Supplementary Table 1. Association of tagging SNPs in genes related to IGF-1 or IL-6 signaling with risk of multiple myeloma

				Main analysis			Secondary analysis	
SNP	Minor allele	Frequency in controls	Genotype	Cases (n=82) N (%)*	Controls (n=164) N (%)*	OR (95% CI)†	Controls (n=2624) N (%)*	OR (95% CI)†
IGF-1 signaling pathway genes								
IGF1								
Haplotype Block 1								
rs7965399	C	3.5	TT	70 (88.6)	145 (92.9)	1.0 (ref)§	2328 (92.8)	1.0 (ref)§
			CT	9 (11.4)	11 (7.1)	2.0 (0.8-5.1)	174 (6.9)	1.8 (0.9-3.6)
			CC	0	0	NC‖	6 (0.2)	NC‖
rs35767	A	13.6	GG	56 (2.7)	116 (73.4)	1.0 (ref)	1740 (70.2)	1.0 (ref)
			AG	20 (26.0)	41 (25.9)	0.9 (0.5-1.7)	678 (27.3)	0.9 (0.5-1.5)
			AA	1 (1.3)	1 (0.6)	1.9 (0.1-32.6)	62 (2.5)	0.5 (0.07-3.9)
Haplotype Block 2								
rs12821878 (HCV11752586)	A	25.0	GG	44 (55.7)	85 (55.2)	1.0 (ref)	1507 (60.6)	1.0 (ref)
			AG	35 (44.3)	61 (39.6)	1.2 (0.7-2.2)**	864 (34.8)	1.4 (0.9-2.2)
			AA	0	8 (5.2)	NC	114 (4.6)	NC
rs1019731	A	15.3	CC	59 (73.8)	115 (71.9)	1.0 (ref)	1919 (75.3)	1.0 (ref)
			CA	19 (23.8)	41 (25.6)	0.9 (0.5-1.8)	588 (23.1)	1.0 (0.6-1.8)
			AA	2 (2.5)	4 (2.5)	0.9 (0.2-5.3)	43 (1.7)	1.6 (0.4-6.6)

rs2195239	G	26.7	CC	43 (55.1)	85 (53.5)	1.0 (ref)	1511 (59.5)	1.0 (ref)
			CG	26 (33.3)	63 (39.6)	0.8 (0.4-1.5)	903 (35.6)	1.0 (0.6-1.7)
			GG	9 (11.5)	11 (6.9)	1.6 (0.6-4.5)	125 (4.9)	2.6 (1.2-5.5)
Haplotype Block 3								
rs10735380 (HCV346219)	G	30.4	AA	39 (49.4)	84 (52.2)	1.0 (ref)	1303 (52.8)	1.0 (ref)
			AG	32 (40.5)	56 (34.8)	1.1 (0.6-1.9)	973 (39.4)	1.1 (0.7-1.8)
			GG	8 (10.1)	21 (13.0)	0.7 (0.3-1.9)	192 (7.8)	1.5 (0.7-3.3)
rs2373722	A	7.0	GG	71 (91.0)	136 (86.1)	1.0 (ref)	2121 (84.8)	1.0 (ref)
			GA	7 (9.0)	22 (13.9)	0.5 (0.2-1.3)	372 (14.9)	0.5 (0.2-1.1)
			AA	0	0	NC	8 (0.3)	NC
rs1549593	T	16.7	GG	56 (74.7)	113 (71.1)	1.0 (ref)	1846 (75.5)	1.0 (ref)
			GT	17 (22.7)	39 (24.5)	0.9 (0.4-1.8)	551 (22.5)	1.0 (0.6-1.8)
			TT	2 (2.7)	7 (4.4)	0.6 (0.1-3.3)	49 (2.0)	1.3 (0.3-5.6)
rs1520220	G	20.3	CC	52 (64.2)	108 (66.3)	1.0 (ref)	1645 (66.2)	1.0 (ref)
			CG	24 (29.6)	44 (27.0)	1.0 (0.5-1.9)	748 (30.1)	1.1 (0.7-1.8)
			GG	5 (6.2)	11 (6.7)	0.7 (0.2-2.5)	91 (3.7)	2.0 (0.8-5.1)
rs5742665 (HCV2801104)	G	12.1	CC	65 (84.4)	126 (78.2)	1.0 (ref)	1883 (75.6)	1.0 (ref)
			CG	12 (15.6)	31 (19.3)	0.9 (0.4-2.0)**	564 (22.6)	0.6 (0.3-1.1)
			GG	0	4 (2.5)	NC	44 (1.8)	NC

