

Supplement Figure legends

sFig. 1. A. WikiPathway of the down-regulated genes in the iAs-induced CSCs. B. Down-regulation of genes for the respiratory chain of mitochondria in the iAs-induced CSCs. The minus numbers indicate fold decrease relative to the non-CSCs of these individual genes.

sFig. 2. Screening of Nrf2 knockout (KO) cells from the BEAS-2B cells subjected to CRISPR-Cas9 gene editing using sgRNA1 and sgRNA2 as indicated, respectively. The successful Nrf2 knockout rates are 15% for sgRNA1 and 60% for sgRNA2, respectively.

sFig. 3. Nrf2 element(s) on the glycolytic genes as exemplified for ENO1, GPI and GAPDH.

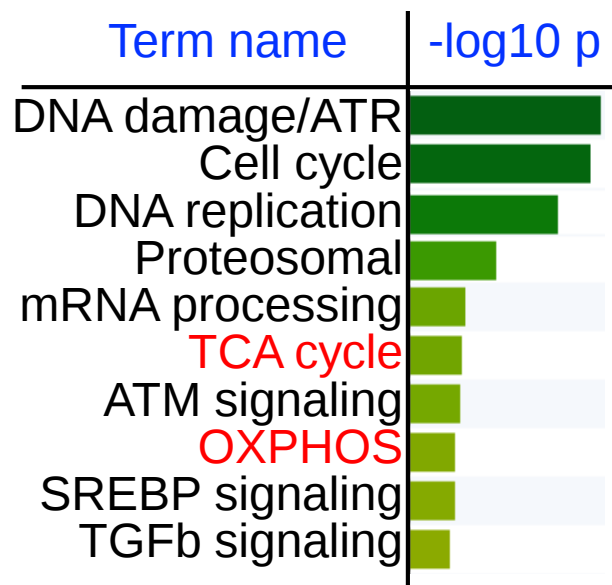
sFig. 4. Identification of a conserved known Nrf2 element at the 32.5 kb upstream of the transcription start site of HIF1 α gene.

sFig. 5. Multiple Nrf2 elements identified at the upstream of the ZEB1 gene.

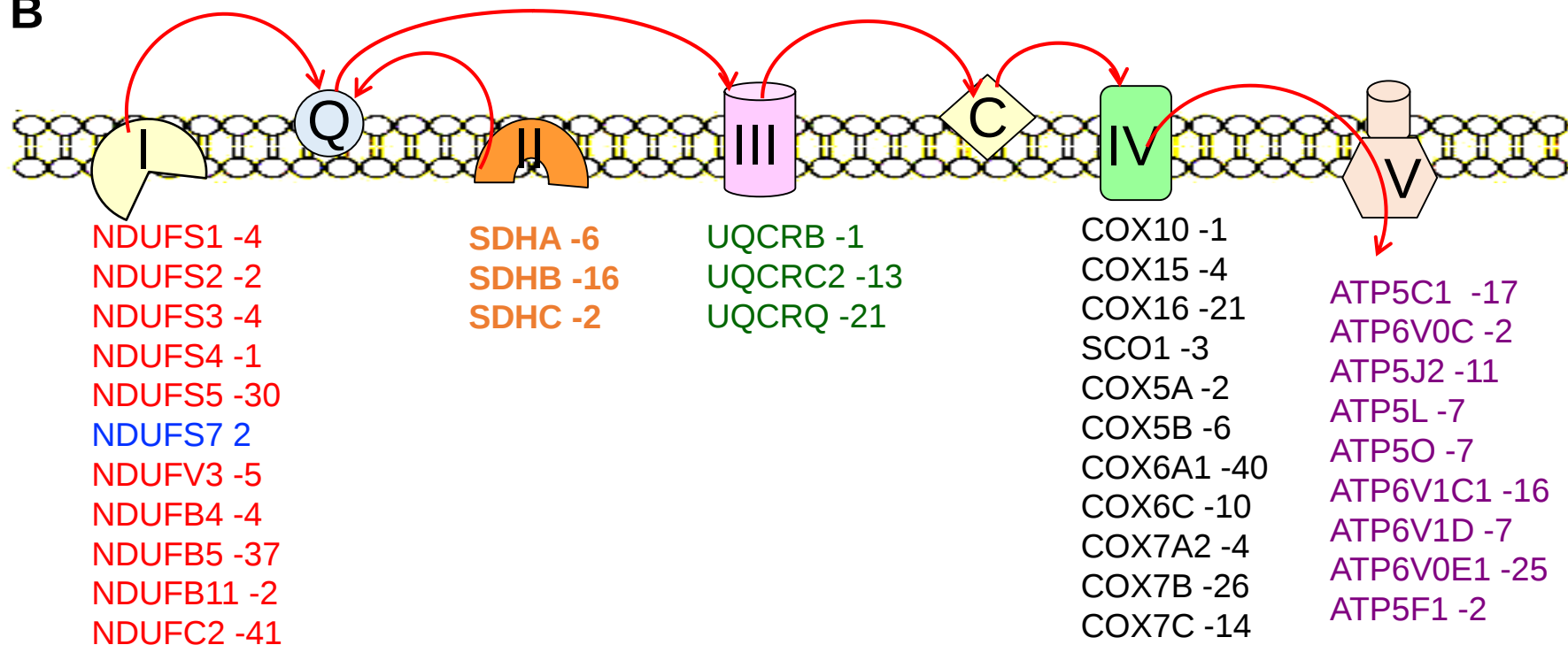
sFig. 6. Known and de novo Nrf2 binding motifs in the gene loci of BACH1, Hes1 and TBC1D7. Red arrows indicate the iAs-induced HIF1 α binding.

