

Supplementary Table 1. Information regarding the horses evaluated in this study.

| Horse name | Life number | Age | Sex | Hair color | Price of the horse (KRW) |
|------------------|-------------|-----|--------|------------|--------------------------|
| JIGUSANG SERYEOK | KOR05218979 | 8 | Female | Chestnut | --- |
| GEUMBIT SESANG | KOR06120650 | 7 | Male | Brown | ₩149,645,000 |

Supplementary Table 2. Information regarding the primers used to validate the methylation state of target gene promoter region by BSP, and assess expression by using real-time RT-PCR.

| Gene | Accession number | Direction | Sequences (5'-3') | Amplify size (bp) |
|--------------------------------|-----------------------|-----------|--------------------------------|-------------------|
| <i>ZNF80</i> (for BSP) | ENSECAT000000506 2 | Forward | GGTTTTGGGATTTGTAGTTTATTG | 203 |
| | | Reverse | AACCTAATCCAACCTACCCCAACT | |
| <i>POU1F1</i> (for BSP) | ENSECAT000000961 5 | Forward | TAAAGGGATTTTTTTGTAGTATAAG | 160 |
| | | Reverse | AAAAAAAATACTACTCCCAAATC | |
| <i>MFGES</i> (for BSP) | ENSECAT000002028 5 | Forward | TAGGGGAGGGGATTAATTTGTTA | 292 |
| | | Reverse | CACCTTAACATCCCAAAAAACTAC | |
| <i>ANAPC1</i> (for BSP) | ENSECAT000002281 0 | Forward | TGTAGTAATAGTTGTTAATGTAGAGATTTG | 421 |
| | | Reverse | AACCTTTCTACTCATAAAATCCAAAC | |
| <i>ANAPC1</i> (for expression) | ENSECAT000002281 0 | Forward | GCAAACACCACCCTAATGCT | 142 |
| | | Reverse | TGCCAGCTTTCCTTCTGTTT | |
| <i>GAPDH</i> | ENSECAT000002372 1 | Forward | ATCTGACCTGCCGCCTGGAG | 68 |
| | | Reverse | CGATGCCTGCTTCACCACCTTC | |

Supplementary Table 3. The general information of read alignment in the genomes of the blood samples collected from the two thoroughbred horses before and after trotting.

| | JIGUSANG SERYEOK | | GEUMBIT SESANG | |
|---|------------------|----------------|-----------------|----------------|
| | Before exercise | After exercise | Before exercise | After exercise |
| Data size (Gb) | 1.20 | 1.19 | 1.15 | 1.20 |
| Total sequenced reads (No.) | 24,489,796 | 24,251,782 | 23,506,720 | 24,489,796 |
| Mapped reads (No.) | 20,888,843 | 20,850,727 | 19,905,128 | 21,304,452 |
| Mapping rate (%) | 85.30 | 85.98 | 84.68 | 86.99 |
| Effective chain depth ¹ | 0.43 | 0.43 | 0.41 | 0.44 |
| Uniquely mapped reads (No.) | 17,847,159 | 17,745,354 | 16,700,660 | 18,540,301 |
| Unique mapping rate (%) ² | 72.88 | 73.17 | 71.05 | 75.71 |
| Total predicted peaks (No.) | 105,303 | 92,969 | 81,140 | 98,210 |
| Average peak length (bp) | 860 | 878 | 889 | 883 |
| Median peak length (bp) | 774 | 791 | 802 | 796 |
| Total length of peaks (bp) | 90,566,979 | 81,629,516 | 72,173,605 | 86,699,687 |
| Peak-covered size in the reference genome (%) | 3.83 | 3.45 | 3.05 | 3.66 |

¹Effective chain depth = total length of mapped reads / the size of the reference genome

²Unique mapping rate = total uniquely mapped reads / total sequenced reads

Supplementary Table 4. Number of different genomic regions in the reference genome (EquCab2).

| | Promoter | 5' UTR | Exon | Intron | 3' UTR | Downstream | Repeat | Others |
|---------|-----------------|---------------|-------------|---------------|---------------|-------------------|---------------|---------------|
| EquCab2 | 27,554 | 12,441 | 205,323 | 178,583 | 11,862 | 27,488 | 2,501,645 | 7,576,494 |

