Lysine Catabolism Reprograms Tumour Immunity through Histone Crotonylation

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This Supplementary information file contains:

- Supplementary Figures 1-9 legends

Due to similar molecular weight of some proteins, the samples derive from the same experiment were run on separate gels in Fig. 1d, 2c, 2e and 2h. Loading controls were run on the same blot.

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experiment were run on separate gels in Extended Data Fig. 8a, Extended Data Fig. 9e, 9l and Extended Data Fig. 10e. Loading controls were run on the same blot.

- Supplementary Tables 1-13 legends

Supplementary Table 1 Quantification of intracellular amino acids normalized to both ISTD and cell number using Mass spectrometry.

Supplementary Table 2 Increased amino acids in GSCs compared to both DGCs and NSCs ($p < 0.01$ and fold change > 2).

Supplementary Table 3 Quantification of intracellular amino acids upon SLC7A2 depletion after normalization to ISTD and cell number.

Supplementary Table 4 Differentially expressed genes upon GCDH depletion in GSCs (adjusted $p < 0.05$ and fold change > 2).

Supplementary Table 5 Differentially expressed genes upon ECHS1 loss in DGCs (adjusted $p < 0.05$ and fold change > 2).

Supplementary Table 6 Differentially expressed genes from GSCs cultured in media with low (0.2 mM) or high (2 mM) L-lysine (adjusted $p < 0.05$ and fold change > 2).

Supplementary Table 7 181 genes designated as "Lysine catabolism-repressed genes".

Supplementary Table 8 Identification of GCDH-interacting proteins based on MS-derived Peptide counts.

Supplementary Table 9 Identification of histone H4 crotonylation from GSCs cultured in media with low (0.2 mM) or high (2 mM) L-lysine.

Supplementary Table 10 Identification of enriched transcriptional factors with selective dependency in GSCs compared to DGCs and NSCs based on a computational biology framework "Lisa".

Supplementary Table 11 Differentially expressed retroelements from GSCs cultured in media with low (0.2 mM) or high (2 mM) L-lysine (adjusted $p < 0.05$ and fold change > 1.5).

Supplementary Table 12 Differentially expressed retroelements upon GCDH depletion in GSCs (adjusted $p < 0.05$ and fold change > 1.5).

Supplementary Table 13 List of siRNA, shRNA and qPCR primer.

Supplementary Fig. 1 Raw data for gels, related to Fig. 1 and Fig. 2.

