

Singh VP, Le B, Khode R, Baker KM, Kumar R: Intracellular angiotensin II production in diabetic rats is correlated with cardiomyocyte apoptosis, oxidative stress, and cardiac fibrosis. *Diabetes* 57:3297–3306, 2008

As printed in the above article, Figures 1 and 2 do not adequately reflect the detail of the images. High-quality versions of Figures 1 and 2 are available as an online-only appendix at <http://diabetes.diabetesjournals.org/cgi/content/full/db08-0805/DC1>.

Nair KS, Bigelow ML, Asmann YW, Chow LS, Coenen-Schimke JM, Klaus KA, Guo Z-K, Sreekumar R, Irving BA: Asian Indians have enhanced skeletal muscle mitochondrial capacity to product ATP in association with severe insulin resistance. *Diabetes* 57:1166–1175, 2008

In the above article, Table 3 (p. 1172) contains an error; the headings for columns 3 and 4 have been reversed. Column 3 should read “Nondiabetic European Americans” and not “Nondiabetic Asian Indians.” Column 4 should read “Nondiabetic Asian Indians” and not “Nondiabetic European Americans.” The correct table appears below. The online version reflects these changes.

TABLE 3

Genes involved in OXPHOS and citrate cycle, the two pathways that were upregulated in nondiabetic Asian Indians compared with nondiabetic European Americans

	Probe set	Nondiabetic European Americans	Nondiabetic Asian Indians	Nondiabetic Asian Indians/ nondiabetic European Americans	<i>P</i>	Accession	Gene name
Oxidative phosphorylation, <i>P</i> = 0.013							
	NDUFB4	7659.66	8172.12	1.067	0.0151	NM_004547	NADH dehydrogenase (ubiquinone) 1 β subcomplex 4,
	COX8A	4522.81	5004.64	1.107	0.0259	NM_004074	Cytochrome c oxidase subunit 8A (ubiquitous)
	COX11	95.54	103.71	1.085	0.0307	AI198212	COX11 homolog
	COX5A	127.38	152.44	1.197	0.0354	BF196691	Cytochrome c oxidase subunit Va
	COX7C	2179.92	2314.60	1.062	0.0416	AA382702	Cytochrome c oxidase subunit VIIc
	ATP5G3	321.71	357.21	1.110	0.0472	AU153583	ATP synthase, H + transporting, mitochondrial F0 complex, subunit C3 (subunit 9)
	NDUFAB1	3916.67	4256.75	1.087	0.0478	NM_005003	NADH dehydrogenase (ubiquinone) 1, α/β subcomplex, 1,
Citrate cycle, <i>P</i> = 0.015							
	SUCLA2	1874.18	1999.18	1.067	0.0442	NM_003850	Succinate-CoA ligase, ADP-forming, β -subunit
	IDH3G	610.71	663.92	1.087	0.0454	NM_004135	Isocitrate dehydrogenase 3 (NAD ⁺)- γ
	ATP5G3	321.71	357.21	1.110	0.0472	AU153583	ATP synthase, H + transporting, mitochondrial F0 complex, subunit C3 (subunit 9)

P values associated with each pathway were calculated by IPA. *P* values associated with each gene were calculated using paired *t* test.