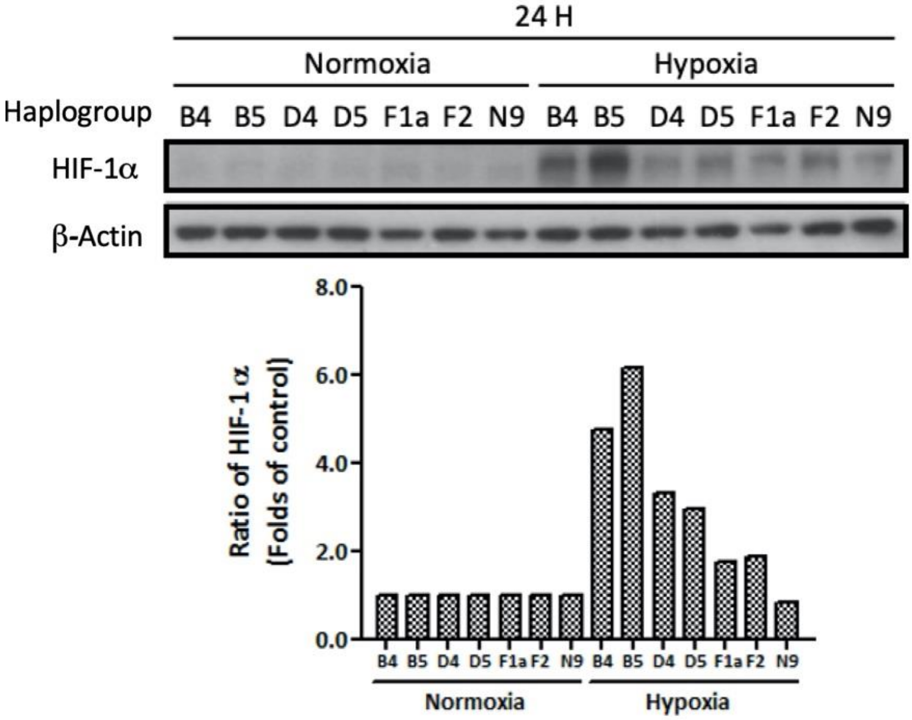
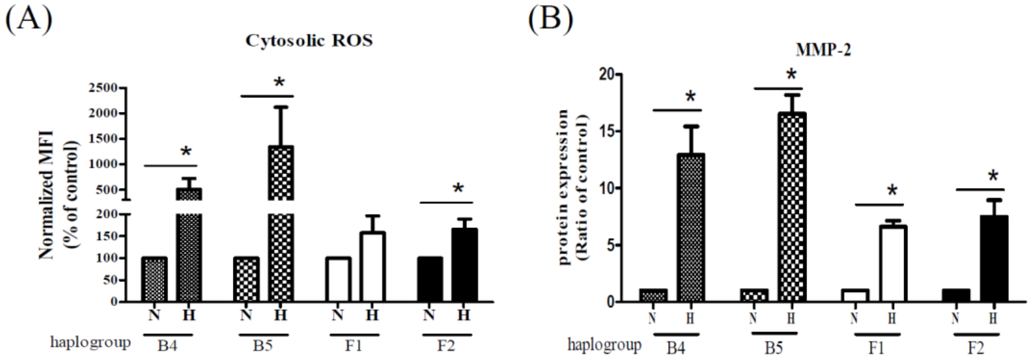
Supplemental tables and figures



Supplemental Figure S1: HIF-1*α* expressions in different cybrids under normoxic and hypoxic conditions. Twenty-four hours after hypoxic treatment, discrepant expressions of HIF-1*α* was observed in cybrid harboring different mtDNA haplogroup (B4, B5, D4, D5, F1a, F2, N9). β-actin was loading control.



Supplemental Figure S2: Comparisons of intracellular ROS generation (**A**), induction of MMP-2 (**B**) in different cybrids under hypoxia-ischemia. DCF-based flow cytometry was used for detecting cytosolic ROS. Protein expression of MMP-2 was assessed by western blot. All data are shown as means ± S.D. (*n* = 4). *$*p < 0.05$.* N was used to represent normoxic and H to represent hypoxic condition for 24 hours.

