Table 4. Fold change comparisons between GeneChip and quantitative reverse transcription PCR data[1]

Gene	GeneChip	TaqMan
UCP3 [2]	-43.3	-65.5
BCL6	-3.5	-3.7
FEZ1	1.7	2.2
PFKFB1	-4.1	-28.7
PHKA1	-4.2	-4.5
FADS1	3.8	6.0

[1] Average fold changes across a subset (5-8 normal and 5-6 NM) of specimens.

[2] GeneChip data for UCP3 represent average of three probe sets.