**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.