RT² Profiler PCR Array (Rotor-Gene® Format)

Human Mitochondrial Energy Metabolism Plus

Cat. no. 330231 PAHS-008YR

For pathway expression analysis

Format	For use with the following real-time cyclers
RT² Profiler PCR Array, Format R	Rotor-Gene Q, other Rotor-Gene cyclers

Description

The Human Mitochondrial Energy Metabolism Plus RT² Profiler PCR Array profiles the expression of 84 key genes involved in mitochondrial respiration, including genes encoding components of the electron transport chain and oxidative phosphorylation complexes. It also determines whether mitochondrial energy metabolism activity is repressed or unchanged in experimental samples. Oxidation of NADH and FADH2, the metabolites from glycolysis and the TCA cycle, occurs via a series of 4 protein complexes embedded in the inner mitochondrial membrane: NADH-coenzyme Q reductase, succinate-coenzyme Q reductase, coenzyme Q-cytochrome c reductase, and cytochrome c oxidase. The free energy generated from these processes drives oxidative phosphorylation and ATP synthesis via a fifth protein complex (ATP synthase). Dysregulation of these processes is a major pathological consequence of cancer progression. Many tumors contain decreased amounts of mitochondrial respiratory chain components, although the exact mechanism for this repression is unclear. However, recent studies demonstrate that the important tumor suppressor p53 induces the expression of COX2, an essential component for cytochrome c oxidase function. Mitochondrial dysfunction also contributes to metabolic syndrome and obesity, where excess ?-oxidation overloads oxidative phosphorylation by generating excessive amounts of NADH. It also includes 16 experimentally derived Signature Biomarker Genes which, along with classification algorithms, are used to generate the activity score. A set of controls present on each array enables data analysis using the ΔΔCT method of relative quantification, assessment of reverse transcription performance, genomic DNA contamination, and PCR performance. Using real-time PCR, research studies can easily and reliably determine mitochondrial energy metabolism activity and analyze the expression of a focused panel of genes involved in mitochondrial energy metabolism with this array.

For further details, consult the *RT² Profiler PCR Array Handbook*.

Shipping and storage

RT² Profiler PCR Arrays in the Rotor-Gene format are shipped at ambient temperature, on dry ice, or blue ice packs depending on destination and accompanying products.

For long term storage, keep plates at –20°C.

Note: Ensure that you have the correct RT² Profiler PCR Array format for your real-time cycler (see table above).

Note: Open the package and store the products appropriately immediately on receipt.

Array layout

The 96 real-time assays in the Rotor-Gene format are located in wells 1–96 of the Rotor-Disc™ (plate A1–A12=Rotor-Disc 1–12, plate B1–B12=Rotor-Disc 13–24, etc.). To maintain data analysis compatibility, wells 97–100 do not contain real-time assays but will contain master mix to account for weight balance.

Gene table: RT² Profiler PCR Array

Position	UniGene	GenBank	Symbol	Description
A01	Hs.298280	NM_004046	ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
A02	Hs.406510	NM_001686	ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
A03	Hs.271135	NM_005174	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
A04	Hs.514870	NM_001688	ATP5F1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1
A05	Hs.80986	NM_005175	ATP5G1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1 (subunit 9)
A06	Hs.524464	NM_001002031	ATP5G2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C2 (subunit 9)
A07	Hs.429	NM_001689	ATP5G3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)
A08	Hs.514465	NM_006356	ATP5H	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
A09	Hs.85539	NM_007100	ATP5I	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit E
A10	Hs.246310	NM_001685	ATP5J	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6
A11	Hs.656515	NM_004889	ATP5J2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F2
A12	Hs.486360	NM_006476	ATP5L	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G
B01	Hs.409140	NM_001697	ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit
B02	Hs.433419	NM_001861	COX4I1	Cytochrome c oxidase subunit IV isoform 1
B03	Hs.401903	NM_004255	COX5A	Cytochrome c oxidase subunit Va
B04	Hs.1342	NM_001862	COX5B	Cytochrome c oxidase subunit Vb
B05	Hs.706889	NM_004373	COX6A1	Cytochrome c oxidase subunit VIa polypeptide 1
B06	Hs.250760	NM_005205	COX6A2	Cytochrome c oxidase subunit VIa polypeptide 2
B07	Hs.431668	NM_001863	COX6B1	Cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)
B08	Hs.351875	NM_004374	COX6C	Cytochrome c oxidase subunit VIc
B09	Hs.70312	NM_001865	COX7A2	Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
B10	Hs.744101	NM_004718	COX7A2L	Cytochrome c oxidase subunit VIIa polypeptide 2 like
B11	Hs.522699	NM_001866	COX7B	Cytochrome c oxidase subunit VIIb
B12	Hs.743989	NM_004074	COX8A	Cytochrome c oxidase subunit VIIIA (ubiquitous)
C01	Hs.289271	NM_001916	CYC1	Cytochrome c-1
C02	Hs.534168	NM_004541	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
C03	Hs.277677	NM_004544	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
C04	Hs.406062	NM_175614	NDUFA11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
C05	Hs.75914	NM_002488	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
C06	Hs.198269	NM_004542	NDUFA3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
C07	Hs.50098	NM_002489	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
C08	Hs.651219	NM_005000	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
C09	Hs.274416	NM_002490	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
C10	Hs.495039	NM_014222	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
C11	Hs.189716	NM_005003	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
C12	Hs.513266	NM_004548	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
D01	Hs.655788	NM_004546	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
D02	Hs.109760	NM_002491	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
D03	Hs.304613	NM_004547	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
D04	Hs.730674	NM_002492	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
D05	Hs.493668	NM_182739	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
D06	Hs.532853	NM_004146	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
D07	Hs.523215	NM_005004	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
D08	Hs.15977	NM_005005	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
D09	Hs.84549	NM_002494	NDUFC1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
D10	Hs.407860	NM_004549	NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
D11	Hs.598436	NM_005006	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
D12	Hs.173611	NM_004550	NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
E01	Hs.502528	NM_004551	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)

