

MIDUS RNA

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Title

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Related Materials

Documentation

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

MR_P6_RNA_SCORE_N863_20210106

Title	MR_P6_RNA_SCORE_N863_20210106
File Name	MR_P6_RNA_SCORE_N863_20210106.sav
Case Quantity	863
Variable Count	26

MRID - MIDUS REFRESHER ID - PUBLIC USE

Type	Numeric (Long)				
Valid	Invalid	Minimum	Maximum	Mean	StdDev
863	0	30024	39977	35068.41	2875.34

RA6RAVAIL - Is Gene Expression data available?

Type	Code
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			Frequency	% of total	% of valid
Valid	1	YES, AVAILABLE	543	62.9%	62.9%
	2	NO, DID NOT CONSENT TO GENETICS	27	3.1%	3.1%
	3	NO, NO CPT SAMPLE	22	2.5%	2.5%
	4	NO, SAMPLE INSUFFICIENT OR ASSAY INVALID	269	31.2%	31.2%
	5	NO, DID NOT SEND A SAMPLE FOR PROCESSING	2	0.2%	0.2%
		Total	863	100.0%	100%

Valid	Invalid	Minimum	Maximum
863	0	1	5

RA6RPLATE - Assay plate number

Type Numeric (Integer)

			Frequency	% of total	% of valid
Missing	98	MISSING	269	31.2%	
	99	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	1	8	4.81	2.2

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

Type Numeric (Double)

Numeric Details Decimals: 1

			Frequency	% of total	% of valid
Missing	98.0	MISSING	269	31.2%	
	99.0	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	3	9.2	5.88	1.46

RA6RAVGR - Sample transcriptome avg correlation with other samples

Type Numeric (Double)

Numeric Details Decimals: 2

			Frequency	% of total	% of valid
Missing	98.00	MISSING	269	31.2%	
	99.00	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0.85	0.93	0.9	0.02


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

Type Numeric (Double)

Numeric Details	Decimals: 4
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			Frequency	% of total	% of valid
Missing	98.0000	MISSING	269	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	


Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-2.13	1.3	0	0.45

 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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.28	1.17	0	0.46

 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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.56	2.55	0	0.61

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.93	1.65	0	0.44

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.33	1.39	0	0.47

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.36	2.38	0	0.55

RA6RCCDKN2A - CDKN2A RNA abundance (centered measure)

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.2%	
	99.00000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.52	3.24	0	0.71

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

Type	Numeric (Double)
Numeric Details	Decimals: 5

			Frequency	% of total	% of valid
Missing	98.00000	MISSING	269	31.2%	
	99.00000	INAPP	51	5.9%	
		Total	320	37.1%	


Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.17	0.95	0	0.39

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	31.2%	
	99.00000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-1.37	1.23	0	0.44

 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	31.2%	
	99.00000	INAPP	51	5.9%	
		Total	320	37.1%	


Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.13	0.53	0	0.12

 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
Missing	98.00000	MISSING	269	31.2%	
	99.00000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.2	3.15	0	0.32

 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	31.2%	
	99.00000	INAPP	51	5.9%	

		Total	320	37.1%	
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Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.54	0.53	0	0.21

 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	31.2%	
	99.00000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	-0.6	1.04	0	0.25

 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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	1.87	7.01	5.4	0.66

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

Type	Numeric (Double)
Numeric Details	Decimals: 4

	Frequency	% of total	% of valid
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Missing	98.0000	MISSING	269	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	8.39	5.59	1.17

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0.11	7.35	5.1	1

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	8.23	3.99	1.24

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	


Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0.6	9.59	7.05	1.38

 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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	


Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	7.51	3.7	1.21

 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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	8.22	5.22	1.47

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

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	31.2%	
	99.0000	INAPP	51	5.9%	
		Total	320	37.1%	

Valid	Invalid	Minimum	Maximum	Mean	StdDev
543	320	0	5.42	2.85	1.18