

Supplementary Materials

Figure S1. Multidimensional scaling (MDS) plot, MDS plot of samples based on genes show the relative similarities of samples to differentially expressed among four groups.

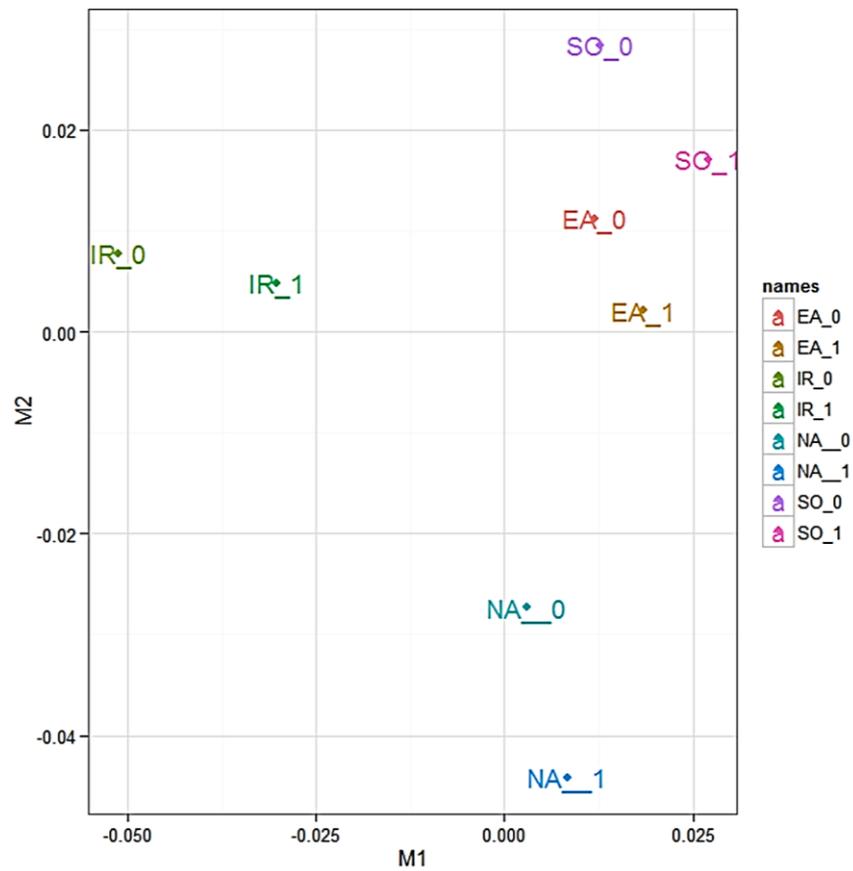


Figure S2. RNA integrity number (RIN) value.

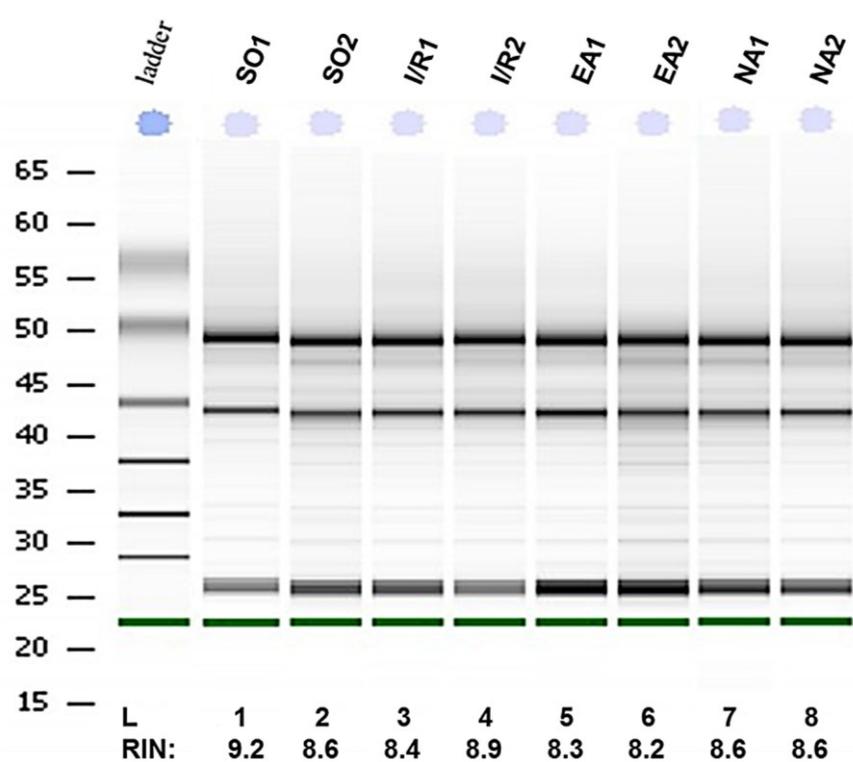


Table S1. Genes up-regulated in I/R group and down-regulated in EA group.

