**Supplementary information：**

**Fig. S1. Dietary restriction (DR) mediates lifespan.** A representative lifespan experiment in triplicates. DR fed flies live longer than fully fed flies (p-value=0.000004), n=100, compared using the log-rank test.

**Fig. S2. The distribution of sequencing coverage over all cytosines on both strands in DR and fully fed flies.** (A) Cumulative coverage, more than 90% of cytosines were covered by at least one sequencing read. (B) The proportion distribution of cytosines sites that have a certain level of sequencing depth, approximately 1.5% of cytosine sites have 40X coverage.

**Table S1. Information of primers used to perform q-PCR.**

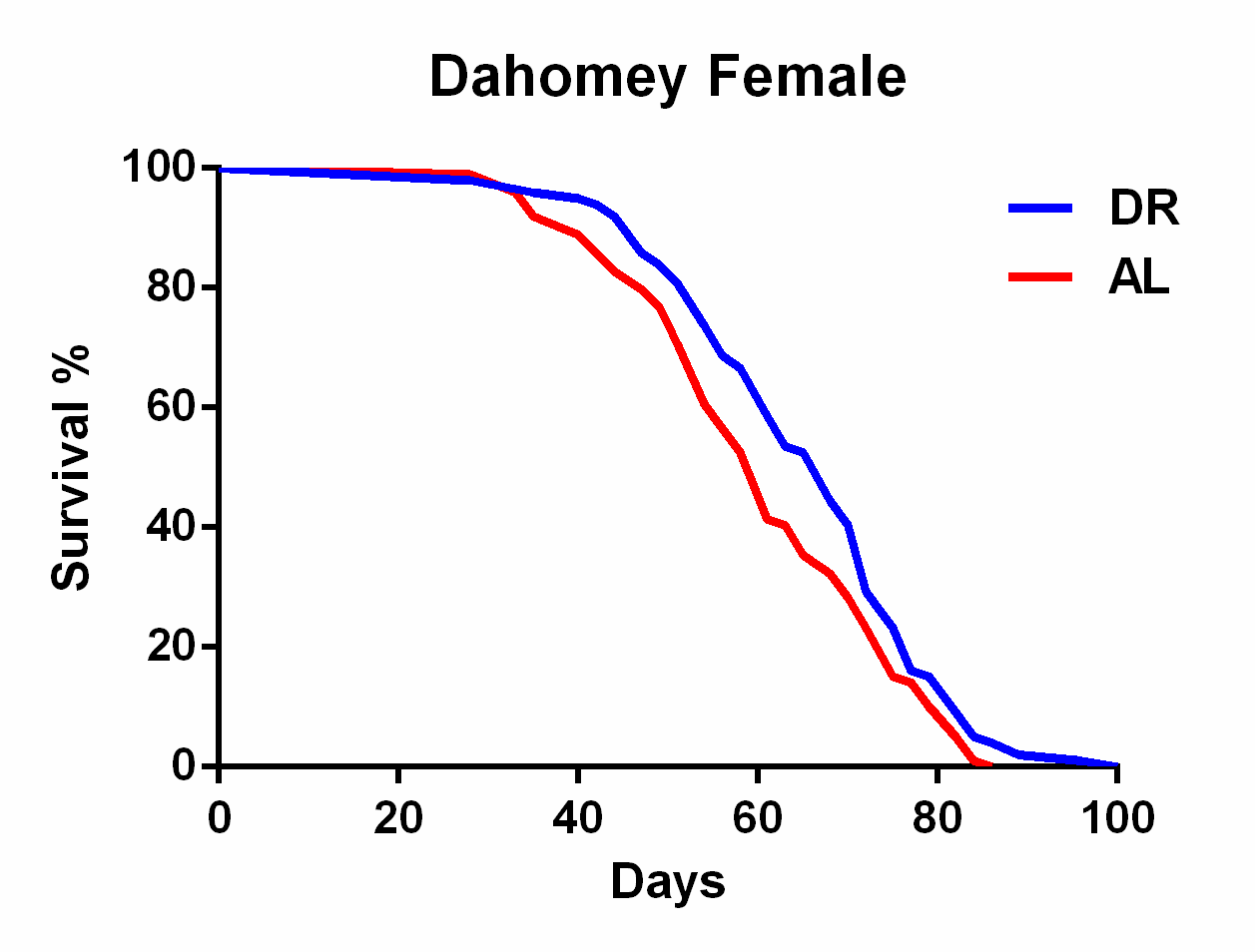
**Table S2. Cytosine methylation in DR and fully fed flies in CG, CHG, and CHH genomic contexts (H = A, T, or C).**

