

Supplemental Table 3

| Name | Size | NES | FDR q-val | AA vs EA |
|---|-------------|------------|------------------|-----------------|
| HALLMARK TARGETS E2F | 193 | 2.81 | <0.010 | Upregulated |
| KEGG RIBOSOME | 83 | 2.74 | <0.010 | Upregulated |
| GO RRNA METABOLIC PROCESS | 239 | 2.73 | <0.010 | Upregulated |
| REACTOME PEPTIDE CHAIN ELONGATION | 82 | 2.72 | <0.010 | Upregulated |
| GO ANAPHASE PROMOTING COMPLEX DEPENDENT CATABOLIC PROCESS | 75 | 2.70 | <0.010 | Upregulated |
| REACTOME TRANSLATION | 143 | 2.70 | <0.010 | Upregulated |
| REACTOME REPLICATION DNA | 179 | 2.69 | <0.010 | Upregulated |
| REACTOME NONSENSE MEDIATED DECA Y ENHANCED BY THE EXON COMPLEX JUNCTION | 101 | 2.69 | <0.010 | Upregulated |

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| REACTOME SRP DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO MEMBRANE | 106 | 2.69 | <0.010 | Upregulated |
| REACTOME INFLUENZA VIRAL RNA TRANSCRIPTION AND REPLICATION | 98 | 2.68 | <0.010 | Upregulated |
| GO NCRNA PROCESSING | 365 | 2.63 | <0.010 | Upregulated |
| REACTOME CELL CYCLE | 355 | 2.62 | <0.010 | Upregulated |
| REACTOME 3 UTR MEDIATED TRANSLATIONAL REGULATION | 102 | 2.58 | <0.010 | Upregulated |
| GO RIBONUCLEOPROTEIN COMPLEX BIOGENESIS | 408 | 2.58 | <0.010 | Upregulated |
| GO OXIDATIVE PHOSPHORYLATION | 82 | 2.57 | <0.010 | Upregulated |

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|---|--------------------------|-----|--------|--------|---------------|
| HALLMARK TARGETS V1 | MYC | 195 | 2.56 | <0.010 | Upregulated |
| REACTOME OF DNA | SYNTHESIS | 83 | 2.55 | <0.010 | Upregulated |
| GO ELONGATION | TRANSLATIONAL | 110 | 2.53 | <0.010 | Upregulated |
| GO ADHESION VIA PLASMA MEMBRANE MOLECULES | HOMOPHILIC CELL ADHESION | 108 | - 2.71 | <0.010 | Downregulated |
| HALLMARK RESPONSE DN | UV | 143 | - 2.61 | <0.010 | Downregulated |
| ATATGCA | MIR448 | 191 | - 2.46 | <0.010 | Downregulated |
| TGCTTTG | MIR330 | 279 | - 2.42 | <0.010 | Downregulated |
| CTTGTAT | MIR381 | 192 | - 2.36 | <0.010 | Downregulated |
| GO CONDUCTION | CARDIAC | 63 | - 2.36 | <0.010 | Downregulated |
| TAATAAT | MIR126 | 188 | - 2.35 | <0.010 | Downregulated |

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|--|-----|-----------|--------|---------------|
| GO REGULATION OF BLOOD CIRCULATION | 202 | - 2.33 | <0.010 | Downregulated |
| TGAATGT MIR181A MIR181B MIR181C MIR181D | 433 | - 2.33 | <0.010 | Downregulated |
| GO REGULATION OF HEART CONTRACTION | 153 | - 2.33 | <0.010 | Downregulated |
| GO MULTICELLULAR ORGANISMAL SIGNALING | 88 | - 2.31 | <0.010 | Downregulated |
| CATTTCA MIR203 | 259 | - 2.28 | <0.010 | Downregulated |
| TTGCACT MIR130A MIR301 MIR130B | 369 | - 2.28 | <0.010 | Downregulated |
| GO REGULATION OF PHOSPHATIDYLINOSITOL 3 KINASE SIGNALING | 110 | - 2.28 | <0.010 | Downregulated |

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|---|-----|-----------|--------|---------------|
| GO MEMBRANE DEPOLARIZATION DURING ACTION POTENTIAL | 26 | - 2.27 | <0.010 | Downregulated |
| TAGCTTT MIR9 | 211 | - 2.27 | <0.010 | Downregulated |
| AAGCACA MIR218 | 347 | - 2.26 | <0.010 | Downregulated |

Name: Gene set name

Size: number of genes in set

NES: Normalized enrichment score

FDR q-val: q value corrected for multiple hypothesis testing

AA vs EA: direction of change in gene set representation in AA tumors as compared to EA tumors