

## #254500 MYELOMA, MULTIPLE

| OMIM Gene ID | HGNC  | UniProtAC |
|--------------|-------|-----------|
| 168461       | CCND1 | P24385    |
| 601837       | LIG4  | P49917    |
| 601900       | IRF4  | Q15306    |

Table 1: OMIM - UniProtAC mapping

### Legend

- N1: #input proteins associated to the significant GO term
- N2: #proteins associated to the significant GO term
- P-value: Bonferroni-corrected p-value of Fisher's exact test
- *red*: go terms not related to the input proteins
- *blue*: go terms related to the input proteins (enriched uniquely by network-based method)
- *green*: go terms ancestors of terms enriched with the standard method (enriched uniquely by network-based method)

## 1 Standard enrichment

| GO Term    | N1 | N2  | P-value    | Description                                                |
|------------|----|-----|------------|------------------------------------------------------------|
| GO:0010165 | 2  | 40  | 0.00147086 | response to X-ray                                          |
| GO:0051301 | 2  | 177 | 0.0293008  | cell division                                              |
| GO:0010212 | 2  | 188 | 0.0330604  | response to ionizing radiation                             |
| GO:0045366 | 1  | 1   | 0.0356092  | regulation of interleukin-13 biosynthetic process          |
| GO:0045368 | 1  | 1   | 0.0356092  | positive regulation of interleukin-13 biosynthetic process |
| GO:0051102 | 1  | 1   | 0.0356092  | DNA ligation involved in DNA recombination                 |

Table 2: Overrepresented GO terms with the standard enrichment

## 2 Network-based enrichment

| GO Term    | N1 | N2  | P-value    | Description                                                        |
|------------|----|-----|------------|--------------------------------------------------------------------|
| GO:0030217 | 3  | 386 | 0.0024217  | T cell differentiation                                             |
| GO:0002244 | 3  | 406 | 0.00281907 | hematopoietic progenitor cell differentiation                      |
| GO:0043369 | 2  | 28  | 0.0032046  | CD4-positive or CD8-positive, alpha-beta T cell lineage commitment |
| GO:0042113 | 3  | 431 | 0.00337401 | B cell activation                                                  |
| GO:0002360 | 2  | 38  | 0.00595869 | T cell lineage commitment                                          |
| GO:0030098 | 3  | 654 | 0.0118163  | lymphocyte differentiation                                         |
| GO:0042110 | 3  | 787 | 0.0206068  | T cell activation                                                  |
| GO:0060740 | 2  | 75  | 0.0235036  | prostate gland epithelium morphogenesis                            |
| GO:0045622 | 2  | 77  | 0.0247816  | regulation of T-helper cell differentiation                        |
| GO:0032259 | 3  | 916 | 0.0325092  | methylation                                                        |
| GO:0002521 | 3  | 929 | 0.0339146  | leukocyte differentiation                                          |
| GO:0031016 | 2  | 100 | 0.0419044  | pancreas development                                               |

Table 3: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.