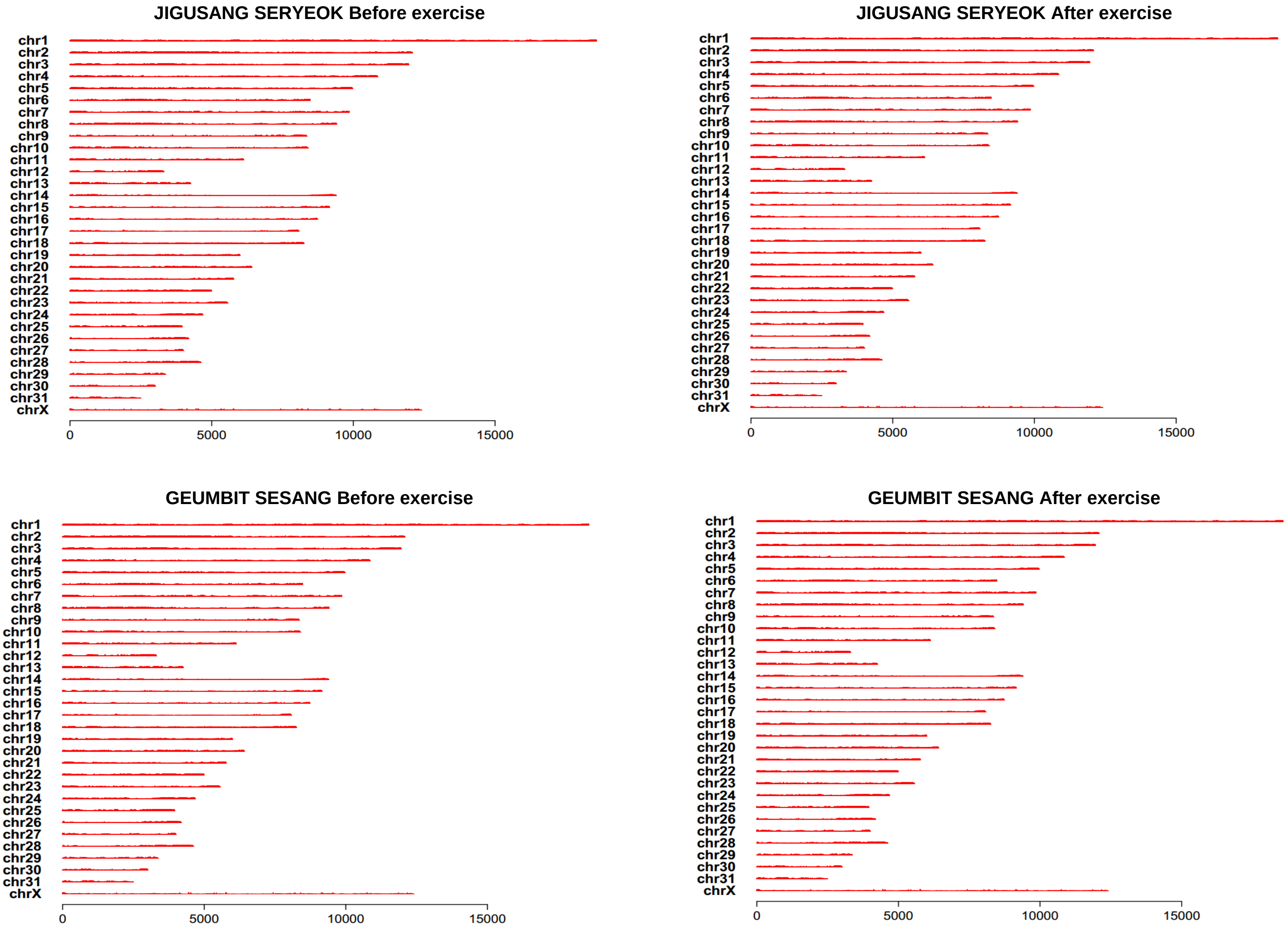
Supplementary Fig. 1.

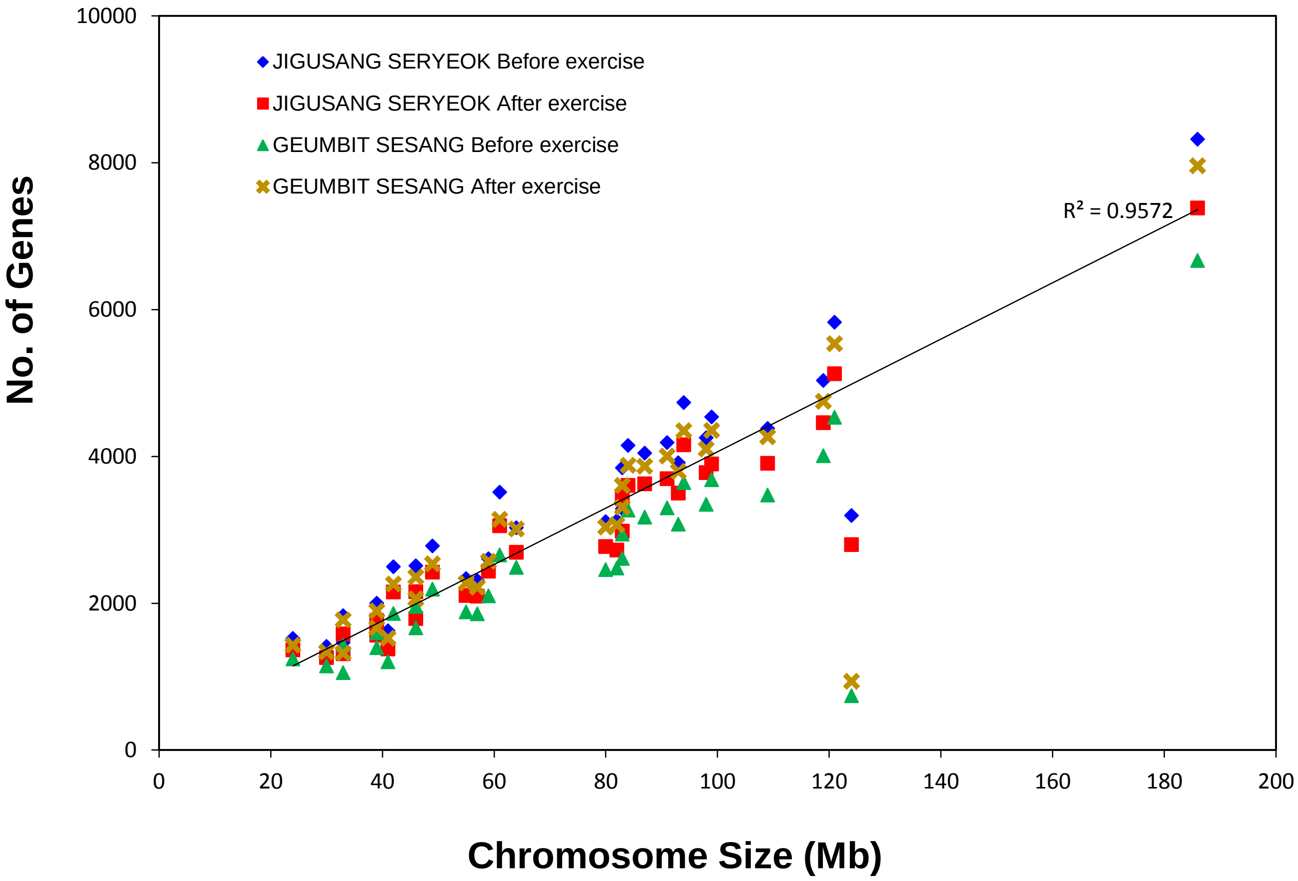

JIGUSANG SERYEOK Before exercise

JIGUSANG SERYEOK After exercise

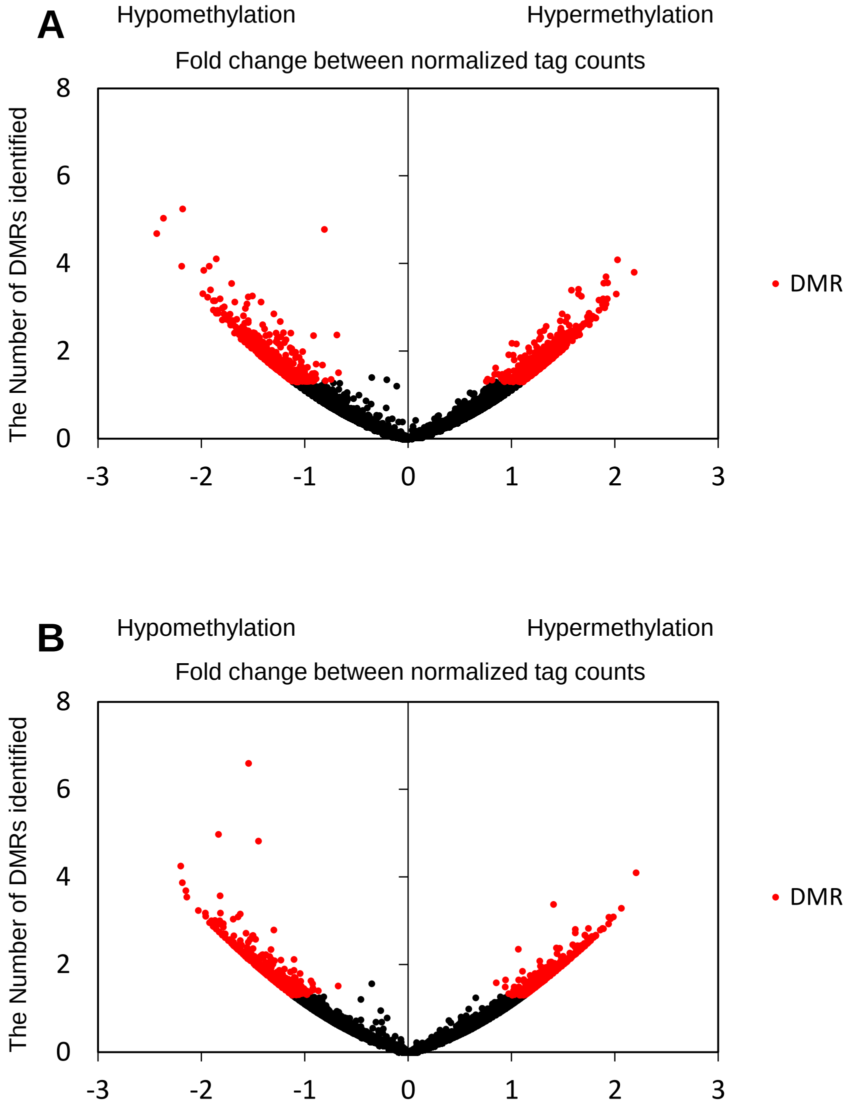
GEUMBIT SESANG Before exercise

GEUMBIT SESANG After exercise

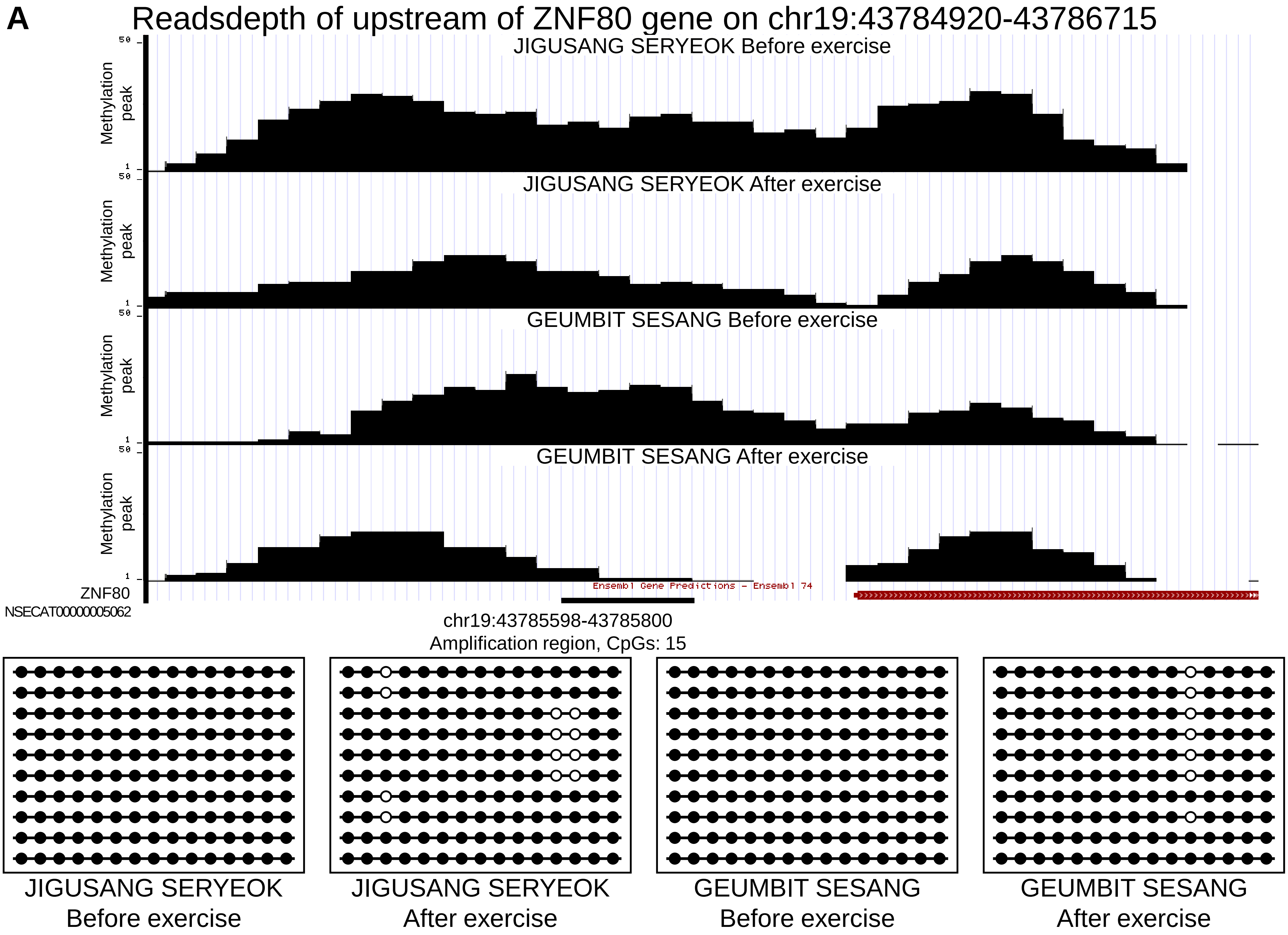
Supplementary Fig. 2.

