

<i>adgrl3.1</i> -/- vs WT	<i>adgrl3.1</i> -/- + ATO vs WT
Cluster 1 Score 26.89 NACHT nucleoside triphosphatase Domain: NACHT SMO1288 Leucine-rich repeat SP1a/Ryanodine receptor SPRY Butyrophyrin-like B30.2/SPRY domain SPRY DOMAIN: B30.2/SPRY domain P-loop containing nucleoside triphosphate hydrolase Intracellular signal transduction PRY Concanavalin A-like lection/ glucanase subgroup	Cluster 1 Score 25.05 NACHT nucleoside triphosphatase Domain: NACHT SMO1288 Leucine-rich repeat SP1a/Ryanodine receptor SPRY Butyrophylin-like P-loop containing nucleoside triphosphate hydrolase SPRY-associated B30.2/SPRY domain Intracellular signal transduction SPRY PRY Concanavalin A-like lectin/glucanase subgroup
Cluster 2 score 5.7 DOMAIN:C2H2-type Zinc finger C2H2-type/integrase DNA-binding domain ZnF-C2H2 RNA polymerase II transcription factor activity, sequence-specific DNA binding Zinc finger RNA polymerase II core promoter proximal region sequence-specific DNA binding Zinc Regulation of transcription from RNA polymerase II promoter Metal-binding Regulation of transcription, DNA-templated Metal ion binding	Cluster 2 Score 5.37 DOMAIN:C2H2-type Zinc finger C2H2-type/integrase DNA-binding domain ZnF C2H2 RNA polymerase II transcription factor activity, sequence-specific DNA binding RNA polymerase II regulatory region sequence-specific DNA binding Zinc-finger RNA polymerase II core promoter proximal region sequence-specific DNA binding Regulation of transcription from RNA polymerase II promoter Zinc Metal-binding Regulation of transcription, DNA-templated Metal ion binding
Cluster 3 Score 2.86 Death-like domain DAPIN domain Domain: Pyrin SMO1289	Cluster 3 Score 3.99 Death-like domain DAPIN domain Domain: Pyrin SMO1289
Cluster 4 Score 2.64 Pentose and glucuronate interconversions Drug metabolism – cytochrome P450 Retinal metabolism Metabolism of xenobiotics by cytochrome P450 Steroid hormone biosynthesis Drug metabolism – other enzymes Porphyrin domain Domain: UDPGT glucuronosyltransferase activity Ascorbate and aldarate metabolism UDP-glucuronosyl/UDP-glucosyltransferase UDP-glycosyltransferase activity Glycosyltransferase Biosynthesis of cofactors Transferase activity, transferring glycosyl groups	Cluster 4 Score 2.65 hyaluronic acid binding Link DOMAIN:Link LINK C-type lectin fold C-type lectin-like Skeletal system development Central nervous system development Extracellular matrix Cell adhesion IGv Cluster 5 Score 2.4 CAAX prenyl protease 1 DOMAIN:Peptidase_M48_N CAAX-box protein processing
Cluster 5 score 2.56 Domain: IG Immunoglobulin subtype IG Immunoglobulin-like fold Immunoglobulin V-set Domain: Ig-like Immunoglobulin-like domain	Cluster 6 Score 2.01 Secreted Extracellular region Extracellular space Cluster 7 Score 1.76 Immunoglobulin subtype Immunoglobulin V-set IG Immunoglobulin-like fold Immunoglobulin-like domain DOMAIN:Ig-like
Cluster 6 Sc.re 2.43 CAAX pernyl protease 1 Domain: Peptidase M48 N CAAX-box protein processing	Cluster 8 Score 1.38 Necroptosis C-type lectin receptor signalling pathway Herpes simplex virus 1 infection NOD-like receptor signalling pathway Toll-like receptor signalling pathway Cluster 9 Score 1.34 Interleukin-1 processing Signalling by interleukins Interleukin-1 family signalling