

## Ontology: BP

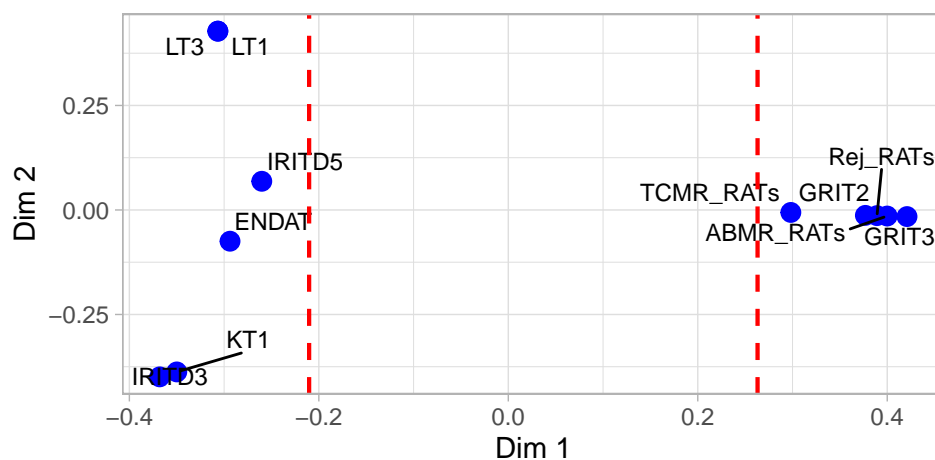
### GO Level: 3

Irrelevance - Threshold matrix of dissimilarities (BP-3):

	ABMR_RATs	ENDAT	GRIT2	GRIT3	IRITD3	IRITD5	KT1	LT1	LT3	Rej_RATs
ENDAT	1.00									
GRIT2	0.58	1.00								
GRIT3	0.47	1.00	0.38							
IRITD3	1.00	0.93	1.00	1.00						
IRITD5	1.00	0.97	1.00	1.00	1.00					
KT1	1.00	0.99	1.00	1.00	0.75	1.00				
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00			
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.83		
Rej_RATs	0.42	1.00	0.61	0.52	1.00	1.00	1.00	1.00	1.00	
TCMR_RATs	0.67	1.00	0.69	0.63	1.00	1.00	1.00	1.00	1.00	0.64

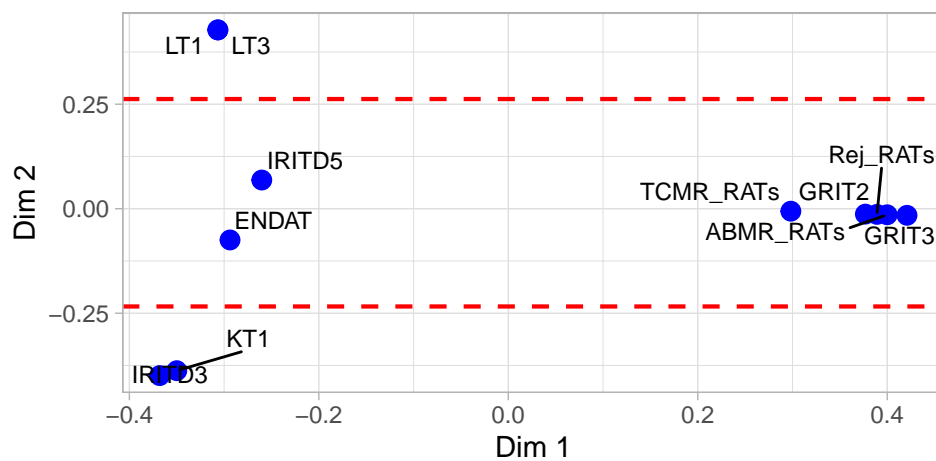
GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-3):

Dimension 1:



	Pseudo_t	Description
GO:0002253	10000	activation of immune response
GO:0002440	10000	production of molecular mediator of immune response
GO:0019882	10000	antigen processing and presentation

Dimension 2:



	Pseudo_t	Description
GO:0097722	10000	sperm motility
GO:0007389	10000	pattern specification process
GO:0050817	10000	coagulation
GO:1900047	10000	negative regulation of hemostasis
GO:0031503	10000	protein-containing complex localization

## GO Level: 4

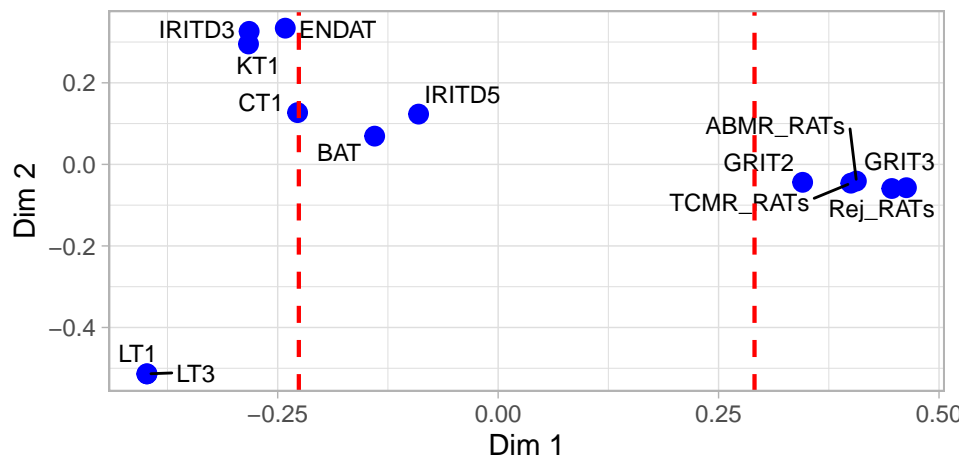
### Irrelevance - Threshold matrix of dissimilarities (BP-4):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	IRITD3	IRITD5	KT1	LT1	LT3
BAT	0.96										
CT1	1.00	1.00									
ENDAT	0.95	1.00	1.00								
GRIT2	0.73	0.99	1.00	0.98							
GRIT3	0.39	0.96	1.00	0.97	0.35						
IRITD3	1.00	1.00	1.00	0.81	1.00	1.00					
IRITD5	0.94	1.00	1.00	0.93	0.95	0.91	0.98				
KT1	1.00	1.00	0.95	0.88	1.00	1.00	0.89	1.00			
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.32	
Rej_RATs	0.27	0.96	1.00	0.97	0.66	0.30	1.00	0.94	1.00	1.00	1.00
TCMR_RATs	0.53	0.96	1.00	0.98	0.59	0.48	0.99	0.92	1.00	1.00	1.00

Rej_RATs	
BAT	
CT1	
ENDAT	
GRIT2	
GRIT3	
IRITD3	
IRITD5	
KT1	
LT1	
LT3	
Rej_RATs	
TCMR_RATs	0.43

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-4):

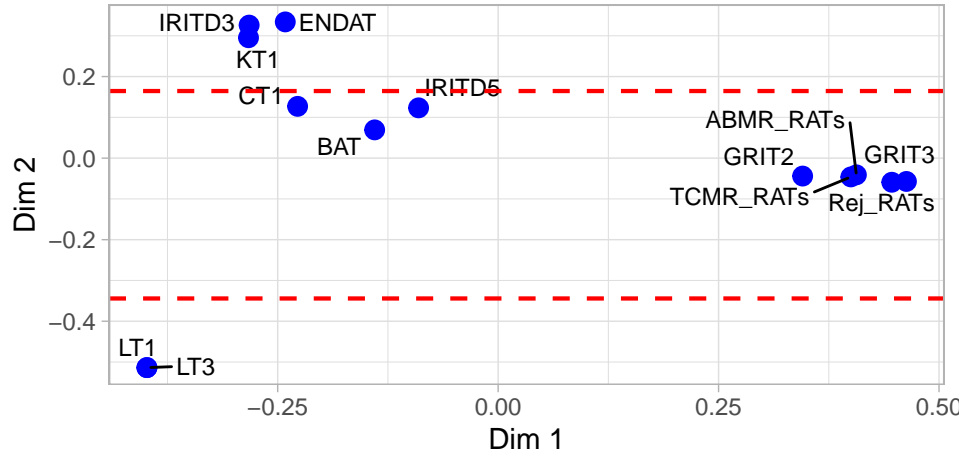
#### Dimension 1:



	Pseudo_t	Description
GO:0002263	10000	cell activation involved in immune response
GO:0050867	10000	positive regulation of cell activation
GO:0002367	10000	cytokine production involved in immune response
GO:0032609	10000	type II interferon production
GO:0001909	10000	leukocyte mediated cytotoxicity

	Pseudo_t	Description
GO: 0031341	10000	regulation of cell killing
GO: 0002443	10000	leukocyte mediated immunity
GO: 0002697	10000	regulation of immune effector process
GO: 0002699	10000	positive regulation of immune effector process
GO: 0002757	10000	immune response-activating signaling pathway
GO: 0002700	10000	regulation of production of molecular mediator of immune response
GO: 0002702	10000	positive regulation of production of molecular mediator of immune response
GO: 0002683	10000	negative regulation of immune system process
GO: 1903706	10000	regulation of hemopoiesis
GO: 0050777	10000	negative regulation of immune response
GO: 0002696	10000	positive regulation of leukocyte activation
GO: 0002764	10000	immune response-regulating signaling pathway
GO: 0070661	10000	leukocyte proliferation
GO: 0002831	10000	regulation of response to biotic stimulus
GO: 0002832	10000	negative regulation of response to biotic stimulus
GO: 0002833	10000	positive regulation of response to biotic stimulus
GO: 0019884	10000	antigen processing and presentation of exogenous antigen
GO: 0048002	10000	antigen processing and presentation of peptide antigen
GO: 0002274	10000	myeloid leukocyte activation
GO: 0002366	10000	leukocyte activation involved in immune response
GO: 0031349	10000	positive regulation of defense response
GO: 0031348	10000	negative regulation of defense response
GO: 0009615	10000	response to virus

## Dimension 2:



	Pseudo_t	Description
GO:0007281	10000	germ cell development
GO:0007288	10000	sperm axoneme assembly
GO:0048515	10000	spermatid differentiation
GO:0120316	10000	sperm flagellum assembly
GO:0007018	10000	microtubule-based movement
GO:0032886	10000	regulation of microtubule-based process
GO:0007389	10000	pattern specification process
GO:0003002	10000	regionalization
GO:0009799	10000	specification of symmetry
GO:0097722	10000	sperm motility
GO:0042073	10000	intraciliary transport
GO:1900047	10000	negative regulation of hemostasis
GO:0001539	10000	cilium or flagellum-dependent cell motility
GO:0007596	10000	blood coagulation
GO:0050878	10000	regulation of body fluid levels
GO:0030317	10000	flagellated sperm motility
GO:0030195	10000	negative regulation of blood coagulation

## GO Level: 5

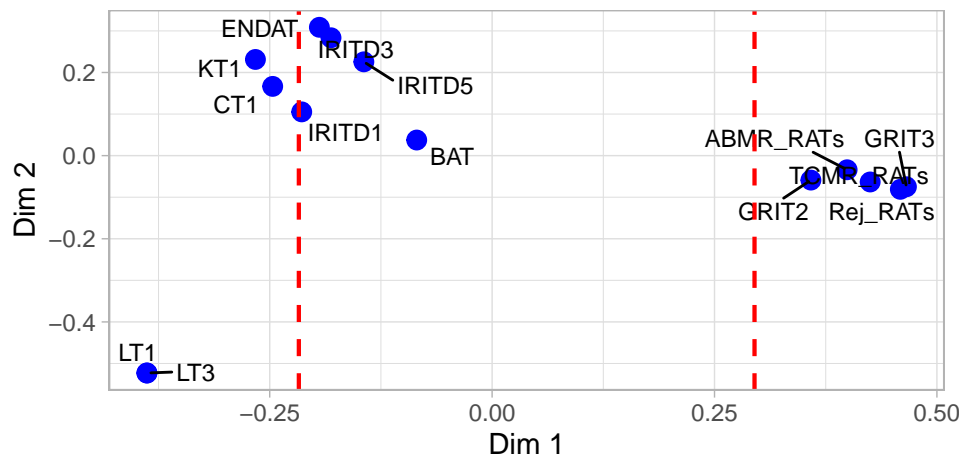
### Irrelevance - Threshold matrix of dissimilarities (BP-5):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	IRITD1	IRITD3	IRITD5	KT1	LT1
BAT	0.95										
CT1	1.00	1.00									
ENDAT	0.89	1.00	1.00								
GRIT2	0.72	0.97	1.00	0.97							
GRIT3	0.48	0.93	1.00	0.97	0.35						
IRITD1	1.00	1.00	1.00	0.97	1.00	1.00					
IRITD3	0.94	1.00	1.00	0.80	0.96	0.96	1.00				
IRITD5	0.96	1.00	1.00	0.88	0.96	0.92	1.00	0.86			
KT1	1.00	1.00	0.85	0.91	1.00	1.00	1.00	0.97	1.00		
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.32
Rej_RATs	0.29	0.95	1.00	0.97	0.65	0.36	1.00	0.97	0.96	1.00	1.00
TCMR_RATs	0.53	0.90	1.00	0.97	0.58	0.43	1.00	0.95	0.94	1.00	1.00

LT3	Rej_RATs	
BAT		
CT1		
ENDAT		
GRIT2		
GRIT3		
IRITD1		
IRITD3		
IRITD5		
KT1		
LT1		
LT3		
Rej_RATs	1.00	
TCMR_RATs	1.00	0.39

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-5):

