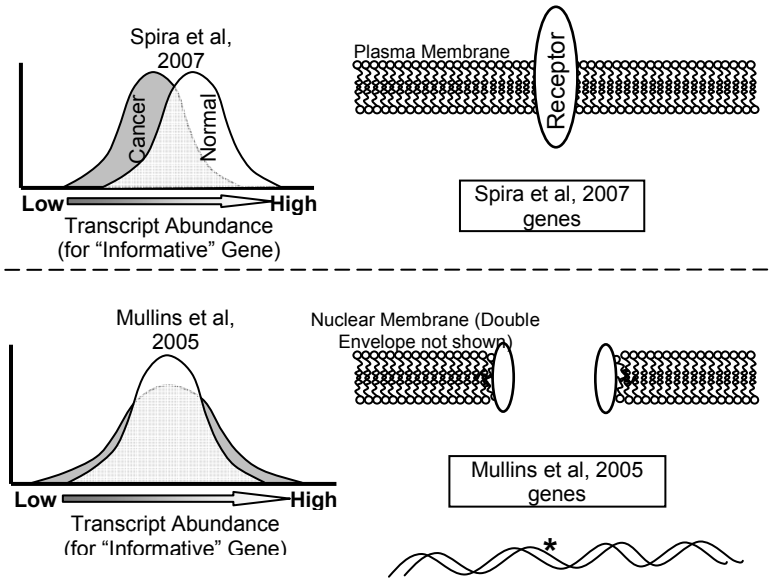
Supplementary Figure 1. Differences in Gene Ontological Terms, Transcript Expression Distribution, and spatial location in the cell between Spira et al, 2007 and Mullins et al, 2005 biomarker gene sets.



Gene Ontology Terms	Percentage of Genes in Respective Biomarkers with GO Terms: Spira et al, 2007	Mullins et al, 2005	Univariate P-value
plasma membrane location (GO:0005886)	30%	0%	4.53E-02
signal transduction cascade (GO:0007165)	30%	0%	1.41E-02
cell signaling and attachment (GO:0007154)	29%	0%	1.67E-02
small molecule transport (GO:0006810)	22%	0%	5.02E-02
cofactor metabolism (GO:0051186)	0%	14%	4.51E-02
coenzyme metabolism (GO:0006732)	0%	14%	4.81E-02
oxidized glutathione reduction (GO:0006749)	0%	17%	4.14E-02
response to endogenous stimulus (GO:0009719)	4%	29%	1.58E-02
response to oxidative stress (GO:0006979)	2%	29%	7.73E-03
DNA repair (GO:0006281)	4%	33%	1.45E-02
mitochondrial location (GO:0005739)	6%	38%	4.57E-02

* = DNA lesion or pro-mutation

GO = Gene Ontology

Transcript Expression Distribution:

Shaded areas represent Cancer (for Spira study, cancer may be over-expressed or under-expressed relative to control group). White areas represent non-cancer group

Univariate P-values represent significant differences in Chemical, Molecular, and cellular location gene category classifiers using web-based FatiGO tool.

Al-Shahrour, F., Diaz-Uriarte, R., and Dopazo, J. FatiGO: a web tool for finding significant associations of Gene Ontology terms with groups of genes. Bioinformatics, 20: 578-580, 2004.

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