

Table S1. Logistic regression models in asbestos-exposed controls and mesothelioma (MM) groups adjusted by age.

Model	Variable	Effect	OR	95% CI		P value	AIC
1	Group	Pre-diagnostic MM	7.98	3.00	21.20	<0.001	210.98
		Manifest MM	12.70	5.36	30.08	<0.001	
		Controls	1				
2	Group	Pre-diagnostic MM	8.07	2.98	21.82	<0.001	205.18
		Manifest MM	17.38	6.88	43.91	<0.001	
		Controls	1				
	MSLN rs3764247 A>C	Non-common genotype	3.12	1.38	7.08	0.006	
		Common genotype (AA)	1				
3	Group	Pre-diagnostic MM	7.98	2.98	21.40	<0.001	209.46
		Manifest MM	15.30	6.21	37.67	<0.001	
		Controls	1				
	MSLN rs3764246 A>G	Non-common genotype	2.12	0.96	4.70	0.063	
		Common genotype (AA)	1				
4	Group	Pre-diagnostic MM	8.29	3.00	22.92	<0.001	201.68
		Manifest MM	25.78	8.96	74.24	<0.001	
		Controls	1				
	MSLN rs2235503 C>A	Non-common genotype	4.77	1.84	12.36	0.001	
		Common genotype (CC)	1				
5	Group	Pre-diagnostic MM	8.78	3.14	24.60	<0.001	200.77
		Manifest MM	30.99	10.19	94.27	<0.001	
		Controls	1				
	Haplotype*	3 mutations	4.86	1.73	13.66	0.003	
		1-2 mutations	0.56	0.18	1.77	0.325	
		No mutation	1				
6	Group	Pre-diagnostic MM	7.80	2.87	21.20	<0.001	204.33
		Manifest MM	20.46	7.72	54.21	<0.001	
		Controls	1				
	MSLN rs1057147 G>A	Non-common genotype	3.51	1.48	8.30	0.004	
		Common genotype (GG)	1				
7	Group	Pre-diagnostic MM	10.65	3.42	33.16	<0.001	203.42
		Manifest MM	35.09	11.06	111.29	<0.001	
		Controls	1				
	MSLN rs3764247 A>C	AC vs. AA	1.28	0.35	4.73	0.707	
		CC vs. AA	1.30	0.18	9.40	0.794	
	MSLN rs3764246 A>G	AG vs. AA	0.65	0.18	2.32	0.504	
		GG vs. AA	0.97	0.07	12.96	0.980	
	MSLN rs2235503 C>A	CA vs. CC	2.27	0.37	14.02	0.378	
		AA vs. CC	17.03	0.82	355.39	0.067	
	MSLN rs1057147 G>A	GA vs. GG	2.04	0.65	6.35	0.221	
		AA vs. GG	1.33	0.25	7.11	0.742	

Model	Variable	Effect	OR	95% CI		P value	AIC
8	Group	Pre-diagnostic MM	9.11	3.13	26.48	<0.001	200.06
		Manifest MM	39.38	11.57	134.02	<0.001	
		Controls					
	Mutations	1 vs. no mutations	0.40	0.10	1.64	0.205	
		2 vs. no mutations	2.36	0.45	12.25	0.308	
		3 vs. no mutations	0.88	0.16	4.83	0.886	
		4 vs. no mutations	5.56	1.51	20.38	0.010	
		5-8 vs. no mutations	9.78	2.61	36.62	0.001	

OR Odds ratio; CI Confidence interval; AIC Akaike Information Criterion

*Haplotype of the three SNPs from 5'-UTR with no mutation (AAC), 1-2 mutations (AGC, AAA, CAC, AGA, CAA, CGC), 3 mutations (CGA)