

Supplemental information

A fingerprint of 2-[¹⁸F]FDG radiometabolites – How tissue-specific metabolism beyond 2-[¹⁸F]FDG-6-P could affect tracer accumulation

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Supplemental information

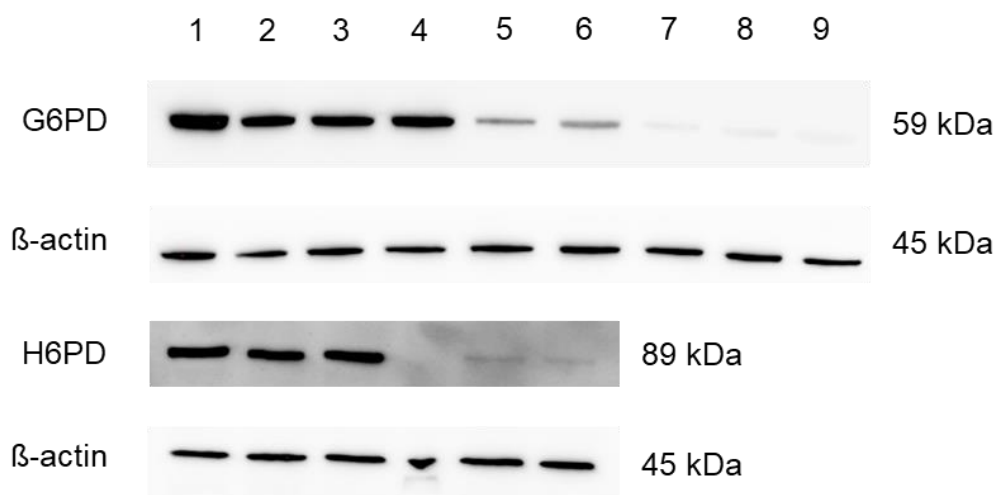
| Time (min) | % A (0.6 M sodium dihydrogen phosphate buffer with 3 % methanol) | % B (3 % methanol in water) |
|------------|---|--------------------------------|
| 0 - 12 | 5 | 95 |
| 13 | 10 | 90 |
| 14 - 18 | 15 | 85 |
| 19 - 32 | 50 | 50 |
| 34 - 35 | 5 | 95 |

Table S1. Gradient profile of the HPLC runs, related to Figure 1.

| Gene | H6PD | G6PD |
|--|---|--------------------|
| Unweighted_meta-Z_of_all_cancers | -3.028058243 | 5.104754536 |
| Adrenocortical_cancer | -0.224 | -1.307 |
| Bladder_cancer | -1.095 | 1.584 |
| Brain_cancer_Astrocytoma | 2.315 | 1.174 |
| Brain_cancer_Glioblastoma | -0.836 | 0.638 |
| Brain_cancer_Glioma | 1.687 | 2.104 |
| Brain_cancer_Medulloblastoma | 0 | 0 |
| Brain_cancer_Meningioma | -0.92 | 0.81 |
| Brain_cancer_Neuroblastoma | -4.873 | 7.427 |
| Breast_cancer | -5.307 | 4.185 |
| Colon_cancer | -0.265 | -0.594 |
| Gastric_cancer | -0.638 | 1.069 |
| Germ_cell_tumors | 0.531 | -1.269 |
| Head_and_neck_cancer | 0.27 | 0.841 |
| Head_and_neck_cancer_Hypopharyngeal_cancer | -0.123 | 0 |
| Head_and_neck_cancer_Oesophageal_cancer | -0.548 | 0 |
| Head_and_neck_cancer_Oral_SCC | 0.848 | 0.205 |
| Hematopoietic_cancer_AML | -1.654 | 1.814 |
| Hematopoietic_cancer_B_ALL | -0.273 | 0.442 |
| Hematopoietic_cancer_Burkitt_lymphoma | 0.668 | -0.29 |
| Hematopoietic_cancer_CLL | 0.072 | 1.544 |
| Hematopoietic_cancer_DLBCL | 0.477 | 0.603 |
| Hematopoietic_cancer_FL | -2.66 | 1.595 |
| Hematopoietic_cancer_Mantle_cell_lymphoma | 0.771 | 2.301 |
| Hematopoietic_cancer_Multiple_myeloma | -0.103 | 2.832 |
| Kidney_cancer | -0.209 | 0 |
| Liver_cancer | -1.438 | -0.824 |
| Liver_cancer_Primary | -0.049 | -0.255 |
| Lung_cancer_ADENO | -0.861 | 2.156 |
| Lung_cancer_LCC | -0.319 | 0.343 |
| Lung_cancer_SCC | -1.922 | 1.712 |
| Lung_cancer_SCLC | 0.258 | 0 |
| Melanoma | 1.114 | 0.319 |
| Melanoma_Metastasis | 1.127 | 1.193 |
| Mesothelioma | -0.479 | 0 |
| Ovarian_cancer | -0.992 | -1.996 |
| Pancreatic_cancer | -1.207 | 0.693 |
| Prostate_cancer | -1.005 | -0.014 |
| Sarcoma_Ewing_sarcoma | -0.375 | 0.446 |
| Sarcoma_Osteosarcoma | -0.674 | 0.397 |
| | higher expression is associated with longer survival | |
| | higher expression is associated with shorter survival | |

