

Table: Mean and median of the variation coefficients (CV) of the signal intensities of probes obtained using the three protocols (NE, OCT and LASER) for each patient. This analysis was computed using intensities signal of the 5,903 probes providing data simultaneously in all experiments. Note that these coefficients of variation are higher in patients (*italics*) that had at least one specimen with lower RNA integrity. Lower coefficient of variation was observed in patients presenting high RNA integrity in all the samples.

# of probes selected	5903	5903
Patient	Mean CV of the full set	Median of the CVs of the full set
2	0.2133	0.1953
3	<i>0.3610</i>	<i>0.3131</i>
6	<i>0.3167</i>	<i>0.2866</i>
<i>11</i>	<i>0.3088</i>	<i>0.2853</i>
102769	0.1976	0.1720

Table: Common biological functional annotations of the probes differentially expressed among samples of high and low RNA integrity. Group 1 includes the underexpressed biological processes in 3-LASER and 6-LASER, group 2 includes the overexpressed biological processes in 3-LASER and 6-LASER specimens together, group 3 consists of the underexpressed significant biological processes in 3-LASER and 6-LASER and the three 11T specimens, group 4 includes the overexpressed biological processes in 3-LASER and 6-LASER plus the three 11T specimens.

Biological process (BP)	Group	Hypergeometric p-value (p<0.05)	Number of probes with a t-test p-value <0.01	Number of probes with annotated BP
antimicrobial humoral response	1	0.000823975	3	17
protein biosynthesis	1	0.003005087	6	131
RNA processing	1	0.004891694	3	31
cell cycle	2	0.02974439	3	9
cholesterol metabolism	2	0.008482575	3	6
complex I (NADH to ubiquinone)	2	0.0339728	5	16
monocarboxylic acid transport	2	0.077468693	3	6
protein biosynthesis	2	1.7285E-06	29	131
protein-nucleus import, translocation	2	0.02105355	3	8
adenylate cyclase activation	3	0.001726151	3	7
cell growth and maintenance	3	0.044215861	2	9
cholesterol metabolism	3	0.01986206	2	6
humoral defense mechanism	3	0.01986206	2	6
protein biosynthesis	3	5.96E-08	21	131
protein folding	3	0.003123224	5	27
translational regulation, initiation	3	0.04440558	3	21
ubiquitin-dependent protein degradation	3	0.008701444	5	34
transcription regulation from Pol	4	0.03073901	18	67

Figure: Hierarchical clustering analysis of the fifteen specimens analyzed. The application of bootstrapping techniques confirmed the robustness of the relatedness of the expression profiles of the samples under study. 2B. Bootstrapping analysis of the group of aliquots obtained by laser microdissection, the sample-handling procedure under evaluation. The laser cluster grouped aliquots of high RNA quality and lower aulity (cases 3T and 6T).