Supplemental Table S1: 24 pair primers for the mitochondrial DNA to perform the gene amplification by polymerase chain reaction.

	primer	**sequence (5'→3')'**		**sequence (3'→5')'**	**PCR product**
1	631	ACATCACCCCATAAACAAATAggTT	931	gCTTCTATTgACTTgggTTAATCg	301
2	1272	AgCAAACCCTgATgAAggCTAC	1781	TATATCTATTgCgCCAggTTTCAAT	510
3	2698	AgAggCgggCATgACACAgCA	3066	gATCACgTAggACTTTAATCgTTgA	369
5	3611	TCCTATTTATTCTAgCCACCTCTAg	3862	ATCATATTATggCCAAgggTCATg	252
6	3916	gAgTCCgAACTAgTCTCAggCT	4255	gAgggggAATgCTggAgATTgTA	340
7	4344	TCgAACCCATCCCTgAgAATCC	4577	gTTTATTTCTAggCCTACTCAggTAA	234
8	4623	TCCACAgAAgCTgCCATCAAgTA	4940	gAgAgTgAggAgAAggCTTACgT	318
9	4989	CAgCTACgCAAAATCTTAgCATAC	5257	TTgggCAAAAAgCCggTTAgCg	269
10	5921	ACTATTCTCTACAAACCACAAAgAC	6284	TgTTCAACCTgTTCCTgCTCCg	364
11	6535	CAgACCgCAACCTCAACACCAC	6807	gTgTgTCTACgTCTATTCCTACTg	273
12	8153	ggggTATACTACggTCAATgCTC	8530	TCATTTTggTTCTCAgggTTTgTTAT	378
13	8628	CAAATATCTCATCAACAACCgACTA	8994	CAgggCTATTggTTgAATgAgTAg	367
14	9044	TAATTggAAgCgCCACCCTAgC	9414	ggCCTTggTATgTgCTTTCTCgT	371
15	9673	gAAACCAAATAATTCAAgCACTgCT	9987	ACCCTCATCAATAgATggAgACAT	315
16	10277	ACCCCTACCATgAgCCCTACAA	10515	gTgAgATggTAAATgCTAgTATAATAT	239
17	12274	AggATAACAgCTATCCATTggTCT	12545	gTggCTCAgTgTCAgTTCgAgAT	272
18	12582	AgACTACTTCTCCATAATATTCATCC	12858	gTATAggATTgCTTgAATggCTgC	277
19	13077	CCACTCAAgCACTATAgTTgTAgC	13591	TCAgggAggTAgCgATgAgAgTA	515
20	13711	gCCggAAgCCTATTCgCAggAT	13980	CAggTTTTggCTCgTAAgAAggC	270
21	14217	CTAATCAACgCCCATAATCATACAA	14562	gTCgggTgTgTTATTATTCTgAATTT	346
22	14829	TCCgCATgATgAAACTTCggCT	15175	ggCCCCTCAgAATgATATTTggC	347
23	15257	gACAgTCCCACCCTCACACgAT	15600	gggACggATCggAgAATTgTgT	344
24	15696	TTCgCCCACTAAgCCAATCACTT	16037	TCCCCATgAAAgAACAgAgAATAgT	342

Supplemental Table S2: The oligonucleotide probes sequences for mtDNA haplogrouping