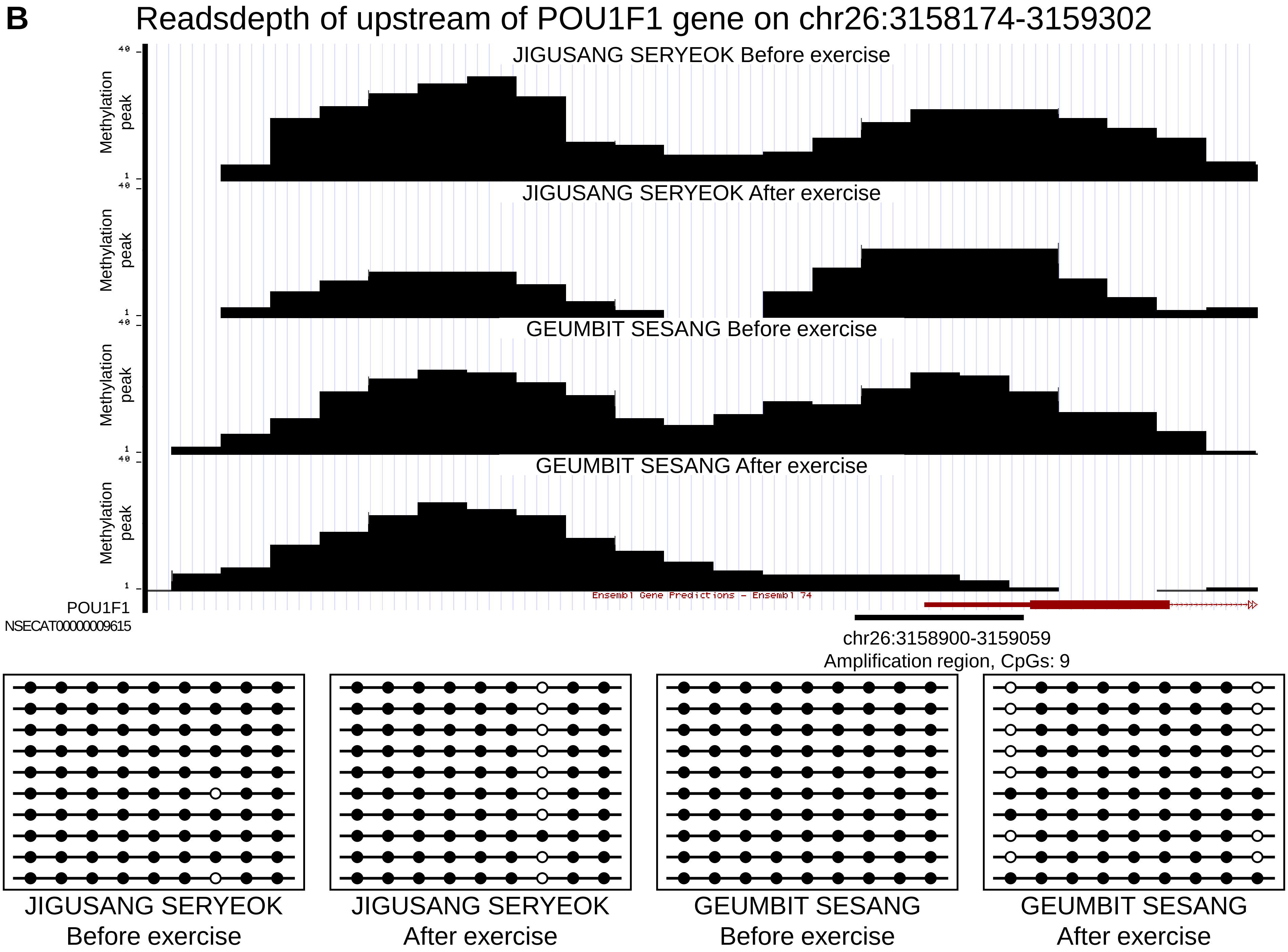


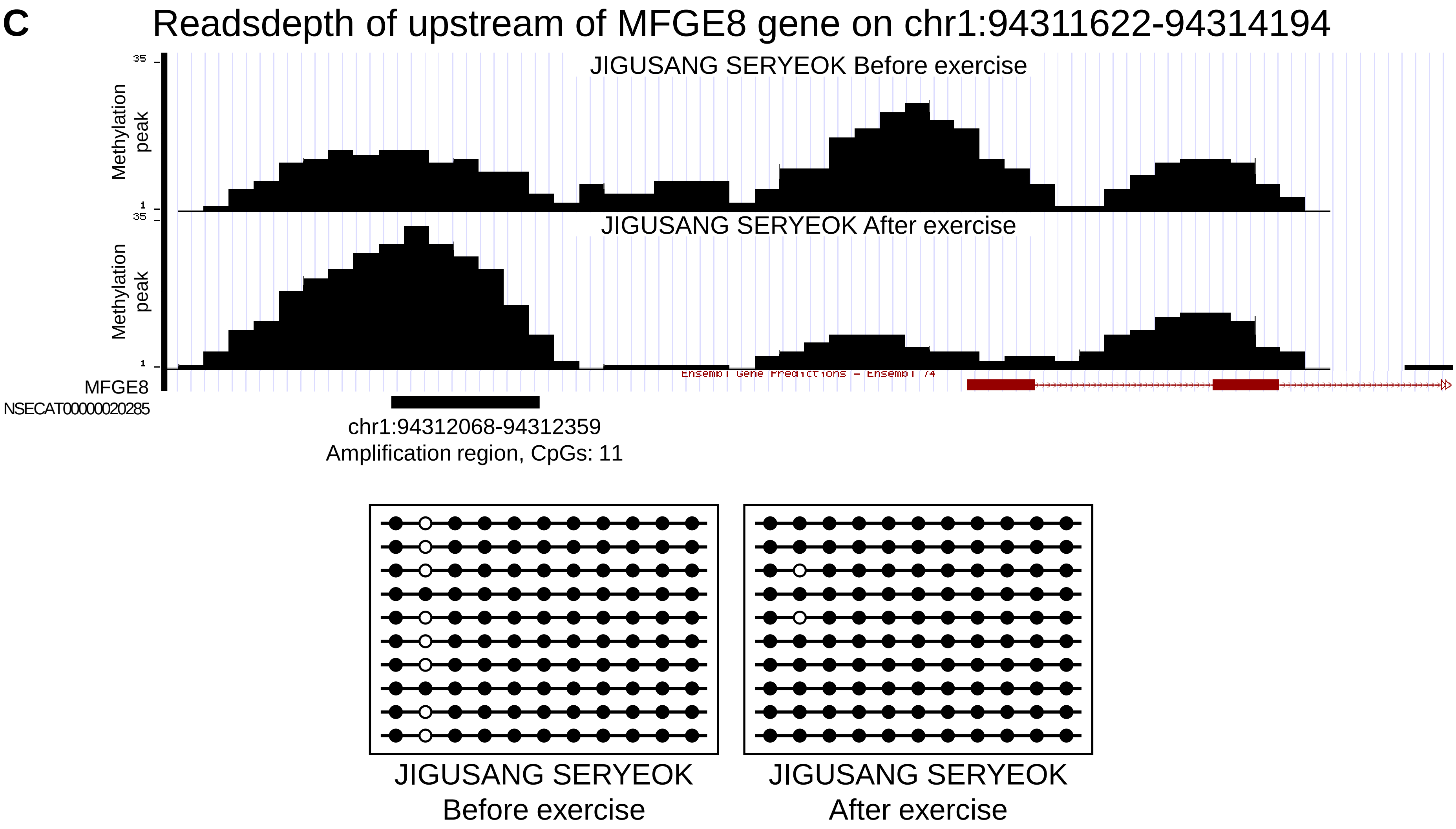
Supplementary Fig. 3.

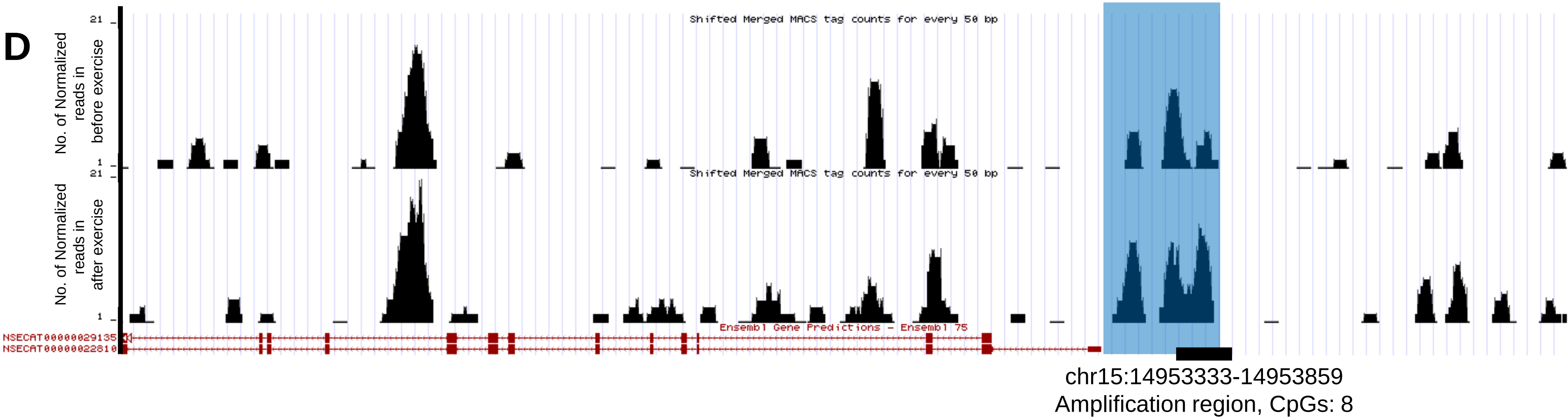


Supplementary Fig. 4.

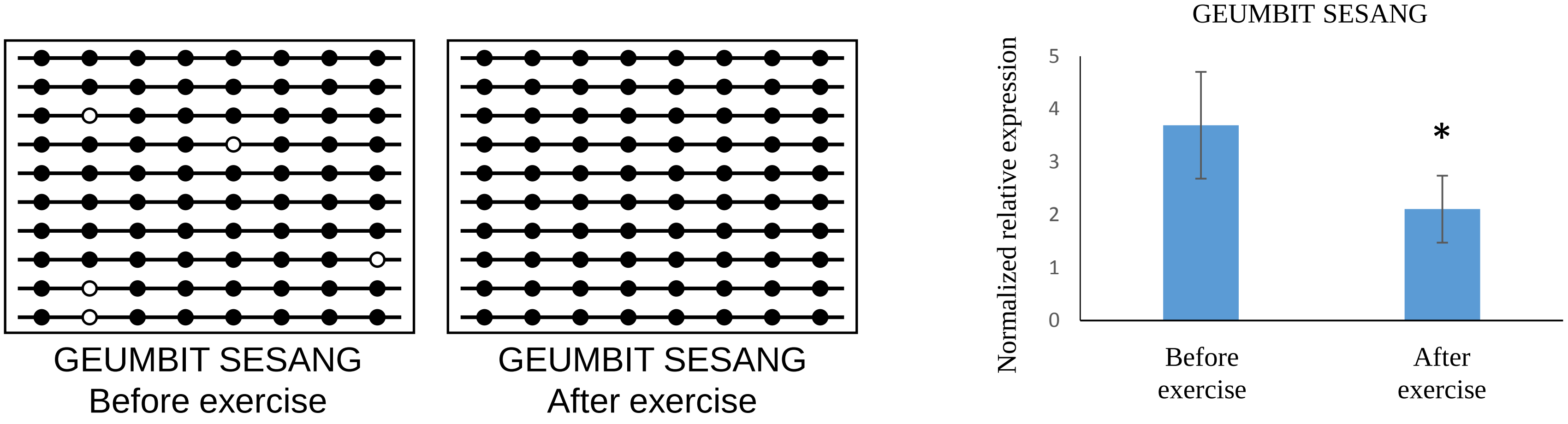



B
Readsdepth of upstream of POU1F1 gene on chr26:3158174-3159302
JIGUSANG SERYEOK Before exercise
JIGUSANG SERYEOK After exercise
GEUMBIT SESANG Before exercise
GEUMBIT SESANG After exercise
Methylation peak
40
1
Ensembl Gene Predictions - Ensembl 74
POU1F1
NSECAT00000009615
chr26:3158900-3159059
Amplification region, CpGs: 9
JIGUSANG SERYEOK Before exercise
JIGUSANG SERYEOK After exercise
GEUMBIT SESANG Before exercise
GEUMBIT SESANG After exercise

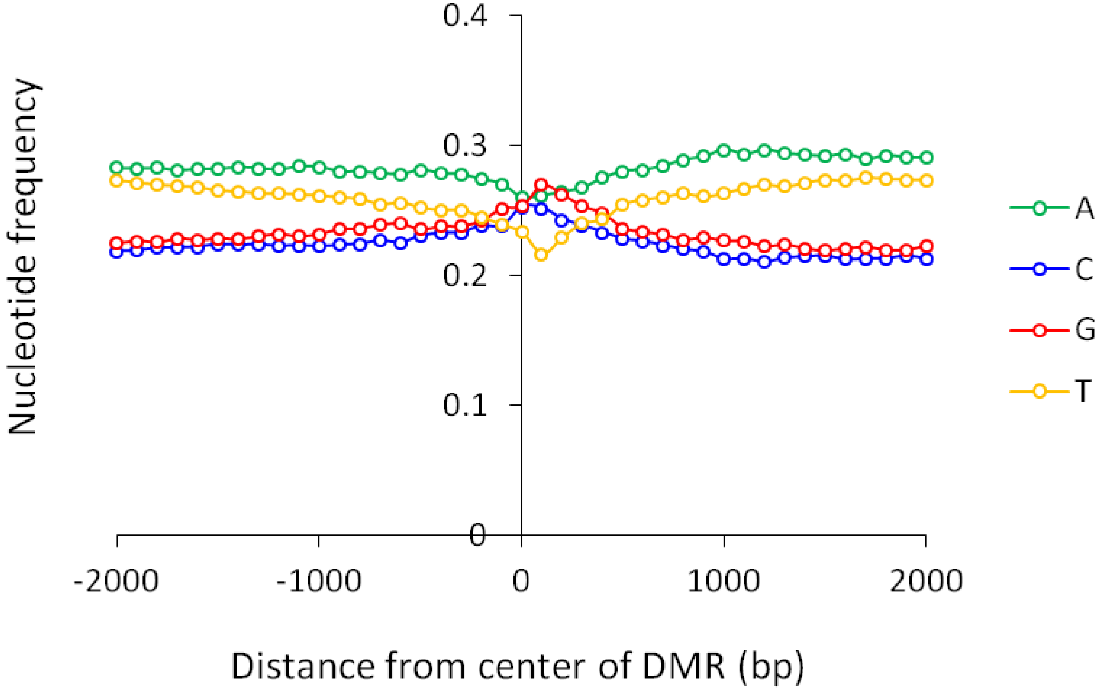

C
Readsdepth of upstream of MFGE8 gene on chr1:94311622-94314194
35
JIGUSANG SERYEOK Before exercise
Methylation peak
1
35
JIGUSANG SERYEOK After exercise
Methylation peak
1
Ensembl Gene Predictions - Ensembl 74
MFGE8
NSECAT00000020285
chr1:94312068-94312359
Amplification region, CpGs: 11
JIGUSANG SERYEOK
Before exercise
JIGUSANG SERYEOK
After exercise



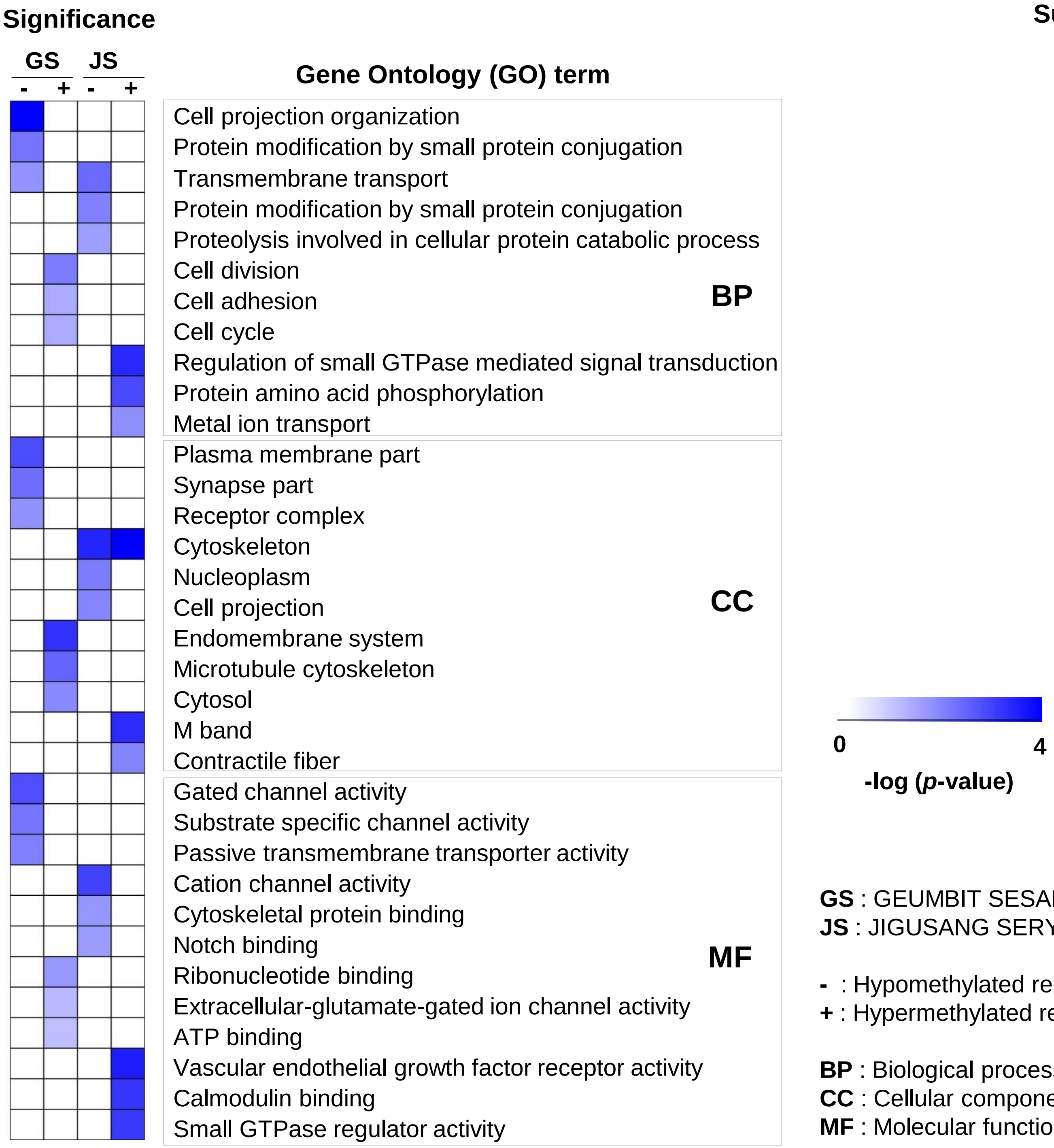
(D) The *ANAPC1* (Anaphase-promoting complex subunit 1) gene is located in chr15:14,841,594-14,951,441. The upstream region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Cell cycle, BP: Cell adhesion, CC: Cytosol. Relative expression levels of *ANAPC1* in pre- and post-exercise samples. The relative expression level of each gene was evaluated by using qRT-PCR, all samples were amplified in triplicate. Results are presented as mean ± SD. A paired Student's *t*-test was performed to obtain *p* values (**p* < 0.05).



Supplementary Fig. 5.



Supplementary Fig. 6.

