# **Data**Sheet



## Clariom<sup>™</sup> S solutions for human, mouse, and rat

Gene-level whole-transcriptome expression profiling solutions for the fastest path to actionable results

Obtain a gene-level view of the transcriptome with Clariom S solutions, providing the fastest, simplest, and most scalable path to measure gene-level expression across the transcriptome. With extensive coverage of all well-annotated genes, compatibility with clinical sample types, scalable formats, and flexible data analysis software, Clariom S solutions are the smartest tools to find expression biomarkers with known function quickly, easily, and cost effectively.

#### Simple, swift biomarker discovery.

- Accurately measure gene-level expression from >20,000 well-annotated genes to get to answers quickly.
- Choose a format that suits your throughput needs, processing from 1 to 192 samples a day.
- Go from data to insight in minutes with intuitive, highly visual, free analysis software designed for the biologist.

#### When you have precious samples, get it right the first time.

- Generate robust expression profiles from as little as 100 pg of total RNA—as few as 10 cells.
- Utilize RNA from various sample types including blood, cells, and fresh/fresh frozen or FFPE tissues.
- Preserve sample integrity and reduce data variability with an assay that does not require a globin or rRNA removal step.
- Save time and money with fully automated sample preparation options.

Clariom S solutions are available in formats for single-sample (cartridge array) processing on the GeneChip® 3000 instrument system and high-throughput, automated (array plate) processing on GeneTitan® Instrument, offering the flexibility to accommodate both small and large cohort studies. The solutions include reagents and fast, simple Transcriptome Analysis Console (TAC) Software to analyze and visualize global expression patterns and pathways.

Content summary	Human <sup>1</sup>	Mouse <sup>1</sup>	Rat <sup>1</sup>	Performance specifications	Human, mouse, ra
Genes <sup>1</sup>	>20,800	>22,100	>22,900	Total RNA input required <sup>3</sup>	100 pg–500 ng
Transcripts <sup>1</sup>	>337,100	>150,300	>129,800	Sensitivity	≥1.5 pM
				Detectable 2-fold change	1:100,000 vs. 1:50,0
Total probes <sup>1</sup>	>211,300	>221,900	>231,800	Dynamic range	~3 logs
Probes targeting genes <sup>1</sup>	>205,800	>221,300	>229,500	Technical replicate signal correlation	≥0.90
Probe length (bases)	25	25	25	Correlation coefficient (intra-lot)	≥0.99
J ( )				cRNA yield	≥20 µg
Probe feature size <sup>1</sup>	5 µm	5 µm	5 µm	cDNA yield	≥6 µg
Background probes	Antigenomic set	Antigenomic set	Antigenomic set	Controls <sup>4,5</sup>	92 ERCC transcripts Poly-A ( <i>dap, lys, phe</i>
Probe orientation <sup>2</sup>	Anti-sense	Anti-sense	Anti-sense	Fluidics script	FS450_0007

#### Get the coverage you require, the reproducibility you need, and the insights you want to act on your discoveries. Now.

1. Numbers are representative annotation as of April, 2016. All numbers have been rounded down to the nearest hundred

2. The probes tiled on the array are designed in the anti-sense orientation, requiring sense-strand labeled targets to be hybridized to the array.

3. Total RNA input requirements are dependent on the amount of available total RNA and sample source. Different assays are required for different input amounts and sample source.

4. Probe sets interrogating external RNA controls present in the Ambion® ERCC RNA Spike-In Control Mixes, P/N 4456740 and 4456739 (purchased from Thermo Fisher Scientific).

5. The arrays contain probe sets for both ERCC and Poly-A spike-in controls. Sequence homology between the two control mixes will result in cross-hybridization of target to the control probes on the arrays. It is important to use only one control probe set when processing the arrays (ERCC or Poly-A controls), but not both.

