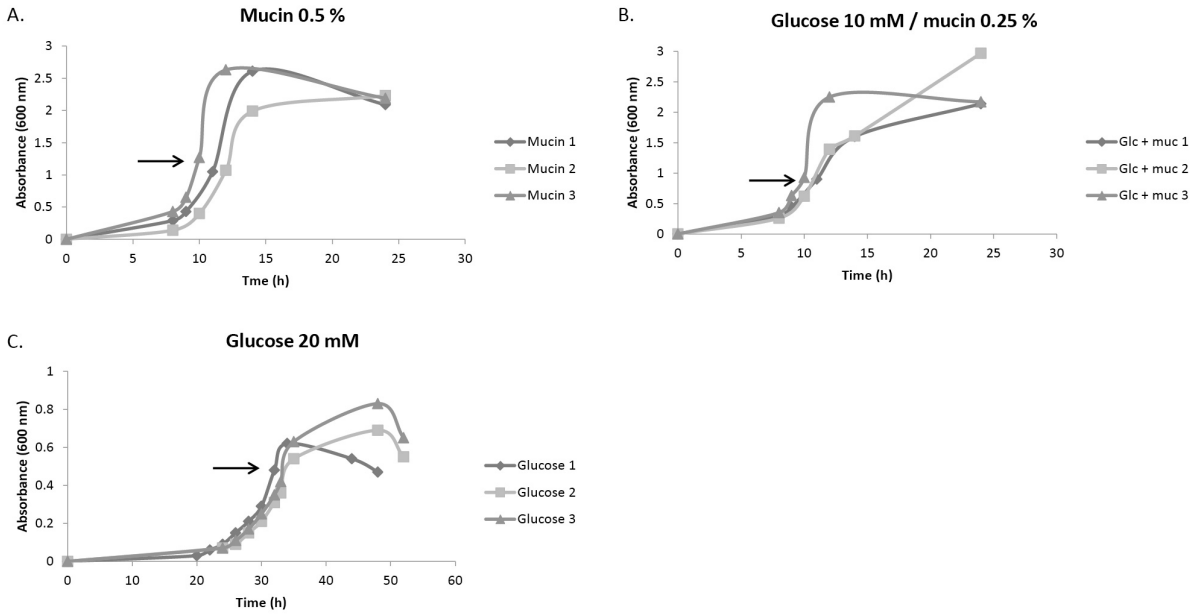

FIG S1. *A. muciniphila* cultures were harvested in mid-exponential phase for RNA-extraction. *A. muciniphila* was grown on mucin (A), a mixture of glucose and mucin (B), or glucose (C). Three replicates of each condition were sampled. Arrows indicate time points for sampling.

