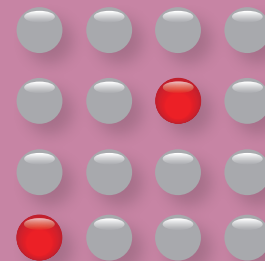


Breast Cancer DSA™ Technical Note



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

The Almac Diagnostics **Breast Cancer DSA™** research tool offers the most comprehensive gene expression analysis platform for the study of breast 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 **Breast Cancer DSA™** research tool provides multiple independent measurements for each transcript.

BREAST CANCER DSA™ Technical Specifications	
Total Probesets on Array	~60,858
Control Probesets	511
Number of Transcripts	~60,000
Feature Size	11 Micron
Probe Length	25-MER
Probe Pairs / Probeset	11

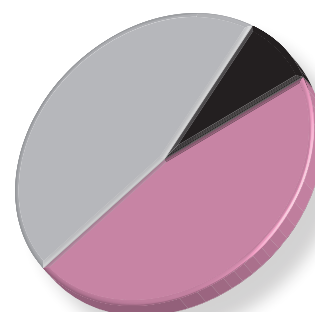
The end result is a tailored research solution providing accurate and reproducible expression data for the transcripts that really matter to your research setting.

ARRAY CONTENT

The **Breast Cancer DSA™** research tool was compared to the NCBI's Reference Sequence (RefSeq) database and it was determined that 55% of the **Breast Cancer DSA™** research tool content is not present in the RefSeq database and 9% of the content represents antisense sequences to annotated transcripts.

BREAST CANCER DSA™ RESEARCH TOOL COMPARED WITH REFSEQ

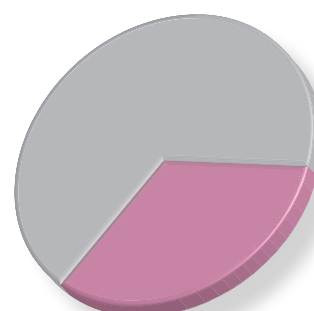
- 45% Similar
- 46% Unique
- 9% Reverse Orientation



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

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

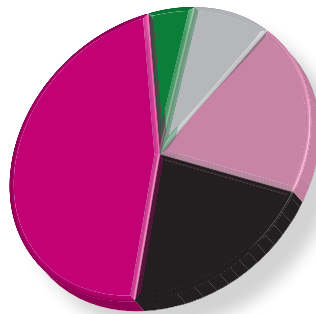
- 67% Similar
- 33% Unique



UNIQUE CONTENT ANALYSIS

Analysis of the unique content of the **Breast Cancer DSA™** research tool (see figure below) demonstrates that 29% corresponds to RefSeq transcripts in both sense and anti-sense orientation.

- 9% RefSeq
- 20% RefSeq Antisense
- 20% Breast Ests
- 46% dbEst
- 5% Genome

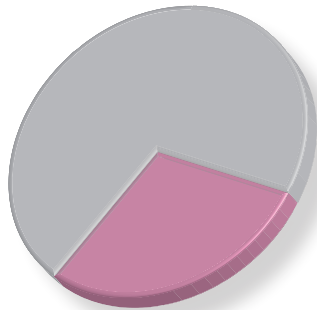


COMPARISONS OF DISEASE TRANSCRIPTOMES

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

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

- 71% Similar
- 29% 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	180	177
Hypothetical protein count	32	33
Cell-cycle-related protein count	0	3
Intercellular signaling-related protein count	23	16
Metabolism-related protein count	55	56
Cytoskeleton, motility and spindle assembly-related protein count	27	26
Proteasome-related protein count	7	13
DNA damage/repair-related protein count	11	15
Cellular signalling-related protein count	30	25
Apoptosis-related protein count	0	3
Chromatin remodelling-related protein count	5	4
Kinase of unknown function count	8	4
Cell surface and intracellular receptors/channel-related protein count	23	21
Transcription-related protein count	36	54
Cancer-related proteins of unknown function count	10	4
Immunoglobulin-related protein count	6	2
Translation-related protein count	9	5
Cellular stress response-related protein count	0	3
Cell-adhesion & extracellular matrix-related protein count	2	6
DNA replication-related protein count	4	2
Other proteins of known function	127	146
	595	618

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