Supplementary Table 5. Frequency of methylation peaks in different genomic regions.

| | | Promoter | 5' UTR | Exon | Intron | 3' UTR | Downstream | Repeat | Others |
|------------------|-----------------|----------|--------|-------|--------|--------|------------|--------|--------|
| JIGUSANG SERYEOK | Before exercise | 0.075 | 0.005 | 0.023 | 0.168 | 0.013 | 0.073 | 0.012 | 0.005 |
| | After exercise | 0.067 | 0.006 | 0.021 | 0.146 | 0.011 | 0.066 | 0.010 | 0.004 |
| GEUMBIT SESANG | Before exercise | 0.056 | 0.004 | 0.019 | 0.128 | 0.009 | 0.056 | 0.009 | 0.004 |
| | After exercise | 0.069 | 0.005 | 0.020 | 0.156 | 0.013 | 0.071 | 0.011 | 0.005 |

Frequency of peaks = Peak distribution / Numbers of different genomic regions in the EquCab2

| | | | | | | | | | | | | | | | |
|------|----------|----------|----|----|--------|--------|------------|------------|---|-----------------|------------|-------|--------|---|-----|
| cm51 | 538267 | 538388 | 32 | 69 | 31,579 | 69,532 | 1.14697293 | 0.02030302 | 0 | HyperExposition | TG00400079 | LIMAD | LABEL1 | C | 29 |
| cm51 | 2014821 | 2014821 | 21 | 46 | 20,724 | 46,427 | 1.0282044 | 0.02030304 | 0 | HyperExposition | TG00400080 | LIMAD | LABEL1 | C | 311 |
| cm51 | 220014 | 220110 | 20 | 47 | 19,737 | 47,625 | 1.2711127 | 0.0203040 | 0 | HyperExposition | TG00400482 | LIMAD | LABEL1 | C | 143 |
| cm51 | 207571 | 207571 | 14 | 23 | 19,855 | 42,321 | 1.02222222 | 0.02030404 | 0 | HyperExposition | TG00400483 | LIMAD | LABEL1 | C | 248 |
| cm51 | 1347424 | 1347538 | 14 | 20 | 13,816 | 30,465 | 1.17969262 | 0.02030505 | 0 | HyperExposition | TG00400490 | LIMAD | LABEL1 | C | 154 |
| cm52 | 5275545 | 5276255 | 16 | 37 | 16,789 | 37,2 | 1.24791799 | 0.02030608 | 0 | HyperExposition | TG00400637 | LIMAD | LABEL1 | C | 411 |
| cm52 | 4572021 | 4572021 | 17 | 41 | 16,776 | 41,554 | 1.39888889 | 0.02030709 | 0 | HyperExposition | TG00400638 | LIMAD | LABEL1 | C | 411 |
| cm52 | 8076884 | 8076882 | 17 | 41 | 16,776 | 41,554 | 1.39888889 | 0.02030709 | 0 | HyperExposition | TG00400639 | LIMAD | LABEL1 | C | 184 |
| cm52 | 3048752 | 3048752 | 14 | 27 | 13,816 | 29,244 | 1.22222222 | 0.02030810 | 0 | HyperExposition | TG00400640 | LIMAD | LABEL1 | C | 184 |
| cm52 | 3048752 | 3048752 | 32 | 66 | 31,579 | 69,532 | 1.0282044 | 0.02030810 | 0 | HyperExposition | TG00400641 | LIMAD | LABEL1 | C | 130 |
| cm52 | 7720800 | 7720800 | 30 | 75 | 30,7 | 76,014 | 1.01935055 | 0.02030911 | 0 | HyperExposition | TG00400688 | LIMAD | LABEL1 | C | 107 |
| cm52 | 34545 | 34545 | 22 | 41 | 21,111 | 46,427 | 1.02222222 | 0.02030911 | 0 | HyperExposition | TG00400689 | LIMAD | LABEL1 | C | 110 |
| cm52 | 1045024 | 1045024 | 14 | 23 | 14,448 | 31,579 | 1.15222222 | 0.02030911 | 0 | HyperExposition | TG00400755 | LIMAD | LABEL1 | C | 74 |
| cm51 | 9156200 | 9156200 | 14 | 23 | 14,448 | 31,579 | 1.0282044 | 0.02030911 | 0 | HyperExposition | TG00400756 | LIMAD | LABEL1 | C | 74 |
| cm51 | 9156200 | 9156200 | 14 | 23 | 14,448 | 31,579 | 1.0282044 | 0.02030911 | 0 | HyperExposition | TG00400757 | LIMAD | LABEL1 | C | 74 |