#### Dimension 1:



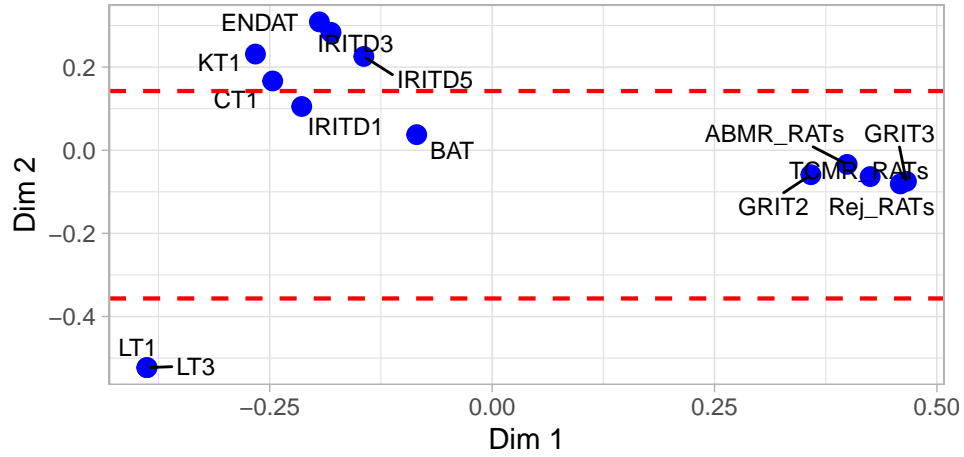
	Pseudo_t	Description
GO:001819	10000	positive regulation of cytokine production
GO:002718	10000	regulation of cytokine production involved in immune response
GO:0032649	10000	regulation of type II interferon production
GO:002720	10000	positive regulation of cytokine production involved in immune response

	Pseudo_	Description
GO:0032729	10000	positive regulation of type II interferon production
GO:0001910	10000	regulation of leukocyte mediated cytotoxicity
GO:0042267	10000	natural killer cell mediated cytotoxicity
GO:0002758	10000	innate immune response-activating signaling pathway
GO:0002460	10000	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002819	10000	regulation of adaptive immune response
GO:0002821	10000	positive regulation of adaptive immune response
GO:0002366	10000	leukocyte activation involved in immune response
GO:0002285	10000	lymphocyte activation involved in immune response
GO:0001909	10000	leukocyte mediated cytotoxicity
GO:0002449	10000	lymphocyte mediated immunity
GO:0002703	10000	regulation of leukocyte mediated immunity
GO:0002704	10000	negative regulation of leukocyte mediated immunity
GO:0002705	10000	positive regulation of leukocyte mediated immunity
GO:0002683	10000	negative regulation of immune system process
GO:0002697	10000	regulation of immune effector process
GO:0019037	10000	regulation of hemopoiesis
GO:0005077	10000	negative regulation of immune response
GO:0002696	10000	positive regulation of leukocyte activation
GO:0002699	10000	positive regulation of immune effector process
GO:0005125	10000	negative regulation of lymphocyte activation
GO:0005125	10000	positive regulation of lymphocyte activation
GO:0002700	10000	regulation of production of molecular mediator of immune response
GO:0002702	10000	positive regulation of production of molecular mediator of immune response
GO:0002757	10000	immune response-activating signaling pathway
GO:0002768	10000	immune response-regulating cell surface receptor signaling pathway
GO:0002832	10000	negative regulation of response to biotic stimulus
GO:0002833	10000	positive regulation of response to biotic stimulus
GO:0004508	10000	regulation of innate immune response
GO:0004582	10000	negative regulation of innate immune response
GO:0004589	10000	positive regulation of innate immune response

	Pseudo_	Description
GO:0031348	10000	negative regulation of defense response
GO:0031349	10000	positive regulation of defense response
GO:0002764	10000	immune response-regulating signaling pathway
GO:0019221	10000	cytokine-mediated signaling pathway
GO:0070665	10000	positive regulation of leukocyte proliferation
GO:0051607	10000	defense response to virus
GO:0002237	10000	response to molecule of bacterial origin
GO:0050900	10000	leukocyte migration
GO:0002478	10000	antigen processing and presentation of exogenous peptide antigen
GO:0022407	10000	regulation of cell-cell adhesion
GO:0045785	10000	positive regulation of cell adhesion
GO:0032102	10000	negative regulation of response to external stimulus
GO:0050727	10000	regulation of inflammatory response
GO:0070663	10000	regulation of leukocyte proliferation
GO:0002228	10000	natural killer cell mediated immunity
GO:0002274	10000	myeloid leukocyte activation
GO:0022409	10000	positive regulation of cell-cell adhesion
GO:0030098	10000	lymphocyte differentiation
GO:0046651	10000	lymphocyte proliferation
GO:0002474	10000	antigen processing and presentation of peptide antigen via MHC class I
GO:0050867	10000	positive regulation of cell activation
GO:0002831	10000	regulation of response to biotic stimulus
GO:0002253	10000	activation of immune response
GO:0031341	10000	regulation of cell killing
GO:0032943	10000	mononuclear cell proliferation
GO:0071219	10000	cellular response to molecule of bacterial origin
GO:0040546	10000	defense response to symbiont
GO:0007159	10000	leukocyte cell-cell adhesion
GO:0032496	10000	response to lipopolysaccharide
GO:1902105	10000	regulation of leukocyte differentiation

## Dimension 2:





	Pseudo_t	Description
GO:0001578	10000	microtubule bundle formation
GO:0060285	10000	cilium-dependent cell motility
GO:0060972	10000	left/right pattern formation
GO:0007281	10000	germ cell development
GO:0007288	10000	sperm axoneme assembly
GO:0048515	10000	spermatid differentiation
GO:0120316	10000	sperm flagellum assembly
GO:0006858	10000	extracellular transport
GO:0099111	10000	microtubule-based transport
GO:0003341	10000	cilium movement
GO:0010970	10000	transport along microtubule
GO:0060632	10000	regulation of microtubule-based movement
GO:0007224	10000	smoothened signaling pathway
GO:0007389	10000	pattern specification process
GO:0007286	10000	spermatid development
GO:0003002	10000	regionalization
GO:0009799	10000	specification of symmetry
GO:0009855	10000	determination of bilateral symmetry
GO:0035720	10000	intraciliary anterograde transport
GO:0030705	10000	cytoskeleton-dependent intracellular transport
GO:0032886	10000	regulation of microtubule-based process
GO:0090660	10000	cerebrospinal fluid circulation
GO:0030317	10000	flagellated sperm motility
GO:1902019	10000	regulation of cilium-dependent cell motility

## GO Level: 6

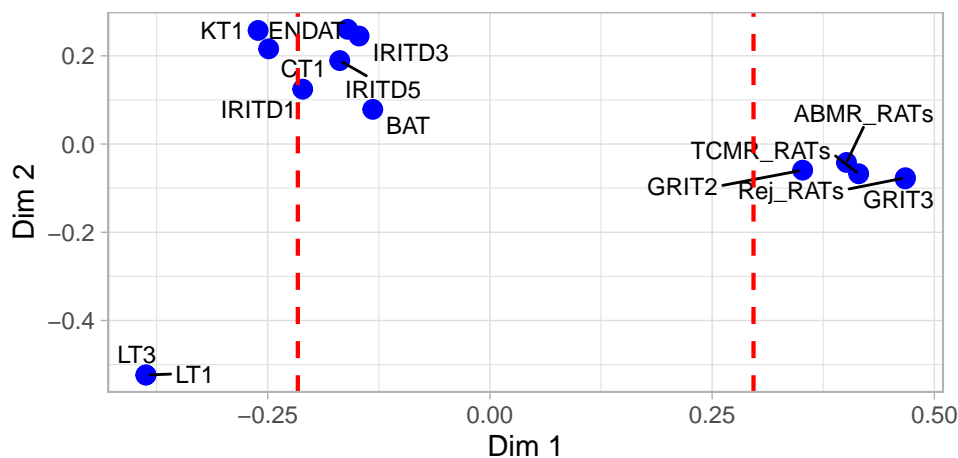
### Irrelevance - Threshold matrix of dissimilarities (BP-6):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	IRITD1	IRITD3	IRITD5	KT1	LT1
BAT	0.98										
CT1	1.00	1.00									
ENDAT	0.89	1.00	1.00								
GRIT2	0.74	0.98	1.00	0.97							
GRIT3	0.49	0.96	1.00	0.96	0.38						
IRITD1	1.00	1.00	1.00	0.98	1.00	1.00					
IRITD3	0.94	1.00	1.00	0.82	0.95	0.95	1.00				
IRITD5	0.98	1.00	1.00	0.94	0.98	0.96	1.00	0.90			
KT1	1.00	1.00	0.83	0.94	1.00	1.00	1.00	0.98	1.00		
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.33
Rej_RATs	0.30	0.98	1.00	0.96	0.60	0.37	1.00	0.95	0.97	1.00	1.00
TCMR_RATs	0.54	0.92	1.00	0.97	0.67	0.44	1.00	0.95	0.97	1.00	1.00

LT3	Rej_RATs	
BAT		
CT1		
ENDAT		
GRIT2		
GRIT3		
IRITD1		
IRITD3		
IRITD5		
KT1		
LT1		
LT3		
Rej_RATs	1.00	
TCMR_RATs	1.00	0.40

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-6):

#### Dimension 1:



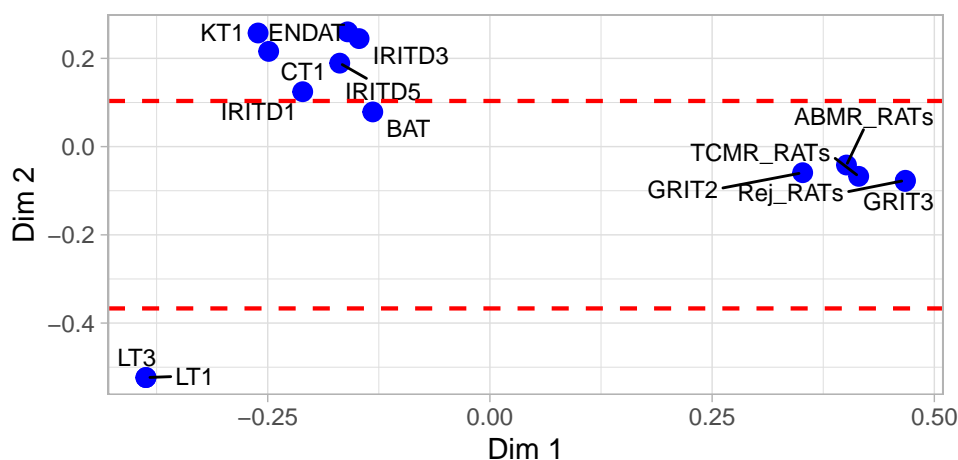
	Pseudo	Description
GO:001819	10000	positive regulation of cytokine production
GO:002718	10000	regulation of cytokine production involved in immune response
GO:0032649	10000	regulation of type II interferon production
GO:002720	10000	positive regulation of cytokine production involved in immune response

	Pseudo	Description
GO:0032729	10000	positive regulation of type II interferon production
GO:0001910	10000	regulation of leukocyte mediated cytotoxicity
GO:0042267	10000	natural killer cell mediated cytotoxicity
GO:0032496	10000	response to lipopolysaccharide
GO:0071219	10000	cellular response to molecule of bacterial origin
GO:0002757	10000	immune response-activating signaling pathway
GO:0002285	10000	lymphocyte activation involved in immune response
GO:0002228	10000	natural killer cell mediated immunity
GO:0002706	10000	regulation of lymphocyte mediated immunity
GO:0002707	10000	negative regulation of lymphocyte mediated immunity
GO:0002708	10000	positive regulation of lymphocyte mediated immunity
GO:0019724	10000	B cell mediated immunity
GO:0002822	10000	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002824	10000	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002105	10000	regulation of leukocyte differentiation
GO:0003131	10000	mononuclear cell differentiation
GO:0050777	10000	negative regulation of immune response
GO:0002696	10000	positive regulation of leukocyte activation
GO:0002699	10000	positive regulation of immune effector process
GO:0051250	10000	negative regulation of lymphocyte activation
GO:0051251	10000	positive regulation of lymphocyte activation
GO:0002700	10000	regulation of production of molecular mediator of immune response
GO:0002703	10000	regulation of leukocyte mediated immunity
GO:0002704	10000	negative regulation of leukocyte mediated immunity
GO:0002702	10000	positive regulation of production of molecular mediator of immune response
GO:0002705	10000	positive regulation of leukocyte mediated immunity
GO:0002758	10000	innate immune response-activating signaling pathway
GO:0002768	10000	immune response-regulating cell surface receptor signaling pathway
GO:0002821	10000	positive regulation of adaptive immune response
GO:0002832	10000	negative regulation of response to biotic stimulus
GO:0002833	10000	positive regulation of response to biotic stimulus

