

MIDUS RNA

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Title

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Related Materials

Documentation

- [MIDUS Refresher Gene Expression README](#)
- [MIDUS Refresher Gene Expression Documentation](#)

MR1_P6_RNA_SCORE

Title	MR1_P6_RNA_SCORE
File Name	MR1_P6_RNA_SCORE_N863_20210923.sav
Case Quantity	863
Variable Count	27

MRID - MIDUS REFRESHER ID - PUBLIC USE

Type	Numeric (Long)				
Valid	Invalid	Minimum	Maximum	Mean	StdDev
863	0	30024	39977	35068.411...	2875.3368...

SAMPLMAJ - Major sample identification

Type	Code	
20	REFRESHER MAIN	
21	REFRESHER MILWAUKEE	

RA6RAVAIL - Is Gene Expression data available?

Type	Code
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Valid			Frequency	% of total	% of valid
	1	YES, AVAILABLE	543	62.92%	62.92%
	2	NO, DID NOT CONSENT TO GENETICS	27	3.13%	3.13%
	3	NO, NO CPT SAMPLE	22	2.55%	2.55%
	4	NO, SAMPLE INSUFFICIENT OR ASSAY INVALID	269	31.17%	31.17%
	5	NO, DID NOT SEND A SAMPLE FOR PROCESSING	2	0.23%	0.23%
		Total	863	100%	100%

Valid	Invalid	Minimum	Maximum
863	0	1	5

RA6RPLATE - Assay plate number

Type	Numeric (Integer)				
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			Frequency	% of total	% of valid
Missing	98	MISSING	269	31.17%	
	99	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	1	8	4.8084714...	2.2036873...

RA6RRIN - RNA integrity number (1-10) for sample

Type	Numeric (Double)				
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Numeric Details	Decimals: 1				
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			Frequency	% of total	% of valid
Missing	98.0	MISSING	269	31.17%	
	99.0	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	3	9.2	5.8767955...	1.4640007...

RA6RAVGR - Sample transcriptome avg correlation with other samples

Type	Numeric (Double)				
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Numeric Details	Decimals: 2				
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			Frequency	% of total	% of valid
Missing	98.00	MISSING	269	31.17%	
	99.00	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0.85	0.93	0.8973296...	0.0198159...

RA6RCCTRA - CTRA composite score (centered log2 gene expression values)

Type	Numeric (Double)				
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Numeric Details	Decimals: 4				
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			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	

		Total	320	37.08%	
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Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-2.1308	1.2965	0.0023635...	0.4545753...

RA6RCINFLAM - CTRA Inflammatory sub-component (centered log2 gene expression values)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.28413	1.17432	0.0035150...	0.4606089...

RA6RCIFNAB - CTRA Interferon/Antibody sub-component (centered log2 gene expression values)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.55794	2.55355	0.0011515...	0.6071401...

RA6RZCTRA - CTRA composite score (z-scored log2 gene expression values)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.9289	1.64994	0.0025524...	0.4383233...

RA6RZINFLAM - CTRA Inflammatory sub-component (z-scored log2 gene expression values)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.33251	1.39099	0.0043086...	0.4665402...

RA6RZIFNAB - CTRA Interferon/Antibody sub-component (z-scored log2 gene expression values)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.35626	2.37893	0.0017563...	0.5468200...

RA6RCCDKN2A - CDKN2A RNA abundance (centered measure)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.51975	3.24465	1.27E-6	0.7052911...

RA6RCDDR30 - 30 DNA Damage Response (DDR30) composite score (average of centered values)

Type	Numeric (Double)
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Numeric Details	Decimals: 5
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			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	


Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.17454	0.9501	-1.29E-7	0.3915073...

 RA6RZDDR30 - 30 DNA Damage Response (DDR30) composite score (average of z-transformed values)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.37446	1.22977	9.21E-8	0.4387049...

 RA6RCSASP10 - 10 Senescence Associated Secretory Phenotype (SASP10) composite score (average of centered values)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.13115	0.52795	4.42E-7	0.1215299...

 RA6RZSASP10 - 10 Senescence Associated Secretory Phenotype (SASP10) composite score (average of z-transformed values)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
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Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.20033	3.15151	-1.03E-6	0.3197746...

RA6RCSASP57 - 57 Senescence Associated Secretory Phenotype (SASP57) composite score (average of centered values)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.54003	0.53403	1.1E-7	0.2101645...

RA6RZSASP57 - 57 Senescence Associated Secretory Phenotype (SASP57) composite score (average of z-transformed values)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.17%	
	99.00000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.59745	1.04385	1.66E-7	0.2501139...

RA6RCD3E - Expression level for CD3E gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	1.868	7.00564	5.4009285...	0.6593612...

RA6RCD3D - Expression level for CD3D gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	8.38828	5.5911142...	1.1664969...

RA6RCD4 - Expression level for CD4 gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0.11246	7.35442	5.1046620...	1E+0

RA6RCD8A - Expression level for CD8A gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	8.23463	3.9865448...	1.2369187...

RA6RCD14 - Expression level for CD14 gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0.5971	9.58999	7.0541234...	1.3758446...

RA6RCD19 - Expression level for CD19 gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	7.50788	3.6992639...	1.2105926...

RA6RFCGR3A - Expression level for FCGR3A gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	8.21584	5.2167539...	1.4739178...

RA6RNCAM1 - Expression level for NCAM1 gene (log2-transform of normalized TPM value)

Type	Numeric (Double)
Numeric Details	Decimals: 4

			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.17%	
	99.0000	INAPP	51	5.91%	
		Total	320	37.08%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	5.4208	2.8529126...	1.1774758...