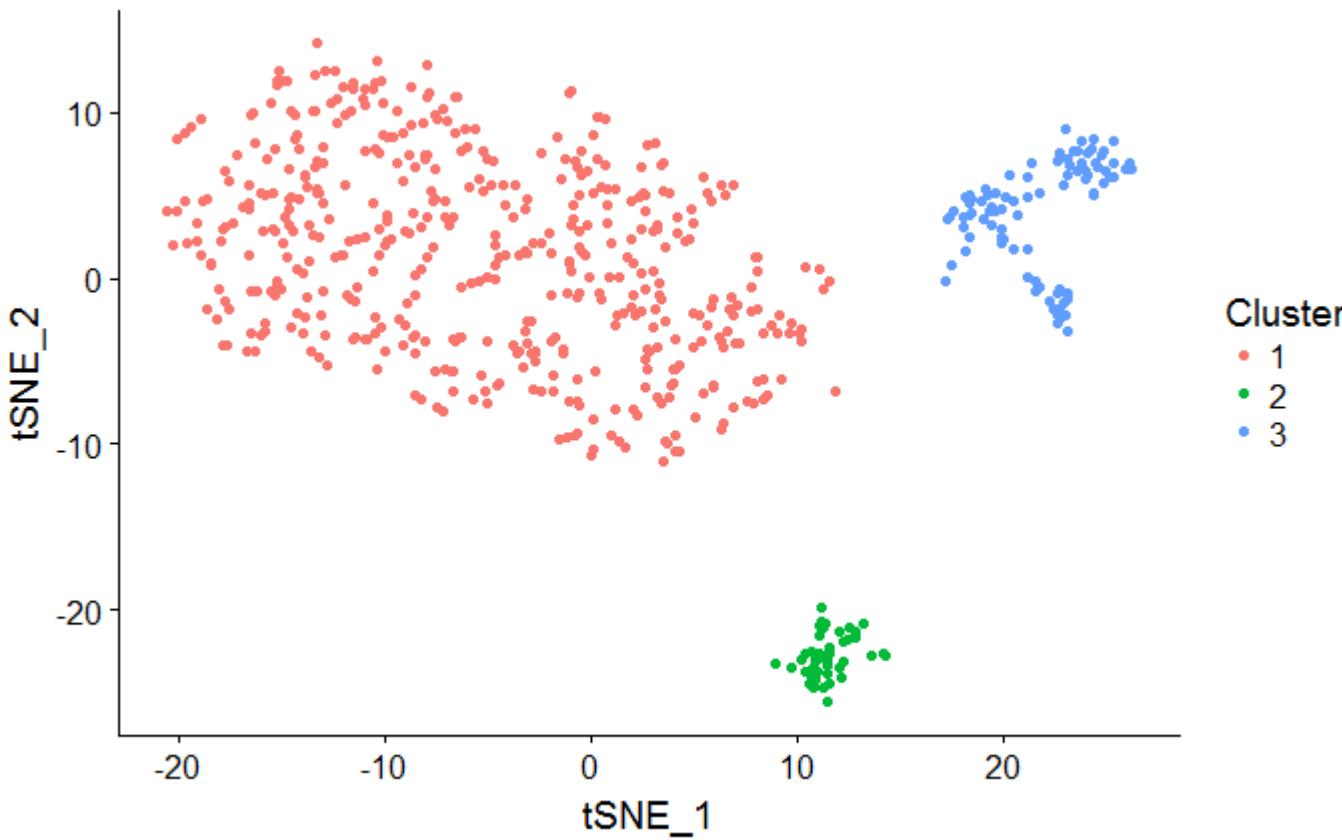


PBMCs Clustering and GO Analysis

Overview

1. Ran tSNE on CD19+ Cells
2. Assigned Cluster Numbers to Each Cell
3. Ran sPLS-DA and PLS-DA using mixOmics and ropls
4. Found highest gene loading values that separated each component
5. Ran GO analysis on variable genes in BiNGO and DAVID
6. Filtered out BiNGO results that matched both component go analyses
7. Created treemaps for both components using filtered BiNGO results
8. Plotted expression distribution based on cluster for AHR, LCK, & CD27

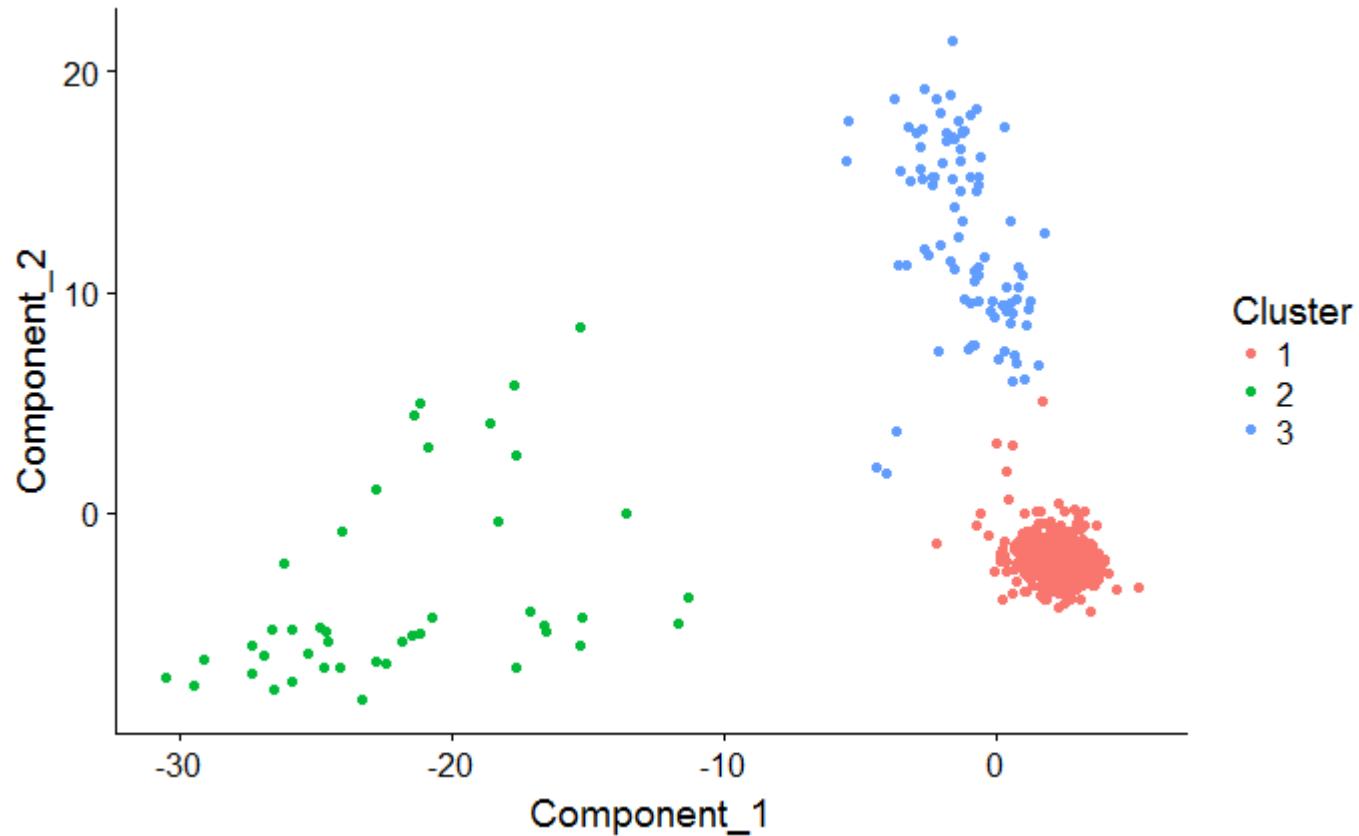
Original tSNE Clustering



tSNE → sPLS-DA (mixOmics)

- tSNE results were used in sPLS-DA supervised clustering of cells
- The gene loading values were found from each gene using mixOmics package
- Loading value vector obtained are assumed to be the diagonal elements of the diagonalizable matrix U^T , and each element is considered an eigenvalue

sPLS-DA Cell Variates



Variable Genes- Comp 1

Decreasing Variation →										
RP11-1143G9.4	FGL2	LST1	PLBD1	TGFBI	CD33	RAB32	NCF2	CSF3R	TIMP2	
CSTA	S100A11	LGALS1	CPVL	TNFSF13B	MGST1	NEAT1	PILRA	KLF4	IFITM3	
AIF1	FCER1G	MS4A6A	MS4A1	KCTD12	IGHD	GIMAP4	CXCL8	CDA	STXBP2	
TYROBP	FCN1	CFP	LGALS3	CLEC12A	SAMHD1	S100A10	FTH1	LILRB2	C4orf48	
CD79A	LGALS2	CD14	CD302	CD37	CD36	IGSF6	VIM	TIMP1	CTSD	
CST3	SRGN	S100A8	PLAUR	BLVRB	FTL	RBP7	SULT1A1	ANXA2	LRP1	
LYZ	S100A12	S100A9	CD68	CFD	CD74	TSPO	RETN	CTD-3252C9.4	ETS2	
CD79B	CLEC7A	SERPINA1	IGHM	IFI30	TNFAIP2	TMSB4X	CD93	GSTP1	LINC01272	
MNDA	S100A6	FYB	ID2	TYMP	IL1B	C10orf54	JAML	LILRA5	RPS5	
VCAN	S100A4	ANXA1	RPS27	CEBPD	HCST	CD300LF	RPL18A	RPL23A	DUSP6	

