**Supplementary figure 1. Generation HGPS monkeys.**

**(A)** Summary of embryo microinjection of BE4max and sgRNA.

**(B)** Photographs of BE #2 and HGPS #3 when they were 3-months old. Scale bar, 0.83 cm.

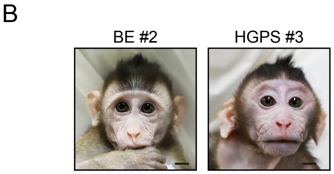
**(C)** Sequencing of the sgRNA-targeted regions in the *LMNA* gene of peripheral blood from the indicated monkeys.

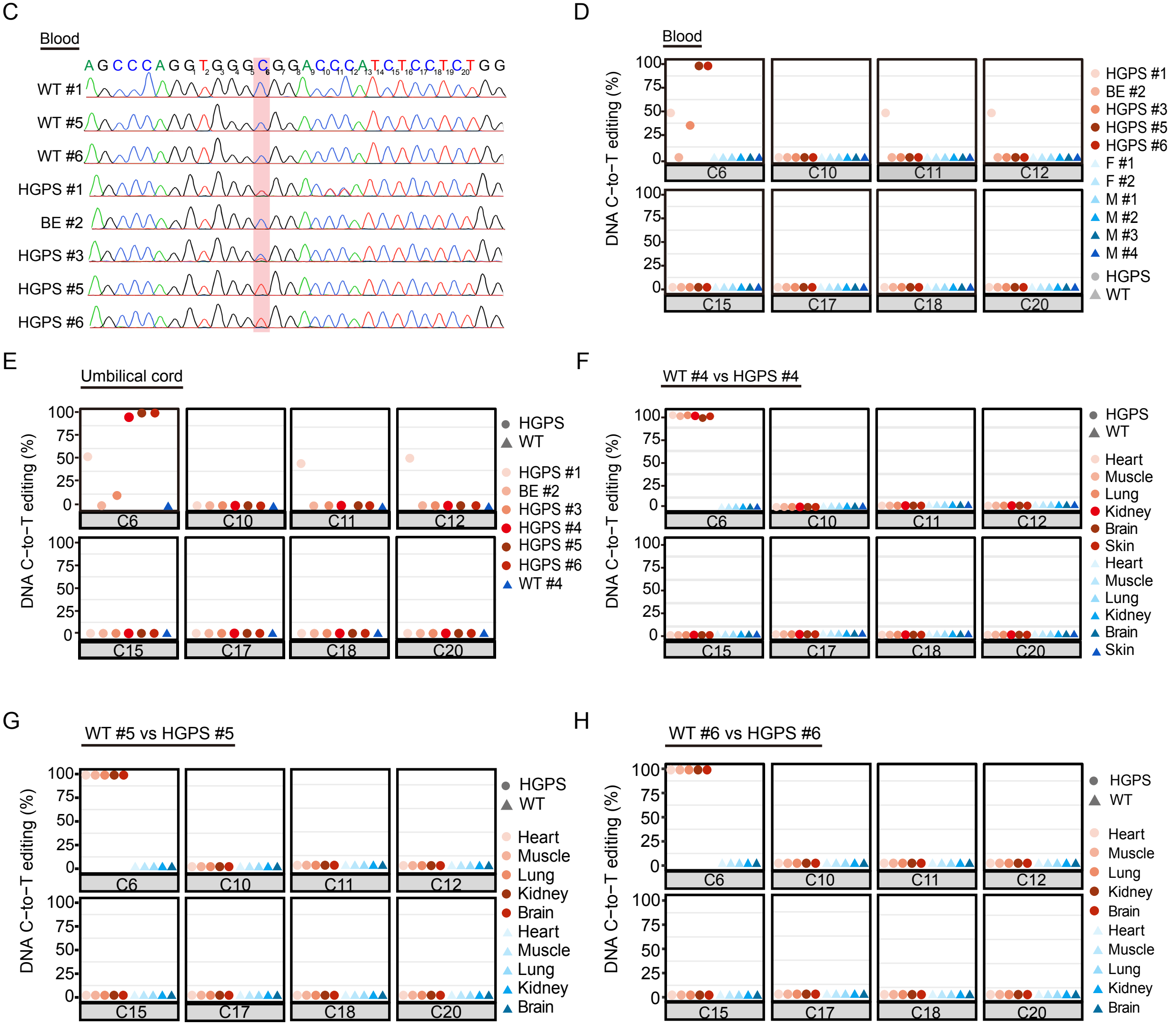
**(D-E)** The on-target editing frequencies at eight cytosine sites within the sgRNA window were analyzed by the WGS data (D, blood; E, umbilical cord).

**(F-H)** Analyzing the on-target editing frequencies at eight cytosine sites within the sgRNA window by the WGS data of each tissue from the HGPS #4 **(F)**, #5 **(G)**, #6 (**H**) monkeys and corresponding WT monkeys.

A

| Oocytes | Injected embryos | Embryos for ET | Pregnancies/ surrogates | Miscarried fetuses | Full-term fetuses | |
|---|---|---|---|---|---|---|
| | | | | | Live | Positive (%) |
| 86 | 68 | 41 | 54.55% (6/11) | 1 | 5 | 4 (80%) |



