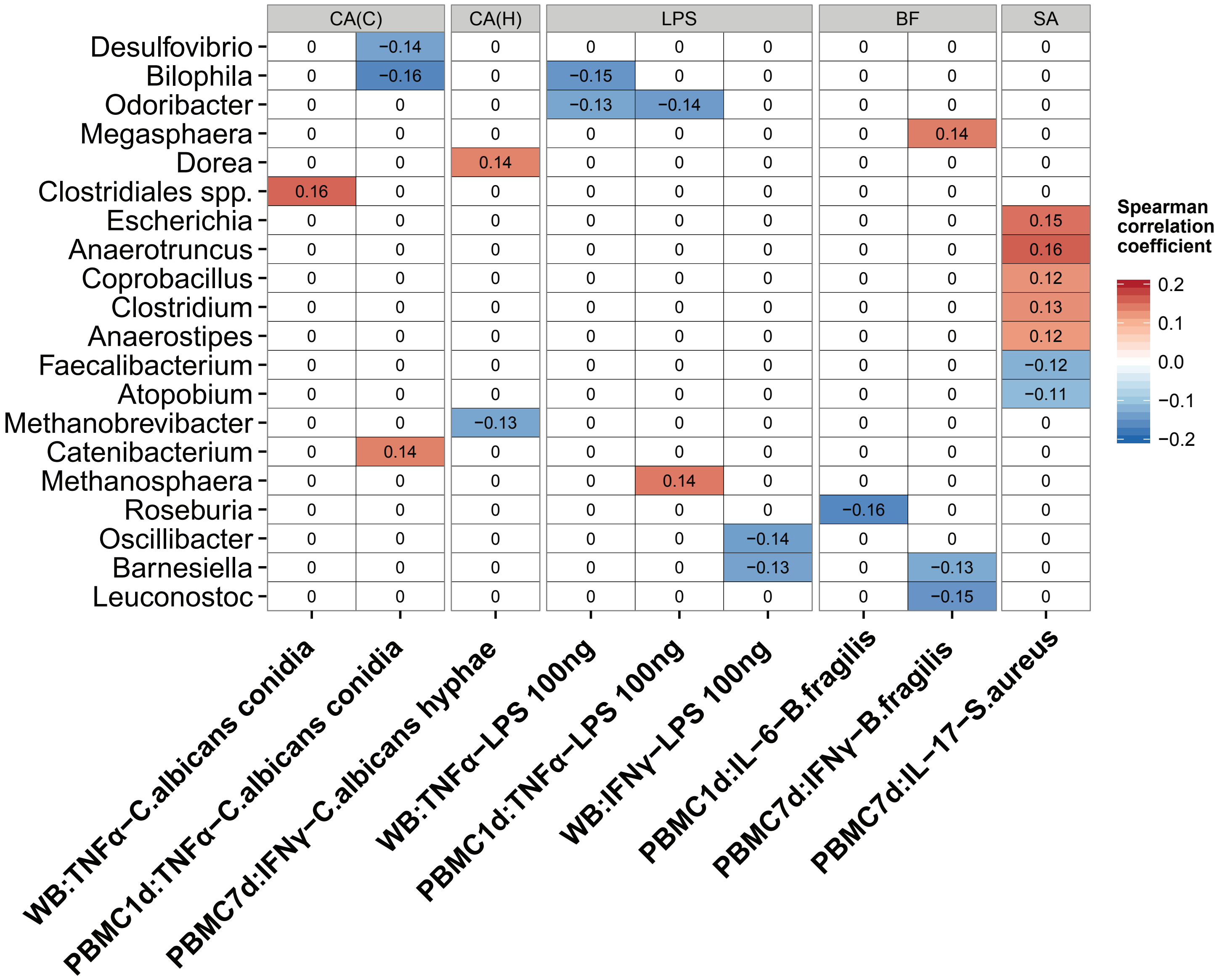
	CA(C)	CA(H)				LPS		BF	SA				
	PBMC7d:IFNγ−C.albicans conidia	PBMC1d:IL-1β−C.albicans hyphae	PBMC1d:IL−6−C.albicans hyphae	PBMC1d:TNFα−C.albicans hyphae	PBMC7d:IFNγ−C.albicans hyphae	WB:TNFα−LPS 100ng	PBMC1d:TNFα−LPS 100ng	PBMC7d:IFNγ−B.fragilis	WB:IFNγ−S.aureus	PBMC7d:IFNγ−S.aureus	WB:IL−6−S.aureus	PBMC7d:IL−17−S.aureus	PBMC7d:IL−22−S.aureus
Bifidobacterium adolescentis	0	0	0	−0.15	0	0	0	0	0	0	0	0	0
Bacteroides xylanisolvens	0	0	−0.16	−0.15	0	0	0	0	0	0	0	0	0
Streptococcus mitis/oralis/pneumoniae group	0	−0.15	0	0	0	0	0	0	0	0	0	0	0
Parabacteroides distasonis	0	−0.15	0	−0.15	0	0	0	0	0	0	0	0	0
Ruminococcus champanellensis	0	0	0	0	−0.13	0	0	0	0	0	0	0	0
Methanobrevibacter smithii	0	0	0	0	−0.13	0	0	0	0	0	0	0	0
Methanobrevibacter sp.	0	0	0	0	−0.12	0	0	0	0	0	0	0	0
Bacteroides salyersiae	0	0	0	0	−0.12	0	0	0	0	0	0	0	0
Dorea sp.	0	0	0	0	−0.12	0	0	0	0	0	0	0	0
Acidaminococcus intestini	0	0	0	0	0	0.13	0	0	0	0	0	0	0
Parabacteroides johnsonii	0	0	0	0	0	0	0	0	0	0	0	−0.14	0
Bacteroides cellulosilyticus	0	0	0	0	0	0	0	0	0	0.15	0	0	0
Methanosphaera stadtmanae	0	0	0	0	0	0	0.14	0	0	0	0	0	0
Lactobacillus acidophilus	0	0	0	0	0	0	0.15	0	0	0	0	0	0
Lachnospiraceae bacterium 3 1 57FAA CT1	−0.15	0	0	0	0	0	0	0	0	0	0	0	0
Ruminococcus gnavus	0	0	0	0	0	0	0	0	0.16	0	0	0	0
Streptococcus parasanguinis	0	0	0	0	0.12	0	0	0	0	0	0	0	0
Dorea longicatena	0	0	0	0	0.12	0	0	0	0	0	0	0	0
Dorea formicigenerans	0	0	0	0	0.12	0	0	0	0	0	0	0	0
Peptostreptococcus sp.	0	0	0	0	0.12	0	0	0	0	0	0	0	0
Streptococcus australis	0	0	0	0	0.13	0	0	0	0	0	0	0	0
Actinomyces turicensis	0	0	0	0	0.13	0	0	0	0	0	0	0	0
Bifidobacterium pseudocatenulatum	0	0	0	0	0.15	0	0	0	0	0	0	0	0
Escherichia sp.	0	0	0	0	0	0	0	0	0	0	0	0.13	0
Bacteroides intestinalis	0	0	0	0	0	0	0	0	0	0	0	0.13	0
Anaerotruncus sp.	0	0	0	0	0	0	0	0	0	0	0	0.14	0
Megasphaera sp.	0	0	0	0	0	0	0	0.15	0	0	0	0	0
Eubacterium limosum	0	0	0	0	0	0	0	0.15	0	0	0	0	0
Bacteroides nordii	0	0	0	0	0	0	0	0.15	0	0	0	0	0
Lachnospiraceae bacterium 8 1 57FAA	0	0	0	0	0	0	0	0	0	−0.15	0	0	0
Bacteroides eggerthii	0	0	0	0	0	0	0	0	0	0	0	0	−0.16
Lachnospiraceae bacterium 5 1 63FAA	0	0	0	0	0	0	0	0	0	0	−0.17	0	0
Clostridium leptum	0	0	0	0	0	−0.16	0	0	0	0	0	0	0
Alistipes finegoldii	0	0	0	0	0	−0.16	0	0	0	0	0	0	0
Bilophila sp.	0	0	0	0	0	−0.15	0	0	0	0	0	0	0
Bilophila wadsworthia	0	0	0	0	0	−0.13	0	0	0	0	0	0	0
Alistipes onderdonkii	0	0	0	0	0	−0.19	0	0	0	0	0	0	0
Enterococcus faecium	0	0	0	0	0	0	−0.18	0	0	0	0	0	0
Collinsella intestinalis	0	0	0	0	0	0	−0.14	0	0	0	0	0	0
Odoribacter splanchnicus	0	0	0	−0.16	0	−0.14	−0.17	0	0	0	0	0	0
Coprococcus comes	0	0.18	0.17	0	0	0	0	0	0	0	0	0	−0.15

Table S2. Related to Figure 3. FDR values for all significant species associations



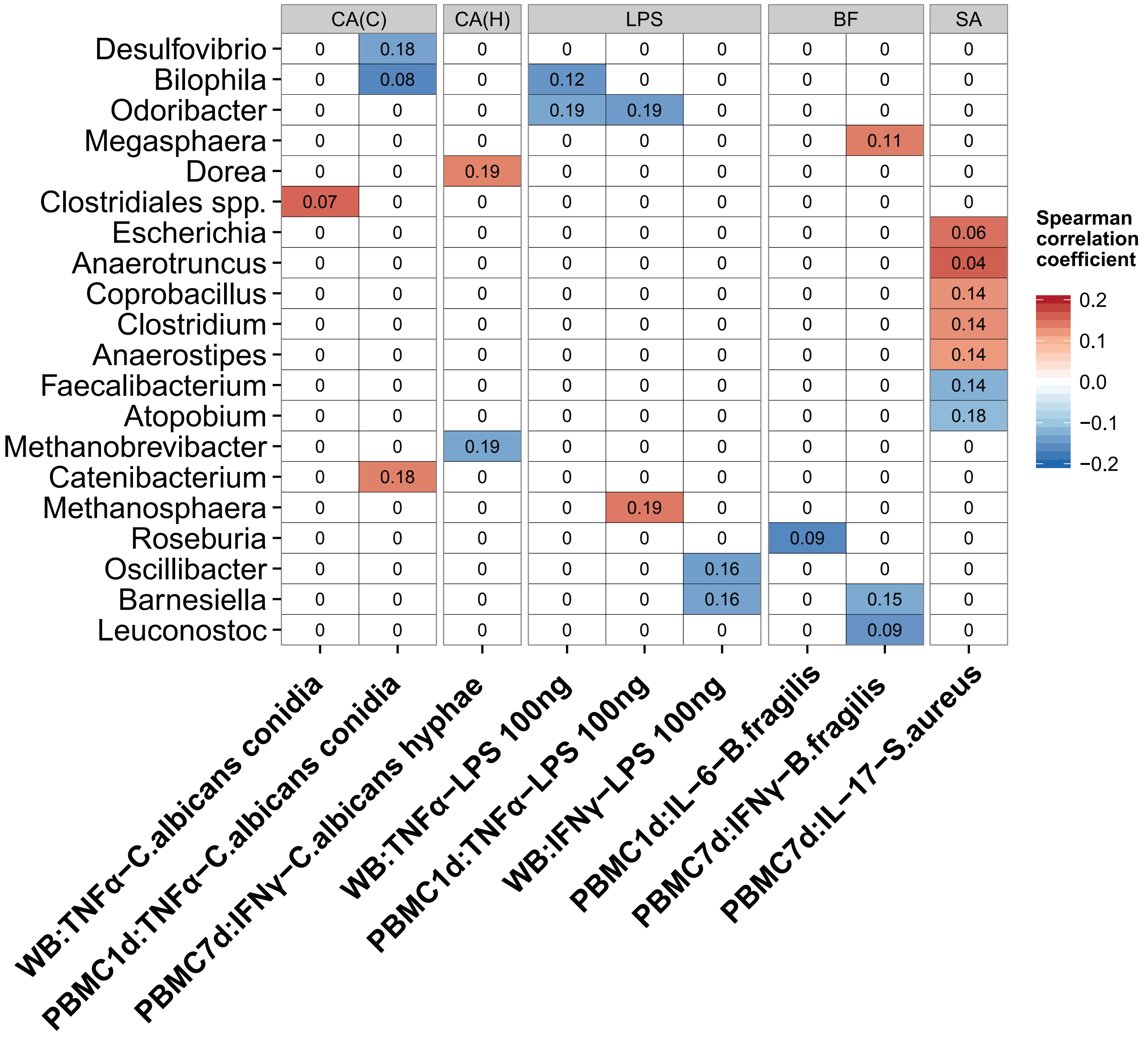
	CA(C)	CA(H)				LPS		BF	SA				
	PBMC7d:IFNγ–C.albicans conidia	PBMC1d:IL–1β–C.albicans hyphae	PBMC1d:IL–6–C.albicans hyphae	PBMC1d:TNFα–C.albicans hyphae	PBMC7d:IFNγ–C.albicans hyphae	WB:TNFα–LPS 100ng	PBMC1d:TNFα–LPS 100ng	PBMC7d:IFNγ–B.fragilis	WB:IFNγ–S.aureus	PBMC7d:IFNγ–S.aureus	WB:IL–6–S.aureus	PBMC7d:IL–17–S.aureus	PBMC7d:IL–22–S.aureus
Bifidobacterium adolescentis	0	0	0	0.19	0	0	0	0	0	0	0	0	0
Bacteroides xylanisolvens	0	0	0.2	0.19	0	0	0	0	0	0	0	0	0
Streptococcus mitis/oralis/pneumoniae group	0	0.2	0	0	0	0	0	0	0	0	0	0	0
Parabacteroides distasonis	0	0.2	0	0.19	0	0	0	0	0	0	0	0	0
Ruminococcus champanellensis	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Methanobrevibacter smithii	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Methanobrevibacter sp.	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Bacteroides salyersiae	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Dorea sp.	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Acidaminococcus intestini	0	0	0	0	0	0.2	0	0	0	0	0	0	0
Parabacteroides johnsonii	0	0	0	0	0	0	0	0	0	0	0	0.2	0
Bacteroides cellulosilyticus	0	0	0	0	0	0	0	0	0	0.15	0	0	0
Methanosphaera stadtmanae	0	0	0	0	0	0	0.2	0	0	0	0	0	0
Lactobacillus acidophilus	0	0	0	0	0	0	0.18	0	0	0	0	0	0
Lachnospiraceae bacterium 3 1 57FAA CT1	0.19	0	0	0	0	0	0	0	0	0	0	0	0
Ruminococcus gnavus	0	0	0	0	0	0	0	0	0.18	0	0	0	0
Streptococcus parasanguinis	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Dorea longicatena	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Dorea formicigenerans	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Peptostreptococcus sp.	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Streptococcus australis	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Actinomyces turicensis	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Bifidobacterium pseudocatenulatum	0	0	0	0	0.16	0	0	0	0	0	0	0	0
Escherichia sp.	0	0	0	0	0	0	0	0	0	0	0	0.2	0
Bacteroides intestinalis	0	0	0	0	0	0	0	0	0	0	0	0.2	0
Anaerotruncus sp.	0	0	0	0	0	0	0	0	0	0	0	0.2	0
Megasphaera sp.	0	0	0	0	0	0	0	0.1	0	0	0	0	0
Eubacterium limosum	0	0	0	0	0	0	0	0.1	0	0	0	0	0
Bacteroides nordii	0	0	0	0	0	0	0	0.1	0	0	0	0	0
Lachnospiraceae bacterium 8 1 57FAA	0	0	0	0	0	0	0	0	0	0.15	0	0	0
Bacteroides eggerthii	0	0	0	0	0	0	0	0	0	0	0	0	0.16
Lachnospiraceae bacterium 5 1 63FAA	0	0	0	0	0	0	0	0	0	0	0.05	0	0
Clostridium leptum	0	0	0	0	0	0.05	0	0	0	0	0	0	0
Alistipes finegoldii	0	0	0	0	0	0.05	0	0	0	0	0	0	0
Bilophila sp.	0	0	0	0	0	0.07	0	0	0	0	0	0	0
Bilophila wadsworthia	0	0	0	0	0	0.2	0	0	0	0	0	0	0
Alistipes onderdonkii	0	0	0	0	0	0.01	0	0	0	0	0	0	0
Enterococcus faecium	0	0	0	0	0	0	0.05	0	0	0	0	0	0
