

Table 1. Recurrent regions of chromosomal alterations (frequency higher than 30%) in murine mesothelioma cells

Alteration	Chromosomal region	Maximum frequency (%)	Start	End	Size (Mb)
Gain	1qA1-qC1.3	31	0	65343589	65
	5qG1.3-qG3	38	124245465	152000000	28
	Chr6*	56			
	Chr8*	50			
	10qC2-qD3	38	92606277	130000000	37
	Chr15*	81			
	16qA1-qB3	31	0	37335257	37
	Chr17*	38			
	Chr19*	75			
Loss	1qH2.1-qH5	38	158533294	188288765	30
	2qE1-qE3	31	88372743	113343671	25
	Chr4*	81			
	Chr7*	63			
	12qA1.1-qE	44	0	105426793	105
	Chr14*	69			

* Several gained or lost regions encompassed whole chromosomes in some murine MMs (Figure 1s.A-C for details, see Figure 1s at <http://ajp.amjpathol.org>).

Table 2. Minimal regions of chromosomal imbalance based on alteration frequency and occurrence of interstitial deletions, amplifications and biallelic deletions in 16 murine mesothelioma cells

Alteration	Chromosomal region	Number of MMs (%)	Start	End	Size (Mb)	Gene number	Gene*	miRNA
Minimal regions of deletion	1qH2.2-qH2.3	6 (38)	162074549	171028275	9	>10	Gas5, Rxrg, Pbx1	Mir214, Mir2134-1, Mir689-1
	4qC4	13 (81)	84800547	89483516	5	>10	Cdkn2a, Cdkn2b	Mir491, Mir31
	4qC7	9 (56)	102961540	114389001	11	>10	Cdkn2c, Faf1	Mir761
	12qC1-qC2	7 (44)	60575140	71056044	10	>10	Sav1	Mir681
	14qB	8 (50)	39021984	43790944	5	>10	-	-
	14qE2.1	11 (69)	85113991	96312501	11	5	Diap3, Tdrd3, Pcdh20, Pcdh9, Klhl1	-
Amplification	8qA1.1	1 (6)	0	23875369	24	>10	Elavl1, Gas6	Mir1968, Mir2144
	8qC5-qD1	1 (6)	91443012	107427526	16	>10	Mmp2, Mmp15, Cdh11, Cdh5, Cdh8	Mir138-2
	15qD1	1 (6)	58895730	66093803	7	>10	Myc	-
Biallelic deletion	1qA1	1 (6)	0	10359697	10	>10	-	-
	4qC4	6 (38)	84800547	89483516	5	>10	Cdkn2a, Cdkn2b	Mir31
	12qC1-qC2	1 (6)	60575140	71056044	10	>10	Sav1	Mir681
	14qB	1 (6)	39021984	43790944	5	>10	-	-

* Genes clearly or potentially involved in oncogenesis are indicated in bold.

Table 3. Recurrent regions of chromosomal alterations (frequency higher than 30%) in human mesothelioma cells

Alteration	Chromosomal region	Maximum frequency (%)	Start	End	Size (Mb)
Gain	5p15.3-p11	51	0	49464271	49
	7p22-p11.2	37	0	57346208	57
	20q11.2-q13.1	34	34168802	43536662	9
Loss	1p36.3-p35	51	0	30383282	30
	1p31-p12	40	75229478	119360570	43
	3p23-p14	63	34981835	64352460	29
	Chr4	54			
	6q14-q27	57	80213243	170629779	90
	8p23-p12	31	1790686	31056165	29
	9p24-q21	91	0	70025358	70
	10p15-p12	37	0	21068361	21
	10q23-q26	37	86173438	135071951	49
	12p13	54	10844968	12614264	2
	13q	60			
	14q11.2-q21	40	0	42832378	43
	14q24-q32	40	76307162	106230236	30
	15q13-q21	40	27018560	44046064	17
	17p13-p11.2	34	5782075	17473056	12
	18q12-q23	46	23824248	75939456	52
	19p13.1-p12	31	18161120	24246700	6
	19q13.2-q13.4	31	47672188	59385609	12
	22q	80			

