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MIDUS 3 RNA Gene Expression

## MIDUS 3 RNA Gene Expression

### **Title**

MIDUS 3 RNA Gene Expression

## Related Materials

## Other

- M3 GeneExpression README
- M3 GeneExpression Documentation

■ M3 RNA Gene Expression				
Title	M3 RNA Gene Expression			
File Name	M3_P6_RNA_Score_N747_20240216.sav			
Case Quantity	747			
Variable Count	28			

## **Topic**

### **Admin**

- M2ID M2 AND MR Public IDs combined in a single variable
- SAMPLMAJ Major sample identification
- · C6RAVAIL Is Gene Expression data available?

## **Technical Variable**

- · C6RPLATE Assay plate number
- C6RMAPPEDREADS Sample RNA quantity (ideally > 5000000)
- C6RMAPPEDPCT Sample RNA quality (% of total RNA sequencing reads that were successfully mapped to the human genome; ideally >= 80% for assay plates 1-30)
- · C6RAVGR Sample transcriptome avg correlation with other samples

## **Composite Score**

- C6RCCTRA CTRA composite score (centered log2 gene expression values)
- · C6RCINFLAM CTRA Inflammatory sub-component (centered log2 gene expression values)
- C6RCIFN CTRA Interferon/Antibody sub-component (centered log2 gene expression values)
- C6RZCTRA CTRA composite score (z-scored log2 gene expression values)
- · C6RZINFLAM CTRA Inflammatory sub-component (z-scored log2 gene expression values)
- C6RZIFN CTRA Interferon/Antibody sub-component (z-scored log2 gene expression values)
- C6RCCDKN2A CDKN2A RNA abundance (centered measure)
- C6RCDDR30 30 DNA Damage Response (DDR30) composite score (average of centered values)
- C6RZDDR30 30 DNA Damage Response (DDR30) composite score (average of z-transformed values)
- · C6RCSASP10 10 Senescence Associated Secretory Phenotype (SASP10) composite score (average of centered values)
- · C6RZSASP10 10 Senescence Associated Secretory Phenotype (SASP10) composite score (average of z-transformed values)
- · C6RCSASP57 57 Senescence Associated Secretory Phenotype (SASP57) composite score (average of centered values)
- C6RZSASP57 57 Senescence Associated Secretory Phenotype (SASP57) composite score (average of z-transformed values)

## **Transcript Variable**

- · C6RCD3E Expression level for CD3E gene (log2-transform of normalized TPM value)
- · C6RCD3D Expression level for CD3D gene (log2-transform of normalized TPM value)
- · C6RCD4 Expression level for CD4 gene (log2-transform of normalized TPM value)
- · C6RCD8A Expression level for CD8A gene (log2-transform of normalized TPM value)
- · C6RCD14 Expression level for CD14 gene (log2-transform of normalized TPM value)
- · C6RCD19 Expression level for CD19 gene (log2-transform of normalized TPM value)
- · C6RFCGR3A Expression level for FCGR3A gene (log2-transform of normalized TPM value)
- · C6RNCAM1 Expression level for NCAM1 gene (log2-transform of normalized TPM value)

## Topic

## Admin

M2ID - MIDUS Core ID - Public use			
Туре	Numeric (Integer)		
Display Values	2		
Stats	1		

Valid	Invalid	Minimum	Maximum	Mean	StdDev
747	0	10019	19193	14673.105	2692.3610

## SAMPLMAJ - Major sample identification Type Code

			Frequency	% of total	% of valid
Valid	1	CORE MAIN RDD	342	45.78%	45.78%
	2	CORE SIBLING	5	0.67%	0.67%
	3	CORE TWIN	284	38.02%	38.02%
	4	CORE CITY OVERSAMPLE	13	1.74%	1.74%
	13	CORE MILWAUKEE	103	13.79%	13.79%
	20	REFRESHER MAIN		0%	0%
	21	REFRESHER MILWAUKEE		0%	0%
		Total	747	100%	100%