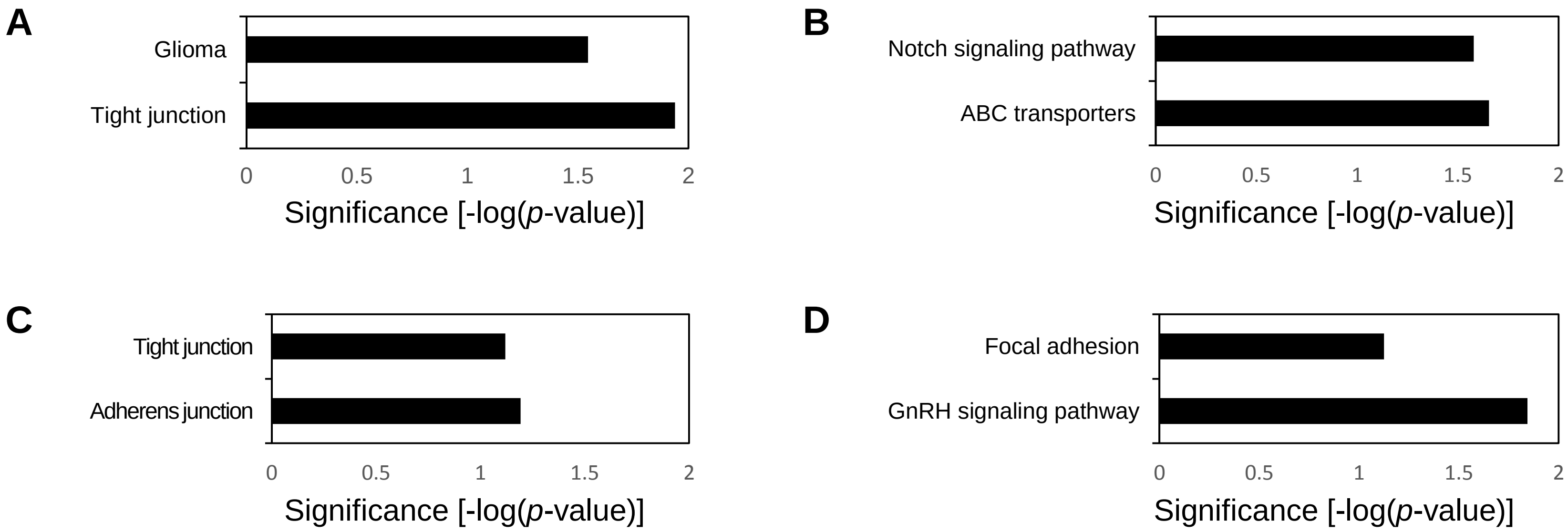


GS : GEUMBIT SESANG
JS : JIGUSANG SERYEOK

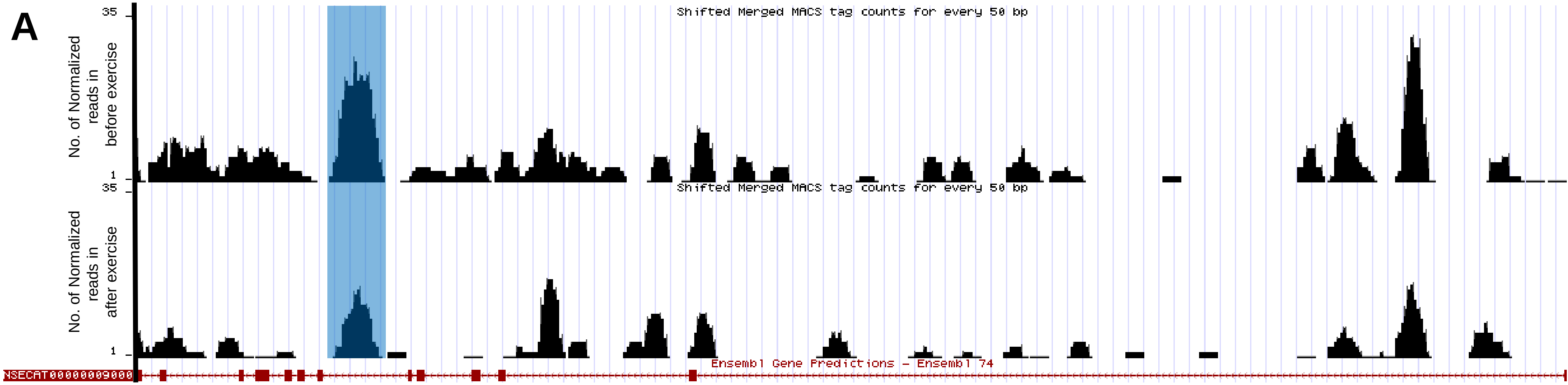
- : Hypomethylated region after exercise
+ : Hypermethylated region after exercise

BP : Biological process
CC : Cellular component
MF : Molecular function

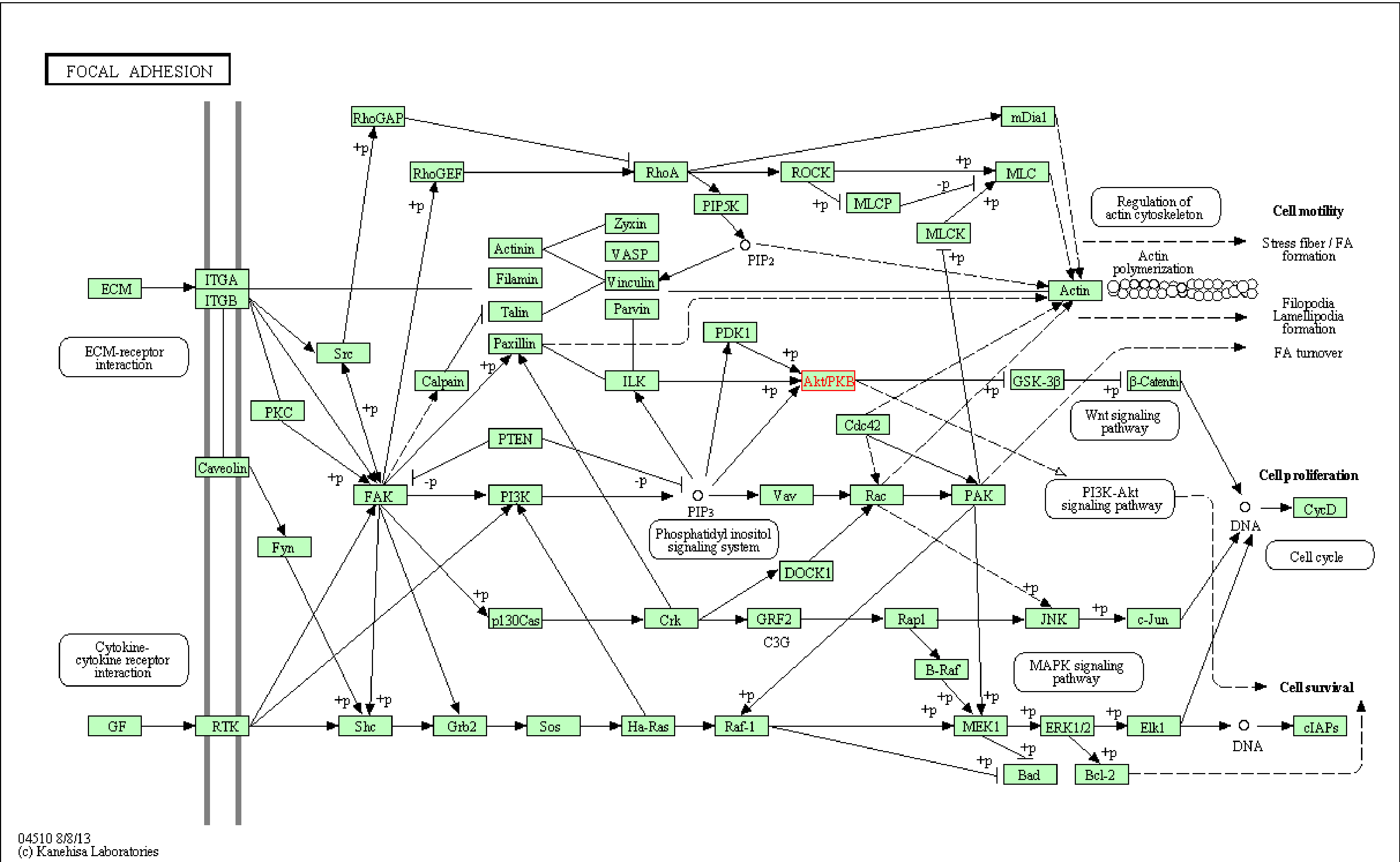
Supplementary Fig. 7.



Supplementary Fig. 8.



(A) The *AKT1* (RAC-alpha serine/threonine-protein kinase 1) gene is located in chr24:46,109,751-46,133,097. The intronic region is hypomethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows: BP: Protein modification by small protein conjugation, BP: Cell projection organization, KEGG: Focal adhesion.


FOCAL ADHESION
RhoGAP
mDia1
RhoGEF
RhoA
ROCK
MLC
PIP5K
MLCP
Zyxin
VASP
Actinin
Filamin
Vinculin
Talin
Parvin
Paxillin
PIP2
MLCK
Regulation of actin cytoskeleton
Cell motility
Stress fiber / FA formation
Actin polymerization
Actin
Filopodia Lamellipodia formation
FA turnover
ECM
ITGA
ITGB
ECM-receptor interaction
Src
PKC
Calpain
ILK
PDK1
Akt/PKB
GSK-3β
β-Catenin
Wnt signaling pathway
Cdc42
PTEN
Caveolin
FAK
PI3K
PIP3
Vav
Rac
PAK
PI3K-Akt signaling pathway
Cell proliferation
DNA
CycD
Phosphatidyl inositol signaling system
DOCK1
Cell cycle
Fyn
p130Cas
Crk
GRF2
C3G
Rap1
JNK
c-Jun
B-Raf
MAPK signaling pathway
Cytokine-cytokine receptor interaction
Cell survival
GF
RTK
Shc
Grb2
Sos
Ha-Ras
Raf-1
MEK1
ERK1/2
Elk1
DNA
cIAPs
Bad
Bcl-2
+p
-p

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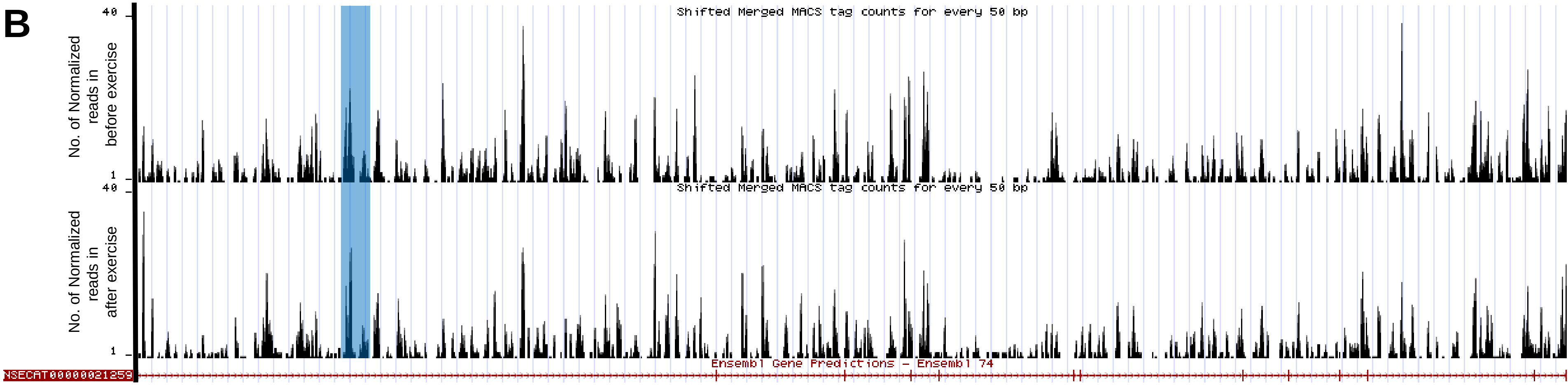
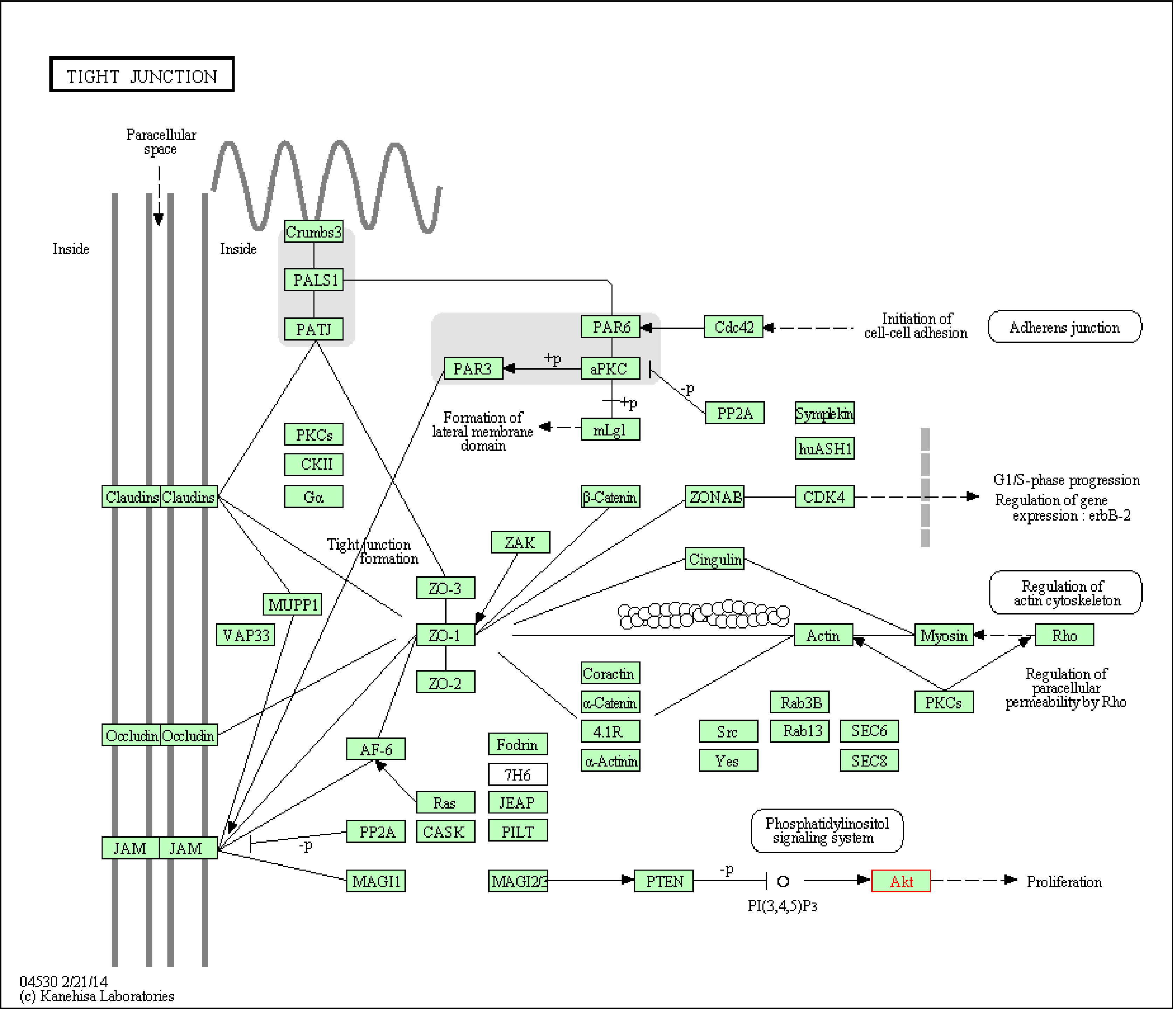
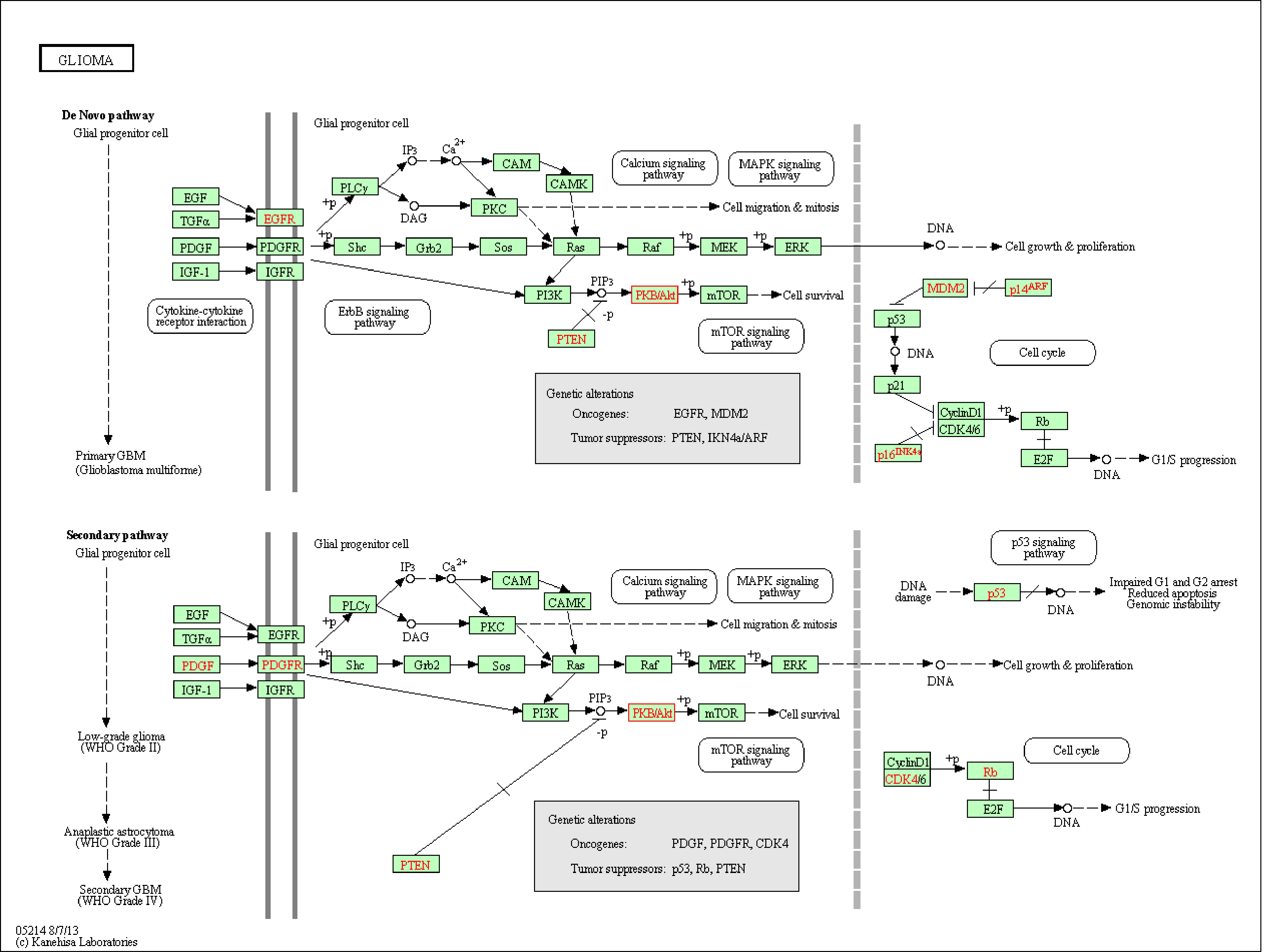
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



(B) The *AKT3* (RAC-gamma serine/threonine-protein kinase 3) gene is located in chr30:1,173,477-1,487,389. The intron region is hypermethylation in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Protein amino acid phosphorylation, KEGG: Tight junction, KEGG: Glioma.