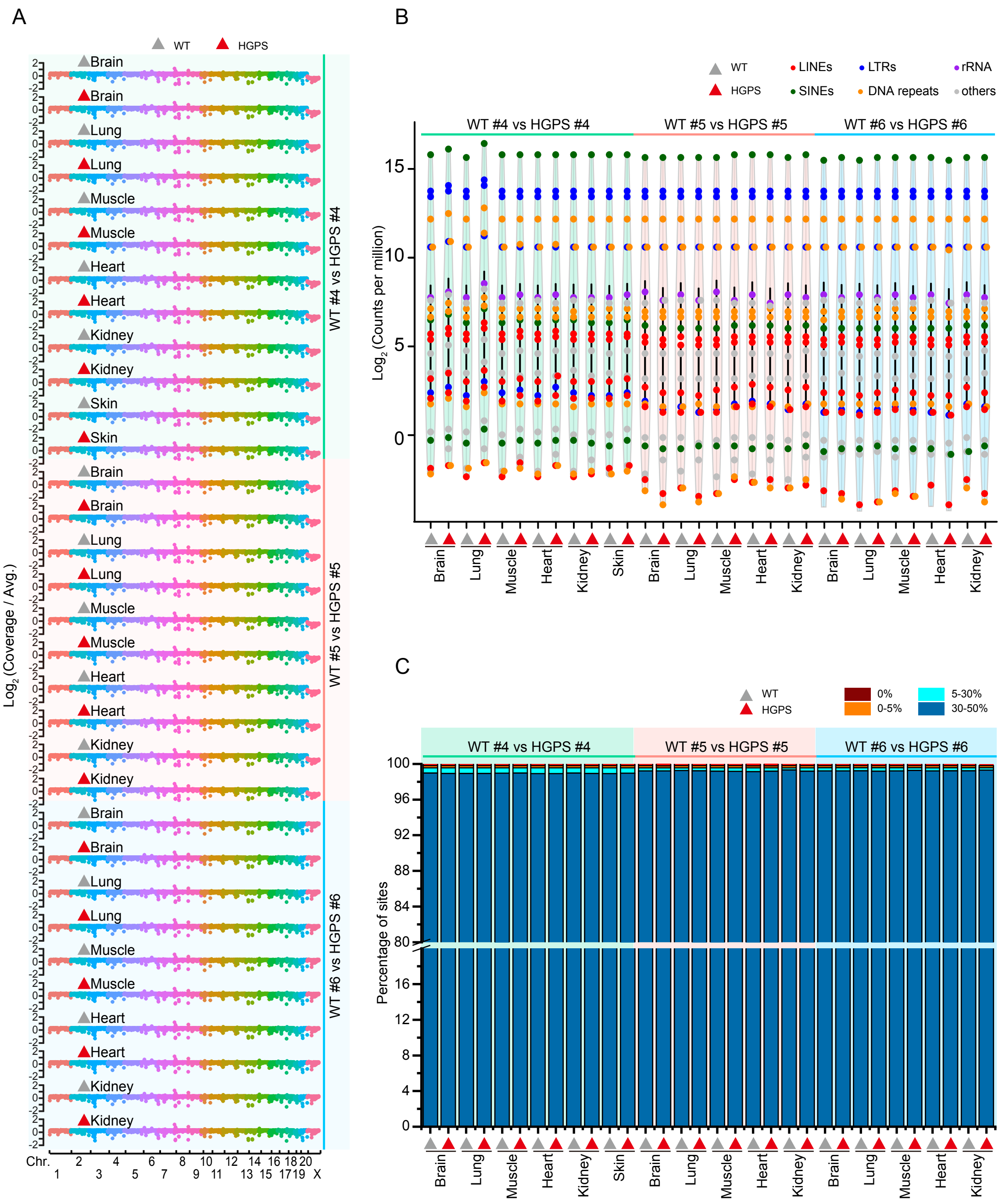


**Supplementary figure 2. *LMNA*$^{G608G}$ did not cause chromosomal instability in various tissues in monkeys.**

**(A)** Whole-genomic sequencing of copy number variations (CNV) in various tissues from WT monkeys and HGPS monkeys. Iridescent point, a 500 kb genomic region of each chromosome.

**(B)** The distribution of different types of repetitive sequences in the genome of various tissues from the WT monkeys and HGPS monkeys. Each type of repeat is marked in the same color: LINE-1, Long Interspersed Element type 1; SINEs, Short Interspersed Elements; LTRs, Long Terminal Repeat (including ERV1, ERV2, EVR3 and other types of LTR); rRNAs and other types of repeat (such as satellite, small nuclear RNA and ‘other’, as annotated in Repbase). The distributions of repeat reads were not significantly different in the WT and HGPS monkeys, according to the two-sided Wilcoxon signed-rank paired test.

**(C)** Heterozygosity distribution of SNVs called from Strelka using various tissues from WT monkeys and HGPS monkeys.


A
WT
HGPS
Brain
Lung
Muscle
Heart
Kidney
Skin
WT #4 vs HGPS #4
WT #5 vs HGPS #5
WT #6 vs HGPS #6
Log2 (Coverage / Avg.)
2
0
-2
Chr.
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
X
B
WT
HGPS
LINEs
SINEs
LTRs
DNA repeats
rRNA
others
WT #4 vs HGPS #4
WT #5 vs HGPS #5
WT #6 vs HGPS #6
Log2 (Counts per million)
15
10
5
0
Brain
Lung
Muscle
Heart
Kidney
Skin
C
WT
HGPS
0%
0-5%
5-30%
30-50%
WT #4 vs HGPS #4
WT #5 vs HGPS #5
WT #6 vs HGPS #6
Percentage of sites
100
96
92
88
84
80
16
12
8
4
0
Brain
Lung
Muscle
Heart
Kidney
Skin