Variation decreases more across each column than within each row

Variable Genes- Comp 2

Decreasing Variation →									
CD3E	HLA-DQB1	LCK	CTSW	CD96	LEPROTL1	DGKZ	RORA	SH2D1A	TMEM204
HLA-DRA	IL32	TRBC1	HLA-DQA1	RGCC	LDLRAP1	DNAJB1	DUSP2	RGS10	OPTN
HLA-DRB1	IL7R	CD79A	MS4A1	CD37	IGHM	GATA3	FAM102A	SARAF	CD6
TRAC	FYB	LEF1	LINC00861	HLA-DMA	B2M	PIK3IP1	TXK	RCAN3	LINC00926
CD3D	TRAT1	CD247	LDHB	TRBC2	CD8A	APBA2	RP11-291B21.2	CCL5	TNFAIP3
CD74	IFITM1	AAK1	CD8B	FLT3LG	TCF7	MEF2C	HLA-DMB	SERINC5	FKBP11
CD3G	LAT	HCST	SLFN5	TC2N	LYAR	KLRB1	ZAP70	MGAT4A	GRAP2
HLA-DPB1	GIMAP7	GZMM	RARRES3	NOSIP	NELL2	IGHD	GZMA	NGFRAP1	ATP1A1
CD7	CD2	CD79B	BCL11B	NUCB2	RGL4	PRKCH	GIMAP1	NMT2	LY86
HLA-DPA1	MAL	AQP3	TRABD2A	TNFRSF25	PIM1	EPHX2	GIMAP6	NKG7	ITM2A

Variation decreases more across each column than within each row

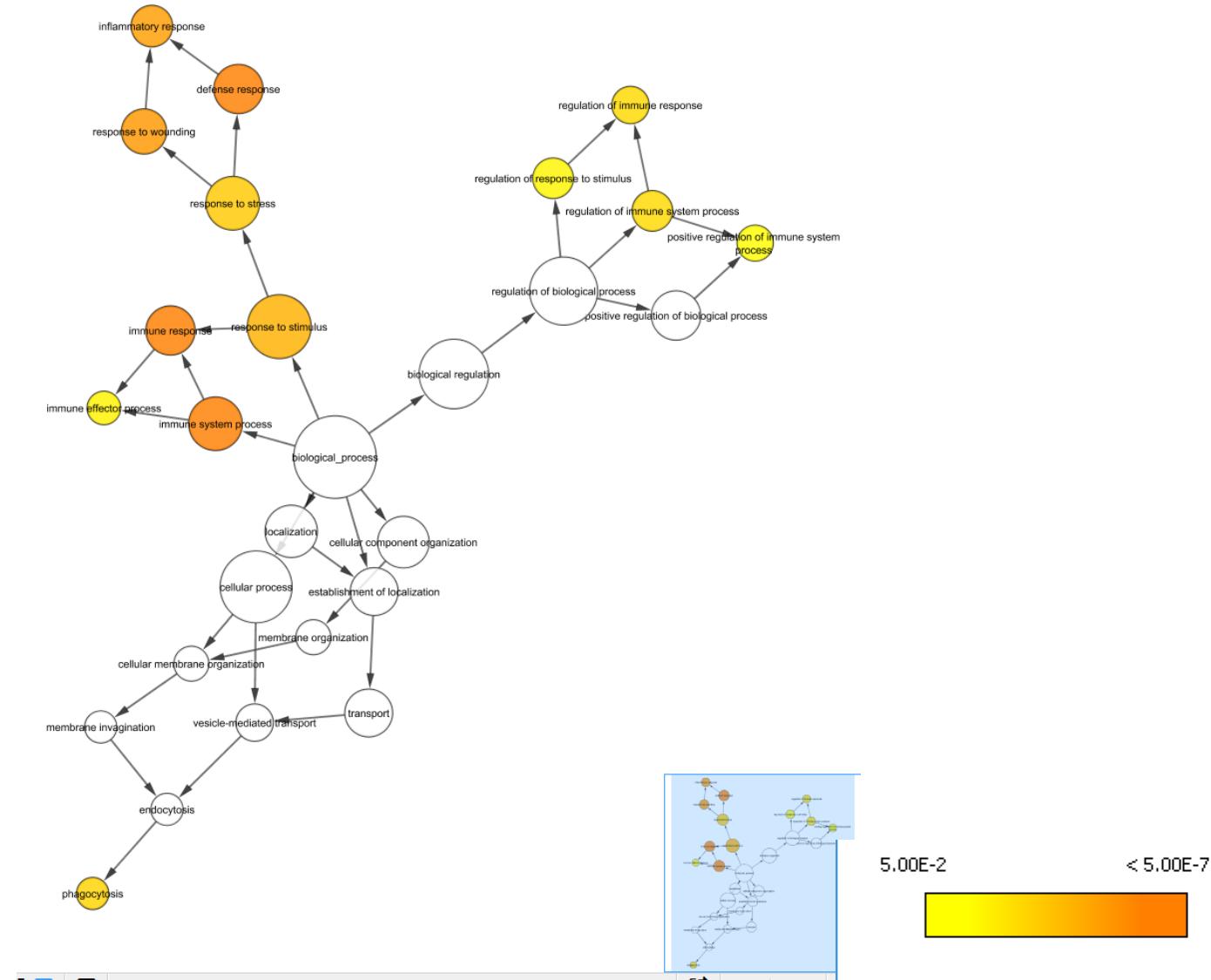
DAVID Results – Component 1

Sublist	Category	Term	# RT	Genes	Count	%<=	P-Value	Bonferroni
	GOTERM_BP_ALL	immune system process	RT	48	0.4	5.4E-17	1.5E-13	
	GOTERM_BP_ALL	immune response	RT	36	0.3	3.1E-14	8.6E-11	
	GOTERM_BP_ALL	regulation of immune system process	RT	32	0.3	1.8E-12	4.8E-9	
	GOTERM_BP_ALL	leukocyte activation	RT	24	0.2	5.4E-8	1.5E-8	
	GOTERM_BP_ALL	cell activation	RT	26	0.2	6.4E-12	1.8E-8	
	GOTERM_BP_ALL	regulation of immune response	RT	26	0.2	6.7E-12	1.8E-8	
	GOTERM_BP_ALL	defense response	RT	32	0.3	2.2E-8	5.9E-8	
	GOTERM_BP_ALL	granulocyte chemotaxis	RT	11	0.1	1.8E-10	5.0E-7	
	GOTERM_BP_ALL	granulocyte migration	RT	11	0.1	5.1E-10	1.4E-6	
	GOTERM_BP_ALL	neutrophil chemotaxis	RT	10	0.1	6.4E-10	1.8E-6	
	GOTERM_BP_ALL	positive regulation of immune system process	RT	24	0.2	8.0E-10	2.2E-6	
	GOTERM_BP_ALL	myeloid leukocyte migration	RT	12	0.1	8.5E-10	2.3E-6	
	GOTERM_BP_ALL	neutrophil migration	RT	10	0.1	1.8E-9	4.9E-6	
	GOTERM_BP_ALL	leukocyte chemotaxis	RT	12	0.1	6.9E-9	1.9E-5	
	GOTERM_BP_ALL	lymphocyte activation	RT	19	0.2	7.1E-9	2.0E-5	
	GOTERM_BP_ALL	cell chemotaxis	RT	13	0.1	9.2E-9	2.6E-5	
	GOTERM_BP_ALL	response to external stimulus	RT	33	0.3	1.1E-8	3.1E-5	
	GOTERM_BP_ALL	innate immune response	RT	21	0.2	1.3E-8	3.6E-5	
	GOTERM_BP_ALL	cell proliferation	RT	31	0.3	1.5E-8	4.1E-5	
	GOTERM_BP_ALL	phagocytosis	RT	13	0.1	2.8E-8	7.7E-5	
	GOTERM_BP_ALL	positive regulation of immune response	RT	18	0.2	1.1E-7	3.1E-4	
	GOTERM_BP_ALL	response to stimulus	RT	70	0.6	1.2E-7	3.4E-4	
	GOTERM_BP_ALL	response to bacterium	RT	16	0.1	1.8E-7	5.0E-4	
	GOTERM_BP_ALL	regulation of leukocyte activation	RT	15	0.1	1.8E-7	5.0E-4	
	GOTERM_BP_ALL	taxis	RT	16	0.1	2.3E-7	6.2E-4	
	GOTERM_BP_ALL	leukocyte proliferation	RT	12	0.1	3.0E-7	8.1E-4	
	GOTERM_BP_ALL	response to other organism	RT	19	0.2	3.3E-7	9.1E-4	
	GOTERM_BP_ALL	response to external biotic stimulus	RT	19	0.2	3.3E-7	9.1E-4	
	GOTERM_BP_ALL	regulation of cell activation	RT	15	0.1	4.2E-7	1.1E-3	
	GOTERM_BP_ALL	single organismal cell adhesion	RT	18	0.2	7.0E-7	1.9E-3	
	GOTERM_BP_ALL	response to biotic stimulus	RT	19	0.2	7.1E-7	1.9E-3	
	GOTERM_BP_ALL	single-organism localization	RT	41	0.3	9.3E-7	2.6E-3	
	GOTERM_BP_ALL	regulation of response to stimulus	RT	41	0.3	1.1E-6	3.0E-3	
	GOTERM_BP_ALL	chemotaxis	RT	15	0.1	1.3E-6	3.6E-3	
	GOTERM_BP_ALL	single organismal cell-cell adhesion	RT	17	0.1	1.3E-6	3.7E-3	
	GOTERM_BP_ALL	regulation of cell proliferation	RT	25	0.2	1.4E-6	3.8E-3	
	GOTERM_BP_ALL	positive regulation of response to stimulus	RT	29	0.2	1.4E-6	3.8E-3	
	GOTERM_BP_ALL	lymphocyte proliferation	RT	11	0.1	1.4E-6	3.9E-3	
	GOTERM_BP_ALL	response to stress	RT	41	0.3	1.5E-6	4.1E-3	