Fig. 1d

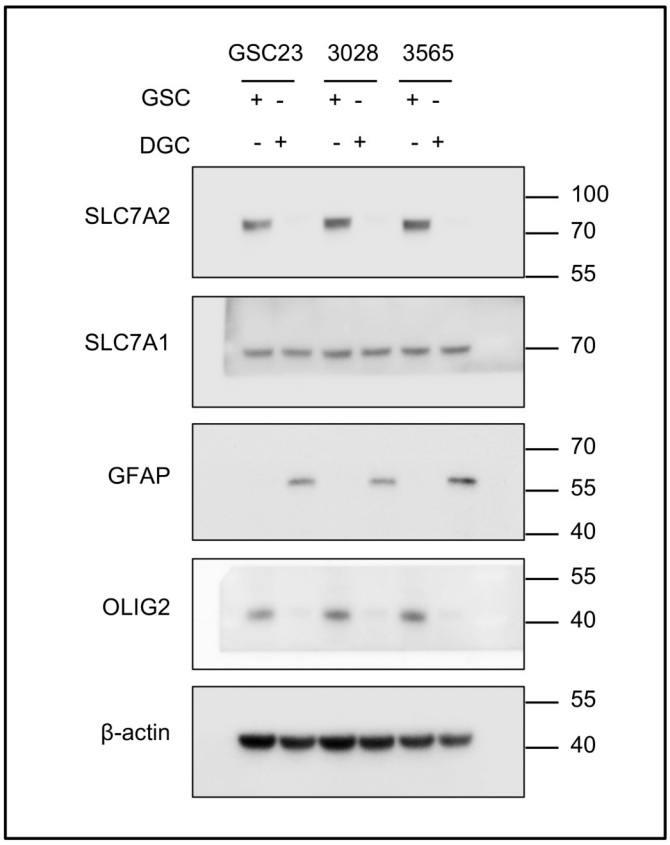


Fig. 2c

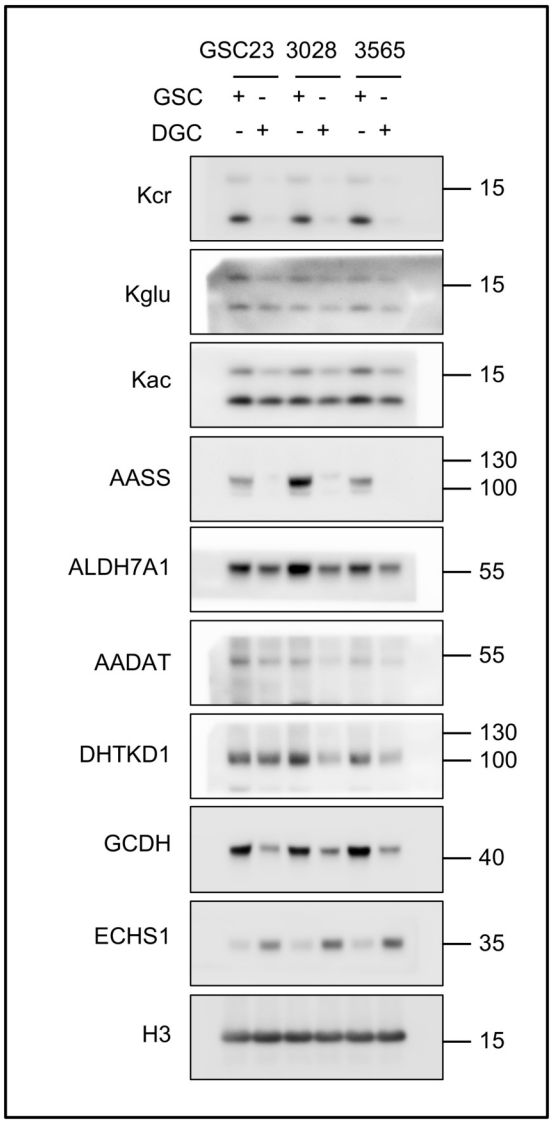


Fig. 2e

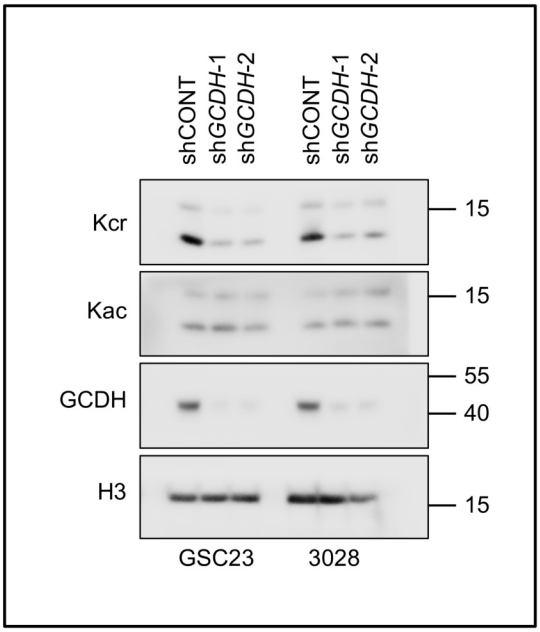
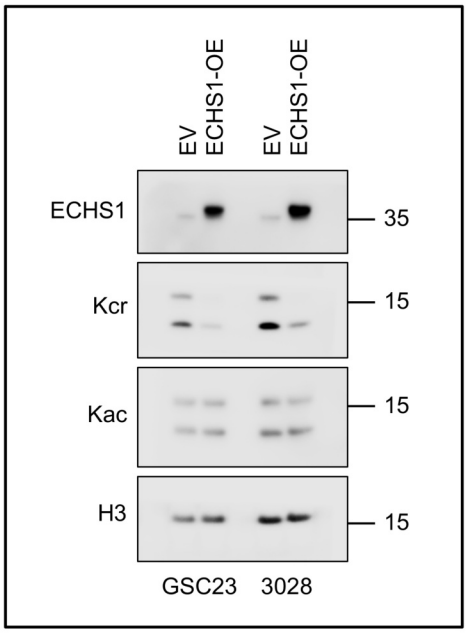


Fig. 2h



Supplementary Fig. 2 Raw data for gels, related to Fig. 3.