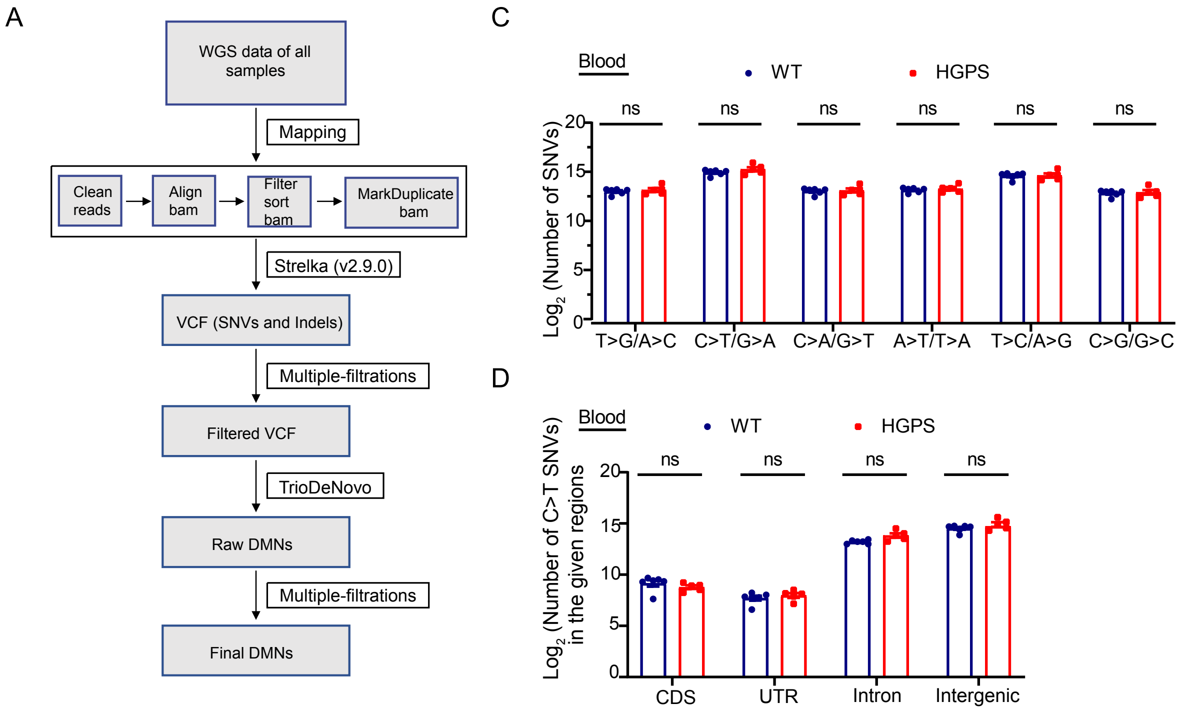
**Supplementary figure 3. *De novo* SNVs and indels analysis in monkeys.**

**(A)** The pipeline for bioinformatics analysis described in the section of Material and Methods.

**(B)** Statistics of SNVs and indels in WT and HGPS samples.

**(C)** Comparing the total number of *de novo* SNVs between WT control samples (WT #1, BC #1, BC #2, BC #3, BC #4, and BC #5) and HGPS monkeys (HGPS #1, BE #2, HGPS #3, HGPS #5, HGPS #6) (*t*-test).

**(D)** Comparing the distribution of indicated mutations in different genomic regions between WT control samples and HGPS monkeys. The sample information is the same as **(C)** (*t*-test).



B

| | ID | SNVs | | | | Indels | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Raw variant calls from Stralka | Filtered variants | Raw DMNs TrioDeNovo | Final DMNs | Raw variant calls from Strelka | Filtered variants | Raw DMNS TrioDeNovo | Final DMNs |
| **WT** | BC #1 | 16506673 | 14178834 | 156880 | 106793 | 232424 | 183051 | 70054 | 7199 |
| | BC #2 | 16628580 | 13776475 | 134035 | 88696 | 218632 | 166243 | 59257 | 6264 |
| | BC #3 | 16513285 | 14176610 | 162986 | 111359 | 234583 | 188628 | 74777 | 7721 |
| | BC #4 | 16493749 | 14323958 | 165406 | 114335 | 233156 | 184799 | 72011 | 3160 |
| | BC #5 | 16540639 | 14422563 | 154860 | 106695 | 232804 | 187347 | 73857 | 7339 |
| | WT #1 | 16864057 | 14594778 | 77751 | 66337 | 236785 | 184262 | 73297 | 6061 |
| **HGPS** | HGPS #1 | 16757527 | 14606401 | 137099 | 119249 | 243499 | 195259 | 100479 | 7900 |
| | HGPS #2 | 16736457 | 14439883 | 99593 | 86556 | 229919 | 174022 | 76339 | 5932 |
| | HGPS #3 | 16673329 | 14919677 | 203574 | 173853 | 263657 | 223263 | 169024 | 13782 |
| | HGPS #5 | 16815272 | 14898835 | 136296 | 112343 | 252639 | 209592 | 113355 | 5356 |
| | HGPS #6 | 16570194 | 14844965 | 95389 | 78059 | 264353 | 224189 | 110120 | 14303 |