sFig. 7. Cooperative regulation of Nrf2 and HIF1 α on NAMPT, CD44 and EGFR. Known and/or de novo Nrf2 motifs were indicated. Red arrows indicate the iAs-induced HIF1 α binding.

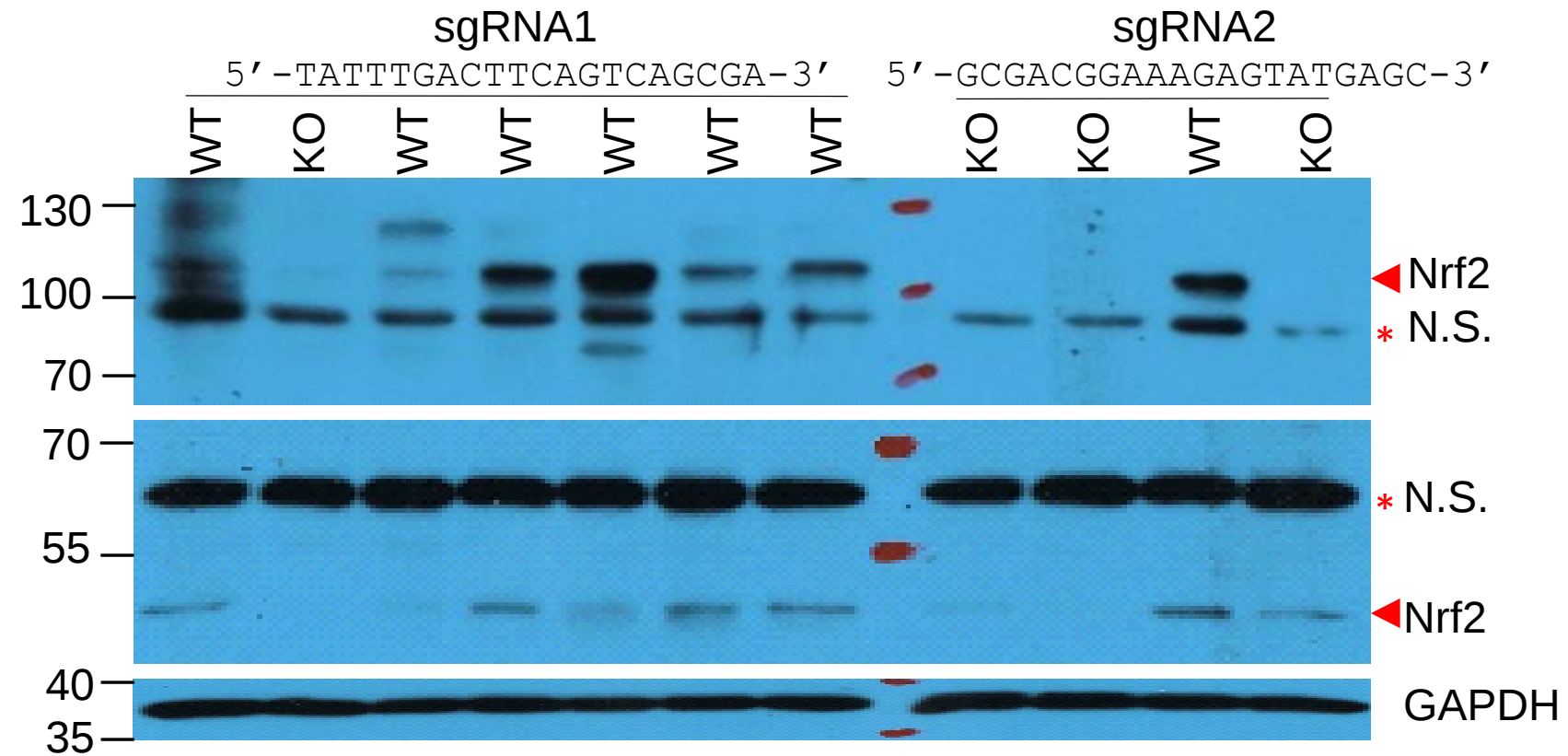
WikiPathway of the
down-regulated genes in
CSCs



