**Supplemental Table 2.** **List of gene sets significantly enriched in both experimental models in response to CR.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Pathway | n genes | Z-score | P value | fdr | Z-score | P value | fdr |
|

|  |
| --- |
| YU MYC TARGETS DN |
| NOJIMA SFRP2 TARGETS DN |
| FOSTER INFLAMMATORY RESPONSE LPS UP |
| SCHLOSSER MYC AND SERUM RESPONSE SYNERGY |
| EBAUER TARGETS OF PAX3 FOXO1 FUSION UP |
| DACOSTA UV RESPONSE VIA ERCC3 UP |
| SCHLOSSER SERUM RESPONSE AUGMENTED BY MYC |
| KEGG ANTIGEN PROCESSING AND PRESENTATION |
| WAMUNYOKOLI OVARIAN CANCER LMP UP |
| MULLIGHAN MLL SIGNATURE 1 UP |
| BIOCARTA LYM PATHWAY |
| APPEL IMATINIB RESPONSE |
| REACTOME COSTIMULATION BY THE CD28 FAMILY |
| SCHUHMACHER MYC TARGETS DN |
| REACTOME MITOCHONDRIAL FATTY ACID BETA OXIDATION |
| IVANOV MUTATED IN COLON CANCER |
|  |
| MILI PSEUDOPODIA HAPTOTAXIS UP |
| KOBAYASHI EGFR SIGNALING 6HR UP |
| SCHLOSSER SERUM RESPONSE DN |
| TING SILENCED BY DICER |
| CHEN HOXA5 TARGETS 9HR UP |
| HAMAI APOPTOSIS VIA TRAIL UP |
| SHEN SMARCA2 TARGETS UP |
| WAMUNYOKOLI OVARIAN CANCER LMP DN |
| GRABARCZYK BCL11B TARGETS UP |
| KANG DOXORUBICIN RESISTANCE DN |

 |

|  |
| --- |
| 49 |
| 23 |
| 140 |
| 23 |
| 140 |
| 230 |
| 74 |
| 41 |
| 160 |
| 254 |
| 10 |
| 27 |
| 42 |
| 6 |
| 9 |
| 5 |
|  |
| 350 |
| 4 |
| 488 |
| 22 |
| 134 |
| 270 |
| 256 |
| 127 |
| 44 |
| 13 |

 |

|  |
| --- |
| 2.280 |
| 2.526 |
| 2.021 |
| 2.821 |
| 2.300 |
| 3.000 |
| 2.443 |
| 3.625 |
| 3.775 |
| 2.619 |
| 1.359 |
| 2.824 |
| 2.373 |
| 1.780 |
| 2.419 |
| 1.330 |
|  |
| -7.807 |
| -3.230 |
| -4.312 |
| -2.501 |
| -4.018 |
| -3.401 |
| -6.440 |
| -2.395 |
| -2.689 |
| -2.256 |

 |

|  |
| --- |
| 0.001 |
| 0.010 |
| 0.016 |
| 0.009 |
| 0.018 |
| 0.009 |
| 0.026 |
| 0.002 |
| 0.001 |
| 0.015 |
| 0.003 |
| 0.030 |
| 0.026 |
| 0.006 |
| 0.010 |
| 0.024 |
|  |
| 2.3E-11 |
| 9.3E-09 |
| 0.000 |
| 0.047 |
| 0.000 |
| 0.003 |
| 2.5E-10 |
| 0.031 |
| 0.016 |
| 0.002 |

 |

|  |
| --- |
| 0.037 |
| 0.130 |
| 0.174 |
| 0.129 |
| 0.183 |
| 0.126 |
| 0.219 |
| 0.039 |
| 0.031 |
| 0.173 |
| 0.056 |
| 0.235 |
| 0.218 |
| 0.095 |
| 0.136 |
| 0.213 |
|  |
| 2.5E-08 |
| 2.0E-06 |
| 0.009 |
| 0.292 |
| 0.006 |
| 0.063 |
| 1.0E-07 |
| 0.237 |
| 0.174 |
| 0.039 |

 |

|  |
| --- |
| 5.014 |
| 4.882 |
| 4.539 |
| 3.974 |
| 3.924 |
| 3.366 |
| 3.274 |
| 3.041 |
| 2.883 |
| 2.630 |
| 2.629 |
| 2.360 |
| 2.277 |
| 1.633 |
| 1.424 |
| 1.215 |
|  |
| -5.562 |
| -5.011 |
| -4.924 |
| -3.307 |
| -3.229 |
| -3.041 |
| -2.664 |
| -2.368 |
| -2.093 |
| -1.893 |

 |

|  |
| --- |
| 0.017 |
| 0.002 |
| 0.003 |
| 0.020 |
| 0.003 |
| 0.020 |
| 0.006 |
| 0.040 |
| 0.020 |
| 0.036 |
| 0.020 |
| 0.035 |
| 0.012 |
| 0.031 |
| 0.035 |
| 0.000 |
|  |
| 6.1E-09 |
| 0.031 |
| 3.4E-05 |
| 0.012 |
| 0.002 |
| 0.011 |
| 0.003 |
| 0.003 |
| 0.042 |
| 0.040 |

 |

|  |
| --- |
| 0.161 |
| 0.042 |
| 0.049 |
| 0.179 |
| 0.053 |
| 0.178 |
| 0.087 |
| 0.258 |
| 0.179 |
| 0.248 |
| 0.178 |
| 0.246 |
| 0.139 |
| 0.230 |
| 0.244 |
| 0.005 |
|  |
| 7.7E-07 |
| 0.231 |
| 0.002 |
| 0.139 |
| 0.042 |
| 0.129 |
| 0.052 |
| 0.056 |
| 0.263 |
| 0.259 |

 |

All gene sets were statistically significant with Z-score > 1.5 in either direction, p<0.05 and false discovery rate <0.3. See Materials and Methods for additional details.