TIGHT JUNCTION
Paracellular space
Inside
Inside
Crumbs3
PALS1
PATJ
PAR6
Cdc42
Initiation of cell-cell adhesion
Adherens junction
PAR3
+p
aPKC
-p
PP2A
Symplekin
+p
Formation of lateral membrane domain
mLgl
huASH1
PKCs
CKII
Gα
Claudins
Claudins
β-Catenin
ZONAB
CDK4
G1/S-phase progression
Regulation of gene expression : erbB-2
ZAK
Tight junction formation
Cingulin
Regulation of actin cytoskeleton
ZO-3
MUPP1
VAP33
ZO-1
Actin
Myosin
Rho
ZO-2
Coractin
α-Catenin
Rab3B
PKCs
Regulation of paracellular permeability by Rho
4.1R
Src
Rab13
SEC6
Occludin
Occludin
AF-6
Fodrin
α-Actinin
Yes
SEC8
7H6
Ras
JEAP
PP2A
CASK
PILT
Phosphatidylinositol signaling system
JAM
JAM
-p
MAGI1
MAGI2/3
PTEN
-p
PI(3,4,5)P3
Akt
Proliferation
04530 2/21/14
(c) Kanehisa Laboratories


GLIOMA
De Novo pathway
Glial progenitor cell
Primary GBM
(Glioblastoma multiforme)
EGF
TGFα
PDGF
IGF-1
EGFR
PDGFR
IGFR
Cytokine-cytokine receptor interaction
Glial progenitor cell
PLCγ
IP3
Ca2+
CAM
CAMK
DAG
PKC
Calcium signaling pathway
MAPK signaling pathway
Cell migration & mitosis
+p
Shc
Grb2
Sos
Ras
Raf
MEK
ERK
DNA
Cell growth & proliferation
ErbB signaling pathway
PI3K
PIP3
PKB/Akt
mTOR
Cell survival
-p
PTEN
mTOR signaling pathway
Genetic alterations
Oncogenes: EGFR, MDM2
Tumor suppressors: PTEN, IKN4a/ARF
MDM2
p14ARF
p53
p21
Cell cycle
CyclinD1
CDK4/6
p16INK4a
Rb
E2F
G1/S progression
Secondary pathway
Glial progenitor cell
Low-grade glioma
(WHO Grade II)
Anaplastic astrocytoma
(WHO Grade III)
Secondary GBM
(WHO Grade IV)
p53 signaling pathway
DNA damage
Impaired G1 and G2 arrest
Reduced apoptosis
Genomic instability
Genetic alterations
Oncogenes: PDGF, PDGFR, CDK4
Tumor suppressors: p53, Rb, PTEN
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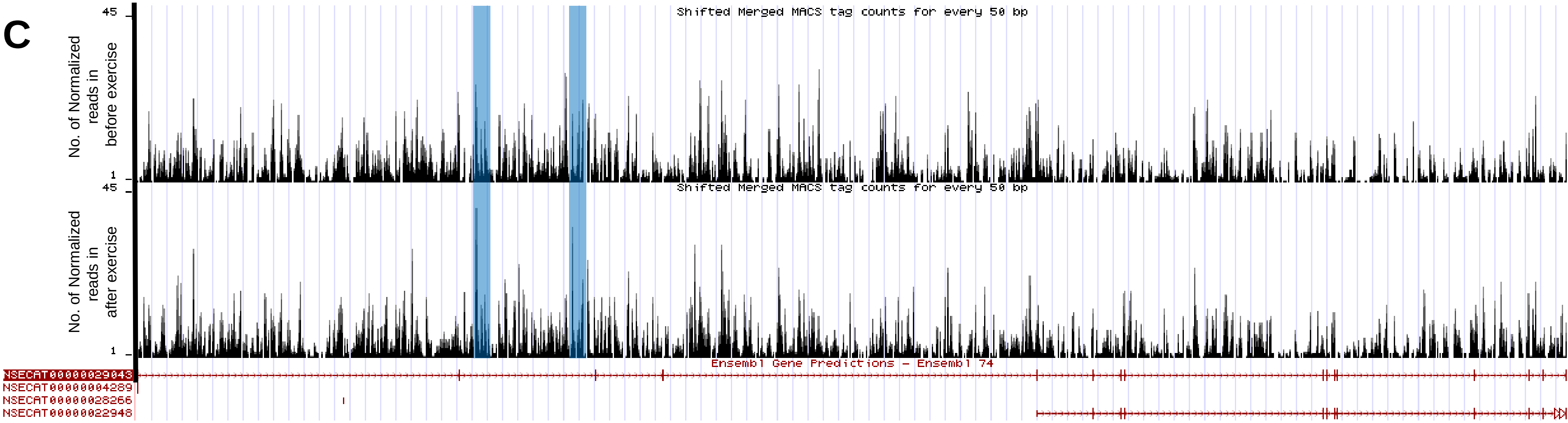
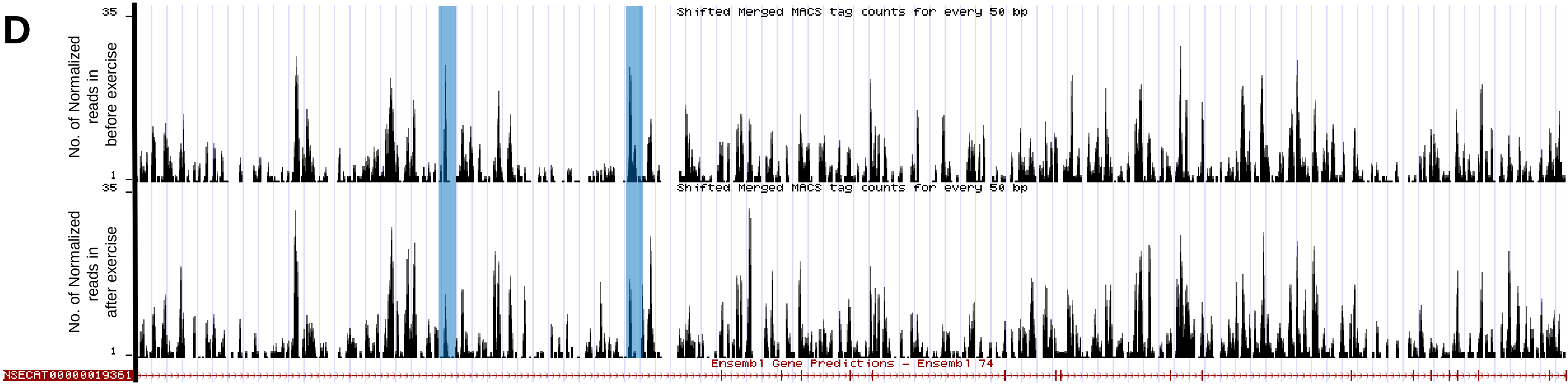
(c) Kanehisa Laboratories

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



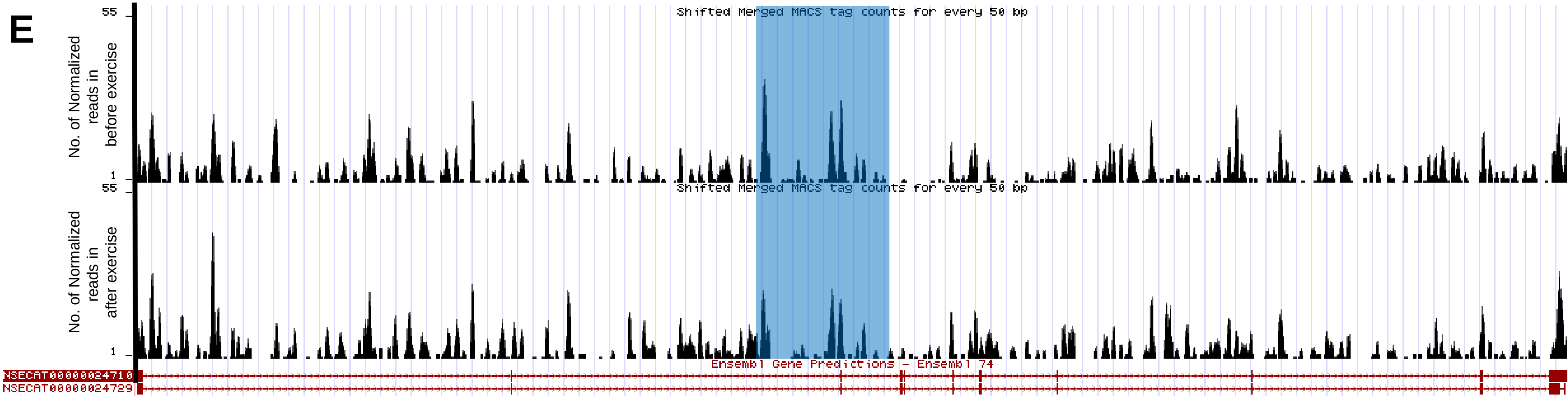
(C) The *GRID1* (Glutamate receptor delta-1) gene is located in chr1:84,021,400-84,686,324. The intron region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. MF: Extracellular-glutamate-gated ion channel activity.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



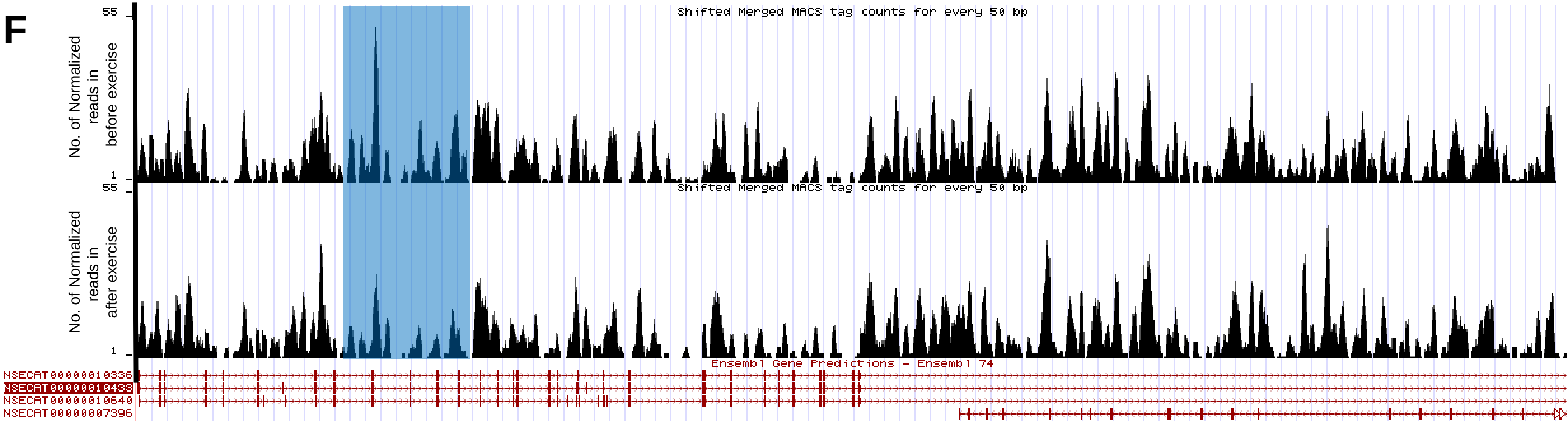
(D) The *GRIK4* (glutamate receptor, ionotropic, kainate 4) gene is located in chr7:28,203,121-28,492,657. The intron region is hypomethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. CC: Receptor complex, CC: Synapse part, CC: Plasma membrane part, MF: Passive transmembrane transporter activity, MF: Substrate specific channel activity, MF: Gated channel activity.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



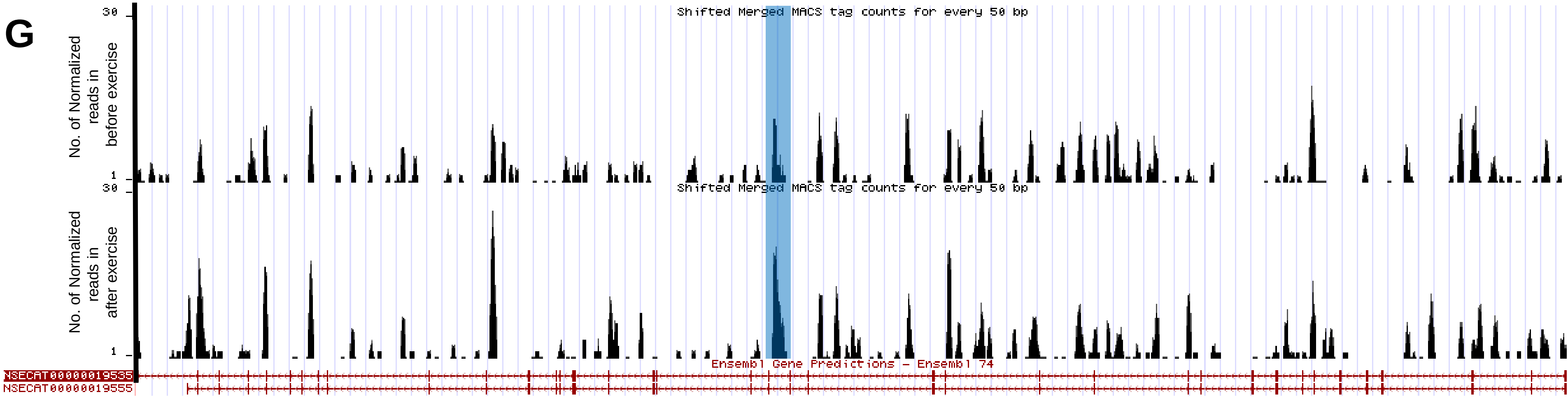
(E) The *GRIN2A* (Glutamate [NMDA] receptor subunit epsilon-1) gene is located in chr13:34,224,912-34,372,429. The intron region is hypomethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. CC: Cell projection, CC: Cytoskeleton, MF: Cation channel activity.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



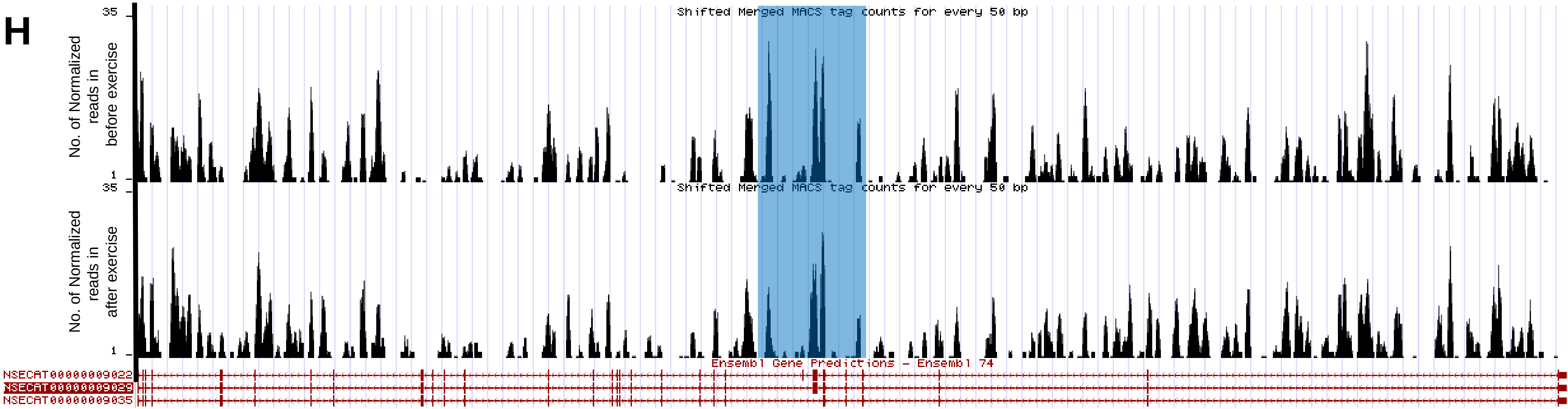
(F) The *ABCC6* (ATP-binding cassette, sub-family C member 9) gene is located in chr13:29,615,992-29,720,039. The intron region is hypomethylated in two horses after exercise. GO and KEGG terms include this gene as follows. BP: Transmembrane transport, KEGG: ABC transporters.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