Haplotype Block 4								
rs2946834	A	32.8	GG	40 (50.0)	81 (49.7)	1.0 (ref)	1134 (45.6)	1.0 (ref)
			GA	33 (41.3)	57 (35.0)	1.3 (0.7-2.3)	1069 (43.0)	0.9 (0.6-1.5)
			AA	7 (8.8)	25 (15.3)	0.5 (0.2-1.4)	282 (11.3)	0.8 (0.3-1.8)
rs4764876	C	27.2	GG	47 (59.5)	90 (56.3)	1.0 (ref)	1361 (54.4)	1.0 (ref)
			GC	27 (34.2)	53 (33.1)	1.0 (0.5-1.8)	981 (39.2)	0.8 (0.5-1.2)
			CC	5 (6.3)	17 (10.6)	0.5 (0.1-1.6)	158 (6.3)	0.9 (0.4-2.3)
rs4764695	G	47.8	AA	25 (31.3)	47 (29.2)	1.0 (ref)	632 (25.0)	1.0 (ref)
			AG	35 (43.8)	74 (46.0)	0.8 (0.4-1.5)	1297 (51.3)	0.7 (0.4-1.2)
			GG	20 (25.0)	40 (24.8)	1.0 (0.4-2.0)	598 (23.7)	0.9 (0.5-1.6)
rs1996656	G	20.0	AA	51 (63.0)	104 (65.0)	1.0 (ref)	1685 (68.4)	1.0 (ref)
			AG	24 (29.6)	48 (30.0)	1.0 (0.6-1.9)	712 (28.9)	1.3 (0.8-2.1)
			GG	6 (7.4)	8 (5.0)	1.6 (0.5-5.2)	68 (2.8)	3.5 (1.4-8.6)
IGFBP1 and IGFBP3‡								
Haplotype Block 1								
rs1022865 (HCV395979)	G	36.7	AA	38 (48.1)	61 (38.6)	1.0 (ref)	1169 (46.3)	1.0 (ref)
			AG	35 (44.3)	78 (49.4)	0.8 (0.5-1.5)	1087 (43.0)	1.0 (0.7-1.7)
			GG	6 (7.6)	19 (12.0)	0.5 (0.2-1.6)	270 (10.7)	0.7 (0.3-1.6)
rs1553009	A	19.1	GG	50 (63.3)	106 (66.3)	1.0 (ref)	1654 (65.1)	1.0 (ref)
			GA	25 (31.7)	47 (29.4)	1.2 (0.6-2.2)	796 (31.4)	1.1 (0.7-1.8)

			AA	4 (5.1)	7 (4.4)	1.3 (0.4-4.5)	89 (3.5)	1.5 (0.5-4.2)
rs35539615 (HCV395975)	G	17.2	CC	47 (61.8)	106 (67.5)	1.0 (ref)	1488 (59.8)	1.0 (ref)
			CG	27 (35.5)	48 (30.6)	1.1 (0.6-2.0)	894 (35.9)	0.9 (0.5-1.4)
			GG	2 (2.6)	3 (1.9)	2.1 (0.3-15.5)	107 (4.3)	0.6 (0.1-2.4)
rs2201638	A	2.9	GG	77 (96.3)	147 (94.2)	1.0 (ref)	2347 (93.4)	1.0 (ref)
			GA	3 (3.8)	9 (5.8)	0.9 (0.2-3.6)	161 (6.4)	0.5 (0.2-1.7)
			AA	0	0	NC	6 (0.2)	NC
rs1065780	A	41.3	GG	28 (35.4)	54 (33.5)	1.0 (ref)	955 (38.0)	1.0 (ref)
			GA	37 (46.8)	81 (50.3)	0.9 (0.5-1.6)	1190 (47.4)	1.2 (0.7-1.9)
			AA	14 (17.7)	26 (16.2)	0.9 (0.4-2.2)	368 (14.6)	1.4 (0.7-2.7)
Haplotype Block 2								
rs4988515	T	6.5	CC	72 (90.0)	142 (87.7)	1.0 (ref)	2263 (91.4)	1.0 (ref)
			CT	8 (10.0)	19 (11.7)	0.8 (0.3-2.2)	206 (8.3)	1.4 (0.7-2.9)
			TT	0	1 (0.6)	NC	7 (0.3)	NC
rs4619	G	37.9	AA	35 (43.8)	57 (36.37)	1.0 (ref)	1046 (42.3)	1.0 (ref)
			AG	33 (41.3)	81 (51.6)	0.7 (0.4-1.3)	1140 (46.1)	1.0 (0.6-1.7)
			GG	12 (15.0)	19 (12.1)	1.0 (0.4-2.5)	285 (11.5)	1.4 (0.7-2.8)
rs1908751	T	25.0	CC	41 (51.3)	88 (55.0)	1.0 (ref)	1248 (49.8)	1.0 (ref)
			CT	33 (41.3)	64 (40.0)	1.2 (0.7-2.2)	1036 (41.3)	1.0 (0.6-1.6)
			TT	6 (7.5)	8 (5.0)	2.0 (0.6-6.2)	224 (8.9)	0.8 (0.4-2.0)