Collinsella intestinalis	0	0	0	0	0	0	0.2	0	0	0	0	0	0
Odoribacter splanchnicus	0	0	0	0.19	0	0.1	0.09	0	0	0	0	0	0
Coprococcus comes	0	0.08	0.14	0	0	0	0	0	0	0	0	0	0.16

Table S3. Related to Figure 3. Correlation coefficients for all significant genus associations



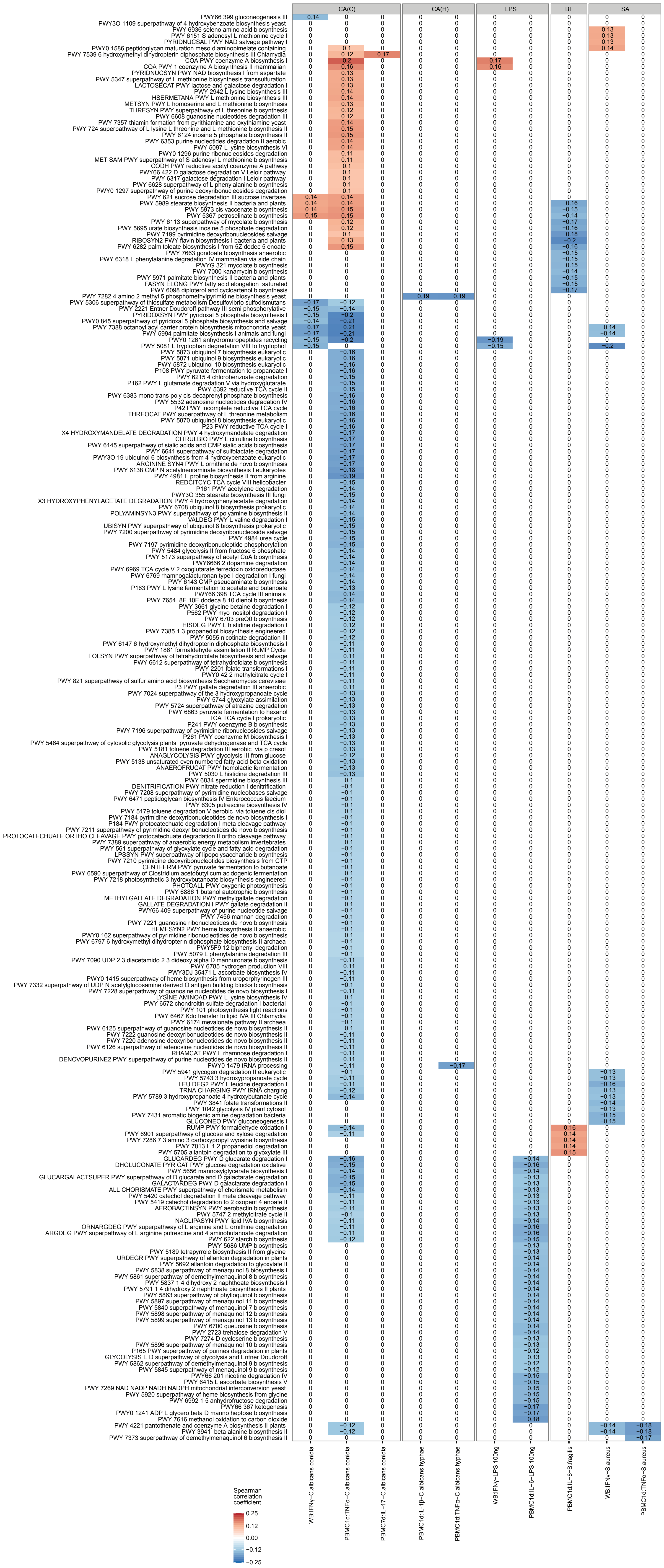
	CA(C)		CA(H)	LPS			BF		SA
	WB:TNFα−C.albicans conidia	PBMC1d:TNFα−C.albicans conidia	PBMC7d:IFNγ−C.albicans hyphae	WB:TNFα−LPS 100ng	PBMC1d:TNFα−LPS 100ng	WB:IFNγ−LPS 100ng	PBMC1d:IL−6−B.fragilis	PBMC7d:IFNγ−B.fragilis	PBMC7d:IL−17−S.aureus
Desulfovibrio	0	−0.14	0	0	0	0	0	0	0
Bilophila	0	−0.16	0	−0.15	0	0	0	0	0
Odoribacter	0	0	0	−0.13	−0.14	0	0	0	0
Megasphaera	0	0	0	0	0	0	0	0.14	0
Dorea	0	0	0.14	0	0	0	0	0	0
Clostridiales spp.	0.16	0	0	0	0	0	0	0	0
Escherichia	0	0	0	0	0	0	0	0	0.15
Anaerotruncus	0	0	0	0	0	0	0	0	0.16
Coprobacillus	0	0	0	0	0	0	0	0	0.12
Clostridium	0	0	0	0	0	0	0	0	0.13
Anaerostipes	0	0	0	0	0	0	0	0	0.12
Faecalibacterium	0	0	0	0	0	0	0	0	−0.12
Atopobium	0	0	0	0	0	0	0	0	−0.11
Methanobrevibacter	0	0	−0.13	0	0	0	0	0	0
Catenibacterium	0	0.14	0	0	0	0	0	0	0
Methanosphaera	0	0	0	0	0.14	0	0	0	0
Roseburia	0	0	0	0	0	0	−0.16	0	0
Oscillibacter	0	0	0	0	0	−0.14	0	0	0
Barnesiella	0	0	0	0	0	−0.13	0	−0.13	0
Leuconostoc	0	0	0	0	0	0	0	−0.15	0

Table S4. Related to Figure 3. FDR values for all significant genus associations



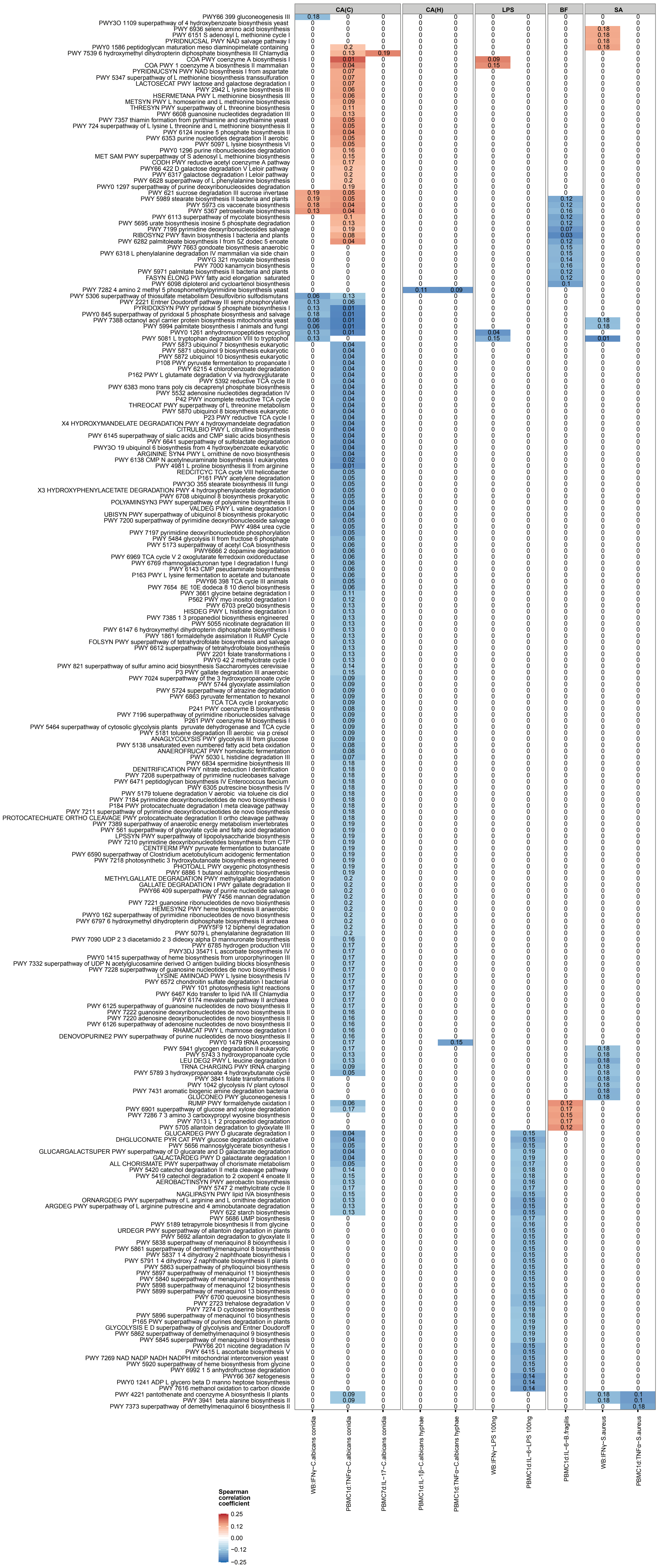
	CA(C)		CA(H)	LPS			BF		SA
	WB:TNFα–C.albicans conidia	PBMC1d:TNFα–C.albicans conidia	PBMC7d:IFNγ–C.albicans hyphae	WB:TNFα–LPS 100ng	PBMC1d:TNFα–LPS 100ng	WB:IFNγ–LPS 100ng	PBMC1d:IL–6–B.fragilis	PBMC7d:IFNγ–B.fragilis	PBMC7d:IL–17–S.aureus
Desulfovibrio	0	0.18	0	0	0	0	0	0	0
Bilophila	0	0.08	0	0.12	0	0	0	0	0
Odoribacter	0	0	0	0.19	0.19	0	0	0	0
Megasphaera	0	0	0	0	0	0	0	0.11	0
Dorea	0	0	0.19	0	0	0	0	0	0
Clostridiales spp.	0.07	0	0	0	0	0	0	0	0
Escherichia	0	0	0	0	0	0	0	0	0.06
Anaerotruncus	0	0	0	0	0	0	0	0	0.04
Coprobacillus	0	0	0	0	0	0	0	0	0.14
Clostridium	0	0	0	0	0	0	0	0	0.14
Anaerostipes	0	0	0	0	0	0	0	0	0.14
Faecalibacterium	0	0	0	0	0	0	0	0	0.14
Atopobium	0	0	0	0	0	0	0	0	0.18
Methanobrevibacter	0	0	0.19	0	0	0	0	0	0
Catenibacterium	0	0.18	0	0	0	0	0	0	0
Methanosphaera	0	0	0	0	0.19	0	0	0	0
Roseburia	0	0	0	0	0	0	0.09	0	0
Oscillibacter	0	0	0	0	0	0.16	0	0	0
Barnesiella	0	0	0	0	0	0.16	0	0.15	0
Leuconostoc	0	0	0	0	0	0	0	0.09	0

Table S5. Related to Figure 4. Correlation coefficients for all significant pathway associations



	CA(C)			CA(H)		LPS		BF	SA	
	WB:IFNγ−C.albicans conidia	PBMC1d:TNFα−C.albicans conidia	PBMC7d:IL−17−C.albicans conidia	PBMC1d:IL−1β−C.albicans hyphae	PBMC1d:TNFα−C.albicans hyphae	WB:IFNγ−LPS 100ng	PBMC1d:IL−6−LPS 100ng	PBMC1d:IL−6−B.fragilis	WB:IFNγ−S.aureus	PBMC1d:TNFα−S.aureus
PWY66 399 gluconeogenesis III	−0.14	0	0	0	0	0	0	0	0	0
PWY3O 1109 superpathway of 4 hydroxybenzoate biosynthesis yeast	0	0	0	0	0	0	0	0	0	0
PWY 6936 seleno amino acid biosynthesis	0	0	0	0	0	0	0	0	0.13	0
PWY 6151 S adenosyl L methionine cycle I	0	0	0	0	0	0	0	0	0.13	0
PYRIDNUCSAL PWY NAD salvage pathway I	0	0	0	0	0	0	0	0	0.13	0
PWY0 1586 peptidoglycan maturation meso diaminopimelate containing	0	0.1	0	0	0	0	0	0	0.14	0
PWY 7539 6 hydroxymethyl dihydropterin diphosphate biosynthesis III Chlamydia	0	0.12	0.17	0	0	0	0	0	0	0
COA PWY coenzyme A biosynthesis I	0	0.2	0	0	0	0.17	0	0	0	0
COA PWY 1 coenzyme A biosynthesis II mammalian	0	0.16	0	0	0	0.16	0	0	0	0
PYRIDNUCSYN PWY NAD biosynthesis I from aspartate	0	0.13	0	0	0	0	0	0	0	0
PWY 5347 superpathway of L methionine biosynthesis transsulfuration	0	0.13	0	0	0	0	0	0	0	0
LACTOSECAT PWY lactose and galactose degradation I	0	0.13	0	0	0	0	0	0	0	0
PWY 2942 L lysine biosynthesis III	0	0.14	0	0	0	0	0	0	0	0
HSERMETANA PWY L methionine biosynthesis III	0	0.14	0	0	0	0	0	0	0	0
METSYN PWY L homoserine and L methionine biosynthesis	0	0.13	0	0	0	0	0	0	0	0
THRESYN PWY superpathway of L threonine biosynthesis	0	0.12	0	0	0	0	0	0	0	0
PWY 6608 guanosine nucleotides degradation III	0	0.12	0	0	0	0	0	0	0	0
PWY 7357 thiamin formation from pyrithiamine and oxythiamine yeast	0	0.14	0	0	0	0	0	0	0	0
PWY 724 superpathway of L lysine L threonine and L methionine biosynthesis II	0	0.15	0	0	0	0	0	0	0	0
PWY 6124 inosine 5 phosphate biosynthesis II	0	0.15	0	0	0	0	0	0	0	0
PWY 6353 purine nucleotides degradation II aerobic	0	0.14	0	0	0	0	0	0	0	0
PWY 5097 L lysine biosynthesis VI	0	0.14	0	0	0	0	0	0	0	0
PWY0 1296 purine ribonucleosides degradation	0	0.11	0	0	0	0	0	0	0	0
MET SAM PWY superpathway of S adenosyl L methionine biosynthesis	0	0.11	0	0	0	0	0	0	0	0
CODH PWY reductive acetyl coenzyme A pathway	0	0.1	0	0	0	0	0	0	0	0
PWY66 422 D galactose degradation V Leloir pathway	0	0.1	0	0	0	0	0	0	0	0
PWY 6317 galactose degradation I Leloir pathway	0	0.1	0	0	0	0	0	0	0	0
PWY 6628 superpathway of L phenylalanine biosynthesis	0	0.1	0	0	0	0	0	0	0	0
PWY0 1297 superpathway of purine deoxyribonucleosides degradation	0	0.1	0	0	0	0	0	0	0	0
PWY 621 sucrose degradation III sucrose invertase	0.14	0.14	0	0	0	0	0	0	0	0
PWY 5989 stearate biosynthesis II bacteria and plants	0.14	0.14	0	0	0	0	0	−0.16	0	0
PWY 5973 cis vaccenate biosynthesis	0.14	0.15	0	0	0	0	0	−0.15	0	0
PWY 5367 petroselinate biosynthesis	0.15	0.15	0	0	0	0	0	−0.14	0	0
PWY 6113 superpathway of mycolate biosynthesis	0	0.12	0	0	0	0	0	−0.17	0	0
PWY 5695 urate biosynthesis inosine 5 phosphate degradation	0	0.12	0	0	0	0	0	−0.16	0	0
PWY 7199 pyrimidine deoxyribonucleosides salvage	0	0.1	0	0	0	0	0	−0.18	0	0
