

Supplemental Table 3. Cellular Processes Increased in MCF7 Cells Treated with Lactate or Ketones.

| Data Set | P-value | Detailed Description |
|---|----------|--|
| <u>1. Lactate-Specific Genes</u> | | |
| <u>Stem Cells</u> | | |
| STEMCELL_NEURAL_UP | 1.31E-13 | Enriched in mouse neural stem cells, compared to differentiated brain |
| STEMCELL_EMBRYONIC_UP | 3.60E-08 | Enriched in mouse embryonic stem cells, compared to differentiated brain and bone marrow cells |
| <u>DNA Damage</u> | | |
| UVC_TTD_ALL_DN | 2.83E-07 | Down-regulated at any timepoint following treatment of XPB/TTD fibroblasts with 3 J/m ² UVC |
| UVC_XPCS_ALL_DN | 7.98E-07 | Down-regulated at any timepoint following treatment of XPB/CS fibroblasts with 3 J/m ² UVC |
| UVC_XPCS_8HR_DN | 1.94E-06 | Down-regulated at 8 hours following treatment of XPB/CS fibroblasts with 3 J/m ² UVC |
| UVC_TTD_4HR_DN | 2.93E-06 | Down-regulated at 4 hours following treatment of XPB/TTD fibroblasts with 3 J/m ² UVC |
| UVC_TTD-XPCS_COMMON_DN with 3 J/m ² UVC | 4.98E-05 | Down-regulated at any timepoint following treatment of both XPB/CS and XPB/TTD fibroblasts |
| UVC_HIGH_ALL_DN a high dose (50 J/m ²) (clusters d1-d9) | 1.24E-03 | Down-regulated at any timepoint following treatment of WS1 human skin fibroblasts with UVC at |
| <u>Key Transcription Factors</u> | | |
| MORF_HDAC2 219 | 3.11E-06 | Neighborhood of HDAC2 histone deacetylase 2 in the MORF expression compendium |
| GGGAGGRR_V\$MAZ_Q6 | 1.02E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif |
| GGGAGGRR which matches annotation for MAZ : MYC-associated zinc finger protein (purine-binding transcription factor) | | |
| SCGGAAGY_V\$ELK1_Q2 | 1.47E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif |
| SCGGAAGY which matches annotation for ELK1 : ELK1, member of ETS oncogene family | | |
| V\$E2F1_Q4_Q1 | 3.28E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif |
| TTTSGCGSG which matches annotation for E2F TFDP1: transcription factor Dp-1 | | |
| TTGTTT_V\$FOXO4_Q1 | 3.72E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif |
| TTGTTT which matches annotation for MLLT7 : myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7 | | |
| GGGCGGR_V\$SP1_Q6 | 3.75E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif |
| GGGCGGR which matches annotation for SP1 : Sp1 transcription factor | | |
| <u>Cancer Prognosis (Poor Survival)</u> | | |
| MOREAUX_TACI_HI_VS_LOW_DN | 1.43E-04 | Genes overexpressed in TACI low patients (poor prognosis in multiple myeloma) |
| HCC_SURVIVAL_GOOD_VS_POOR_DN | 1.82E-04 | Genes highly expressed in hepatocellular carcinoma with poor survival. |
| <u>2. Ketone-Specific Genes</u> | | |
| <u>Stem Cells</u> | | |
| STEMCELL_HEMATOPOIETIC_UP | 7.49E-04 | Enriched in mouse hematopoietic stem cells, compared to differentiated brain and bone marrow |
| <u>Key Transcription Factors</u> | | |
| CAGGTG_V\$E12_Q6 | 7.97E-05 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif |
| CAGGTG which matches annotation for TCF3 : transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) | | |

