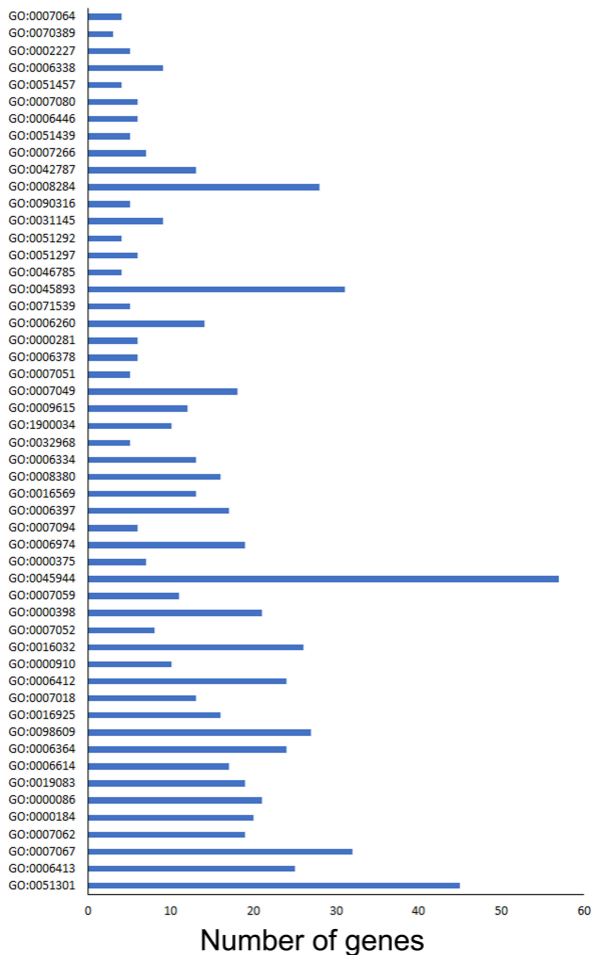


Supplementary Figure 13



Supplementary Figure 14

Supplementary Table 10. Dysregulated pathways identified in tumors induced by *SMC1A* wild-type with $p < 0.01$.

Pathway Description	P-value
GO:0006695~cholesterol biosynthetic process	1,50E-08
GO:0006364~rRNA processing	5,00E-06
GO:0008299~isoprenoid biosynthetic process	9,00E-06
GO:0001568~blood vessel development	1,00E-04
GO:0008283~cell proliferation	1,60E-04
GO:0007155~cell adhesion	2,00E-04
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	3,70E-04
GO:0006418~tRNA aminoacylation for protein translation	9,20E-04
GO:0006260~DNA replication	1,40E-03
GO:0046777~protein autophosphorylation	1,50E-03
GO:0006366~transcription from RNA polymerase II promoter	1,50E-03
GO:0008610~lipid biosynthetic process	1,80E-03
GO:0045893~positive regulation of transcription DNA-templated	2,90E-03
GO:0007005~mitochondrion organization	3,50E-03
GO:0032869~cellular response to insulin stimulus	3,50E-03
GO:0050900~leukocyte migration	3,50E-03
GO:0035329~hippo signaling	3,90E-03
GO:0000079~regulation of cyclin-dependent protein serine/threonine kinase activity	4,20E-03
GO:0009636~response to toxic substance	6,70E-03
GO:0000082~G1/S transition of mitotic cell cycle	7,50E-03
GO:0051216~cartilage development	8,80E-03
GO:0009267~cellular response to starvation	1,10E-02
GO:2000505~regulation of energy homeostasis	1,10E-02
GO:0048286~lung alveolus development	1,10E-02
GO:0009168~purine ribonucleoside monophosphate biosynthetic process	1,30E-02
GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway	1,40E-02
GO:0071504~cellular response to heparin	1,50E-02
GO:0008033~tRNA processing	1,50E-02

Supplementary Table 11. Dysregulated pathways identified in tumors induced by *SMC1A* c.A2027G with $p < 0.01$.

Pathway Description	P-value
GO:0051301~cell division	1,30E-13
GO:0006413~translational initiation	5,40E-11
GO:0007067~mitotic nuclear division	6,60E-10
GO:0007062~sister chromatid cohesion	1,50E-08
GO:0000184~nuclear-transcribed mRNA catabolic process nonsense-mediated decay	2,70E-08
GO:0000086~G2/M transition of mitotic cell cycle	5,50E-08
GO:0019083~viral transcription	5,60E-08
GO:0006614~SRP-dependent cotranslational protein targeting to membrane	1,40E-07
GO:0006364~rRNA processing	1,60E-06
GO:0098609~cell-cell adhesion	3,00E-06
GO:0016925~protein sumoylation	1,30E-05
GO:0007018~microtubule-based movement	2,20E-05
GO:0006412~translation	2,60E-05
GO:0000910~cytokinesis	3,40E-05
GO:0016032~viral process	4,80E-05
GO:0007052~mitotic spindle organization	6,00E-05
GO:0000398~mRNA splicing via spliceosome	9,80E-05
GO:0007059~chromosome segregation	1,10E-04
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	1,70E-04
GO:0000375~RNA splicing via transesterification reactions	1,70E-04
GO:0006974~cellular response to DNA damage stimulus	3,50E-04
GO:0007094~mitotic spindle assembly checkpoint	5,00E-04
GO:0006397~mRNA processing	5,20E-04
GO:0016569~covalent chromatin modification	5,60E-04
GO:0008380~RNA splicing	6,80E-04
GO:0006334~nucleosome assembly	8,80E-04
GO:0032968~positive regulation of transcription elongation from RNA polymerase II promoter	1,10E-03
GO:1900034~regulation of cellular response to heat	1,10E-03
GO:0009615~response to virus	1,50E-03
GO:0007049~cell cycle	1,50E-03
GO:0007051~spindle organization	1,90E-03
GO:0006378~mRNA polyadenylation	2,50E-03
GO:0000281~mitotic cytokinesis	2,90E-03
GO:0006260~DNA replication	3,00E-03
GO:0071539~protein localization to centrosome	3,00E-03
GO:0045893~positive regulation of transcription DNA-templated	4,10E-03
GO:0046785~microtubule polymerization	4,20E-03
GO:0051297~centrosome organization	4,80E-03

GO:0051292~nuclear pore complex assembly	5,30E-03
GO:0031145~anaphase-promoting complex-dependent catabolic process	6,00E-03
GO:0090316~positive regulation of intracellular protein transport	6,40E-03
GO:0008284~positive regulation of cell proliferation	6,70E-03
GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	7,10E-03
GO:0007266~Rho protein signal transduction	7,40E-03
GO:0051439~regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	7,50E-03
GO:0006446~regulation of translational initiation	7,70E-03
GO:0007080~mitotic metaphase plate congression	8,60E-03
GO:0051457~maintenance of protein location in nucleus	9,20E-03
GO:0006338~chromatin remodeling	9,90E-03
GO:0002227~innate immune response in mucosa	1,00E-02
GO:0070389~chaperone cofactor-dependent protein refolding	1,10E-02
GO:0007064~mitotic sister chromatid cohesion	1,10E-02