**Table S3. Summary of differentially methylated regions (DMRs).**

**Table S4. Bisulfite sequencing result from Drosophila**

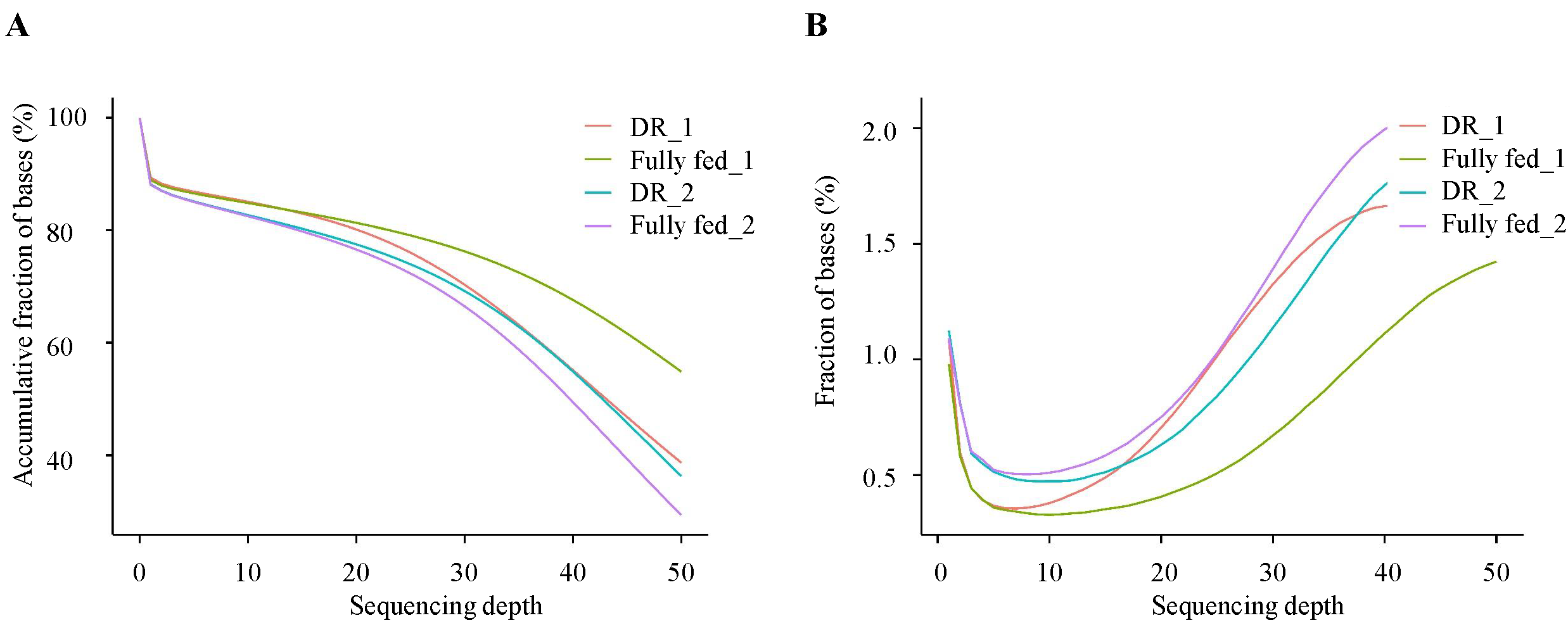
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**1. Fig. S1.**



**Fig S1. Dietary restriction (DR) mediates lifespan.** A representative lifespan experiment in triplicates. DR fed flies live longer than fully fed flies (p-value=0.000004), n=100, compared using the log-rank test.