Valid	Invalid	Minimum	Maximum
747	0	1	13

C6RAVAIL - Is Gene Expression data available?			
Туре	Code		
ForwardSkip	IF <u>C6RAVAIL</u> = 2 TO 5, SKIP <u>C6RPLATE</u> TO <u>C6RNCAM1</u>		
Display Values	1		
Stats	1		

Frequency	% of total	% of valid

Valid	1	YES, AVAILABLE	672	89.96%	89.96%
	2	NO, DID NOT CONSENT TO GENETICS	10	1.34%	1.34%
	3	NO, NO CPT SAMPLE	8	1.07%	1.07%
4	4	NO, SAMPLE INSUFFICIENT OR ASSAY INVALID	49	6.56%	6.56%
	5	NO, DID NOT SEND A SAMPLE FOR PROCESSING	8	1.07%	1.07%
		Total	747	100%	100%

Valid	Invalid	Minimum	Maximum
747	0	1	5

## Technical Variable

C6RPLATE - Assay plate number			
Туре	Numeric (Integer)		
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)		
Display Values	1		
Stats	1		

			Frequency	% of total	% of valid
Missing	98	MISSING	49	6.56%	
	99	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	11	42	25.132440	10.035942

C6RMAPPEDREADS - Sample RNA quantity (ideally > 5000000)				
Type Numeric (Integer)				
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)			
Display Values	2			
Stats	2			

		Frequency	% of total	% of valid
Missing	9999998 MISSING	49	6.56%	
	9999999 INAPP	26	3.48%	
	Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	5319373	37313415	13613949	2914738.8

 $^{56}$  C6RMAPPEDPCT - Sample RNA quality (% of total RNA sequencing reads that were successfully mapped to the human genome; ideally >= 80% for assay plates 1-30)

Туре	Numeric (Double)
Numeric Details	Decimals: 4

Frequency	% of total	% of valid

Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0.3893	0.99	0.8984495	0.1132771

## Type Numeric (Double) Numeric Details Decimals: 4 BackwardSkip (CGRAVAIL = 2,3,4,5) Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0.52	0.954	0.8281857	0.0904647

## Composite Score

C6RCCTRA - CTRA composite score (centered log2 gene expression values)				
Туре	Numeric (Double)			
Numeric Details	Decimals: 5			
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)			
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'			
Display Values	2			
Stats	2			

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-2.94124	2.1073	-9.62E-5	0.6785659

	C6RCINFLAM - CTRA Inflammatory sub-component (centered log2 gene expression values)			
Туре	Numeric (Double)			
Numeric Details	Decimals: 5			
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)			
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'			
Display Values	2			
Stats	2			

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-3.36915	2.57488	-0.003651	0.9727407

# C6RCIFN - CTRA Interferon/Antibody sub-component (centered log2 gene expression values) Type Numeric (Double) Numeric Details Decimals: 5 BackwardSkip (C6RAVAIL = 2,3,4,5) Notes Computed Variable, see 'M3\_P6\_GeneExpression\_Documentation' Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-4.28869	2.40257	-0.003554	0.9988600

## 🌃 C6RZCTRA - CTRA composite score (z-scored log2 gene expression values)

Туре	Numeric (Double)
Numeric Details	Decimals: 5
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-1.2327	1.13959	3.86E-4	0.3036184

## C6RZINFLAM - CTRA Inflammatory sub-component (z-scored log2 gene expression values)

Туре	Numeric (Double)
Numeric Details	Decimals: 5
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-1.53594	1.57165	-0.001352	0.4327122

# Type Numeric (Double) Numeric Details Decimals: 5 BackwardSkip (C6RAVAIL = 2,3,4,5) Notes Computed Variable, see 'M3\_P6\_GeneExpression\_Documentation' Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-1.91605	1.04797	-0.001738	0.4249600

## Type Numeric (Double) Numeric Details Decimals: 5 BackwardSkip (C6RAVAIL = 2,3,4,5) Notes Computed Variable, see 'M3\_P6\_GeneExpression\_Documentation' Display Values 2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

2

Stats

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-2.29309	9.24376	-0.005190	2.4859624