Fig. 3b

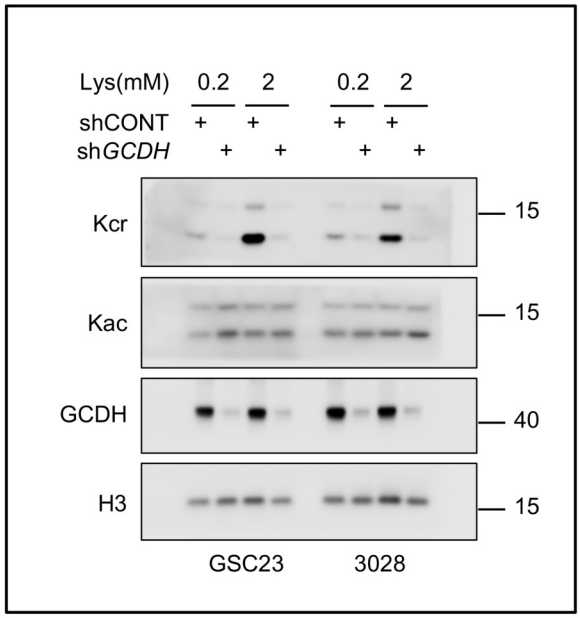


Fig. 3f

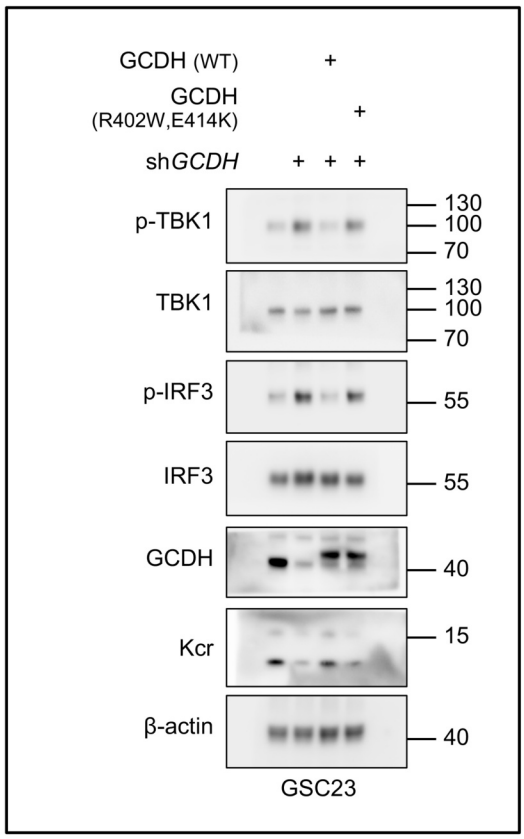


Fig. 3h

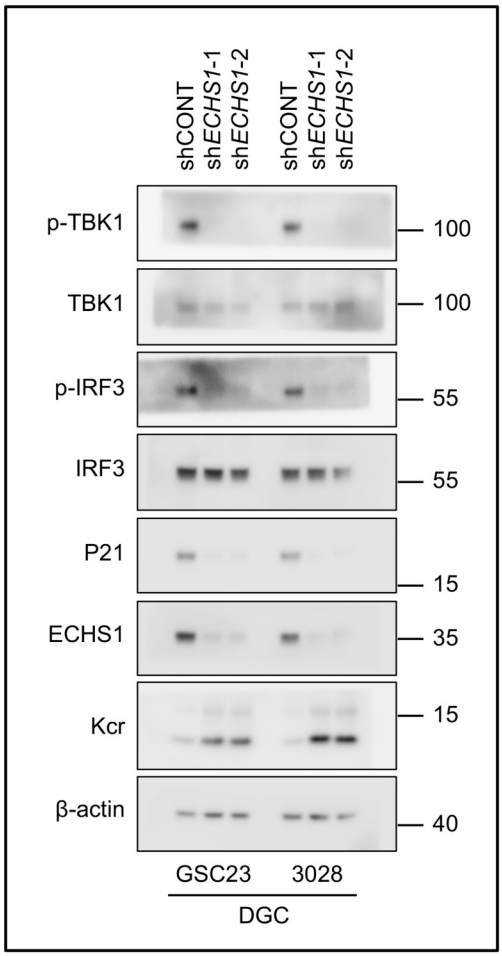
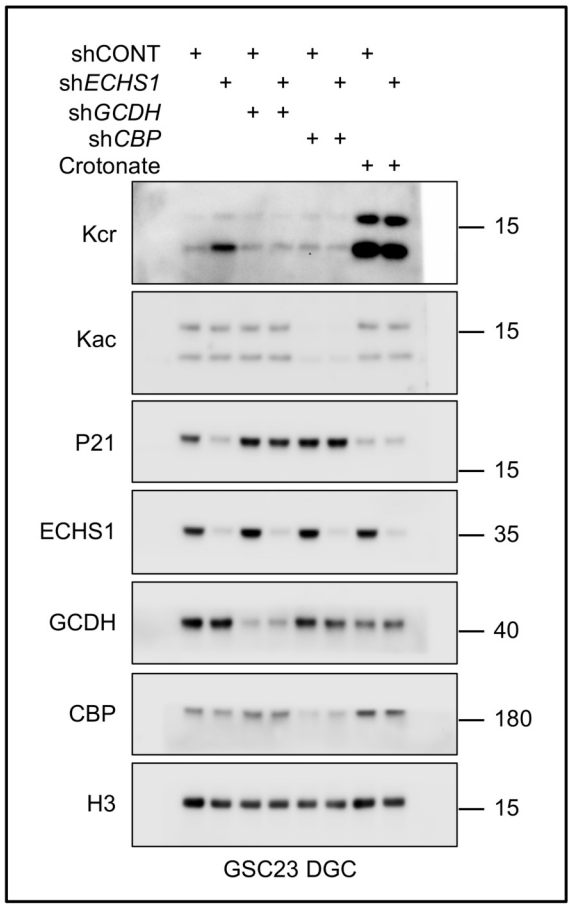


Fig. 3j



Supplementary Fig. 3 Raw data for gels, related to Fig. 4.