RIBOSYN2 PWY flavin biosynthesis I bacteria and plants	0	0.13	0	0	0	0	0	−0.2	0	0
PWY 6282 palmitoleate biosynthesis I from 5Z dodec 5 enoate	0	0.15	0	0	0	0	0	−0.16	0	0
PWY 7663 gondoate biosynthesis anaerobic	0	0	0	0	0	0	0	−0.15	0	0
PWY 6318 L phenylalanine degradation IV mammalian via side chain	0	0	0	0	0	0	0	−0.15	0	0
PWYG 321 mycolate biosynthesis	0	0	0	0	0	0	0	−0.15	0	0
PWY 7000 kanamycin biosynthesis	0	0	0	0	0	0	0	−0.14	0	0
PWY 5971 palmitate biosynthesis II bacteria and plants	0	0	0	0	0	0	0	−0.15	0	0
FASYN ELONG PWY fatty acid elongation saturated	0	0	0	0	0	0	0	−0.15	0	0
PWY 6098 diploterol and cycloartenol biosynthesis	0	0	0	0	0	0	0	−0.17	0	0
PWY 7282 4 amino 2 methyl 5 phosphomethylpyrimidine biosynthesis yeast	0	0	0	−0.19	−0.19	0	0	0	0	0
PWY 5306 superpathway of thiosulfate metabolism Desulfovibrio sulfodismutans	−0.17	−0.12	0	0	0	0	0	0	0	0
PWY 2221 Entner Doudoroff pathway III semi phosphorylative	−0.15	−0.14	0	0	0	0	0	0	0	0
PYRIDOXSYN PWY pyridoxal 5 phosphate biosynthesis I	−0.15	−0.2	0	0	0	0	0	0	0	0
PWY0 845 superpathway of pyridoxal 5 phosphate biosynthesis and salvage	−0.14	−0.21	0	0	0	0	0	0	0	0
PWY 7388 octanoyl acyl carrier protein biosynthesis mitochondria yeast	−0.17	−0.21	0	0	0	0	0	0	−0.14	0
PWY 5994 palmitate biosynthesis I animals and fungi	−0.17	−0.21	0	0	0	0	0	0	−0.14	0
PWY0 1261 anhydromuropeptides recycling	−0.15	−0.2	0	0	0	−0.19	0	0	0	0
PWY 5081 L tryptophan degradation VIII to tryptophol	−0.15	0	0	0	0	−0.15	0	0	−0.2	0
PWY 5873 ubiquinol 7 biosynthesis eukaryotic	0	−0.16	0	0	0	0	0	0	0	0
PWY 5871 ubiquinol 9 biosynthesis eukaryotic	0	−0.16	0	0	0	0	0	0	0	0
PWY 5872 ubiquinol 10 biosynthesis eukaryotic	0	−0.16	0	0	0	0	0	0	0	0
P108 PWY pyruvate fermentation to propanoate I	0	−0.16	0	0	0	0	0	0	0	0
PWY 6215 4 chlorobenzoate degradation	0	−0.15	0	0	0	0	0	0	0	0
P162 PWY L glutamate degradation V via hydroxyglutarate	0	−0.15	0	0	0	0	0	0	0	0
PWY 5392 reductive TCA cycle II	0	−0.15	0	0	0	0	0	0	0	0
PWY 6383 mono trans poly cis decaprenyl phosphate biosynthesis	0	−0.16	0	0	0	0	0	0	0	0
PWY 5532 adenosine nucleotides degradation IV	0	−0.16	0	0	0	0	0	0	0	0
P42 PWY incomplete reductive TCA cycle	0	−0.16	0	0	0	0	0	0	0	0
THREOCAT PWY superpathway of L threonine metabolism	0	−0.16	0	0	0	0	0	0	0	0
PWY 5870 ubiquinol 8 biosynthesis eukaryotic	0	−0.16	0	0	0	0	0	0	0	0
P23 PWY reductive TCA cycle I	0	−0.16	0	0	0	0	0	0	0	0
X4 HYDROXYMANDELATE DEGRADATION PWY 4 hydroxymandelate degradation	0	−0.17	0	0	0	0	0	0	0	0
CITRULBIO PWY L citrulline biosynthesis	0	−0.17	0	0	0	0	0	0	0	0
PWY 6145 superpathway of sialic acids and CMP sialic acids biosynthesis	0	−0.17	0	0	0	0	0	0	0	0
PWY 6641 superpathway of sulfolactate degradation	0	−0.17	0	0	0	0	0	0	0	0
PWY3O 19 ubiquinol 6 biosynthesis from 4 hydroxybenzoate eukaryotic	0	−0.17	0	0	0	0	0	0	0	0
ARGININE SYN4 PWY L ornithine de novo biosynthesis	0	−0.17	0	0	0	0	0	0	0	0
PWY 6138 CMP N acetylneuraminate biosynthesis I eukaryotes	0	−0.18	0	0	0	0	0	0	0	0
PWY 4981 L proline biosynthesis II from arginine	0	−0.19	0	0	0	0	0	0	0	0
REDCITCYC TCA cycle VIII helicobacter	0	−0.15	0	0	0	0	0	0	0	0
P161 PWY acetylene degradation	0	−0.14	0	0	0	0	0	0	0	0
PWY3O 355 stearate biosynthesis III fungi	0	−0.15	0	0	0	0	0	0	0	0
X3 HYDROXYPHENYLACETATE DEGRADATION PWY 4 hydroxyphenylacetate degradation	0	−0.14	0	0	0	0	0	0	0	0
PWY 6708 ubiquinol 8 biosynthesis prokaryotic	0	−0.14	0	0	0	0	0	0	0	0
POLYAMINSYN3 PWY superpathway of polyamine biosynthesis II	0	−0.14	0	0	0	0	0	0	0	0
VALDEG PWY L valine degradation I	0	−0.15	0	0	0	0	0	0	0	0
UBISYN PWY superpathway of ubiquinol 8 biosynthesis prokaryotic	0	−0.15	0	0	0	0	0	0	0	0
PWY 7200 superpathway of pyrimidine deoxyribonucleoside salvage	0	−0.15	0	0	0	0	0	0	0	0
PWY 4984 urea cycle	0	−0.15	0	0	0	0	0	0	0	0
PWY 7197 pyrimidine deoxyribonucleotide phosphorylation	0	−0.15	0	0	0	0	0	0	0	0
PWY 5484 glycolysis II from fructose 6 phosphate	0	−0.14	0	0	0	0	0	0	0	0
PWY 5173 superpathway of acetyl CoA biosynthesis	0	−0.14	0	0	0	0	0	0	0	0
PWY6666 2 dopamine degradation	0	−0.14	0	0	0	0	0	0	0	0
PWY 6969 TCA cycle V 2 oxoglutarate ferredoxin oxidoreductase	0	−0.14	0	0	0	0	0	0	0	0
PWY 6769 rhamnogalacturonan type I degradation I fungi	0	−0.14	0	0	0	0	0	0	0	0
PWY 6143 CMP pseudaminate biosynthesis	0	−0.14	0	0	0	0	0	0	0	0
P163 PWY L lysine fermentation to acetate and butanoate	0	−0.13	0	0	0	0	0	0	0	0
PWY66 398 TCA cycle III animals	0	−0.14	0	0	0	0	0	0	0	0
PWY 7654 8E 10E dodeca 8 10 dienol biosynthesis	0	−0.14	0	0	0	0	0	0	0	0
PWY 3661 glycine betaine degradation I	0	−0.12	0	0	0	0	0	0	0	0
P562 PWY myo inositol degradation I	0	−0.12	0	0	0	0	0	0	0	0
PWY 6703 preQ0 biosynthesis	0	−0.12	0	0	0	0	0	0	0	0
HISDEG PWY L histidine degradation I	0	−0.12	0	0	0	0	0	0	0	0
PWY 7385 1 3 propanediol biosynthesis engineered	0	−0.12	0	0	0	0	0	0	0	0
PWY 5055 nicotinate degradation III	0	−0.12	0	0	0	0	0	0	0	0
PWY 6147 6 hydroxymethyl dihydropterin diphosphate biosynthesis I	0	−0.11	0	0	0	0	0	0	0	0
PWY 1861 formaldehyde assimilation II RuMP Cycle	0	−0.11	0	0	0	0	0	0	0	0
FOLSYN PWY superpathway of tetrahydrofolate biosynthesis and salvage	0	−0.11	0	0	0	0	0	0	0	0
PWY 6612 superpathway of tetrahydrofolate biosynthesis	0	−0.11	0	0	0	0	0	0	0	0
PWY 2201 folate transformations I	0	−0.11	0	0	0	0	0	0	0	0
PWY0 42 2 methylcitrate cycle I	0	−0.11	0	0	0	0	0	0	0	0
PWY 821 superpathway of sulfur amino acid biosynthesis Saccharomyces cerevisiae	0	−0.11	0	0	0	0	0	0	0	0
P3 PWY gallate degradation III anaerobic	0	−0.11	0	0	0	0	0	0	0	0