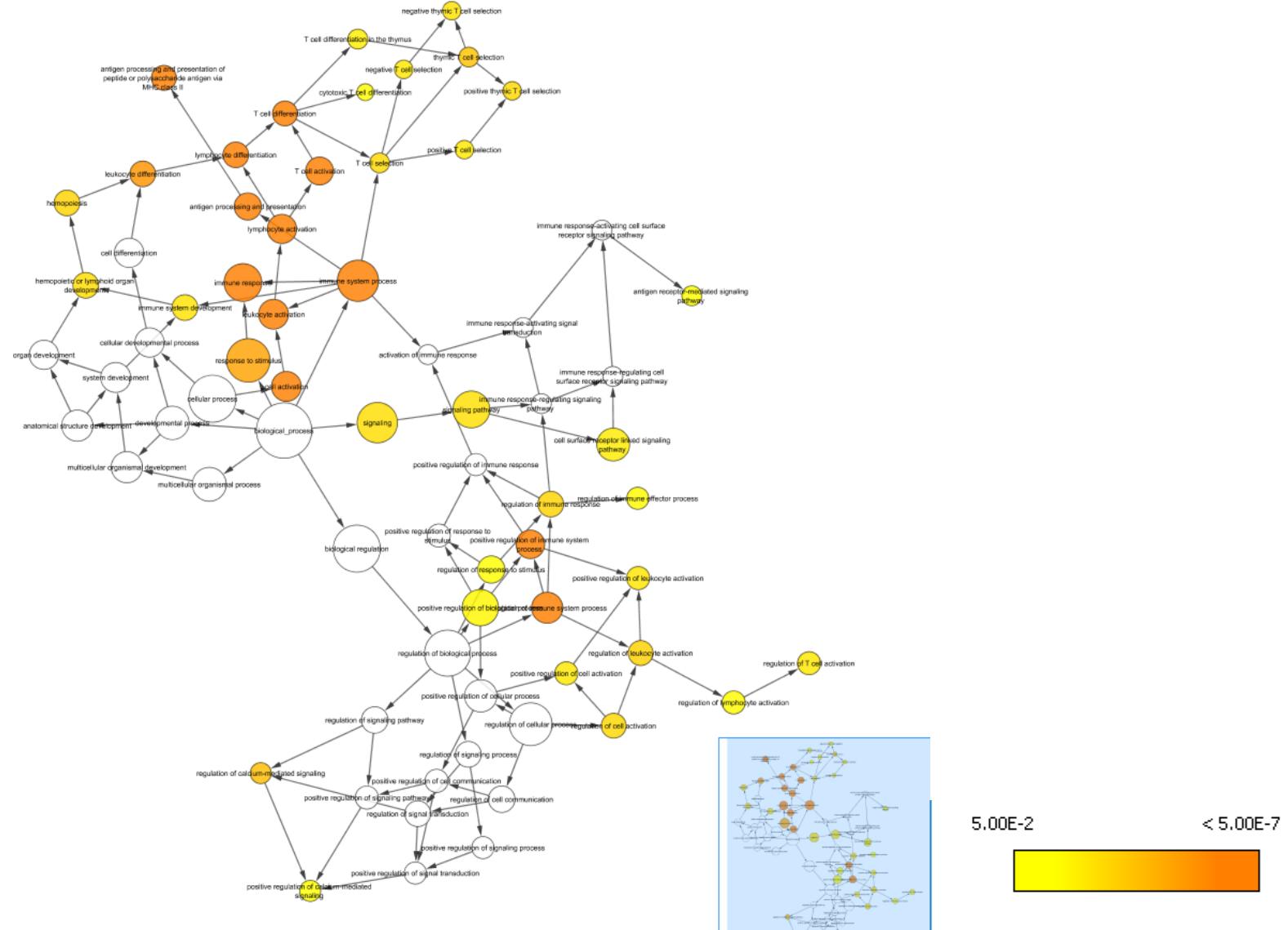
DAVID Results – Component 2

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Bonferroni
		GOTERM_BP_ALL lymphocyte activation	RT		40	40.8	2.5E- 32	6.9E-29
		GOTERM_BP_ALL immune response	RT		53	54.1	6.9E- 32	1.9E-28
		GOTERM_BP_ALL cell activation	RT		44	44.9	1.8E- 31	4.8E-28
		GOTERM_BP_ALL leukocyte activation	RT		40	40.8	7.6E- 30	2.1E-26
		GOTERM_BP_ALL immune system process	RT		59	60.2	2.9E- 28	8.0E-25
		GOTERM_BP_ALL antigen receptor-mediated signaling pathway	RT		26	26.5	1.1E- 26	3.0E-23
		GOTERM_BP_ALL regulation of immune response	RT		40	40.8	1.3E- 26	3.6E-23
		GOTERM_BP_ALL regulation of immune system process	RT		46	46.5	2.7E- 26	7.4E-23
		GOTERM_BP_ALL T cell aggregation	RT		31	31.6	9.4E- 26	2.6E-22
		GOTERM_BP_ALL T cell activation	RT		31	31.6	9.4E- 26	2.6E-22
		GOTERM_BP_ALL lymphocyte aggregation	RT		31	31.6	1.0E- 25	2.8E-22
		GOTERM_BP_ALL leukocyte aggregation	RT		31	31.6	1.6E- 25	4.3E-22
		GOTERM_BP_ALL positive regulation of immune system process	RT		39	39.8	1.2E- 24	3.3E-21
		GOTERM_BP_ALL leukocyte cell-cell adhesion	RT		31	31.6	1.6E- 24	4.3E-21
		GOTERM_BP_ALL positive regulation of leukocyte activation	RT		26	26.5	2.8E- 23	7.5E-20
		GOTERM_BP_ALL regulation of cell activation	RT		30	30.6	5.1E- 23	1.4E-19
		GOTERM_BP_ALL positive regulation of cell activation	RT		26	26.5	5.6E- 23	1.5E-19
		GOTERM_BP_ALL regulation of lymphocyte activation	RT		28	28.6	7.7E- 23	2.1E-19
		GOTERM_BP_ALL positive regulation of lymphocyte activation	RT		25	25.5	9.2E- 23	2.5E-19
		GOTERM_BP_ALL positive regulation of immune response	RT		33	33.7	1.2E- 22	3.2E-19
		GOTERM_BP_ALL regulation of leukocyte activation	RT		29	29.6	1.4E- 22	3.7E-19
		GOTERM_BP_ALL immune response-activating cell surface receptor signaling pathway	RT		26	26.5	1.6E- 21	4.5E-18
		GOTERM_BP_ALL single organismal cell-cell adhesion	RT		32	32.7	8.9E- 21	2.4E-17
		GOTERM_BP_ALL T cell receptor signaling pathway	RT		20	20.4	1.2E- 20	3.3E-17
		GOTERM_BP_ALL immune response-regulating cell surface receptor signaling pathway	RT		26	26.5	1.3E- 20	3.4E-17
		GOTERM_BP_ALL positive regulation of T cell activation	RT		21	21.1	3.8E- 20	1.1E-16
		GOTERM_BP_ALL positive regulation of cell-cell adhesion	RT		22	22.4	4.7E- 20	1.3E-16
		GOTERM_BP_ALL single organism cell adhesion	RT		32	32.7	7.1E- 20	2.0E-16
		GOTERM_BP_ALL positive regulation of leukocyte cell-cell adhesion	RT		21	21.4	8.2E- 20	2.2E-16
		GOTERM_BP_ALL regulation of cell-cell adhesion	RT		25	25.5	1.0E- 19	2.7E-16
		GOTERM_BP_ALL regulation of T cell activation	RT		23	23.5	1.1E- 19	3.1E-16
		GOTERM_BP_ALL activation of immune response	RT		28	28.6	1.5E- 19	4.1E-16
		GOTERM_BP_ALL immune response-activating signal transduction	RT		27	27.6	1.8E- 19	4.9E-16
		GOTERM_BP_ALL regulation of leukocyte cell-cell adhesion	RT		23	23.5	3.1E- 19	8.4E-16
		GOTERM_BP_ALL immune response-regulating signaling pathway	RT		27	27.6	8.7E- 19	2.4E-15
		GOTERM_BP_ALL regulation of response to stimulus	RT		58	59.2	1.3E- 18	3.7E-15
		GOTERM_BP_ALL adaptive immune response	RT		23	23.5	1.6E- 16	3.0E-13
		GOTERM_BP_ALL T cell costimulation	RT		14	14.3	2.1E- 16	6.1E-13