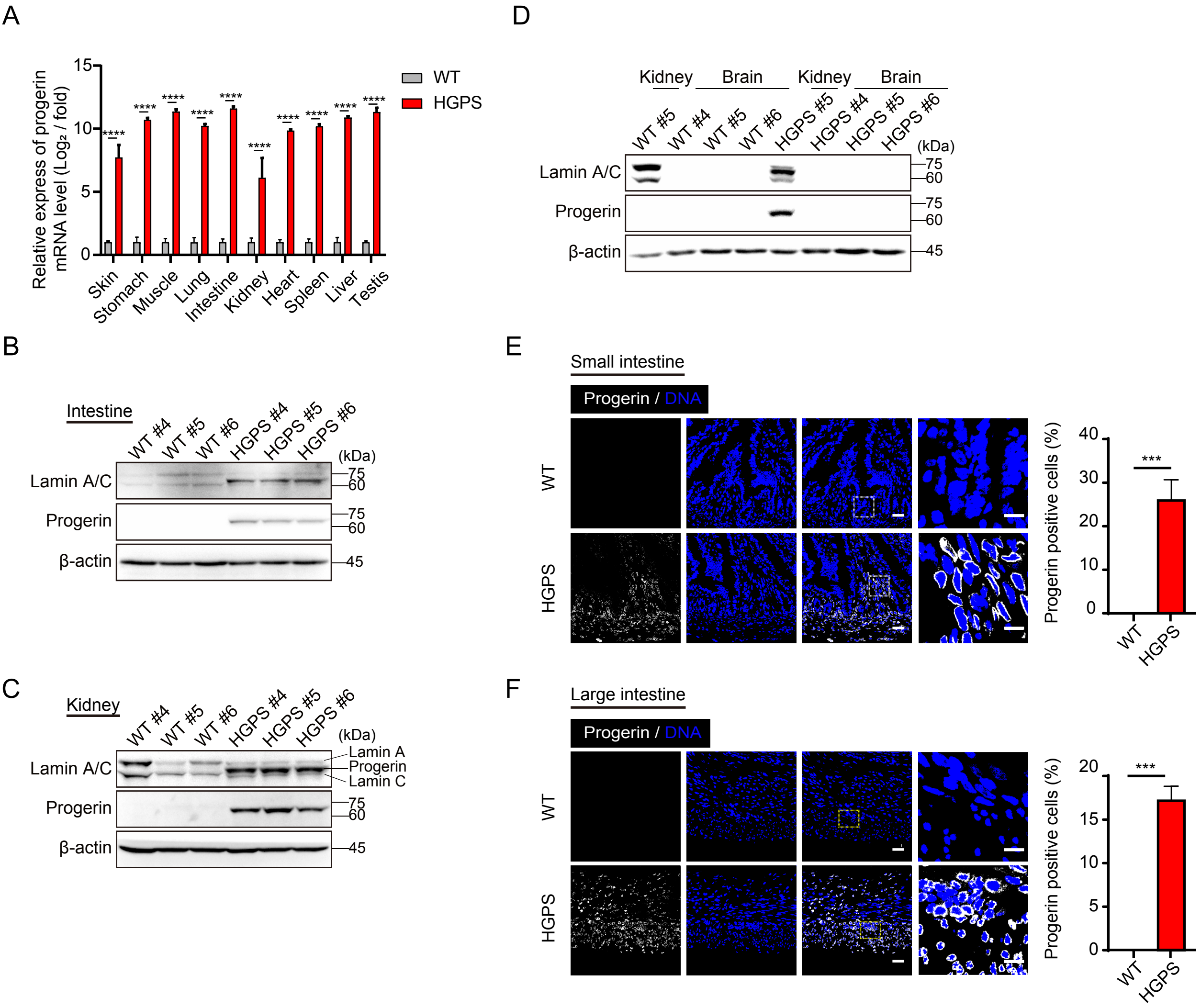
**Supplementary figure 4. Expression of progerin in various tissues of HGPS monkeys.**

**(A)** Quantitative analysis of progerin mRNA expression in various tissues of WT #4 and HGPS #4 monkeys by qPCR. The data from the HGPS monkeys were normalized to the corresponding data obtained from the WT monkeys. Data are mean ± SD. n = 4 wells per condition, *****P* < 0.0001 (two-way ANOVA).

**(B-C)** Western blots showed the expression of progerin in the intestine and kidney of HGPS monkeys. For uncropped gels, refer to Source Data.

**(D)** Western blot showed the absence of progerin in the brain of HGPS monkeys. For uncropped gels, refer to Source Data.

**(E-F)** Immunofluorescence staining showed the expression of progerin in the small intestine (**E**), and large intestine **(F)** of HGPS monkeys. Scale bar, 25 μm, (zoom: 10 μm). Data are mean ± SD. n = 3 monkeys (WT #4, #5, #6 versus HGPS #4, #5, #6). ****P* < 0.001 (*t*-test).


A
Relative express of progerin mRNA level (Log₂ / fold)
0
5
10
15
WT
HGPS
****
Skin
Stomach
Muscle
Lung
Intestine
Kidney
Heart
Spleen
Liver
Testis
B
Intestine
WT #4
WT #5
WT #6
HGPS #4
HGPS #5
HGPS #6
(kDa)
Lamin A/C
Progerin
β-actin
75
60
45
C
Kidney
WT #4
WT #5
WT #6
HGPS #4
HGPS #5
HGPS #6
(kDa)
Lamin A/C
Lamin A
Progerin
Lamin C
Progerin
β-actin
75
60
45
D
Kidney
Brain
Kidney
Brain
WT #5
WT #4
WT #5
WT #6
HGPS #5
HGPS #4
HGPS #5
HGPS #6
(kDa)
Lamin A/C
Progerin
β-actin
75
60
45
E
Small intestine
Progerin / DNA
WT
HGPS
Progerin positive cells (%)
0
10
20
30
40
***
WT
HGPS
F
Large intestine
Progerin / DNA
WT
HGPS
Progerin positive cells (%)
0
5
10
15
20
***
WT
HGPS

**Supplementary figure 5. Characterization of HGPS monkeys.**

**(A)** Head circumference of WT and HGPS monkeys after birth. Data was displayed as mean ± SD, n = 3 (WT #1, #5, #6 versus HGPS #1, #5, #6), $^{ns}P > 0.5$ (two-way ANOVA)

