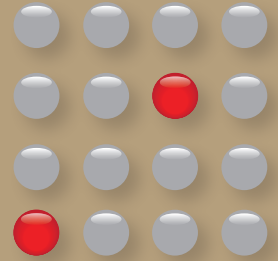
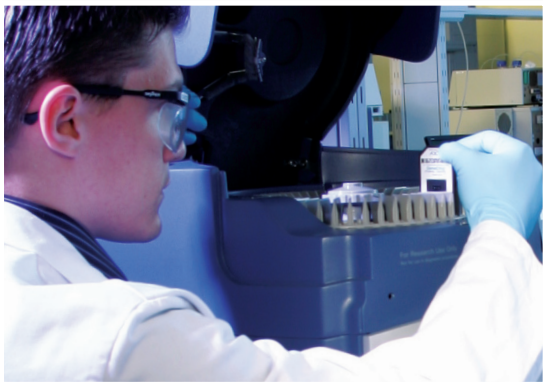


Lung Cancer DSA™ Technical Note



The Almac Diagnostics Lung Cancer DSA™ research tool offers the most comprehensive platform available for the study of Lung Cancer.

The Almac Diagnostics **Lung Cancer DSA™** research tool offers the most comprehensive gene expression analysis platform for the study of lung cancer with over 60,000 biologically relevant transcripts available for interrogation, tens of thousands of which are unavailable on leading generic arrays.



Based upon the Affymetrix GeneChip® technology, the **Lung Cancer DSA™** research tool provides multiple independent measurements for each transcript.

LUNG CANCER DSA™ Technical Specifications	
Total Probesets on Array	~60,416
Control Probesets	489
Number of Transcripts	~60,300
Feature Size	11 Micron
Probe Length	25-MER
Probe Pairs / Probeset	11

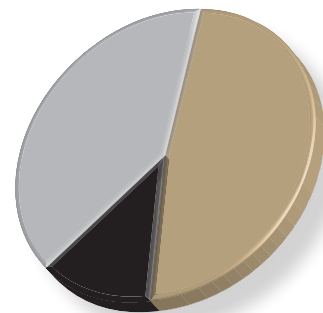
The end result is a tailored research solution providing accurate and reproducible expression data for the transcripts that really matter to your research setting.

ARRAY CONTENT

The **Lung Cancer DSA™** research tool was compared to the NCBI's Reference Sequence (RefSeq) database and it was determined that 52% of the **Lung Cancer DSA™** research tool content is not present in the RefSeq database and 13% of the content represents antisense sequences to annotated transcripts.

LUNG CANCER DSA™ RESEARCH TOOL COMPARED WITH REFSEQ

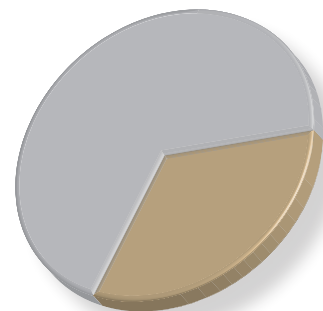
- 48% Similar
- 39% Unique
- 13% Reverse Orientation



Sequence analysis comparing the **Lung Cancer DSA™** research tool with a leading commercially available microarray clearly highlights the extent of its unique content (see figure below).

LUNG CANCER DSA™ RESEARCH TOOL COMPARED WITH A LEADING GENERIC ARRAY

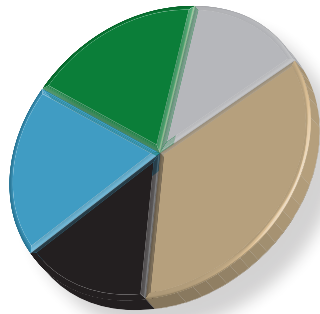
- 68% Similar
- 32% Unique



UNIQUE CONTENT ANALYSIS

Analysis of the unique content of the **Lung Cancer DSA™** research tool (see figure below) demonstrates that (48%) corresponds to RefSeq transcripts in both sense and anti-sense orientation.

- 14% RefSeq
- 34% RefSeq Antisense
- 15% Lung Ests
- 19% dbEst
- 18% Genome

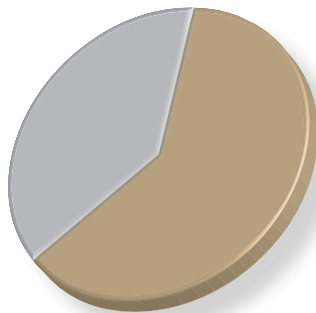


COMPARISONS OF DISEASE TRANSCRIPTOMES

Comparison of the content of the **Lung Cancer DSA™** research tool with the **Breast Cancer DSA™** research tool demonstrates unequivocally the differences between disease transcriptomes.

LUNG CANCER DSA™ RESEARCH TOOL COMPARED WITH BREAST CANCER DSA™ RESEARCH TOOL

- 62% Similar
- 38% Unique



PROTEIN HOMOLOGY ANALYSIS

Protein homology analysis as shown in the table, reveals that a large proportion of the unique transcripts are likely to be protein coding and are involved in processes closely related to cancer initiation and development. A similar proportion are transcripts with antisense homology to these cancer-related proteins and represent sequences with important regulatory potential.

PROTEIN HOMOLOGY ANALYSIS	SENSE	ANTISENSE
Uncharacterised protein count	768	1078
Hypothetical protein count	79	287
Cell-cycle-related protein count	10	1
Intercellular signaling-related protein count	40	27
Metabolism-related protein count	107	54
Cytoskeleton, motility and spindle assembly-related protein count	110	50
Proteasome-related protein count	14	9
DNA damage/repair-related protein count	40	13
Cellular signalling-related protein count	75	56
Apoptosis-related protein count	4	19
Chromatin remodelling-related protein count	10	1
Kinase of unknown function count	15	8
Cell surface and intracellular receptors/channel-related protein count	41	22
Transcription-related protein count	66	58
Cancer-related proteins of unknown function count	20	16
Immunoglobulin-related protein count	6	1
Translation-related protein count	21	7
Cellular stress response-related protein count	0	2
Cell-adhesion & extracellular matrix-related protein count	22	6
DNA replication-related protein count	7	2
Other proteins of known function	270	274
	1725	1991

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