Table 4. Amplification and biallelic deletions in human mesothelioma cells

Alteration	Chromosomal region	Number of MMs (N _T = 35)	Start	End	Size (Mb)	Gene number	Gene*	miRNA
Amplification	1p34.2-p34.1	1	40464163	43936177	3	>10	CDC20	MIR30E, MIR30C1
	2p12	1	75046439	76197958	1	5	POLE4, TACR1, FAM176A, MRPL19, C2orf3	-
	4q31.2	1	147916169	150226685	2	>10	-	MIR548G
	5p15.3	1	0	2692035	3	>10	TERT	-
	7p21-p15	1	9198514	29922960	21	>10	TWIST1, GPNMB, IL6, NPY, HNRNPA2B1, HOXA9, HOXA13	MIR1302-6, MIR1183, MIR148A, MIR196B
	7p14	1	39469174	43369192	4	>10	-	-
	9p24	1	442668	8228482	8	>10	RLN2, KDM4C	MIR101-2
	10q26	1	123070217	126566539	3	>10	FGFR2	-
	19q12-q13.1	1	33184604	38838451	6	>10	-	-
	20q13.3	1	54336834	57746514	3	>10	AURKA	MIR296, MIR298
Biallelic deletion	1p21	2	101859311	105068099	3	8	OLFM3, COL11A1, RNPC3, AMY2B, AMY2A, AMY1A, AMY1B, AMY1C	-
	4p15.3	1	12344454	13298102	1	3	RAB28, NKX3-2, BOD1L	-
	5q34	1	166908572	170038731	3	>10	-	MIR103-1, MIR103-1AS, MIR218-2, MIR585
	9p23	2	8228482	13419660	5	4	PTPRD , TYRP1, C9orf150, MPDZ	-
	9p21	22	20172510	22317110	2	>10	CDKN2A, CDKN2B	MIR31, MIR491
	10q26	1	126566539	131109233	5	>10	-	-
	11q22-q23	1	106448945	114320480	8	>10	ATM, SDHD, ZBTB16, PPP2R1B	MIR34B, MIR34C
	13q21	1	65415360	70465908	5	3	PCDH9, KLHL1, DACH1	-
	16p13.3	1	5147035	8712134	4	4	A2BP1, TMEM114, C16orf68, ABAT	-
	18p11.3	1	5196459	7203642	2	6	ZFP161, EPB41L3, TTMA, L3MBTL4, ARHGAP28, LAMA1	-
	22q11.2	3	19570585	20084258	1	9	SNAP29, CRKL, AIFM3, LZTR1, THAP7, P2RX6, SLC7A4, GGT2, RIMBP3B	MIR649
	22q12	1	28155132	28374240	<1	1	RFPL1, NEFH, THOC5, NIPSNAP1, NF2	-

* Genes clearly or potentially involved in oncogenesis are indicated in bold.

Table 5. Comparison of chromosomal alterations (frequency higher than 30%) between human and murine mesothelioma cells

Alteration	Human					Mouse	
	Chromosomal region	Maximum frequency (%)	Start	End	Size (Mb)	Chromosomal region	Maximum frequency (%)
Gain	5p15.3-p13	49	7387737	39283396	32	15qA1-qB3.1	75
	7p22-p21	37	188237	12020141	12	5qG2 / 6qA1	38 / 58
	7p15-p14	37	24340863	30917523	7	6qB2.3-qB3	44
Loss	1p36.3-p35	51	2058046	29574368	28	4qD2.3-4qE2	63
	3p21-p14	60	52571782	63683864	11	14qA1 / 14qA3	38 / 38
	6q15-q16	40	89148060	100061960	11	4qA3-qA5	38
	8p21	31	22048391	26316410	4	14qD1	44
	9p24-p13	91	8228482	36895443	29	4qA5-B1 / 4qC3-C5	44 / 81
	10q23	34	86679954	87489928	1	14qA3-qB	38
	10q26	37	121395903	127901902	7	7qF2-F3	56
	13q12	57	19505755	19703538	0	14qC3	44
	13q14-q33	57	42908596	101265081	58	14qD1-qE2.3	69
	14q11.2-q21	40	19150554	42832378	24	12qB3-qC1 / 14qC1-qC2	44 / 44
	14q24-q32	37	77705005	94277131	17	12qD3-qE	38
	19q13.2-q13.4	31	50052470	54919450	5	7qA2 / 7qB3	56 / 56
Biallelic deletion	9p21	63	20172510	22317110	2	4qC4	40