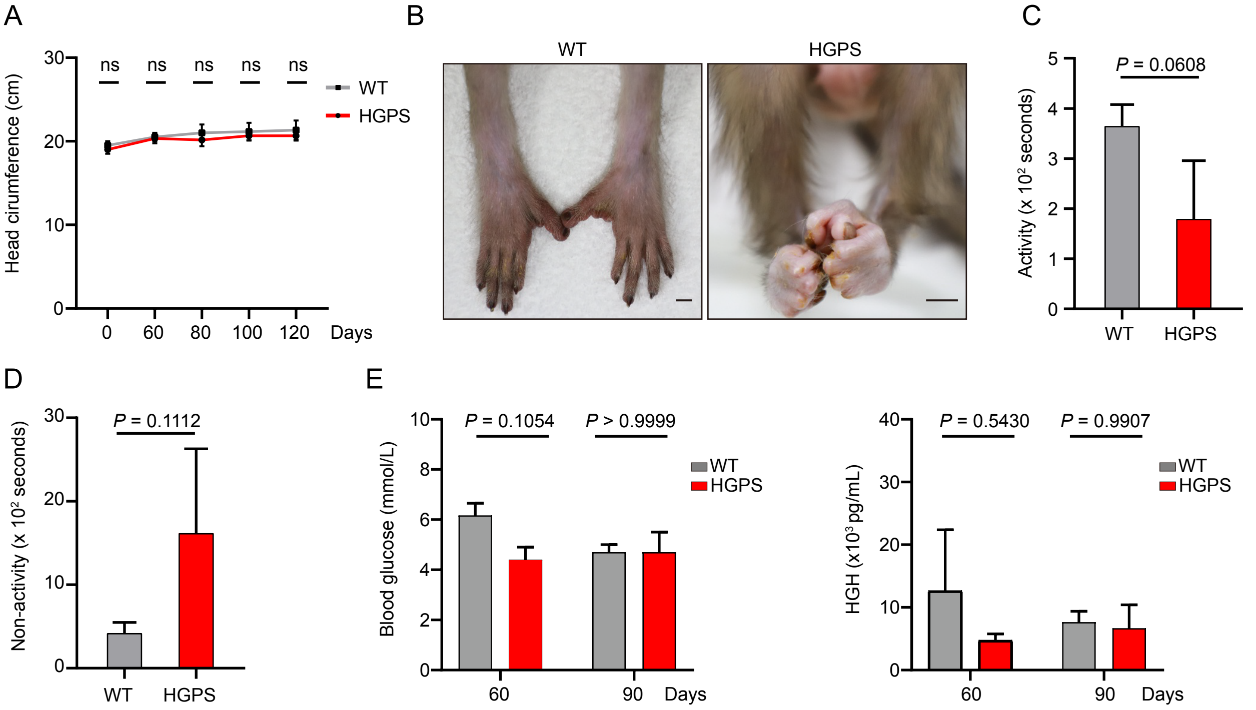
**(B)** Representative photographs showing the appearance of toe malformation in HGPS monkey at 87 days of age. Scale bar, 0.32 cm.

**(C)** A reduction of activity in HGPS monkeys. Data was presented as mean ± SD, n = 3 (WT #1, #5, #6 versus HGPS #1, #5, #6), $P = 0.0608$ (*t*-test).

**(D)** An increase of non-activity in HGPS monkeys. Data was presented as mean ± SD, n = 3 (WT #1, #5, #6 versus HGPS #1, #5, #6), $P = 0.1112$ (*t*-test).

**(E)** There was no difference in blood glucose and HGH (human growth hormone) between WT monkeys and HGPS monkeys. Data was displayed as mean ± SD, n = 3 (WT #1, #5, #6 versus HGPS #1, #5, #6), $^{ns}P > 0.05$ (two-way ANOVA).

**(F)** Summary of phenotypes observed in monkeys. The number of “+” indicated the different level of phenotype manifestation. HGPS #3 didn’t exhibit any typical phenotype of HGPS, possibly due to a low mutation frequency of 11~35%. (N.A. represented not appear).