BiNGO Results – Component 1



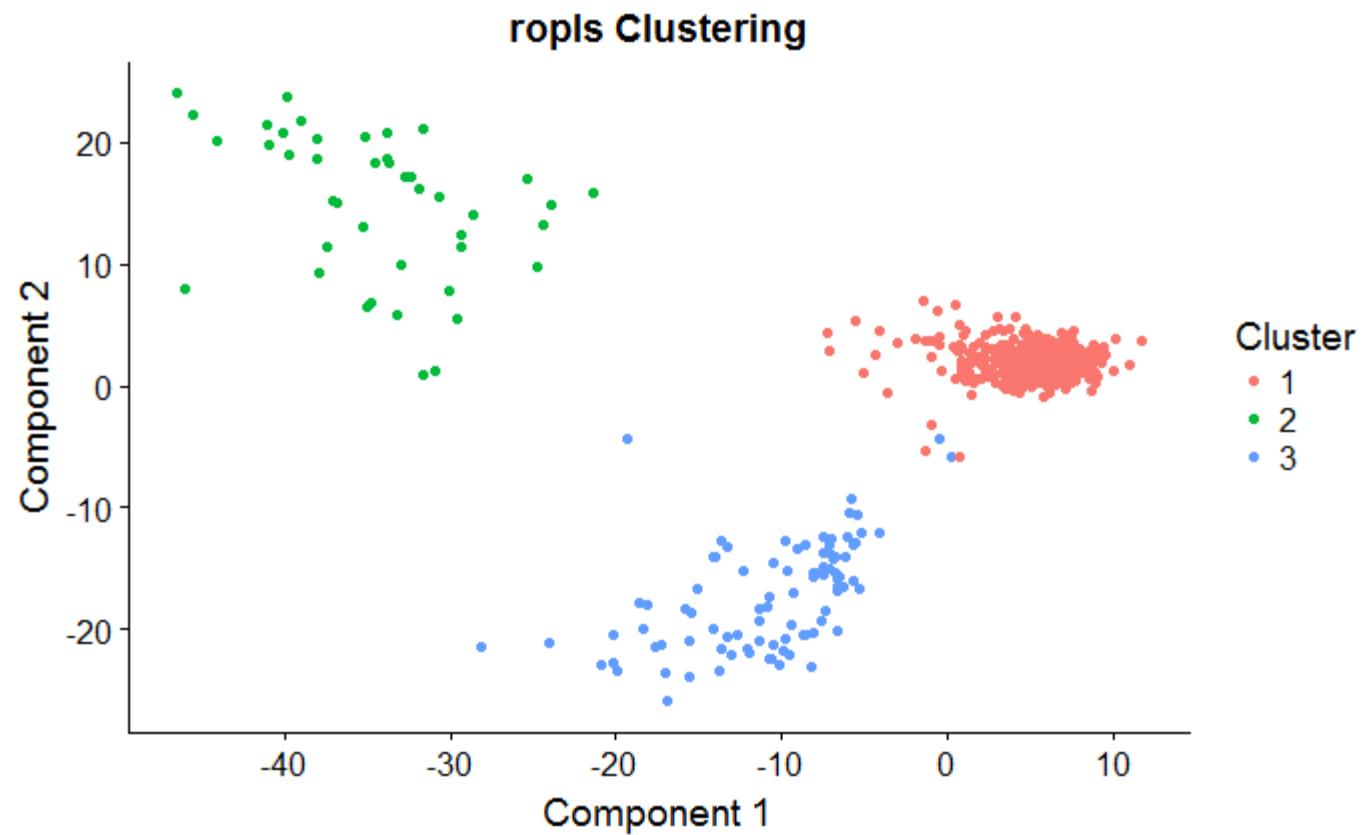
BiNGO Results – Component 2



tSNE → PLS-DA (ropls)

- tSNE results were used in PLS-DA supervised clustering of cells
- The gene loading values were found from each gene using ropls package
- Loading value vector obtained are assumed to be the diagonal elements of the diagonalizable matrix P , and each element is considered an eigenvalue

PLS-DA (ropls) Clustering



Variable Genes- Comp 1

Decreasing Variation →									
↓ Decreasing Variation ↓									
CD79A	FCER1G	S100A12	ANXA1	CD68	NEAT1	CFD	PILRA	CTD-3252C9.4	TCL1A
CD79B	CST3	IGHM	LST1	PLBD1	CEBPD	C10orf54	RPS5	RAB32	ITGB2
TYROBP	VCAN	RPS27	CFP	HCST	GIMAP4	TMSB4X	FTL	IFITM3	GSTP1
CSTA	FYB	ID2	IGHD	KCTD12	VIM	C4orf48	CD93	NCF2	STXBP2
RP11-1143G9.4	FCN1	MS4A1	S100A8	CLEC12A	TYMP	CD33	CD300LF	HLA-DQB1	HNMT
S100A11	FGL2	CLEC7A	CD74	RPL18A	TNFSF13B	MGST1	IL1B	LINC00926	CTSD
SRGN	LYZ	CD37	PLAUR	S100A10	IFI30	RBP7	IGSF6	GAPDH	JAML
S100A4	MNDA	MS4A6A	CD14	SAMHD1	CD36	TSPO	TIMP1	CXCL8	HLA-DRA
AIF1	LGALS1	LGALS3	CD302	CPVL	TGFBI	CD19	HLA-DPA1	LINC01272	KLF4
S100A6	LGALS2	SERPINA1	S100A9	BLVRB	ANXA2	HLA-DPB1	TNFAIP2	SULT1A1	LILRB2

Variation decreases more across each column than within each row

Variable Genes- Comp 2

Decreasing Variation →									
↓ Decreasing Variation									
HLA-DRA	IL7R	LEF1	CTSS	CST3	PLBD1	CD68	LYAR	EPHX2	RPL31
HLA-DRB1	HLA-DPB1	MAL	LINC00861	AQP3	FLT3LG	TYMP	CPVL	S100A12	TYROBP
CD3E	HLA-DPA1	CD247	SLFN5	CD8B	NOSIP	PIK3IP1	FGL2	RPS27	NELL2
TRAC	IFITM1	CTSW	GZMM	CD96	CD14	MS4A6A	GPX1	RBP7	RGL4
CD3D	CD2	TRBC1	CSTA	TRABD2A	IFI30	BCL11B	SERPINA1	HCST	OAZ1
CD3G	TRAT1	HLA-DQA1	TRBC2	S100A9	TNFRSF25	RPS27A	FCN1	SPI1	FCER1G
CD74	LAT	RP11-1143G9.4	RPS3	CYBA	NUCB2	LST1	MGST1	DNAJB1	PIM1
IL32	LCK	FTH1	AAK1	LGALS2	LDLRAP1	RPS29	S100A8	APBA2	GRN
HLA-DQB1	GIMAP7	FYB	LDHB	HLA-DMA	RARRES3	MALAT1	LEPROTL1	TCF7	VCAN
CD7	FTL	MNDA	CLEC7A	TC2N	CD302	LYZ	CFP	RGCC	PILRA

