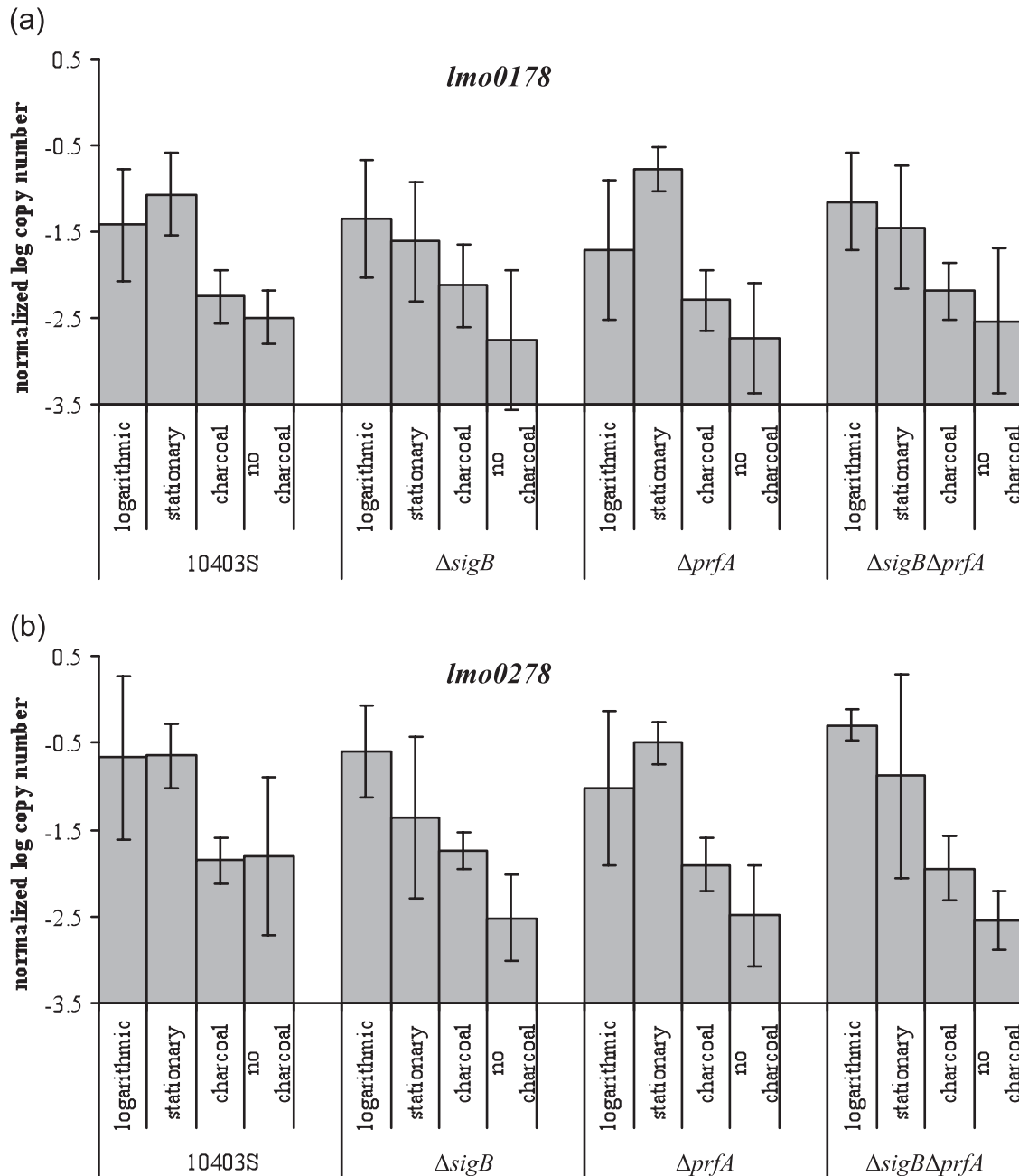


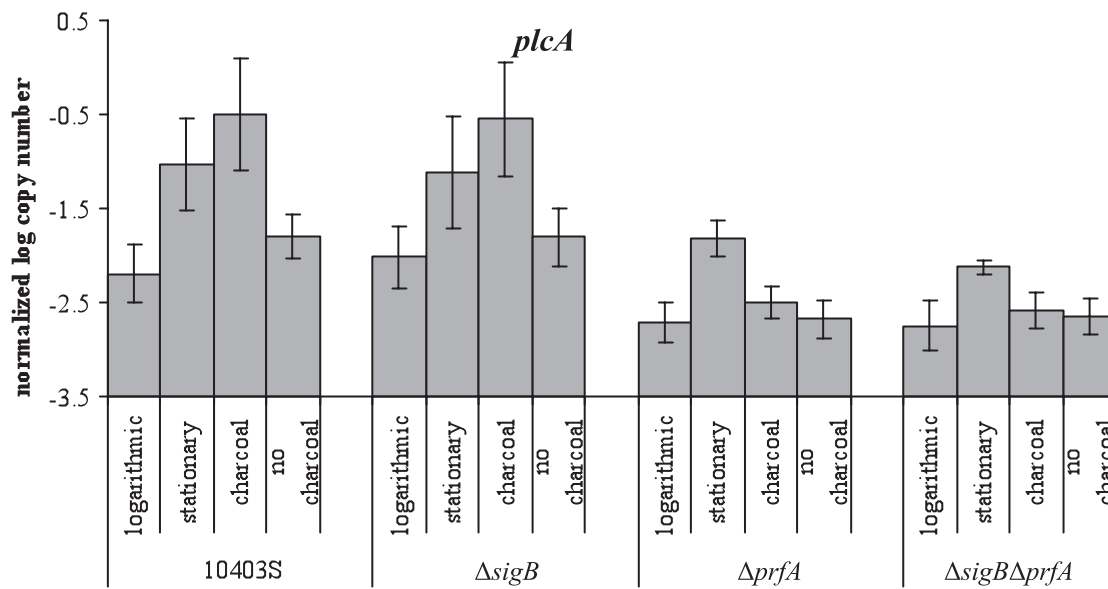
SUPPLEMENTAL TABLE S1. STATISTICAL ANALYSES OF THE EFFECTS OF STRAIN, CONDITION, AND INTERACTIONS BETWEEN STRAIN AND CONDITIONS ON TRANSCRIPT LEVELS FOR DIFFERENT GROUP I, II, AND III GENES

<i>Condition</i>	<i>Gene</i>	<i>p-values for</i>		
		<i>Strain</i>	<i>Condition</i>	<i>Strain × Condition</i>