Data sources			
	Human	Mouse	Rat
Ensembl	>20,000	>21,700	>20,500
VEGA	>19,900	>14,700	_
NONCODE	>12,200	>9,200	-
IncRNAWiki	>12,000	_	_
UCSC Genes	>19,800	>21,000	_
AceView	>10,800	_	>18,000
miTranscriptome	>10	-	-
RefSeq	>19,500	>20,800	>16,500
MGC	>17,100	>17,300	>6,400
MGI	-	>21,300	_
RGD	-	-	>21,700
Consensus CDS	>18,500	_	_
RNA Central	>1,100	-	-
circBase	>11,500	_	_
Human Body Map	>400	-	-
lincRNAdb	>10	>10	>2
Publication-specific gene sets <sup>2,3,4,5</sup>	>3,000	-	>8,020
Non-overlapping orthologous mouse gene and transcript models <sup>1</sup>	_	_	>20

1. Numbers are representative annotation as of April, 2016. All numbers have been rounded down to the nearest hundred.

2. Luo, H., et al. Comprehensive characterization of 10,571 mouse large intergenic noncoding RNAs from whole transcriptome sequencing. PLoS ONE 8(8):e70835 (2013).

3. Chalmel, F., et al. High-resolution profiling of novel transcribed regions during rat spermatogenesis. Biology of Reproduction 91(1):5 (2014).

4. Williams, W. P., et al. Increased levels of B1 and B2 SINE transcripts in mouse fibroblast cells due to minute virus of mice infection. Virology **327**(2):233-241 (2004).

5. Guo, J. U., et al. Expanded identification and characterization of mammalian circular RNAs. Genome Biology **15**(7):409 (2014).

#### **Ordering information**

Assays for 100 pg-50 ng of total RNA isolated from whole blood, cultured cells, and fresh/fresh frozen or FFPE tissues.

Part number	Product description	Pack size (reactions)
902928		12
902929	Clariom <sup>™</sup> S Pico Assay, human	30
902932	Clariom™ S Pico Assay, mouse	12
902933		30
902936	Clariom <sup>™</sup> S Pico Assay, rat	12
902937	Cianoffi S Fico Assay, rat	30
900720	GeneChip <sup>®</sup> Hybridization, Wash, and Stain Kit	30

Assays for 50–500 ng of total RNA isolated from whole blood, cultured cells, and fresh/fresh frozen tissues.

Part number	Product description	Pack size (reactions)
902926	Clariom <sup>™</sup> S Assay, human	10
902927		30
902930	Clariom <sup>™</sup> S Assay, mouse	10
902931	Cianom S Assay, mouse	30
902934	Clariam™ S. Accay rat	10
902935	Clariom <sup>™</sup> S Assay, rat	30
900720	GeneChip <sup>®</sup> Hybridization, Wash, and Stain Kit	30

#### **Ordering information (continued)**

Assays for 100 pg–50 ng of total RNA isolated from whole blood analysis on GeneTitan Instrument.

Part number	Product description	Pack size (reactions)
902963	Clarion <sup>™</sup> S Dico Accay HT human	241
902964	Clariom™ S Pico Assay HT, human	96
902965	Clariom™ S Pico Assay HT, mouse	241
902966		96
902967	Clariom <sup>™</sup> S Pico Assay HT, rat	241
902968		96
901622	GeneChip <sup>®</sup> Hybridization, Wash, and Stain Kit	96

1. The library preparation portion of this assay contains enough material to process 24 samples on the Beckman FX Biomek® FX<sup>P</sup> Target Prep Express, or 30 samples using the manual protocol.

### Assays for 50–500 ng of total RNA isolated from whole blood, cultured cells, and fresh/fresh frozen tissues for analysis on GeneTitan Instrument.

Part number	Product description	Pack size (reactions)
902969	Clariom™ S Assay HT, human	241
902970	Cianom - 5 Assay m, numan	96
902971	Clariom™ S Assay HT, mouse	24 <sup>1</sup>
902972	Cianom - 5 Assay m, mouse	96
902973	Clariom™ S Assay HT, rat	241
902974	Cianoni - 5 Assay III, Tat	96
901622	GeneChip <sup>®</sup> Hybridization, Wash, and Stain Kit	96

1. The library preparation portion of this assay contains enough material to process 24 samples on the Beckman FX Biomek® FX<sup>®</sup> Target Prep Express, or 30 samples using the manual protocol.

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P/N EMI07387 Rev. 2

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#### Assays for 100 pg-50 ng of total RNA isolated from whole blood, cultured cells, and fresh/fresh frozen or FFPE tissues for