Variation decreases more across each column than within each row

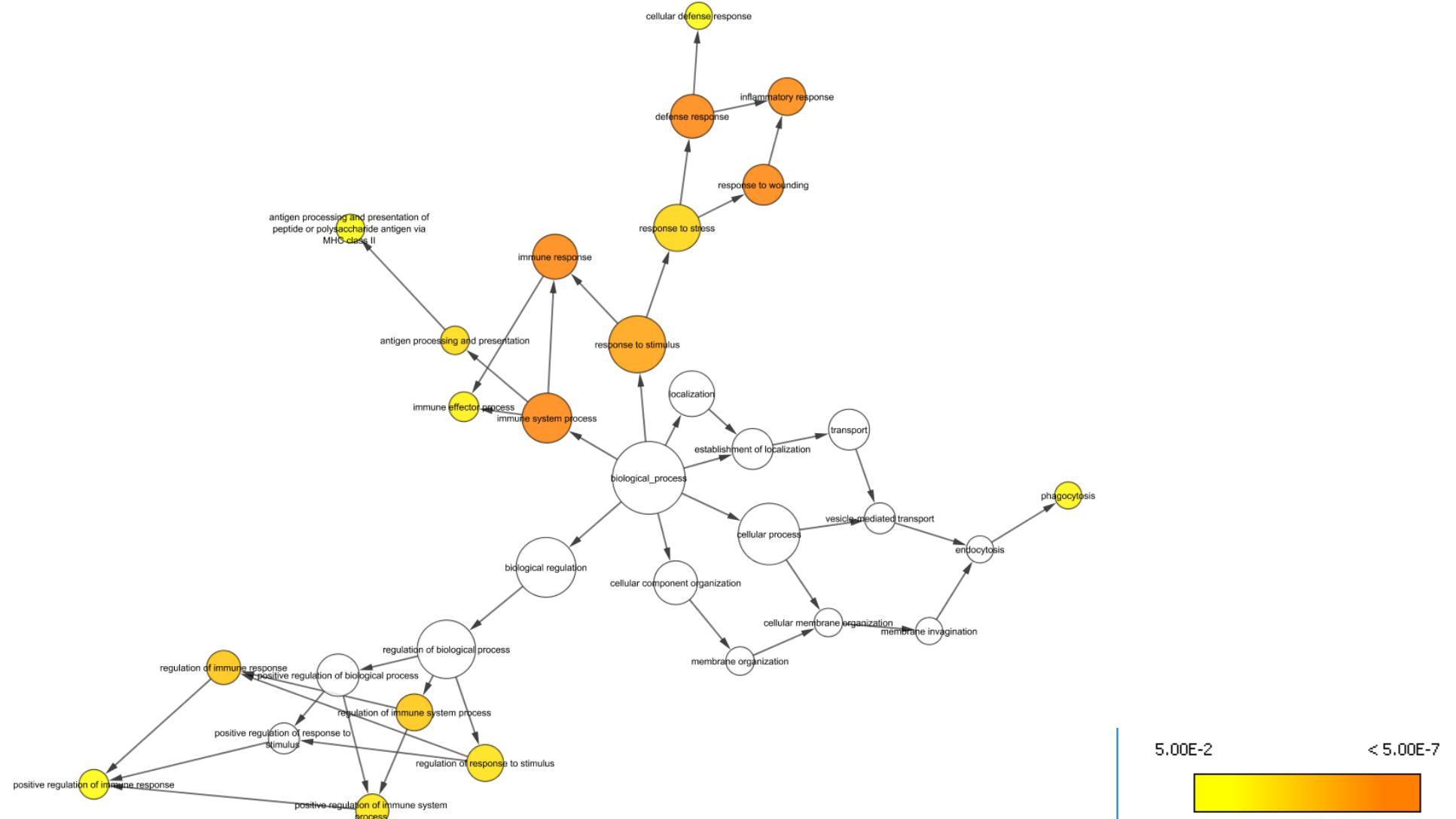
DAVID Results – Component 1

441 chart records							Download File	
Sublist	Category	Term	RT	Genes	Count	%	P-Value	Bonferroni
	GOTERM_BP_ALL	immune system process	RT		52	53.1	1.1E-20	3.0E-17
	GOTERM_BP_ALL	immune response	RT		41	41.6	8.5E-19	2.3E-15
	GOTERM_BP_ALL	regulation of immune response	RT		32	32.7	1.4E-17	3.7E-14
	GOTERM_BP_ALL	leukocyte activation	RT		29	29.6	6.3E-17	3.0E-13
	GOTERM_BP_ALL	regulation of immune system process	RT		37	37.8	6.6E-17	3.0E-13
	GOTERM_BP_ALL	cell activation	RT		31	31.6	1.2E-17	3.0E-13
	GOTERM_BP_ALL	defense response	RT		37	37.8	1.6E-15	4.2E-12
	GOTERM_BP_ALL	positive regulation of immune system process	RT		30	30.6	4.9E-15	1.4E-11
	GOTERM_BP_ALL	lymphocyte activation	RT		24	24.5	1.9E-13	5.2E-10
	GOTERM_BP_ALL	positive regulation of immune response	RT		24	24.5	6.9E-13	1.9E-9
	GOTERM_BP_ALL	innate immune response	RT		26	26.5	7.6E-13	2.1E-9
	GOTERM_BP_ALL	regulation of leukocyte activation	RT		19	19.4	3.6E-11	9.9E-8
	GOTERM_BP_ALL	activation of immune response	RT		20	20.4	6.1E-11	1.7E-7
	GOTERM_BP_ALL	single organism cell adhesion	RT		23	23.5	7.2E-11	2.0E-7
	GOTERM_BP_ALL	leukocyte cell-cell adhesion	RT		19	19.4	8.0E-11	2.2E-7
	GOTERM_BP_ALL	regulation of cell activation	RT		19	19.4	1.1E-10	3.0E-7
	GOTERM_BP_ALL	single organismal cell-cell adhesion	RT		22	22.4	3.3E-10	3.6E-7
	GOTERM_BP_ALL	granulocyte chemotaxis	RT		11	11.2	1.6E-10	4.5E-7
	GOTERM_BP_ALL	immune response-regulating signaling pathway	RT		19	19.4	2.8E-10	7.7E-7
	GOTERM_BP_ALL	regulation of lymphocyte activation	RT		17	17.3	4.3E-10	1.2E-6
	GOTERM_BP_ALL	granulocyte migration	RT		11	11.2	4.5E-10	1.2E-6
	GOTERM_BP_ALL	neutrophil chemotaxis	RT		10	10.2	5.8E-10	1.6E-6
	GOTERM_BP_ALL	myeloid leukocyte migration	RT		12	12.3	7.5E-10	2.0E-6
	GOTERM_BP_ALL	immune response-activating signal transduction	RT		18	18.4	8.6E-10	2.3E-6
	GOTERM_BP_ALL	neutrophil migration	RT		10	10.2	1.6E-9	4.4E-6
	GOTERM_BP_ALL	leukocyte aggregation	RT		17	17.3	1.8E-9	4.9E-6
	GOTERM_BP_ALL	response to stress	RT		46	46.5	2.5E-9	6.7E-6
	GOTERM_BP_ALL	immune response-regulating cell surface receptor signaling pathway	RT		16	16.3	2.6E-9	7.0E-6
	GOTERM_BP_ALL	leukocyte proliferation	RT		14	14.3	2.6E-9	7.2E-6
	GOTERM_BP_ALL	positive regulation of response to stimulus	RT		33	33.7	5.0E-9	1.4E-5
	GOTERM_BP_ALL	leukocyte chemotaxis	RT		12	12.3	6.1E-9	1.7E-5
	GOTERM_BP_ALL	immune response-activating cell surface receptor signaling pathway	RT		15	15.3	7.7E-9	2.1E-5
	GOTERM_BP_ALL	cell chemotaxis	RT		13	13.3	8.2E-9	2.2E-5
	GOTERM_BP_ALL	positive regulation of leukocyte activation	RT		14	14.3	9.4E-9	2.5E-5
	GOTERM_BP_ALL	regulation of leukocyte proliferation	RT		12	12.3	1.3E-8	3.4E-5
	GOTERM_BP_ALL	positive regulation of cell activation	RT		14	14.3	1.3E-8	3.6E-5
	GOTERM_BP_ALL	lymphocyte proliferation	RT		13	13.3	1.4E-8	3.8E-5
	GOTERM_BP_ALL	mononuclear cell proliferation	RT		13	13.3	1.5E-8	4.1E-5
	GOTERM_BP_ALL	regulation of response to stimulus	RT		44	44.9	2.2E-8	6.1E-5

