

GO enrichment map of biological processes altered in prephenotype dt27J mice. mRNA expression profiling of P4 WT (n = 3) and dt27J (n = 3) DRGs. Genes were clustered based on GO term, and an enrichment map of those biological processes up-regulated (left) or down-regulated



Ryan S D et al. J Cell Biol doi:10.1083/jcb.201107096

Figure 3. Biological processes and protein complexes associated with sensitivity to elesclomol.



Blackman RK, Cheung-Ong K, Gebbia M, Proia DA, et al. (2012) Mitochondrial Electron Transport Is the Cellular Target of the Oncology Drug Elesciomol. PLoS ONE 7(1): e29798. doi:10.1371/journal.pone.0029798 http://www.plosone.org/article/info:doi/10.1371/journal.pone.0029798



Figure 4. Network of enriched GO terms derived from differentially expressed genes between schizophrenia and control using GOseq software.



Wu JQ, Wang X, Beveridge NJ, Tooney PA, et al. (2012) Transcriptome Sequencing Revealed Significant Alteration of Cortical Promoter Usage and Splicing in Schizophrenia. PLoS ONE 7(4): e36351. doi:10.1371/journal.pone.0036351 http://www.plosone.org/article/info:doi/10.1371/journal.pone.0036351



Figure 2. A network map of the enriched GO terms in the perturbed subnetworks.



Liang D, Han G, Feng X, Sun J, et al. (2012) Concerted Perturbation Observed in a Hub Network in Alzheimer's Disease. PLoS ONE 7(7): e40498. doi:10.1371/journal.pone.0040498 http://www.plosone.org/article/info:doi/10.1371/journal.pone.0040498



Autism paper, Merico et al.









a. Enrichment map of pSNV function, FDR p<0.01

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b. top-50 genes with pSNVs, RNA processing