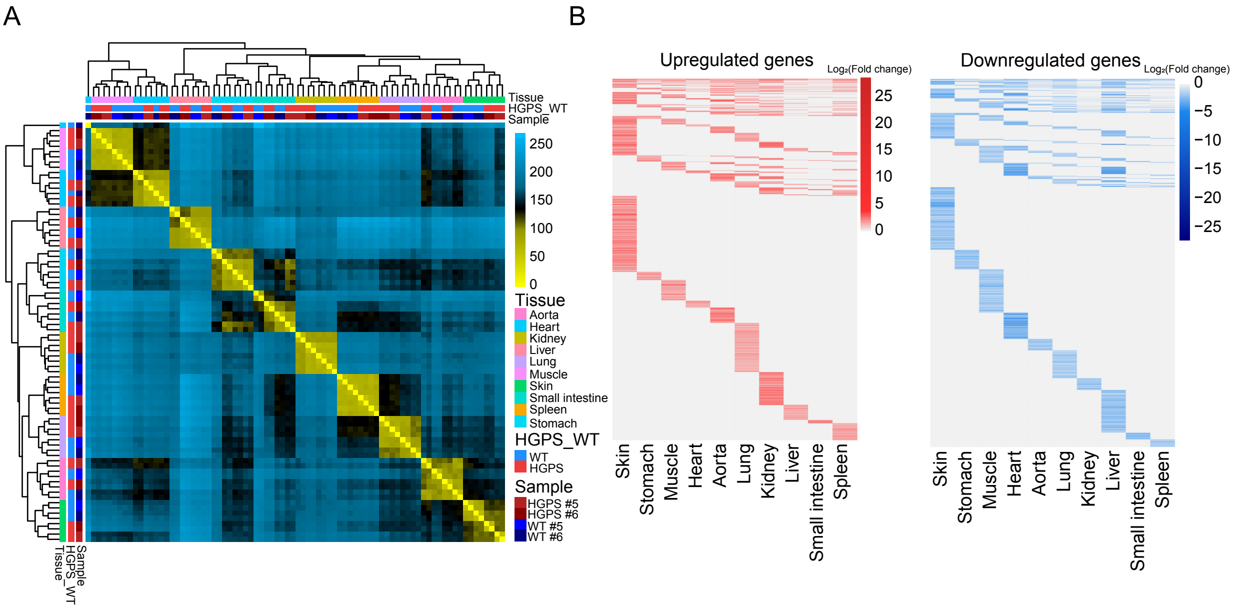
F

| Phenotype | HGPS #1 | BE #2 | HGPS #3 | HGPS #4 | HGPS #5 | HGPS #6 |
|---|---|---|---|---|---|---|
| Sex | Female | Female | Female | Male | Male | Female |
| Age of presentation (months) | 4 | 4 | 4 | 0 | 4 | 4 |
| Weight (g) | 500 | 500 | 950 | 260 | 470 | 410 |
| Height (cm) | 17 | 17 | 17 | 14 | 16 | 15.5 |
| Body mass index (g/$cm^2$) | 1.73 | 1.73 | 12.38 | 1.33 | 1.84 | 1.71 |
| Alopecia | + | - | - | N.A. | ++ | ++ |
| Scleroderma-like skin atrophy | + | - | - | N.A. | + | ++ |
| Decrustation | ++ | - | - | N.A. | + | +++ |
| Mottled pigmentation of the skin | + | - | - | N.A. | ++ | ++ |
| Eyes proptosis | + | - | - | N.A. | + | ++ |
| Tear ducts sensitive | + | - | - | N.A. | - | ++ |
| Nasal discharge | + | - | - | N.A. | + | ++ |
| Panting hard | + | - | - | N.A. | + | ++ |
| Micrognathia | + | - | - | N.A. | + | + |
| Disarry teeth | + | - | - | N.A. | + | + |
| Coracoid mouth | + | - | - | N.A. | + | + |
| Recurrent diarrhea | + | - | - | N.A. | + | ++ |
| Acro-osteolysis | + | - | - | N.A. | ++ | ++ |
| Joint stiffness/arthritis | + | - | - | N.A. | ++ | ++ |

**Supplementary figure 6. Transcriptome features of HGPS monkeys.**

**(A)** Heat map showed the Euclidean distance between WT monkeys and HGPS monkeys in indicated tissues based on the expression levels of all coding genes. The color keys from blue to yellow indicated low to high Euclidean distance. Two experimental repeats are shown.

**(B)** Heat maps showed upregulated genes (left panel) and downregulated genes (right panel) between WT monkeys and HGPS monkeys in various tissues. The color keys from white to red and blue to white indicated low to high $\log_2$ (fold change) for upregulated and downregulated genes between WT monkeys (WT #5 and #6) and HGPS monkeys (HGPS #5 and #6), respectively.

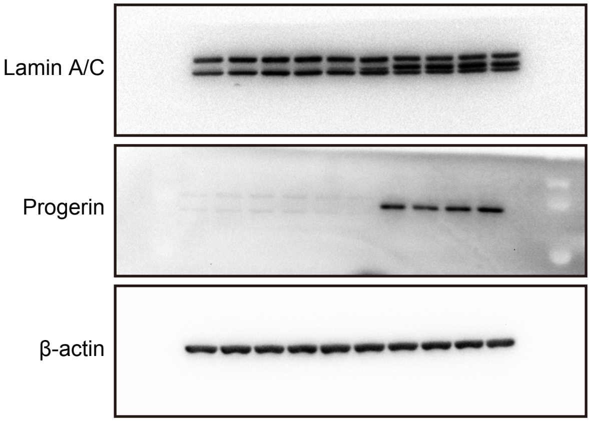

A
Tissue
HGPS_WT
Sample
250
200
150
100
50
0
Tissue
Aorta
Heart
Kidney
Liver
Lung
Muscle
Skin
Small intestine
Spleen
Stomach
HGPS_WT
WT
HGPS
Sample
HGPS #5
HGPS #6
WT #5
WT #6
Sample
HGPS_WT
Tissue
B
Upregulated genes
Log₂(Fold change)
25
20
15
10
5
0
Skin
Stomach
Muscle
Heart
Aorta
Lung
Kidney
Liver
Small intestine
Spleen
Downregulated genes
Log₂(Fold change)
0
−5
−10
−15
−20
−25
Skin
Stomach
Muscle
Heart
Aorta
Lung
Kidney
Liver
Small intestine
Spleen

**Source data. The original photograph involved in the representative figures of WB.**

**(A-E)** The enlarged screenshots of indicated WB results shown in figure 2C **(A)**, figure 2D **(B)**, supplementary figure 4B **(C)**, supplementary figure 4C **(D)**, and supplementary figure 4D **(E)**.

