# Exploring the Mechanisms of Acupuncture-Induced Lowering of Blood Pressure through Positron Emission Tomography and RNA Sequencing of the PVH

Jing Li[1, 2, 4], Chong Peng[2, 5], Dongjian Lai[4], Yajing Fang[3], Daihong Luo[6], Zun-ming Zhou[5], Chenyun Li[4], Xin-sheng Lai[3, 4*]

1. Integrative Cancer Centre, The First Affiliated Hospital of Guangzhou University of Chinese Medicine, Guangzhou, Guangdong, 510405, China

2. Postdoctoral Research Station of Guangzhou University of Chinese Medicine, Guangzhou, Guangdong, 510405, China

3. Rehabilitation Center, The First Affiliated Hospital of Guangzhou University of Chinese Medicine, Guangzhou, Guangdong, 510405, China

4. Clinical School of Acupuncture and Rehabilitation, Guangzhou University of Chinese Medicine, Guangzhou, Guangdong, 510405, China

5. Department of Gastroenterology, The First Affiliated Hospital of Guangzhou University of Chinese Medicine, Guangzhou, Guangdong, 510405, China

6. Shenzhen Hospital of Beijing University of Chinese Medicine, Shenzhen, Guangdong, 518100, China

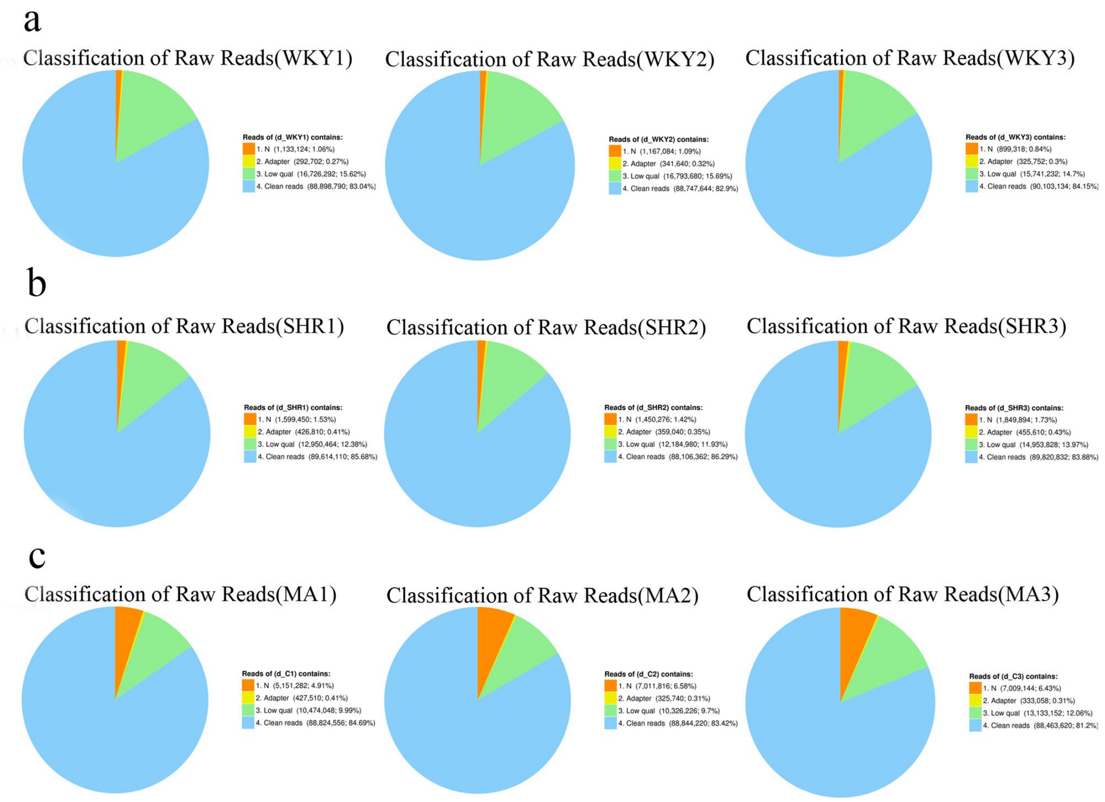
*Correspondence: lai1023@163.com

**Supplementary Table 1.** Primer sequence information.

| Gene | Primer sequences |
|---|---|
| *Ednra* | F: GCTCTAGATAGGTAGCAACGTGGCTT |
| *Ednra* | R: GCTCTAGAGCCCCAAAACTTGTCAAC |
| *Ccr5* | F: TCCTGACCACCTTCCAGGAA |
| *Ccr5* | R: GCAGCAGTGTGTCATCCCAA |
| *Angptl2* | F: TGTCAACTCCAAAGAGCCCG |
| *Angptl2* | R: GTCTCGATCTGCCGCTTCTG |
| *Gnb3* | F: TCTACAACCTCAAATCCCGC |
| *Gnb3* | R: TCTCAATGTCCCACAAGGC |
| *Erbb2* | F: GAGACAGAGCTAAGGAAGCTGA |
| *Erbb2* | R: ACGGGGATTTTCACGTTCTCC |
| *Klotho* | F: TCCCTCCTTTACCTGAGAAC |
| *Klotho* | R: CGGATGGCAGAGAAATCAAC |
| *Gpr81* | F: GGCTGAGAAAAGCGGTATGA |
| *Gpr81* | R: TCGTTAACTCTCTCCGAGCTAGA |
| *Cyp1b1* | F: CACTGCCAACACCTCTGTCTT |
| *Cyp1b1* | R: CAAGGAGCTCCATGGACTCT |
| *β-actin* | F: TCACCCACACTGTGCCCATC |
| *β-actin* | R: AGCTGTAGCCACGCTCGGTC |

**Supplementary Table 2.** Quality metrics f clean reads.

| Sample | Total Raw Reads(Mbp) | Total Clean Reads(Mbp) | Total Clean Bases(Gbp) | Clean Reads Q20(%) | Clean Reads Q30(%) | Clean Reads Ratio(%) |
|---|---|---|---|---|---|---|
| WKY1 | 107.05 | 88.9 | 8.89 | 97.64 | 91.29 | 83.04 |
| WKY2 | 107.05 | 88.75 | 8.87 | 97.56 | 91.05 | 82.9 |
| WKY3 | 107.07 | 90.1 | 9.01 | 97.74 | 91.44 | 84.15 |
| SHR1 | 104.59 | 89.61 | 8.96 | 97.7 | 91.34 | 85.68 |
| SHR2 | 102.1 | 88.11 | 8.81 | 97.76 | 91.47 | 86.29 |
| SHR3 | 107.08 | 89.82 | 8.98 | 97.42 | 90.86 | 83.88 |
| MA1 | 104.88 | 88.82 | 8.88 | 97.66 | 91.52 | 84.69 |
| MA2 | 106.51 | 88.84 | 8.88 | 97.63 | 91.39 | 83.42 |
| MA3 | 108.94 | 88.46 | 8.85 | 97.35 | 90.6 | 81.2 |



**Supplementary Figure. 1** A summary of the original RNA-Seq data. The original data performance of the WKY(A), SHR(B), and MA(C) group is shown in the pie chart (n = 3). N: The total amount of reads that contain more than 5% unknown N base (the N reads ratio); adaptor: The total amount of reads that contain adaptors (the adaptor ratio); low quality: More than 20% of the bases in the total read have a quality score lower than 15 (a low quality read ratio); clean reads: Reads filtered with N reads; reads have adaptors and low quality reads (a clean read ratio).