

ESI4. Enriched go-terms among the significantly expressed genes between changing copper levels in response to interaction effect of the change in the copper level and the deletion of *CCC2*.

INTERACTION EFFECT		Enriched GO-Biological Process Terms	
		CCC2Δ/ CCC2Δ	Reference strain
UP	High Cu vs Low Cu	Arginine metabolic process (p-val≤ 2.89e-2) Carboxylic acid metabolic process (p-val≤ 5.43e-3)	Iron ion homeostasis (p-val≤ 3.04e-2) Siderophore transport (p-val≤ 2.19e-2)
	High Cu vs Cu Def	ATP synthesis coupled electron transport (p-val≤ 1.41e-2)	Iron ion homeostasis (p-val≤ 5.98e-3) Siderophore transport (p-val≤ 1.11e-2) "de novo" NAD biosynthetic process from tryptophan (p-val≤ 3.55e-2) "de novo" UMP biosynthetic process (p-val≤ 4.27e-2) Response to copper ion (p-val≤ 3.55e-2) Cellular cell wall organization or biogenesis (p-val≤ 3.55e-2) Nucleotide biosynthetic process (p-val≤ 1.27e-2) Regulation of sporulation (p-val≤ 4.27e-2)
DOWN	High Cu vs Cu Def	Iron ion homeostasis (p-val≤ 4.63e-3) Siderophore transport (p-val≤ 1.52e-6)	
	Low Cu vs Cu Def	Arginine metabolic process (p-val≤ 2.20e-03) Ornithine (p-val≤ 8.34e-3) and urea (p-val≤ 5.24e-3) metabolic process Drug membrane transport (p-val≤ 8.34e-3) Cellular keton metabolic process (p-val≤ 9.47e-3) "de novo" UMP biosynthetic process (p-val≤ 7.83e-3)	