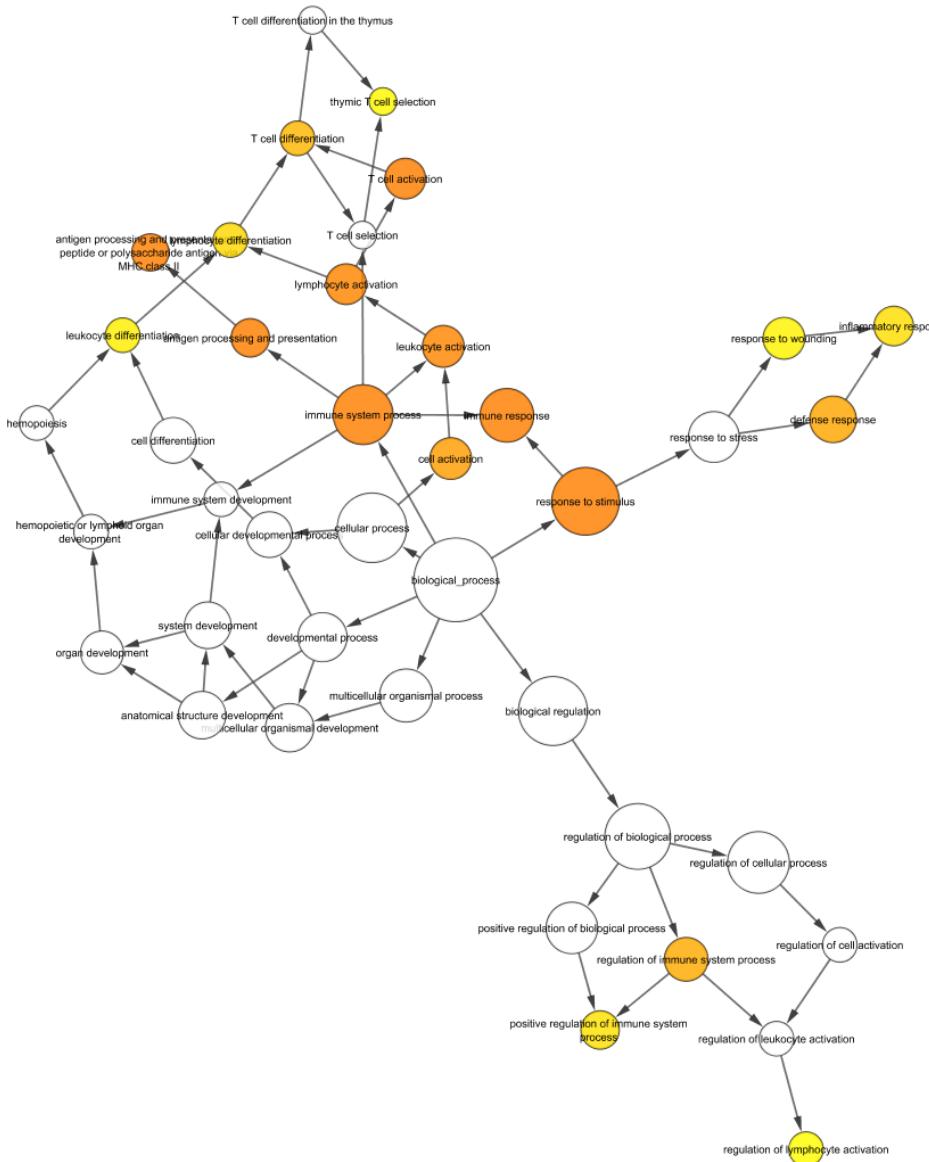
DAVID Results – Component 2

340 chart records						
Sublist	Category	Term	RT	Genes	Count	%
Download File						
		GOTERM_BP_ALL immune response	RT		47	47.5 2.3E-24 5.6E-21
		GOTERM_BP_ALL immune system process	RT		53	53.5 2.8E-21 7.0E-18
		GOTERM_BP_ALL regulation of immune system process	RT		40	40.4 1.8E-19 4.6E-16
		GOTERM_BP_ALL regulation of immune response	RT		34	34.3 2.0E-19 5.0E-16
		GOTERM_BP_ALL leukocyte aggregation	RT		26	26.3 7.0E-19 1.8E-15
		GOTERM_BP_ALL leukocyte cell-cell adhesion	RT		26	26.3 4.5E-18 1.1E-14
		GOTERM_BP_ALL leukocyte activation	RT		30	30.3 8.5E-18 2.1E-14
		GOTERM_BP_ALL cell activation	RT		32	32.3 1.9E-17 4.7E-14
		GOTERM_BP_ALL lymphocyte activation	RT		28	28.3 2.1E-17 5.6E-14
		GOTERM_BP_ALL activation of immune response	RT		26	26.3 6.5E-17 2.0E-13
		GOTERM_BP_ALL positive regulation of immune system process	RT		32	32.3 8.4E-17 2.8E-13
		GOTERM_BP_ALL T cell activation	RT		24	24.2 4.2E-17 2.8E-13
		GOTERM_BP_ALL T cell aggregation	RT		24	24.2 9.2E-17 2.8E-13
		GOTERM_BP_ALL lymphocyte aggregation	RT		24	24.2 9.7E-17 2.8E-13
		GOTERM_BP_ALL single organismal cell-cell adhesion	RT		28	28.3 4.2E-16 1.1E-12
		GOTERM_BP_ALL T cell receptor signaling pathway	RT		17	17.2 4.8E-16 1.1E-12
		GOTERM_BP_ALL immune response-activating signal transduction	RT		24	24.2 1.1E-15 2.8E-12
		GOTERM_BP_ALL positive regulation of immune response	RT		27	27.3 1.1E-15 2.8E-12
		GOTERM_BP_ALL single organism cell adhesion	RT		28	28.3 2.8E-15 7.0E-12
		GOTERM_BP_ALL antigen receptor-mediated signaling pathway	RT		18	18.2 3.9E-15 9.7E-12
		GOTERM_BP_ALL immune response-regulating signaling pathway	RT		24	24.2 4.3E-15 1.1E-11
		GOTERM_BP_ALL immune response-activating cell surface receptor signaling pathway	RT		21	21.2 4.7E-15 1.2E-11
		GOTERM_BP_ALL T cell costimulation	RT		13	13.1 1.4E-14 3.5E-11
		GOTERM_BP_ALL lymphocyte costimulation	RT		13	13.1 1.4E-14 4.0E-11
		GOTERM_BP_ALL defense response	RT		36	36.4 1.6E-14 4.1E-11
		GOTERM_BP_ALL immune response-regulating cell surface receptor signaling pathway	RT		21	21.2 2.3E-14 5.7E-11
		GOTERM_BP_ALL regulation of leukocyte activation	RT		21	21.2 4.5E-13 1.1E-9
		GOTERM_BP_ALL regulation of lymphocyte activation	RT		20	20.2 4.7E-13 1.2E-9
		GOTERM_BP_ALL positive regulation of leukocyte activation	RT		18	18.2 6.3E-13 1.6E-9
		GOTERM_BP_ALL positive regulation of cell activation	RT		18	18.2 1.0E-12 2.5E-9
		GOTERM_BP_ALL regulation of cell activation	RT		21	21.2 1.6E-12 4.0E-9
		GOTERM_BP_ALL regulation of cell-cell adhesion	RT		19	19.2 1.8E-12 4.9E-9
		GOTERM_BP_ALL positive regulation of cell-cell adhesion	RT		16	16.2 3.9E-12 9.7E-9
		GOTERM_BP_ALL regulation of T cell activation	RT		17	17.2 4.5E-12 1.1E-8
		GOTERM_BP_ALL positive regulation of T cell activation	RT		15	15.2 5.0E-12 1.5E-8
		GOTERM_BP_ALL cell-cell adhesion	RT		29	29.3 6.0E-12 1.5E-8
		GOTERM_BP_ALL regulation of leukocyte cell-cell adhesion	RT		17	17.2 9.0E-12 2.3E-8
		GOTERM_BP_ALL positive regulation of leukocyte cell-cell adhesion	RT		15	15.2 9.6E-12 2.4E-8
		GOTERM_BP_ALL positive regulation of response to stimulus	RT		37	37.4 1.6E-11 4.0E-8