| cm51 | 1835642 | 1835770 | 15 | 27 | 14,803 | 32,1 | 1.41012101 | 0.02030911 | 0 | HyperExposition | TG00400854 | LIMAD | LABEL1 | C | 69 |
| cm51 | 1835642 | 1835770 | 15 | 27 | 14,803 | 32,1 | 1.41012101 | 0.02030911 | 0 | HyperExposition | TG00400855 | LIMAD | LABEL1 | C | 113 |
| cm51 | 2833489 | 2833274 | 23 | 63 | 22,807 | 63,851 | 1.46255154 | 0.02030911 | 0 | HyperExposition | TG00401468 | LIMAD | LABEL1 | C | 254 |
| cm51 | 2833489 | 2833274 | 23 | 63 | 22,807 | 63,851 | 1.46255154 | 0.02030911 | 0 | HyperExposition | TG00401469 | LIMAD | LABEL1 | C | 254 |
| cm51 | 9232000 | 9232054 | 16 | 36 | 15,771 | 35,473 | 1.05491454 | 0.02031102 | 0 | HyperExposition | TG00400320 | LIMAD | LABEL1 | C | 480 |
| cm51 | 9232000 | 9232054 | 22 | 60 | 21,111 | 46,427 | 1.22222222 | 0.02031102 | 0 | HyperExposition | TG00400321 | LIMAD | LABEL1 | C | 480 |
| cm51 | 4238767 | 4238763 | 31 | 77 | 30,522 | 78,041 | 1.59173890 | 0.02032306 | 0 | HyperExposition | TG00400389 | LIMAD | LABEL1 | C | 130 |
| cm51 | 10270828 | 10270814 | 26 | 63 | 26,624 | 61,624 | 1.46255154 | 0.02032306 | 0 | HyperExposition | TG00400423 | LIMAD | LABEL1 | C | 147 |
| cm51 | 7720800 | 7720800 | 30 | 75 | 30,553 | 81,122 | 1.33091388 | 0.02032678 | 0 | HyperExposition | TG00400224 | LIMAD | LABEL1 | C | 239 |
| cm51 | 7720800 | 7720800 | 30 | 75 | 30,553 | 81,122 | 1.33091388 | 0.02032678 | 0 | HyperExposition | TG00400225 | LIMAD | LABEL1 | C | 239 |
| cm51 | 14388 | 14388 | 21 | 42 | 21,728 | 46,427 | 1.02222222 | 0.02032678 | 0 | HyperExposition | TG00400427 | LIMAD | LABEL1 | C | 275 |
| cm51 | 4238767 | 4238763 | 14 | 28 | 13,816 | 28,718 | 1.0282044 | 0.02032678 | 0 | HyperExposition | TG00400922 | LIMAD | LABEL1 | C | 17 |
| cm51 | 2463200 | 2462267 | 25 | 66 | 24,421 | 66,802 | 1.43617467 | 0.02032701 | 0 | HyperExposition | TG00401952 | LIMAD | LABEL1 | C | 17 |
| cm51 | 2463200 | 2462267 | 25 | 66 | 24,421 | 66,802 | 1.43617467 | 0.02032701 | 0 | HyperExposition | TG00401953 | LIMAD | LABEL1 | C | 17 |
| cm51 | 1726562 | 1726254 | 22 | 50 | 20,724 | 50,676 | 1.22222222 | 0.02032816 | 0 | HyperExposition | TG00400511 | LIMAD | LABEL1 | C | 80 |
| cm51 | 2657876 | 2658261 | 24 | 47 | 23,523 | 50,676 | 1.1717076 | 0.02032816 | 0 | HyperExposition | TG00400586 | LIMAD | LABEL1 | C | 80 |
| cm51 | 3611700 | 3612269 | 16 | 44 | 15,789 | 44,556 | 1.49526120 | 0.02032816 | 0 | HyperExposition | TG00400937 | LIMAD | LABEL1 | C | 240 |
| cm51 | 3611700 | 3612269 | 16 | 44 | 15,789 | 44,556 | 1.49526120 | 0.02032816 | 0 | HyperExposition | TG00400938 | LIMAD | LABEL1 | C | 240 |
| cm51 | 3707202 | 3708954 | 15 | 36 | 14,803 | 38,514 | 1.37042203 | 0.02032816 | 0 | HyperExposition | TG00400939 | LIMAD | LABEL1 | C | 240 |
| cm51 | 134467 | 134461 | 15 | 36 | 14,803 | 38,514 | 1.1124844 | 0.02032816 | 0 | HyperExposition | TG00400940 | LIMAD | LABEL1 | C | 240 |
| cm51 | 4932288 | 4932398 | 15 | 36 | 14,803 | 38,514 | 1.37042203 | 0.02032816 | 0 | HyperExposition | TG00400941 | LIMAD | LABEL1 | C | 240 |
