

**Supplementary Table 3. Functional annotation for genes that were differentially expressed in EZH2-depleted cells**

Category	Term	Count	%	P Value
GOTERM_BP_AL	GO:0008219~cell death	36	7.86%	1.89E-04
GOTERM_BP_AL	GO:0016265~death	36	7.86%	1.89E-04
GOTERM_BP_AL	GO:0006915~apoptosis	34	7.42%	2.74E-04
GOTERM_BP_AL	GO:0012501~programmed cell death	34	7.42%	3.23E-04
GOTERM_BP_AL	GO:0048522~positive regulation of cellular process	40	8.73%	3.32E-04
GOTERM_BP_AL	GO:0042981~regulation of apoptosis	26	5.68%	3.67E-04
GOTERM_BP_AL	GO:0043067~regulation of programmed cell death	26	5.68%	4.36E-04
GOTERM_BP_AL	GO:0006950~response to stress	42	9.17%	4.47E-04
GOTERM_BP_AL	GO:0048518~positive regulation of biological process	42	9.17%	7.02E-04
GOTERM_BP_AL	GO:0051649~establishment of cellular localization	35	7.64%	0.001045
GOTERM_BP_AL	GO:0050794~regulation of cellular process	124	27.07%	0.001345
GOTERM_BP_AL	GO:0051641~cellular localization	35	7.64%	0.001668
GOTERM_BP_AL	GO:0046907~intracellular transport	29	6.33%	0.00228
GOTERM_BP_AL	GO:0050789~regulation of biological process	130	28.38%	0.002681
GOTERM_BP_AL	GO:0006917~induction of apoptosis	13	2.84%	0.002735
GOTERM_BP_AL	GO:0012502~induction of programmed cell death	13	2.84%	0.002829
GOTERM_BP_AL	GO:0009719~response to endogenous stimulus	19	4.15%	0.003665
GOTERM_BP_AL	GO:0008152~metabolic process	227	49.56%	0.003933
GOTERM_BP_AL	GO:0043065~positive regulation of apoptosis	14	3.06%	0.004215
GOTERM_BP_AL	GO:0043068~positive regulation of programmed cell death	14	3.06%	0.004492
GOTERM_BP_AL	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	8	1.75%	0.004962
GOTERM_BP_AL	GO:0044238~primary metabolic process	207	45.20%	0.005305
GOTERM_BP_AL	GO:0006974~response to DNA damage stimulus	16	3.49%	0.005536
GOTERM_BP_AL	GO:0009987~cellular process	303	66.16%	0.005548
GOTERM_BP_AL	GO:0048523~negative regulation of cellular process	39	8.52%	0.006037
GOTERM_BP_AL	GO:0009889~regulation of biosynthetic process	12	2.62%	0.006245
GOTERM_BP_AL	GO:0009967~positive regulation of signal transduction	10	2.18%	0.006802
GOTERM_BP_AL	GO:0048519~negative regulation of biological process	40	8.73%	0.007038
GOTERM_BP_AL	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	8	1.75%	0.007672
GOTERM_BP_AL	GO:0031326~regulation of cellular biosynthetic process	11	2.40%	0.009143
GOTERM_BP_AL	GO:0043283~biopolymer metabolic process	140	30.57%	0.009472
GOTERM_BP_AL	GO:0048468~cell development	41	8.95%	0.009911
GOTERM_BP_AL	GO:0065007~biological regulation	137	29.91%	0.010043
GOTERM_BP_AL	GO:0043170~macromolecule metabolic process	181	39.52%	0.011299
GOTERM_BP_AL	GO:0044237~cellular metabolic process	204	44.54%	0.011486
GOTERM_BP_AL	GO:0043627~response to estrogen stimulus	4	0.87%	0.011927
GOTERM_BP_AL	GO:0044248~cellular catabolic process	23	5.02%	0.012718
GOTERM_BP_AL	GO:0006396~RNA processing	19	4.15%	0.012909
GOTERM_BP_AL	GO:0045184~establishment of protein localization	27	5.90%	0.013775
GOTERM_BP_AL	GO:0010467~gene expression	100	21.83%	0.013859
GOTERM_BP_AL	GO:0022613~ribonucleoprotein complex biogenesis and assembly	11	2.40%	0.01456
GOTERM_BP_AL	GO:0016070~RNA metabolic process	84	18.34%	0.014865
GOTERM_BP_AL	GO:0008104~protein localization	28	6.11%	0.01577
GOTERM_BP_AL	GO:0006886~intracellular protein transport	17	3.71%	0.017902
GOTERM_BP_AL	GO:0006979~response to oxidative stress	7	1.53%	0.019261
GOTERM_BP_AL	GO:0016043~cellular component organization and biogenesis	76	16.59%	0.019942
GOTERM_BP_AL	GO:0015031~protein transport	25	5.46%	0.020591
GOTERM_BP_AL	GO:0006996~organelle organization and biogenesis	38	8.30%	0.021843
GOTERM_BP_AL	GO:0044265~cellular macromolecule catabolic process	15	3.28%	0.024294
GOTERM_BP_AL	GO:0042221~response to chemical stimulus	22	4.80%	0.027038
GOTERM_BP_AL	GO:0007243~protein kinase cascade	16	3.49%	0.028014
GOTERM_BP_AL	GO:0009966~regulation of signal transduction	21	4.59%	0.029045
GOTERM_BP_AL	GO:0051098~regulation of binding	4	0.87%	0.030125
GOTERM_BP_AL	GO:0009059~macromolecule biosynthetic process	30	6.55%	0.03034
GOTERM_BP_AL	GO:0033036~macromolecule localization	28	6.11%	0.03134
GOTERM_BP_AL	GO:0007249~I-kappaB kinase/NF-kappaB cascade	8	1.75%	0.031904
GOTERM_BP_AL	GO:0030154~cell differentiation	53	11.57%	0.033051
GOTERM_BP_AL	GO:0048869~cellular developmental process	53	11.57%	0.033051
GOTERM_BP_AL	GO:0006281~DNA repair	12	2.62%	0.03452

GOTERM_BP_AL\GO:0006417~regulation of translation	9	1.97%	0.038851
GOTERM_BP_AL\GO:0043285~biopolymer catabolic process	14	3.06%	0.04016
GOTERM_BP_AL\GO:0051179~localization	84	18.34%	0.04124
GOTERM_BP_AL\GO:0006613~cotranslational protein targeting to membrane	3	0.66%	0.04197
GOTERM_BP_AL\GO:0022618~protein-RNA complex assembly	7	1.53%	0.043078
GOTERM_BP_AL\GO:0010039~response to iron ion	2	0.44%	0.043528
GOTERM_BP_AL\GO:0051128~regulation of cellular component organization and biogenesis	6	1.31%	0.046515
GOTERM_BP_AL\GO:0048545~response to steroid hormone stimulus	4	0.87%	0.047327