Supplemental Table 1. Smallest significant regions with copy number changes in malignant mesothelioma cell lines

Region[a]	Cytoband location	Region Length	CN change[b]	No. of genes[c]	Percentage of cell lines[d]	p-value[e]	Percentage of CNV Overlap[f]
chr9:21,973,222-22,354,257	9p21.3	381,035	Loss	4	100	0	0
chr13:28,852,665-28,941,613	13q12.2 - q12.3	88,948	Loss	2	82	0.003	83
chr16:6,770,326-6,961,633	16p13.3	191,307	Loss	1[h]	76	0	0
chr1:4,507,843-5,027,751	1p36.32	519,908	Loss	2	71	0.028	0
chr1:5,847,675-12,907,136	1p36.31 - p36.21	7,059,461	Loss	99; 5[g]	71	0.028	6
chr6:32,469,084-32,538,937	6p21.32	69,853	Loss	3	47	0	100
chr9:71,234,232-72,423,412	9q21.11 - q21.12	1,189,180	Loss	10	47	0	7
chr16:7,249,315-7,284,367	16p13.3	35,052	Loss	1[h]	47	0.001	58
chr16:6,245,937-6,299,769	16p13.3	53,832	Loss	1[h]	41	0.014	0
chr1:157,398,349-157,805,740	1q23.1	407,391	Gain	7	65	0	2
chr1:157,883,449-158,092,535	1q23.1	209,086	Gain	3	65	0	0
chr5:784,423-808,109	5p15.33	23,686	Gain	1	65	0.004	100
chr17:37,876,495-38,184,266	17q12 - q21.1	307,771	Gain	13; 1[g]	65	0.032	0
chr17:40,863,774-41,005,303	17q21.2 - q21.31	141,529	Gain	12	65	0.032	0
chr17:44,221,384-44,418,461	17q21.31	197,077	Gain	4	65	0.032	100
chr8:145,637,777-145,733,477	8q24.3	95,700	Gain	10	59	0	3
chr20:60,953,791-61,286,207	20q13.33	332,416	Gain	8; 2[g]	59	0.027	15
chr3:162,486,527-162,637,386	3q26.1	150,859	Gain	1	53	0	76
chr8:39,229,932-39,398,576	8p11.22	168,644	Gain	3	53	0	100
chr7:72,490,276-73,992,274	7q11.23	1,501,998	Gain	40; 2[g]	47	0.002	3
chr7:99,867,651-100,068,777	7q22.1	201,126	Gain	10	47	0.002	20
chr19:0-616,511	19p13.3	616,511	Gain	18; 1[g]	47	0.002	22
chr6:31,552,127-31,574,180	6p21.33	22,053	Gain	1	41	0	0
chr1:44,289,519-44,550,931	1p34.1	261,412	Gain	9	35	0.043	2
chr3:195,425,989-195,467,168	3q29	41,179	Gain	3; 1[g]	35	0.002	100
chr16:71,114,287-71,204,647	16q22.2	90,360	Gain	1	35	0.001	0
				Total:			
				265 genes			
				and 12 miRNAs			

[a] Smalllest significant regions, by STAC (see materials and methods) with the highest frequency above the % of cut-off line.
Cut-off line =0 (no minimal number of cell lines required).

[b] Copy number change.

[c] For gene list please see Supplemental Table 2.

[d] Percentage of the 17 malignant mesothelioma cell lines showing the copy number change.

[e] p-value less than or equal to 0.05. FASST segmentation, significant threshold 0.0001.

[f] Copy number variation according to the Database of Genomic Variants (DGV) (Toronto), most stringent DGV from Nexus CN 6.0.

[g] Gene; miRNA. For miRNA list please see Supplemental Table 2

[h] These 3 areas target the same gene, *RBFOX1/A2BP1.*