| cm51 | 4932288 | 4932398 | 15 | 36 | 14,803 | 38,514 | 1.37042203 | 0.02032816 | 0 | HyperExposition | TG00400942 | LIMAD | LABEL1 | C | 240 |
| cm51 | 520615 | 520578 | 16 | 30 | 15,789 | 35,446 | 1.0282044 | 0.02032816 | 0 | HyperExposition | TG00400927 | LIMAD | LABEL1 | C | 17 |
| cm51 | 412618 | 412618 | 14 | 23 | 14,448 | 31,579 | 1.0282044 | 0.02032816 | 0 | HyperExposition | TG00400928 | LIMAD | LABEL1 | C | 17 |
| cm51 | 448440 | 448501 | 15 | 30 | 20,724 | 50,676 | 1.22691604 | 0.02032816 | 0 | HyperExposition | TG00400927 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400928 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400929 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400930 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400931 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400932 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400933 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400934 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400935 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400936 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400937 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400938 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400939 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400940 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400941 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400942 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400943 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400944 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400945 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400946 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400947 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400948 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400949 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400950 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400951 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400952 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400953 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400954 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400955 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400956 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400957 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400958 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400959 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400960 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400961 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400962 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400963 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400964 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400965 | LIMAD | LABEL1 | C | 287 |
| cm51 | 457919 | 457919 | 14 | 23 | 13,816 | 31,579 | 1.17969262 | 0.02032816 | 0 | HyperExposition | TG00400966 | LIMAD | LABEL1 | C | 28 |