	Pseudo	Description
GO:0045088	10000	regulation of innate immune response
GO:0045824	10000	negative regulation of innate immune response
GO:0045089	10000	positive regulation of innate immune response
GO:0050727	10000	regulation of inflammatory response
GO:1903037	10000	regulation of leukocyte cell-cell adhesion
GO:1903039	10000	positive regulation of leukocyte cell-cell adhesion
GO:0002764	10000	immune response-regulating signaling pathway
GO:0019221	10000	cytokine-mediated signaling pathway
GO:0070665	10000	positive regulation of leukocyte proliferation
GO:0002440	10000	production of molecular mediator of immune response
GO:0022409	10000	positive regulation of cell-cell adhesion
GO:1903706	10000	regulation of hemopoiesis
GO:0030217	10000	T cell differentiation
GO:0045619	10000	regulation of lymphocyte differentiation
GO:0022407	10000	regulation of cell-cell adhesion
GO:0045785	10000	positive regulation of cell adhesion
GO:0031348	10000	negative regulation of defense response
GO:0031349	10000	positive regulation of defense response
GO:0032102	10000	negative regulation of response to external stimulus
GO:0071222	10000	cellular response to lipopolysaccharide
GO:0032944	10000	regulation of mononuclear cell proliferation
GO:0032946	10000	positive regulation of mononuclear cell proliferation
GO:0046651	10000	lymphocyte proliferation
GO:0042098	10000	T cell proliferation
GO:0046631	10000	alpha-beta T cell activation
GO:0050863	10000	regulation of T cell activation
GO:0050870	10000	positive regulation of T cell activation
GO:0070663	10000	regulation of leukocyte proliferation
GO:0030098	10000	lymphocyte differentiation
GO:0050670	10000	regulation of lymphocyte proliferation
GO:0050671	10000	positive regulation of lymphocyte proliferation

	Pseudo_t	Description
GO:0050867	10000	positive regulation of cell activation
GO:0002819	10000	regulation of adaptive immune response
GO:0002253	10000	activation of immune response
GO:0009615	10000	response to virus
GO:00040546	10000	defense response to symbiont
GO:00051607	10000	defense response to virus

## Dimension 2:



	Pseudo_t	Description
GO:00035082	10000	axoneme assembly
GO:00060972	10000	left/right pattern formation
GO:00003351	10000	epithelial cilium movement involved in extracellular fluid movement
GO:00003352	10000	regulation of cilium movement
GO:00060294	10000	cilium movement involved in cell motility
GO:00044782	10000	cilium organization
GO:0007224	10000	smoothened signaling pathway
GO:0007281	10000	germ cell development
GO:0007286	10000	spermatid development
GO:00048515	10000	spermatid differentiation
GO:000120316	10000	sperm flagellum assembly
GO:00003002	10000	regionalization
GO:00009799	10000	specification of symmetry
GO:00009855	10000	determination of bilateral symmetry
GO:00007368	10000	determination of left/right symmetry
GO:00042073	10000	intraciliary transport
GO:00010970	10000	transport along microtubule
GO:00060632	10000	regulation of microtubule-based movement
GO:00030705	10000	cytoskeleton-dependent intracellular transport
GO:00030317	10000	flagellated sperm motility
GO:0001902019	10000	regulation of cilium-dependent cell motility
GO:00007288	10000	sperm axoneme assembly
GO:00060295	10000	regulation of cilium movement involved in cell motility

## GO Level: 7

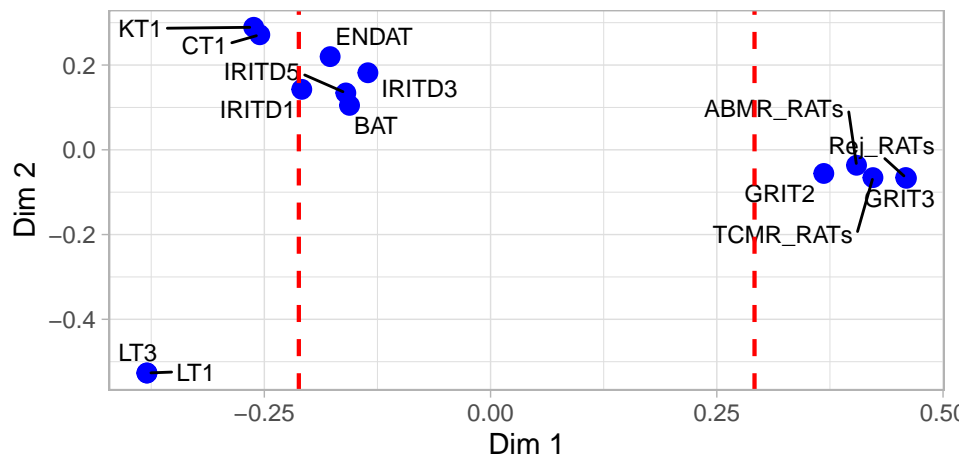
### Irrelevance - Threshold matrix of dissimilarities (BP-7):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	IRITD1	IRITD3	IRITD5	KT1	LT1
BAT	0.98										
CT1	1.00	1.00									
ENDAT	0.91	1.00	1.00								
GRIT2	0.71	1.00	1.00	0.99							
GRIT3	0.49	0.97	1.00	0.98	0.42						
IRITD1	0.99	1.00	1.00	0.97	1.00	1.00					
IRITD3	0.94	1.00	1.00	0.86	0.96	0.95	1.00				
IRITD5	1.00	1.00	1.00	0.98	0.97	0.96	1.00	0.96			
KT1	1.00	1.00	0.79	0.96	1.00	1.00	1.00	1.00	1.00		
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.33
Rej_RATs	0.37	0.98	1.00	0.97	0.58	0.41	1.00	0.95	0.97	1.00	1.00
TCMR_RATs	0.52	0.96	1.00	0.99	0.64	0.47	1.00	0.97	0.98	1.00	1.00
LT3 Rej_RATs											

BAT		
CT1		
ENDAT		
GRIT2		
GRIT3		
IRITD1		
IRITD3		
IRITD5		
KT1		
LT1		
LT3		
Rej_RATs	1.00	
TCMR_RATs	1.00	0.44

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-7):

#### Dimension 1:



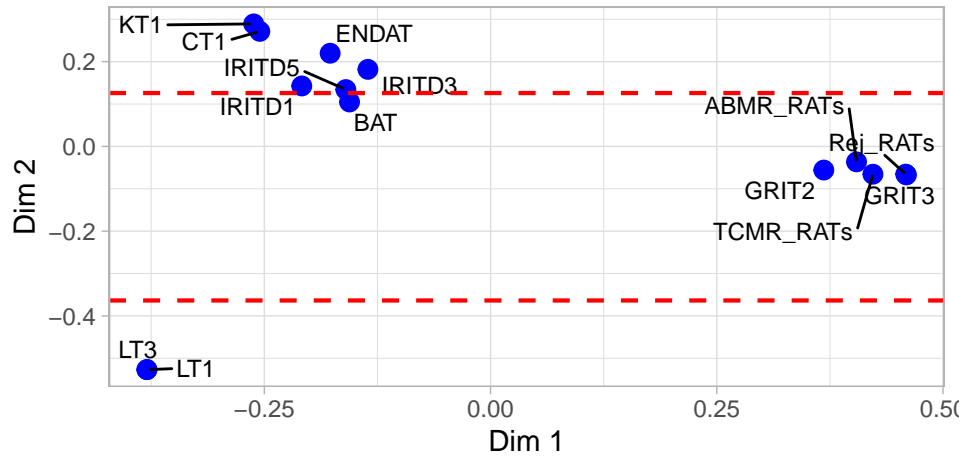
	Pseudo	Description
GO:001819	10000	positive regulation of cytokine production
GO:002367	10000	cytokine production involved in immune response
GO:0032609	10000	type II interferon production
GO:002718	10000	regulation of cytokine production involved in immune response

	Pseudo	Description
GO:0032649	10000	regulation of type II interferon production
GO:0002720	10000	positive regulation of cytokine production involved in immune response
GO:0032729	10000	positive regulation of type II interferon production
GO:0002758	10000	innate immune response-activating signaling pathway
GO:0042267	10000	natural killer cell mediated cytotoxicity
GO:0002757	10000	immune response-activating signaling pathway
GO:0002700	10000	regulation of production of molecular mediator of immune response
GO:0002702	10000	positive regulation of production of molecular mediator of immune response
GO:1902105	10000	regulation of leukocyte differentiation
GO:1903131	10000	mononuclear cell differentiation
GO:0002696	10000	positive regulation of leukocyte activation
GO:0051250	10000	negative regulation of lymphocyte activation
GO:0051251	10000	positive regulation of lymphocyte activation
GO:0002704	10000	negative regulation of leukocyte mediated immunity
GO:0002705	10000	positive regulation of leukocyte mediated immunity
GO:0001910	10000	regulation of leukocyte mediated cytotoxicity
GO:0002706	10000	regulation of lymphocyte mediated immunity
GO:0002707	10000	negative regulation of lymphocyte mediated immunity
GO:0002708	10000	positive regulation of lymphocyte mediated immunity
GO:0002768	10000	immune response-regulating cell surface receptor signaling pathway
GO:0002821	10000	positive regulation of adaptive immune response
GO:0002822	10000	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002824	10000	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0045824	10000	negative regulation of innate immune response
GO:0045089	10000	positive regulation of innate immune response
GO:0019221	10000	cytokine-mediated signaling pathway
GO:0070665	10000	positive regulation of leukocyte proliferation
GO:0051607	10000	defense response to virus
GO:0002237	10000	response to molecule of bacterial origin
GO:0016064	10000	immunoglobulin mediated immune response
GO:0022409	10000	positive regulation of cell-cell adhesion

	Pseudo	Description
GO:19 03037	10000	regulation of leukocyte cell-cell adhesion
GO:19 03039	10000	positive regulation of leukocyte cell-cell adhesion
GO:19 03706	10000	regulation of hemopoiesis
GO:00 30217	10000	T cell differentiation
GO:00 45619	10000	regulation of lymphocyte differentiation
GO:00 45580	10000	regulation of T cell differentiation
GO:00 31348	10000	negative regulation of defense response
GO:00 31349	10000	positive regulation of defense response
GO:00 45088	10000	regulation of innate immune response
GO:00 50727	10000	regulation of inflammatory response
GO:00 71222	10000	cellular response to lipopolysaccharide
GO:00 32946	10000	positive regulation of mononuclear cell proliferation
GO:00 50670	10000	regulation of lymphocyte proliferation
GO:00 50671	10000	positive regulation of lymphocyte proliferation
GO:00 42102	10000	positive regulation of T cell proliferation
GO:00 42129	10000	regulation of T cell proliferation
GO:00 46633	10000	alpha-beta T cell proliferation
GO:00 42098	10000	T cell proliferation
GO:00 46631	10000	alpha-beta T cell activation
GO:00 50863	10000	regulation of T cell activation
GO:00 50870	10000	positive regulation of T cell activation
GO:00 02228	10000	natural killer cell mediated immunity
GO:00 36037	10000	CD8-positive, alpha-beta T cell activation
GO:00 46634	10000	regulation of alpha-beta T cell activation
GO:00 46635	10000	positive regulation of alpha-beta T cell activation
GO:00 02253	10000	activation of immune response
GO:00 32944	10000	regulation of mononuclear cell proliferation
GO:01 40546	10000	defense response to symbiont
GO:00 30098	10000	lymphocyte differentiation

## Dimension 2:





	Pseudo_t	Description
GO:	10000	left/right pattern formation
0060972		
GO:	10000	epithelial cilium movement involved in determination of left/right asymmetry
0060287		
GO:	10000	cerebrospinal fluid circulation
0090660		
GO:	10000	regulation of cilium beat frequency
0003356		
GO:	10000	regulation of cilium movement involved in cell motility
0060295		
GO:	10000	smoothened signaling pathway
0007224		
GO:	10000	spermatid development
0007286		
GO:	10000	spermatid differentiation
0048515		
GO:	10000	sperm flagellum assembly
0120316		
GO:	10000	determination of bilateral symmetry
0009855		
GO:	10000	determination of left/right symmetry
0007368		
GO:	10000	intraciliary transport
0042073		
GO:	10000	transport along microtubule
0010970		
GO:	10000	protein localization to cilium
0061512		
GO:	10000	sperm axoneme assembly
0007288		
GO:	10000	axonemal dynein complex assembly
0070286		
GO:	10000	intraciliary anterograde transport
0035720		
GO:	10000	cilium assembly
0060271		
GO:	10000	flagellated sperm motility
0030317		
GO:	10000	regulation of cilium movement
0003352		
GO:	10000	cilium organization
0044782		

## GO Level: 8

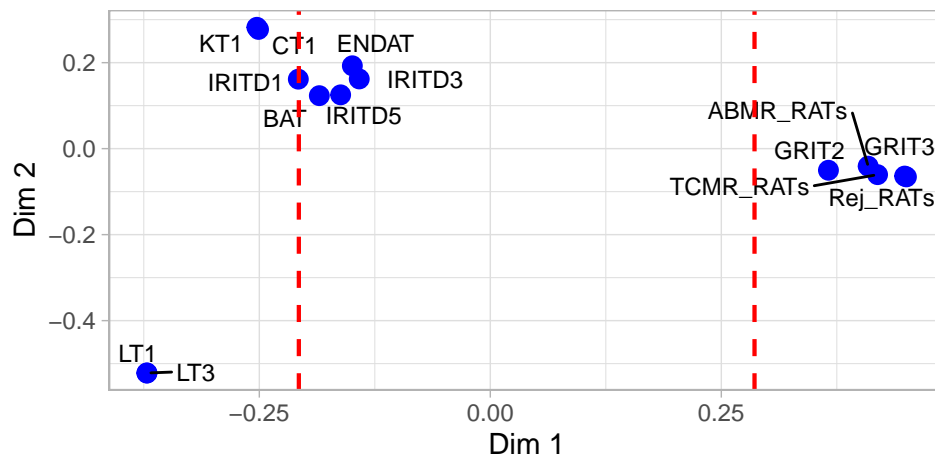
### Irrelevance - Threshold matrix of dissimilarities (BP-8):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	IRITD1	IRITD3	IRITD5	KT1	LT1
BAT	0.99										
CT1	1.00	1.00									
ENDAT	0.91	1.00	1.00								
GRIT2	0.72	1.00	1.00	0.97							
GRIT3	0.52	0.99	1.00	0.97	0.44						
IRITD1	0.99	1.00	1.00	0.94	1.00	1.00					
IRITD3	0.95	1.00	1.00	0.89	0.97	0.97	1.00				
IRITD5	1.00	1.00	1.00	0.98	0.98	0.96	1.00	0.99			
KT1	1.00	1.00	0.80	0.99	1.00	1.00	1.00	1.00	1.00		
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.40
Rej_RATs	0.36	1.00	1.00	0.97	0.65	0.46	1.00	0.97	0.98	1.00	1.00
TCMR_RATs	0.55	0.97	1.00	0.98	0.60	0.53	1.00	0.96	0.99	1.00	1.00