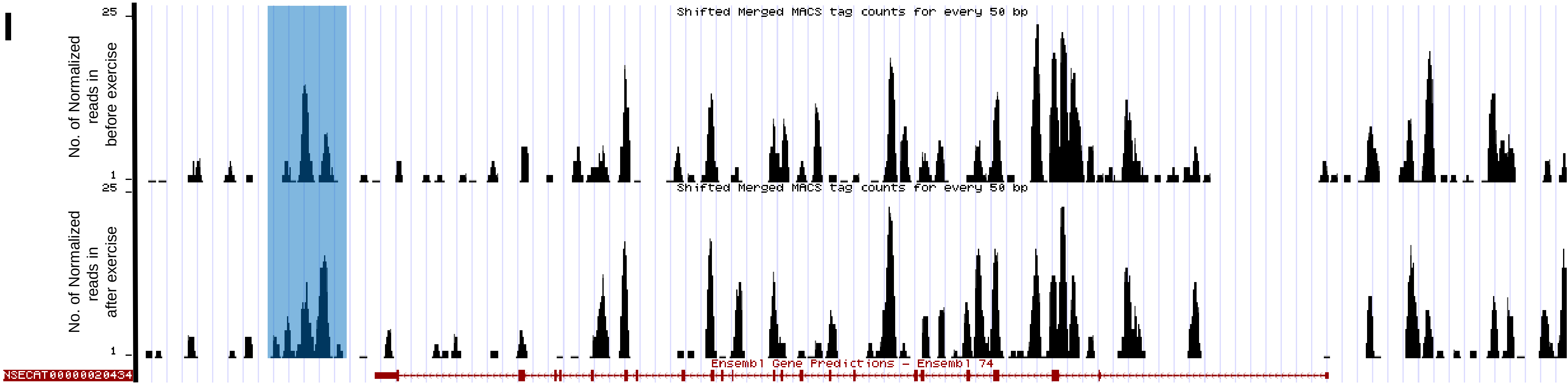
(G) The *ABCC9* (ATP-binding cassette, sub-family C member 9) gene is located in chr6:47,951,001-48,065,838. The intron region is hypermethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Metal ion transport.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

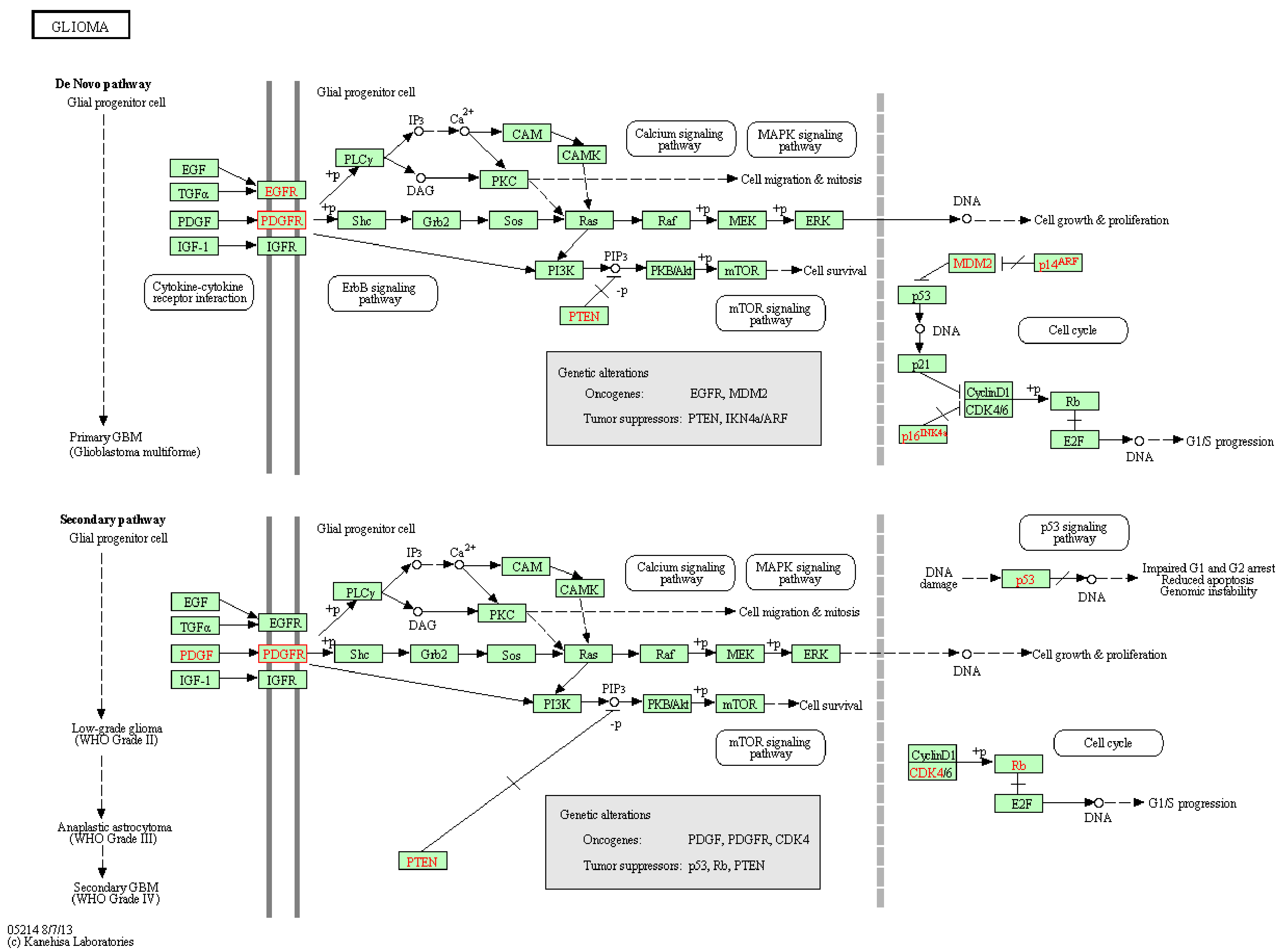


(H) The *UBE4B* (Ubiquitin conjugation factor E4 B) gene is located in chr2:41,135,015-41,256,326. The intron region is hypomethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Proteolysis involved in cellular protein catabolic process, BP: Protein modification by small protein conjugation.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



(I) The *PDGFRA* (Platelet-derived growth factor receptor A) gene is located in chr3:78,140,545-78,182,493. The downstream regions is hypermethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Protein amino acid phosphorylation, MF: Vascular endothelial growth factor receptor activity, KEGG: Glioma.


GLIOMA
De Novo pathway
Glial progenitor cell
Primary GBM
(Glioblastoma multiforme)
EGF
TGFα
PDGF
IGF-1
EGFR
PDGFR
IGFR
Cytokine-cytokine receptor interaction
Glial progenitor cell
PLCγ
IP3
Ca2+
CAM
CAMK
DAG
PKC
+p
Shc
Grb2
Sos
Ras
Raf
MEK
ERK
Calcium signaling pathway
MAPK signaling pathway
Cell migration & mitosis
DNA
Cell growth & proliferation
ErbB signaling pathway
PI3K
PIP3
-p
PKB/Akt
mTOR
Cell survival
PTEN
mTOR signaling pathway
Genetic alterations
Oncogenes: EGFR, MDM2
Tumor suppressors: PTEN, IKN4a/ARF
MDM2
p14ARF
p53
DNA
p21
Cell cycle
CyclinD1
CDK4/6
p16INK4a
Rb
E2F
DNA
G1/S progression
Secondary pathway
Glial progenitor cell
Low-grade glioma
(WHO Grade II)
Anaplastic astrocytoma
(WHO Grade III)
Secondary GBM
(WHO Grade IV)
EGF
TGFα
PDGF
IGF-1
EGFR
PDGFR
IGFR
Glial progenitor cell
PLCγ
IP3
Ca2+
CAM
CAMK
DAG
PKC
Shc
Grb2
Sos
Ras
Raf
MEK
ERK
Calcium signaling pathway
MAPK signaling pathway
Cell migration & mitosis
DNA
Cell growth & proliferation
PI3K
PIP3
PKB/Akt
mTOR
Cell survival
PTEN
mTOR signaling pathway
p53 signaling pathway
DNA damage
p53
DNA
Impaired G1 and G2 arrest
Reduced apoptosis
Genomic instability
Cell cycle
CyclinD1
CDK4/6
Rb
E2F
DNA
G1/S progression
Genetic alterations
Oncogenes: PDGF, PDGFR, CDK4
Tumor suppressors: p53, Rb, PTEN
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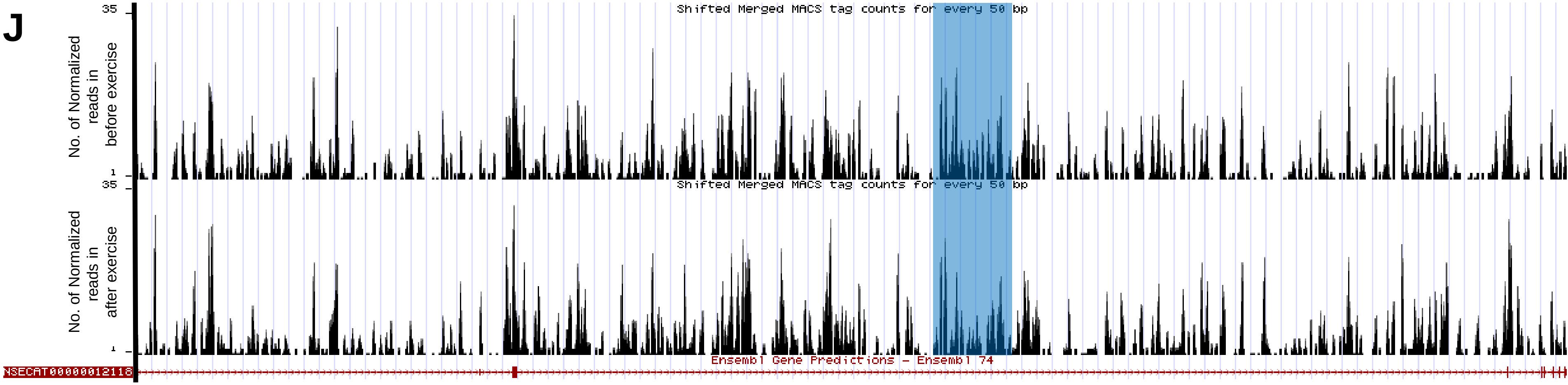
(c) Kanehisa Laboratories

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

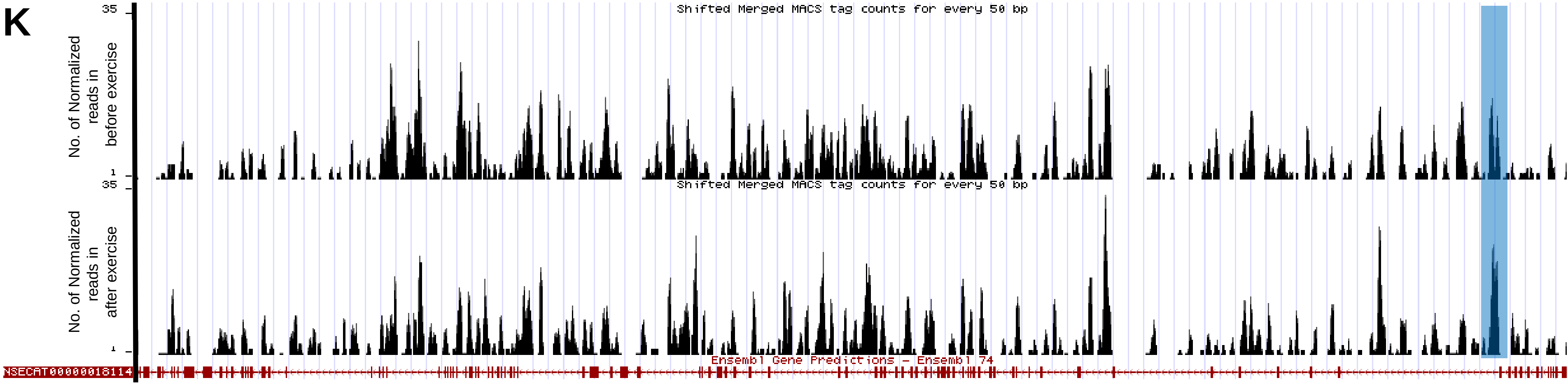
J



(J) The *KCND3* (Potassium voltage-gated channel subfamily D member 3) gene is located in chr5:56,363,110-56,634,447. The intron region is hypomethylated JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Transmembrane transport, CC: Cell projection, MF: Cation channel activity.

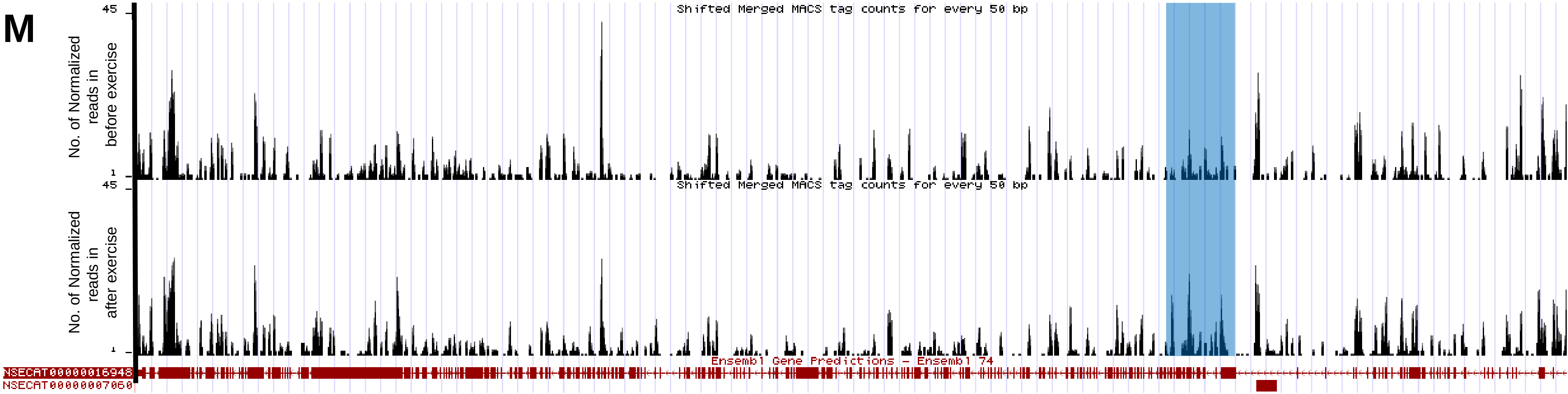
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

K



(K) The *OBSCN* (Obscurin) gene is located in chr14:93,349,768-93,500,127. The intron region is hypermethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Protein amino acid phosphorylation, BP: Regulation of small GTPase mediated signal transduction, CC: Contractile fiber, CC: M band, MF: Small GTPase regulator activity.

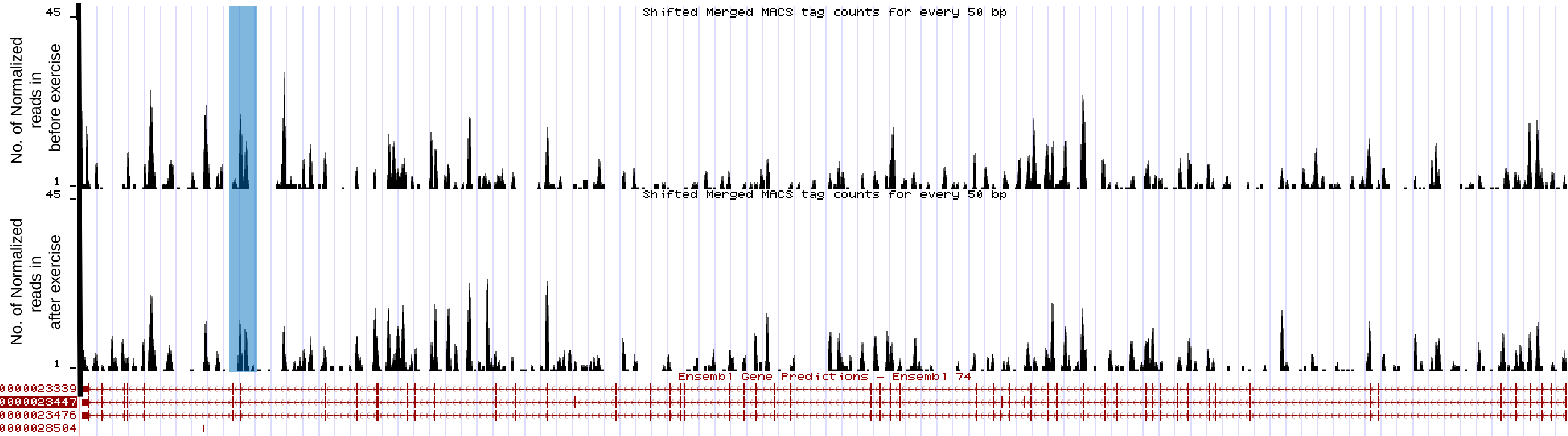
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



(M) The *TTN* (Titin, also known as Connectin) gene is located in chr18:56,684,352-56,950,669. The exon region is hypermethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Protein amino acid phosphorylation, BP: Regulation of small GTPase mediated signal transduction, CC: Contractile fiber, CC: M band, CC: Cytoskeleton, MF: Small GTPase regulator activity, MF: Calmodulin binding.