Supplementary Table 7. The list of negatively-correlated genes between expression level and methylation level.

Differentially expressed genes (DEGs) from RNA-Seq

| Gene | Locus | GS FPKM (A) | GS FPKM (B) | Log2(B/A) | P-value | Expression change after exercise in GS |
|----------|--------------------------|-------------|-------------|---------------|-------------|--|
| FOXP2 | Chr4:71764132-72012020 | 0.0680683 | 0 | -1.79769e+308 | 0.0369233 | Low-expressed |
| GXYLT2 | Chr16:17474065-17553670 | 0.223271 | 0 | -1.79769e+308 | 0.0335125 | Low-expressed |
| SH2D4B | Chr1:88561674-88654379 | 0.131498 | 0 | -1.79769e+308 | 0.0335125 | Low-expressed |
| SLC5A3 | Chr26:30639217-30670146 | 6.52548 | 10.0874 | 0.628406 | 0.0433971 | High-expressed |
| TMEM150B | Chr10:24471616-24498340 | 11.2547 | 18.1067 | 0.685998 | 0.0489095 | High-expressed |
| DEDD2 | Chr10:13553003-13573408 | 17.423 | 30.137 | 0.790539 | 0.00105037 | High-expressed |
| C1orf21 | Chr5:21315334-21458065 | 6.19695 | 12.24 | 0.98197 | 0.0135391 | High-expressed |
| NLRP12 | Chr10:22834672-22866121 | 2.2363 | 6.33784 | 1.50288 | 0.000012507 | High-expressed |
| LRP11 | Chr31:16978002-17011735 | 0.240771 | 0.700482 | 1.54069 | 0.027201 | High-expressed |
| ANGPT1 | Chr9:51942202-52181014 | 0 | 0.0859218 | 1.79769e+308 | 0.0345177 | High-expressed |
| FSTL4 | Chr14:42281899-42486963 | 0 | 0.0164148 | 1.79769e+308 | 0.0384396 | High-expressed |
| Gene | Locus | JS FPKM (A) | JS FPKM (B) | Log2(B/A) | P-value | Expression change after exercise in JS |
| NCKAP5 | Chr18:16876570-17702260 | 0.125461 | 0.0128215 | -3.2906 | 0.0245383 | Low-expressed |
| PHC3 | Chr19:10518569-10590129 | 15.2939 | 6.11646 | -1.32218 | 0.00593945 | Low-expressed |
| SLC16A6 | Chr11:12371268-12389919 | 23.1525 | 10.8843 | -1.08892 | 0.0121751 | Low-expressed |
| CACNA1D | Chr16:34062865-34381927 | 0.0377868 | 0 | -1.79769e+308 | 0.0436843 | Low-expressed |
| GNAL | Chr8:38096950-38193302 | 0.238902 | 0 | -1.79769e+308 | 0.0371067 | Low-expressed |
| SCUBE2 | Chr7:78361864-78421344 | 0.0569065 | 0 | -1.79769e+308 | 0.0433786 | Low-expressed |
| TNFRSF21 | Chr20:45737669-45803833 | 2.8901 | 6.04327 | 1.06421 | 0.0259256 | High-expressed |
| CCS | Chr12:26545317-26556416 | 17.7861 | 37.2994 | 1.0684 | 0.0297999 | High-expressed |
| TGM2 | Chr22:28368451-28401055 | 11.1224 | 25.4011 | 1.19142 | 0.00117231 | High-expressed |
| UNC93A | Chr31:7737541-7780641 | 12.8184 | 30.5082 | 1.25099 | 0.0287247 | High-expressed |
| CYSTM1 | Chr14:36525183-36642135 | 24.9577 | 75.159 | 1.59046 | 0.0483555 | High-expressed |
| NFKBIA | Chr1:172073462-172075841 | 204.95 | 899.854 | 2.13442 | 9.07634E-06 | High-expressed |
| CORO6 | Chr11:43380047-43389316 | 0.139187 | 0.678452 | 2.28522 | 0.0043599 | High-expressed |