Fig. 4b

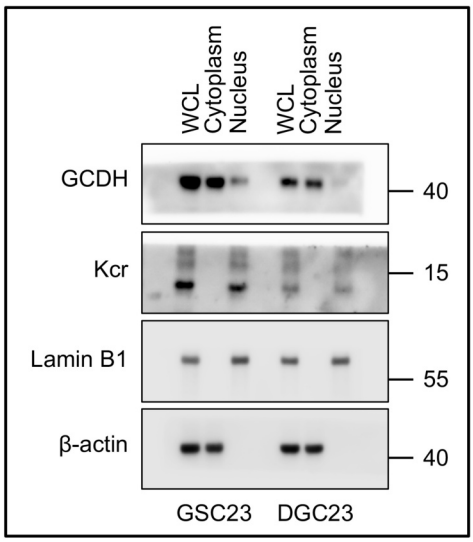


Fig. 4c

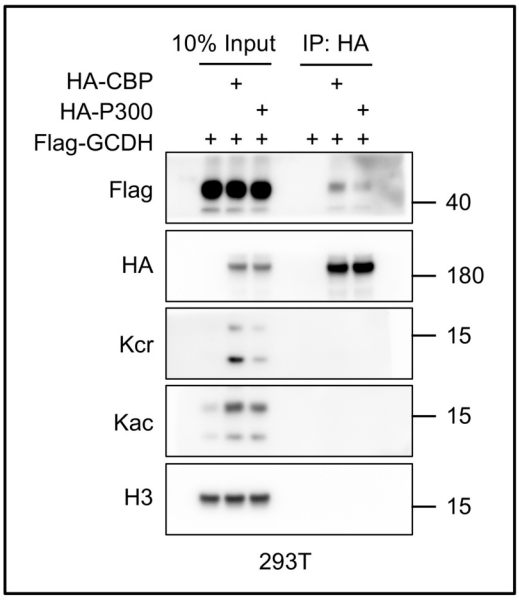


Fig. 4d

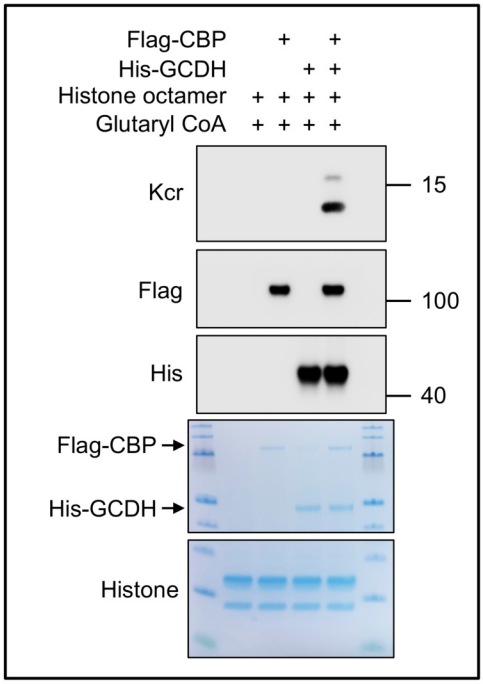


Fig. 4e

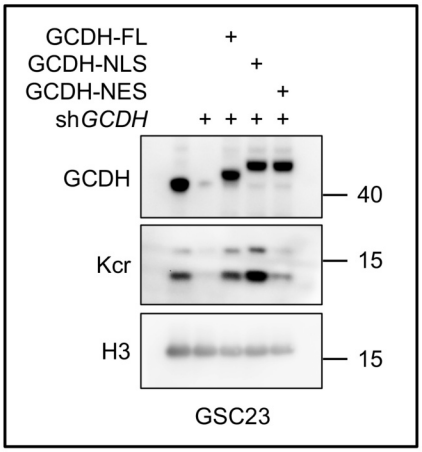


Fig. 4g

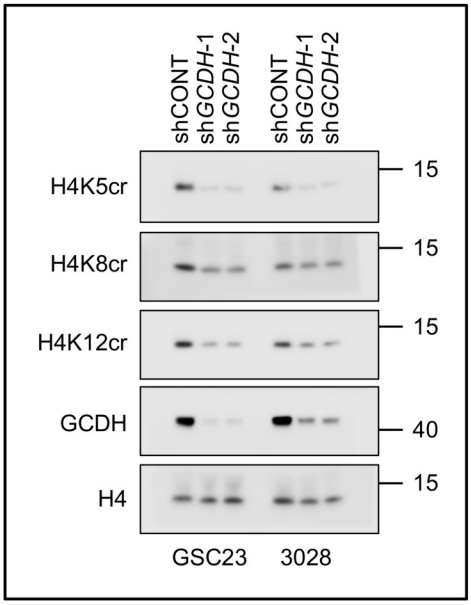


Fig. 4h

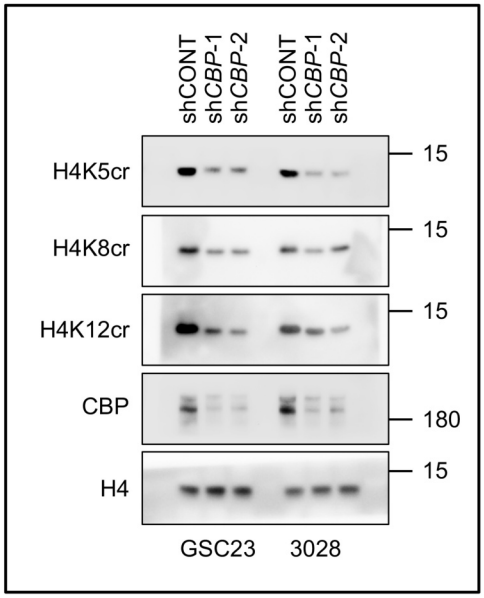
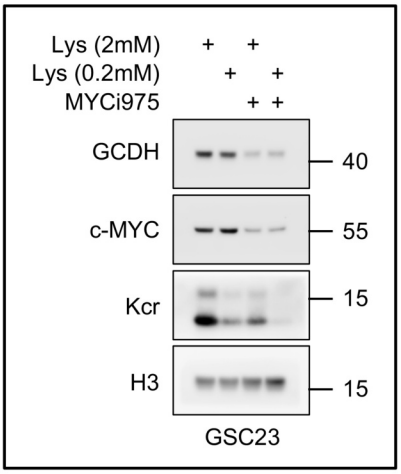


Fig. 4i



Supplementary Fig. 4 Raw data for gels and gating strategy of CD8⁺ T cells, related to Fig. 5.

Fig. 5g

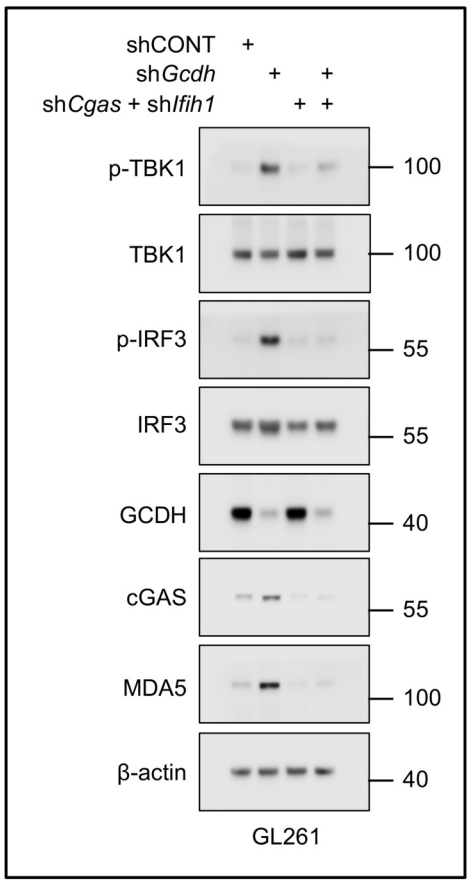
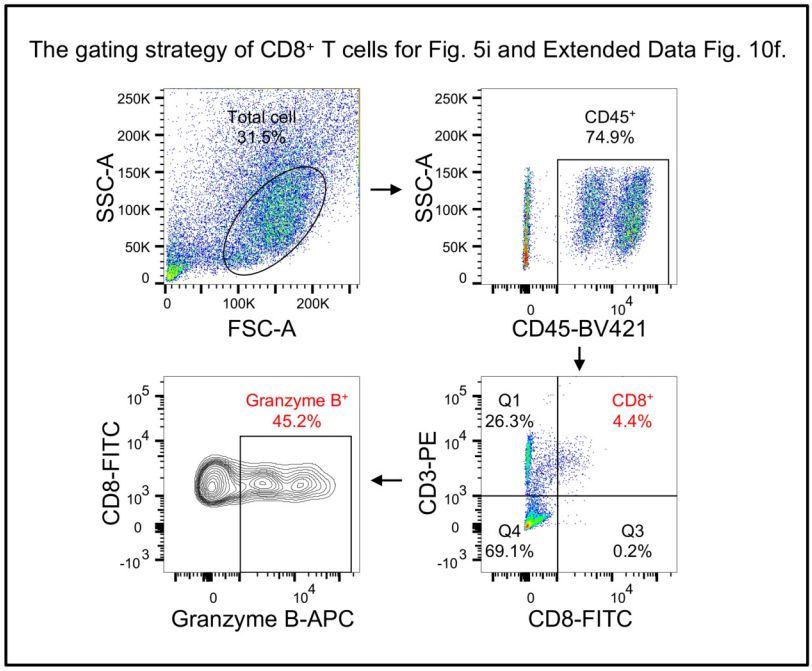
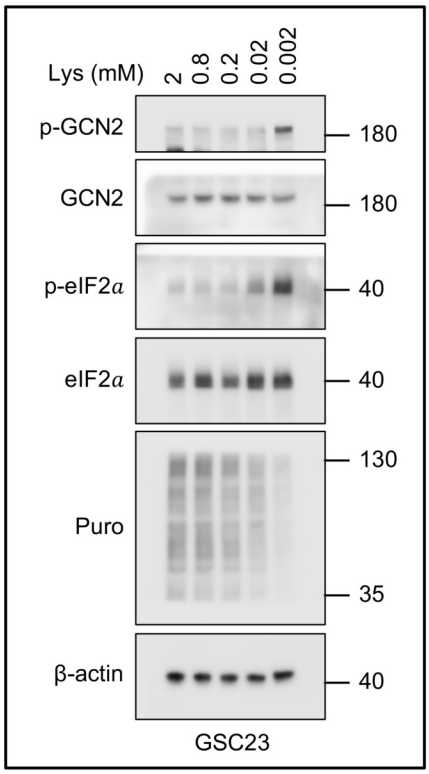