Probe for hybridization				Probe for hybridization		
position	purpose	sequence (5'→3')		position	purpose	sequence (5'→3')
663	a	GCTAATAGAAAGGCCAGGA		8701	a	AGTGTTGTGTATGGCTATCATT
681	a	TGTAATCTTACTGAGAGCTAAT		8701	b(N)	AGTGTTGTGTATGGTTATCAT
681	b	TGTAATCTTACTAAGAGCTAA		8793	a	CGGACTCCTGCCCCACTCA
752	a	CGTGCTTGATGCTTATTCCTTTTGA		8794	a	TGGTGTAAATGAGTAAGGCAGG
1382	a	GGCTATCGTAGTTGTCTGGG		9123	a	GATTTCTAGGATAGTTAGTAGAAT
1438	a	AGCACTCTACTCTTAGTTTACT		9219	p	ATCACATGCCTATCATATAGTA
1442	a	AACTAAGCACTCTATTCTCAGT		9296	a	CTAATGACCTCCGGTCTAGCC
1647	p	AGGAGATTTCAACTTAACTTGA		9452	a	TTCGATACGGAATAATCCTATT
3010	a	ATCAGGACATCCCAATGGTG		9774	p	ATGCCGTCGGAAATGGTGA
3010	b	ATCAGGACATCCCGATGGT		9950	a	ATTTTGTAGATGTGGTCTGACTA
3027	a	TGCAGCCGCTATCAAAGG		9968	a	GACTATTTCTGTATGTTTC
3644	a	GGATTGAGTAAGCGGCT		10310	a	ACTATTAGTGGTAGGTTAGTT
3667	p	TAGTTTGAGTTTGATGCTCA		10310	b	TATTAGTGGCAGGTTAGTTGTT
3714	a	GAGATTGTTTGGGCCACTGCT		10320	a	CCACTAATAATTATGTCATCCC
3714	b	GAGATTGTTTGGGCTACTGCT		10397	a	TACCAATTCAGCCCAGTCTAAT
3970	a	GGCTATGAAGAATAAGGCGA		10400	m	TACCAATTCAGCTCAGTCT
4048	a	CTAGGAACAACATATAACGCACTC		10400	m-1	ACTATATACCAATTCAGCTCAGT
4048	b	CTAGGAACAACATATGACGCACTC		10400	n-1	ACTATATACCAATTCGGTTCAGT
4071	a	GACAAAATATGTTGTATAGAGTTC		10454	a	GACTCATTAAATTATGACAATCATA
4071	b	ACAAAATATGTTGTGTAGAGTTC		12338	a	AAGTAACAACCATGCACACTA
4086	a	AAGTAGGGTCTTGGTAACAAAATA		12372	a	TAACCCTAACTTCCCTAATTC
4386	a	GGTGTGGTAGGTGGCAC		12406	a	ATCCTTACCACCCTCATTAACC
4386	b	GGGTGTGATAGGTGGC		12501	a	CAACAATATTCATATGCCTAG
4491	a	CTGGCCCAACCCATCATCTA		12501	b	ACAACAATATTCATGTGCCT
4715	a	TTATGGTTCATTGCCCGGAG		12630	a	CGTTACATGATCCATCATAGA
4820	a	TTCTGAGTCCCAGAAGTTACCC		12630	a	CGTTACATGATCCATCATAGA
4833	a	AGGTTACCCAAGGCGCCCCT		12705	a	CTACTCATCTTCCTAATTACC
4850	a	CTGACATCCGGTCTGCTT		12775	p	TAGGAATTATATCCTTCTTGC
4883	a	AACTAGCCCCTATCTCAAT		13156	p	CTAAGCATAGTGTTAGAGTTTG
4895	a	CCATCTCAATCATGTACCAA		13263	a	TATTATGAGTCCTAGCTGACTTG
4895	b	ATCTCAATCATATACCAAATC		13928	a	GGATTCTACCCTACCATCA
5108	a	TTATCCTAACTACCACCGCA		13928	b	GATTCTACCCTAGCATCA
5147	a	CTCCAGCACCACAACC		13942	a	ATCACACACCGCGCAAT
5178	a	TGAAACAAGATAACATGAC		14308	a	TAATAGTGTAGGGAGCTGAAT
5178	b	CTGAAACAAGCTAACATGA		14343	p	GTGGGTGAAAGAGTATGATG
5231	a	TCCCTAGGAGGCCTACCCCC		14476	a	CTGTAGTATATCCAAAAACAACC
5301	a	TAGCCTCATCGTCCCCACCAT		14569	a	ACACACCCGACCACACCACTAA
6146	a	GCTTTGGCAACTGGCTAGTTC		14893	a	TGCATGGCTAGGAACAGTCCT
6179	a	GTGCCCCCGATATAGCGTTT		14893	b	GCATGGCTAGGAATAGTCC
6680	a	CTCCCATATTGTAACCTACTACT		14979	a	AAGGTAGCGGATGGTTCAGC
6752	a	CAATTGGCTTCCTGGGGTT		15346	a	CACCTCCTATTCTTACACGAAA
6752	b	CAATTGGCTTCCTAGGGTTT		15440	a	ACGCCCTCGGCCTACTTCT
8272	a	TGGGCTCTAGAGGTGGTGCTAT		15487	a	TATTCTCACCTGACCTCCT
8272	b	CTCTAGAGGGGGTAGAGGTGGTGCT		15524	a	TTATACCCTAGCCGACC
8392	a	GTAATTATGGTGGGTCATACG		15535	a	CCAACCCCTTAAATACCCCTC
8584	a	TACCCGCCACAGTACTGATCA		15535	b	AACCCCTTAAACACCCCTCC
8684	a	ATCATTTGTTTTGAGATTAGTTT		15924	a	GTTTTCATCTCCGGCTTACAAG