PWY 7024 superpathway of the 3 hydroxypropanoate cycle	0	−0.13	0	0	0	0	0	0	0	0
PWY 5744 glyoxylate assimilation	0	−0.13	0	0	0	0	0	0	0	0
PWY 5724 superpathway of atrazine degradation	0	−0.13	0	0	0	0	0	0	0	0
PWY 6863 pyruvate fermentation to hexanol	0	−0.13	0	0	0	0	0	0	0	0
TCA TCA cycle I prokaryotic	0	−0.13	0	0	0	0	0	0	0	0
P241 PWY coenzyme B biosynthesis	0	−0.13	0	0	0	0	0	0	0	0
PWY 7196 superpathway of pyrimidine ribonucleosides salvage	0	−0.13	0	0	0	0	0	0	0	0
P261 PWY coenzyme M biosynthesis I	0	−0.13	0	0	0	0	0	0	0	0
PWY 5464 superpathway of cytosolic glycolysis plants pyruvate dehydrogenase and TCA cycle	0	−0.13	0	0	0	0	0	0	0	0
PWY 5181 toluene degradation III aerobic via p cresol	0	−0.13	0	0	0	0	0	0	0	0
ANAGLYCOLYSIS PWY glycolysis III from glucose	0	−0.12	0	0	0	0	0	0	0	0
PWY 5138 unsaturated even numbered fatty acid beta oxidation	0	−0.13	0	0	0	0	0	0	0	0
ANAEROFRUCAT PWY homolactic fermentation	0	−0.13	0	0	0	0	0	0	0	0
PWY 5030 L histidine degradation III	0	−0.13	0	0	0	0	0	0	0	0
PWY 6834 spermidine biosynthesis III	0	−0.1	0	0	0	0	0	0	0	0
DENITRIFICATION PWY nitrate reduction I denitrification	0	−0.1	0	0	0	0	0	0	0	0
PWY 7208 superpathway of pyrimidine nucleobases salvage	0	−0.1	0	0	0	0	0	0	0	0
PWY 6471 peptidoglycan biosynthesis IV Enterococcus faecium	0	−0.1	0	0	0	0	0	0	0	0
PWY 6305 putrescine biosynthesis IV	0	−0.1	0	0	0	0	0	0	0	0
PWY 5179 toluene degradation V aerobic via toluene cis diol	0	−0.1	0	0	0	0	0	0	0	0
PWY 7184 pyrimidine deoxyribonucleotides de novo biosynthesis I	0	−0.1	0	0	0	0	0	0	0	0
P184 PWY protocatechuate degradation I meta cleavage pathway	0	−0.1	0	0	0	0	0	0	0	0
PWY 7211 superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	0	−0.1	0	0	0	0	0	0	0	0
PROTOCATECHUATE ORTHO CLEAVAGE PWY protocatechuate degradation II ortho cleavage pathway	0	−0.1	0	0	0	0	0	0	0	0
PWY 7389 superpathway of anaerobic energy metabolism invertebrates	0	−0.1	0	0	0	0	0	0	0	0
PWY 561 superpathway of glyoxylate cycle and fatty acid degradation	0	−0.1	0	0	0	0	0	0	0	0
LPSSYN PWY superpathway of lipopolysaccharide biosynthesis	0	−0.1	0	0	0	0	0	0	0	0
PWY 7210 pyrimidine deoxyribonucleotides biosynthesis from CTP	0	−0.1	0	0	0	0	0	0	0	0
CENTFERM PWY pyruvate fermentation to butanoate	0	−0.1	0	0	0	0	0	0	0	0
PWY 6590 superpathway of Clostridium acetobutylicum acidogenic fermentation	0	−0.1	0	0	0	0	0	0	0	0
PWY 7218 photosynthetic 3 hydroxybutanoate biosynthesis engineered	0	−0.1	0	0	0	0	0	0	0	0
PHOTOALL PWY oxygenic photosynthesis	0	−0.1	0	0	0	0	0	0	0	0
PWY 6886 1 butanol autotrophic biosynthesis	0	−0.1	0	0	0	0	0	0	0	0
METHYLGALLATE DEGRADATION PWY methylgallate degradation	0	−0.1	0	0	0	0	0	0	0	0
GALLATE DEGRADATION I PWY gallate degradation II	0	−0.1	0	0	0	0	0	0	0	0
PWY66 409 superpathway of purine nucleotide salvage	0	−0.1	0	0	0	0	0	0	0	0
PWY 7456 mannan degradation	0	−0.1	0	0	0	0	0	0	0	0
PWY 7221 guanosine ribonucleotides de novo biosynthesis	0	−0.1	0	0	0	0	0	0	0	0
HEMESYN2 PWY heme biosynthesis II anaerobic	0	−0.1	0	0	0	0	0	0	0	0
PWY0 162 superpathway of pyrimidine ribonucleotides de novo biosynthesis	0	−0.1	0	0	0	0	0	0	0	0
PWY 6797 6 hydroxymethyl dihydropterin diphosphate biosynthesis II archaea	0	−0.1	0	0	0	0	0	0	0	0
PWY5F9 12 biphenyl degradation	0	−0.1	0	0	0	0	0	0	0	0
PWY 5079 L phenylalanine degradation III	0	−0.1	0	0	0	0	0	0	0	0
PWY 7090 UDP 2 3 diacetamido 2 3 dideoxy alpha D mannuronate biosynthesis	0	−0.11	0	0	0	0	0	0	0	0
PWY 6785 hydrogen production VIII	0	−0.11	0	0	0	0	0	0	0	0
PWY3DJ 35471 L ascorbate biosynthesis IV	0	−0.11	0	0	0	0	0	0	0	0
PWY0 1415 superpathway of heme biosynthesis from uroporphyrinogen III	0	−0.11	0	0	0	0	0	0	0	0
PWY 7332 superpathway of UDP N acetylglucosamine derived O antigen building blocks biosynthesis	0	−0.1	0	0	0	0	0	0	0	0
PWY 7228 superpathway of guanosine nucleotides de novo biosynthesis I	0	−0.11	0	0	0	0	0	0	0	0
LYSINE AMINOAD PWY L lysine biosynthesis IV	0	−0.1	0	0	0	0	0	0	0	0
PWY 6572 chondroitin sulfate degradation I bacterial	0	−0.1	0	0	0	0	0	0	0	0
PWY 101 photosynthesis light reactions	0	−0.1	0	0	0	0	0	0	0	0
PWY 6467 Kdo transfer to lipid IVA III Chlamydia	0	−0.1	0	0	0	0	0	0	0	0
PWY 6174 mevalonate pathway II archaea	0	−0.1	0	0	0	0	0	0	0	0
PWY 6125 superpathway of guanosine nucleotides de novo biosynthesis II	0	−0.1	0	0	0	0	0	0	0	0
PWY 7222 guanosine deoxyribonucleotides de novo biosynthesis II	0	−0.11	0	0	0	0	0	0	0	0
PWY 7220 adenosine deoxyribonucleotides de novo biosynthesis II	0	−0.11	0	0	0	0	0	0	0	0
PWY 6126 superpathway of adenosine nucleotides de novo biosynthesis II	0	−0.11	0	0	0	0	0	0	0	0
RHAMCAT PWY L rhamnose degradation I	0	−0.11	0	0	0	0	0	0	0	0
DENOVOPURINE2 PWY superpathway of purine nucleotides de novo biosynthesis II	0	−0.11	0	0	0	0	0	0	0	0
PWY0 1479 tRNA processing	0	−0.11	0	0	−0.17	0	0	0	0	0
PWY 5941 glycogen degradation II eukaryotic	0	−0.1	0	0	0	0	0	0	−0.13	0
PWY 5743 3 hydroxypropanoate cycle	0	−0.11	0	0	0	0	0	0	−0.13	0
LEU DEG2 PWY L leucine degradation I	0	−0.11	0	0	0	0	0	0	−0.16	0
TRNA CHARGING PWY tRNA charging	0	−0.12	0	0	0	0	0	0	−0.13	0
PWY 5789 3 hydroxypropanoate 4 hydroxybutanate cycle	0	−0.14	0	0	0	0	0	0	−0.13	0
PWY 3841 folate transformations II	0	0	0	0	0	0	0	0	−0.14	0
PWY 1042 glycolysis IV plant cytosol	0	0	0	0	0	0	0	0	−0.13	0
PWY 7431 aromatic biogenic amine degradation bacteria	0	0	0	0	0	0	0	0	−0.15	0
GLUCONEO PWY gluconeogenesis I	0	0	0	0	0	0	0	0	−0.15	0
RUMP PWY formaldehyde oxidation I	0	−0.14	0	0	0	0	0	0.16	0	0