Fig. 5i and Extended Data Fig. 10f.



Supplementary Fig. 5 Raw data for gels, related to Extended Data Fig. 1, Extended Data Fig. 2 and Extended Data Fig. 3.

Extended Data Fig. 1g



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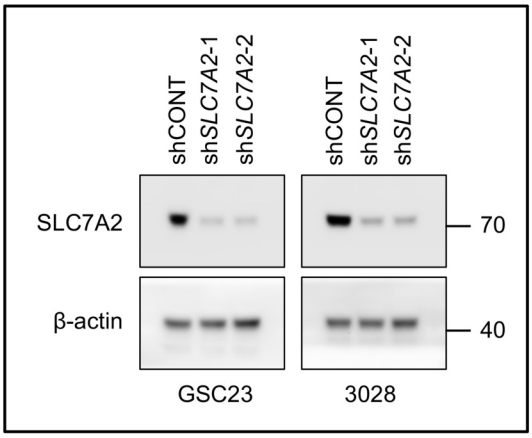
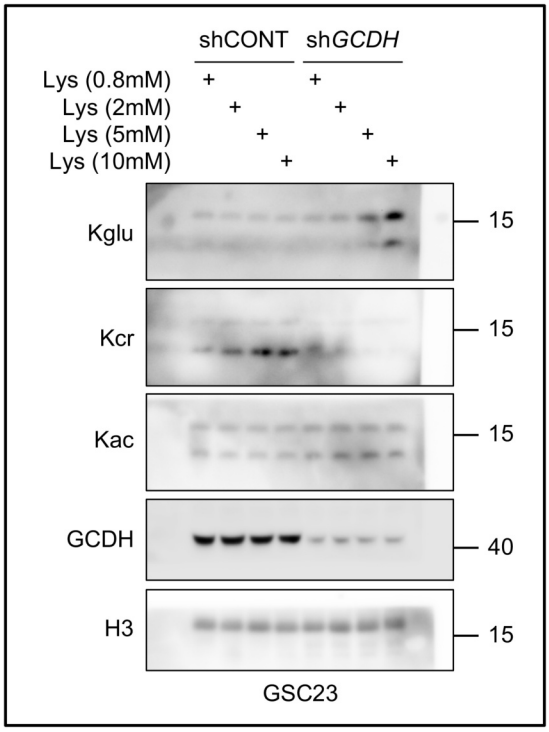


Extended Data Fig. 2q



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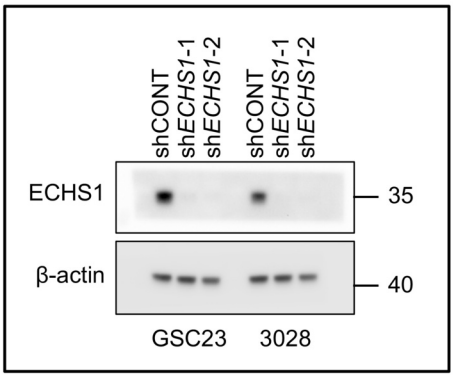

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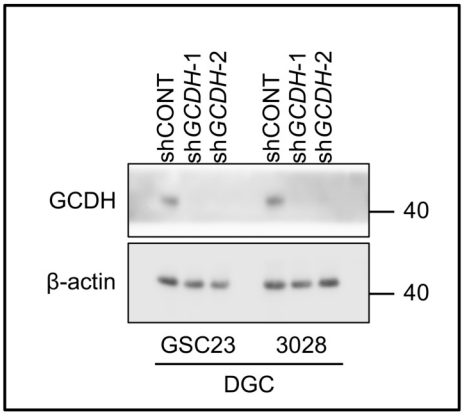