	LT3	Rej_RATs
BAT		
CT1		
ENDAT		
GRIT2		
GRIT3		
IRITD1		
IRITD3		
IRITD5		
KT1		
LT1		
LT3		
Rej_RATs	1.00	
TCMR_RATs	1.00	0.48

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-8):

#### Dimension 1:

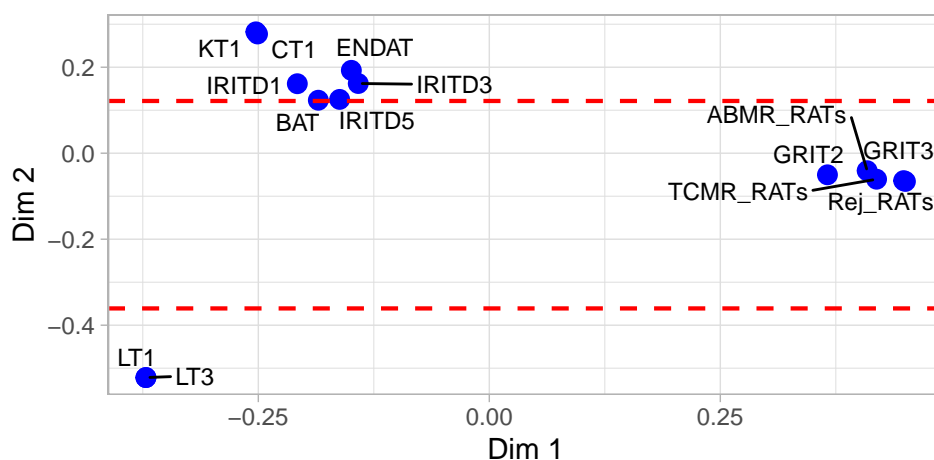


	Pseudo	Description
GO:001819	10000	positive regulation of cytokine production
GO:002718	10000	regulation of cytokine production involved in immune response
GO:0032649	10000	regulation of type II interferon production
GO:002720	10000	positive regulation of cytokine production involved in immune response

	Pseudo	Description
GO:0032729	10000	positive regulation of type II interferon production
GO:0002758	10000	innate immune response-activating signaling pathway
GO:0042267	10000	natural killer cell mediated cytotoxicity
GO:0032496	10000	response to lipopolysaccharide
GO:0071219	10000	cellular response to molecule of bacterial origin
GO:0002757	10000	immune response-activating signaling pathway
GO:0002105	10000	regulation of leukocyte differentiation
GO:0003131	10000	mononuclear cell differentiation
GO:0051250	10000	negative regulation of lymphocyte activation
GO:0051251	10000	positive regulation of lymphocyte activation
GO:0002702	10000	positive regulation of production of molecular mediator of immune response
GO:0002707	10000	negative regulation of lymphocyte mediated immunity
GO:0002708	10000	positive regulation of lymphocyte mediated immunity
GO:0002824	10000	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0003039	10000	positive regulation of leukocyte cell-cell adhesion
GO:0030217	10000	T cell differentiation
GO:0045619	10000	regulation of lymphocyte differentiation
GO:0045580	10000	regulation of T cell differentiation
GO:0045824	10000	negative regulation of innate immune response
GO:0045089	10000	positive regulation of innate immune response
GO:0032946	10000	positive regulation of mononuclear cell proliferation
GO:0050670	10000	regulation of lymphocyte proliferation
GO:0050671	10000	positive regulation of lymphocyte proliferation
GO:0001185	10000	regulation of CD8-positive, alpha-beta T cell activation
GO:0042102	10000	positive regulation of T cell proliferation
GO:0042129	10000	regulation of T cell proliferation
GO:0046633	10000	alpha-beta T cell proliferation
GO:0046640	10000	regulation of alpha-beta T cell proliferation
GO:0002228	10000	natural killer cell mediated immunity
GO:0045088	10000	regulation of innate immune response
GO:0036037	10000	CD8-positive, alpha-beta T cell activation

	Pseudo_t	Description
GO:0046634	10000	regulation of alpha-beta T cell activation
GO:0046635	10000	positive regulation of alpha-beta T cell activation
GO:0050870	10000	positive regulation of T cell activation
GO:0050863	10000	regulation of T cell activation
GO:0051607	10000	defense response to virus
GO:0030098	10000	lymphocyte differentiation

Dimension 2:



	Pseudo_t	Description
GO:0001578	10000	microtubule bundle formation
GO:0003356	10000	regulation of cilium beat frequency
GO:0060295	10000	regulation of cilium movement involved in cell motility
GO:0048515	10000	spermatid differentiation
GO:0120316	10000	sperm flagellum assembly
GO:0060287	10000	epithelial cilium movement involved in determination of left/right asymmetry
GO:0007368	10000	determination of left/right symmetry
GO:0042073	10000	intraciliary transport
GO:0035720	10000	intraciliary anterograde transport
GO:0060271	10000	cilium assembly
GO:0007286	10000	spermatid development
GO:0035082	10000	axoneme assembly
GO:0044458	10000	motile cilium assembly

	Pseudo_t	Description
GO: 1905515	10000	non-motile cilium assembly
GO: 0036158	10000	outer dynein arm assembly
GO: 0036159	10000	inner dynein arm assembly
GO: 0007288	10000	sperm axoneme assembly

## GO Level: 9

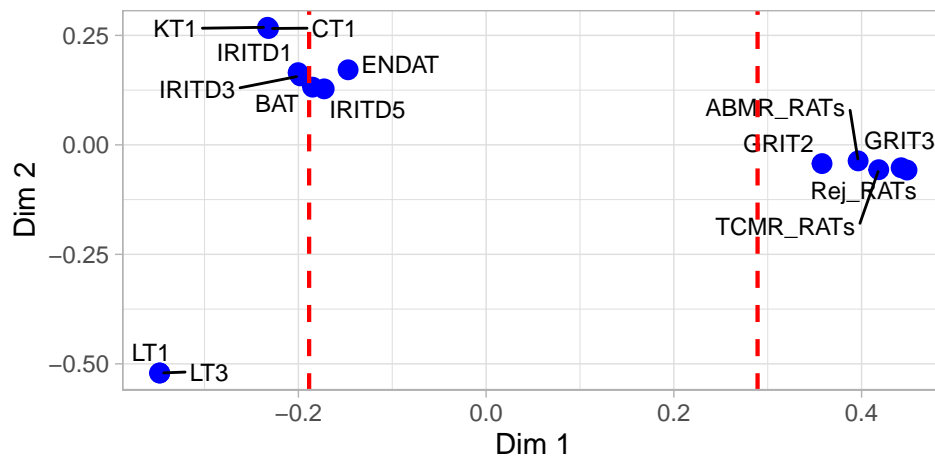
### Irrelevance - Threshold matrix of dissimilarities (BP-9):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	IRITD1	IRITD3	IRITD5	KT1	LT1
BAT	1.00										
CT1	1.00	1.00									
ENDAT	0.92	1.00	1.00								
GRIT2	0.77	1.00	1.00	0.98							
GRIT3	0.61	1.00	1.00	0.97	0.51						
IRITD1	1.00	1.00	1.00	0.94	1.00	1.00					
IRITD3	1.00	1.00	1.00	0.96	1.00	1.00	1.00				
IRITD5	1.00	1.00	1.00	1.00	1.00	0.97	1.00	1.00			
KT1	1.00	1.00	0.83	0.99	1.00	1.00	1.00	1.00	1.00		
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.46
Rej_RATs	0.42	1.00	1.00	0.98	0.70	0.53	1.00	1.00	0.99	1.00	1.00
TCMR_RATs	0.63	0.99	1.00	1.00	0.64	0.56	1.00	1.00	1.00	1.00	1.00

BAT		
CT1		
ENDAT		
GRIT2		
GRIT3		
IRITD1		
IRITD3		
IRITD5		
KT1		
LT1		
LT3		
Rej_RATs	1.00	
TCMR_RATs	1.00	0.55

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-9):

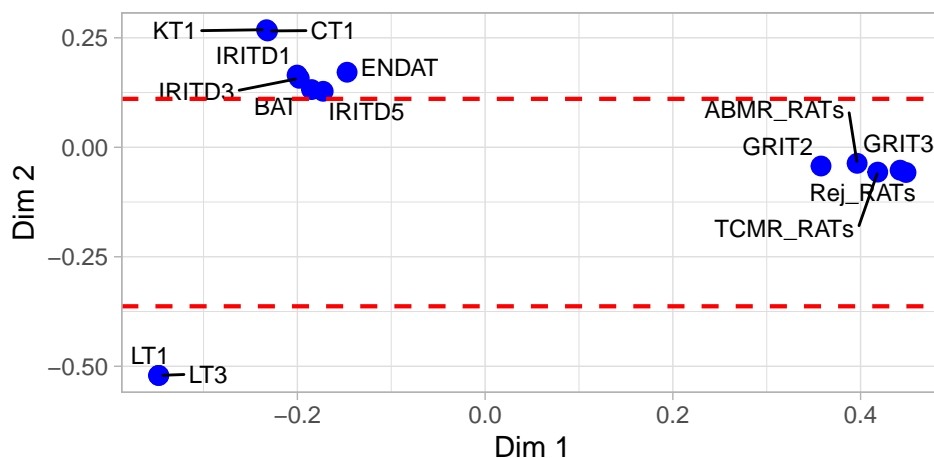
#### Dimension 1:



	Pseudo_t	Description
GO:0002720	10000	positive regulation of cytokine production involved in immune response
GO:0032729	10000	positive regulation of type II interferon production
GO:0002758	10000	innate immune response-activating signaling pathway
GO:0042267	10000	natural killer cell mediated cytotoxicity
GO:0030217	10000	T cell differentiation
GO:0045619	10000	regulation of lymphocyte differentiation
GO:0045580	10000	regulation of T cell differentiation
GO:0050671	10000	positive regulation of lymphocyte proliferation

	Pseudo_t	Description
GO:2001185	10000	regulation of CD8-positive, alpha-beta T cell activation
GO:0042102	10000	positive regulation of T cell proliferation
GO:0046640	10000	regulation of alpha-beta T cell proliferation
GO:0045089	10000	positive regulation of innate immune response
GO:0045824	10000	negative regulation of innate immune response
GO:0046635	10000	positive regulation of alpha-beta T cell activation
GO:0042129	10000	regulation of T cell proliferation
GO:0046634	10000	regulation of alpha-beta T cell activation
GO:0050870	10000	positive regulation of T cell activation
GO:0030098	10000	lymphocyte differentiation

## Dimension 2:



	Pseudo_t	Description
GO:0035082	10000	axoneme assembly
GO:0120316	10000	sperm flagellum assembly
GO:0060287	10000	epithelial cilium movement involved in determination of left/right asymmetry
GO:0007288	10000	sperm axoneme assembly
GO:0070286	10000	axonemal dynein complex assembly
GO:0035720	10000	intraciliary anterograde transport
GO:0007286	10000	spermatid development
GO:0044458	10000	motile cilium assembly
GO:1905515	10000	non-motile cilium assembly

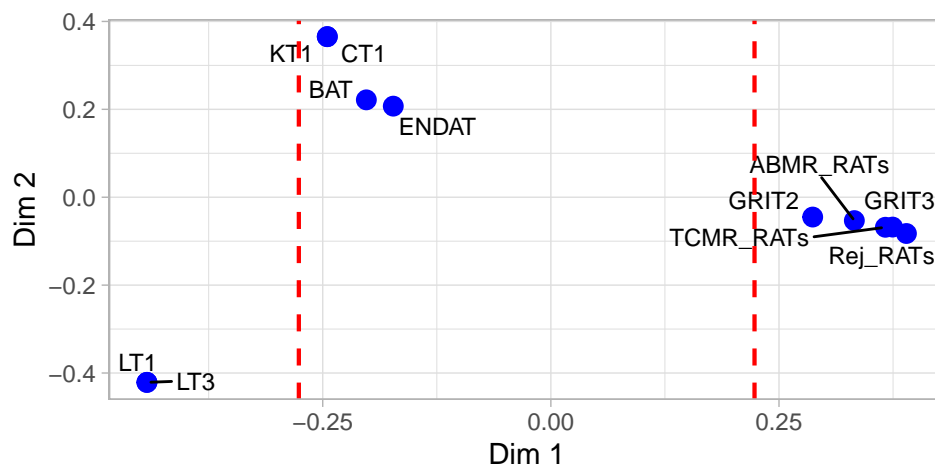
## GO Level: 10

### Irrelevance - Threshold matrix of dissimilarities (BP-10):

	ABMR_RATs	BAT	CT1	ENDAT	GRIT2	GRIT3	KT1	LT1	LT3	Rej_RATs
BAT	1.00									
CT1	1.00	1.00								
ENDAT	0.96	1.00	1.00							
GRIT2	0.83	1.00	1.00	0.99						
GRIT3	0.70	1.00	1.00	0.97	0.60					
KT1	1.00	1.00	0.91	1.00	1.00	1.00				
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00			
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.52		
Rej_RATs	0.47	1.00	1.00	1.00	0.75	0.62	1.00	1.00	1.00	
TCMR_RATs	0.67	0.98	1.00	1.00	0.69	0.58	1.00	1.00	1.00	0.61

