Data Supplement (Web only)

Table 1. Probability of MMR gene mutation according to PREMM$_{1,2,6}$ by type of gene and ascertainment

PREMM$_{1,2,6}$ categories	Total N	(%)	No Mutation N	(%)	*MLH1* Mutation N	(%)	*MSH2* Mutation N	(%)	*MSH6* Mutation N	(%)
OVERALL COHORT (n=1651)										
< 5%	836	(50.6)	823	(58.3)	3	(3.3)	6	(4.8)	4	(16.7)
5-9%	331	(20.1)	306	(21.7)	9	(10.0)	10	(8.0)	6	(25.0)
10-19%	174	(10.5)	151	(10.7)	9	(10.0)	9	(7.2)	5	(20.8)
20-29%	68	(4.1)	44	(3.1)	6	(6.7)	13	(10.4)	5	(20.8)
30-39%	53	(3.2)	28	(2.0)	9	(10.0)	15	(12.0)	1	(4.2)
≥ 40%	189	(11.5)	60	(4.2)	54	(60.0)	72	(57.6)	3	(12.5)
Total	1651	(100)	1412	(100)	90	(100)	125	(100)	24	(100)
POPULATION-BASED (n=1181)										
< 5%	738	(62.5)	731	(66.4)	2	(7.4)	2	(4.6)	3	(30)
5-9%	239	(20.2)	225	(20.4)	5	(18.5)	5	(11.6)	4	(40)
10-19%	99	(8.4)	92	(8.4)	3	(11.1)	3	(7.0)	1	(10)
20-29%	31	(2.6)	20	(1.8)	4	(14.8)	6	(14.0)	1	(10)
30-39%	18	(1.5)	10	(0.9)	1	(3.7)	6	(14.0)	1	(10)
≥ 40%	56	(4.7)	23	(2.1)	12	(44.4)	21	(48.8)	0	0
Total	1181	(100)	1101	(100)	27	(100)	43	(100)	10	(100)
CLINIC-BASED (n=470)										
< 5%	98	(20.9)	92	(29.6)	1	(1.6)	4	(4.9)	1	(7.1)
5-9%	92	(19.6)	81	(26.1)	4	(6.4)	5	(6.1)	2	(14.3)
10-19%	75	(16.0)	59	(19.0)	6	(9.5)	6	(7.3)	4	(28.6)
20-29%	37	(7.9)	24	(7.7)	2	(3.2)	7	(8.5)	4	(28.6)
30-39%	35	(7.5)	18	(5.8)	8	(12.7)	9	(11.0)	0	(0)
≥ 40%	133	(28.3)	37	(11.9)	42	(66.7)	51	(62.2)	3	(21.4)
Total	470	(100)	311	(100)	63	(100)	82	(100)	14	(100)

MMR=mismatch repair