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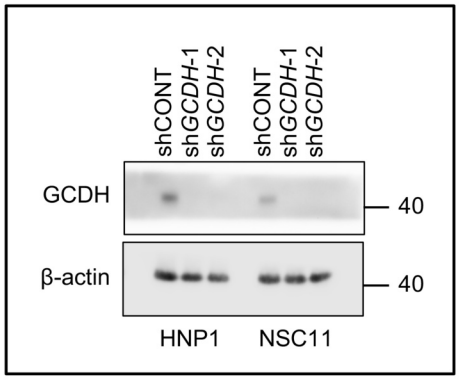
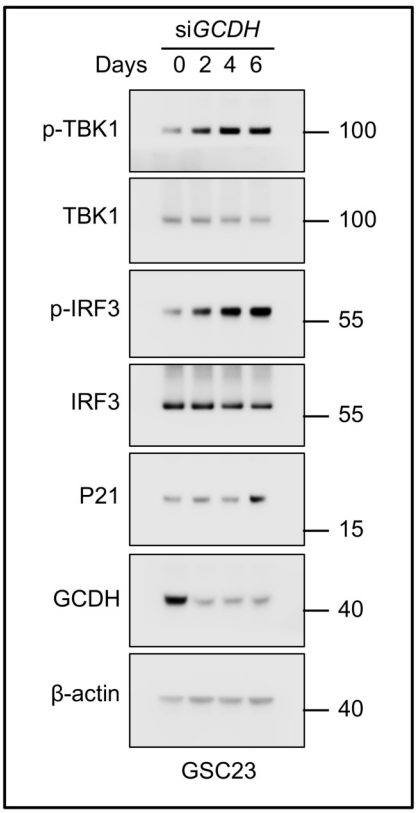
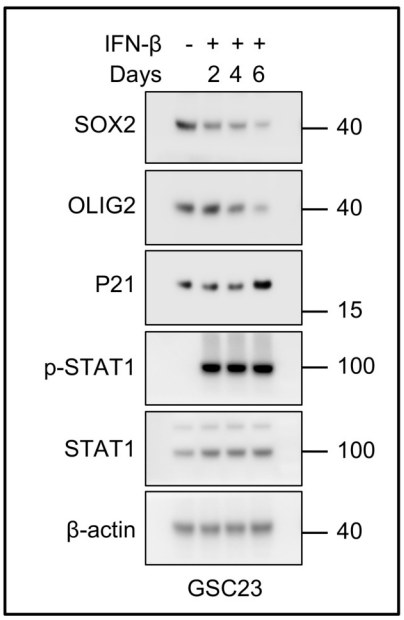


Supplementary Fig. 6 Raw data for gels, related to Extended Data Fig. 5.

Extended Data Fig. 5a



Extended Data Fig. 5c



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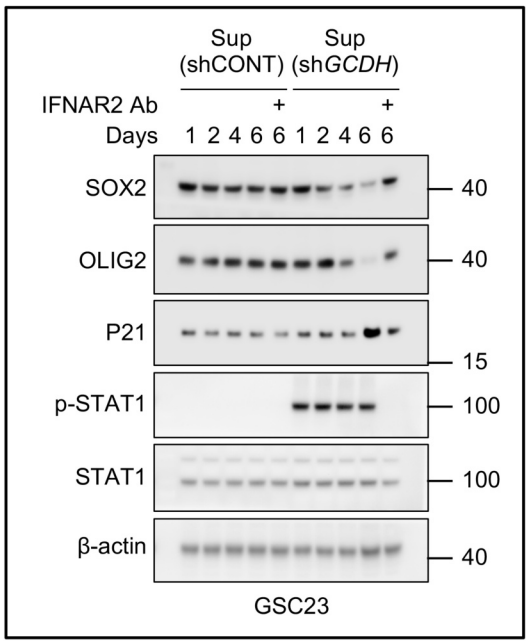
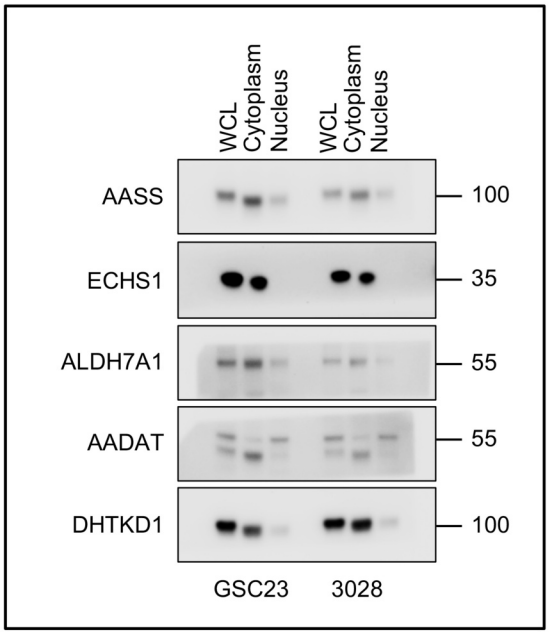


Supplementary Fig. 7 Raw data for gels, related to Extended Data Fig. 6.

Extended Data Fig. 6b



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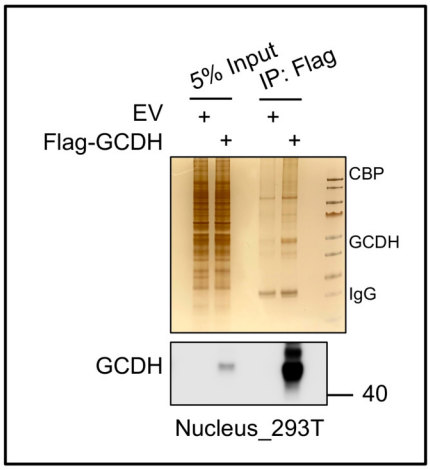

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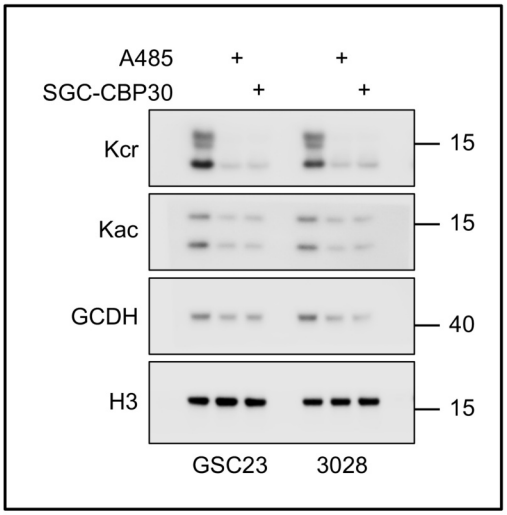