Pathway	Genes
Parkinson's disease	SEPT5, ATP5D, NDUFB7, NDUFB8, NDUFA7, CYC1, ATP5G2, ATP5G1, COX5B, ATP5G3, VDAC3, NDUFB2, NDUFS7, GP1BB, NDUFS8, COX6A1
Oxidative phosphorylation	ATP5D, NDUFB7, NDUFB8, NDUFA7, CYC1, ATP5G2, ATP5G1, COX5B, ATP5G3, NDUFB2, NDUFS7, NDUFS8, COX6A1, ATP5L
Huntington's disease	ATP5D, NDUFB7, NDUFB8, NDUFA7, CYC1, ATP5G2, ATP5G1, COX5B, ATP5G3, VDAC3, NDUFB2, NDUFS7, NDUFS8, COX6A1
Alzheimer's disease	ATP5D, NDUFB7, NDUFB8, NDUFA7, CYC1, ATP5G2, ATP5G1, COX5B, ATP5G3, NDUFB2, NDUFS7, NDUFS8, COX6A1, CACNA1C
Focal adhesion	CAV3, PGF, BCAR1, COL5A3, FLNC, COL5A1, MYL9, VEGFB, LAMA5, COL6A2, COL1A2, RHOC, COL1A1
Cardiac muscle contraction	ACTC1, MYL3, CYC1, COX6A1, MYH6, TNNI3, CACNA1C, COX5B
ECM-receptor interaction	SEPT5, GP1BB, LAMA5, COL1A2, COL6A2, COL1A1, COL5A3, COL5A1, SDC3
MAPK signaling pathway	MAP2K3, HSPA1B, FLNC, CDC25B, DUSP5, DUSP14, GADD45G, JUND, HSPB1, CACNA1C, NFATC2, PLA2G5
Gap junction	TUBB5, TUBB6, TUBA4A, TUBA1B, TUBA1C, TUBB3
Vascular smooth muscle contraction	KCNMB4, ACTC1, ADORA2A, RHOC, CACNA1C, PLA2G5, MYL9
Hypertrophic cardiomyopathy	ACTC1, MYL3, MYH6, TNNI3, CACNA1C

Table S2. Genes down-regulated in I/R group and up-regulated in EA group.

Pathway	Genes
NOD-like receptor signaling pathway	CCL12, XIAP, IL18, CASP1, CARD6, CHUK
Cytosolic DNA-sensing pathway	TBK1, IL18, IL33, CASP1, CHUK
p53 signaling pathway	CCNE2, IGF1, RRM2B, PTEN, SESN3
Leukocyte transendothelial migration	VCAM1, CYBB, GNAI1, RAP1B, JAM2, PIK3R1
Small cell lung cancer	CCNE2, XIAP, PTEN, CHUK, PIK3R1
Apoptosis	TNFSF10, XIAP, IL1RAP, CHUK, PIK3R1
Prostate cancer	CCNE2, IGF1, PTEN, CHUK, PIK3R1
Natural killer cell mediated cytotoxicity	CD48, TNFSF10, CD244, FCGR2B, PIK3R1
Cytokine-cytokine receptor interaction	TNFSF10, CXCL13, IL18, IL1RAP, LIFR, KITLG, IL13RA1
Long-term depression	GNAQ, GNAI1, IGF1, GUCY1B3
Adipocytokine signaling pathway	CD36, ACSL4, ACSL3, CHUK
B cell receptor signaling pathway	FCGR2B, RASGRP3, CHUK, PIK3R1

Table S3. Genes down-regulated in I/R group and up-regulated in NA group.

Pathway	Genes
Apoptosis	TNFSF10, XIAP, IL1RAP, PIK3R1
Natural killer cell mediated cytotoxicity	TNFSF10, CD244, FCGR2B, PIK3R1
Cytokine-cytokine receptor interaction	TNFSF10, CXCL13, IL1RAP, LIFR, IL13RA1
Leukocyte transendothelial migration	VCAM1, CYBB, RAP1B, PIK3R1
Renal cell carcinoma	HIF1A, RAP1B, PIK3R1

Table S4. Genes up-regulated in I/R group and down-regulated in NA group.

Pathway	Genes
ECM-receptor interaction	SEPT5, GP1BB, COL1A1, COL5A3, COL5A1
Parkinson's disease	SEPT5, GP1BB, COX5B, VDAC3, NDUFB2
MAPK signaling pathway	FOS, JUND, NR4A1, FLNC, NFATC2
Keratan sulfate biosynthesis	B3GNT7, CHST1

Table S5. Number of total reads and mapped reads.

Group	Fastq_Name	Total Reads	Mapped Reads	%
SO_0	11_ACTTGA_L002_R1_001.fastq	39862003	37318902	93.62
SO_1	12_GGCTAC_L003_R1_001.fastq	40442143	37702209	93.23
IR_0	13_TAGCTT_L002_R1_001.fastq	30662110	28700545	93.60
IR_1	14_GTGGCC_L003_R1_001.fastq	43356297	40111978	92.52
EA_0	15_GGCTAC_L002_R1_001.fastq	41608188	38659922	92.91
EA_1	16_CGTACG_L002_R1_001.fastq	41844123	38578194	92.20
NA_0	17_GTGGCC_L002_R1_001.fastq	35675554	33309894	93.37
NA_1	18_CGTACG_L003_R1_001.fastq	20577495	19105240	92.85

Table S6. Primer sequences for Real-time PCR.

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (°C)	Product (bp)
Gja1	CACTAGCCATTGTGGACCAG	CTAGATCTCCAGGTCATCAGG	58	158
Vegfb	CGCGGATCCGCCCTGTCTCCCAGCCTG	CCGGAATTCTAAGCCCCGCCCTTGGCAAC	60	200
Bcl-2	AACATCGCCCTGTGGATGACTG	GCTGATTCGACGTTTTGCCTGA	56	112
Cav3	GCTGATTCGACGTTTTGCCTGA	GCTGATTCGACGTTTTGCCTGA	62	137
Adora1	TACATTGGCATCGAGGTCCTC ATT	GAGCTCTGGGTGAGGATGAGGAC	54	196
Adora2a	TCAGAATTCTAATGGTITACTAA	TTCAAGCTTGGIACCAIAIGCAA	57	129
GAPDH	TGCCCAGAATATCATCCC	AGGTCAGATCCACAACAG	59	134