Table 6. Minimal regions of chromosomal alterations in human mesothelioma cells

Alteration (Loss)	Chromosomal region	Maximum frequency (%)	Start	End	Size (Mb)	Gene number	Gene*	miRNA
Human / mouse comparison	1p36.3	(human/mouse) 51 / 63	4356069	6292626	2	>10	CHD5	-
	1p36.1	46 / 50	19083345	20986850	2	>10	NBL1	MIR1290
	9p21	91 / 81	20172510	22317110	2	>10	CDKN2A, CDKN2B	MIR31, MIR491
	13q21	49 / 69	62637997	70465908	8	3	PCDH9, KLHL1, DACH1	-
Interstitial deletions in humans	1p22-p21	(human) 40	92918111	101318454	8	>10	-	MIR760, MIR137, MIR553
	3p21	60	45214909	50409942	5	>10	SETD2, MST1R, PLXNB1, RASSF1, RBM5, SEMA3B, SEMA3F, HYAL1, HYAL2	MIR1226, MIR2115, MIR711, MIR425, MIR191, MIR566
	4p16-p15.3	46	9614707	12344454	3	5	SLC2A9, WDR1, ZNF518B, CLNK, HS3ST1	MIR572
	4q13	49	63518558	65274228	2	1	TECRL	-
	4q22-23	54	92471635	101247956	9	>10	BMPR1B, UNC5C	-
	6q22	57	115807782	120525326	5	>10	-	MIR548B
	6q24-q25	51	144840012	155794638	11	>10	LATS1, AKAP12	-
	9p22	49	14010653	14732051	1	4	NFIB, ZDHHC21, CER1, FREM1	-
	9p11.1	43	42843412	66195312	23	4	ANKRD20A3, FAM75A6, CNTNAP3B, FAM75A7	-
	10q23-q24	37	87489928	108067973	21	>10	BMPR1A, SNCG, PTEN, FAS, LGI1, NFKB2, SUFU	MIR346, MIR107, MIR607, MIR1287, MIR608, MIR146B, MIR1307, MIR936, MIR609
	12p13	54	11584100	12614264	1	6	ETV6, BCL2L14, LRP6, MANSC1, LOH12CR1, DUSP16	MIR1244
	13q13	60	31067328	33059957	2	9	RXFP2, FRY, ZAR1L, BRCA2, N4BP2L1, N4BP2L2, PDS5B, KL, STARD13	-
15q14-q21	40	30654132	44046064	13	>10	THBS1	MIR1233, MIR626, MIR627	
High frequency in humans	22q12-q13	80	32678146	42309461	10	>10	EP300, BIK	MIR658, MIR659, MIR1281, MIR33a

* Genes clearly or potentially involved in oncogenesis are indicated in bold.

Table 7. Percentage of cases showing gene alterations in human and murine mesothelioma cells

Human/murine gene	Alterations frequency in humans (%)	Alterations frequency in mice (%)	P value*
<i>TP53/Trp53</i>	20	25	0.72
<i>NF2/Nf2</i>	46	75	0.07
<i>CDKN2A/Cdkn2a</i>	82	56	0.09
<i>CDKN2B/Cdkn2b</i>	76	60	0.43

* Fisher's exact test