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (BP-10):

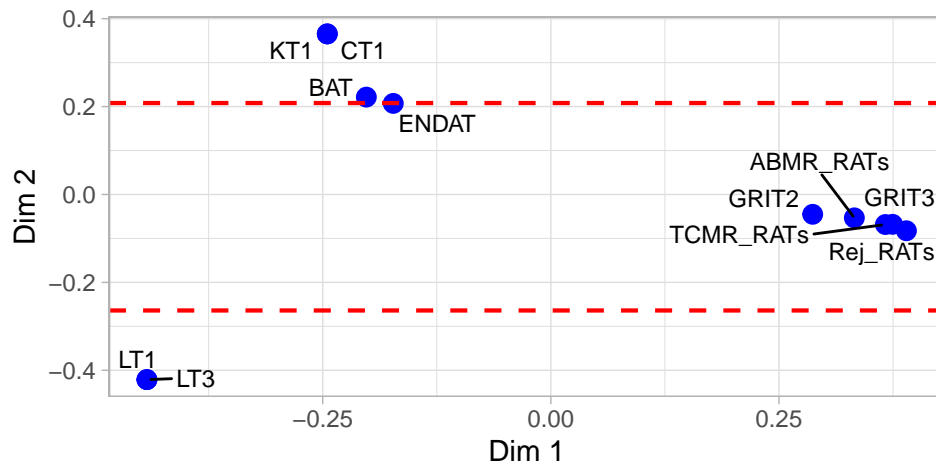
#### Dimension 1:



	Pseudo_t	Description
GO:0002758	10000	innate immune response-activating signaling pathway
GO:0120316	10000	sperm flagellum assembly
GO:0030217	10000	T cell differentiation
GO:0045619	10000	regulation of lymphocyte differentiation
GO:0045580	10000	regulation of T cell differentiation
GO:0007288	10000	sperm axoneme assembly
GO:0070286	10000	axonemal dynein complex assembly
GO:0042102	10000	positive regulation of T cell proliferation
GO:0046640	10000	regulation of alpha-beta T cell proliferation
GO:0046635	10000	positive regulation of alpha-beta T cell activation
GO:2001185	10000	regulation of CD8-positive, alpha-beta T cell activation
GO:0036158	10000	outer dynein arm assembly
GO:0036159	10000	inner dynein arm assembly

#### Dimension 2:





	Pseudo_t	Description
GO:0120316	10000	sperm flagellum assembly
GO:0007288	10000	sperm axoneme assembly
GO:0070286	10000	axonemal dynein complex assembly
GO:0036158	10000	outer dynein arm assembly
GO:0036159	10000	inner dynein arm assembly

## Ontology: CC

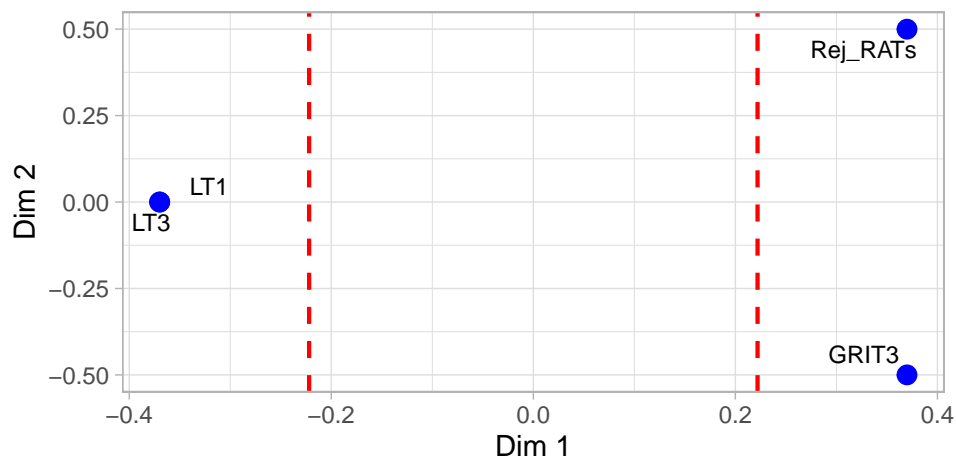
### GO Level: 3

Irrelevance - Threshold matrix of dissimilarities (CC-3):

	GRIT3	LT1	LT3
LT1	1.0		
LT3	1.0	0.9	
Rej_RATs	1.0	1.0	1.0

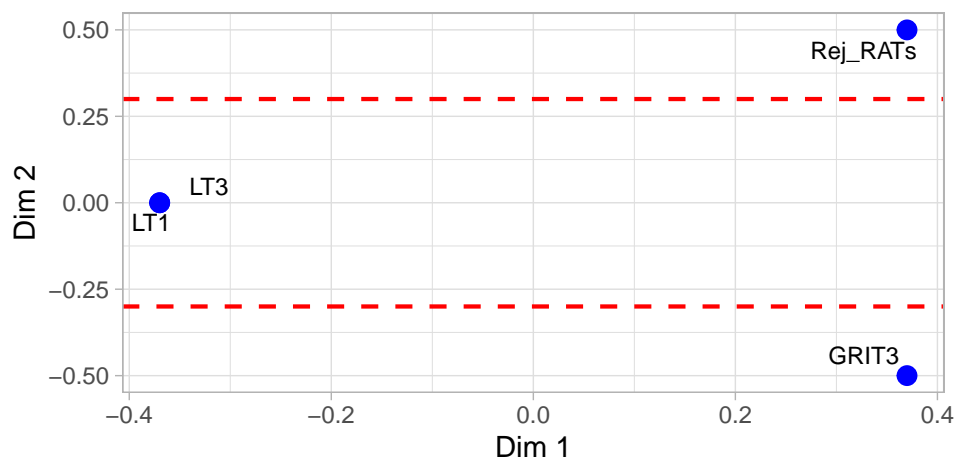
GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-3):

Dimension 1:



	Pseudo_t	Description
GO:0002177	10000	manchette
GO:0005875	10000	microtubule associated complex
GO:0005930	10000	axoneme
GO:0019774	10000	proteasome core complex, beta-subunit complex
GO:0030990	10000	intraciliary transport particle
GO:0030992	10000	intraciliary transport particle B
GO:0035869	10000	ciliary transition zone
GO:0036038	10000	MKS complex
GO:0097228	10000	sperm principal piece
GO:0097542	10000	ciliary tip
GO:0097546	10000	ciliary base

Dimension 2:



	Pseudo_t	Description
GO:0001772	10000	immunological synapse
GO:0072562	10000	blood microparticle
GO:1904090	10000	peptidase inhibitor complex

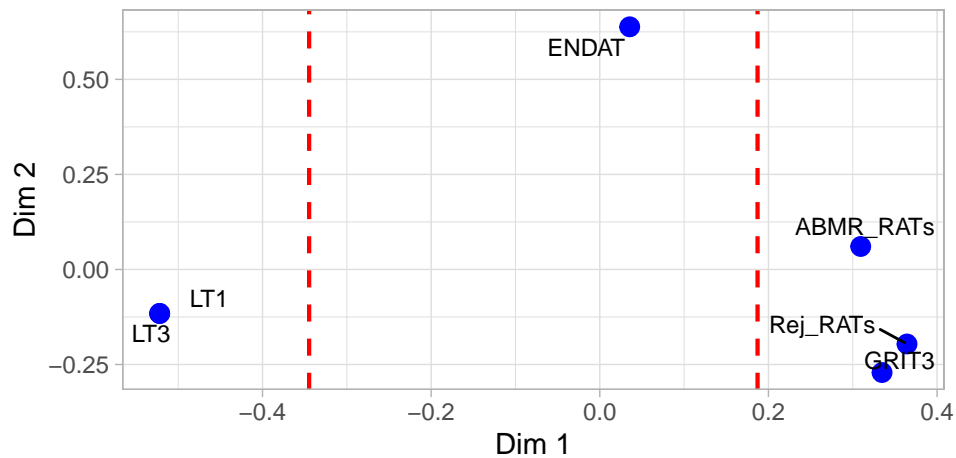
## GO Level: 4

### Irrelevance - Threshold matrix of dissimilarities (CC-4):

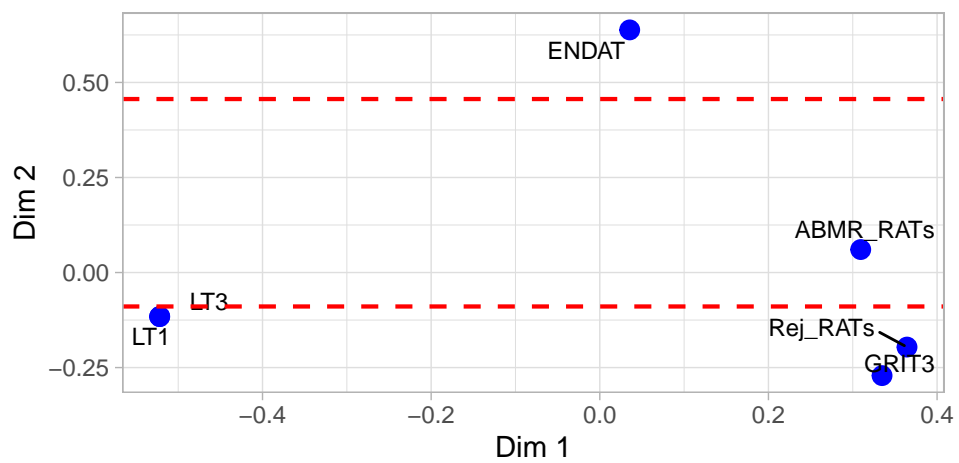
	ABMR_RATs	ENDAT	GRIT3	LT1	LT3
ENDAT	0.89				
GRIT3	0.80	1.00			
LT1	1.00	1.00	1.00		
LT3	1.00	1.00	1.00	0.59	
Rej_RATs	0.72	0.97	0.65	1.00	1.00

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-4):

#### Dimension 1:



#### Dimension 2:



	Pseudo_t	Description
GO:0098857	10000	membrane microdomain

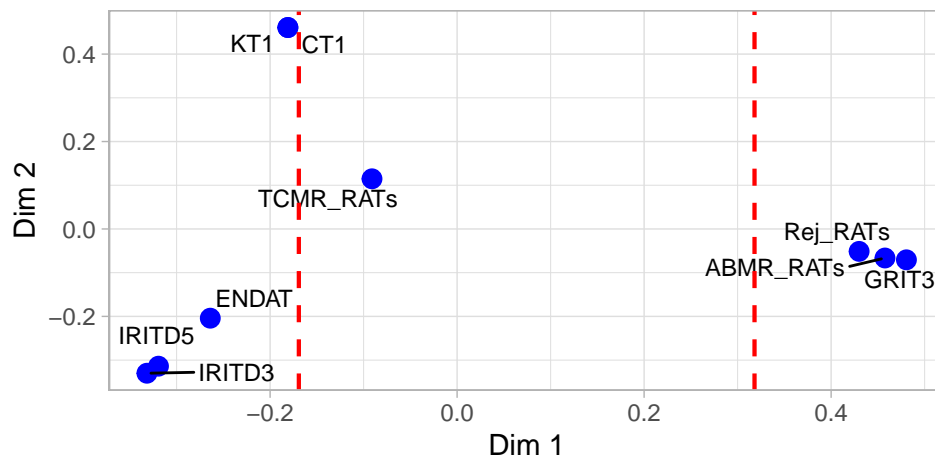
## GO Level: 5

### Irrelevance - Threshold matrix of dissimilarities (CC-5):

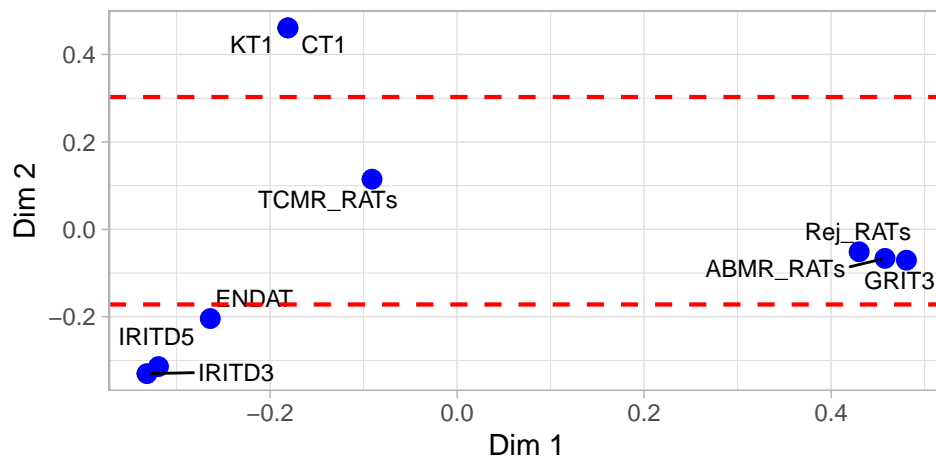
	ABMR_RATs	CT1	ENDAT	GRIT3	IRITD3	IRITD5	KT1	Rej_RATs
CT1	1.00							
ENDAT	1.00	1.00						
GRIT3	0.56	1.00	1.00					
IRITD3	1.00	1.00	0.87	1.00				
IRITD5	1.00	1.00	0.91	1.00	0.76			
KT1	1.00	0.84	1.00	1.00	1.00	1.00		
Rej_RATs	0.68	1.00	1.00	0.62	1.00	1.00	1.00	
TCMR_RATs	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.96

