TABLE 3. Mapping of transposon insertions sites that result in white phenotype in *C. sakazakii* ES5

COG functional category[a]	COG functional class	Annotation[b,c]	
		Homologue	Gene product
Mutation in pigment operon			
H: coenzyme transport and metabolism	Geranylgeranyl pyrophosphate synthase	*crtE*	Geranylgeranyl pyrophosphate synthase
GC: carbohydrate transport and metabolism/signal transduction mechanisms	Glucosyl transferases, related to UDP-glucosyltransferase	*crtX*	Zeaxanthin glucosyl transferase
R/E: general function prediction only/amino acid transport and metabolism	Acetyltransferase/choline dehydrogenase and related flavoproteins	*crtY*	Lycopene cyclase
Q: secondary metabolites biosynthesis, transport and catabolism	Phytoene dehydrogenase and related proteins	*crtI*	Phytoene dehydrogenase
I: lipid transport and metabolism	Phytoene/squalene synthase	*crtB*	Phytoene synthase
Mutation outside pigment operon			
C: energy production and conversion	F_oF_1-type ATP synthase, subunit alpha	ESA_04012	F_oF_1 ATP synthase subunit alpha
	F_oF_1-type ATP synthase, subunit beta	ESA_04006	F_oF_1 ATP synthase subunit beta
	F_oF_1-type ATP synthase, subunit gamma	ESA_04007	F_oF_1 ATP synthase subunit gamma
	F_oF_1-type ATP synthase, subunit epsilon (mitochondrial delta subunit)	ESA_04005	F_oF_1 ATP synthase subunit epsilon
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acetyltransferase (E1) component, and related enzymes	ESA_02622	*sucA* 2-oxoglutarate dehydrogenase E1 component
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acetyltransferase (E2) component, and related enzymes	ESA_02621	Dihydrolipoamide acetyltransferase
	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acetyltransferase (E3) component, and related enzymes	ESA_03222	*aceF* dihydrolipoamide acetyltransferase
	Malate/lactate dehydrogenases	ESA_03622	Malate dehydrogenase
	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	ESA_02624	Succinate dehydrogenase flavoprotein subunit
P: inorganic ion transport and metabolism	Na^+/H^+ antiporter	ESA_03316	pH-dependent sodium/proton antiporter
T: signal transduction mechanisms	cAMP-binding proteins, catabolite gene activator, and regulatory subunit of cAMP-dependent protein kinases	ESA_04376	cAMP regulatory protein
	DnaK suppressor protein	ESA_03194	DnaK transcriptional regulator DksA
S: function unknown	Uncharacterized conserved protein	ESA_04343 (Ent638_3811)[d]	Hypothetical protein (intracellular growth attenuator IgA, *Enterobacter* sp. 638)[d]
		ESA_03563 (ETA_03450)[d]	Hypothetical protein (YhbC-like protein, *Erwinia tasmaniensis* Et1/99)[d]
		ESA_00549 (AAG53883)[d]	Hypothetical protein (sigma factor RpoS, *Escherichia coli*)[d]

[a] NCBI clusters of orthologous groups (COG) of proteins.
[b] *Cronobacter sakazakii* ES5 BAC 9E10 for mutations within the pigment operon (accession no. AM384990.1).
[c] NCBI assembly ATCC BAA-894 *C. sakazakii* complete genome for mutations outside pigment operon (accession no. CP000783.1).
[d] Closest annotated homolog.

(data not shown), consistently with the results for LB, all mutant strains showed significantly increased maximum rates of growth (μmax_{wt}, 0.14; $\mu max_{\Delta crtX}$, 0.22; $\mu max_{\Delta crtE}$, 0.24; and $\mu max_{\Delta crtY}$, 0.19; $P = 0.000$).

Cold stress experiments were performed by growing Δ*crtE*, Δ*crtX*, and Δ*crtY* in LB and M9 medium at 10°C (for results in M9, see Fig. 1B). Under these conditions, no significant differences in maximum specific growth rates were detected for Δ*crtY*, Δ*crtE*, and Δ*crtX* in both LB and M9 compared to those of the wild type (in LB, $\mu max_{wt} = 0.04$, $\mu max_{\Delta crtX} = 0.03$, $\mu max_{\Delta crtE} = 0.03$, and $\mu max_{\Delta crtY} = 0.04$; in M9, $\mu max_{wt} = 0.01$, $\mu max_{\Delta crtX} = 0.01$, $\mu max_{\Delta crtE} = 0.01$, and $\mu max_{\Delta crtY} = 0.01$).

To evaluate growth under acidic conditions, wild-type and