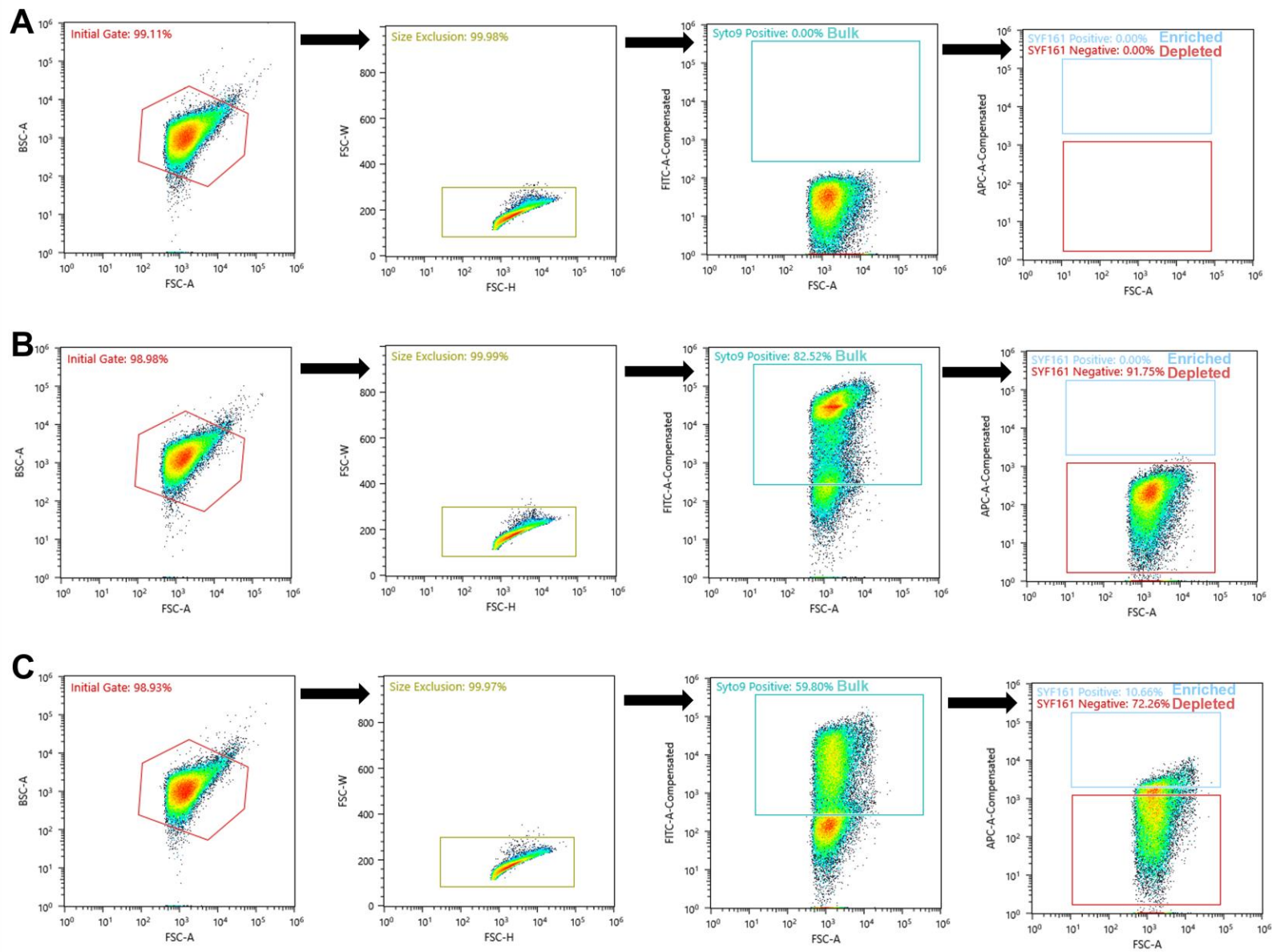
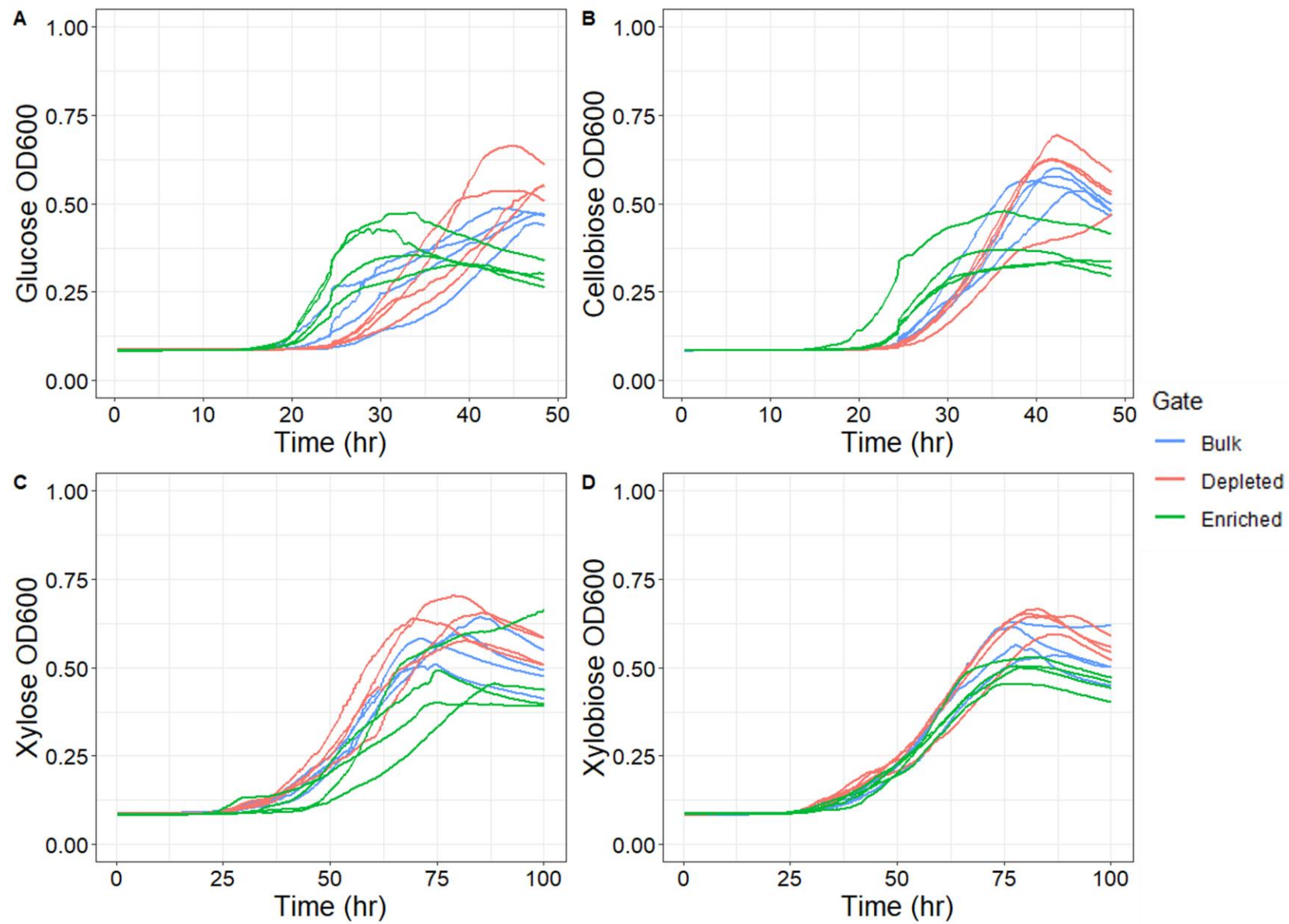


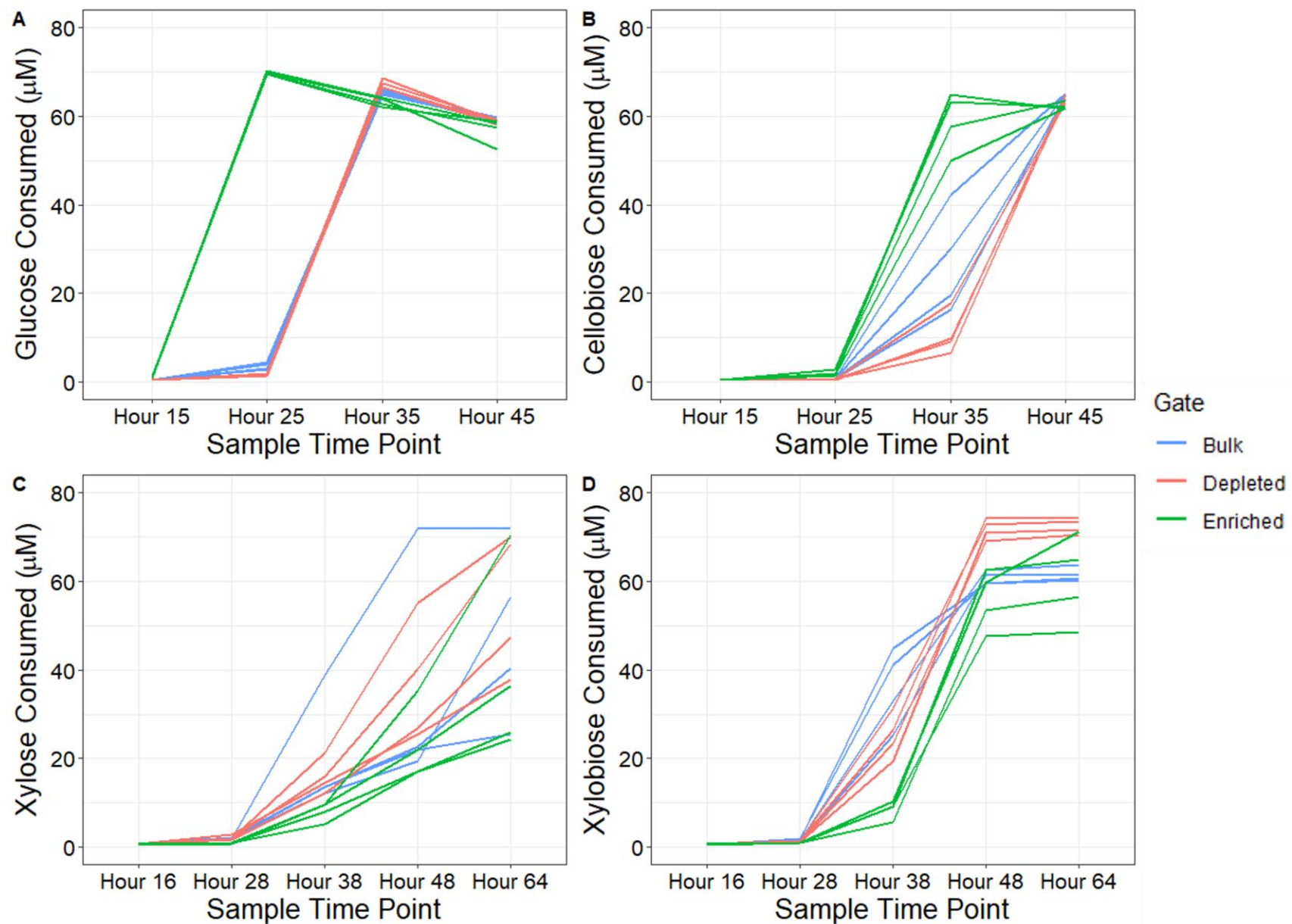
**SI Figure 1.** Sony SH800 sorter plots for sorting with GH4a activity-based probe. **(A)** Original set of sorter gates determined with an unlabeled control sample. **(B)** Sorter gates to determine biological events only containing the Syto59 signal. **(C)** Final sorter gates used to sort biological events containing signal from GH4a-ABP. Black arrows direction of nested plots.