PWY 6901 superpathway of glucose and xylose degradation	0	−0.11	0	0	0	0	0	0.14	0	0
PWY 7286 7 3 amino 3 carboxypropyl wyosine biosynthesis	0	0	0	0	0	0	0	0.14	0	0
PWY 7013 L 1 2 propanediol degradation	0	0	0	0	0	0	0	0.14	0	0
PWY 5705 allantoin degradation to glyoxylate III	0	0	0	0	0	0	0	0.15	0	0
GLUCARDEG PWY D glucarate degradation I	0	−0.16	0	0	0	0	−0.14	0	0	0
DHGLUCONATE PYR CAT PWY glucose degradation oxidative	0	−0.15	0	0	0	0	−0.16	0	0	0
PWY 5656 mannosylglycerate biosynthesis I	0	−0.14	0	0	0	0	−0.14	0	0	0
GLUCARGALACTSUPER PWY superpathway of D glucarate and D galactarate degradation	0	−0.15	0	0	0	0	−0.13	0	0	0
GALACTARDEG PWY D galactarate degradation I	0	−0.15	0	0	0	0	−0.13	0	0	0
ALL CHORISMATE PWY superpathway of chorismate metabolism	0	−0.14	0	0	0	0	−0.13	0	0	0
PWY 5420 catechol degradation II meta cleavage pathway	0	−0.11	0	0	0	0	−0.13	0	0	0
PWY 5419 catechol degradation to 2 oxopent 4 enoate II	0	−0.11	0	0	0	0	−0.13	0	0	0
AEROBACTINSYN PWY aerobactin biosynthesis	0	−0.11	0	0	0	0	−0.13	0	0	0
PWY 5747 2 methylcitrate cycle II	0	−0.1	0	0	0	0	−0.13	0	0	0
NAGLIPASYN PWY lipid IVA biosynthesis	0	−0.11	0	0	0	0	−0.14	0	0	0
ORNARGDEG PWY superpathway of L arginine and L ornithine degradation	0	−0.11	0	0	0	0	−0.16	0	0	0
ARGDEG PWY superpathway of L arginine putrescine and 4 aminobutanoate degradation	0	−0.11	0	0	0	0	−0.16	0	0	0
PWY 622 starch biosynthesis	0	−0.12	0	0	0	0	−0.15	0	0	0
PWY 5686 UMP biosynthesis	0	0	0	0	0	0	−0.13	0	0	0
PWY 5189 tetrapyrrole biosynthesis II from glycine	0	0	0	0	0	0	−0.13	0	0	0
URDEGR PWY superpathway of allantoin degradation in plants	0	0	0	0	0	0	−0.14	0	0	0
PWY 5692 allantoin degradation to glyoxylate II	0	0	0	0	0	0	−0.14	0	0	0
PWY 5838 superpathway of menaquinol 8 biosynthesis I	0	0	0	0	0	0	−0.14	0	0	0
PWY 5861 superpathway of demethylmenaquinol 8 biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 5837 1 4 dihydroxy 2 naphthoate biosynthesis I	0	0	0	0	0	0	−0.14	0	0	0
PWY 5791 1 4 dihydroxy 2 naphthoate biosynthesis II plants	0	0	0	0	0	0	−0.14	0	0	0
PWY 5863 superpathway of phylloquinol biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 5897 superpathway of menaquinol 11 biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 5840 superpathway of menaquinol 7 biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 5898 superpathway of menaquinol 12 biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 5899 superpathway of menaquinol 13 biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 6700 queuosine biosynthesis	0	0	0	0	0	0	−0.14	0	0	0
PWY 2723 trehalose degradation V	0	0	0	0	0	0	−0.14	0	0	0
PWY 7274 D cycloserine biosynthesis	0	0	0	0	0	0	−0.13	0	0	0
PWY 5896 superpathway of menaquinol 10 biosynthesis	0	0	0	0	0	0	−0.13	0	0	0
P165 PWY superpathway of purines degradation in plants	0	0	0	0	0	0	−0.12	0	0	0
GLYCOLYSIS E D superpathway of glycolysis and Entner Doudoroff	0	0	0	0	0	0	−0.13	0	0	0
PWY 5862 superpathway of demethylmenaquinol 9 biosynthesis	0	0	0	0	0	0	−0.12	0	0	0
PWY 5845 superpathway of menaquinol 9 biosynthesis	0	0	0	0	0	0	−0.12	0	0	0
PWY66 201 nicotine degradation IV	0	0	0	0	0	0	−0.15	0	0	0
PWY 6415 L ascorbate biosynthesis V	0	0	0	0	0	0	−0.15	0	0	0
PWY 7269 NAD NADP NADH NADPH mitochondrial interconversion yeast	0	0	0	0	0	0	−0.15	0	0	0
PWY 5920 superpathway of heme biosynthesis from glycine	0	0	0	0	0	0	−0.15	0	0	0
PWY 6992 1 5 anhydrofructose degradation	0	0	0	0	0	0	−0.15	0	0	0
PWY66 367 ketogenesis	0	0	0	0	0	0	−0.17	0	0	0
PWY0 1241 ADP L glycero beta D manno heptose biosynthesis	0	0	0	0	0	0	−0.17	0	0	0
PWY 7616 methanol oxidation to carbon dioxide	0	0	0	0	0	0	−0.18	0	0	0
PWY 4221 pantothenate and coenzyme A biosynthesis II plants	0	−0.12	0	0	0	0	0	0	−0.14	−0.18
PWY 3941 beta alanine biosynthesis II	0	−0.12	0	0	0	0	0	0	−0.14	−0.18
PWY 7373 superpathway of demethylmenaquinol 6 biosynthesis II	0	0	0	0	0	0	0	0	0	−0.17

Table S6. Related to Figure 4. FDR values for all significant pathway associations



	CA(C)			CA(H)		LPS		BF	SA	
	WB:IFNγ−C.albicans conidia	PBMC1d:TNFα−C.albicans conidia	PBMC7d:IL−17−C.albicans conidia	PBMC1d:IL−1β−C.albicans hyphae	PBMC1d:TNFα−C.albicans hyphae	WB:IFNγ−LPS 100ng	PBMC1d:IL−6−LPS 100ng	PBMC1d:IL−6−B.fragilis	WB:IFNγ−S.aureus	PBMC1d:TNFα−S.aureus
PWY66 399 gluconeogenesis III	0.18	0	0	0	0	0	0	0	0	0
PWY3O 1109 superpathway of 4 hydroxybenzoate biosynthesis yeast	0	0	0	0	0	0	0	0	0	0
PWY 6936 seleno amino acid biosynthesis	0	0	0	0	0	0	0	0	0.18	0
PWY 6151 S adenosyl L methionine cycle I	0	0	0	0	0	0	0	0	0.18	0
PYRIDNUCSAL PWY NAD salvage pathway I	0	0	0	0	0	0	0	0	0.18	0
PWY0 1586 peptidoglycan maturation meso diaminopimelate containing	0	0.2	0	0	0	0	0	0	0.18	0
PWY 7539 6 hydroxymethyl dihydropterin diphosphate biosynthesis III Chlamydia	0	0.13	0.19	0	0	0	0	0	0	0
COA PWY coenzyme A biosynthesis I	0	0.01	0	0	0	0.09	0	0	0	0
COA PWY 1 coenzyme A biosynthesis II mammalian	0	0.04	0	0	0	0.15	0	0	0	0
PYRIDNUCSYN PWY NAD biosynthesis I from aspartate	0	0.07	0	0	0	0	0	0	0	0
PWY 5347 superpathway of L methionine biosynthesis transsulfuration	0	0.07	0	0	0	0	0	0	0	0
LACTOSECAT PWY lactose and galactose degradation I	0	0.07	0	0	0	0	0	0	0	0
PWY 2942 L lysine biosynthesis III	0	0.06	0	0	0	0	0	0	0	0
HSERMETANA PWY L methionine biosynthesis III	0	0.06	0	0	0	0	0	0	0	0
METSYN PWY L homoserine and L methionine biosynthesis	0	0.09	0	0	0	0	0	0	0	0
THRESYN PWY superpathway of L threonine biosynthesis	0	0.11	0	0	0	0	0	0	0	0