C6RCDDR30 - 30 DNA Damage Response (DDR30) composite score (average of centered values)		
Туре	Numeric (Double)	
Numeric Details	Decimals: 5	
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)	
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'	
Display Values	2	
Stats	2	

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-4.29225	2.11738	-0.005526	1.2270858

# Type Numeric (Double) Numeric Details Decimals: 5 BackwardSkip (C6RAVAIL = 2,3,4,5) Notes Computed Variable, see 'M3\_P6\_GeneExpression\_Documentation' Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-1.73718	0.89373	-0.002183	0.4842768

## $^{\&\&}$ C6RCSASP10 - 10 Senescence Associated Secretory Phenotype (SASP10) composite score (average of centered values)

Туре	Numeric (Double)
Numeric Details	Decimals: 5
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-0.53225	2.12463	4.69E-4	0.4519743

## $^{\&\&}$ C6RZSASP10 - 10 Senescence Associated Secretory Phenotype (SASP10) composite score (average of z-transformed values)

Туре	Numeric (Double)
Numeric Details	Decimals: 5
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'

Display Values	2	
Stats	2	

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-0.31404	3.26159	6.73E-4	0.3736719

🅯 C6RCSASP57 - 57 Senescence Associated Secretory Phenotype (SASP57) composite score (average of centered values)

Туре	Numeric (Double)
Numeric Details	Decimals: 5
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-1.64281	1.37589	-0.001827	0.5395554

C6RZSASP57 - 57 Senescence Associated Secretory Phenotype (SASP57) composite score (average of z-transformed values)

Туре	Numeric (Double)
Numeric Details	Decimals: 5
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Notes	Computed Variable, see 'M3_P6_GeneExpression_Documentation'
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	49	6.56%	
	99.00000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	-0.81829	0.82615	-8.68E-4	0.2677405

Transcript Variable

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Туре	Numeric (Double)
Numeric Details	Decimals: 4
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0	15.9196	8.6614361	1.7492620

## C6RCD3D - Expression level for CD3D gene (log2-transform of normalized TPM value) Type Numeric (Double) Numeric Details Decimals: 4 BackwardSkip (C6RAVAIL = 2,3,4,5) Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0	17.8885	8.8263584	1.9511795

## C6RCD4 - Expression level for CD4 gene (log2-transform of normalized TPM value) Type Numeric (Double) Numeric Details Decimals: 4 BackwardSkip (C6RAVAIL = 2,3,4,5) Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	2.3171	17.6255	9.0022623	1.4054494

SCERCD8A - Expression level for CD8A gene (log2-transform of normalized TPM value)				
Туре	Numeric (Double)			
Numeric Details	Decimals: 4			

BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)
Display Values	2
Stats	2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0	12.825	6.5003101	2.7182129

## C6RCD14 - Expression level for CD14 gene (log2-transform of normalized TPM value) Type Numeric (Double) Numeric Details Decimals: 4 BackwardSkip (C6RAVAIL = 2,3,4,5) Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	2.4792	14.8701	10.237504	1.5692914

## C6RCD19 - Expression level for CD19 gene (log2-transform of normalized TPM value) Type Numeric (Double) Numeric Details Decimals: 4 BackwardSkip (C6RAVAIL = 2,3,4,5) Display Values 2 Stats 2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0	12.9862	4.5474974	3.0048791

C6RFCGR3A - Expression level for FCGR3A gene (log2-transform of normalized TPM value)				
Туре	Numeric (Double)			
Numeric Details	Decimals: 4			
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)			
Display Values	2			

## Stats 2

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	1.0312	17.3325	8.8689779	1.7611260

C6RNCAM1 - Expression level for NCAM1 gene (log2-transform of normalized TPM value)				
Туре	Numeric (Double)			
Numeric Details	Decimals: 4			
BackwardSkip	( <u>C6RAVAIL</u> = 2,3,4,5)			
Display Values	2			
Stats	2			

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	49	6.56%	
	99.0000	INAPP	26	3.48%	
		Total	75	10.04%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
672	75	0	12.8588	5.6667651	2.8042307