|  |
| --- |
| **Relative expression compared to fibroblasts** |
|  |  |  | **ALDH+** | **ALDH-** |
| **Gene** | **UACC 903** | **1205 Lu** | **1205 Lu** | **1205 Lu** |
| **ALDH1A1** | 6.299 | 6.365 | 11.728 | 1.072 |
| **ALDH1A2** | 6.748 | 3.119 | 7.208 | 1.089 |
| **ALDH1A3** | 5.332 | 7.845 | 11.001 | 1.816 |
| **ALDH1B1** | 1.83 | 1.799 | 1.482 | 1.734 |
| **ALDH1L1** | 3.758 | 1.913 | 5.351 | 1.28 |
| **ALDH1L2** | 1.053 | 1.774 | 1.898 | 1.686 |
| **ALDH2** | 6.18 | 6.929 | 9.818 | 1.843 |
| **ALDH3A1** | 7.047 | 9.698 | 11.118 | 1.592 |
| **ALDH3A2** | 1.297 | 1.965 | 1.722 | 1.007 |
| **ALDH3B1** | 1.021 | 1.294 | 1.892 | 1.438 |
| **ALDH3B2** | 1.246 | 1.991 | 1.887 | 1.752 |
| **ALDH4A1** | 1.855 | 1.116 | 1.493 | 1.041 |
| **ALDH5A1** | 5.89 | 7.93 | 8.038 | 1.383 |
| **ALDH6A1** | 1.416 | 1.948 | 1.893 | 1.304 |
| **ALDH7A1** | 1.174 | 1.19 | 1.973 | 1.779 |
| **ALDH8A1** | 1.06 | 1.659 | 1.558 | 1.517 |
| **ALDH9A1** | 1.951 | 1.07 | 1.54 | 1.688 |
| **ALDH16A1** | 1.189 | 1.028 | 1.967 | 1.406 |
| **ALDH18A1** | 11.432 | 6.609 | 10.708 | 1.179 |
| **GAPDH** | 1.307 | 1.051 | 1.003 | 1.195 |

**Supplementary table 1.** RT-PCR analysis of the expression of ALDH isoforms in melanoma cell lines and isolated ALDH+ and ALDH- cells. ALDH+ and ALDH- cells were isolated from 1205 Lu melanoma cell line using the Aldered dye as described in materials and methods. RT-PCR analysis was performed to evaluate the expression of various ALDH isoforms in melanoma cells and are compared to that of fibroblasts (FF2441).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **PDB ID** | **Atoms** | **Residues** | **RMSD (Å)** | **Description** | **Organism** |
| **4WB9 (Query)****4URH** | 33  26 | 13  14 | 2.24  6.87 | Crystal structure of human ALDH1A1 complexed with NADHCrystal structure of high-resolution structure of partially oxidized *D. fructosivorans* NiFe-hydrogenase | *Homo sapiens*  *Desulfovibrio fructosivorans* |

**Supplementary table 2.** KS100 has no human off-target effects based on the Erebus algorithm. The specificity of KS100 was evaluated using the binding scaffold of KS100 to ALDH1A1, 2 and 3A1 and querying in the Erebus program to identify similar substructural scaffolds in the PDB database.