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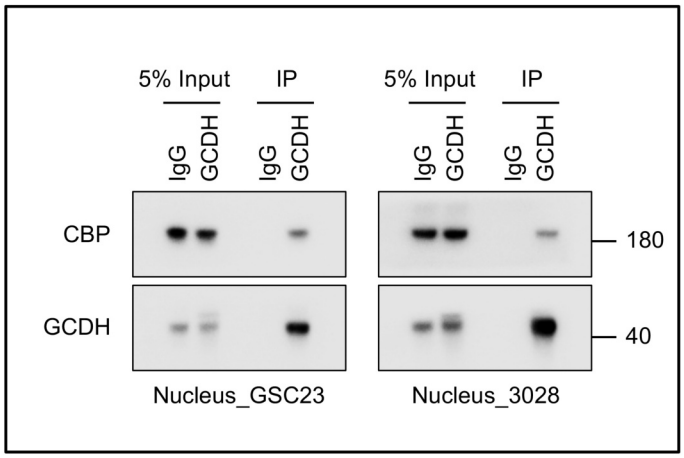

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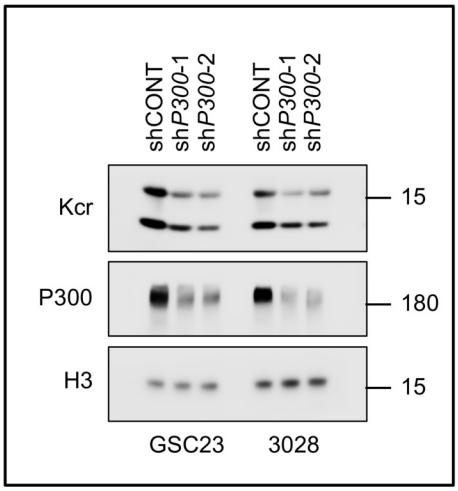

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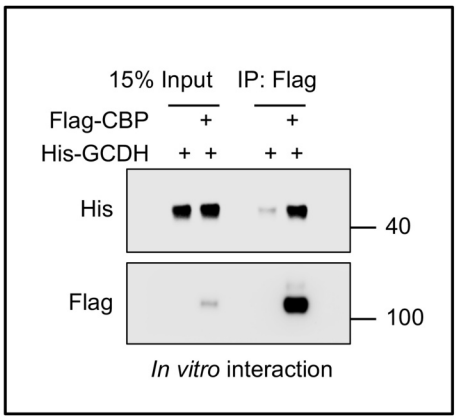

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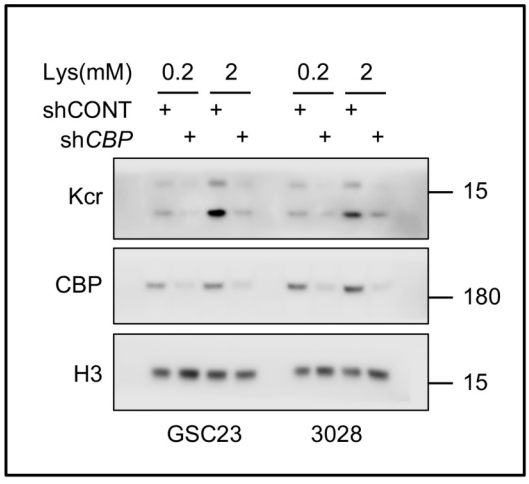
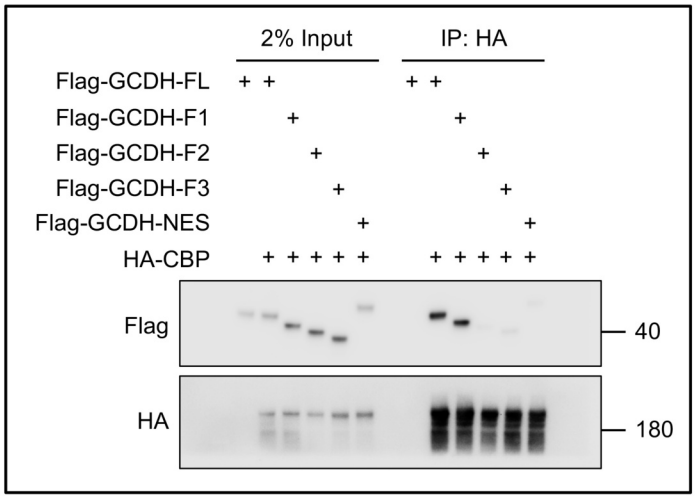


Supplementary Fig. 8 Raw data for gels, related to Extended Data Fig. 6 and Extended Data Fig. 7.

Extended Data Fig. 6k



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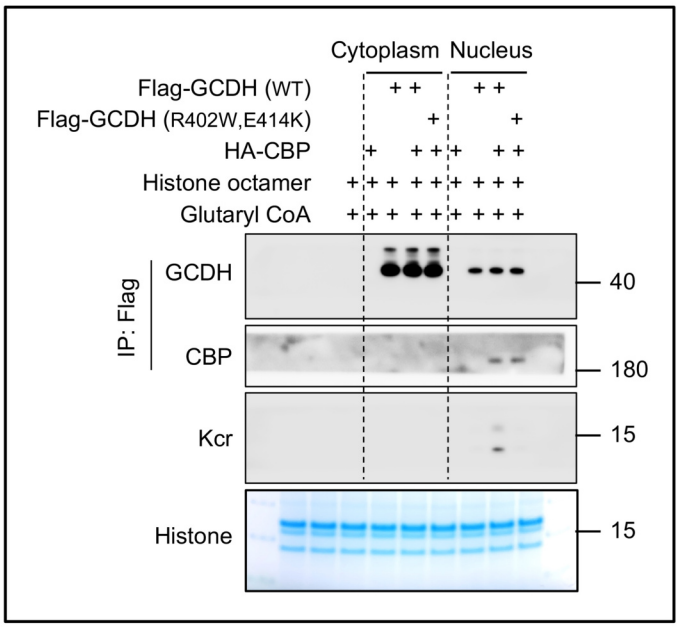