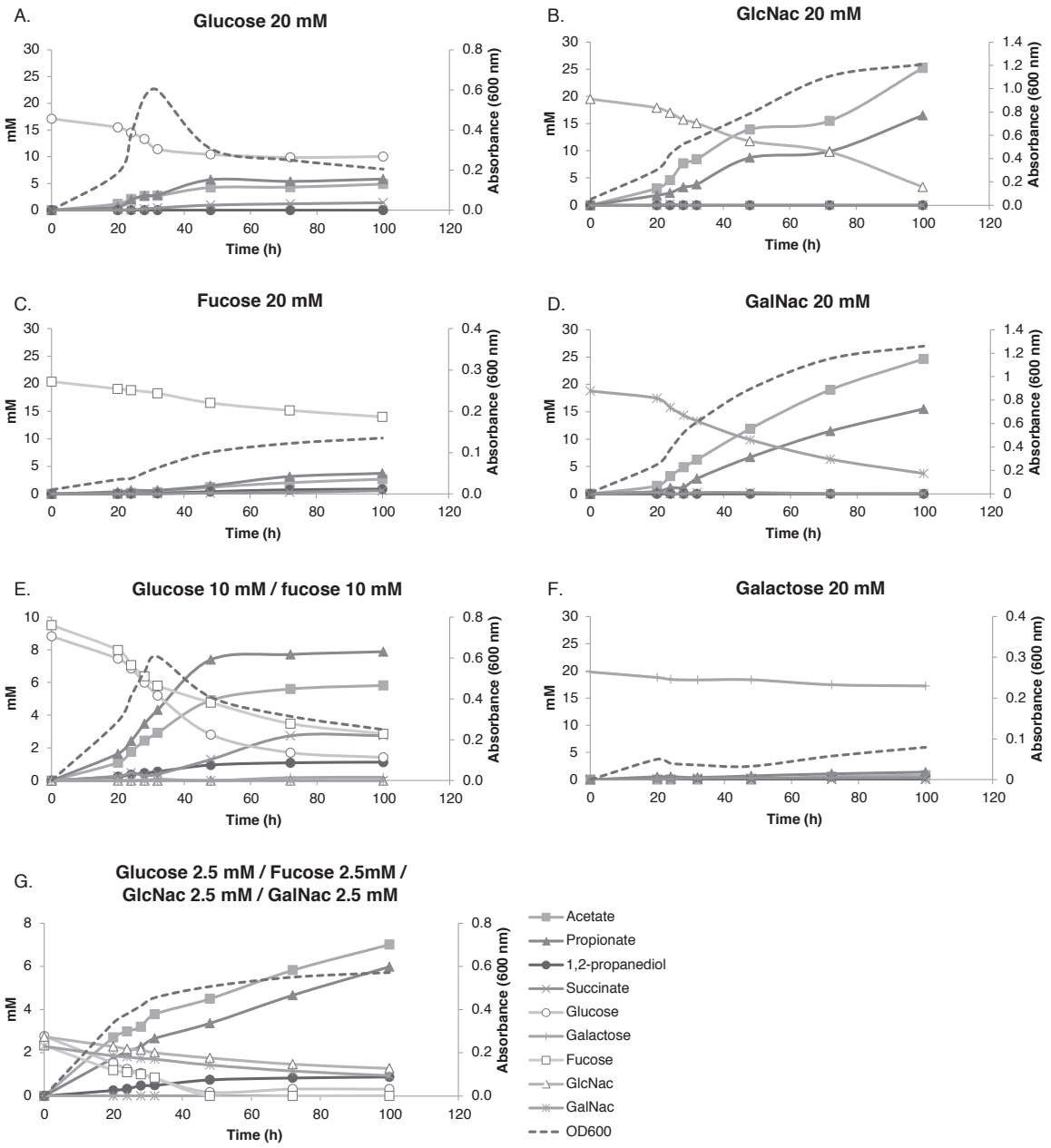

FIG S2. *A. muciniphila* utilization of glucose and mucin-derived sugars. *A. muciniphila* is able to efficiently grow on glucose, N-acetylglucosamine (GlcNAc) and N-acetylgalactosamine (GalNAc). Highest yields are reached when grown on GlcNAc or GalNAc. Galactose and fucose degradation by *A. muciniphila* is weak. However, in a mixture glucose and fucose are the preferred substrates. Values represent mean of three replicate experiments.

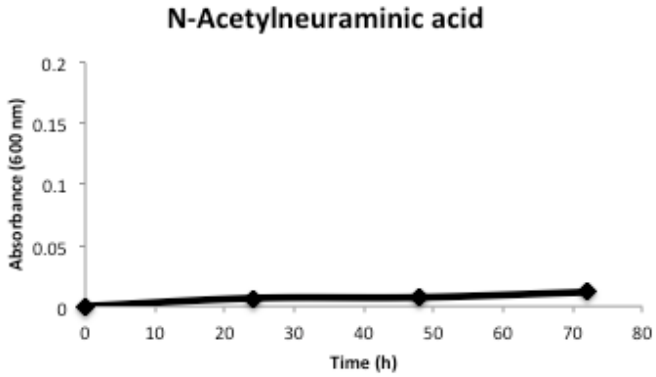

FIG S3. ***A. muciniphila*** **is not able to grow on N-acetylneuraminic acid as the sole carbon source.**

