

**Exploration and validation of the prognostic value of mitophagy and mitochondrial dynamics-related genes in cervical cancer**

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## Supplementary Materials

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Table S3 Heterogeneity test results

| x        | method                          | Q               | Q_df | Q_pval      |
|----------|---------------------------------|-----------------|------|-------------|
| ROGDI    | Inverse<br>variance<br>weighted | 75.841<br>07334 | 109  | 0.993406525 |
| PLOD3    | Inverse<br>variance<br>weighted | 42.250<br>90972 | 17   | 0.000616937 |
| SBK1     | Inverse<br>variance<br>weighted | 29.674<br>68723 | 51   | 0.992652562 |
| SLC39A10 | Inverse<br>variance<br>weighted | 63.301<br>2572  | 70   | 0.701404181 |

Table S4 Horizontal multiple validity test results

| x        | egger_intercept | se          | pval        |
|----------|-----------------|-------------|-------------|
| ROGDI    | 0.00516478      | 0.009701075 | 0.595547792 |
| PLOD3    | 0.020973873     | 0.048481838 | 0.671070527 |
| SBK1     | 0.019576969     | 0.014855644 | 0.193572298 |
| SLC39A10 | -0.00959603     | 0.013844593 | 0.490557968 |

Table S5 Directionality test results

| x     | ENSEMBL                | correct_causal_direction | steiger_pval |
|-------|------------------------|--------------------------|--------------|
| ROGDI | eqtl-a-ENSG00000067836 | TRUE                     | 0            |

|          |                        |      |   |
|----------|------------------------|------|---|
| PLOD3    | eqtl-a-ENSG00000106397 | TRUE | 0 |
| SBK1     | eqtl-a-ENSG00000188322 | TRUE | 0 |
| SLC39A10 | eqtl-a-ENSG00000196950 | TRUE | 0 |

Table S6 proportional hazards (PH) hypothetical test

|           | chisq       | df | p           |
|-----------|-------------|----|-------------|
| riskScore | 0.217801378 | 1  | 0.640720289 |
| Smoking   | 6.369253477 | 3  | 0.09496392  |
| T         | 1.025616916 | 2  | 0.598811478 |
| N         | 0.031388238 | 1  | 0.859377012 |
| M         | 3.64E-11    | 1  | 0.999995184 |

Table S8 Primer sequence

| primer   |   | sequence               |
|----------|---|------------------------|
| PLOD3    | F | ATGGTGTCTTTGTCGACCC    |
| PLOD3    | R | TGTCTTGGGAGCAAGGTGAC   |
| SLC39A10 | F | GTACCGAGCGGAGAGGAGAT   |
| SLC39A10 | R | CAGGGCCATGGTCATGTTCT   |
| SBK1     | F | CCGCGATGGAGCGCA        |
| SBK1     | R | CCGGATCCTGGATGTGGAAG   |
| GAPDH    | F | CGAAGGTGGAGTCAACGGATTT |
| GAPDH    | R | ATGGGTGGAATCATATTGGAAC |