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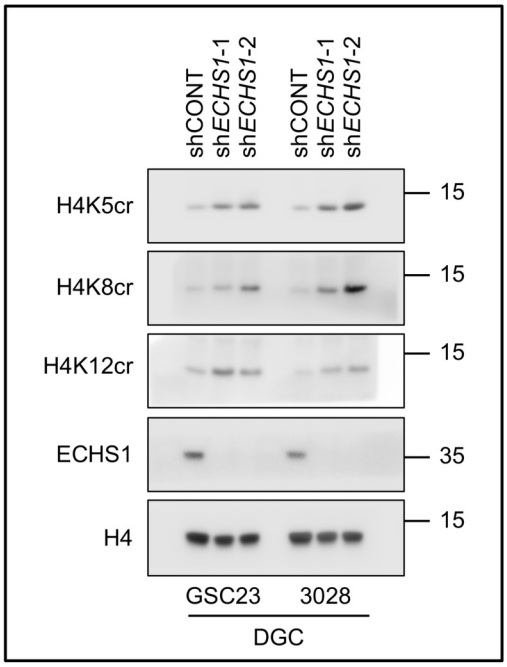

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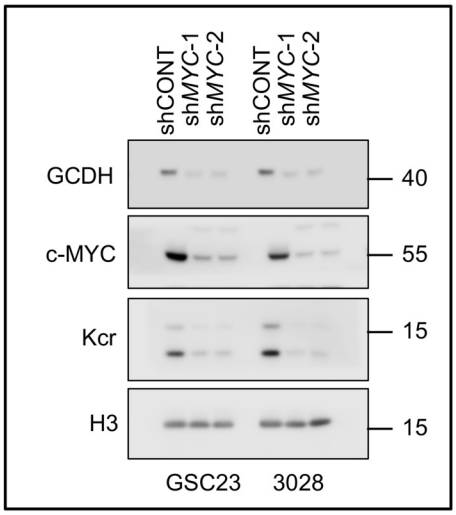
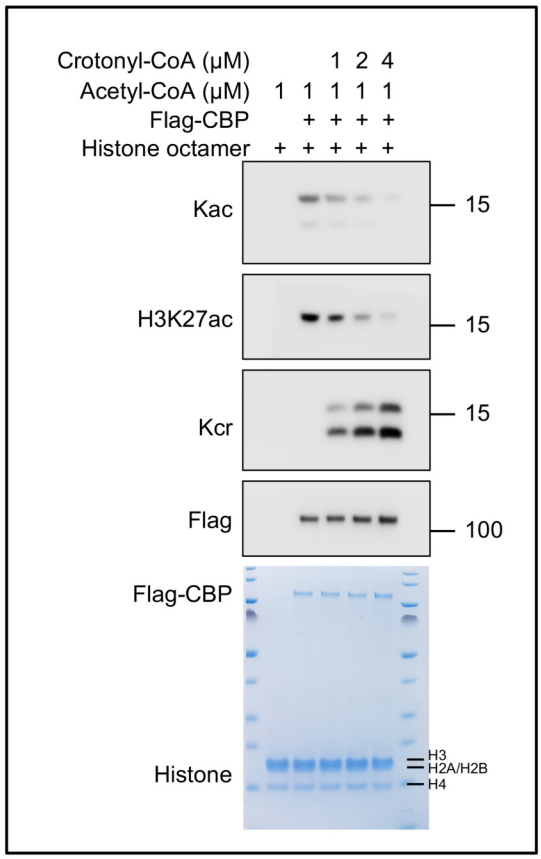


Supplementary Fig. 9 Raw data for gels, related to Extended Data Fig. 8, Extended Data Fig. 9 and Extended Data Fig. 10.

Extended Data Fig. 8a



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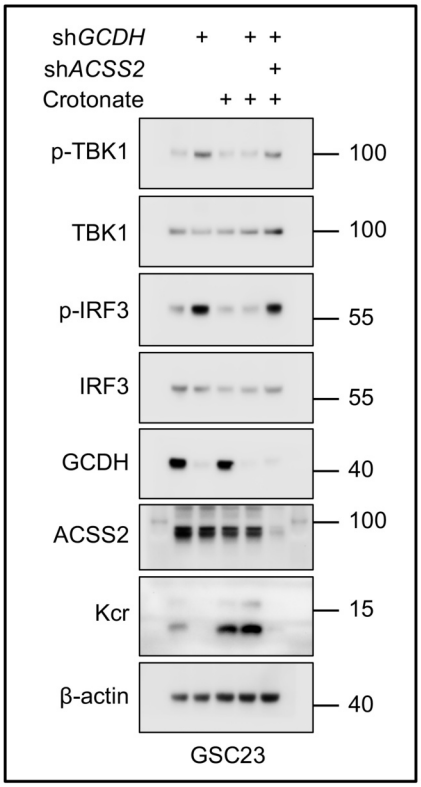

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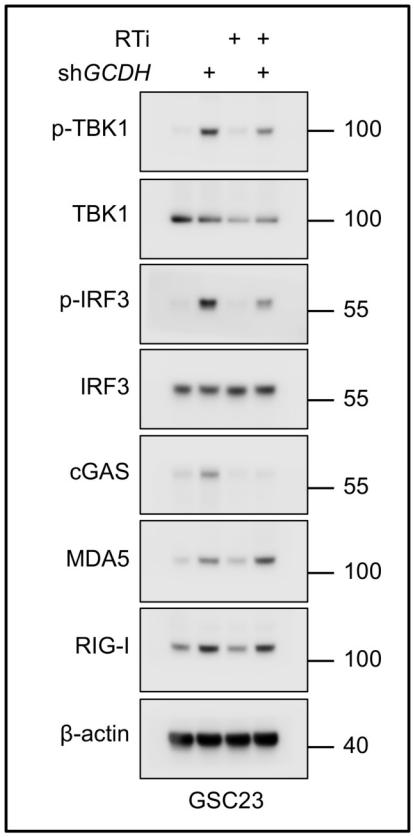

Extended Data Fig. 10e