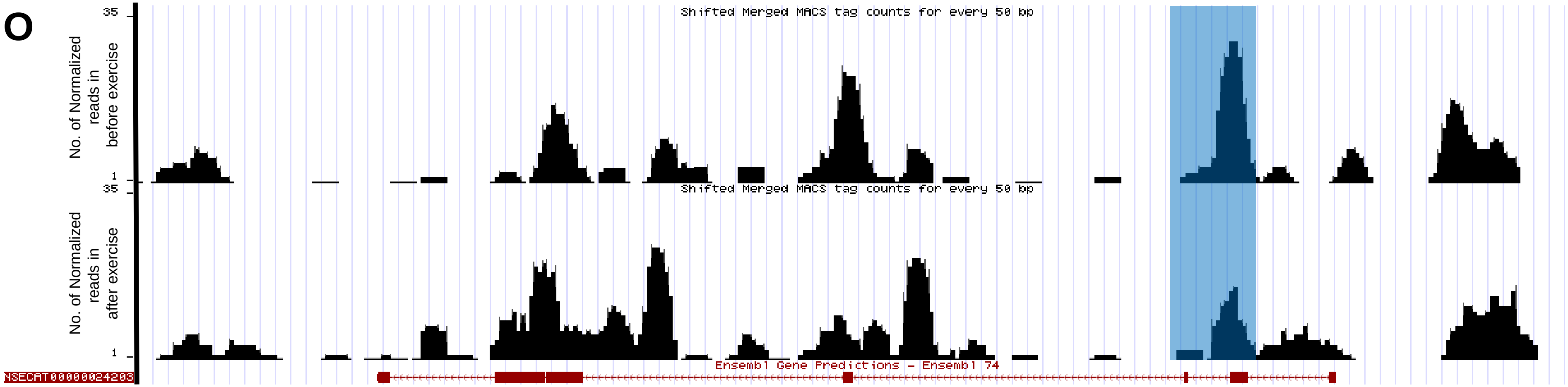
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

N



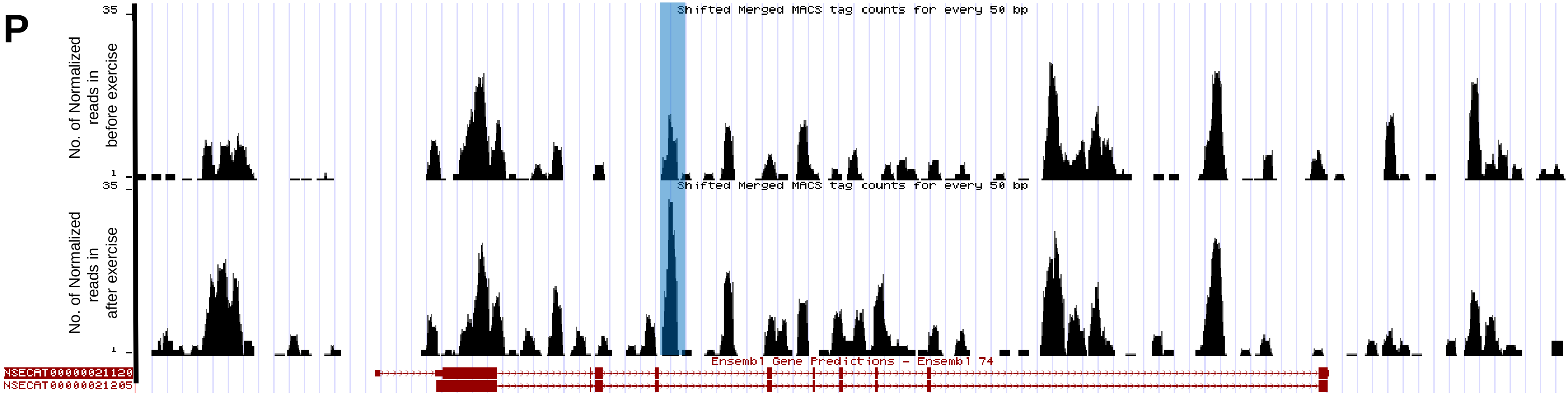
(N) The *TLN2* (Talin 2) gene is located in chr1:129,230,635-129,422,024. The intron region is hypomethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. CC: Cell projection, CC: Cytosleleton, MF: Cytoskeletal protein binding.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



(O) The *CHRNA2* (Neuronal acetylcholine receptor subunit alpha-2) gene is located in chr2:56,053,752-56,064,776. The intron region is hypomethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. CC: Receptor complex, CC: Synapse part, CC: Plasma membrane part, MF: Passive transmembrane transporter activity, MF: Substrate specific channel activity, MF: Gated channel activity.

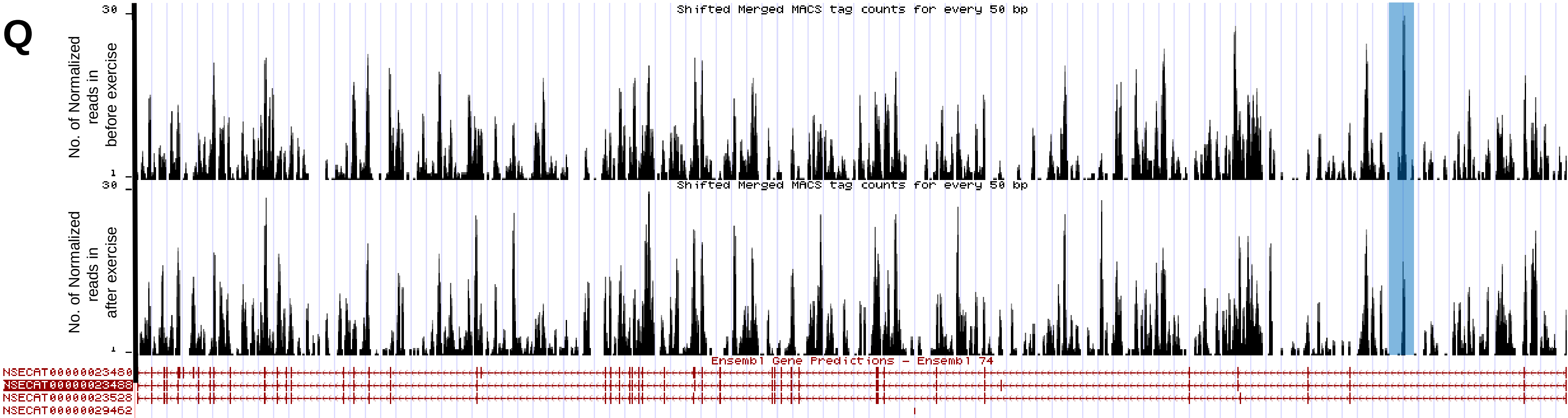
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



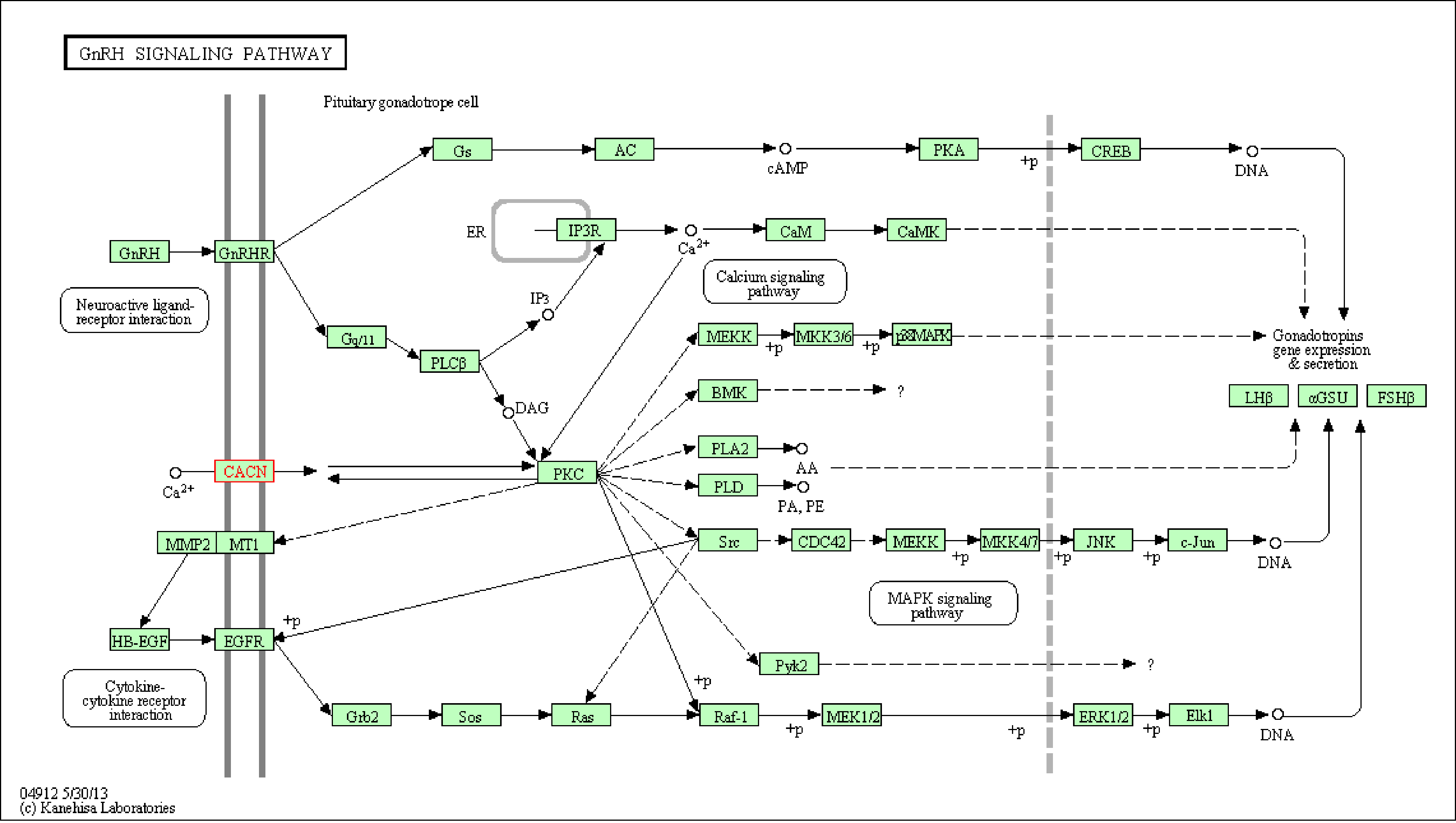
(P) The *PIK3CG* (phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma) gene is located in chr4:6,928,944-6,959,751. The intron region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. CC: Cytosol, MF: ATP binding, MF: Ribonucleotide binding.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

Q



(Q) The *CACNA1C* (Calcium channel, voltage-dependent, L type, alpha 1C subunit) gene is located in chr6:28,057,667-28,285,464. The intron region is hypomethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Transmembrane transport, CC: Synapse part, CC: Plasma membrane part, MF: Passive transmembrane transporter activity, MF: Substrate specific channel activity, MF: Gated channel activity, KEGG: GnRH signaling pathway.



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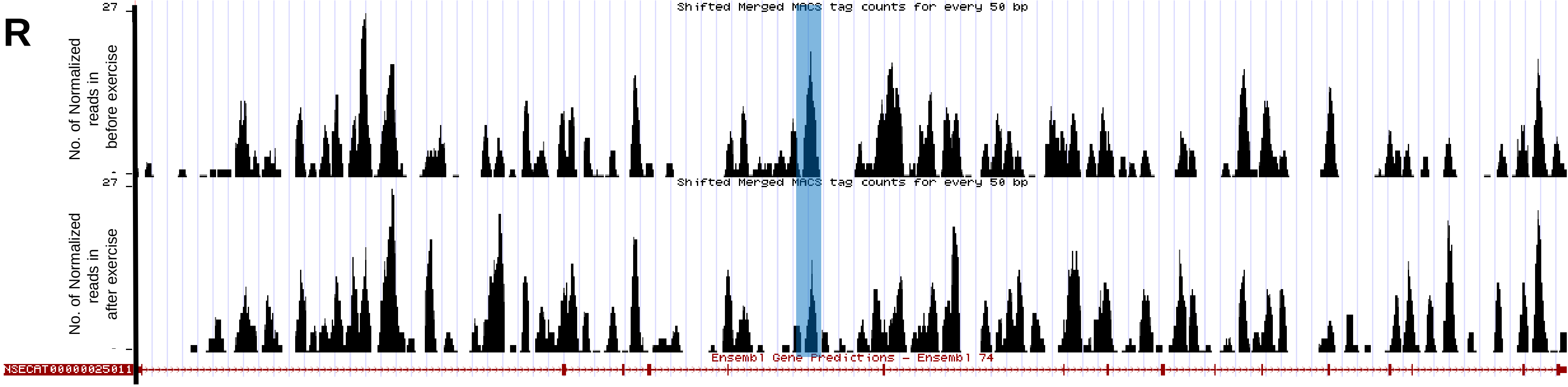
(c) Kanehisa Laboratories

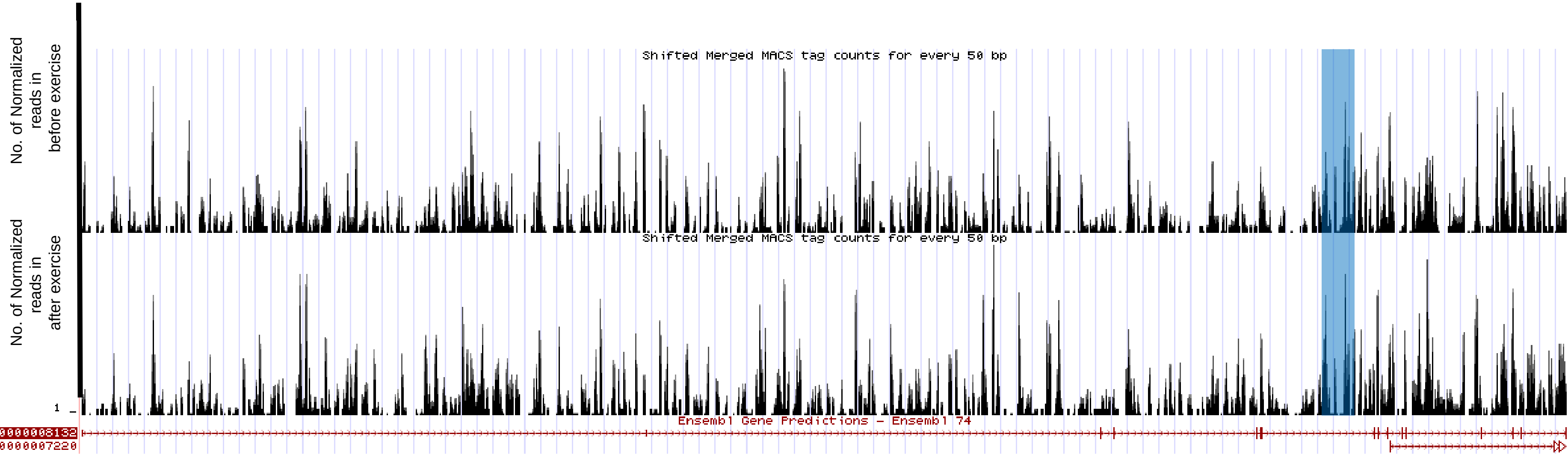
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



