Table 1s. Comparison of recurrent regions of chromosomal alterations with published data.

Alteration	CGH array (33 cultured cells)	CGH[21] (90 tumors)	CGH array[22] (17 tumors)	CGH array[23] (26 tumors)	ROMA[24] (22 tumors)	SNP array[26] (23 tumors)	SNP array[25] (22 cultured cells)
Gain		1q23-q32 (16%)	1q (44%)			1q23 (35%) 1q32 (22%)	
	5p15.3-p11 (51%)		5p (44%)		5p14 (55%)	5p (22%)	
	7p22-p11.2 (37%)	7p14–p15 (14%)	7p (44%)			7p14-p15 (22%)	
		8q22–q23 (18%)	8q24 (56%)		8q23-q24 (36%)	8q22-q23 (20%) 8q24 (22%)	
		15q22–q25 (14%)				15q22-q25 (17%)	
				17q21.32-q25 (27%)	17q21-q23 (24%)		17q23.2 (55%)
					18q12.1 (36%)		
			20p (33%)			20p (9%)	
	20q11.2-q13.1 (34%)*						
Loss	1p36.3-p35 (51%)		1p36.33 (11%) 1p36.1 (33%)		1p36.22-p36.23 (36%) 1p36.11-p36.12 (55%)	1p36.1 (30%) 1p36.33 (39%)	1p36.3-p36.2 (55%)
	1p31-p12 (40%)	1p21 (21%)	1p21.3 (56%)	1p31.1-p13.2 (42%)	1p13.2-p13.3 (36%)	1p21.3 (30%)	1p22.3-p22.1 (82%)
	3p23-p14 (63%)	3p21 (16%)	3p21.3 (33%)	3p22.1-p14.2 (42%)	3p21.31 (27%) 3p14.3-p14.2 (32%)	3p21.3 (43%)	3p22.1-p21.31 (77%)
	Chr4 (54%)	4q31–q32 (29%) 4p12–p13 (25%)	4q22 (56%) 4q34-q35.2 (33%)			4p12 (26%) 4q22 (30%) 4q31-q32 (35%)	Chr4 (53%)
	6q14-q27 (57%)	6q22 (16%)	6q25 (44%)	6q22.1 (58%)		6q22 (26%) 6q25 (39%)	
	8p23-p12 (31%)						
	9p24-q21 (91%)	9p21 (34%)	9p21.3 (100%)	9p21.3 (65%)	9p21.3 (32%) 9p21.1 (36%)	9p21 (39%)	9p21.3 (100%)
					9q34.11 (41%)		
	10p15-p12 (37%)	10p13–p15 (16%)	10p (44%)			10p13 (9%)	
	10q23-q26 (37%)*						
							11q23.2-q23.3 (64%)
	12p13 (54%)						
	13q (60%)	13q13–q14 (19%)	13q33.2 (44%)	13q11-q14.12 (35%)		13q13-14 (17%)	13q12.2-q13.2 (73%)
	14q11.2-q21 (40%)	14q12–q24 (23%)				14q12-q24 (22%)	
	14q24-q32 (40%)		14q32.13 (56%)	14q22.1-32 (38%)		14q32.13 (17%)	14q32.2 (73%)
	15q13-q21 (40%)*						15q15.1 (55%)
	17p13-p11.2 (34%)	17p13–p12 (16%)			17p13.1 (46%)	17p12 (17%)	
					17q21.31 (32%)		
	18q12-q23 (46%)		18q (33%)			18q (13%)	18q12.3 (59%)
	19p13.1-p12 (31%)				19p13.2 (55%)		
	19q13.2-q13.4 (31%)				19q13.32 (55%)		
	22q (80%)	22q (32%)	22q (33%)	22q11-q12.3 (35%)	22q12.2 (74%)	22q (43%)	Chr22 (78%)

* Alterations in these genomic regions have been previously observed by Kivipensas *et al.* (1996) [19] and De Rienzo *et al.* (2001) [20] by CGH and polymorphic DNA marker analysis in primary tumors

Legends to supplementary figures

Figure 1s. Schematic diagram of recurrent regions of chromosomal alterations in murine mesothelioma cells.

The start position in the mouse genome (NCBI Build 36), the cytogenetic location and the alteration frequency of each BAC clones are shown on the left columns. Each other vertical column represents one individual MM, in which alteration was detected in the corresponding region: Open circle (○), no evidence of loss or gain; large black circle (●), heterozygous loss; black square (■), homozygous loss; open circle with a central dot (⊙), gain; open square with a central dot (▣), high level gain; small black circle (•), not informative; dark grey shaded area, region of loss; light grey shaded area, region of gain. Number of MMs with homozygous loss or high level gain are also specified. Regions containing homozygous loss or high level gain, and minimal regions of chromosomal alterations are framed with a thin and a thick line, respectively. Putative tumor suppressor genes (in bold), others genes and miRNAs located in these regions are indicated on the right side. **A.** 1qA1-qC1.3, 1qH2.1-qH5, 2qE1-qE3, Chr4; **B.** 5qG1.3-qG3, Chr6, Chr7, Chr8, 10qC2-qD3; **C.** 12qA1.1-qE, Chr15, 16qA1-qB3, Chr17, Chr19.

Figure 2s. Schematic diagram of recurrent regions of chromosomal alterations in human mesothelioma cells and corresponding syntenic regions in mouse mesothelioma cells.

The start position in the human genome (NCBI Build 36), the cytogenetic location and the alteration frequency of each BAC clones are shown on the left columns. Each other vertical column represents one individual MM, in which alteration was detected in the corresponding region: Open circle (○), no evidence of loss or gain; large black circle (●), heterozygous loss; black square (■), homozygous loss; open circle with a central dot (⊙), gain; open square with a central dot (▣), high level gain; small black circle (•), not informative; dark grey shaded area, region of loss; light grey shaded area, region of gain. Number of MMs with homozygous loss or high level gain are also specified. Corresponding mouse chromosomal regions are shown when alteration frequency of BAC clones were higher than 30%. Regions containing homozygous loss or high level gain, and minimal regions of chromosomal alterations are framed by thin and thick lines,

respectively. Putative tumor suppressor genes (in bold), others genes and miRNAs located in these regions are indicated on the right side. **A.** 1p36.3-p35 (part 1); **B.** 1p36.3-p35 (part 2); **C.** 1p31-p12; **D.** 3p23-p14; **E.** chr4 (parts 1 and 2); **F.** chr4 (part 3), 5p15.3-p11; **G.** 6q14-q27; **H.** 7p22-p11.2, 8p23-p12; **I.** 9p24-q21; **J.** 10p15-p12; 10q23-q26; **K.** 12p13; **L.** 13q (part 1); **M.** 13q (part 2); **N.** 14q11.2-q21, 14q24-q32; **O.** 15q13-q21, 17p13-p11.2, 18q12-q23; **P.** 19p13.1-p12, 19q13.2-q13.4, 20q11.2-q13.1; **Q.** Chr22.