Supplementary Table S1: Yoshida et al. A Statistical Framework for Genome-Wide Discovery of Biomarker Splice Variations with GeneChip Human Exon 1.0 ST Arrays

sample no	cel file name	part number	patient no	tissue type	gender	age	differentiation
1	1-1T.CEL	R8235090-PT	1	Tumor	Μ	58	Well
2	2-1N.CEL	R8235090-PN	1	Normal	Μ	58	Normal
3	3-2T.CEL	R8235090-PT	2	Tumor	\mathbf{F}	75	Moderate
4	4-2N.CEL	R8235090-PN	2	Normal	\mathbf{F}	75	Normal
5	5-3T.CEL	R8235090-PT	3	Tumor	Μ	67	Moderate
6	6-3N.CEL	R8235090-PN	3	Normal	Μ	67	Normal
7	7-4T.CEL	R8235090-PT	4	Tumor	Μ	75	Well
8	8-4N.CEL	R8235090-PN	4	Normal	Μ	75	Normal
9	9-5T.CEL	R8235090-PT	5	Tumor	\mathbf{F}	33	Well
10	10-5N.CEL	R8235090-PN	5	Normal	\mathbf{F}	33	Normal
11	11-6T.CEL	R8235090-PT	6	Tumor	Μ	68	Poo
12	12-6N.CEL	R8235090-PN	6	Normal	Μ	68	Normal
13	13-7T.CEL	R8235090-PT	7	Tumor	\mathbf{F}	53	Poor
14	14-7N.CEL	R8235090-PN	7	Normal	\mathbf{F}	53	Normal
15	15-8T.CEL	R8235090-PT	8	Tumor	\mathbf{F}	62	Well
16	16-8N.CEL	R8235090-PN	8	Normal	\mathbf{F}	62	Normal
17	17-9T.CEL	R8235090-PT	9	Tumor	Μ	79	Moderate
18	18-9N.CEL	R8235090-PN	9	Normal	Μ	79	Normal
19	19-10T.CEL	R8235090-PT	10	Tumor	\mathbf{F}	60	Moderate
20	20-10N.CEL	R8235090-PN	10	Normal	F	60	Normal

Table 1: Sample information sheet. The Affymetrix provides the third party developers of the data analysis tools 20 exon expression profiles of normal control and tumor cells which are isolated from different 10 individuals with colon cancer. Each profile and individual are denoted by the cell file name in the second colomn and the patient ID in the fifth colomn.