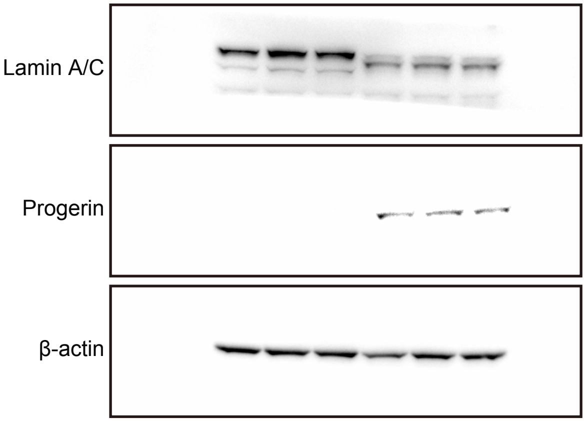
A

Figure 2C



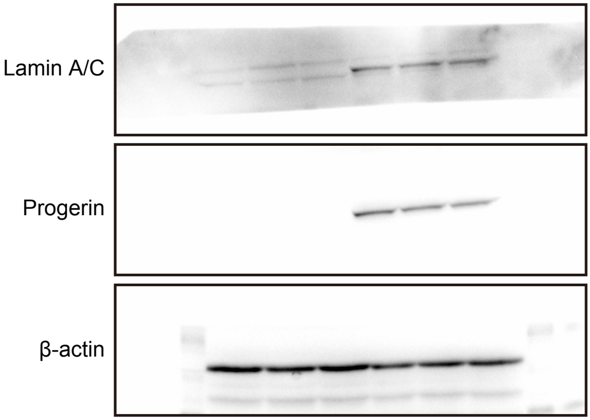
B

Figure 2D



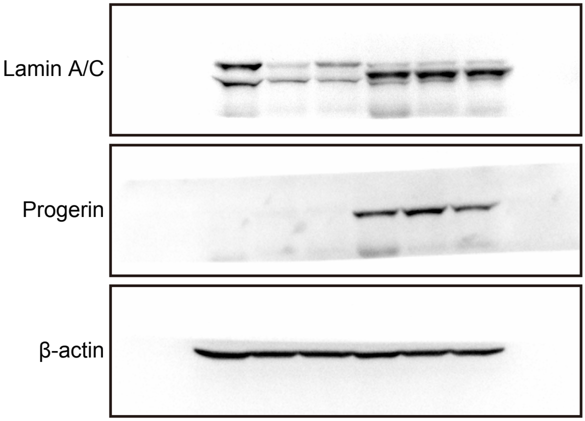
C

Supplementary figure 4B



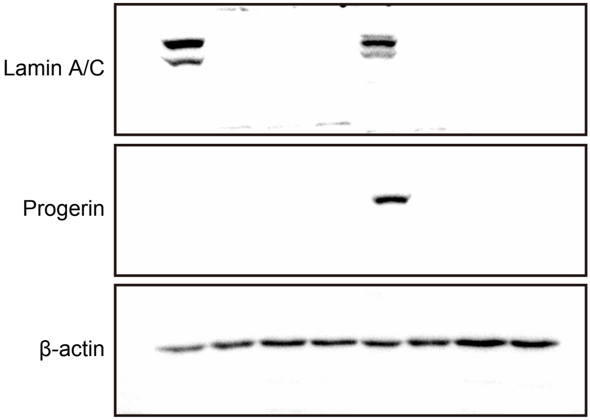
D

Supplementary figure 4C



E

Supplementary figure 4D



# Supplementary Tables

## Table S1

| ID | Sex | Gestation cycle (days) | Birth weight (kg) | Birth height (cm) | Body mass index (kg/cm$^2$) (x10$^{-3}$) | Life span (days) |
|---|---|---|---|---|---|---|
| **HGPS #1** | ♀ | 159 | 0.325 | 13 | 1.92 | alive |
| **BE #2** | ♀ | 159 | 0.4 | 14.5 | 1.9 | alive |
| **HGPS #3** | ♀ | 161 | 0.415 | 14 | 2.12 | alive |
| **HGPS #4** | ♂ | 146 | 0.26 | 14 | 1.33 | 0 |
| **HGPS #5** | ♂ | 166 | 0.36 | 14 | 1.84 | 151 |
| **HGPS #6** | ♀ | 165 | 0.43 | 14 | 2.19 | 132 |
| **WT #1** | ♀ | 155 | 0.36 | 14 | 1.84 | alive |
| **WT #4** | ♂ | 145 | 0.31 | 14 | 1.58 | 0 |
| **WT #5** | ♂ | 155 | 0.4 | 14.1 | 2.01 | 136 |
| **WT #6** | ♀ | 155 | 0.36 | 13.8 | 1.89 | 158 |

**Table S1. Summary of monkeys' information.** Summary of monkey cohorts used in this study.

## Table S2

| **Sample type** | **Monkey** | **G5** | **C6** | **G7** | **G8** | **A9** | **C10** | **C11** | **C12** | **A13** |
|---|---|---|---|---|---|---|---|---|---|---|
| **Blood** | WT #1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #1 | 0 | 0.49 | 0 | 0 | 0 | 0 | 0.48 | 0.46 | 0 |
| | BE #2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #3 | 0 | 0.35 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | F1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | F2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | F3 | 0 | 0 | 0 | 0.02 | 0 | 0 | 0 | 0 | 0 |
| | M1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | M2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | M3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | M4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | M5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Umbilical cord** | WT #4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #1 | 0 | 0.53 | 0 | 0 | 0 | 0 | 0.55 | 0.55 | 0 |
| | BE #2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #3 | 0 | 0.11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #4 | 0 | 0.96 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Heart** | WT #4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #4 | 0 | 0.97 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | WT #6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Muscle** | WT #4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #4 | 0 | 0.96 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Brain** | WT #4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #4 | 0 | 0.94 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Lung** | WT #4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #4 | 0 | 0.97 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Kidney** | WT #4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #4 | 0 | 0.96 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | WT #6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | HGPS #6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Table S2.** Summarized the base editing frequency in seven tissues.

## Table S3

| No. of mismatches | PAM | | | CDS | Off-targets in mutant monkey | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | UTR | | | | | |
| | | | | Intron | | | | | |
| | NGG | NAG | NNN | Intergenic | HGPS #1 | BE #2 | HGPS #3 | HGPS #5 | HGPS #6 |
| 0 | 1 | 0 | 0 | 1 | N.A. | N.A. | N.A. | N.A. | N.A. |
| | | | | 0 | N.A. | N.A. | N.A. | N.A. | N.A. |
| | | | | 0 | N.A. | N.A. | N.A. | N.A. | N.A. |
| | | | | 0 | N.A. | N.A. | N.A. | N.A. | N.A. |
| 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 | 0 | 0 | 0 |
| | | | | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 0 | 0 | 7 | 1 | 0 | 0 | 0 | 0 | 0 |
| | | | | 1 | 0 | 0 | 0 | 0 | 0 |
| | | | | 1 | 0 | 0 | 0 | 0 | 0 |
| | | | | 4 | 0 | 0 | 0 | 0 | 0 |
| 3 | 9 | 6 | 71 | 3 | 0 | 0 | 0 | 0 | 0 |
| | | | | 5 | 0 | 0 | 0 | 0 | 0 |
| | | | | 37 | 0 | 0 | 0 | 0 | 0 |
| | | | | 41 | 1 | 0 | 0 | 0 | 0 |
| 4 | 70 | 70 | 926 | 52 | 0 | 0 | 0 | 0 | 0 |
| | | | | 27 | 0 | 0 | 0 | 0 | 0 |
| | | | | 430 | 3 | 2 | 0 | 1 | 1 |
| | | | | 557 | 0 | 0 | 2 | 2 | 2 |
| 5 | 781 | 671 | 8871 | 495 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | 263 | 0 | 0 | 0 | 0 | 0 |
| | | | | 4065 | 7 | 8 | 8 | 9 | 10 |
| | | | | 5500 | 8 | 7 | 17 | 8 | 9 |