BiNGO Results – Component 1

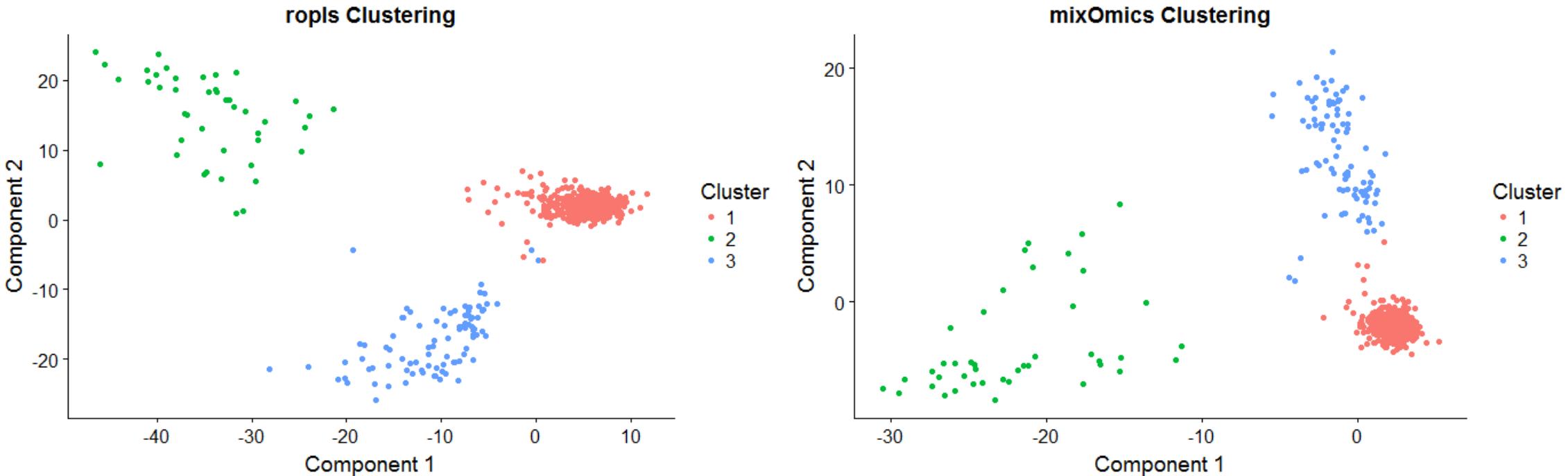


BiNGO Results – Component 2



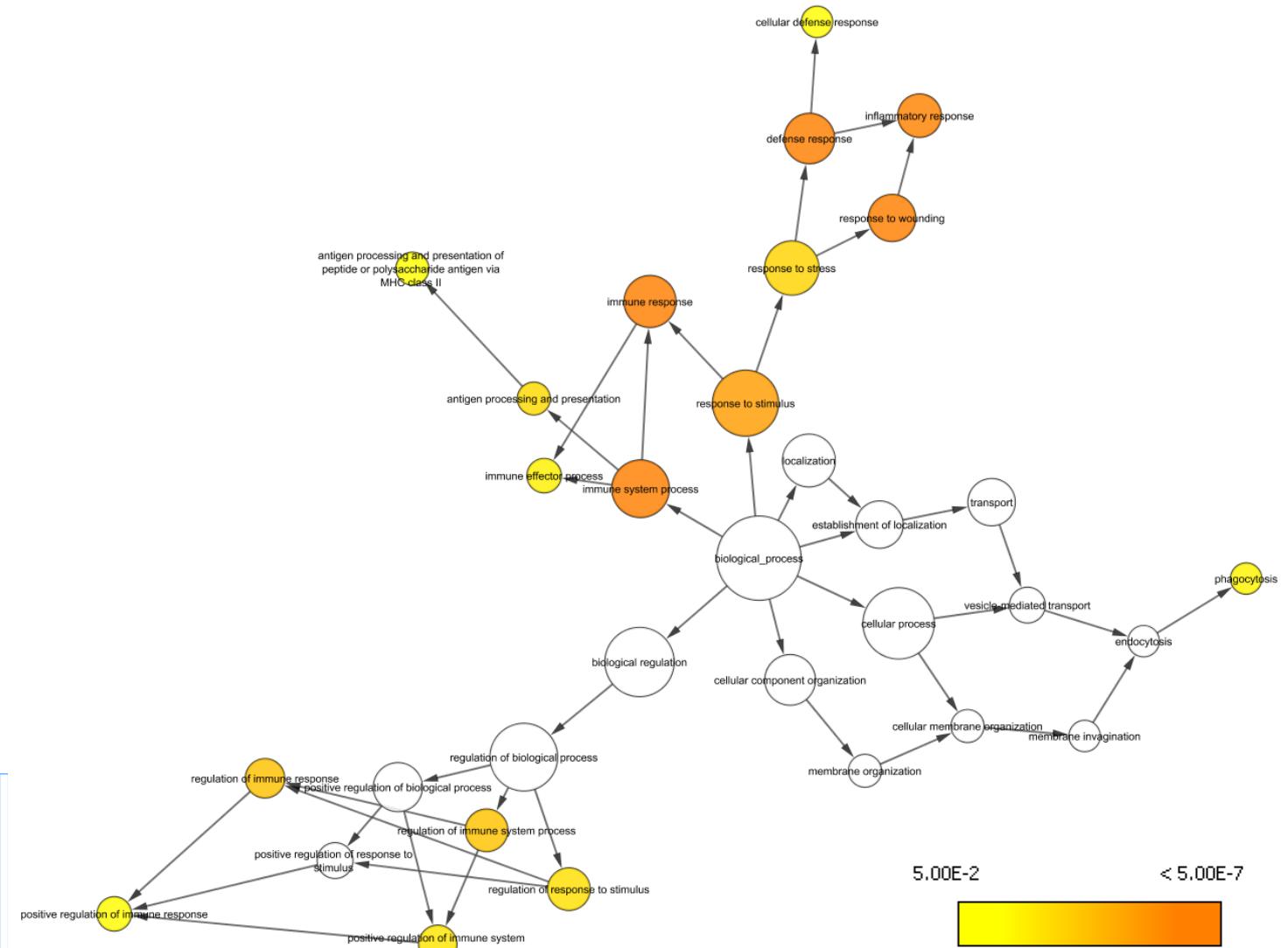
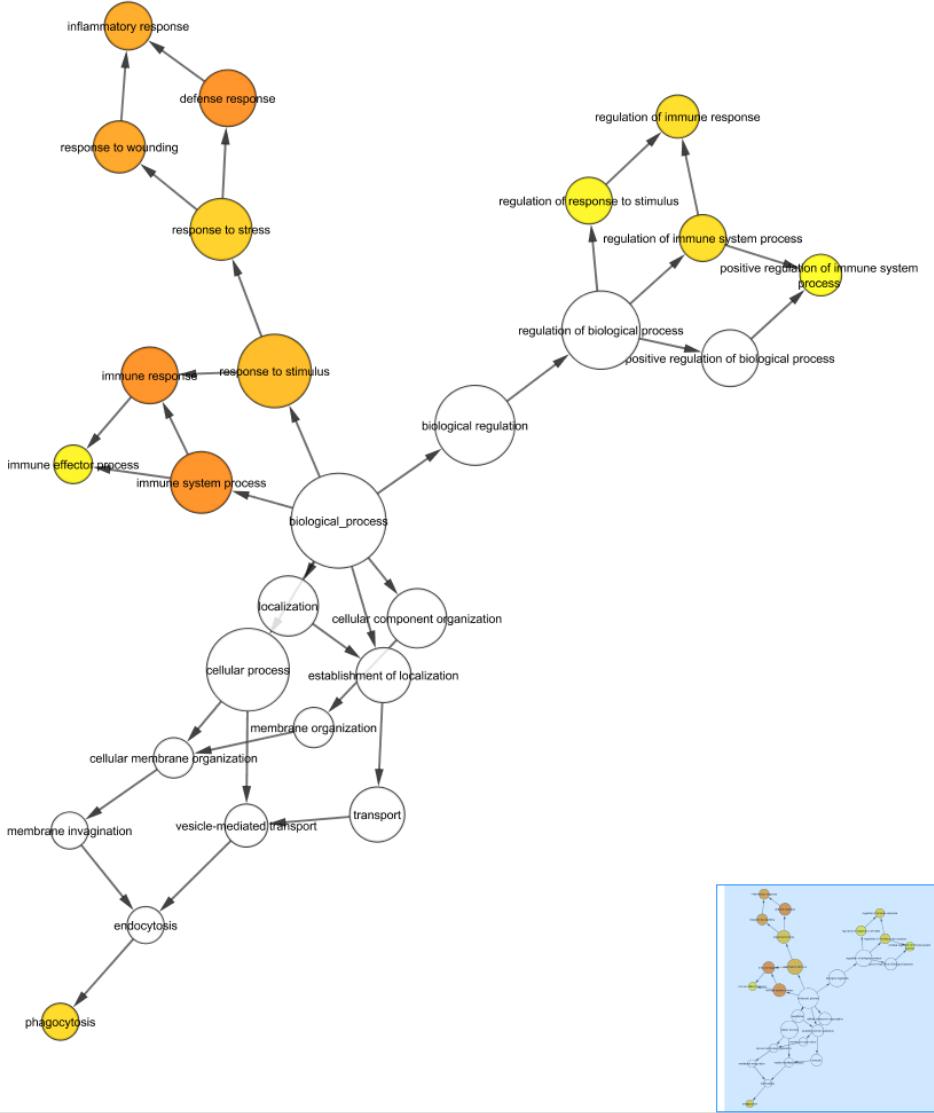
mixOmics and ropls comparison

- 90% match for variable genes along component 1
- 57% match for variable genes along component 2



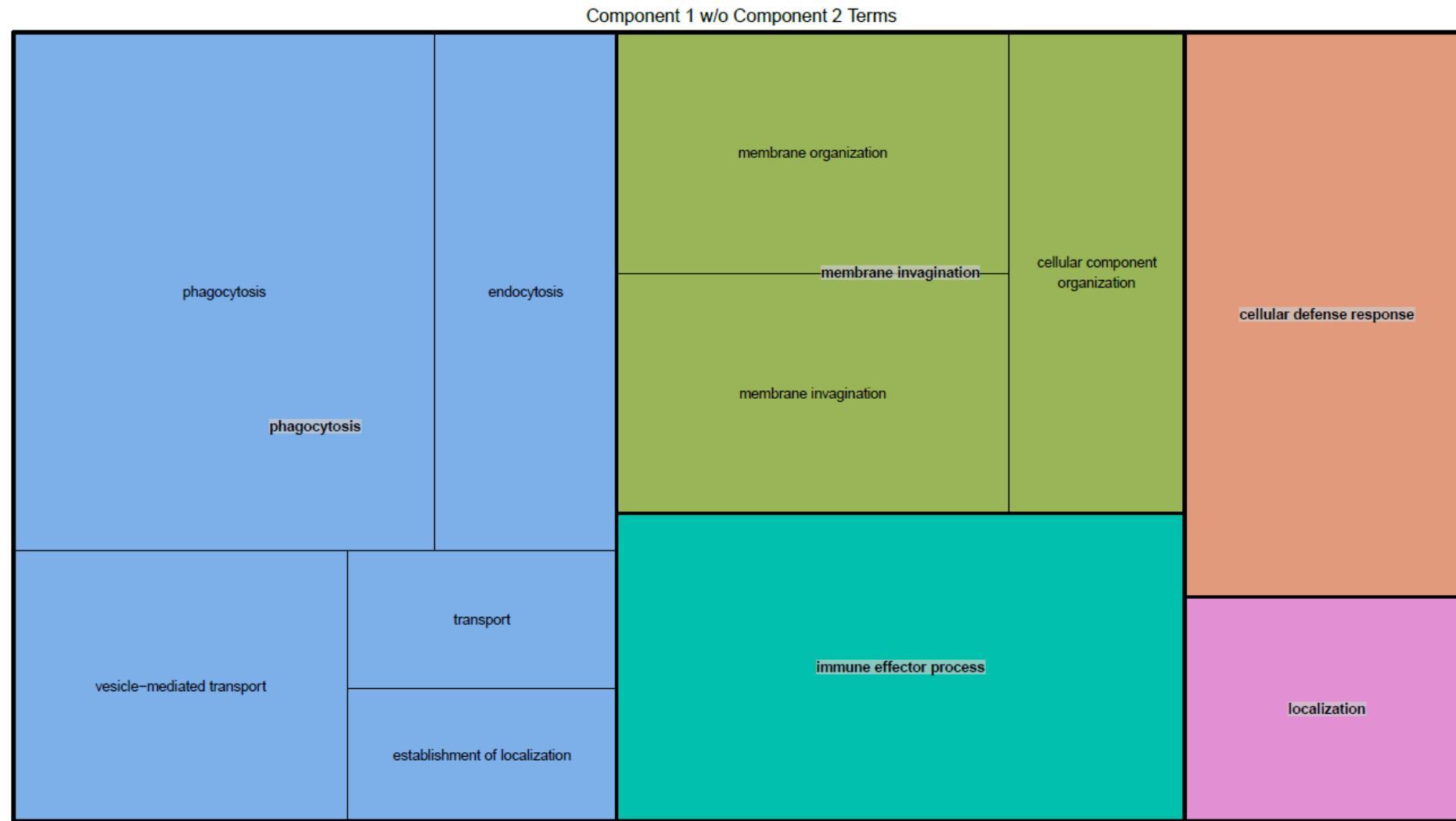
- Cluster 2 varies from Clusters 1 and 3 along the first component
- Cluster 3 negatively deviates from Clusters 1 and 2 in ropls, and positively deviates in the mixOmics clustering

