SUPPLEMENTARY TABLES

Supplementary Table 1. Genes of interest related to NAD⁺ metabolism and proliferation used for analysis of RNA sequencing results.

| Gene name | Gene description |
|-----------|---|
| LMNB1 | lamin B1 [Source:HGNC Symbol;Acc:HGNC:6637) |
| TP53 | tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998) |
| HMGB1 | high mobility group box 1 [Source:HGNC Symbol;Acc:HGNC:4983] |
| COKN2A | cyclin dependent kinase inhibitor 2A [Source:HGNC Symbol;Acc:HGNC:1787] |
| COKN1A | cyclin dependent kinase inhibitor 1A [Source:HGNC Symbol;Acc:HGNC:1784] |
| PCNA | proliferating cell nuclear antigen [Source:HGNC Symbol;Acc:HGNC:8729) |
| CSF2 | colony stimulating factor 2 [Source:HGNC Symbol;Acc:HGNC:2434] |
| MCM2 | minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:HGNC:6944] |
| MCM3 | minichromosome maintenance complex component 3 [Source:HGNC Symbol;Acc:HGNC:6945] |
| NMNAT1 | nicotinamide nucleotide adenylyltransferase1 [Source:HGNC Symbol;Acc:HGNC:17877] |
| NMNAT2 | nicotinamide nucleotide adenylyltransferase2 [Source:HGNC Symbol;Acc:HGNC:16789] |
| NMNAT3 | nicotinamide nucleotide adenylyltransferase3 [Source:HGNC Symbol;Acc:HGNC:20989] |
| NAMPT | nicotinamide phosphoribosy ltransferase [Source:HGNC Symbol;Acc:HGNC:30092] |
| NMRK1 | nicotinamide riboside kinase 1 [Source:HGNC Symbol;Acc:HGNC:26057] |
| NMRK2 | nicotinamide riboside kinase 2 [Source:HGNC Symbol;Acc:HGNC:17871] |
| NNMT | nicotinamide N-methyltransferase [Source:HGNC Symbol;Acc:HGNC:7861] |
| ID01 | indoleamine2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:HGNC:6059] |
| TD02 | tryptophan 2,3-dioxygenase [Source:HGNC Symbol;Acc:HGNC:11708] |
| KMO | kynurenine 3-monooxygenase [Source:HGNC Symbol;Acc:HGNC:638]1 |
| KYNU | kynureninase [Source:HGNC Symbol;Acc:HGNC:6469) |
| ACMSO | aminocarboxymuconate semialdehyde decarboxylase [Source:HGNC Symbol;Acc:HGNC:19288] |
| NAPRT | nicotinate phosphoribosyltransferase [Source:HGNCSymbol;Acc:HGNC:30450] |
| NAOSYN1 | NAO synthetase 1 [Source:HGNC Symbol;Acc:HGNC:29832] |
| QPRT | quinolinate phosphoribosyltransferase[Source:HGNC Symbol;Acc:HGNC:9755] |
| NAOK | NAO kinase [Source:HGNC Symbol;Acc:HGNC:29831] |
| SARM1 | sterile alpha and TIR motif containing 1 [Source:HGNC Symbol;Acc:HGNC:17074] |
| SIRT1 | sirtuin 1 [Source:HGNC Symbol;Acc:HGNC:14929] |
| SIRT2 | sirtuin 2 [Source:HGNC Symbol;Acc:HGNC:10886] |
| SIRT3 | sirtuin 3 [Source:HGNC Symbol;Acc:HGNC:1493]1 |
| SIRT4 | sirtuin 4 [Source:HGNC Symbol;Acc:HGNC:14932] |
| SIRT5 | sirtuin 5 [Source:HGNC Symbol;Acc:HGNC:14933] |
| SIRT6 | sirtuin 6 [Source:HGNC Symbol;Acc:HGNC:14934] |
| SIRT7 | sirtuin 7 [Source:HGNC Symbol;Acc:HGNC:14935] |
| COX5A | cytochrome c oxidase subunit 5A [Source:HGNC Symbol;Acc:HGNC:2267) |
| CYC1 | cytochrome c1 [Source:HGNC Symbol;Acc:HGNC:2579] |
| PARP1 | poly(AOP-ribose) polymerase 1 [Source:HGNC Symbol;Acc:HGNC:27]0 |
| PARP2 | poly(AOP-ribose) polymerase 2 [Source:HGNC Symbol;Acc:HGNC:272] |

