

<i>Probe Set</i>	<i>Description</i>	<i>% Correct</i>
40808_at	chromogranin A (parathyroid secretory protein 1)	1.0%
40825_at	microtubule-associated protein, RP/EB family, member 3	1.0%
32254_at	Cluster Incl AL050223:Homo sapiens mRNA; cDNA DKFZp586L1323	1.0%
36148_at	Cluster Incl U48437:Human amyloid precursor-like protein 1 mRNA	1.0%
40165_at	cutaneous T-cell lymphoma-associated tumor antigen se20-4	1.0%
916_at	protein tyrosine phosphatase, receptor type, N	1.0%
41107_at	syntaphilin	99.5%
41675_at	KIAA0656 gene product	99.5%
35742_at	KIAA0430 gene product	99.5%

Table 1: The Best Individual Transcript Sequences to Indicate Membership/Non-membership in the Pulmonary Carcinoid Class.

<i>Probe Set</i>	<i>Description</i>	<i>% Correct</i>
41231_f_at	high-mobility group (nonhistone chromosomal) protein 17	1.0%
31935_s_at	Cluster Incl U75968:Human clone C3 CHL1 protein (CHLR1) mRNA	99.5%
39990_at	ISL1 transcription factor, LIM/homeodomain, (islet-1) †	99.5%
37302_at	centromere protein F (350/400kD, mitotin)	99.5%
1809_at	CDC7 (cell division cycle 7, <i>S. cerevisiae</i> , homolog)-like 1	99.5%
893_at	ubiquitin carrier protein	99.5%

Table 2: The Best Individual Transcript Sequences to Indicate Membership/Non-membership in the SCLC Class.

<i>Probe Set</i>	<i>Description</i>	<i>% Correct</i>
37398_at	Cluster Incl AA100961:zn40b06.s1 Homo sapiens cDNA	99.0%
36569_at	tetranectin (plasminogen-binding protein) ‡	98.5%
35868_at	advanced glycosylation end product-specific receptor ‡	98.0%
39631_at	epithelial membrane protein 2	98.0%
37196_at	cadherin 5, type 2, VE-cadherin (vascular epithelium)	97.5%
32542_at	four and a half LIM domains 1	97.5%
1814/15_at	transforming growth factor, beta receptor II (70-80kD) †	97.5%
38177_at	receptor (calcitonin) activity modifying protein 2	97.0%
34708_at	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen)	97.0%
1596_g_at	TEK tyrosine kinase, endothelial	97.0%

Table 3: The Best Individual Transcript Sequences to Indicate Membership/Non-membership in the Normal Lung Sample Class. † indicates that the transcript sequence was previously identified as biologically important in Garber et. al's paper; ‡ that it was identified in Bhattejee et al.'s paper.

<i>Probe Set</i>	<i>Description</i>	<i>% Correct</i>
31791_at	tumor protein 63 kDa with strong homology to p53 †‡	98%
36133_at	Cluster Incl AL031058:Human DNA sequence	94.5%
38608_at	Cluster Incl AA010777:ze22f06.r1 Homo sapiens cDNA, 5 end	93.5%
39581_at	Cluster Incl AA570193:nf38c11.s1 Homo sapiens cDNA	93.1%
40304_at	bullous pemphigoid antigen 1 (230/240kD) †	93.1%
41619_at	novel putative protein sim. to YIL091C yeast hyp. 84 kD prot.	93.1%
33267_at	Cluster Incl AF035315:Homo sapiens clone 23664 and 23905 mRNA seq.	93.1%
1898_at	ataxia-telangiectasia group D-associated protein †	93.1%
863_g_at	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5	93.1%
601_s_at	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)	93.1%

Table 4: The Best Individual Transcript Sequences to Indicate Membership/Non-membership in the Squamous Class. † indicates that the transcript sequence was previously identified as biologically important in Garber et. al’s paper; ‡ that it was identified in Bhattejee et al.’s paper.

<i>Probe Set</i>	<i>Description</i>	<i>% Correct</i>
33218_at	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2	80.8%
36209_at	bromodomain-containing 2	80.3%
35531_at	ligand of neuronal nitric oxide synthase w/carboxyl-terminal PDZ domain	79.3%
1814/15_at	transforming growth factor, beta receptor II (70-80kD) †	78.8%
34352_at	Cluster Incl AA631698:np79a08.s1 Homo sapiens cDNA	78.3%
1802_s_at	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2	78.3%
32640_at	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor †	77.3%
37406_at	microtubule-associated protein, RP/EB family, member 2	77.3%
40717_at	cathepsin L2	77.3%

Table 5: The Best Individual Transcript Sequences to Indicate Membership/Non-membership in the Adenocarcinoma Class. † indicates that the transcript sequence was previously identified as biologically important in Garber et. al’s paper; ‡ that it was identified in Bhattejee et al.’s paper.