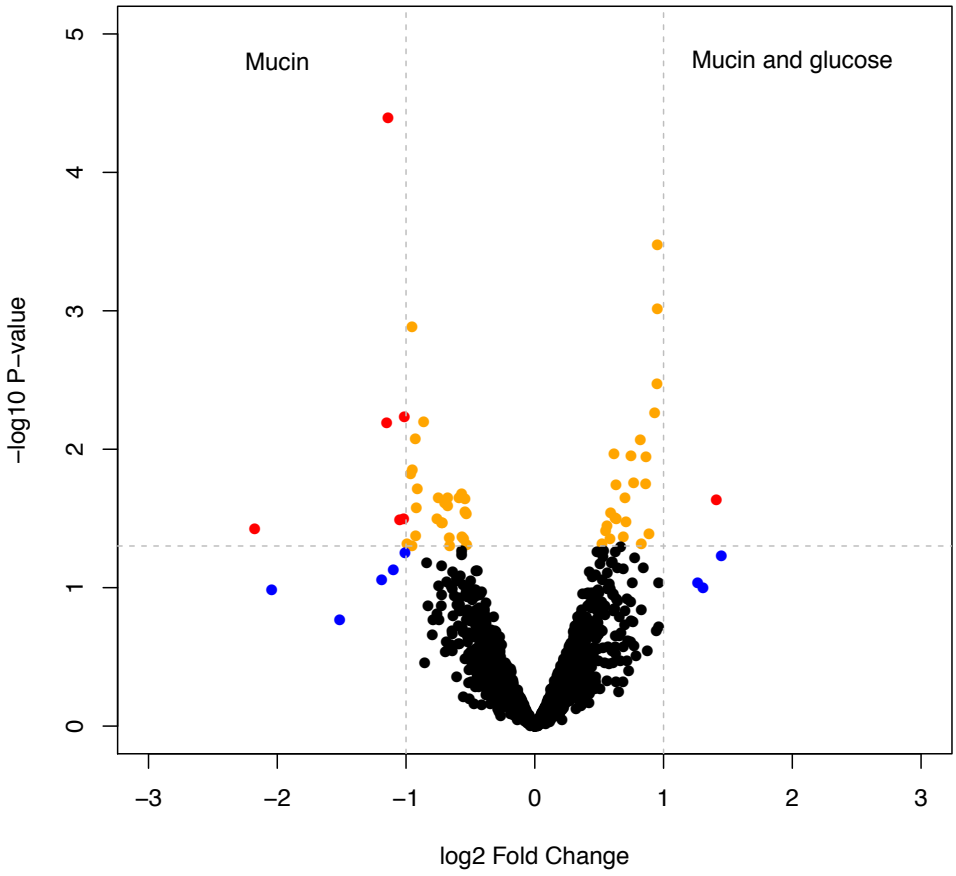

FIG S4. Volcano plot of the distribution of gene expression for *A. muciniphila* grown on mucin vs. mixture of mucin and glucose. Positive fold change indicates upregulation in the mixture condition. Red data points indicate genes having $p < 0.05$ and fold change ≥ 2.

