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Erratum: Global transcriptomic responses of *Escherichia coli* K-12 to volatile organic compounds

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In this Article, the shaded cells and bold numbers in Table 3 have been omitted. The correct Table 3 appears below as Table 1.

Treatment	ID	Gene	B	CHP	CP	DMA	DMS	NMP	NMS	T	Gene description	ISC/SUF
b dms	b1679	sufE	1.49	0.71	0.80	0.79	1.02	-0.02	-0.91	0.91	Sulfur acceptor protein	SUF
b cp dma dms	b1680	sufS	1.83	0.68	1.21	1.21	1.35	0.28	0.36	0.91	Cysteine desulfurase, SufE induced	SUF
b cp dma dms	b1681	sufD	1.72	0.88	1.46	1.11	1.14	0.33	-0.16	0.71	Component of SufBCD Fe-S cluster assembly scaffold	SUF
b cp dms	b1682	sufC	1.77	0.99	1.97	1.11	1.30	0.42	-0.67	0.92	SufBCD Fe-S cluster assembly scaffold protein	SUF
b chp cp dma dms nmp t	b1683	sufB	2.71	1.54	3.12	1.87	2.02	1.44	0.11	1.77	Component of SufBCD Fe-S cluster assembly scaffold	SUF
b cp dma dms t	b1684	sufA	3.01	1.57	4.06	2.12	2.30	1.73	0.76	2.36	Fe-S cluster assembly protein	SUF
b chp cp nms	b2525	fdx	1.03	1.31	1.27	0.59	0.45	0.67	1.69	0.48	[2Fe-2S] ferredoxin	ISC
b chp cp nms	b2526	hscA	1.11	1.03	1.22	0.74	0.62	0.88	1.9	0.76	DnaK-like molecular chaperone specific for IscU	ISC
b chp cp nmp nms t	b2527	hscB	1.43	1.38	1.69	0.89	0.93	1.27	2.44	1.16	IscU-specific HscA co-chaperone Hsc56	ISC
chp cp nmp nms	b2528	iscA	0.97	1.05	1.33	0.41	0.51	1.39	1.52	0.72	FeS cluster assembly protein	ISC
b chp cp nmp nms t	b2529	iscU	1.31	1.50	1.78	0.59	0.62	1.79	2.07	1.14	Iron-sulfur cluster assembly scaffold protein	ISC
b chp cp dms nmp nms t	b2530	iscS	1.62	1.58	1.94	0.97	1.05	2.69	2.48	1.64	Cysteine desulfurase (tRNA sulfurtransferase)	ISC
b chp cp dma dms nmp nms t	b2531	iscR*	1.91	1.62	2.17	1.38	1.32	3.81	3.07	2.00	Isc operon repressor; suf operon activator	Regulator
chp cp nmp nms t	b3414	nfuA	0.66	1.31	1.71	0.5	0.23	1.75	1.41	1.32	Fe/S biogenesis protein; putative scaffold/chaperone	Fe/S carrier
b chp cp dms nmp nms	b4705	mntS	1.14	2.06	2.34	0.89	1.12	2.64	2.97	0.94	Mn(2)-response protein, MntR-repressed	Oxidative stress
b chp cp dma dms nmp nms t	b1778	msrB*	1.63	1.33	1.07	1.39	1.05	1.76	1.93	2.52	Methionine sulfoxide reductase B (EC:1.8.4.12)	Oxidative stress
b chp cp dma dms nmp nms	b0950	pqiA*	1.33	1.07	1.1	1.03	1.08	1.4	1.99	0.83	Paraquat-inducible, SoxRS-regulated inner membrane protein	Oxidative stress
b cp nmp nms	b0951	pqiB	1.14	0.8	1.05	0.75	0.71	1.19	1.5	0.77	Paraquat-inducible, SoxRS-regulated MCE domain protein	Oxidative stress
b chp cp dma dms nmp nms t	b2294	yfbU*	**-1.84**	**-1.36**	**-1.18**	**-1.11**	**-1.39**	**-1.70**	**-1.99**	**-1.43**	UPF0304 family protein; K09161 hypothetical protein	Oxidative stress
b dms nmp t	b3238	yhcN	1.92	1.11	1.39	1.39	1.6	2.25	1.26	1.69	Cadmium and peroxide resistance protein	Oxidative stress
b chp cp dma dms nmp nms t	b3495	uspA*	**-1.79**	**-1.63**	**-1.49**	**-1.29**	**-1.63**	**-2**	**-3.16**	**-1.4**	Universal stress global response regulator A	Usps
nms	b1895	uspC	0.78	0.34	0.75	-0.03	-0.24	0.61	**-1.44**	-0.55	Universal stress induced protein C	Usps
chp nms	b3923	uspD	-0.74	**-1.23**	-0.83	-0.73	-0.83	-0.58	**-2.03**	-0.42	Universal stress-induced protein D	Usps
b dma dms t	b1333	uspE*	7.16	1.96	1.39	5.79	6.71	-5.12	-1.81	6.96	Universal stress-induced protein E	Usps
b dma dms t	b1376	uspF	3.79	-0.09	-0.36	2.23	3.75	-6.06	-2.75	4.16	Universal stress-induced protein F, ATP-binding protein	Usps
b dma nmp nms t	b0607	uspG*	**-1.48**	-0.25	-0.03	**-1.62**	-0.88	**-1.18**	**-2.4**	**-1.48**	Universal stress protein UP12	Usps

Table 1.

As a result, the table legend "*E. coli* contains the ISC and SUF Fe/S assembly system. Treatment: Chemical treatment associated with the DE genes; ID: Gene ID; the shaded cells and bolded numbers are not shown in the table. Genes marked with "*": Gene promoter-fused GFP assays performed"

should read:

"*E. coli* contains the ISC and SUF Fe/S assembly system. Treatment: Chemical treatment associated with the DE genes; ID: Gene ID; Shaded cells: up regulated DE genes; Bolded number: down regulated DE genes; Genes marked with "*": Gene promoter-fused GFP assays performed"

In addition, there is an error in the 'Results and Discussion' section.

"The cytoplasmic putrescine transporter protein, encoded by *PpotFGHI*, was significantly up regulated following n-butanol, DMA, NMP and T treatment."

should read:

"The cytoplasmic putrescine transporter protein, encoded by *potFGHI*, was significantly up regulatedfollowing n-butanol, DMA, NMP and T treatment."


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