Source: PRECOG database Stanford 2021

Table S2. Relationship between G6PD/H6PD gene expression and survival across different cancer types, related to Figure 5.



Amount of siRNA applied and time course of silencing:

G6PD

1: control
 2: 12.5 nM, 24 h
 3: 25 nM, 24 h
 4: 50 nM, 24 h
 5: 12.5 nM, 48 h

H6PD

1-3: control
 4-6: 12.5 nM, 72 h

6: 50 nM, 48 h
 7: 12.5 nM, 72 h
 8: 25 nM, 72 h
 9: 50 nM, 72 h

Figure S1. Western blots of preliminary tests with SMARTpool ON-TARGETplus siRNAs to find the optimal concentration for G6PD/H6PD knockdown in HT29 cells, related to Figure 7.

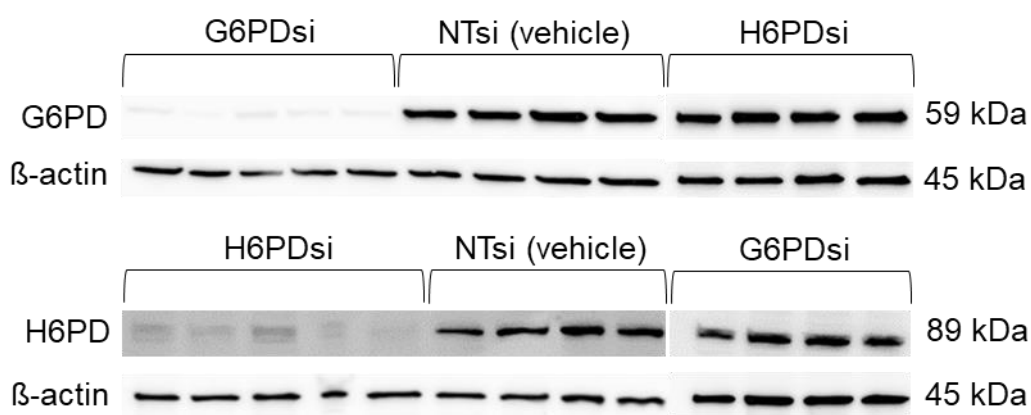


Figure S2. Representative western blots that exclude compensatory overexpression of the respective other enzyme after knockdown with siRNA (samples from different experiments), related to Figure 7.

