**Supplementary Table S2: Gene Set Variation Analysis (GSVA) between primary dnMBC tumors vs. eBC.** The hallmark pathways, mean difference, raw p-value, and FDR-corrected p-value are reported. The direction of the mean difference is dnMBC vs. eBC. A negative value means a downregulation of the hallmark pathways in dnMBC tumors and a positive value means an upregulation of the hallmark pathways in dnMBC tumors compared to eBC tumors. The p-values were calculated using a paired-test. FDR: false discovery rate.

|  |  |  |  |
| --- | --- | --- | --- |
| **Hallmarks** | **Mean difference** | **P-values** | |
| **Raw** | **FDR** |
| HALLMARK\_HEME\_METABOLISM | -0.010 | 0.018 | 0.396 |
| HALLMARK\_UV\_RESPONSE\_UP | -0.018 | 0.020 | 0.396 |
| HALLMARK\_ANDROGEN\_RESPONSE | -0.015 | 0.031 | 0.396 |
| HALLMARK\_PANCREAS\_BETA\_CELLS | -0.031 | 0.036 | 0.396 |
| HALLMARK\_KRAS\_SIGNALING\_DN | -0.012 | 0.047 | 0.396 |
| HALLMARK\_PROTEIN\_SECRETION | -0.013 | 0.048 | 0.396 |
| HALLMARK\_PI3K\_AKT\_MTOR\_SIGNALING | -0.010 | 0.056 | 0.396 |
| HALLMARK\_MTORC1\_SIGNALING | -0.016 | 0.087 | 0.422 |
| HALLMARK\_GLYCOLYSIS | -0.010 | 0.095 | 0.422 |
| HALLMARK\_REACTIVE\_OXIGEN\_SPECIES\_PATHWAY | -0.016 | 0.097 | 0.422 |
| HALLMARK\_MYC\_TARGETS\_V1 | -0.019 | 0.098 | 0.422 |
| HALLMARK\_ADIPOGENESIS | -0.011 | 0.113 | 0.422 |
| HALLMARK\_INTERFERON\_ALPHA\_RESPONSE | -0.035 | 0.115 | 0.422 |
| HALLMARK\_PEROXISOME | -0.009 | 0.118 | 0.422 |
| HALLMARK\_CHOLESTEROL\_HOMEOSTASIS | -0.012 | 0.131 | 0.435 |
| HALLMARK\_FATTY\_ACID\_METABOLISM | -0.009 | 0.190 | 0.591 |
| HALLMARK\_ESTROGEN\_RESPONSE\_LATE | -0.013 | 0.201 | 0.591 |
| HALLMARK\_P53\_PATHWAY | -0.005 | 0.221 | 0.613 |
| HALLMARK\_ANGIOGENESIS | -0.013 | 0.255 | 0.613 |
| HALLMARK\_HEDGEHOG\_SIGNALING | -0.011 | 0.266 | 0.613 |
| HALLMARK\_OXIDATIVE\_PHOSPHORYLATION | -0.011 | 0.270 | 0.613 |
| HALLMARK\_MYC\_TARGETS\_V2 | -0.013 | 0.281 | 0.613 |
| HALLMARK\_INTERFERON\_GAMMA\_RESPONSE | -0.020 | 0.282 | 0.613 |
| HALLMARK\_SPERMATOGENESIS | -0.009 | 0.310 | 0.629 |
| HALLMARK\_IL2\_STAT5\_SIGNALING | -0.010 | 0.314 | 0.629 |
| HALLMARK\_MYOGENESIS | -0.010 | 0.335 | 0.644 |
| HALLMARK\_COAGULATION | -0.009 | 0.388 | 0.701 |
| HALLMARK\_HYPOXIA | -0.007 | 0.400 | 0.701 |
| HALLMARK\_XENOBIOTIC\_METABOLISM | -0.005 | 0.406 | 0.701 |
| HALLMARK\_UNFOLDED\_PROTEIN\_RESPONSE | -0.005 | 0.442 | 0.707 |
| HALLMARK\_APICAL\_JUNCTION | -0.007 | 0.449 | 0.707 |
| HALLMARK\_MITOTIC\_SPINDLE | -0.005 | 0.452 | 0.707 |
| HALLMARK\_DNA\_REPAIR | -0.005 | 0.466 | 0.707 |
| HALLMARK\_KRAS\_SIGNALING\_UP | -0.010 | 0.523 | 0.767 |
| HALLMARK\_TGF\_BETA\_SIGNALING | 0.005 | 0.537 | 0.767 |
| HALLMARK\_ESTROGEN\_RESPONSE\_EARLY | -0.007 | 0.578 | 0.803 |
| HALLMARK\_E2F\_TARGETS | -0.010 | 0.607 | 0.818 |
| HALLMARK\_COMPLEMENT | -0.006 | 0.629 | 0.818 |
| HALLMARK\_G2M\_CHECKPOINT | -0.008 | 0.638 | 0.818 |
| HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB | 0.005 | 0.713 | 0.891 |
| HALLMARK\_NOTCH\_SIGNALING | 0.003 | 0.779 | 0.930 |
| HALLMARK\_IL6\_JAK\_STAT3\_SIGNALING | 0.004 | 0.789 | 0.930 |
| HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION | 0.005 | 0.816 | 0.930 |
| HALLMARK\_UV\_RESPONSE\_DN | 0.002 | 0.820 | 0.930 |
| HALLMARK\_BILE\_ACID\_METABOLISM | -0.001 | 0.853 | 0.930 |
| HALLMARK\_INFLAMMATORY\_RESPONSE | -0.002 | 0.875 | 0.930 |
| HALLMARK\_APOPTOSIS | -0.001 | 0.880 | 0.930 |
| HALLMARK\_WNT\_BETA\_CATENIN\_SIGNALING | -0.001 | 0.907 | 0.930 |
| HALLMARK\_APICAL\_SURFACE | -0.001 | 0.911 | 0.930 |
| HALLMARK\_ALLOGRAFT\_REJECTION | 0.001 | 0.973 | 0.973 |