PWY 6608 guanosine nucleotides degradation III	0	0.13	0	0	0	0	0	0	0	0
PWY 7357 thiamin formation from pyrithiamine and oxythiamine yeast	0	0.05	0	0	0	0	0	0	0	0
PWY 724 superpathway of L lysine L threonine and L methionine biosynthesis II	0	0.05	0	0	0	0	0	0	0	0
PWY 6124 inosine 5 phosphate biosynthesis II	0	0.04	0	0	0	0	0	0	0	0
PWY 6353 purine nucleotides degradation II aerobic	0	0.05	0	0	0	0	0	0	0	0
PWY 5097 L lysine biosynthesis VI	0	0.05	0	0	0	0	0	0	0	0
PWY0 1296 purine ribonucleosides degradation	0	0.16	0	0	0	0	0	0	0	0
MET SAM PWY superpathway of S adenosyl L methionine biosynthesis	0	0.15	0	0	0	0	0	0	0	0
CODH PWY reductive acetyl coenzyme A pathway	0	0.17	0	0	0	0	0	0	0	0
PWY66 422 D galactose degradation V Leloir pathway	0	0.2	0	0	0	0	0	0	0	0
PWY 6317 galactose degradation I Leloir pathway	0	0.2	0	0	0	0	0	0	0	0
PWY 6628 superpathway of L phenylalanine biosynthesis	0	0.2	0	0	0	0	0	0	0	0
PWY0 1297 superpathway of purine deoxyribonucleosides degradation	0	0.19	0	0	0	0	0	0	0	0
PWY 621 sucrose degradation III sucrose invertase	0.19	0.05	0	0	0	0	0	0	0	0
PWY 5989 stearate biosynthesis II bacteria and plants	0.19	0.05	0	0	0	0	0	0.12	0	0
PWY 5973 cis vaccenate biosynthesis	0.18	0.04	0	0	0	0	0	0.12	0	0
PWY 5367 petroselinate biosynthesis	0.13	0.04	0	0	0	0	0	0.16	0	0
PWY 6113 superpathway of mycolate biosynthesis	0	0.1	0	0	0	0	0	0.12	0	0
PWY 5695 urate biosynthesis inosine 5 phosphate degradation	0	0.13	0	0	0	0	0	0.12	0	0
PWY 7199 pyrimidine deoxyribonucleosides salvage	0	0.19	0	0	0	0	0	0.07	0	0
RIBOSYN2 PWY flavin biosynthesis I bacteria and plants	0	0.08	0	0	0	0	0	0.03	0	0
PWY 6282 palmitoleate biosynthesis I from 5Z dodec 5 enoate	0	0.04	0	0	0	0	0	0.12	0	0
PWY 7663 gondoate biosynthesis anaerobic	0	0	0	0	0	0	0	0.15	0	0
PWY 6318 L phenylalanine degradation IV mammalian via side chain	0	0	0	0	0	0	0	0.15	0	0
PWYG 321 mycolate biosynthesis	0	0	0	0	0	0	0	0.14	0	0
PWY 7000 kanamycin biosynthesis	0	0	0	0	0	0	0	0.16	0	0
PWY 5971 palmitate biosynthesis II bacteria and plants	0	0	0	0	0	0	0	0.12	0	0
FASYN ELONG PWY fatty acid elongation saturated	0	0	0	0	0	0	0	0.12	0	0
PWY 6098 diploterol and cycloartenol biosynthesis	0	0	0	0	0	0	0	0.1	0	0
PWY 7282 4 amino 2 methyl 5 phosphomethylpyrimidine biosynthesis yeast	0	0	0	0.11	0.09	0	0	0	0	0
PWY 5306 superpathway of thiosulfate metabolism Desulfovibrio sulfodismutans	0.06	0.13	0	0	0	0	0	0	0	0
PWY 2221 Entner Doudoroff pathway III semi phosphorylative	0.13	0.06	0	0	0	0	0	0	0	0
PYRIDOXSYN PWY pyridoxal 5 phosphate biosynthesis I	0.13	0.01	0	0	0	0	0	0	0	0
PWY0 845 superpathway of pyridoxal 5 phosphate biosynthesis and salvage	0.18	0.01	0	0	0	0	0	0	0	0
PWY 7388 octanoyl acyl carrier protein biosynthesis mitochondria yeast	0.06	0.01	0	0	0	0	0	0	0.18	0
PWY 5994 palmitate biosynthesis I animals and fungi	0.06	0.01	0	0	0	0	0	0	0.18	0
PWY0 1261 anhydromuropeptides recycling	0.13	0.01	0	0	0	0.04	0	0	0	0
PWY 5081 L tryptophan degradation VIII to tryptophol	0.13	0	0	0	0	0.15	0	0	0.01	0
PWY 5873 ubiquinol 7 biosynthesis eukaryotic	0	0.04	0	0	0	0	0	0	0	0
PWY 5871 ubiquinol 9 biosynthesis eukaryotic	0	0.04	0	0	0	0	0	0	0	0
PWY 5872 ubiquinol 10 biosynthesis eukaryotic	0	0.04	0	0	0	0	0	0	0	0
P108 PWY pyruvate fermentation to propanoate I	0	0.04	0	0	0	0	0	0	0	0
PWY 6215 4 chlorobenzoate degradation	0	0.04	0	0	0	0	0	0	0	0
P162 PWY L glutamate degradation V via hydroxyglutarate	0	0.04	0	0	0	0	0	0	0	0
PWY 5392 reductive TCA cycle II	0	0.04	0	0	0	0	0	0	0	0
PWY 6383 mono trans poly cis decaprenyl phosphate biosynthesis	0	0.04	0	0	0	0	0	0	0	0
PWY 5532 adenosine nucleotides degradation IV	0	0.04	0	0	0	0	0	0	0	0
P42 PWY incomplete reductive TCA cycle	0	0.04	0	0	0	0	0	0	0	0
THREOCAT PWY superpathway of L threonine metabolism	0	0.04	0	0	0	0	0	0	0	0
PWY 5870 ubiquinol 8 biosynthesis eukaryotic	0	0.04	0	0	0	0	0	0	0	0
P23 PWY reductive TCA cycle I	0	0.04	0	0	0	0	0	0	0	0
X4 HYDROXYMANDELATE DEGRADATION PWY 4 hydroxymandelate degradation	0	0.04	0	0	0	0	0	0	0	0
CITRULBIO PWY L citrulline biosynthesis	0	0.04	0	0	0	0	0	0	0	0
PWY 6145 superpathway of sialic acids and CMP sialic acids biosynthesis	0	0.04	0	0	0	0	0	0	0	0
PWY 6641 superpathway of sulfolactate degradation	0	0.04	0	0	0	0	0	0	0	0
PWY3O 19 ubiquinol 6 biosynthesis from 4 hydroxybenzoate eukaryotic	0	0.04	0	0	0	0	0	0	0	0
ARGININE SYN4 PWY L ornithine de novo biosynthesis	0	0.04	0	0	0	0	0	0	0	0
PWY 6138 CMP N acetylneuraminate biosynthesis I eukaryotes	0	0.02	0	0	0	0	0	0	0	0
PWY 4981 L proline biosynthesis II from arginine	0	0.01	0	0	0	0	0	0	0	0
REDCITCYC TCA cycle VIII helicobacter	0	0.05	0	0	0	0	0	0	0	0
P161 PWY acetylene degradation	0	0.05	0	0	0	0	0	0	0	0
PWY3O 355 stearate biosynthesis III fungi	0	0.05	0	0	0	0	0	0	0	0
X3 HYDROXYPHENYLACETATE DEGRADATION PWY 4 hydroxyphenylacetate degradation	0	0.05	0	0	0	0	0	0	0	0
PWY 6708 ubiquinol 8 biosynthesis prokaryotic	0	0.05	0	0	0	0	0	0	0	0
POLYAMINSYN3 PWY superpathway of polyamine biosynthesis II	0	0.05	0	0	0	0	0	0	0	0
VALDEG PWY L valine degradation I	0	0.04	0	0	0	0	0	0	0	0
UBISYN PWY superpathway of ubiquinol 8 biosynthesis prokaryotic	0	0.04	0	0	0	0	0	0	0	0
PWY 7200 superpathway of pyrimidine deoxyribonucleoside salvage	0	0.05	0	0	0	0	0	0	0	0
PWY 4984 urea cycle	0	0.05	0	0	0	0	0	0	0	0
PWY 7197 pyrimidine deoxyribonucleotide phosphorylation	0	0.05	0	0	0	0	0	0	0	0
PWY 5484 glycolysis II from fructose 6 phosphate	0	0.06	0	0	0	0	0	0	0	0
PWY 5173 superpathway of acetyl CoA biosynthesis	0	0.06	0	0	0	0	0	0	0	0