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|----------------------|----------|--|
| TGACAGNY_V\$MEIS1_01 | 3.33E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGACAGNY which matches annotation for MEIS1 : Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) |
| GGGTGGRR_V\$PAX4_03 | 4.16E-04 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GGGTGGRR which matches annotation for PAX4 : paired box gene 4 |
| MORF_ATF2_258 | 8.02E-04 | Neighborhood of ATF2 activating transcription factor 2 in the MORF expression compendium |

3. Common Intersecting Genes (Upregulated by both Lactate and Ketones)

DNA Damage

| | | |
|---|----------|--|
| UVC_XPCS_ALL_DN | 2.60E-13 | Down-regulated at any timepoint following treatment of XPB/CS fibroblasts with 3 J/m ² UVC |
| UVC_XPCS_8HR_DN | 7.33E-12 | Down-regulated at 8 hours following treatment of XPB/CS fibroblasts with 3 J/m ² UVC |
| UVC_TTD_ALL_DN | 2.47E-08 | Down-regulated at any timepoint following treatment of XPB/TTD fibroblasts with 3 J/m ² UVC |
| UVC_XPCS_4HR_DN | 3.21E-07 | Down-regulated at 4 hours following treatment of XPB/CS fibroblasts with 3 J/m ² UVC |
| UVC_TTD_4HR_DN | 3.38E-07 | Down-regulated at 4 hours following treatment of XPB/TTD fibroblasts with 3 J/m ² UVC |
| UVB_NHEK1_DN | 2.68E-06 | Downregulated by UV-B light in normal human epidermal keratinocytes |
| UVC_TTD_8HR_DN | 1.27E-05 | Down-regulated at 8 hours following treatment of XPB/TTD fibroblasts with 3 J/m ² UVC |
| UVC_TTD-XPCS_COMMON_DN with 3 J/m ² UVC | 6.54E-04 | Down-regulated at any timepoint following treatment of both XPB/CS and XPB/TTD fibroblasts |
| UVB_NHEK3_C5 | 9.27E-04 | Regulated by UV-B light in normal human epidermal keratinocytes, cluster 5 |

Stem Cells

| | | |
|---------------------------|----------|--|
| STEMCELL_EMBRYONIC_UP | 7.26E-08 | Enriched in mouse embryonic stem cells, compared to differentiated brain and bone marrow cells |
| STEMCELL_NEURAL_UP | 1.29E-07 | Enriched in mouse neural stem cells, compared to differentiated brain and bone marrow cells |
| STEMCELL_HEMATOPOIETIC_UP | 2.93E-06 | Enriched in mouse hematopoietic stem cells, compared to differentiated brain and bone marrow |

Key Transcription Factors

| | | |
|----------------------|----------|--|
| GGGCGGR_V\$SP1_Q6 | 1.16E-07 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif GGGCGGR which matches annotation for SP1 : Sp1 transcription factor |
| CAGGTG_V\$E12_Q6 | 1.30E-06 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CAGGTG which matches annotation for TCF3 : transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) |
| TGGAAA_V\$NFAT_Q4_01 | 6.09E-06 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TGGAAA which matches annotation for NFAT NFATC |
| CTTTGT_V\$LEF1_Q2 | 1.61E-05 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif CTTTGT which matches annotation for LEF1 : lymphoid enhancer-binding factor 1 |
| TTGTTT_V\$FOXO4_01 | 7.86E-05 | Genes with promoter regions [-2kb,2kb] around transcription start site containing the motif TTGTTT which matches annotation for MLL7 : myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7 |

Cancer Associated Genes

| | | |
|--------------------|----------|--|
| BRCA_ER_NEG | 3.48E-04 | Genes whose expression is consistently negatively correlated with estrogen receptor status in breast cancer - higher expression is associated with ER-negative tumors |
| BRCA_ER_POS | 6.77E-04 | Genes whose expression is consistently positively correlated with estrogen receptor status in breast cancer - higher expression is associated with ER-positive tumors |
| BRENTANI_SIGNALING | 1.05E-03 | Cancer related genes involved in the cell signaling |