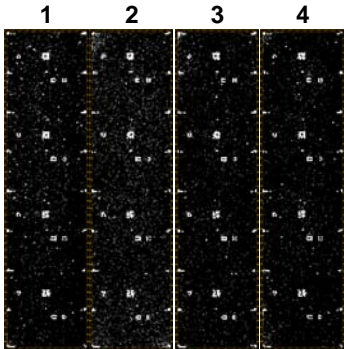


Rapid Genotyping with the Influenza A Detection System, ElectraSense™ Reader and the Re-Usable Combimatrix Microarray

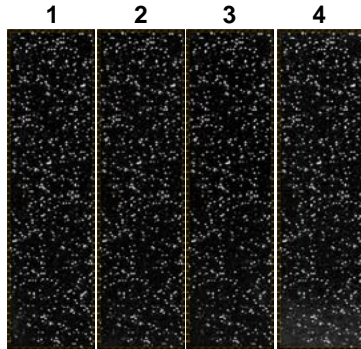
Step 1: Quality Control

Experimental microarrays are thoroughly tested to pass quality control standards which are specific for the ElectraSense™ Reader. Functionality and reproducibility are ensured through the CombiMatrix quality control process.



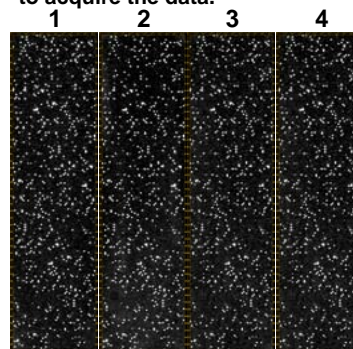
Assay 1: Gene Expression

Microarrays were first hybridized for 18 hours with a population of biotin labeled non-specific RNA generated from K562 (human CML cell line) and known concentrations of Lambda RNA. After an 18 hour hybridization the arrays were read using the ElectraSense™ Reader.



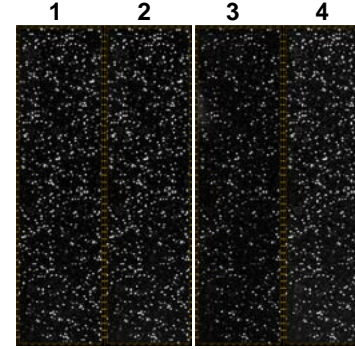
Assay 2: Strip and Rapid Genotyping

Microarrays were chemically stripped of hybridized K562 RNA, the same chips were re-hybridized with Viral RNA which was reverse transcribed and PCR amplified using the CombiMatrix Influenza A Detection System. The hybridization time was one hour after which the ElectraSense Reader™ was used to acquire the data.



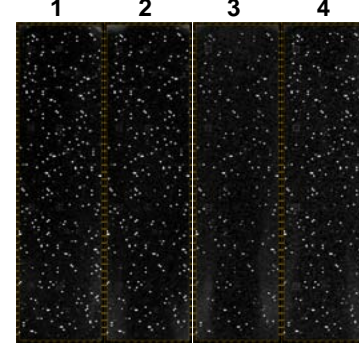
Assay 3: Strip and Gene Expression

After stripping of the influenza RNA the same set of microarrays were again re-hybridized with K562 RNA and Lambda RNA spike-in controls to assess performance. No residual influenza PCR products were detectable.

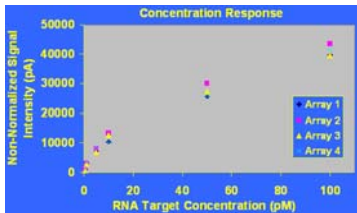


Assay 4: Strip and Rapid Genotype

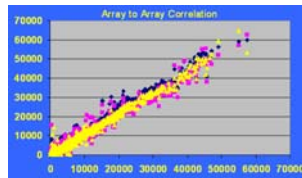
The third and final strip was performed and a different influenza sub-type (H4N8) was hybridized to the array and data collected using the ElectraSense™ Reader. Each of the four chips made the proper call of H4N8. In most cases a signal to noise ratio of 10 was indicated.



CombiMatrix Influenza A Detection System:
Influenza A Research Microarrays
ElectraSense™ Reader
ElectraSense™ Software

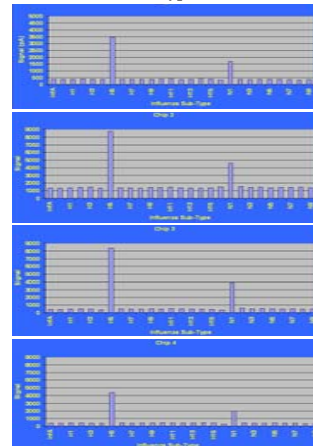


Spike-in Lambda RNA concentrations of 1 and 0.375 pM were distinguishable with an average signal to noise ratio of 5:1 and 2:1 respectively.

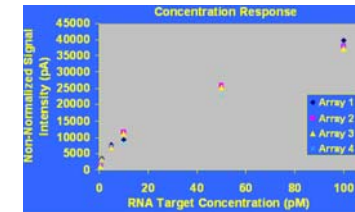


Average Pearson Correlation between the 4 arrays was 0.98.

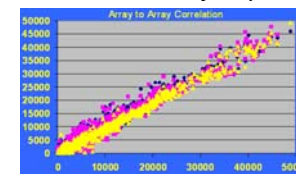
All arrays successfully called the proper influenza subtype (H5N1)



	H5 Call S/N Ratio	N1 Call S/N Ratio
Array 1	9.5	4.6
Array 2	5.7	3.0
Array 3	18	8.5
Array 4	10	5.1

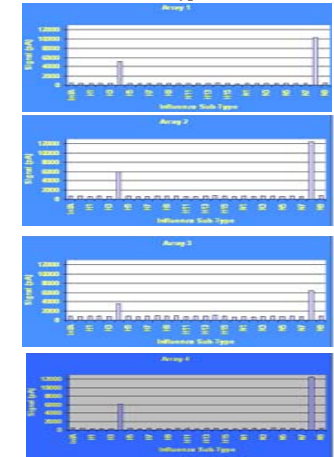


Spike-in RNA concentrations of 1 and 0.375 pM were distinguishable with an average signal to noise ratio of 4.5:1 and 1.7:1 respectively.



Average Pearson Correlation between the four microarrays was 0.98.

All arrays successfully called the proper influenza subtype (H4N8)



	H4 Call S/N Ratio	N8 Call S/N Ratio
Array 1	15	30
Array 2	4.8	8.7
Array 3	11	22
Array 4	19	40