Charcoal	<i>plcA</i>	<0.0001	<0.0001	0.0002
	<i>lmo0178</i>	NS	0.0013	NS
	<i>lmo0278</i>	NS	0.0103	NS
	<i>opuCA</i>	<0.0001	0.0069	NS
	<i>bsh</i>	<0.0001	NS	NS
	<i>lmo0596</i>	<0.0001	0.0432	NS
	<i>lmo0654</i>	0.0304	NS	NS
Growth phase	<i>plcA</i>	<0.0001	<0.0001	NS
	<i>lmo0178</i>	NS	NS	NS
	<i>lmo0278</i>	NS	NS	NS
	<i>opuCA</i>	<0.0001	0.0001	NS
	<i>bsh</i>	<0.0001	<0.0001	NS
	<i>lmo0596</i>	<0.0001	NS	NS
	<i>lmo0654</i>	0.0004	0.0072	NS

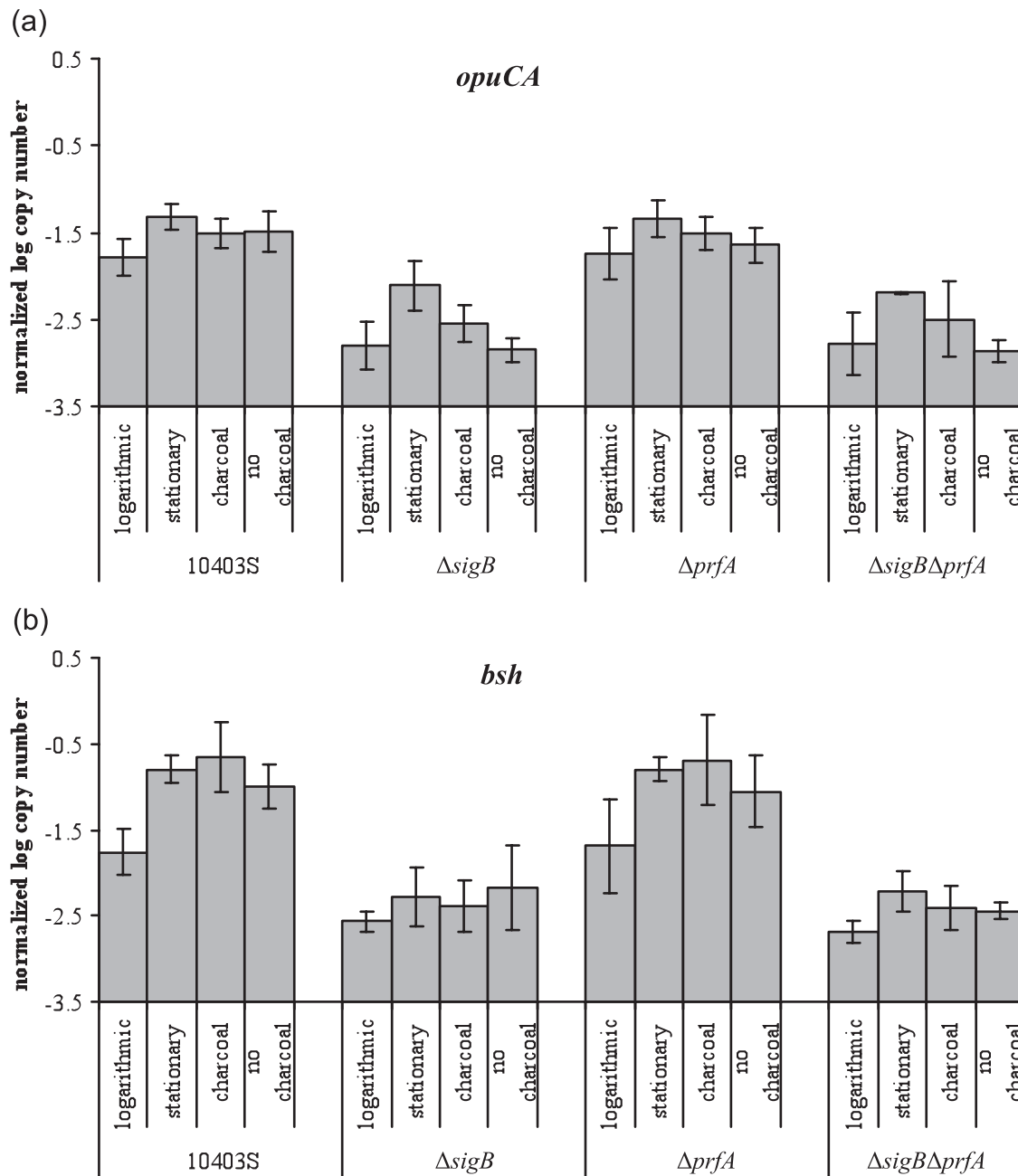
“Charcoal” indicates that statistical analyses were performed on transcript levels for cells grown in the presence or absence of charcoal; “Growth phase” indicates that statistical analyses were performed on transcript levels for cells grown to log phase or stationary phase. NS, not significant.