BiNGO Comparison –Component 1

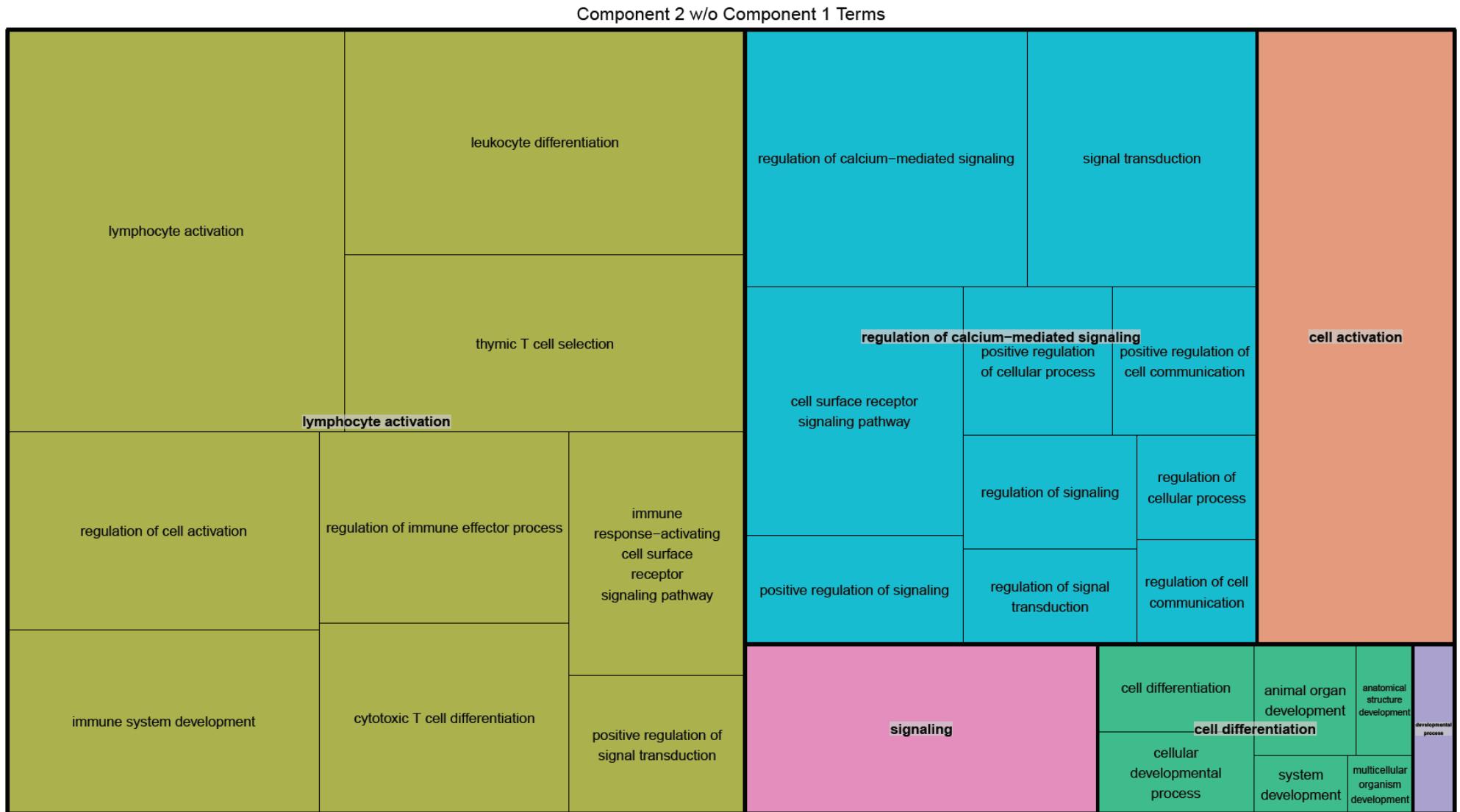


BiNGO → REVIGO: Comp 1

This treemap depicts the GO terms obtained from both component 1 axes



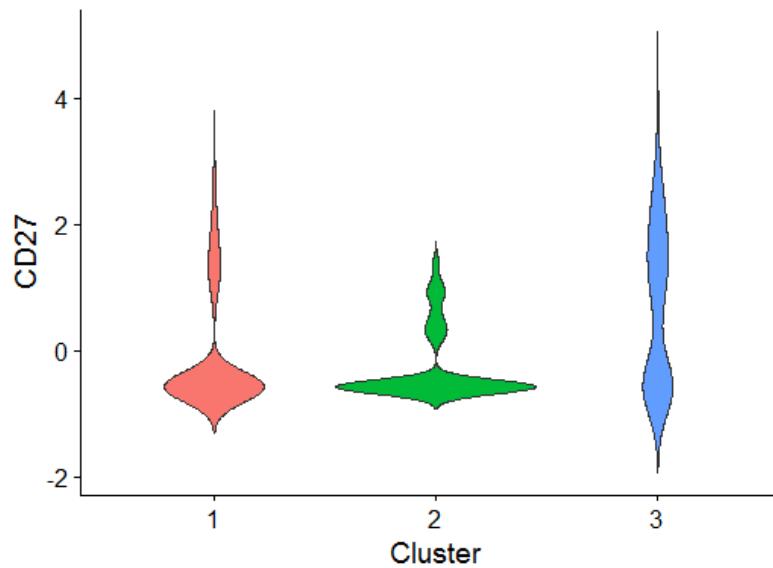
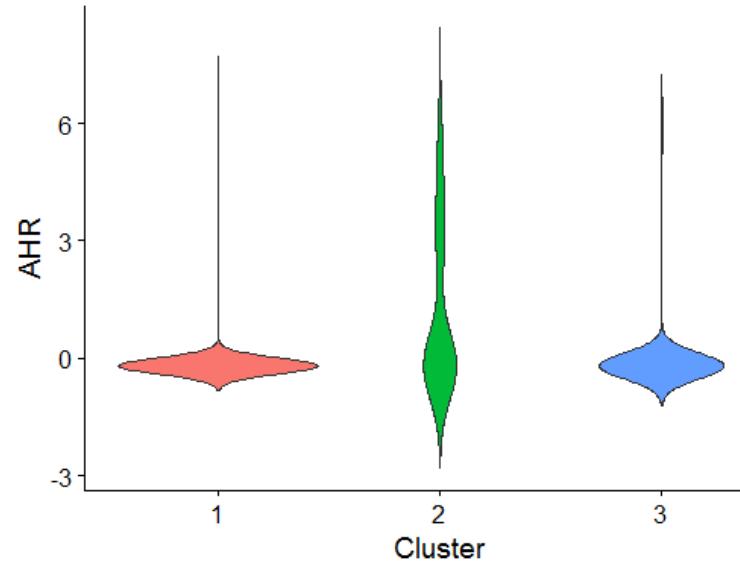
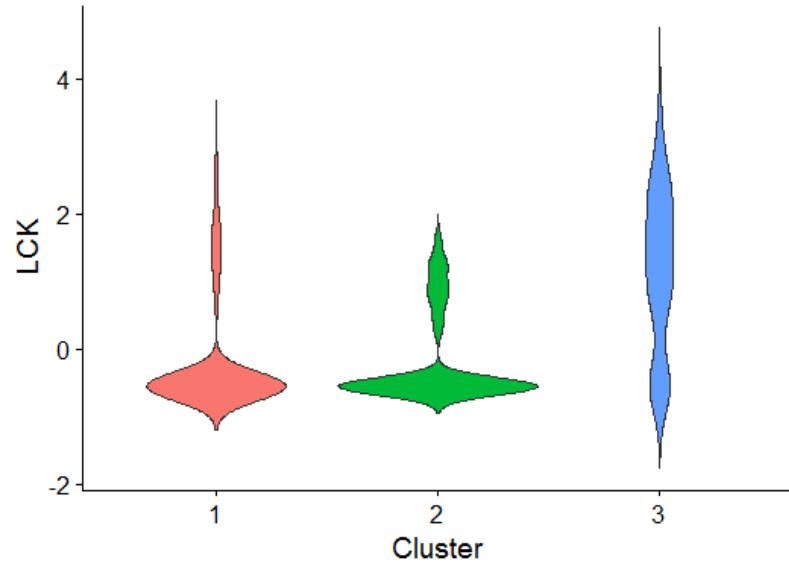
BiNGO → REVIGO: Comp 2



BiNGO Comparison

- **Component 1**
 - Endocytosis/Phagocytosis is a process derived from the variable genes
 - Membrane invagination – infolding of membrane
 - Could be involved in the Phagocytosis process?
- **Component 2**
 - Some sort of activation process is occurring
 - Ca^{2+} transport and signaling is responsible for the variation among the component 2 axis

Genes and Clusters



- AHR is prevalent in Cluster 2, and deficient in Clusters 1&3
- LCK and CD27 have similar expression level distributions in each cluster