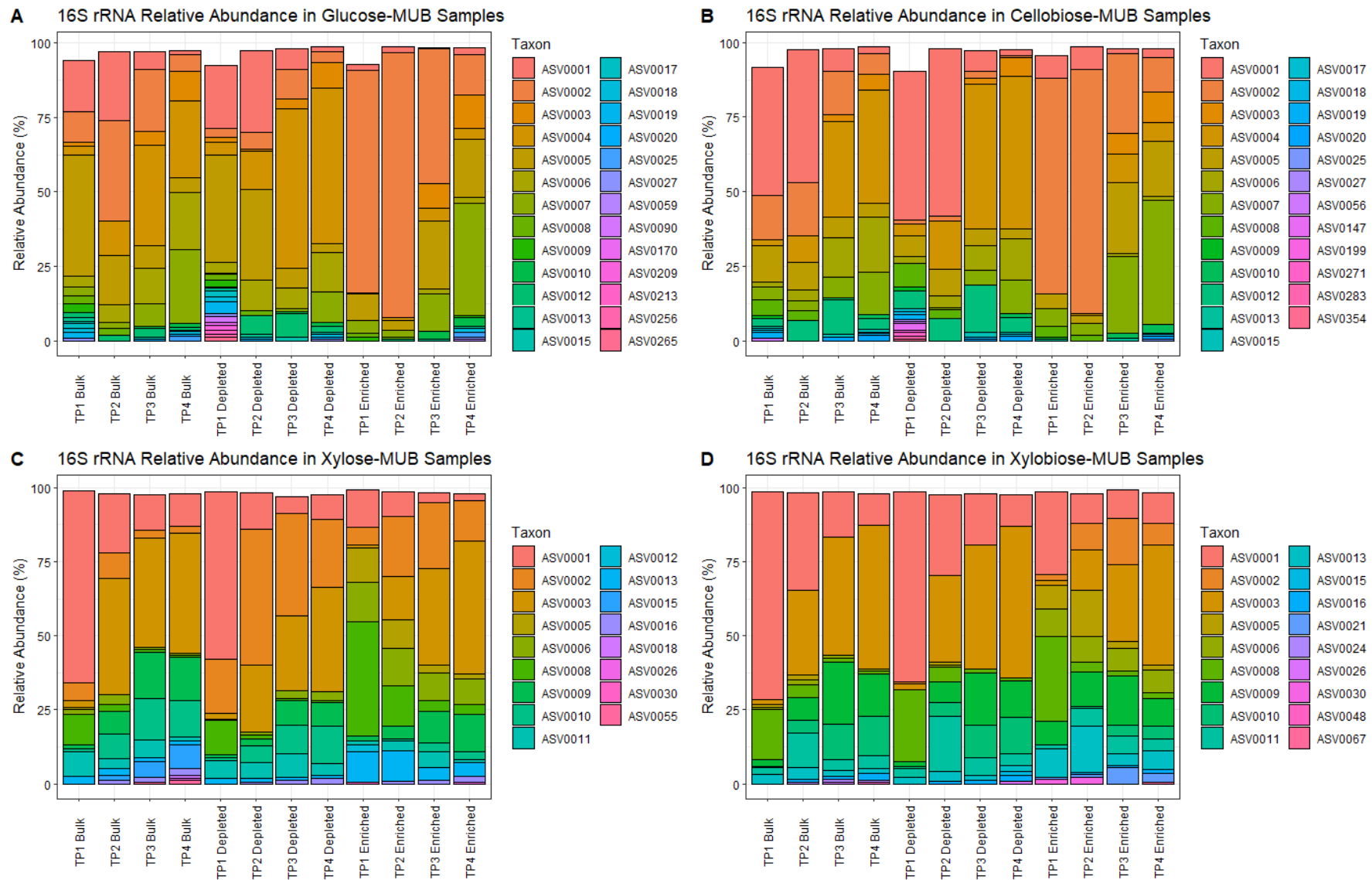
**SI Figure 2.** Sony SH800 sorter plots for sorting with SYF161 activity-based probe. **(A)** Original set of sorter gates determined with an unlabeled control sample. **(B)** Sorter gates to determine biological events only containing the Syto9 signal. **(C)** Final sorter gates used to sort biological events containing signal from SYF161-ABP. Black arrows direction of nested plots.