Differentially methylated regions (DMRs) from MeDIP-Seq

| Locus | Region | GS #No. of nomalized tag (C) | GS #No. of nomalized tag (D) | log2(D/C) | Methylation change after exercise in GS |
|--------------------------|----------|------------------------------|------------------------------|--------------|---|
| chr4:71883226-71884016 | Intron | 8.382902233 | 14.0235048 | 0.742325248 | Hypermethylation |
| chr16:17523312-17524090 | Intron | 11.97557462 | 25.88954732 | 1.112274858 | Hypermethylation |
| chr1:88634905-88636084 | Intron | 19.16091939 | 29.12574073 | 0.604127954 | Hypermethylation |
| chr26:30659825-30660957 | CDS | 22.75359177 | 14.0235048 | -0.698247343 | Hypomethylation |
| chr10:24493821-24494734 | Intron | 25.1487067 | 11.86604252 | -1.083645352 | Hypomethylation |
| chr10:13551779-13552578 | Promoter | 17.3645832 | 9.169214675 | -0.921277702 | Hypomethylation |
| chr5:21365884-21366919 | Intron | 23.35237051 | 12.94477366 | -0.851199266 | Hypomethylation |
| chr10:22835202-22837013 | Intron | 46.10596228 | 29.6651063 | -0.636186375 | Hypomethylation |
| chr31:17006150-17006808 | CDS | 17.3645832 | 10.78731138 | -0.686812448 | Hypomethylation |
| chr9:52167932-52168543 | Intron | 16.76580447 | 8.629849105 | -0.95811447 | Hypomethylation |
| chr14:42281774-42282989 | Intron | 24.54992797 | 14.56287037 | -0.75342405 | Hypomethylation |
| Chr | Region | JS #No. of nomalized tag (C) | JS #No. of nomalized tag (D) | log2(D/C) | Methylation change after exercise in JS |
| chr18:17202202-17202867 | Intron | 15.12845826 | 23.66816689 | 0.645683003 | Hypermethylation |
| chr19:10559357-10560782 | Intron | 13.44751845 | 27.61286137 | 1.038000426 | Hypermethylation |
| chr11:12380345-12382804 | CDS | 19.61096441 | 47.89986156 | 1.288361001 | Hypermethylation |
| chr16:34245727-34246767 | Intron | 10.64595211 | 18.59641684 | 0.804719688 | Hypermethylation |
| chr8:38130307-38130965 | Intron | 10.08563884 | 15.77877793 | 0.645683003 | Hypermethylation |
| chr7:78395986-78397691 | Intron | 13.44751845 | 28.17638916 | 1.067146771 | Hypermethylation |
| chr20:45739955-45740750 | CDS | 17.93002461 | 11.83408345 | -0.599429495 | Hypomethylation |
| chr12:26546342-26548572 | Intron | 57.7122667 | 32.68461142 | -0.82026645 | Hypomethylation |
| chr22:28401186-28402536 | Promoter | 40.90286863 | 26.48580581 | -0.626982625 | Hypomethylation |
| chr31:7775322-7776231 | Intron | 28.57597671 | 18.03288906 | -0.66417226 | Hypomethylation |
| chr14:36605515-36606545 | Intron | 17.36971134 | 11.27055566 | -0.624015133 | Hypomethylation |
| chr1:172074178-172075231 | Intron | 19.61096441 | 10.1435001 | -0.951104933 | Hypomethylation |
| chr11:43384670-43385728 | CDS | 26.33472364 | 16.90583349 | -0.639445174 | Hypomethylation |

Supplementary Table 8. Distribution and frequency of methylation peaks over repeats in the genome.

| Repeat class | Repeats in the genome | No. of peaks | | | | Frequency of peaks | | | |
|----------------|-----------------------|------------------|----------------|-----------------|----------------|--------------------|----------------|-----------------|----------------|
| | | JIGUSANG SERYEOK | | GEUMBIT SESANG | | JIGUSANG SERYEOK | | GEUMBIT SESANG | |
| | | Before exercise | After exercise | Before exercise | After exercise | Before exercise | After exercise | Before exercise | After exercise |
| DNA | 364,428 | 2,458 | 2,227 | 1,787 | 2,407 | 0.007 | 0.006 | 0.005 | 0.007 |
| LINE | 1,246,366 | 18,338 | 15,468 | 13,565 | 17,457 | 0.015 | 0.012 | 0.011 | 0.014 |
| Low complexity | 252,740 | 393 | 343 | 298 | 358 | 0.002 | 0.001 | 0.001 | 0.001 |
| LTR | 436,921 | 3,826 | 3,743 | 3,042 | 3,779 | 0.009 | 0.009 | 0.007 | 0.009 |
| RC | 2,424 | 12 | 19 | 10 | 12 | 0.005 | 0.008 | 0.004 | 0.005 |
| RNA | 696 | 4 | 4 | 6 | 3 | 0.006 | 0.006 | 0.009 | 0.004 |
| rRNA | 445 | 13 | 10 | 11 | 11 | 0.029 | 0.022 | 0.025 | 0.025 |
| Satellite | 1,344 | 59 | 61 | 65 | 71 | 0.044 | 0.045 | 0.048 | 0.053 |
| scRNA | 73 | 1 | 1 | - | 1 | 0.014 | 0.014 | - | 0.014 |
| Simple repeat | 199,308 | 1,213 | 1,024 | 800 | 1,032 | 0.006 | 0.005 | 0.004 | 0.005 |
| SINE | 990,165 | 16,339 | 13,931 | 12,763 | 14,225 | 0.017 | 0.014 | 0.013 | 0.014 |
| snRNA | 989 | 9 | 10 | 8 | 16 | 0.009 | 0.010 | 0.008 | 0.016 |
| srpRNA | 25 | 2 | 1 | 2 | 1 | 0.080 | 0.040 | 0.080 | 0.040 |
| tRNA | 14,097 | 51 | 56 | 49 | 55 | 0.004 | 0.004 | 0.003 | 0.004 |
| Unknown | 8,133 | 40 | 42 | 30 | 46 | 0.005 | 0.005 | 0.004 | 0.006 |
| Total | 3,518,154 | 42,758 | 36,940 | 32,436 | 39,474 | 0.012 | 0.010 | 0.009 | 0.011 |