**2. Fig. S2.**



**Fig. S2.** **The distribution of sequencing coverage over all cytosines on both strands in DR and fully fed flies.** (A) Cumulative coverage, more than 90% of cytosines were covered by at least one sequencing read. (B) The proportion distribution of cytosines sites that have a certain level of sequencing depth, approximately 1.5% of cytosine sites have 40X coverage.

**3. Table S1. Information of primers used to perform q-PCR.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene symbol | Primer sequence (5'to3') | Amplicon length/bp | Annealing temperature (℃) | Flybase ID |
| d*sir2*-F | CGGCCTCGTGCACCAAGTGT | 91 | 63.3 | FBgn0024291 |
| d*sir2*-R | CACTGCGGGCACACCGGAAT |  |  |  |
| *grappa*-F | GTCTTAGTCACGGTCACAGCA | 148 | 63.3 | FBgn0264495 |
| *grappa*-R | CCAGACAAAGTCGTGCGAAG |  |  |  |
| Act5C-F | CTCGCCACTTGCGTTTACAGT | 318 | 63.3 | FBgn0000042 |
| Act5C-R | TCCATATCGTCCCAGTTGGTC |  |  |  |

**4. Table S2. Cytosine methylation in DR and fully fed flies in CG, CHG, and CHH genomic contexts (H = A, T, or C).**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | raw reads | clean reads | mapping rate(%) | average coverage(X) | C | mC | mC percent(%) | CG | mCG(Mb) | mCG percent(%) | CHG | mCHG | mCHG percent(%) | CHH | mCHH | mCHH percent(%) |
| DR | 45900184(5.74Gb) | 37121781(4.64Gb) | 61.62 | 32.29 | 8.43E+08 | 3E+06 | 0.00399114 | 1.68E+08 | 610209 | 0.3643 | 1.58E+08 | 620417 | 0.392 | 513679516 | 2133149 | 0.4153 |
| Fully fed | 42642287(5.33Gb) | 34064372(4.26Gb) | 62.49 | 29.63 | 7.86E+08 | 3E+06 | 0.00419988 | 1.56E+08 | 603281 | 0.3861 | 1.48E+08 | 609940 | 0.4133 | 478699870 | 2087179 | 0.436 |

**5. Table S3. Summary of differentially methylated regions (DMRs).**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| DMR id | chrom | DMR start | DMR end | mC sites | DR methylation Level | Fully fed methylation Level | DR depth | Fully fed depth | *P* value |
| DMR\_2R\_20966699 | 2R | 20966699 | 20966753 | 11 | 0 | 0.1 | 22.73 | 5.45 | 4.26E-05 |

**6. Table S4. Bisulfite sequencing result from *Drosophila***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | | | | |
| Sample | Mapping efficiency (%) | Average sequence coverage | BS Conversion Rate (%) | Reference |
| w1118,0-2h embryos | 57 | 32.0× | 99.75 | Raddatz *et al.* 2013 |
| Dnmt2149,0-2h embryos | 52 | 23.6× | 99.42 | Raddatz *et al.* 2013 |
| 7d adult with DR | 61.62 | 34.69× | 99.72 | present result |
| 7d adult with fully fed diets | 62.49 | 36.79× | 99.7 | present result |

**References**

Raddatz, G., P. M. Guzzardo, N. Olova, M. R. Fantappié, M. Rampp *et al.*, 2013 *Dnmt2-*dependent methylomes lack defined DNA methylation patterns. Proceedings of the National Academy of Sciences 110**:** 8627-8631.