PWY6666 2 dopamine degradation	0	0.06	0	0	0	0	0	0	0	0
PWY 6969 TCA cycle V 2 oxoglutarate ferredoxin oxidoreductase	0	0.06	0	0	0	0	0	0	0	0
PWY 6769 rhamnogalacturonan type I degradation I fungi	0	0.06	0	0	0	0	0	0	0	0
PWY 6143 CMP pseudaminate biosynthesis	0	0.06	0	0	0	0	0	0	0	0
P163 PWY L lysine fermentation to acetate and butanoate	0	0.06	0	0	0	0	0	0	0	0
PWY66 398 TCA cycle III animals	0	0.05	0	0	0	0	0	0	0	0
PWY 7654 8E 10E dodeca 8 10 dienol biosynthesis	0	0.06	0	0	0	0	0	0	0	0
PWY 3661 glycine betaine degradation I	0	0.11	0	0	0	0	0	0	0	0
P562 PWY myo inositol degradation I	0	0.12	0	0	0	0	0	0	0	0
PWY 6703 preQ0 biosynthesis	0	0.13	0	0	0	0	0	0	0	0
HISDEG PWY L histidine degradation I	0	0.13	0	0	0	0	0	0	0	0
PWY 7385 1 3 propanediol biosynthesis engineered	0	0.13	0	0	0	0	0	0	0	0
PWY 5055 nicotinate degradation III	0	0.13	0	0	0	0	0	0	0	0
PWY 6147 6 hydroxymethyl dihydropterin diphosphate biosynthesis I	0	0.13	0	0	0	0	0	0	0	0
PWY 1861 formaldehyde assimilation II RuMP Cycle	0	0.13	0	0	0	0	0	0	0	0
FOLSYN PWY superpathway of tetrahydrofolate biosynthesis and salvage	0	0.13	0	0	0	0	0	0	0	0
PWY 6612 superpathway of tetrahydrofolate biosynthesis	0	0.13	0	0	0	0	0	0	0	0
PWY 2201 folate transformations I	0	0.13	0	0	0	0	0	0	0	0
PWY0 42 2 methylcitrate cycle I	0	0.13	0	0	0	0	0	0	0	0
PWY 821 superpathway of sulfur amino acid biosynthesis Saccharomyces cerevisiae	0	0.14	0	0	0	0	0	0	0	0
P3 PWY gallate degradation III anaerobic	0	0.15	0	0	0	0	0	0	0	0
PWY 7024 superpathway of the 3 hydroxypropanoate cycle	0	0.09	0	0	0	0	0	0	0	0
PWY 5744 glyoxylate assimilation	0	0.09	0	0	0	0	0	0	0	0
PWY 5724 superpathway of atrazine degradation	0	0.09	0	0	0	0	0	0	0	0
PWY 6863 pyruvate fermentation to hexanol	0	0.09	0	0	0	0	0	0	0	0
TCA TCA cycle I prokaryotic	0	0.09	0	0	0	0	0	0	0	0
P241 PWY coenzyme B biosynthesis	0	0.08	0	0	0	0	0	0	0	0
PWY 7196 superpathway of pyrimidine ribonucleosides salvage	0	0.09	0	0	0	0	0	0	0	0
P261 PWY coenzyme M biosynthesis I	0	0.09	0	0	0	0	0	0	0	0
PWY 5464 superpathway of cytosolic glycolysis plants pyruvate dehydrogenase and TCA cycle	0	0.09	0	0	0	0	0	0	0	0
PWY 5181 toluene degradation III aerobic via p cresol	0	0.09	0	0	0	0	0	0	0	0
ANAGLYCOLYSIS PWY glycolysis III from glucose	0	0.09	0	0	0	0	0	0	0	0
PWY 5138 unsaturated even numbered fatty acid beta oxidation	0	0.08	0	0	0	0	0	0	0	0
ANAEROFRUCAT PWY homolactic fermentation	0	0.08	0	0	0	0	0	0	0	0
PWY 5030 L histidine degradation III	0	0.07	0	0	0	0	0	0	0	0
PWY 6834 spermidine biosynthesis III	0	0.18	0	0	0	0	0	0	0	0
DENITRIFICATION PWY nitrate reduction I denitrification	0	0.18	0	0	0	0	0	0	0	0
PWY 7208 superpathway of pyrimidine nucleobases salvage	0	0.18	0	0	0	0	0	0	0	0
PWY 6471 peptidoglycan biosynthesis IV Enterococcus faecium	0	0.18	0	0	0	0	0	0	0	0
PWY 6305 putrescine biosynthesis IV	0	0.18	0	0	0	0	0	0	0	0
PWY 5179 toluene degradation V aerobic via toluene cis diol	0	0.18	0	0	0	0	0	0	0	0
PWY 7184 pyrimidine deoxyribonucleotides de novo biosynthesis I	0	0.18	0	0	0	0	0	0	0	0
P184 PWY protocatechuate degradation I meta cleavage pathway	0	0.18	0	0	0	0	0	0	0	0
PWY 7211 superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	0	0.18	0	0	0	0	0	0	0	0
PROTOCATECHUATE ORTHO CLEAVAGE PWY protocatechuate degradation II ortho cleavage pathway	0	0.18	0	0	0	0	0	0	0	0
PWY 7389 superpathway of anaerobic energy metabolism invertebrates	0	0.19	0	0	0	0	0	0	0	0
PWY 561 superpathway of glyoxylate cycle and fatty acid degradation	0	0.19	0	0	0	0	0	0	0	0
LPSSYN PWY superpathway of lipopolysaccharide biosynthesis	0	0.19	0	0	0	0	0	0	0	0
PWY 7210 pyrimidine deoxyribonucleotides biosynthesis from CTP	0	0.19	0	0	0	0	0	0	0	0
CENTFERM PWY pyruvate fermentation to butanoate	0	0.19	0	0	0	0	0	0	0	0
PWY 6590 superpathway of Clostridium acetobutylicum acidogenic fermentation	0	0.19	0	0	0	0	0	0	0	0
PWY 7218 photosynthetic 3 hydroxybutanoate biosynthesis engineered	0	0.19	0	0	0	0	0	0	0	0
PHOTOALL PWY oxygenic photosynthesis	0	0.19	0	0	0	0	0	0	0	0
PWY 6886 1 butanol autotrophic biosynthesis	0	0.19	0	0	0	0	0	0	0	0
METHYLGALLATE DEGRADATION PWY methylgallate degradation	0	0.2	0	0	0	0	0	0	0	0
GALLATE DEGRADATION I PWY gallate degradation II	0	0.2	0	0	0	0	0	0	0	0
PWY66 409 superpathway of purine nucleotide salvage	0	0.2	0	0	0	0	0	0	0	0
PWY 7456 mannan degradation	0	0.2	0	0	0	0	0	0	0	0
PWY 7221 guanosine ribonucleotides de novo biosynthesis	0	0.2	0	0	0	0	0	0	0	0
HEMESYN2 PWY heme biosynthesis II anaerobic	0	0.2	0	0	0	0	0	0	0	0
PWY0 162 superpathway of pyrimidine ribonucleotides de novo biosynthesis	0	0.2	0	0	0	0	0	0	0	0
PWY 6797 6 hydroxymethyl dihydropterin diphosphate biosynthesis II archaea	0	0.2	0	0	0	0	0	0	0	0
PWY5F9 12 biphenyl degradation	0	0.2	0	0	0	0	0	0	0	0
PWY 5079 L phenylalanine degradation III	0	0.2	0	0	0	0	0	0	0	0
PWY 7090 UDP 2 3 diacetamido 2 3 dideoxy alpha D mannuronate biosynthesis	0	0.16	0	0	0	0	0	0	0	0
PWY 6785 hydrogen production VIII	0	0.17	0	0	0	0	0	0	0	0
PWY3DJ 35471 L ascorbate biosynthesis IV	0	0.17	0	0	0	0	0	0	0	0
PWY0 1415 superpathway of heme biosynthesis from uroporphyrinogen III	0	0.17	0	0	0	0	0	0	0	0
PWY 7332 superpathway of UDP N acetylglucosamine derived O antigen building blocks biosynthesis	0	0.17	0	0	0	0	0	0	0	0
PWY 7228 superpathway of guanosine nucleotides de novo biosynthesis I	0	0.17	0	0	0	0	0	0	0	0
LYSINE AMINOAD PWY L lysine biosynthesis IV	0	0.17	0	0	0	0	0	0	0	0
PWY 6572 chondroitin sulfate degradation I bacterial	0	0.17	0	0	0	0	0	0	0	0