Supplementary Table 9. DMR-containing gene lists after GO and KEGG analysis of the two horses before and after exercise.

| Category | Term | P-value | Genes | Count |
|---------------|--|-------------|--|-------|
| GOTERM_BP_FAT | Metal ion transport | 0.004663668 | SLC12A8, SLC8A2, SLC39A11, KCNB1, TRPC7, SFXN4, SFXN1, TCN2, KCNIP1, SFXN5, CACNA2D4, KCNMB2, KCNQ5, ABCC9, KCNN3, SCN8A, CHRNA10 | 17 |
| GOTERM_BP_FAT | Protein amino acid phosphorylation | 7.03E-04 | PRKCA, PIK3CG, OBSCN, CDK5R1, FLT3, NLK, STRADA, PRKCH, EIF2A, TTN, CDKL5, CAMKK1, DAPK1, MAP4K3, IRAK3, PTK2, COL4A3BP, PDGFRA, SPTBN1, PDGFRB, GRK4, EIF2AK4, AKT3, NEK7 | 24 |
| GOTERM_BP_FAT | Regulation of small GTPase mediated signal transduc | 2.96E-04 | OBSCN, ARHGEF7, KIAA1244, PREX1, IQGAP2, PSD4, TTN, DNMBP, ADAP1, TBC1D16, GARNL3, RASGRF2, GIT2, RASA3 | 14 |
| GOTERM_CC_FAT | Contractile fiber | 0.003515576 | OBSCN, CDK5R1, SYNE1, TNNT1, MYH11, SPTBN1, MYOM1, TTN | 8 |
| GOTERM_CC_FAT | M band | 3.27E-04 | OBSCN, SPTBN1, MYOM1, TTN | 4 |
| GOTERM_CC_FAT | Cytoskeleton | 8.54E-05 | DNAH11, MAD1L1, PARD3, LMNB1, CNN3, CDC14A, DNAH14, FAM110B, IQGAP2, DNAH2, TTN, STAU1, PTK2, SORBS1, CDK5RAP2, MYOM1, IFNGR1, ZW10, NF2, MICAL2, KIF18B, SPATC1, SEPT10, DNMBP, DAPK1, ARPC1A, SYNE1, EPB41L1, TNNT1, CST6, TBCA, SPAG5, CGN, FRMD4A, MCPH1, NINL, MYH11, PEBP1, CLIP1, SPTBN1, PDE4DIP, ADD1 | 42 |
| GOTERM_MF_FAT | Small GTPase regulator activity | 4.74E-04 | OBSCN, ARHGEF7, KIAA1244, PREX1, IQGAP2, PSD4, TTN, DNMBP, ADAP1, TBC1D16, MAP4K3, GARNL3, RASGRF2, GIT2 | 14 |
| GOTERM_MF_FAT | Calmodulin binding | 4.19E-04 | SLC8A2, CNN3, KCNN3, MYH11, IQGAP2, SPTBN1, TTN, CAMKK1, ADD1, DAPK1 | 10 |
| GOTERM_MF_FAT | Vascular endothelial growth factor receptor activity | 2.14E-04 | NRP2, FLT3, PDGFRA, PDGFRB | 4 |
| KEGG_PATHWAY | Tight junction | 0.011503665 | PRKCA, INADL, PARD3, EPB41L1, CGN, MYH11, PRKCH, AKT3 | 8 |
| KEGG_PATHWAY | Glioma | 0.028459795 | PRKCA, PIK3CG, PDGFRA, PDGFRB, AKT3 | 5 |