JFYL007vsOKYL029 Biological Process – rankScore 25 ,pval < 0.01 <-- RankScore / total number of genes --> translational termination 11 6 chaperone-mediated protein complex assembly 22 cellular response to unfolded protein 15 protein refolding 8 12 chaperone cofactor-dependent protein refolding 23 8 Golgi organization 17 ubiquitin-dependent ERAD pathway 22 18 ubiquitin-dependent protein catabolic process 10 ΑII 3077 protein N-linked glycosylation 16 DNA replication, removal of RNA primer 16 peptidyl-tyrosine dephosphorylation 10 5 50% 75% 25% 0% 100% Genes Molecular Function – rankScore 25 ,pval < 0.01 <-- RankScore total number of genes --> oxidoreductase activity, acting on the CH-CH 6 group of donors misfolded protein binding 5 copper ion binding 3 protein folding chaperone 19 GO terms thiol-dependent ubiquitin-specific protease 14 activity pyridoxal phosphate binding 20 ΑII 3077 guanyl-nucleotide exchange factor activity 24 13 protein tyrosine phosphatase activity 8 25% 50% 75% 0% 100% Genes Cellular Component – rankScore 25 ,pval < 0.01 <-- RankScore total number of genes --> peroxisomal membrane preribosome, small subunit precursor 5 perinuclear region of cytoplasm nuclear membrane 18 5 large ribosomal subunit GO terms preribosome, large subunit precursor 5 14 nuclear pore 22 9 endoplasmic reticulum membrane 23 38 24 29 peroxisome ΑII 3077 spindle pole 3 nuclear envelope 15 12 50% 25% 75% 0% 100% Genes Up (p<0.01) Up (p>0.01) Down (p>0.01) Direction Down (p<0.01)