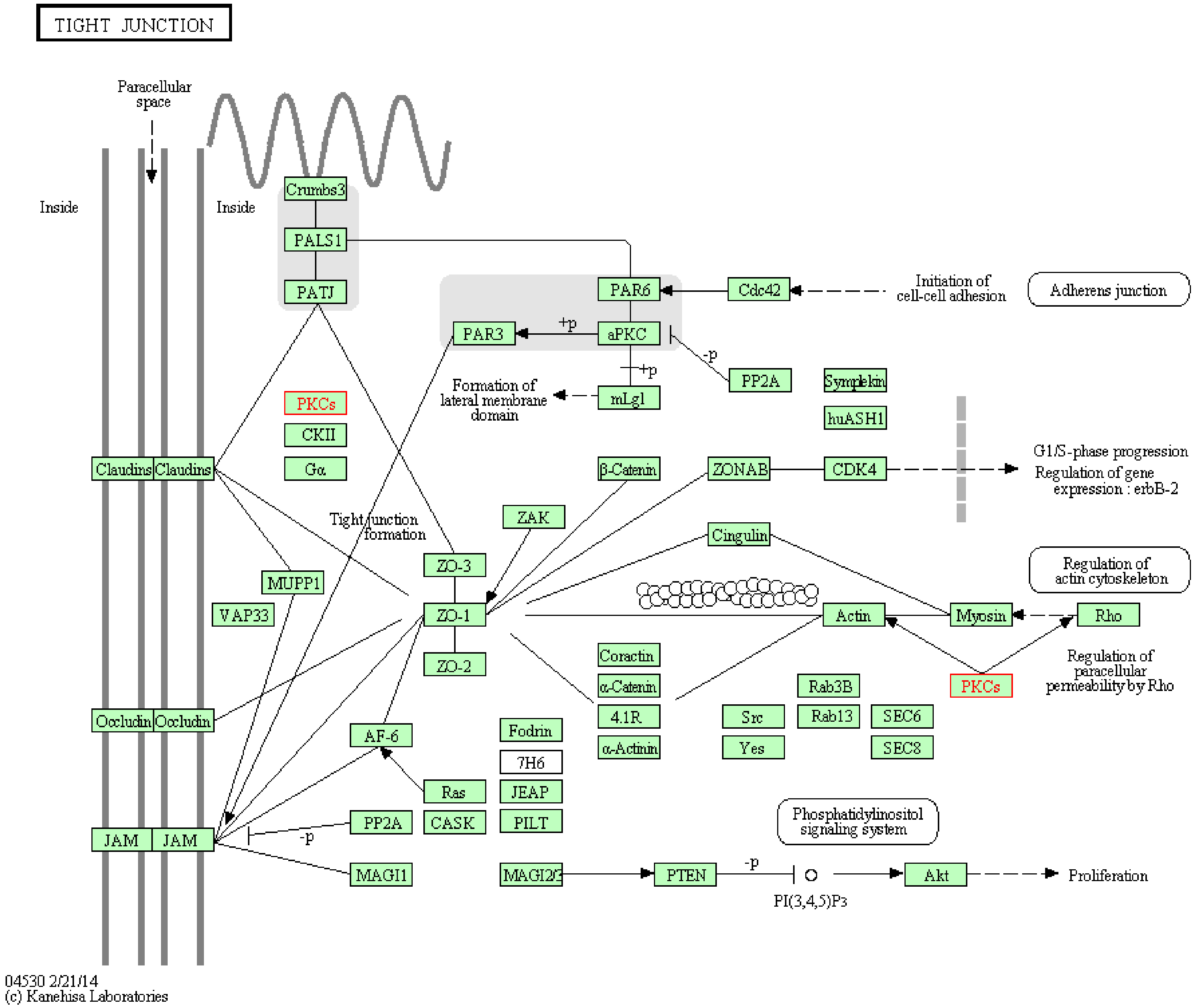
(R) The *SVOP* (SV2-Related Protein) gene is located in chr8:12,056,855-12,120,245. The intron region is hypomethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Transmembrane transport, CC: Synapse part, CC: Plasma membrane part.

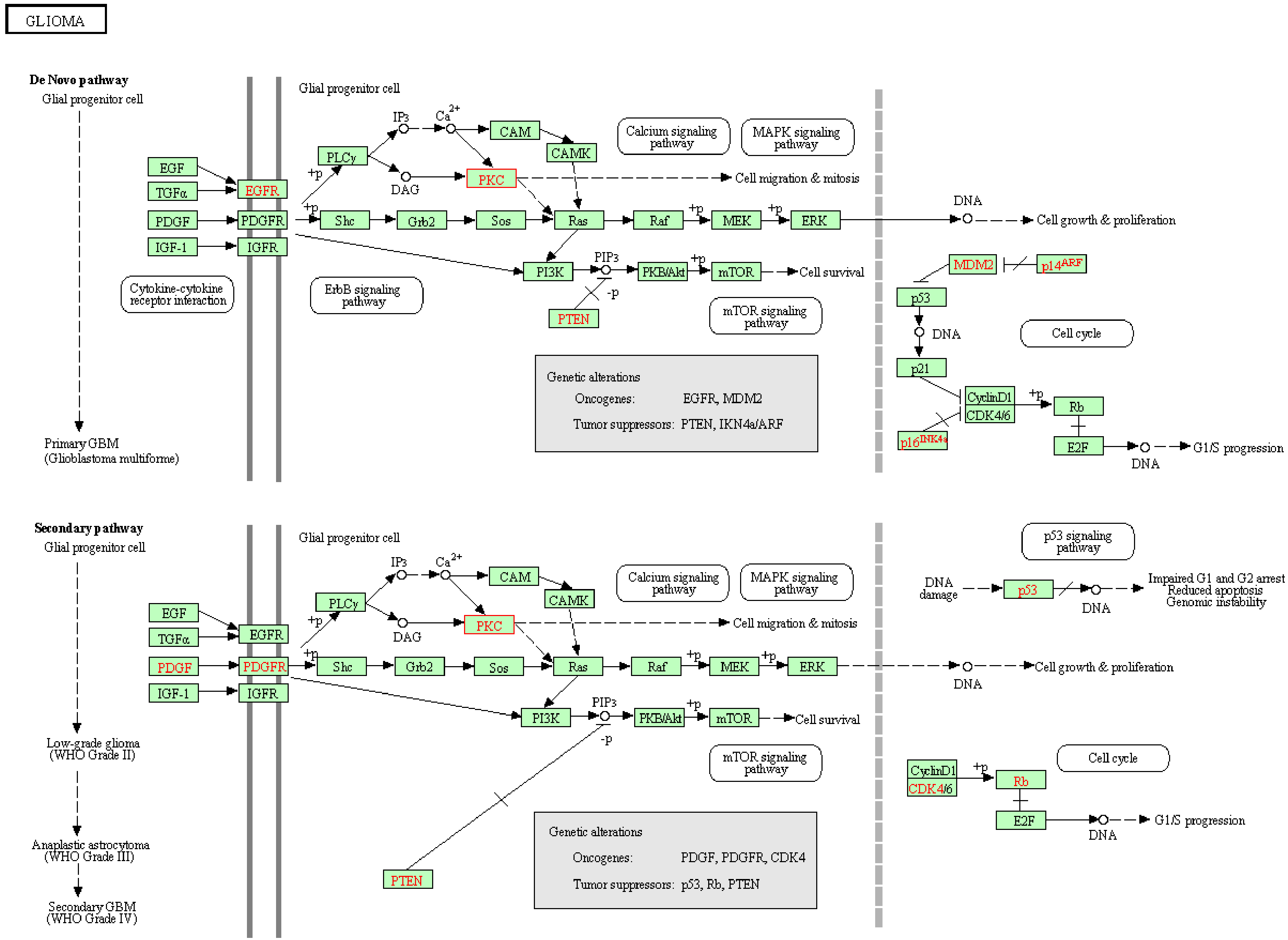
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

S



(S) The *PRKCA* (Protein kinase C alpha) gene is located in chr11:13,417,359-13,812,648. The intron region is hypermethylated in JIGUSANG SERYEOK after exercise. GO and KEGG terms include this gene as follows. BP: Protein amino acid phosphorylation, KEGG: Tight junction, KEGG: Glioma.


TIGHT JUNCTION
Paracellular space
Inside
Inside
Crumbs3
PALS1
PATJ
PAR6
Cdc42
Initiation of cell-cell adhesion
Adherens junction
PAR3
+p
aPKC
-p
PP2A
Symplekin
+p
Formation of lateral membrane domain
mLgl
huASH1
PKCs
CKII
Gα
Claudins
Claudins
β-Catenin
ZONAB
CDK4
G1/S-phase progression
Regulation of gene expression : erbB-2
Tight junction formation
ZAK
Cingulin
Regulation of actin cytoskeleton
ZO-3
MUPP1
VAP33
ZO-1
Actin
Myosin
Rho
ZO-2
Coractin
α-Catenin
Rab3B
PKCs
Regulation of paracellular permeability by Rho
Occludin
Occludin
4.1R
Src
Rab13
SEC6
AF-6
Fodrin
α-Actinin
Yes
SEC8
7H6
Ras
JEAP
PP2A
CASK
PILT
-p
Phosphatidylinositol signaling system
JAM
JAM
MAGI1
MAGI2/3
PTEN
-p
Akt
Proliferation
PI(3,4,5)P3
04530 2/21/14
(c) Kanehisa Laboratories


GLIOMA
De Novo pathway
Glial progenitor cell
Primary GBM
(Glioblastoma multiforme)
EGF
TGFα
PDGF
IGF-1
EGFR
PDGFR
IGFR
Cytokine-cytokine receptor interaction
Glial progenitor cell
PLCγ
+p
IP3
Ca2+
DAG
CAM
CAMK
PKC
Calcium signaling pathway
MAPK signaling pathway
Cell migration & mitosis
Shc
Grb2
Sos
Ras
Raf
MEK
ERK
DNA
Cell growth & proliferation
PI3K
PIP3
-p
PTEN
PKB/Akt
mTOR
Cell survival
ErbB signaling pathway
mTOR signaling pathway
MDM2
p14ARF
p53
DNA
p21
Cell cycle
CyclinD1
CDK4/6
p16INK4a
Rb
E2F
DNA
G1/S progression
Genetic alterations
Oncogenes: EGFR, MDM2
Tumor suppressors: PTEN, IKN4a/ARF
Secondary pathway
Glial progenitor cell
Low-grade glioma
(WHO Grade II)
Anaplastic astrocytoma
(WHO Grade III)
Secondary GBM
(WHO Grade IV)
EGF
TGFα
PDGF
IGF-1
EGFR
PDGFR
IGFR
Glial progenitor cell
PLCγ
IP3
Ca2+
DAG
CAM
CAMK
PKC
Calcium signaling pathway
MAPK signaling pathway
Cell migration & mitosis
Shc
Grb2
Sos
Ras
Raf
MEK
ERK
DNA
Cell growth & proliferation
PI3K
PIP3
PKB/Akt
mTOR
Cell survival
mTOR signaling pathway
PTEN
p53 signaling pathway
DNA damage
p53
DNA
Impaired G1 and G2 arrest
Reduced apoptosis
Genomic instability
Cell cycle
CyclinD1
CDK4/6
Rb
E2F
DNA
G1/S progression
Genetic alterations
Oncogenes: PDGF, PDGFR, CDK4
Tumor suppressors: p53, Rb, PTEN

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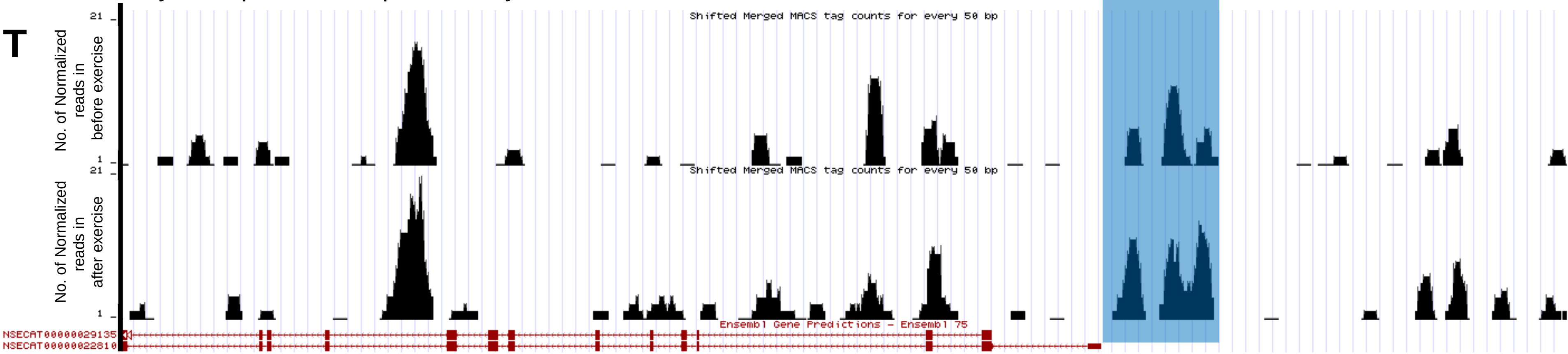
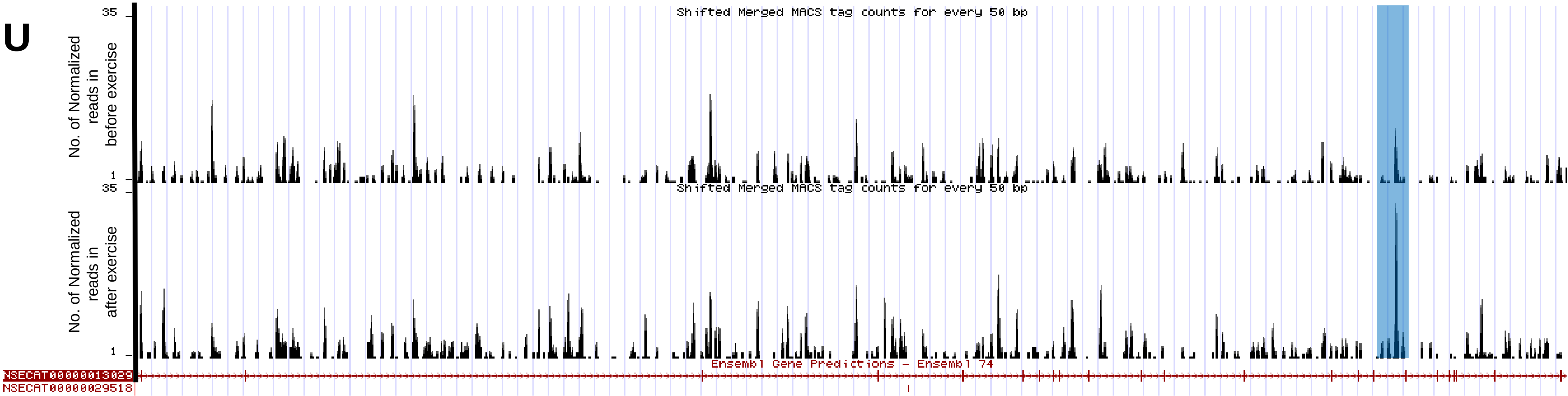
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



(T) The *ANAPC1* (Anaphase-promoting complex subunit 1) gene is located in chr15:14,841,594-14,951,441. The upstream region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Cell cycle, BP: Cell adhesion, CC: Cytosol.

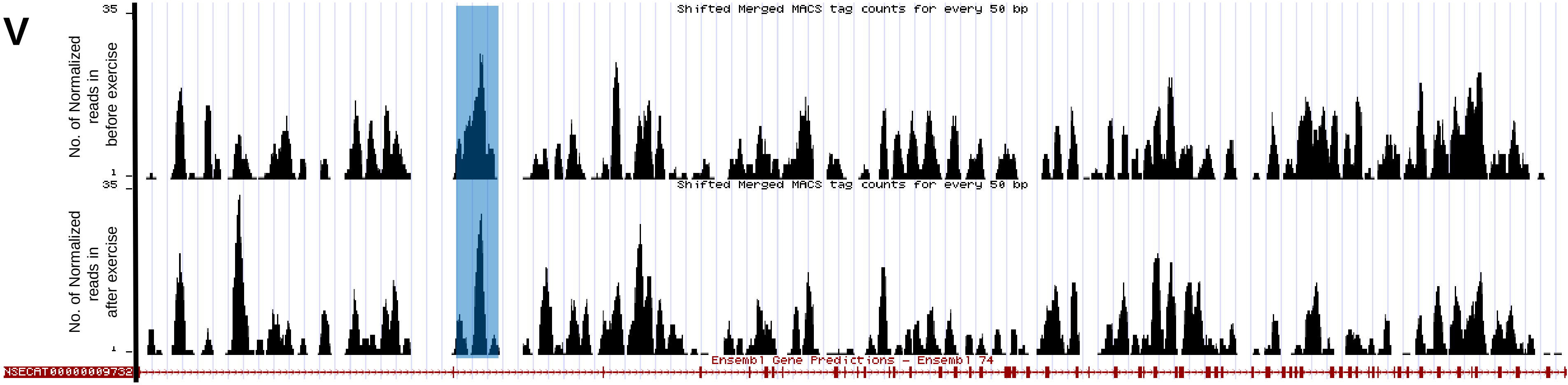
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



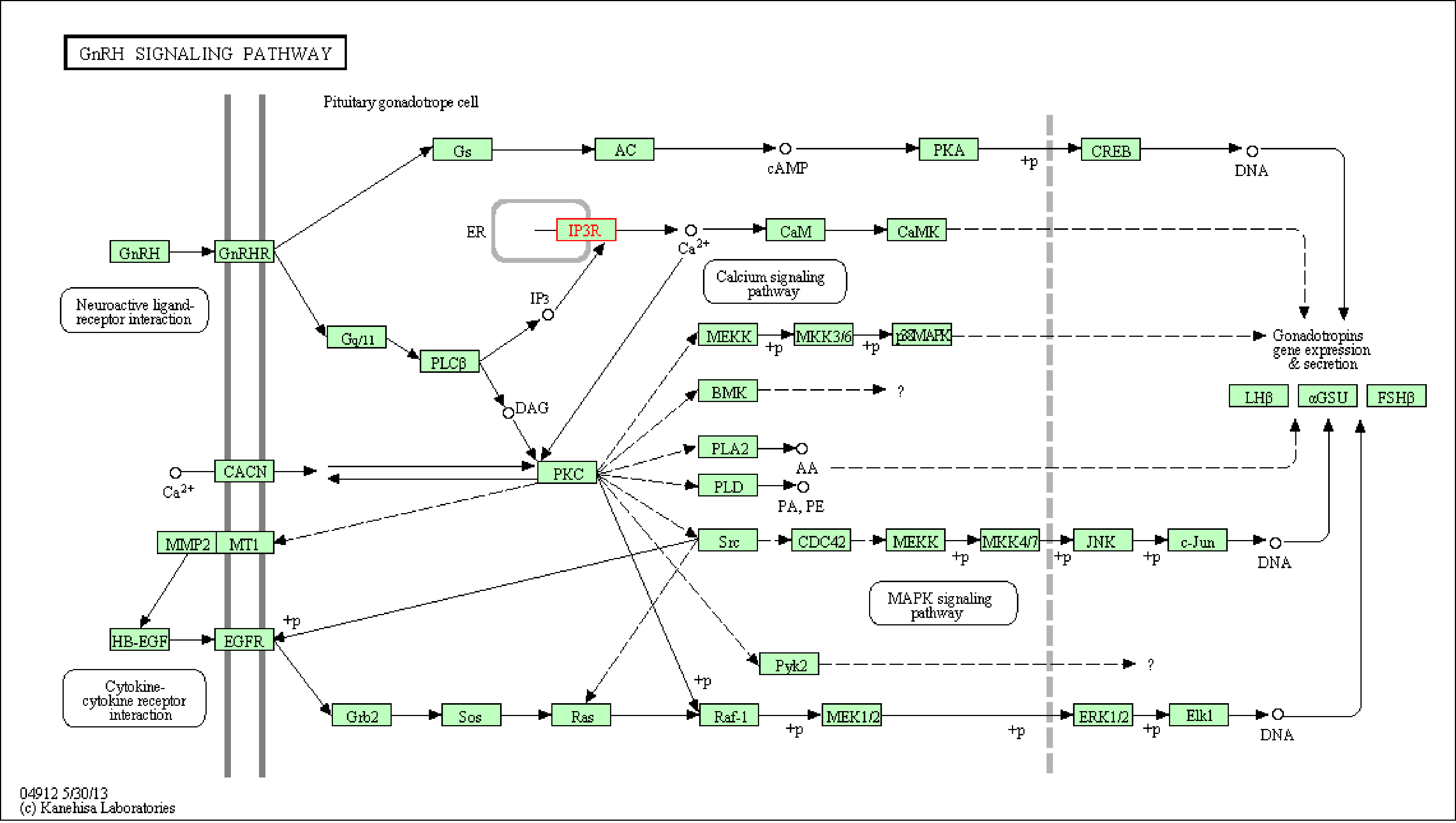
(U) The *DLG1* (Disks large homolog 1) gene is located in chr19:32,456,460-32,709,089. The intron region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Cell adhesion, CC: Cytosol, CC: Endomembrane system.

Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

V



(V) The *ITPR3* (Inositol 1,4,5-trisphosphate receptor, type 3) gene is located in chr20:33,949,360-34,014,422. The intron region is hypomethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Transmembrane transport, CC: Plasma membrane part, MF: Passive transmembrane transporter activity, MF: Substrate specific channel activity, MF: Gated channel activity, KEGG: GnRH signaling pathway.


GnRH SIGNALING PATHWAY
Pituitary gonadotrope cell
Gs
AC
cAMP
PKA
+p
CREB
DNA
ER
IP3R
Ca^{2+}
CaM
CaMK
GnRH
GnRHR
Calcium signaling pathway
Neuroactive ligand-receptor interaction
IP_3
Gq/11
PLCβ
MEKK
+p
MKK3/6
+p
p38MAPK
Gonadotropins gene expression & secretion
BMK
?
DAG
LHβ
αGSU
FSHβ
PLA2
AA
CACN
PKC
Ca^{2+}
PLD
PA, PE
MMP2
MT1
Src
CDC42
MEKK
+p
MKK4/7
+p
JNK
+p
c-Jun
DNA
MAPK signaling pathway
+p
HB-EGF
EGFR
Pyk2
?
Cytokine-cytokine receptor interaction
+p
Grb2
Sos
Ras
Raf-1
+p
MEK1/2
+p
ERK1/2
+p
Elk1
DNA
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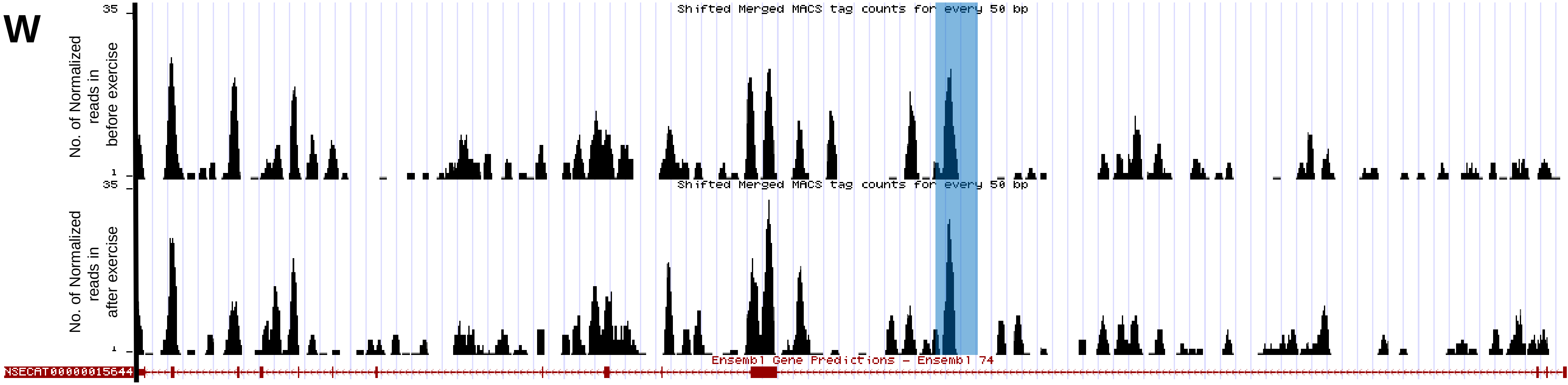
(c) Kanehisa Laboratories

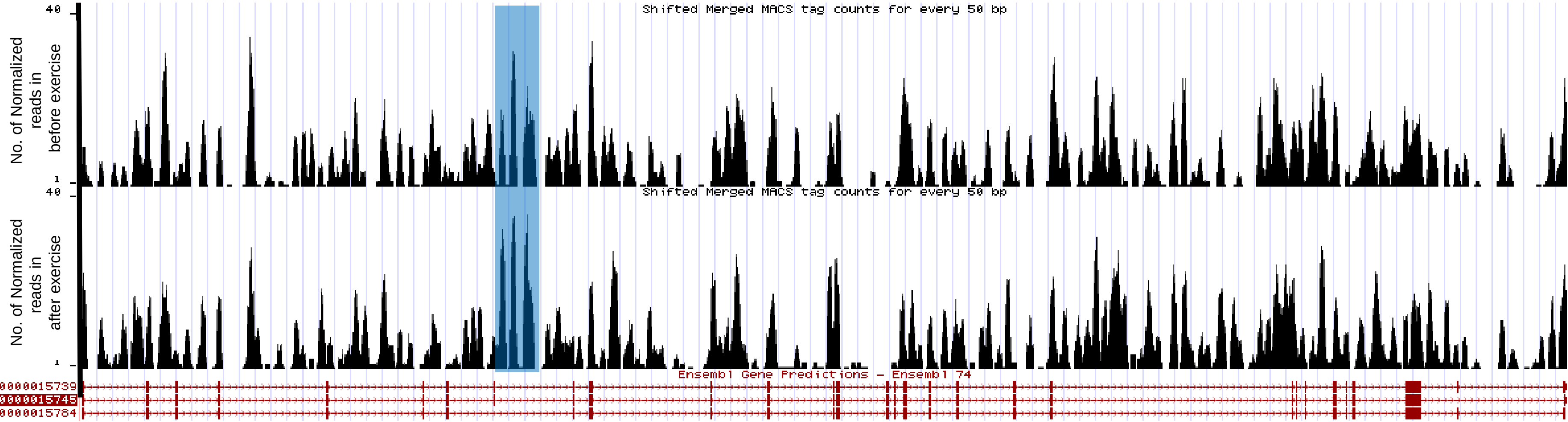
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.



(W) The *TACC1* (Transforming acidic coiled-coil-containing protein 1) gene is located in chr27:6,993,558-7,052,436. The intron region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Cell cycle, BP: Cell division, CC: Microtubule cytoskeleton.

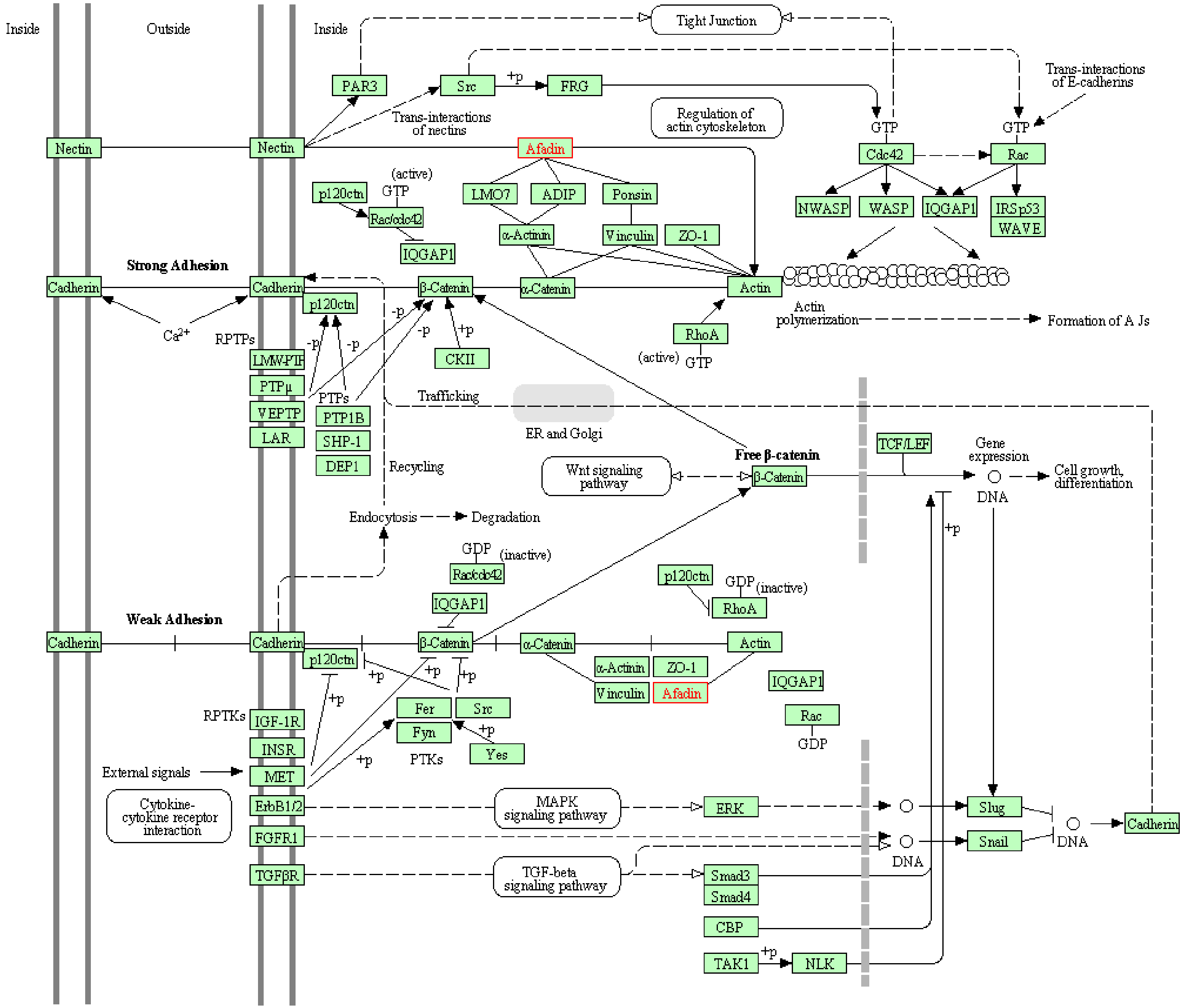
Supplementary Fig. 8. Visualization of methylation peaks in exercise-related genes. A total of 23 genes in two horses were selected and the methylation peaks were provided by the UCSC Genome Browser custom tracks.

X



(X) The *MLLT4* gene is located in chr31:8,143,543-8,237,290. The intron region is hypermethylated in GEUMBIT SESANG after exercise. GO and KEGG terms include this gene as follows. BP: Cell adhesion, CC: Cytosol, KEGG: Adherens junction, KEGG: Tight junction.

ADHERENS JUNCTION



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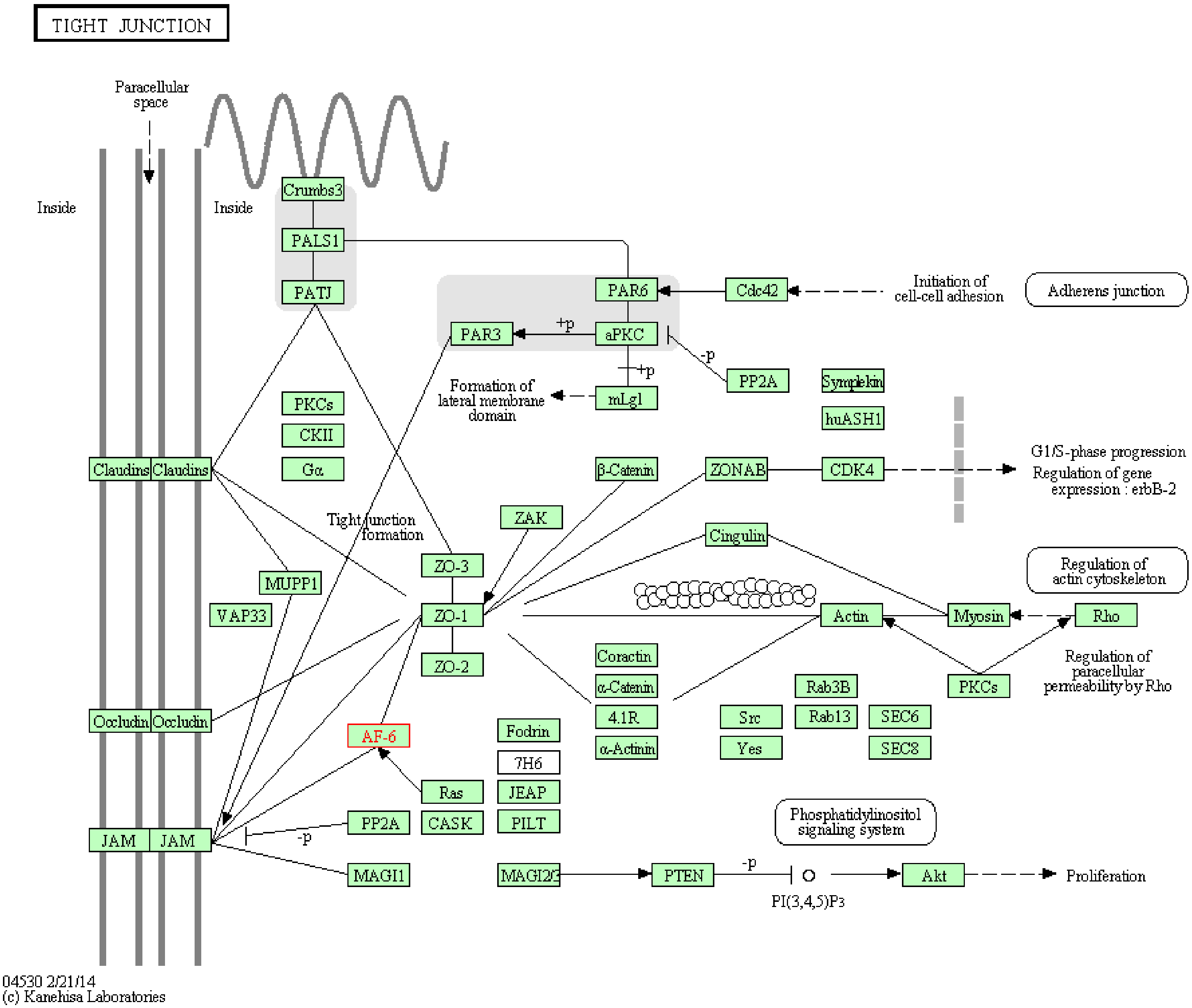
(c) Kanehisa Laboratories


TIGHT JUNCTION
Paracellular space
Inside
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Crumbs3
PALS1
PATJ
PAR6
Cdc42
Initiation of cell-cell adhesion
Adherens junction
PAR3
+p
aPKC
-p
PP2A
Symplekin
+p
Formation of lateral membrane domain
mLgl
huASH1
PKCs
CKII
Gα
Claudins
Claudins
β-Catenin
ZONAB
CDK4
G1/S-phase progression
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Regulation of actin cytoskeleton
MUPP1
VAP33
ZO-1
Actin
Myosin
Rho
ZO-2
Coractin
Regulation of paracellular permeability by Rho
α-Catenin
Rab3B
PKCs
Occludin
Occludin
4.1R
Src
Rab13
SEC6
AF-6
Fodrin
α-Actinin
Yes
SEC8
7H6
Ras
JEAP
PP2A
CASK
PILT
Phosphatidylinositol signaling system
JAM
JAM
-p
MAGI1
MAGI2/3
PTEN
-p
Akt
Proliferation
PI(3,4,5)P3
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