Position	UniGene	GenBank	Symbol	Description
E02	Hs.528222	NM_002495	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
E03	Hs.632385	NM_004552	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
E04	Hs.408257	NM_004553	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
E05	Hs.211914	NM_024407	NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)
E06	Hs.90443	NM_002496	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
E07	Hs.7744	NM_007103	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
E08	Hs.464572	NM_021074	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
E09	Hs.473937	NM_021075	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
E10	Hs.437403	NM_021129	PPA1	Pyrophosphatase (inorganic) 1
E11	Hs.440475	NM_004168	SDHA	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
E12	Hs.465924	NM_003000	SDHB	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
F01	Hs.444472	NM_003001	SDHC	Succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
F02	Hs.744039	NM_003002	SDHD	Succinate dehydrogenase complex, subunit D, integral membrane protein
F03	Hs.8372	NM_006830	UQCR11	Ubiquinol-cytochrome c reductase, complex III subunit XI
F04	Hs.119251	NM_003365	UQCRC1	Ubiquinol-cytochrome c reductase core protein I
F05	Hs.528803	NM_003366	UQCRC2	Ubiquinol-cytochrome c reductase core protein II
F06	Hs.743307	NM_006003	UQCRFS1	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
F07	Hs.481571	NM_006004	UQCRH	Ubiquinol-cytochrome c reductase hinge protein
F08	Hs.146602	NM_014402	UQCRQ	Ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa
F09	Hs.24684	NM_020801	ARRDC3	Arrestin domain containing 3
F10	Hs.516788	NM_001040445	ASB1	Ankyrin repeat and SOCS box containing 1
F11	Hs.514682	NM_182580	CYB561D1	Cytochrome b-561 domain containing 1
F12	Hs.515210	NM_006145	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1
G01	Hs.713645	NM_001955	EDN1	Endothelin 1
G02	Hs.110571	NM_015675	GADD45B	Growth arrest and DNA-damage-inducible, beta
G03	Hs.702139	NM_005345	HSPA1A	Heat shock 70kDa protein 1A
G04	Hs.719966	NM_005346	HSPA1B	Heat shock 70kDa protein 1B
G05	Hs.634058	NM_182492	LRP5L	Low density lipoprotein receptor-related protein 5-like
G06	N/A	r4_NC_012920	MitoH1	Polycistronic_H1_3
G07	N/A	r3_NC_012920	MitoH2_12106	Polycistronic_H2_200_12106_1
G08	N/A	r2_NC_012920	MitoH2_14573	Polycistronic_H2_200_14573_3
G09	N/A	r1_NC_012920	MitoH2_4162	Polycistronic_H2_200_4162_1
G10	N/A	r5_NC_012920	MitoH2_5726	Polycistronic_H2_200_5726_3
G11	Hs.640266	NR_004407	RNU11	RNU11
G12	Hs.729700	NM_052901	SLC25A25	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25
H01	Hs.520640	NM_001101	ACTB	Actin, beta
H02	Hs.534255	NM_004048	B2M	Beta-2-microglobulin
H03	Hs.544577	NM_002046	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
H04	Hs.412707	NM_000194	HPRT1	Hypoxanthine phosphoribosyltransferase 1
H05	Hs.546285	NM_001002	RPLP0	Ribosomal protein, large, P0
H06	N/A	SA_00105	HGDC	Human Genomic DNA Contamination
H07	N/A	SA_00104	RTC	Reverse Transcription Control
H08	N/A	SA_00104	RTC	Reverse Transcription Control
H09	N/A	SA_00104	RTC	Reverse Transcription Control
H10	N/A	SA_00103	PPC	Positive PCR Control
H11	N/A	SA_00103	PPC	Positive PCR Control
H12	N/A	SA_00103	PPC	Positive PCR Control

Related products

For optimal performance, RT² Profiler PCR Arrays should be used together with the RT² First Strand Kit for cDNA synthesis and RT² SYBR® Green qPCR Mastermixes for PCR.

Product	Contents	Cat. no.
RT² First Strand Kit (12)	Enzymes and reagents for cDNA synthesis	330401
RT² SYBR Green ROX™ FAST Mastermix (2)*	For 2 x 96 assays in 96-well plates; suitable for use with the Rotor-Gene Q and other Rotor-Gene cyclers	330620

* Larger kit sizes available; please inquire.

RT^2 Profiler PCR Array products are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

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