Genetic variants and signatures of selective sweep of Hanwoo population (Korean native cattle)
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**Supplementary Figure 1.** Distribution of each variant at the chromosome level. The x-axis of panel a) represents the chromosome number and the y-axis represents the chromosomal proportion of variants. Panel b, c, d) show the number of SNPs, INDELs, and CNVs, number of SNPs, INDELs, and CNVs fit the linear regression with chromosomal length. The R-squared values are 0.9622, 0.9717, and 0.8776.
Supplementary Figure 2. Proportion of each variant. Panel a) length of reference genome, panel b) count of SNP, panel c) length of CNV and panel d) count of INDEL.
Supplementary Figure 3. Distribution of each variant count within 10M bin.
**Supplementary Figure 4.** Detailed distribution of SNPs. Bar colors are as follows: yellow, exon region; green, synonymous SNPs; blue, non-synonymous SNPs; pink, intron SNPs; grey, intergenic SNPs. Panel a) *BoLA* and panel b) *GPR180* are on highly variable region of Figure 2. Panel c) *RCN2* is identified as a selective sweep gene by LD-based $\omega$ statistics and SFS-based $\Lambda$ statistics.
Supplementary Figure 5. Correlation among various variants and repeat elements. The correlation values are represented as colors, where range of colors (from red to blue) shows the range of correlation values. The blue color represents positive correlation between them, the red color means negative correlation between them.
Supplementary Figure 6. Histogram of variant quality. A) SNP, B) INEL
Supplementary Figure 7. Histogram of INDEL length.
Supplementary Figure 8. Distribution of CNV length.
Supplementary Figure 9A. Distribution of repeat element count (each 1M bin).
Supplementary Figure 9B. Distribution of repeat element count (each 1M bin).
Supplementary Figure 10. Contig map. Highly variable region marked as red line. A) chr23: 23-31Mb, B) chr12: 69-77Mb.
Supplementary Figure 11. Site frequency spectrum (SFS) of each variants.
**Supplementary Table 1.** Depth of aligned reads.

| Sample ID  | Length of mapped reads | Depth  |
|------------|-------------------------|--------|
| Sample 1   | 33,368,106,938          | 12.64  |
| Sample 2   | 33,280,536,546          | 12.61  |
| Sample 3   | 37,026,364,021          | 14.02  |
| Sample 4   | 34,418,405,645          | 13.04  |
| Sample 5   | 36,252,079,703          | 13.73  |
| Sample 6   | 38,681,093,570          | 14.65  |
| Sample 7   | 40,373,295,400          | 15.29  |
| Sample 8   | 38,302,265,874          | 14.51  |
| Sample 9   | 40,994,015,656          | 15.53  |
| Sample 10  | 40,369,688,670          | 15.29  |
| Sample 11  | 40,786,434,996          | 15.45  |
| Sample 12  | 37,387,121,377          | 14.16  |
| **Average**| **37,603,284,033**      | **14.24** |
**Supplementary Table 2.** Number of 3 kinds of variants.

| Chromosome | Length         | SNPs | Change rate | INDELS | Change rate | CNVs  | Change rate |
|------------|----------------|------|-------------|--------|-------------|-------|-------------|
| Autosome   | 2,512,082,506  |      |             |        |             |       |             |
| 1          | 158,337,067    | 951,682 | 166 | 116,542 | 1,358 | 241 | 657,000   |
| 2          | 137,060,424    | 769,456 | 178 | 93,014  | 1,473 | 183 | 748,964   |
| 3          | 121,430,405    | 751,302 | 161 | 84,287  | 1,440 | 159 | 763,713   |
| 4          | 120,829,699    | 736,948 | 163 | 88,842  | 1,360 | 161 | 750,495   |
| 5          | 121,191,424    | 682,000 | 177 | 80,386  | 1,507 | 188 | 644,635   |
| 6          | 119,458,736    | 713,808 | 167 | 88,316  | 1,352 | 180 | 663,659   |
| 7          | 112,638,659    | 618,603 | 182 | 74,718  | 1,507 | 172 | 654,875   |
| 8          | 113,384,836    | 637,221 | 177 | 77,957  | 1,456 | 162 | 699,906   |
| 9          | 105,705,250    | 600,264 | 176 | 74,342  | 1,421 | 131 | 806,933   |
| 10         | 104,305,016    | 610,408 | 170 | 70,959  | 1,469 | 121 | 862,024   |
| 11         | 107,310,763    | 603,234 | 177 | 70,293  | 1,526 | 147 | 730,005   |
| 12         | 91,163,125     | 621,266 | 146 | 71,123  | 1,281 | 154 | 591,968   |
| 13         | 84,240,350     | 485,950 | 173 | 55,082  | 1,529 | 85  | 991,062   |
| 14         | 84,648,390     | 491,074 | 172 | 58,029  | 1,458 | 99  | 855,034   |
| 15         | 85,296,676     | 546,086 | 156 | 62,085  | 1,373 | 139 | 613,645   |
| 16         | 81,724,687     | 477,614 | 171 | 54,997  | 1,485 | 99  | 825,501   |
| 17         | 75,158,596     | 471,290 | 159 | 55,269  | 1,359 | 112 | 671,058   |
| 18         | 66,004,023     | 385,437 | 171 | 42,701  | 1,545 | 68  | 970,647   |
| 19         | 64,057,457     | 375,841 | 170 | 41,604  | 1,539 | 63  | 1,016,785 |
| 20         | 72,042,655     | 434,344 | 165 | 52,239  | 1,379 | 124 | 580,989   |
| 21         | 71,599,096     | 420,917 | 170 | 47,882  | 1,495 | 84  | 852,370   |
| 22         | 61,435,874     | 350,737 | 175 | 41,479  | 1,481 | 67  | 916,953   |
| 23         | 52,530,062     | 422,898 | 124 | 44,581  | 1,178 | 87  | 603,793   |
| 24         | 62,714,930     | 407,537 | 153 | 47,273  | 1,326 | 86  | 729,243   |
| 25         | 42,904,170     | 274,418 | 156 | 29,085  | 1,475 | 37  | 1,159,572 |
| 26         | 51,681,464     | 313,010 | 165 | 35,768  | 1,444 | 80  | 646,018   |
| 27         | 45,407,902     | 298,638 | 152 | 35,852  | 1,266 | 59  | 769,625   |
| 28         | 46,312,546     | 307,270 | 150 | 34,705  | 1,334 | 70  | 661,607   |
| 29         | 51,505,224     | 366,167 | 140 | 38,704  | 1,330 | 87  | 592,014   |
**Supplementary Table 3.** Nucleotide diversity of gene in highly variable region.

| Gene    | Nucleotide diversity ($\pi$) |
|---------|-----------------------------|
| BIRC3   | 8.85                        |
| CLDN10  | 8.85                        |
| DCT     | 14.80                       |
| DNAJC3  | 0.68                        |
| DZIP1   | 12.74                       |
| GPC6    | 28.18                       |
| GPR180  | 1.13                        |
| HS6ST3  | 37.07                       |
| RAP2A   | 4.27                        |
| Average | 12.95                       |