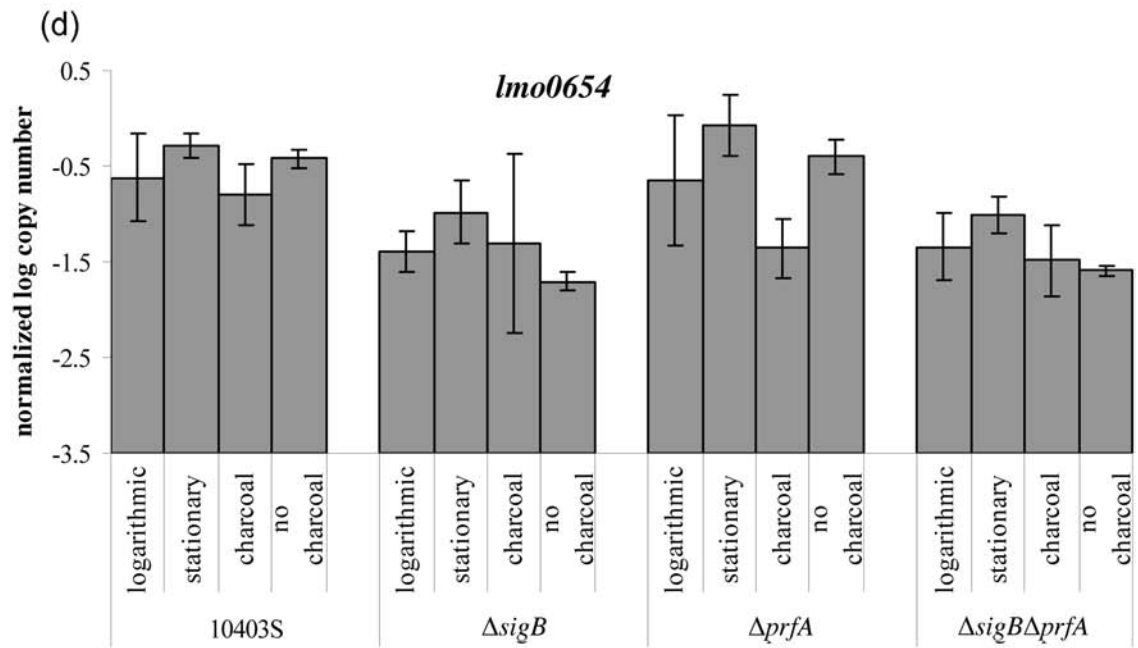
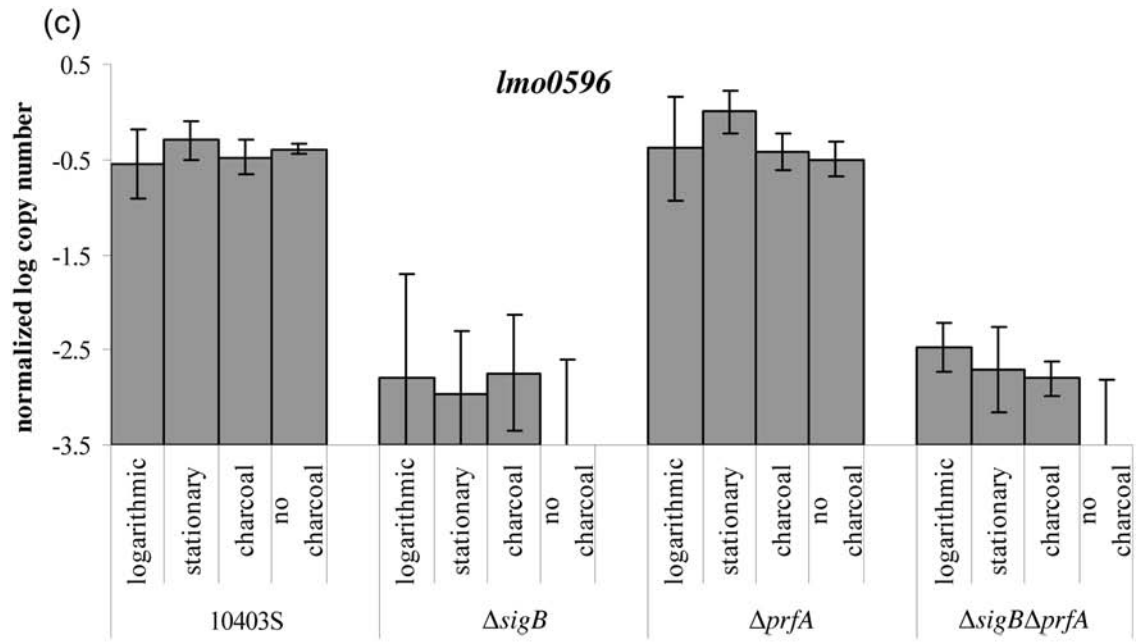
SUPPLEMENTAL FIG. S1. Transcript levels for the group II genes (a) *lmo0178* and (b) *lmo0278* in the *L. monocytogenes* parent strain 10403S and in isogenic $\Delta sigB$, $\Delta prfA$, and $\Delta sigB\Delta prfA$ strains grown to either (i) log phase (OD600 = 0.4; labeled as “logarithmic”) or (ii) stationary phase (OD600 = 2.0; labeled as “stationary”), or exposed to either (i) BHI + 0.2% activated charcoal or (ii) BHI alone. Normalized log copy numbers shown on the Y-axis represent log-transformed transcript levels for *lmo0178* and *lmo0278* normalized to the geometric mean of the transcript levels for the housekeeping genes *rpoB* and *gap*. Data shown represent the mean of qRT-PCR data collected from three to four independent RNA extractions; error bars represent one standard deviation. The data presented in this figure are also shown in Figs. 1 and 2 of this manuscript; the data are arranged differently here to allow for comparisons between transcript levels for a given gene in a given mutant strain.



SUPPLEMENTAL FIG. S2. Transcript levels for the group I gene *plcA* in the *L. monocytogenes* parent strain 10403S and in isogenic $\Delta sigB$, $\Delta prfA$, and $\Delta sigB\Delta prfA$ strains grown to either (i) logarithmic phase (OD600 = 0.4; labeled as “logarithmic”) or (ii) stationary phase (OD600 = 2.0; labeled as “stationary”), or exposed to either (i) BHI + 0.2% activated charcoal or (ii) BHI alone. Normalized log copy numbers shown on the Y-axis represent log-transformed transcript levels for *plcA* normalized to the