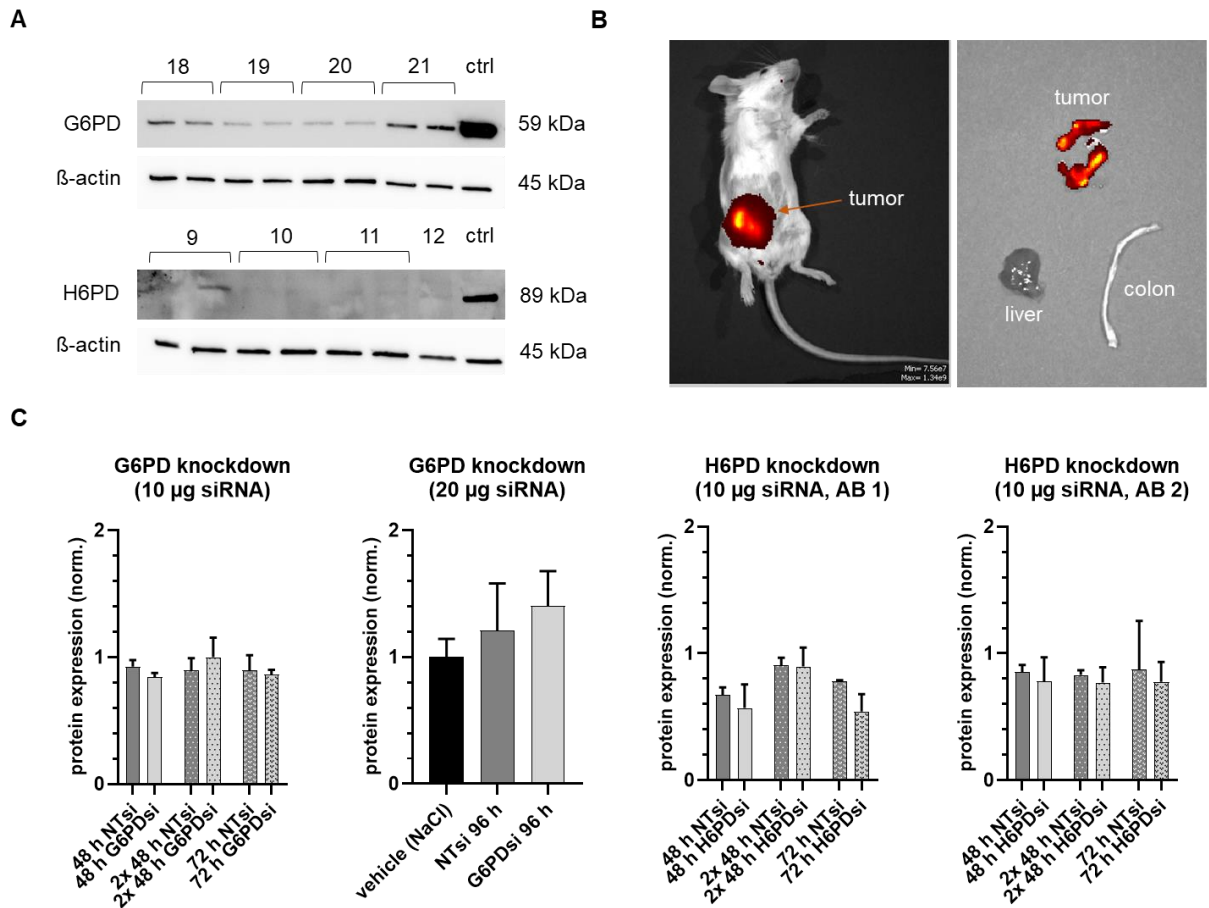


Figure S3. Attempts for *in vivo* knockdown of G6PD/H6PD were not successful, related to Figure 7. (A) Western blot analysis determining the most effective siRNAs within the tested pool. (B) Post-mortem IVIS® images showing successful siRNA injection and good distribution in HT29 tumor, and (C) summary of western blot analyses of G6PD/H6PD knockdown ($n = 3$ each, NTsi = non-targeting siRNA, AB 1 = proteintech antibody, AB 2 = abcam antibody). Bar graph data are represented as mean \pm SD.