PWY 101 photosynthesis light reactions	0	0.17	0	0	0	0	0	0	0	0
PWY 6467 Kdo transfer to lipid IVA III Chlamydia	0	0.17	0	0	0	0	0	0	0	0
PWY 6174 mevalonate pathway II archaea	0	0.17	0	0	0	0	0	0	0	0
PWY 6125 superpathway of guanosine nucleotides de novo biosynthesis II	0	0.17	0	0	0	0	0	0	0	0
PWY 7222 guanosine deoxyribonucleotides de novo biosynthesis II	0	0.16	0	0	0	0	0	0	0	0
PWY 7220 adenosine deoxyribonucleotides de novo biosynthesis II	0	0.16	0	0	0	0	0	0	0	0
PWY 6126 superpathway of adenosine nucleotides de novo biosynthesis II	0	0.16	0	0	0	0	0	0	0	0
RHAMCAT PWY L rhamnose degradation I	0	0.16	0	0	0	0	0	0	0	0
DENOVOPURINE2 PWY superpathway of purine nucleotides de novo biosynthesis II	0	0.16	0	0	0	0	0	0	0	0
PWY0 1479 tRNA processing	0	0.17	0	0	0.15	0	0	0	0	0
PWY 5941 glycogen degradation II eukaryotic	0	0.17	0	0	0	0	0	0	0.18	0
PWY 5743 3 hydroxypropanoate cycle	0	0.13	0	0	0	0	0	0	0.18	0
LEU DEG2 PWY L leucine degradation I	0	0.13	0	0	0	0	0	0	0.18	0
TRNA CHARGING PWY tRNA charging	0	0.09	0	0	0	0	0	0	0.18	0
PWY 5789 3 hydroxypropanoate 4 hydroxybutanate cycle	0	0.05	0	0	0	0	0	0	0.18	0
PWY 3841 folate transformations II	0	0	0	0	0	0	0	0	0.18	0
PWY 1042 glycolysis IV plant cytosol	0	0	0	0	0	0	0	0	0.18	0
PWY 7431 aromatic biogenic amine degradation bacteria	0	0	0	0	0	0	0	0	0.18	0
GLUCONEO PWY gluconeogenesis I	0	0	0	0	0	0	0	0	0.18	0
RUMP PWY formaldehyde oxidation I	0	0.06	0	0	0	0	0	0.12	0	0
PWY 6901 superpathway of glucose and xylose degradation	0	0.17	0	0	0	0	0	0.17	0	0
PWY 7286 7 3 amino 3 carboxypropyl wyosine biosynthesis	0	0	0	0	0	0	0	0.15	0	0
PWY 7013 L 1 2 propanediol degradation	0	0	0	0	0	0	0	0.17	0	0
PWY 5705 allantoin degradation to glyoxylate III	0	0	0	0	0	0	0	0.12	0	0
GLUCARDEG PWY D glucarate degradation I	0	0.04	0	0	0	0	0.15	0	0	0
DHGLUCONATE PYR CAT PWY glucose degradation oxidative	0	0.04	0	0	0	0	0.15	0	0	0
PWY 5656 mannosylglycerate biosynthesis I	0	0.05	0	0	0	0	0.15	0	0	0
GLUCARGALACTSUPER PWY superpathway of D glucarate and D galactarate degradation	0	0.04	0	0	0	0	0.19	0	0	0
GALACTARDEG PWY D galactarate degradation I	0	0.04	0	0	0	0	0.19	0	0	0
ALL CHORISMATE PWY superpathway of chorismate metabolism	0	0.05	0	0	0	0	0.17	0	0	0
PWY 5420 catechol degradation II meta cleavage pathway	0	0.14	0	0	0	0	0.18	0	0	0
PWY 5419 catechol degradation to 2 oxopent 4 enoate II	0	0.15	0	0	0	0	0.18	0	0	0
AEROBACTINSYN PWY aerobactin biosynthesis	0	0.13	0	0	0	0	0.16	0	0	0
PWY 5747 2 methylcitrate cycle II	0	0.17	0	0	0	0	0.17	0	0	0
NAGLIPASYN PWY lipid IVA biosynthesis	0	0.15	0	0	0	0	0.15	0	0	0
ORNARGDEG PWY superpathway of L arginine and L ornithine degradation	0	0.13	0	0	0	0	0.15	0	0	0
ARGDEG PWY superpathway of L arginine putrescine and 4 aminobutanoate degradation	0	0.13	0	0	0	0	0.15	0	0	0
PWY 622 starch biosynthesis	0	0.13	0	0	0	0	0.15	0	0	0
PWY 5686 UMP biosynthesis	0	0	0	0	0	0	0.17	0	0	0
PWY 5189 tetrapyrrole biosynthesis II from glycine	0	0	0	0	0	0	0.16	0	0	0
URDEGR PWY superpathway of allantoin degradation in plants	0	0	0	0	0	0	0.15	0	0	0
PWY 5692 allantoin degradation to glyoxylate II	0	0	0	0	0	0	0.15	0	0	0
PWY 5838 superpathway of menaquinol 8 biosynthesis I	0	0	0	0	0	0	0.15	0	0	0
PWY 5861 superpathway of demethylmenaquinol 8 biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 5837 1 4 dihydroxy 2 naphthoate biosynthesis I	0	0	0	0	0	0	0.15	0	0	0
PWY 5791 1 4 dihydroxy 2 naphthoate biosynthesis II plants	0	0	0	0	0	0	0.15	0	0	0
PWY 5863 superpathway of phylloquinol biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 5897 superpathway of menaquinol 11 biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 5840 superpathway of menaquinol 7 biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 5898 superpathway of menaquinol 12 biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 5899 superpathway of menaquinol 13 biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 6700 queuosine biosynthesis	0	0	0	0	0	0	0.15	0	0	0
PWY 2723 trehalose degradation V	0	0	0	0	0	0	0.15	0	0	0
PWY 7274 D cycloserine biosynthesis	0	0	0	0	0	0	0.19	0	0	0
PWY 5896 superpathway of menaquinol 10 biosynthesis	0	0	0	0	0	0	0.18	0	0	0
P165 PWY superpathway of purines degradation in plants	0	0	0	0	0	0	0.19	0	0	0
GLYCOLYSIS E D superpathway of glycolysis and Entner Doudoroff	0	0	0	0	0	0	0.19	0	0	0
PWY 5862 superpathway of demethylmenaquinol 9 biosynthesis	0	0	0	0	0	0	0.19	0	0	0
PWY 5845 superpathway of menaquinol 9 biosynthesis	0	0	0	0	0	0	0.19	0	0	0
PWY66 201 nicotine degradation IV	0	0	0	0	0	0	0.15	0	0	0
PWY 6415 L ascorbate biosynthesis V	0	0	0	0	0	0	0.15	0	0	0
PWY 7269 NAD NADP NADH NADPH mitochondrial interconversion yeast	0	0	0	0	0	0	0.15	0	0	0
PWY 5920 superpathway of heme biosynthesis from glycine	0	0	0	0	0	0	0.15	0	0	0
PWY 6992 1 5 anhydrofructose degradation	0	0	0	0	0	0	0.15	0	0	0
PWY66 367 ketogenesis	0	0	0	0	0	0	0.14	0	0	0
PWY0 1241 ADP L glycero beta D manno heptose biosynthesis	0	0	0	0	0	0	0.14	0	0	0
PWY 7616 methanol oxidation to carbon dioxide	0	0	0	0	0	0	0.14	0	0	0
PWY 4221 pantothenate and coenzyme A biosynthesis II plants	0	0.09	0	0	0	0	0	0	0.18	0.1
PWY 3941 beta alanine biosynthesis II	0	0.09	0	0	0	0	0	0	0.18	0.1
PWY 7373 superpathway of demethylmenaquinol 6 biosynthesis II	0	0	0	0	0	0	0	0	0	0.18

Table S7. Related to Figure 4. Correlation coefficients for all significant GO category associations

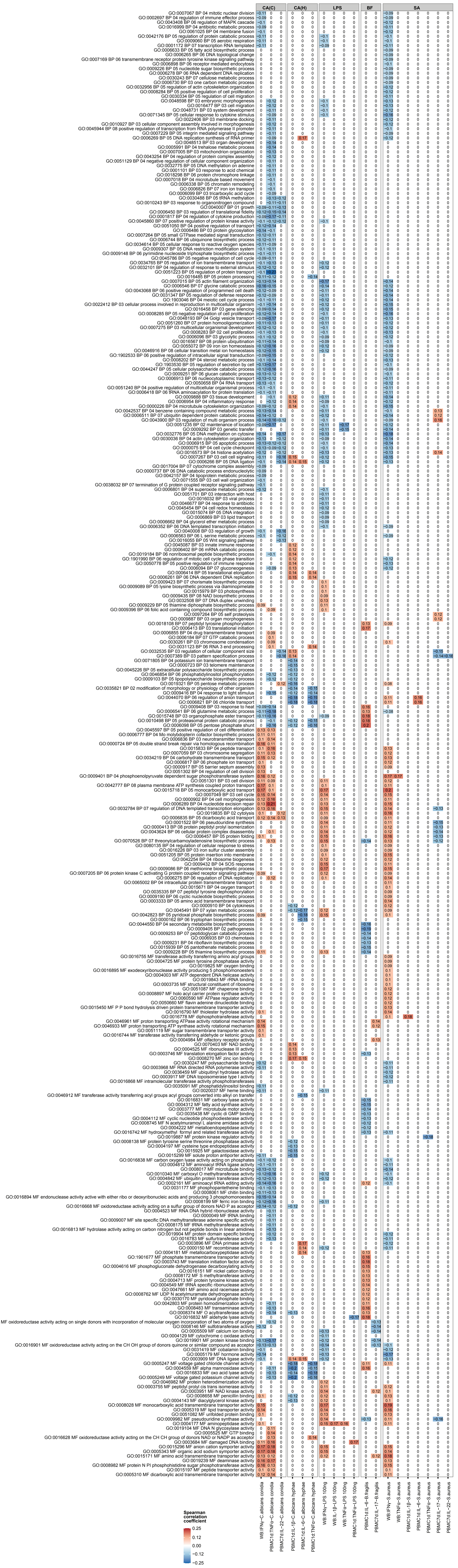


Table S8. Related to Figure 4. FDR values for all significant GO category associations