**Table S3. The predicted off-target sites.** Whole-genome sequencing data did not reveal notable mutations in the potential off-target sites predicted based on sequences similar to the sgRNA sequence. The presumed PAM sequences and genomic locations of these sites are shown.

## Table S4.

|  | HGPS #1 | BE #2 | HGPS #3 | HGPS #5 | HGPS #6 | WT #1 | WT #2 | WT #3 |
|---|---|---|---|---|---|---|---|---|
| **WBC ($10^9$/L)** | 11.20 | 12.10 | 20.40 | 14.20 | 16.90 | 12.60 | 11.10 | 25.80 |
| **Lymph ($10^9$/L)** | 5.60 | 4.00 | 12.90 | 6.20 | 9.20 | 7.70 | 8.60 | 15.60 |
| **Mon ($10^9$/L)** | 1.10 | 1.30 | 3.40 | 0.90 | 2.60 | 2.00 | 0.80 | 5.30 |
| **Gran ($10^9$/L)** | 4.00 | 6.80 | 4.10 | 7.10 | 5.10 | 2.90 | 1.70 | 4.90 |
| **Lymph (%)** | 50.30 | 32.70 | 62.80 | 44.00 | 54.50 | 61.50 | 77.60 | 60.40 |
| **Mon (%)** | 9.80 | 11.10 | 16.90 | 6.60 | 15.60 | 15.80 | 6.80 | 20.60 |
| **Gran (%)** | 39.90 | 56.20 | 20.30 | 49.40 | 29.90 | 22.70 | 15.60 | 19.00 |
| **RBC ($10^{12}$/L)** | 6.73 | 6.98 | 6.79 | 5.66 | 5.94 | 6.31 | 6.85 | 6.41 |
| **HGB (g/dL)** | 11.00 | 15.10 | 14.90 | 12.70 | 13.40 | 13.80 | 15.80 | 14.00 |
| **HCT (%)** | 40.70 | 51.80 | 51.30 | 43.20 | 47.00 | 47.30 | 51.20 | 51.80 |
| **MCV (fL)** | 60.60 | 74.30 | 75.60 | 76.50 | 79.20 | 75.10 | 77.70 | 80.90 |
| **MCH (pg)** | 16.30 | 21.60 | 21.90 | 22.40 | 22.50 | 21.80 | 23.00 | 21.80 |
| **MCHC (g/dL)** | 27.00 | 29.10 | 29.00 | 29.30 | 28.50 | 29.10 | 29.60 | 27.00 |
| **RDW (%)** | 14.20 | 14.40 | 15.30 | 14.70 | 16.20 | 14.20 | 15.40 | 16.30 |
| **PLT ($10^9$/L)** | 812.00 | 657.00 | 336.00 | 466.00 | 674.00 | 724.00 | 554.00 | 728.00 |
| **MPV (fL)** | 8.00 | 8.10 | 8.50 | 8.90 | 9.50 | 9.00 | 8.40 | 7.80 |
| **PDW** | 17.00 | 17.00 | 17.00 | 16.80 | 16.70 | 17.00 | 17.40 | 16.90 |
| **PCT (%)** | 0.65 | 0.53 | 0.29 | 0.41 | 0.64 | 0.65 | 0.47 | 0.57 |
| **URIC< (μmol/L)** | 8.00 | 6.00 | 6.00 | 6.00 | 6.00 | 6.00 | 6.00 | 6.00 |
| **CREA (μmol/L)** | 28.00 | 48.00 | 36.00 | 57.00 | 64.00 | 35.00 | 35.00 | 56.00 |
| **TBIL (μmol/L)** | 2.00 | 5.00 | 2.00 | 7.00 | 6.00 | 2.00 | 2.00 | 4.00 |
| **CHOL(mmol/L)** | 3.41 | 2.92 | 3.56 | 6.87 | 3.12 | 4.31 | 5.82 | 2.92 |
| **TRIG (mmol/L)** | 0.68 | 0.36 | 1.02 | 0.99 | 1.10 | 0.42 | 0.71 | 0.32 |
| **UREA (mmol/L)** | 6.70 | 3.10 | 2.40 | 6.40 | 4.50 | 4.40 | 7.90 | 6.70 |
| **AST (U/L)** | 17.00 | 11.00 | 0.00 | 18.00 | 14.00 | 11.00 | 29.00 | 57.00 |
| **ALT (U/L)** | 26.00 | 23.00 | 36.00 | 36.00 | 29.00 | 56.00 | 77.00 | 61.00 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **GLU (mmol/L)** | 7.93 | 4.26 | 4.33 | 1.58 | 2.62 | 4.57 | 3.50 | 3.81 |

**Table S4. Summary of serum analysis.**

**Table S5. Summary of upregulated DEGs between WT and HGPS monkeys.**

**Table S6. Summary of downregulated DEGs between WT and HGPS monkeys.**