B



sFig. 2

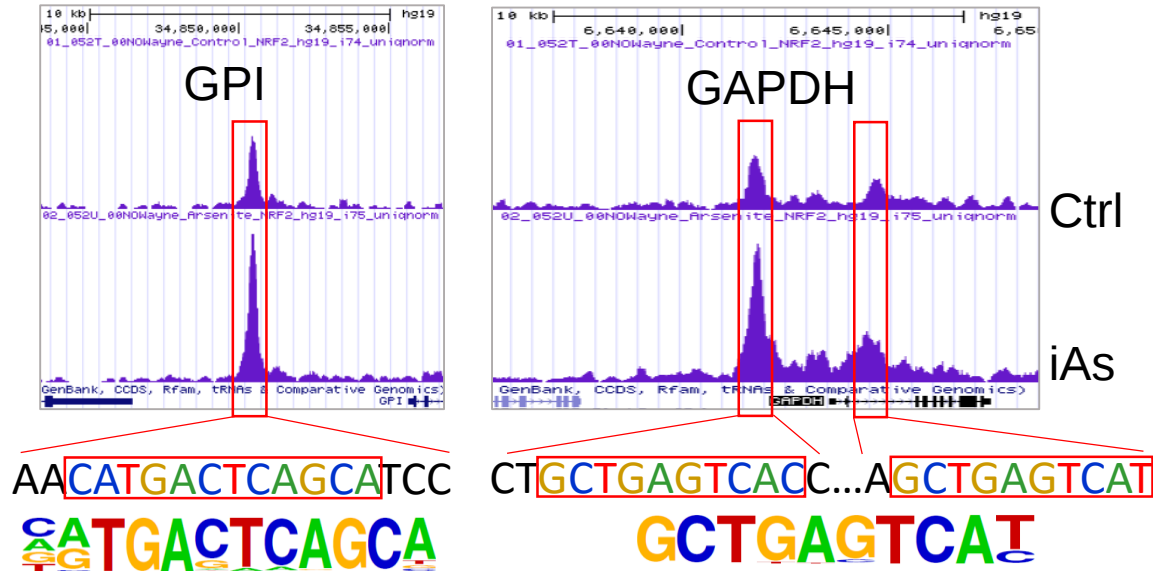
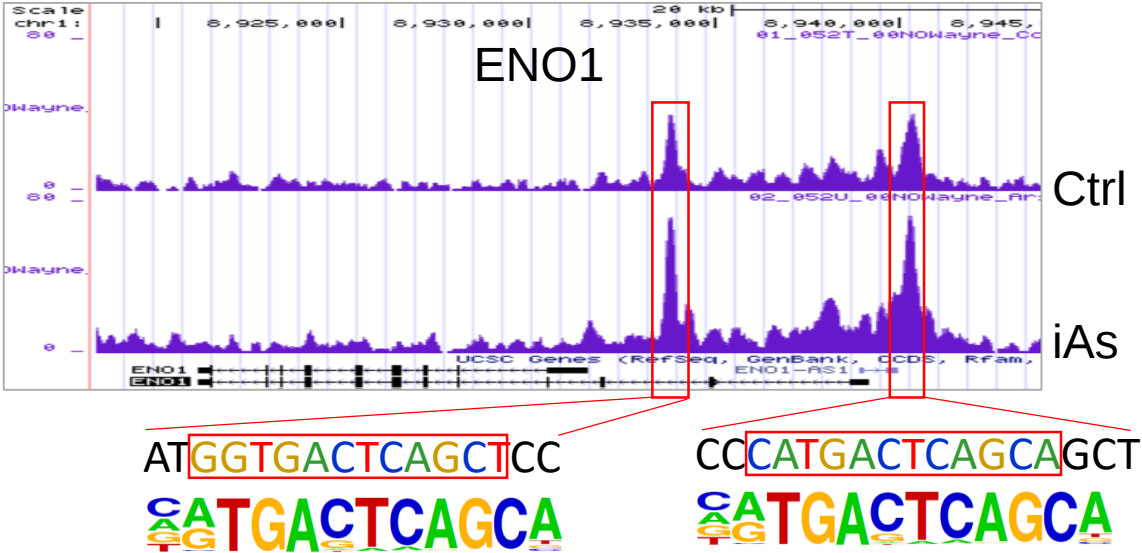