| Cell line name | Genotype | Age (Years) | Sex |
|------------------------|--------------------------------|-------------|---------|
| Primary fibroblasts | | | |
| AG10803A | Apparently healthy individual | 22 | Male |
| AG16146A | Apparently healthy individual | 31 | Male |
| AG026028 | Apparently healthy individual | 35 | Female |
| NF1 (WT 1) | Apparently healthy individual | 42 | Male |
| FN2 (WT 2) | Apparently healthy individual | 58 | Male |
| AG06300D | Werner Syndrome | 37 | Male |
| AG12795C | Werner Syndrome | 19 | Male |
| WF8L (WS 1) | Werner Syndrome | 43 | Male |
| WF9A (WS 2) | Werner Syndrome | 47 | Male |
| Mesenchymal stem cells | | | |
| GM440 | Control | 20 | Male |
| BM-MSC | Control | Unknown | Unknown |
| WS797 | WRN KO (from AG12797, Coriell) | 36 | Male |
| WS780 | WRN KO (from AG00780, Coriell) | 60 | Male |

Supplementary Table 2. Overview of the mesenchymal stem cell lines and primary fibroblasts used in the study.

The table shows the cell line name, the genotype, age of the donors or the cells (in years), and the sex of the donors.

Supplementary Table 3. Shared transcription factor targets between WRN and NMNAT1-3 based on ChIP sequencing datasets from the ENCODE Transcription factor target database [6].

| Gene name Function (GeneCards) BACH1 Transcription factor | |
|--|----|
| BACH1 Transcription factor | |
| 1 | |
| BHLHE40 Control of circadian rhythm | |
| CHD1 Chromatin regulation | |
| CHD2 Chromatin regulation | |
| CHO? Helicase function, DNA binding | |
| CTCF Transcriptional activator or Transcriptional repressor via histone binding | |
| E2F6 Transcription factor, cell cycle regulation | |
| EGR1 Transcription regulation | |
| EP300 Histone acetyltransferase | |
| EZH2 Maintaining the transcriptional repressive state of genes over successive cell generations | |
| GTF2F1 Chromatin regulation, RNA pol II initiation | |
| H2AFZ Histone family, nucleosome | |
| HDAC2 Histone deacetylase family | |
| HDAC6 Histone deacetylase | |
| JUN Transcription factor | |
| JUND Transcription factor | |
| KDM4A Histone demethylase | |
| KDMSB Histone demethylase | |
| MAX MYC associated | |
| MAZ Transcription factor, regulation of gene expression; regulation of signal transduction; and transcription by RNA polymerase II | n |
| MYC Nuclear phosphoprotein that plays a role in cell cycle progression, apoptosis and cellular transformat | on |
| MYOG Muscle-specific transcription factor | |
| MX11 Inhibitor of transcriptional activity of MYC by competing for MAX | |

| PHFB | Histone lysine demethylase |
|--------|--|
| POLR2A | RNA pol II |
| RAD21 | Double-strand break repair |
| RBBPS | Regulates cell proliferation, histone methyltransferase |
| RCOR1 | Interacts with REST, neuronal cell differentation |
| REST | Transcription factor, chromatin regulation, cancer |
| SAP30 | Histone deacetylase, cancer |
| SIN3A | Transcription factor, chromatin regulation |
| SMC3 | Chromatin regulation |
| TAF1 | Transcription factor, RNA pol II initiation |
| TBP | Transcription factor |
| TCF12 | Participate in regulating lineage-specific gene expression |
| TEAD4 | Transcriptional enhancer |
| USF1 | Transcription factor |
| ZNF143 | Transcription factor, chromatin regulation |
| YY1 | Transcription factor, chromatin regulation |

Our analysis showed that WRN has 110 targets, NMNAT1 has 140 targets, NMNAT2 has 53 targets, and NMNAT3 has 74 targets (lists of all targets in Supplementary File 2). 39 targets are shared between WRN and all three NMNATs shown here.