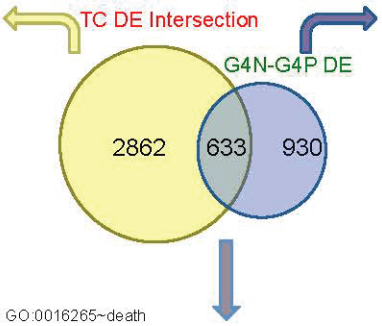
Supplementary Figure 6

1	GO:0022402~cell cycle process	4.22E-28
2	GO:0000166~nucleotide binding	2.57E-18
3	GO:0005694~chromosome	1.04E-12
4	GO:0000775~centromeric region	8.93E-11
5	GO:0015630~microtubule cytoskeleton	5.15E-10
6	GO:0005524~ATP binding	4.52E-11
7	GO:0015630~microtubule cytoskeleton	5.15E-10
8	GO:0033554~cellular response to stress	2.77E-09
9	GO:0009057~macromolecule catabolic process	1.14E-06
10	GO:0031974~membrane-enclosed lumen	3.08E-07



1	GO:0005576~extracellular region	1.90E-04
2	GO:0006954~inflammatory response	6.00E-06
3	GO:0009891~positive regulation of biosynthetic process	4.71E-07
4	GO:0006928~cell motion	2.85E-05
5	GO:0005125~cytokine activity	0.030476127
6	GO:0003924~GTPase activity	0.048559491
7	GO:0000904~cell morphogenesis involved in differentiation	3.23E-04
8	GO:0006935~chemotaxis	8.40E-05
9	GO:0042995~cell projection	0.027832105
10	GO:0051090~regulation of transcription factor activity	0.002246178

1	GO:0016265~death	2.48E-08
2	GO:0006897~endocytosis	8.47E-07
3	GO:0001817~regulation of cytokine production	8.25E-06
4	GO:0030100~regulation of endocytosis	7.68E-05
5	GO:0030695~GTPase regulator activity	1.22E-07
6	GO:0050867~positive regulation of cell activation	2.10E-09
7	GO:0043067~regulation of programmed cell death	3.51E-06
8	GO:0008092~cytoskeletal protein binding	5.87E-04
9	GO:0042325~regulation of phosphorylation	1.35E-05
10	GO:0000267~cell fraction	7.50E-04