Supplemental Table S3: Summary of the major non-synonymous mtDNA variants in the coding region of various mitochondrial haplogroups**.**

mtDNA SNP (A-A change)	**Locus**	**Macro-haplogroup N**						**Macro-haplogroup M**							
		A	**B4**	**B5**	**F1**	**F2**	**N9a**	**C**	**D4**	D5	E	G	M7b	M7c	M8a
		(*n* = 5)	(*n* = 10)	(*n* = 10)	(*n* = 10)	(*n* = 10)	(*n* = 5)	(*n* = 5)	(*n* = 10)	(*n* = 10)	(*n* = 5)	(*n* = 5)	(*n* = 10)	(*n* = 10)	(*n* = 5)
G4048A (Asp-Asn)	ND1	—	—	—	—	—	—	—	—	—	—	—	—	80% A	—
A4824G (Thr-Ala)	ND2	100% G	—	—	—	—	—	—	—	—	—	—	—	—	—
A4833G (Thr-Ala)	ND2	—	—	—	—	—	—	—	—	—	—	100% G	—	—	—
C5178A (Leu-Met)	ND2	—	—	—	—	—	—	—	100% A	100% A	—	—	—	—	—
A5301G (Ile-Val)	ND2	—	—	—	—	—	—	—	—	100% G	—	—	—	—	—
T5442C (Phe-Leu)	ND2	—	—	—	—	—	—	—	—	—	—	—	—	100% C	—
G5460A (Ala-Thr)	ND2	—	—	—	—	—	—	—	—	—	—	—	—	80% A	—
G7598A (Ala-Thr)	COX2	—	—	—	—	—	—	—	—	—	100% A	—	—	—	—
G7853A (Val-Ile)	COX2	—	—	—	—	—	—	—	—	—	—	—	90% A	—	—
G8584A (Ala-Thr)	ATP6	—	—	100% A	—	—	—	80% A	—	—	—	—	—	—	80% A
C8684T (Thr-Ile)	ATP6	—	—	—	—	—	—	—	—	—	—	—	—	—	100% T
A8701G (Thr-Ala)	ATP6	—	—	—	—	—	—	100% G	100% G	100% G	100% G	100% G	100% G	100% G	100% G
C8794T (His-Tyr)	ATP6	100% T	—	—	—	—	—	—	—	—	—	—	—	—	—
G9053A (Ser-Asn)	ATP6	—	—	—	100% G	—	—	—	—	—	—	—	—	—	—
A10398G (Thr-Ala)	ND3	—	—	100% G	—	—	—	100% G	100% G	100% G	100% G	100% G	100% G	100% G	100% G
T10609C (Met-Thr)	ND4L	—	—	—	100% G	—	—	—	—	—	—	—	—	—	—
G11969A (Ala-Thr)	ND4	—	—	—	—	—	—	100% A	—	—	—	—	—	—	—
T12338C (Met-Thr)	ND5	—	—	—	—	100% C	—	—	—	—	—	—	—	—	—
A12358G (Thr-Ala)	ND5	—	—	—	—	—	100% G	—	—	—	—	—	—	—	—
G12406A (Val-Ile)	ND5	—	—	—	100% A	—	—	—	—	—	—	—	—	—	—
T12811C (Tyr-His)	ND5	—	—	—	—	—	—	—	—	—	—	—	80% C	—	—
A13263G (Gln-His)	ND5	—	—	—	—	—	—	100% G	—	—	—	—	—	—	—
G13708A (Ala-Thr)	ND5	—	—	—	—	100% A	—	—	—	—	—	—	—	—	—
G13759A (Ala-Thr)	ND5	—	—	—	100% A	—	—	—	—	—	—	—	—	—	—
G13928C (Ser-Asn)	ND5	—	—	—	100% C	100% C	—	—	—	—	—	—	—	—	—
T14318C (Asn-Ser)	ND5	—	—	—	—	—	—	100% C	—	—	—	—	—	—	—
T15204C (Ile-Thr)	CytB	—	—	—	—	—	—	100% C	—	—	—	—	—	—	—

SNP: single nucleotide polymorphism; A-A: amino acid; "—" denotes 100% wild-type; Ala: Alanine; Asn: asparagine; Asp: aspartic acid; Gln: glutamine; His: histidine;. Ile: isoleucine; Leu: leucine; Met: methionine; Phe: phenylalanine; Ser: serine; Thr: threonine; Tyr: tyrosine; Val: valine; ND1~5: NADH dehydrogenase subunit 1~5; ATP6: ATP synthase 6; COX2: cytochrome c oxidase subunit II; CytB: cytochrome b.