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-5):

#### Dimension 1:



#### Dimension 2:



	Pseudo_t	Description
GO:0005759	10000	mitochondrial matrix
GO:0005777	10000	peroxisome
GO:0009925	10000	basal plasma membrane
GO:0016323	10000	basolateral plasma membrane
GO:0016324	10000	apical plasma membrane
GO:0031091	10000	platelet alpha granule
GO:0031907	10000	microbody lumen
GO:0042579	10000	microbody
GO:0062023	10000	collagen-containing extracellular matrix

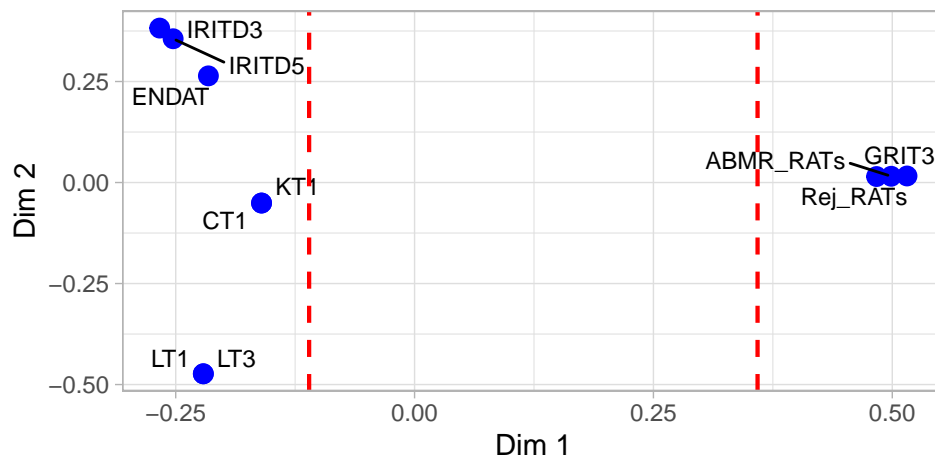
## GO Level: 6

### Irrelevance - Threshold matrix of dissimilarities (CC-6):

	ABMR_RATs	CT1	ENDAT	GRIT3	IRITD3	IRITD5	KT1	LT1	LT3
CT1	1.00								
ENDAT	1.00	1.00							
GRIT3	0.48	1.00	1.00						
IRITD3	1.00	1.00	0.85	1.00					
IRITD5	1.00	1.00	0.91	1.00	0.73				
KT1	1.00	0.81	1.00	1.00	1.00	1.00			
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00		
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.66	
Rej_RATs	0.59	1.00	1.00	0.54	1.00	1.00	1.00	1.00	1.00

### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-6):

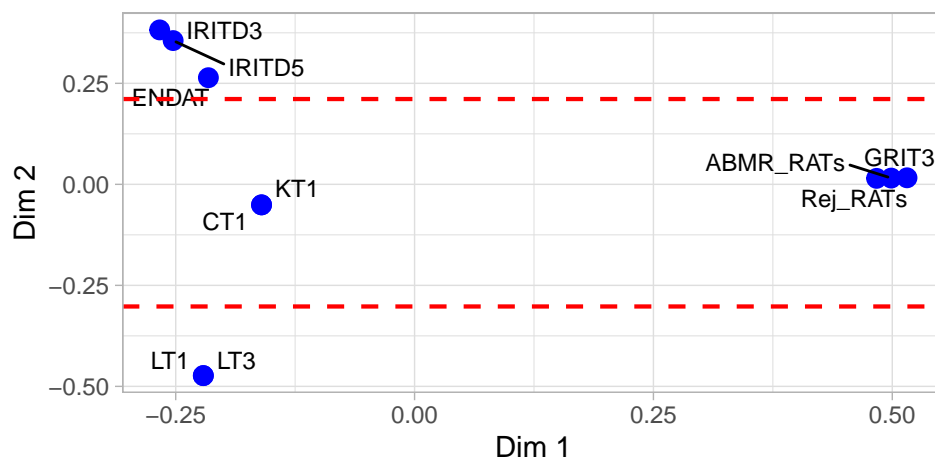
#### Dimension 1:



	Pseudo_t	Description
GO:0005774	10000	vacuolar membrane
GO:0005802	10000	trans-Golgi network
GO:0012507	10000	ER to Golgi transport vesicle membrane
GO:0030133	10000	transport vesicle
GO:0030134	10000	COPII-coated ER to Golgi transport vesicle
GO:0030135	10000	coated vesicle
GO:0030136	10000	clathrin-coated vesicle
GO:0030658	10000	transport vesicle membrane
GO:0030662	10000	coated vesicle membrane
GO:0030666	10000	endocytic vesicle membrane
GO:0031901	10000	early endosome membrane
GO:0032588	10000	trans-Golgi network membrane
GO:0042611	10000	MHC protein complex
GO:0042613	10000	MHC class II protein complex
GO:0045334	10000	clathrin-coated endocytic vesicle
GO:0045335	10000	phagocytic vesicle
GO:0055038	10000	recycling endosome membrane
GO:0098553	10000	luminal side of endoplasmic reticulum membrane
GO:0098576	10000	luminal side of membrane
GO:0098791	10000	Golgi apparatus subcompartment
GO:0098852	10000	lytic vacuole membrane

#### Dimension 2:





	Pseudo_t	Description
GO:0005604	10000	basement membrane
GO:0005788	10000	endoplasmic reticulum lumen
GO:0005814	10000	centriole
GO:0005879	10000	axonemal microtubule
GO:0031093	10000	platelet alpha granule lumen
GO:0031514	10000	motile cilium
GO:0032838	10000	plasma membrane bounded cell projection cytoplasm
GO:0035869	10000	ciliary transition zone
GO:0036064	10000	ciliary basal body
GO:0036157	10000	outer dynein arm
GO:0062023	10000	collagen-containing extracellular matrix
GO:0097014	10000	ciliary plasm
GO:0097542	10000	ciliary tip
GO:0097546	10000	ciliary base
GO:0120293	10000	dynein axonemal particle

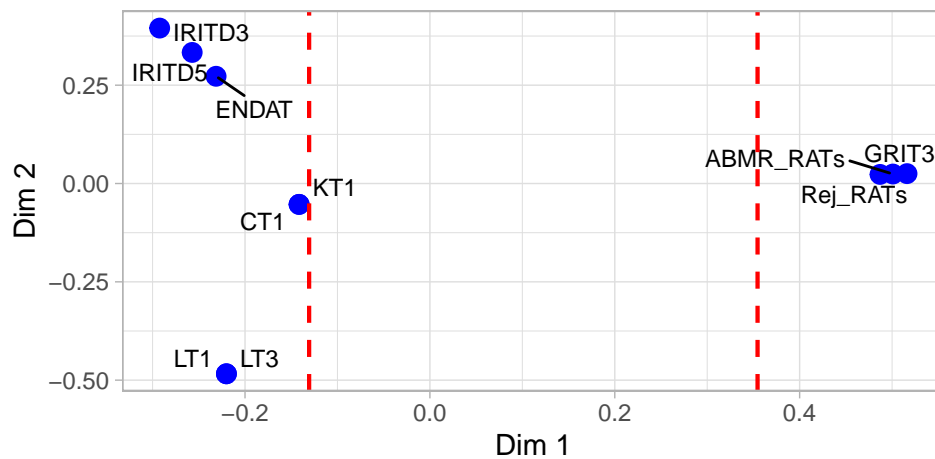
## GO Level: 7

### Irrelevance - Threshold matrix of dissimilarities (CC-7):

	ABMR_RATs	CT1	ENDAT	GRIT3	IRITD3	IRITD5	KT1	LT1	LT3
CT1	1.00								
ENDAT	1.00	1.00							
GRIT3	0.47	1.00	1.00						
IRITD3	1.00	1.00	0.79	1.00					
IRITD5	1.00	1.00	0.94	1.00	0.71				
KT1	1.00	0.86	1.00	1.00	1.00	1.00			
LT1	1.00	1.00	1.00	1.00	1.00	1.00	1.00		
LT3	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.64	
Rej_RATs	0.57	1.00	1.00	0.52	1.00	1.00	1.00	1.00	1.00

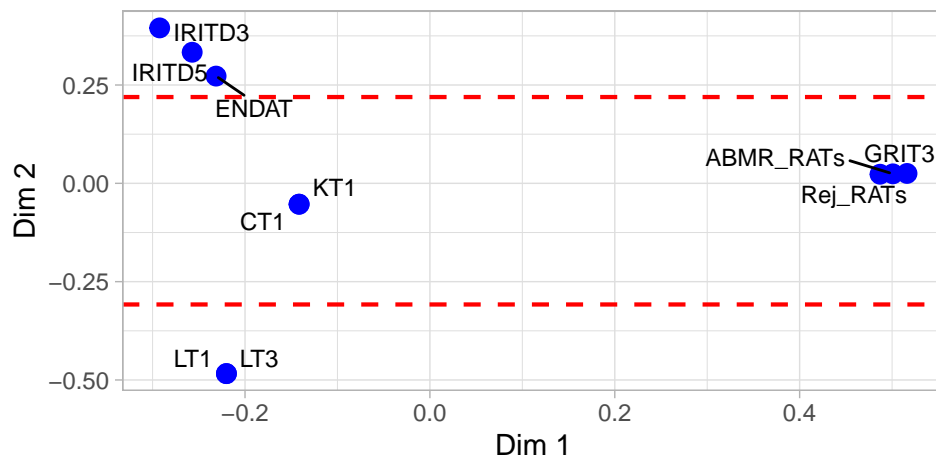
### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-7):

#### Dimension 1:



	Pseudo_t	Description
GO:0005765	10000	lysosomal membrane
GO:0005774	10000	vacuolar membrane
GO:0005802	10000	trans-Golgi network
GO:0012507	10000	ER to Golgi transport vesicle membrane
GO:0030134	10000	COPII-coated ER to Golgi transport vesicle
GO:0030136	10000	clathrin-coated vesicle
GO:0030658	10000	transport vesicle membrane
GO:0030662	10000	coated vesicle membrane
GO:0030665	10000	clathrin-coated vesicle membrane
GO:0030666	10000	endocytic vesicle membrane
GO:0030669	10000	clathrin-coated endocytic vesicle membrane
GO:0030670	10000	phagocytic vesicle membrane
GO:0031901	10000	early endosome membrane
GO:0032588	10000	trans-Golgi network membrane
GO:0042613	10000	MHC class II protein complex
GO:0045334	10000	clathrin-coated endocytic vesicle
GO:0045335	10000	phagocytic vesicle
GO:0055038	10000	recycling endosome membrane
GO:0098553	10000	luminal side of endoplasmic reticulum membrane
GO:0098791	10000	Golgi apparatus subcompartment
GO:0098852	10000	lytic vacuole membrane

#### Dimension 2:



	Pseudo_t	Description
GO:0005604	10000	basement membrane
GO:0005788	10000	endoplasmic reticulum lumen
GO:0005874	10000	microtubule
GO:0005930	10000	axoneme
GO:0031091	10000	platelet alpha granule
GO:0031093	10000	platelet alpha granule lumen
GO:0036038	10000	MKS complex
GO:0097014	10000	ciliary plasm
GO:0097729	10000	9+2 motile cilium

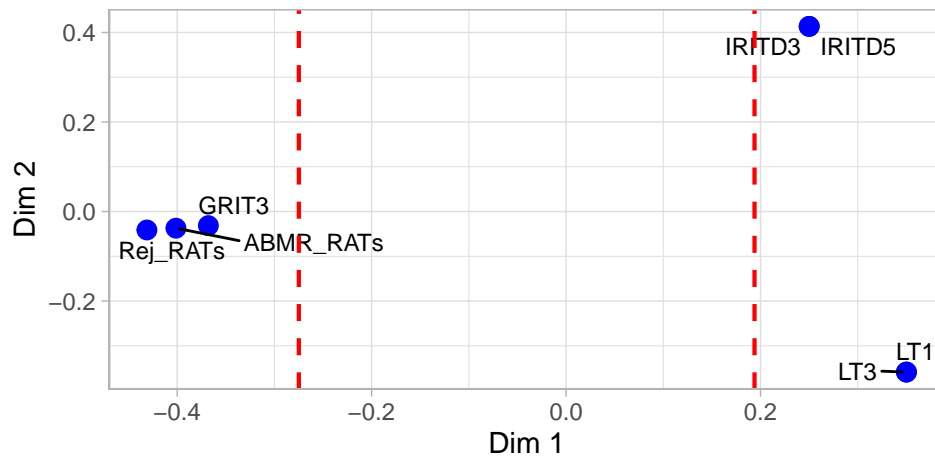
## GO Level: 8

### Irrelevance - Threshold matrix of dissimilarities (CC-8):

	ABMR_RATs	GRIT3	IRITD3	IRITD5	LT1	LT3
GRIT3	0.76					
IRITD3	1.00	1.00				
IRITD5	1.00	1.00	0.93			
LT1	1.00	1.00	1.00	1.00		
LT3	1.00	1.00	1.00	1.00	0.84	
Rej_RATs	0.61	0.68	1.00	1.00	1.00	1.00

