

SUPPLEMENTARY TABLES

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Supplementary Table 1. Summary of culture duration and cumulative population doubling level (PDL) values used to construct growth curves.

| Passage | Group | Cumulative culture days | Cumulative PDL |
|---------|--------|-------------------------|----------------|
| p0 | young | 6 | 3.76 |
| p1 | young | 9 | 6.34 |
| p2 | young | 12 | 8.60 |
| p3 | young | 18 | 11.41 |
| p4 | young | 23 | 15.00 |
| p5 | young | 29 | 18.26 |
| p6 | young | 28 | 17.13 |
| p7 | middle | 52 | 27.31 |
| p8 | middle | 65 | 32.53 |
| p9 | middle | 55 | 37.44 |
| p10 | middle | 58 | 35.79 |
| p11 | middle | 76 | 41.02 |
| p12 | middle | 75 | 41.89 |
| p13 | middle | 82 | 44.89 |
| p14 | middle | 89 | 47.89 |
| p12 | old | 167 | 62.65 |
| p13 | old | 185 | 66.48 |
| p14 | old | 196 | 71.88 |
| p15 | old | 240 | 75.45 |
| p16 | old | 253 | 77.45 |
| p17 | old | 247 | 77.24 |

Supplementary Table 1 shows the correspondence between passage number, cumulative PDL, culture duration, and classification into young, middle, and old groups. Classification was based on cumulative PDL to more accurately represent biological aging, as passage number does not always reflect the actual replication history (e.g., repeated subculture at low seeding density). This table supports Supplementary Figure 1.

Supplementary Table 2. Estimated breakpoints and bootstrap confidence intervals for senescence-related genes.

| Gene | Breakpoint | | Bootstrap 95% CI | | Group |
|----------|-----------------|-------------------------|------------------|-------|--------|
| | segmented model | grid search, visualized | lower | upper | |
| CDKN1A | 39.7 | 37.5 | 15.6 | 54.7 | middle |
| CDKN2A | 67.4 | 69.0 | 28.2 | 69 | old |
| IL6 | 19.6 | 47.9 | 17.3 | 53.2 | middle |
| CXCL8 | 45.3 | 47.9 | 28.7 | 61.8 | middle |
| MMP1 | 22.4 | 36.5 | 19.7 | 68.4 | middle |
| MMP3 | 47.9 | 47.9 | 19.5 | 62.6 | middle |
| SERPINE1 | 69.0 | 69.0 | 15.6 | 69 | old |
| LMNB1 | 39.1 | 37.5 | 18 | 59.9 | middle |

Breakpoints were estimated using segmented regression models fitted to $\log_2(\text{TPM} + 1)$ expression values across cumulative PDLs. Grid search breakpoints correspond to the values visualized in Supplementary Figure 2 (blue dashed lines), selected by minimizing residual sum of squares. Bootstrap confidence intervals (B = 1000) reflect uncertainty in breakpoint estimation.