geometric mean of the transcript levels for the housekeeping genes *rpoB* and *gap*. Data shown represent the mean of qRT-PCR data collected from three to four independent RNA extractions; error bars represent one standard deviation. The data presented in this figure are also shown in Figs. 1 and 2 of this manuscript; the data are arranged differently here to allow comparisons between transcript levels for a given gene in a given mutant strain.



SUPPLEMENTAL FIG. S3. Transcript levels for the group III genes (a) *opuCA*, (b) *bsh*, (c) *lmo0596*, and (d) *lmo0654* in the *L. monocytogenes* parent strain 10403S and isogenic $\Delta sigB$, $\Delta prfA$, and $\Delta sigB\Delta prfA$ strains grown to either (i) logarithmic phase (OD600 = 0.4; labeled as “logarithmic”) or (ii) stationary phase (OD600 = 2.0; labeled as “stationary”), or exposed to either (i) BHI + 0.2% activated charcoal or (ii) BHI alone. Normalized log copy numbers shown on the Y-axis represent log-transformed transcript levels for a given target gene normalized to the geometric mean of the transcript levels for the housekeeping genes *rpoB* and *gap*. Data shown represent the mean of qRT-PCR data collected from three to four independent RNA extractions; error bars represent one standard deviation (data for genes *lmo0596* and *lmo0654* when grown without charcoal represent two independent RNA extractions). The data presented in this figure are also shown in Figs. 1 and 2 of this manuscript; the data are arranged differently in this figure to allow comparisons between transcript levels for a given gene in a given mutant strain.



SUPPLEMENTAL FIG. S3. (continued)