

Table S1. Topological analysis results of main target network.

| Targets | Degree | Betweenness | Closeness |
|----------|--------|-------------|-------------|
| TP53 | 117 | 0.055373284 | 0.795918367 |
| AKT1 | 117 | 0.04963017 | 0.795918367 |
| TNF | 112 | 0.046052317 | 0.776119403 |
| IL6 | 110 | 0.041614556 | 0.768472906 |
| VEGFA | 109 | 0.03820015 | 0.76097561 |
| CASP3 | 102 | 0.024361759 | 0.735849057 |
| IL1B | 99 | 0.02340656 | 0.728971963 |
| EGFR | 95 | 0.026241713 | 0.71559633 |
| MYC | 94 | 0.019600855 | 0.712328767 |
| ESR1 | 93 | 0.025129339 | 0.705882353 |
| PTGS2 | 92 | 0.026761069 | 0.705882353 |
| HIF1A | 92 | 0.013973436 | 0.702702703 |
| MMP9 | 89 | 0.026755905 | 0.693333333 |
| EGF | 87 | 0.017712971 | 0.68722467 |
| HSP90AA1 | 85 | 0.024082187 | 0.684210526 |
| CCND1 | 84 | 0.010874663 | 0.67826087 |
| PTEN | 82 | 0.014592393 | 0.672413793 |
| SRC | 82 | 0.008720338 | 0.672413793 |
| PPARG | 82 | 0.026125668 | 0.672413793 |
| CXCL8 | 79 | 0.008244547 | 0.663829787 |
| ERBB2 | 77 | 0.019298793 | 0.658227848 |
| CCL2 | 77 | 0.009824196 | 0.655462185 |
| FOS | 76 | 0.009270428 | 0.655462185 |
| IL10 | 73 | 0.007278643 | 0.647302905 |
| CASP8 | 71 | 0.008450925 | 0.639344262 |
| BCL2L1 | 69 | 0.005797696 | 0.634146341 |
| RELA | 65 | 0.005690601 | 0.626506024 |
| HMOX1 | 65 | 0.005732155 | 0.624 |
| MAPK1 | 63 | 0.006975278 | 0.621513944 |
| SERPINE1 | 57 | 0.00558362 | 0.604651163 |
| AR | 56 | 0.005933897 | 0.6 |
| PPARA | 54 | 0.012369688 | 0.6 |
| CRP | 50 | 0.010112801 | 0.590909091 |

Table S2. The enrichment pathways corresponding to intersection genes.

| Description | Count | Pvalue |
|--|-------|------------------------|
| Pathways in cancer | 65 | 4.17×10 ⁻⁷² |
| Lipid and atherosclerosis | 42 | 1.31×10 ⁻⁵⁴ |
| AGE-RAGE signaling pathway in diabetic complications | 31 | 3.27×10 ⁻⁴⁷ |
| IL-17 signaling pathway | 25 | 3.21×10 ⁻³⁶ |
| PI3K-Akt signaling pathway | 36 | 5.43×10 ⁻³⁶ |
| TNF signaling pathway | 24 | 2.81×10 ⁻³² |
| Colorectal cancer | 20 | 8.06×10 ⁻²⁸ |
| MAPK signaling pathway | 28 | 3.21×10 ⁻²⁷ |
| Coronavirus disease - COVID-19 | 25 | 1.01×10 ⁻²⁵ |
| Toll-like receptor signaling pathway | 18 | 1.27×10 ⁻²² |
| ErbB signaling pathway | 17 | 1.42×10 ⁻²² |
| Amoebiasis | 17 | 3.97×10 ⁻²¹ |
| NF-kappa B signaling pathway | 17 | 5.64×10 ⁻²¹ |
| Th17 cell differentiation | 17 | 1.11×10 ⁻²⁰ |
| T cell receptor signaling pathway | 16 | 2.31×10 ⁻¹⁹ |
| NOD-like receptor signaling pathway | 17 | 1.20×10 ⁻¹⁶ |
| JAK-STAT signaling pathway | 15 | 7.78×10 ⁻¹⁵ |
| Inflammatory bowel disease | 10 | 1.50×10 ⁻¹² |
| Th1 and Th2 cell differentiation | 10 | 5.38×10 ⁻¹¹ |
| Inflammatory mediator regulation of TRP channels | 8 | 4.70×10 ⁻⁰⁸ |

Table S3. The affinity scores of quercetin with the top 10 targets.

| Targets | Affinity |
|---------------|----------|
| TP53 | -7.438 |
| AKT1 | -6.724 |
| TNF- α | -7.401 |
| IL-6 | -7.318 |
| VEGFA | -7.42 |
| CASP3 | -7.535 |
| IL-1 β | -7.599 |
| EGFR | -6.91 |
| MYC | -6.752 |
| ESR1 | -9.298 |