**SI Figure 3.** Optical density plots for the continuous plate reader assay (OD600). **(A)** GH4a sorted populations with glucose-MUB. **(B)** GH4a sorted populations with cellobiose-MUB. **(C)** SYF161 sorted populations with xylose-MUB. **(D)** SYF161 sorted populations with xylobiose-MUB.



**SI Figure 4.** Discrete kinetic plots for substrate consumed ( $\mu\text{M}$ ) at distinct time points. **(A)** Glucose-MUB incubated samples that were sampled at 15, 25, 35, and 45-hours during the incubation. **(B)** Cellobiose-MUB incubated samples that were sampled at 15, 25, 35, and 45-hours during the incubation. **(C)** Xylose-MUB incubated samples that were sampled at 16, 28, 38, 48, and 64-hours during the incubation. **(D)** Xylobiose-MUB incubated samples that were sampled at 16, 28, 38, 48, and 64-hours during the incubation.



**SI Figure 5.** 16S rRNA gene relative abundances for averaged sorted incubations. Incubations from three sorter populations samples at four time points. Taxa represented as amplicon sequence variant (ASV) for taxa above 0.5 % relative abundance in the averaged samples. **(A)** Glucose-MUB incubated samples sampled at 15, 25, 35, and 45-hours during the incubation. **(B)** Cellobiose-MUB incubated samples that were sampled at 15, 25, 35, and 45-hours during the incubation. **(C)** Xylose-MUB incubated samples that were sampled at 16, 28, 38, 48, and 64-hours during the incubation. **(D)** Xylobiose-MUB incubated samples that were sampled at 16, 28, 38, 48, and 64-hours during the incubation.



**Supplementary Table 1. PERMANOVA analysis of relative abundance community composition for FACS incubated samples.** Pairwise comparison between sample types were compared by PERMANOVA using Bray Curtis dissimilarity with Holm p-value adjustment.

Time point	Sample comparison	Glucose			Cellobiose			Xylose			Xylobiose		
		F Model	R2	Adjusted p value	F Model	R2	Adjusted p value	F Model	R2	Adjusted p value	F Model	R2	Adjusted p value
TP1	Bulk v Depleted	1.57	0.0892	0.063	2.93	0.164	0.011	3.92	0.151	0.046	6.93	0.240	0.003
	Bulk v Enriched	72.48	0.801	0.003	41.96	0.688	0.003	71.07	0.764	0.003	90.69	0.805	0.003
	Enriched v Depleted	36.60	0.696	0.003	52.99	0.768	0.003	48.18	0.687	0.003	57.28	0.723	0.003
TP2	Bulk v Depleted	28.65	0.566	0.003	18.21	0.453	0.003	13.32	0.377	0.006	2.48	0.101	0.071
	Bulk v Enriched	97.46	0.816	0.003	278.69	0.927	0.003	14.62	0.399	0.003	21.43	0.493	0.003
	Enriched v Depleted	817.79	0.974	0.003	456.05	0.954	0.003	8.32	0.274	0.006	24.96	0.531	0.003
TP3	Bulk v Depleted	25.70	0.539	0.003	8.91	0.288	0.003	17.30	0.440	0.003	2.95	0.118	0.043
	Bulk v Enriched	59.95	0.732	0.003	18.86	0.462	0.003	13.87	0.387	0.003	9.54	0.303	0.003
	Enriched v Depleted	159.68	0.879	0.003	36.18	0.622	0.003	4.95	0.184	0.019	10.25	0.318	0.003
TP4	Bulk v Depleted	25.82	0.540	0.003	3.24	0.134	0.03	8.79	0.305	0.006	0.85	0.037	0.463
	Bulk v Enriched	74.09	0.771	0.003	30.51	0.629	0.003	9.25	0.316	0.003	12.57	0.364	0.003
	Enriched v Depleted	166.07	0.883	0.003	38.57	0.694	0.003	6.01	0.215	0.008	13.57	0.381	0.003