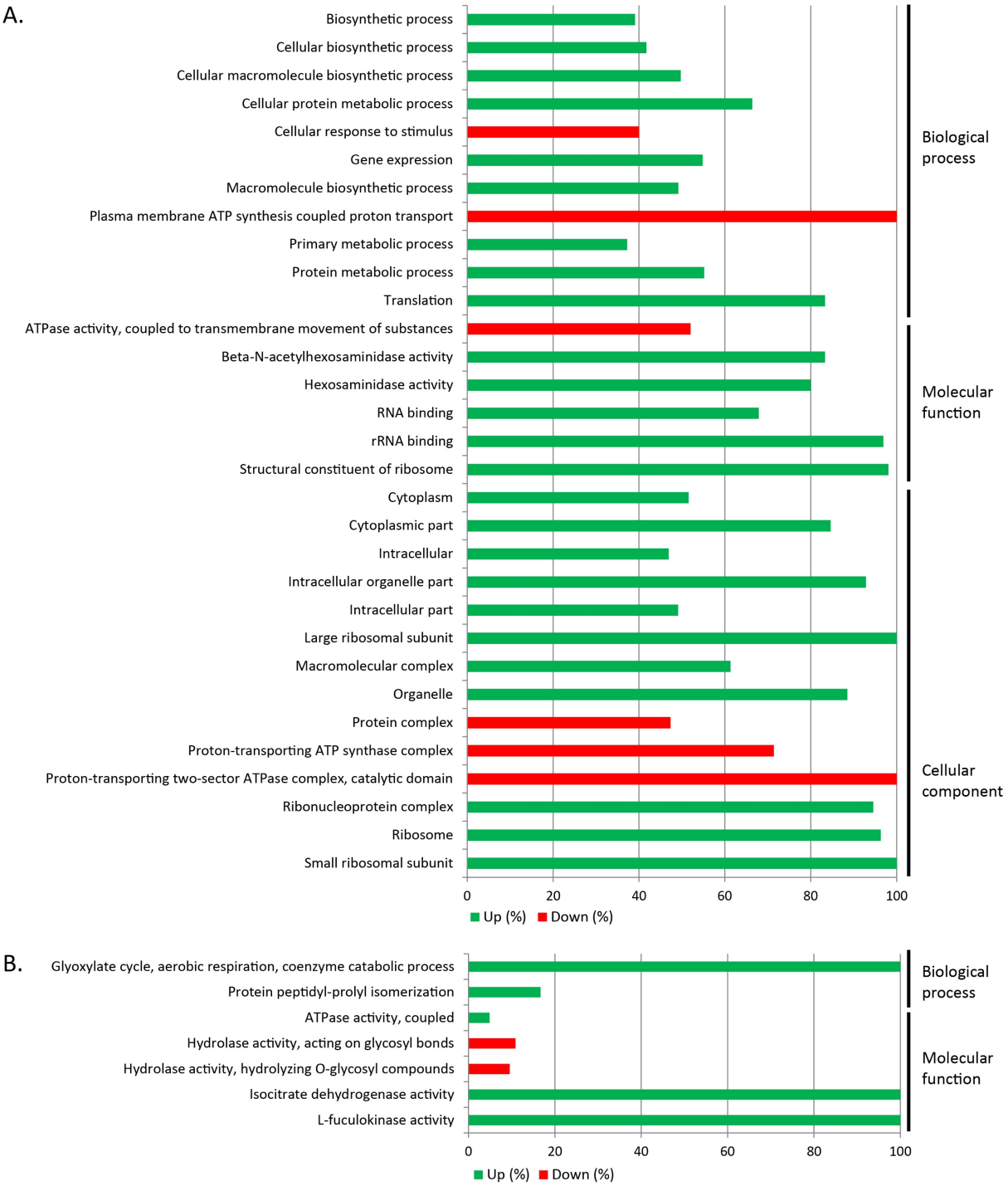

FIG S5. Functionally grouped gene ontology of genes differentially expressed in mucin and glucose. Each bar represents the ratio of the number of differentially expressed genes belonging to the GO terms shown in the y-axis. (A) *A. muciniphila* grown on mucin vs. glucose. Green, upregulated in mucin; red, downregulated in mucin. (B) *A. muciniphila* grown on mucin vs. mixture (mucin+glucose). Green, upregulated in mixture; red, downregulated in mixture.

	Acetate		Propionate		Succinate		1,2-propanediol	
	10-12 h	24 h	10-12 h	24 h	10-12 h	24 h	10-12 h	24 h
Mucin 0.5 %	6.1 ± 2.4	17.1 ± 3.6	4.1 ± 2.3	12.4 ± 3.6	1.8 ± 1.0	0.1 ± 0.1	0.0 ± 0.0	0.7 ± 0.1
Glucose 10 mM / mucin 0.25 %	6.0 ± 3.7	12.2 ± 3.0	3.1 ± 4.0	12.8 ± 5.0	2.0 ± 0.6	1.1 ± 0.5	0.1 ± 0.1	0.1 ± 0.2

Table S1. Fermentation end products of *A. muciniphila* during growth on different substrates. Samples were obtained during mid-exponential phase (~10-12 h incubation, used for transcriptome analysis) and in stationary phase (24 h incubation). Values represent means of triplicate cultures with standard deviations. N.D., not detected.

	Glucose		Fucose		Galactose	
	10-12 h	24 h	10-12 h	24 h	10-12 h	24 h
Mucin 0.5 %	N.D.	N.D.	0.1 ± 0.1	N.D.	0.1 ± 0.1	N.D.
Glucose 10 mM / mucin 0.25 %	-1.7 ± 0.6	-8.3 ± 0.0	N.D.	N.D.	0.3 ± 0.2	0.0 ± 0.1

Table S2. Degradation of sugars in *A. muciniphila* cultures during growth on different substrates. Values represent means of triplicate cultures with standard deviations. N.D., not detected.

	Glucose		Acetate		Propionate		Succinate	
	32-33 h	48 h	32-33 h	48 h	32-33 h	48 h	32-33 h	48 h
Glucose 20 mM	-4.9 ± 0.9	-11.5 ± 2.8	1.7 ± 0.7	5.5 ± 0.6	1.6 ± 0.1	8.0 ± 0.9	0.6 ± 0.1	1.8 ± 0.2

Table S3. Glucose degradation and fermentation end products of *A. muciniphila* during growth on glucose. Samples were obtained during mid-exponential phase (~32-33 h incubation, used for transcriptome analysis) and in stationary phase (48 h incubation). Values represent means of triplicate cultures with standard deviations.

	Glucose			Mucin			Mucin + glucose		
	1	2	3	1	2	3	1	2	3
Total no. of reads	11047878	10545771	18497197	11645389	17180153	11743614	16724960	14660237	17949331
Total no. of reads mapped to the genome	10302029	10206943	17953823	11459340	16915727	11596495	16215886	14271680	17217612
Percentage of reads mapped to the genome	93.2	96.8	97.1	98.4	98.5	98.7	97.0	97.3	95.9
Total no. of reads mapped to protein coding regions	7063596	6904150	12096349	8399083	11766433	8157964	12130637	9767040	11811538

Table S4. Summary of the RNA-Seq raw data analysis for transcriptome analysis of *A. muciniphila* grown on glucose, mucin and a mixture of mucin and glucose.