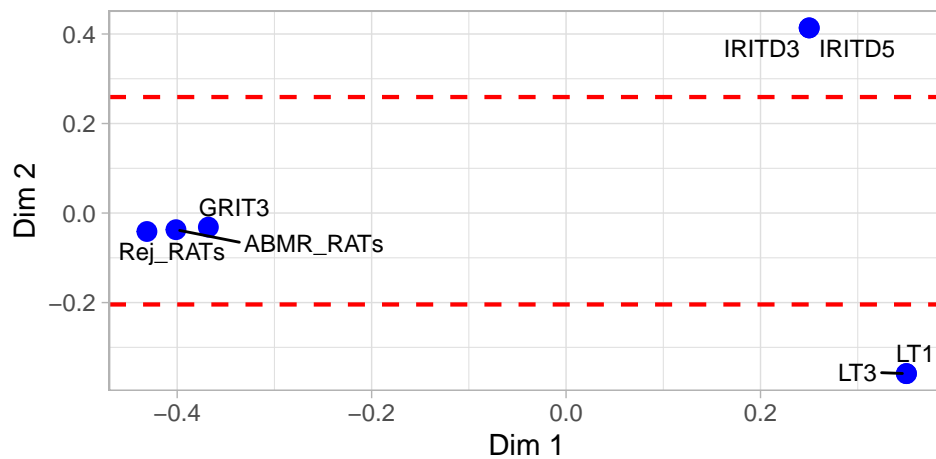
### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-8):

#### Dimension 1:



	Pseudo_t	Description
GO:0005765	10000	lysosomal membrane
GO:0005802	10000	trans-Golgi network
GO:0012507	10000	ER to Golgi transport vesicle membrane
GO:0030133	10000	transport vesicle
GO:0030135	10000	coated vesicle
GO:0030658	10000	transport vesicle membrane
GO:0030662	10000	coated vesicle membrane
GO:0030665	10000	clathrin-coated vesicle membrane
GO:0030666	10000	endocytic vesicle membrane
GO:0030669	10000	clathrin-coated endocytic vesicle membrane
GO:0030670	10000	phagocytic vesicle membrane
GO:0031901	10000	early endosome membrane
GO:0032588	10000	trans-Golgi network membrane
GO:0045334	10000	clathrin-coated endocytic vesicle
GO:0055038	10000	recycling endosome membrane
GO:0098553	10000	luminal side of endoplasmic reticulum membrane
GO:0098852	10000	lytic vacuole membrane

#### Dimension 2:



	Pseudo_t	Description
GO:0002177	10000	manchette
GO:0005858	10000	axonemal dynein complex
GO:0005874	10000	microtubule
GO:0005875	10000	microtubule associated complex
GO:0005879	10000	axonemal microtubule
GO:0005881	10000	cytoplasmic microtubule
GO:0005930	10000	axoneme
GO:0031091	10000	platelet alpha granule
GO:0031093	10000	platelet alpha granule lumen
GO:0034774	10000	secretory granule lumen
GO:0036126	10000	sperm flagellum
GO:0060205	10000	cytoplasmic vesicle lumen
GO:0070820	10000	tertiary granule
GO:1904724	10000	tertiary granule lumen

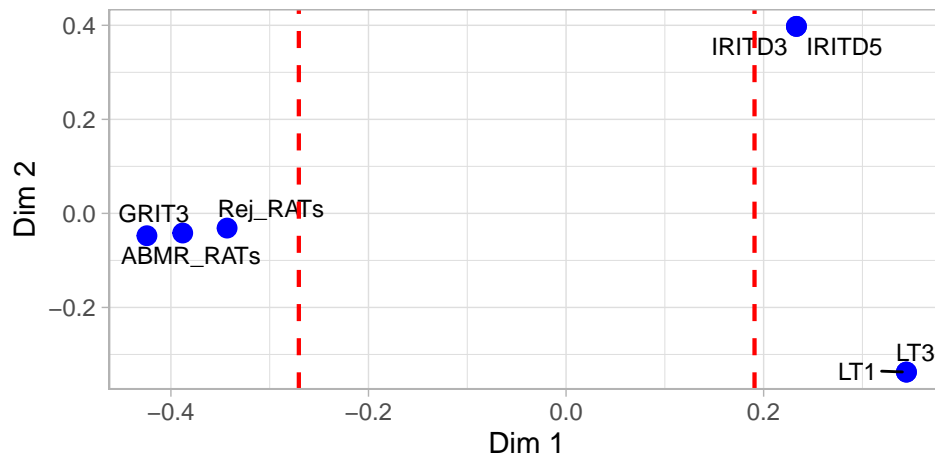
## GO Level: 9

### Irrelevance - Threshold matrix of dissimilarities (CC-9):

	ABMR_RATs	GRIT3	IRITD3	IRITD5	LT1	LT3
GRIT3	0.65					
IRITD3	1.00	1.00				
IRITD5	1.00	1.00	0.99			
LT1	1.00	1.00	1.00	1.00		
LT3	1.00	1.00	1.00	1.00	0.89	
Rej_RATs	0.73	0.81	1.00	1.00	1.00	1.00

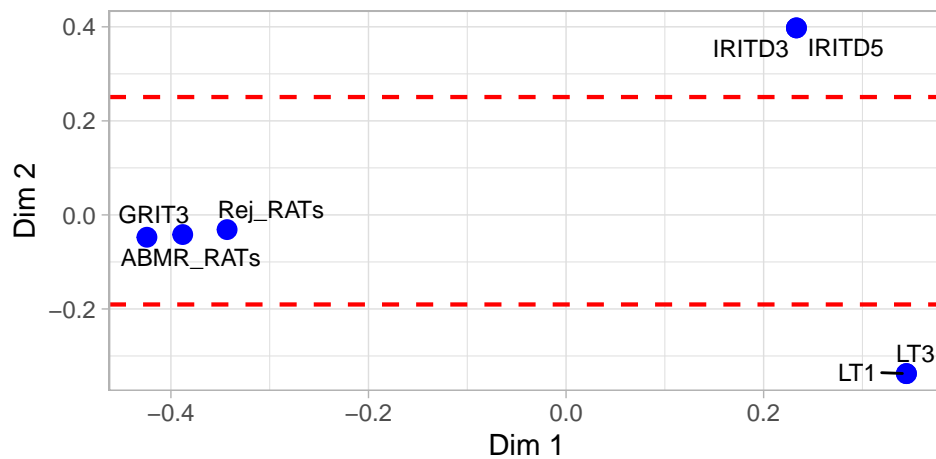
### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-9):

#### Dimension 1:



	Pseudo_t	Description
GO:0005765	10000	lysosomal membrane
GO:0012507	10000	ER to Golgi transport vesicle membrane
GO:0030134	10000	COPII-coated ER to Golgi transport vesicle
GO:0030136	10000	clathrin-coated vesicle
GO:0030658	10000	transport vesicle membrane
GO:0030662	10000	coated vesicle membrane
GO:0030665	10000	clathrin-coated vesicle membrane
GO:0030666	10000	endocytic vesicle membrane
GO:0030669	10000	clathrin-coated endocytic vesicle membrane
GO:0030670	10000	phagocytic vesicle membrane
GO:0031901	10000	early endosome membrane
GO:0032588	10000	trans-Golgi network membrane
GO:0045334	10000	clathrin-coated endocytic vesicle
GO:0045335	10000	phagocytic vesicle
GO:0055038	10000	recycling endosome membrane
GO:0098553	10000	luminal side of endoplasmic reticulum membrane

#### Dimension 2:



	Pseudo_t	Description
GO:0005814	10000	centriole
GO:0005858	10000	axonemal dynein complex
GO:0005879	10000	axonemal microtubule
GO:0005881	10000	cytoplasmic microtubule
GO:0030286	10000	dynein complex
GO:0031093	10000	platelet alpha granule lumen
GO:0034774	10000	secretory granule lumen
GO:0036064	10000	ciliary basal body
GO:0036157	10000	outer dynein arm
GO:0097228	10000	sperm principal piece
GO:1904724	10000	tertiary granule lumen

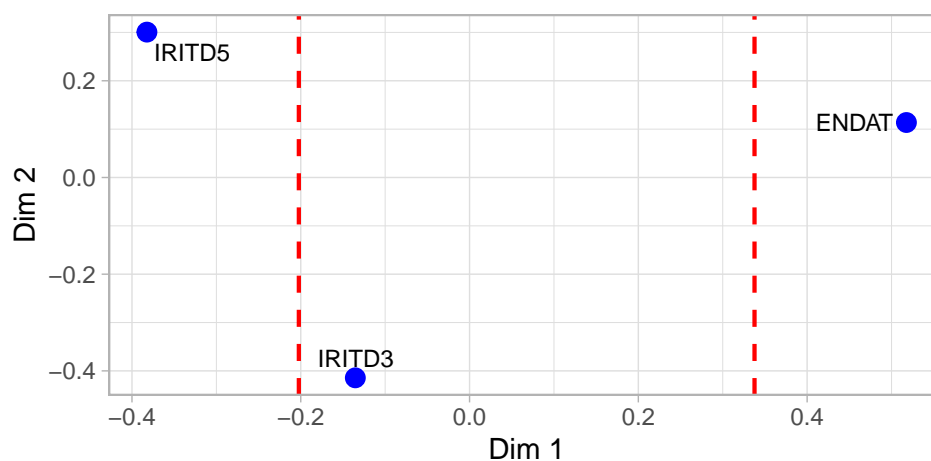
## GO Level: 10

Irrelevance - Threshold matrix of dissimilarities (CC-10):

```
ENDAT IRITD3
IRITD3 0.84
IRITD5 0.92 0.76
```

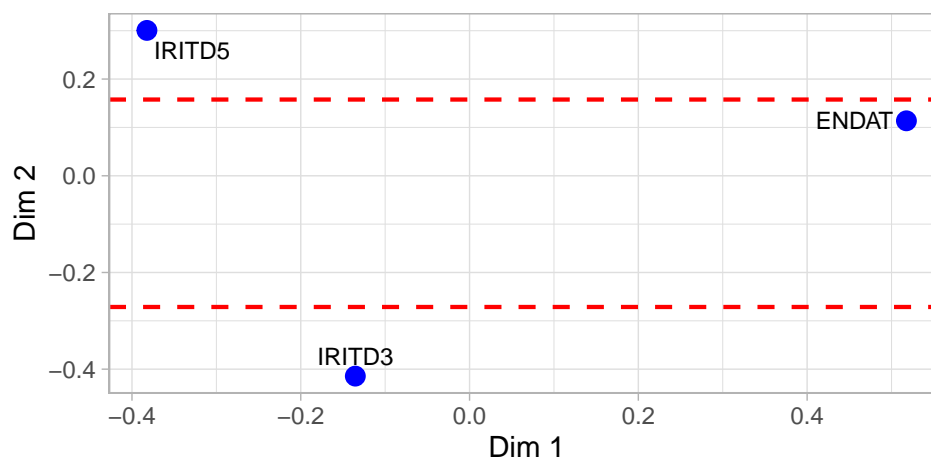
GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (CC-10):

Dimension 1:



	Pseudo_t	Description
GO:0031092	10000	platelet alpha granule membrane
GO:0034774	10000	secretory granule lumen
GO:0035580	10000	specific granule lumen
GO:0070820	10000	tertiary granule

Dimension 2:



	Pseudo_t	Description
GO:0035580	10000	specific granule lumen



## Ontology: MF

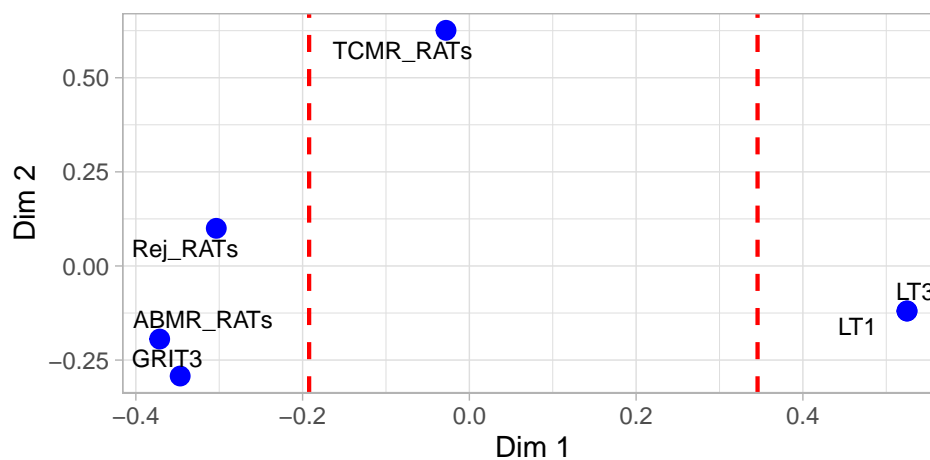
### GO Level: 4

#### Irrelevance - Threshold matrix of dissimilarities (MF-4):

	ABMR_RATs	GRIT3	LT1	LT3	Rej_RATs
GRIT3	0.56				
LT1	1.00	1.00			
LT3	1.00	1.00	0.62		
Rej_RATs	0.69	0.77	1.00	1.00	
TCMR_RATs	0.95	1.00	1.00	1.00	0.85