Sources of Nrf2 antibodies for screening:

Upper panel: 12721 Cell Signaling D1Z9C XP Rabbit mAb

Lower panel: sc-365949 A-10 Mouse mAb

sFig.3



ATGCTGAGTCAT

Scale chr14: 50 kb hg19

62,130,000| 62,140,000| 62,150,000| 62,160,000| 62,170,000| 62,180,000| 62,190,000| 62,200,000| 62,210,000| 62,220,000

01_052T_00NOWayne_Control1_NRF2_hg19_i74_uniqnorm

HIF1 α

02_052U_00NOWayne_Arsenite_NRF2_hg19_i75_uniqnorm

03_052R_00NOWayne_Control1_HIF1a_hg19_i72_uniqnorm

04_052S_00NOWayne_Arsenite_HIF1a_hg19_i73_uniqnorm

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

HIF1A

HIF1B

Ctrl,

Nrf2

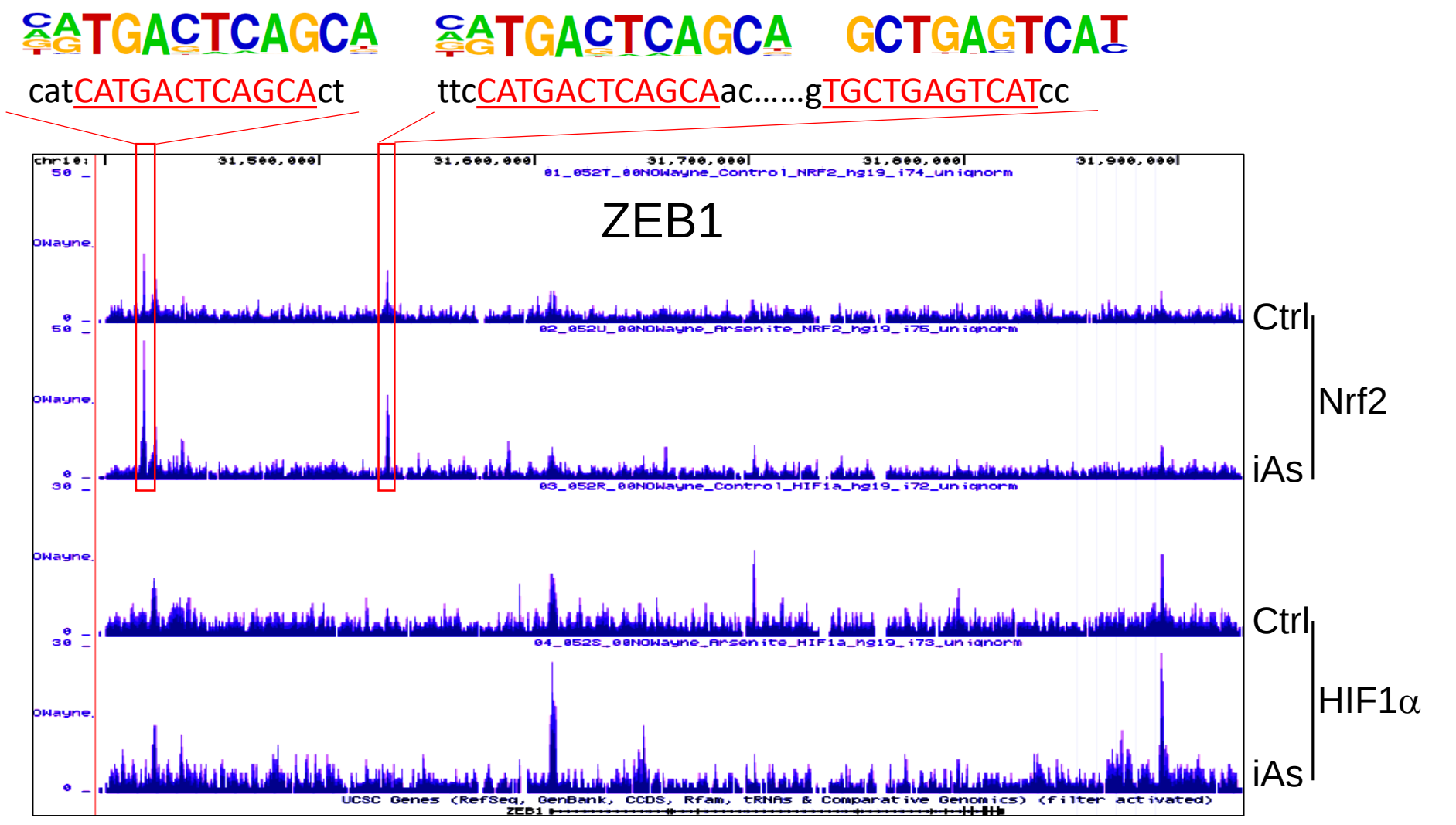
iAs

Ctrl,

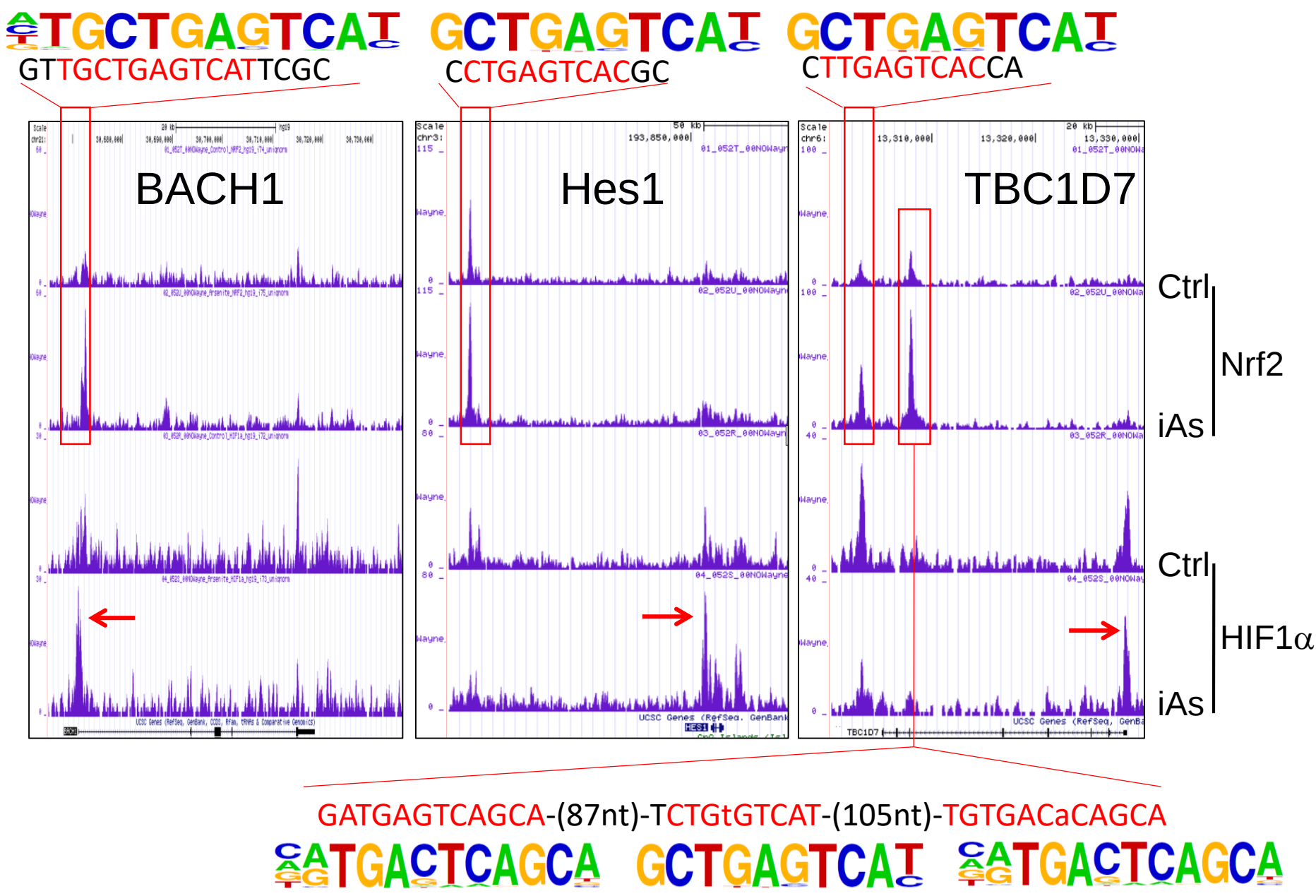
HIF1 α

iAs

sFig. 5



sFig. 6



sFig. 7