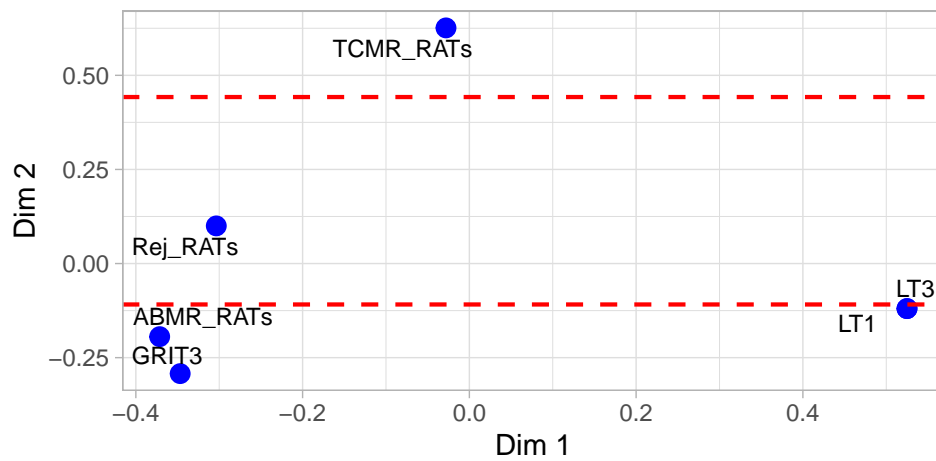
#### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (MF-4):

##### Dimension 1:



	Pseudo_t	Description
GO:0008569	10000	minus-end-directed microtubule motor activity
GO:0023023	10000	MHC protein complex binding
GO:0042277	10000	peptide binding
GO:0042605	10000	peptide antigen binding
GO:0042608	10000	T cell receptor binding
GO:0045504	10000	dynein heavy chain binding
GO:0045505	10000	dynein intermediate chain binding
GO:0051959	10000	dynein light intermediate chain binding
GO:0140375	10000	immune receptor activity

##### Dimension 2:



	Pseudo_t	Description
GO:0015026	10000	coreceptor activity

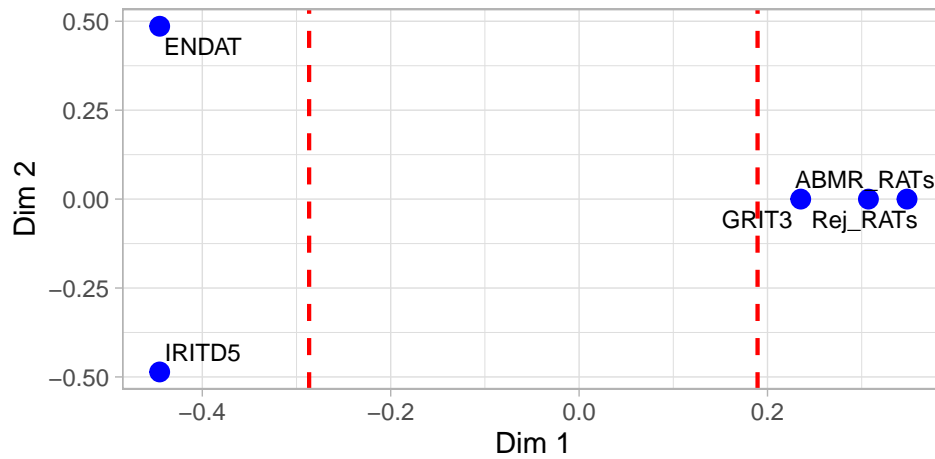
## GO Level: 5

### Irrelevance - Threshold matrix of dissimilarities (MF-5):

	ABMR_RATs	ENDAT	GRIT3	IRITD5
ENDAT	1.00			
GRIT3	0.79	1.00		
IRITD5	1.00	0.97	1.00	
Rej_RATs	0.71	1.00	0.88	1.00

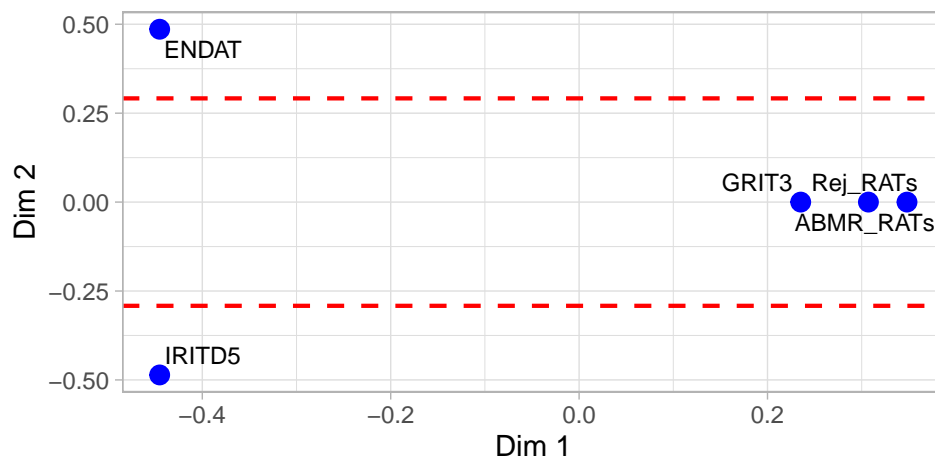
### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (MF-5):

#### Dimension 1:



	Pseudo_t	Description
GO:0001664	10000	G protein-coupled receptor binding
GO:0005126	10000	cytokine receptor binding
GO:0023026	10000	MHC class II protein complex binding
GO:0032395	10000	MHC class II receptor activity
GO:0042605	10000	peptide antigen binding
GO:0042608	10000	T cell receptor binding
GO:0048407	10000	platelet-derived growth factor binding

#### Dimension 2:



	Pseudo_t	Description
GO: 0001228	10000	DNA-binding transcription activator activity, RNA polymerase II-specific
GO: 0004713	10000	protein tyrosine kinase activity
GO: 0008201	10000	heparin binding
GO: 0008656	10000	cysteine-type endopeptidase activator activity involved in apoptotic process
GO: 0016504	10000	peptidase activator activity
GO: 0016641	10000	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor
GO: 0019199	10000	transmembrane receptor protein kinase activity
GO: 0030414	10000	peptidase inhibitor activity
GO: 0050700	10000	CARD domain binding
GO: 0071813	10000	lipoprotein particle binding

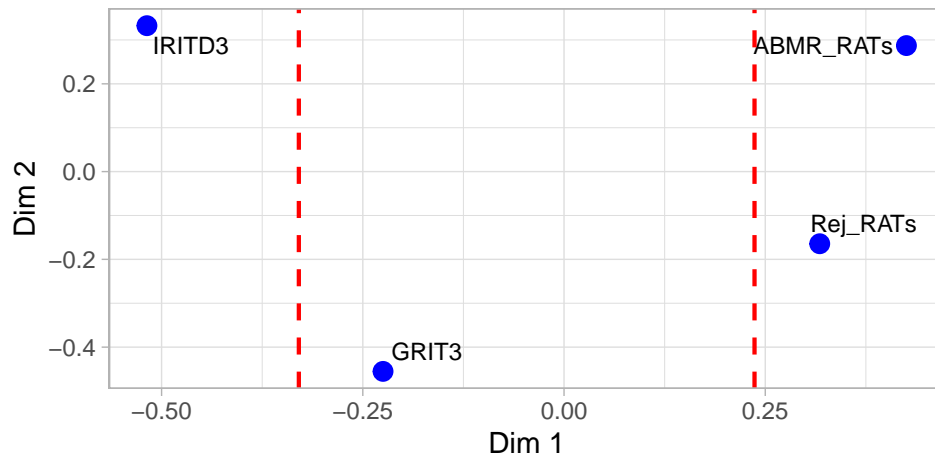
## GO Level: 6

### Irrelevance - Threshold matrix of dissimilarities (MF-6):

	ABMR_RATs	GRIT3	IRITD3
GRIT3	0.99		
IRITD3	1.00	0.89	
Rej_RATs	0.73	0.81	1.00

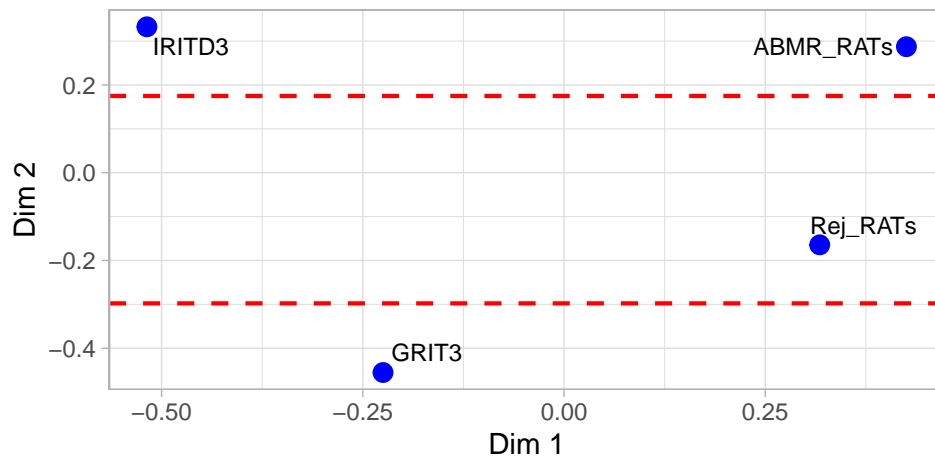
### GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (MF-6):

#### Dimension 1:



	Pseudo_t	Description
GO:0004859	10000	phospholipase inhibitor activity
GO:0005125	10000	cytokine activity
GO:0005525	10000	GTP binding
GO:0019001	10000	guanyl nucleotide binding
GO:0019843	10000	rRNA binding
GO:0032561	10000	guanyl ribonucleotide binding
GO:0042288	10000	MHC class I protein binding
GO:0042379	10000	chemokine receptor binding
GO:0098641	10000	cadherin binding involved in cell-cell adhesion

#### Dimension 2:



	Pseudo_t	Description
GO:0003725	10000	double-stranded RNA binding

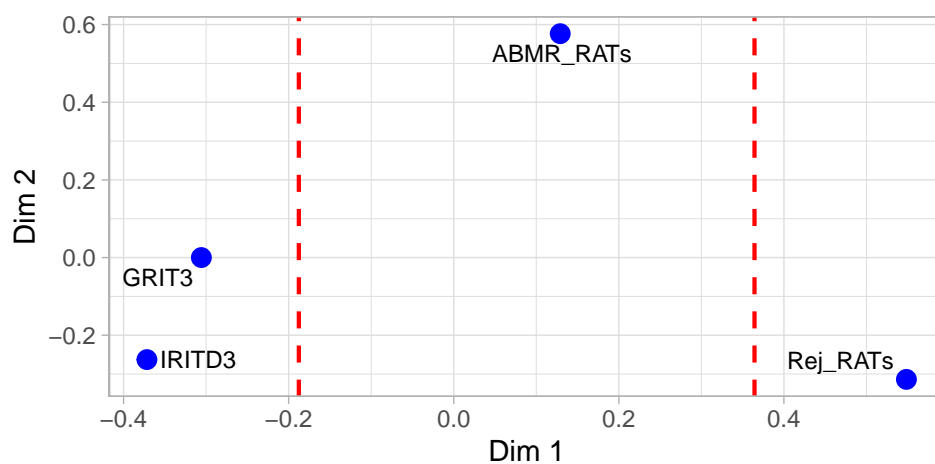
## GO Level: 7

Irrelevance - Threshold matrix of dissimilarities (MF-7):

	ABMR_RATs	GRIT3	IRITD3
GRIT3	0.92		
IRITD3	1.00	0.83	
Rej_RATs	1.00	0.99	1.00

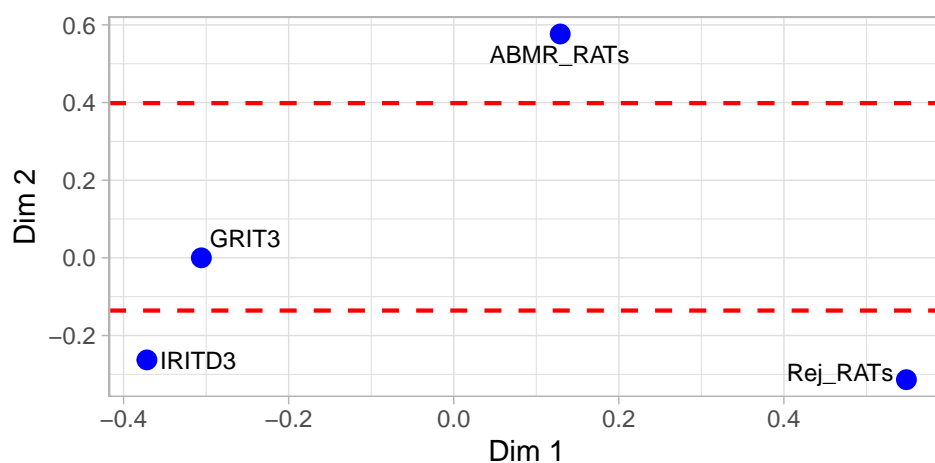
GO terms associated with the dissimilarities in the dimensions of the MDS - Biplot (MF-7):

Dimension 1:



	Pseudo_t	Description
GO:0005525	10000	GTP binding
GO:0019001	10000	guanyl nucleotide binding
GO:0032561	10000	guanyl ribonucleotide binding
GO:0048020	10000	CCR chemokine receptor binding

Dimension 2:



	Pseudo_t	Description
GO:0005525	0.8408964	GTP binding
GO:0008009	0.8408964	chemokine activity
GO:0019001	0.8408964	guanyl nucleotide binding

	Pseudo_t	Description
GO:0032561	0.8408964	guanyl ribonucleotide binding
GO:0045236	0.8408964	CXCR chemokine receptor binding
GO:0048020	0.8408964	CCR chemokine receptor binding
GO:0098641	0.8408964	cadherin binding involved in cell-cell adhesion