rs2270628	T	23.1	CC	55 (68.8)	94 (59.5)	1.0 (ref)	1601 (64.4)	1.0 (ref)
			CT	21 (26.3)	55 (34.8)	0.7 (0.4-1.3)	787 (31.6)	0.9 (0.5-1.4)
			TT	4 (5.0)	9 (5.7)	0.7 (0.2-2.7)	99 (4.0)	1.3 (0.5-3.8)
Haplotype Block 3								
rs3110697	A	45.7	GG	20 (25.0)	45 (27.8)	1.0 (ref)	858 (34.6)	1.0 (ref)
			GA	41 (51.3)	86 (53.1)	1.1 (0.5-2.1)	1177 (47.4)	1.6 (0.9-2.7)
			AA	19 (23.8)	31 (19.1)	1.5 (0.7-3.4)	448 (18.0)	2.0 (1.1-3.7)
rs2854746	C	38	GG	33 (42.9)	59 (37.3)	1.0 (ref)	887 (37.1)	1.0 (ref)
			GC	33 (42.9)	78 (49.4)	0.7 (0.4-1.3)	1159 (48.4)	0.9 (0.5-1.4)
			CC	11 (14.3)	21 (13.3)	0.8 (0.3-2.1)	348 (14.5)	0.9 (0.4-1.8)
rs2854744	T	46.5	GG	20 (25.3)	43 (27.7)	1.0 (ref)	667 (27.2)	1.0 (ref)
			GT	42 (53.2)	80 (51.6)	1.1 (0.6-2.2)	1304 (53.2)	1.1 (0.7-1.9)
			TT	17 (21.5)	32 (20.7)	1.0 (0.5-2.4)	479 (19.6)	1.2 (0.7-2.4)
rs2132570	T	21.1	GG	46 (59.0)	92 (59.7)	1.0 (ref)	1553 (62.8)	1.0 (ref)
			GT	28 (35.9)	59 (38.3)	1.1 (0.6-1.9)	811 (32.8)	1.2 (0.7-1.9)
			TT	4 (5.1)	3 (2.0)	3.0 (0.6-14.2)	109 (4.4)	1.4 (0.5-4.0)
SNPs not within a defined haplotype block								
rs6670	A	23.6	TT	50 (63.3)	93 (58.5)	1.0 (ref)	1577 (62.7)	1.0 (ref)
			TA	26 (32.9)	57 (35.9)	0.9 (0.5-1.6)	822 (32.7)	1.1 (0.7-1.7)
			AA	3 (3.8)	9 (5.7)	0.5 (0.1-2.7)	116 (4.6)	0.8 (0.3-2.8)

rs2453839	C	20.7	TT	51 (63.8)	103 (63.6)	1.0 (ref)	1636 (65.0)	1.0 (ref)
			TC	25 (31.3)	51 (31.5)	0.9 (0.5-1.8)	789 (31.3)	1.0 (0.6-1.6)
			CC	4 (5.0)	8 (4.9)	1.1 (0.3-4.0)	93 (3.7)	1.3 (0.5-3.8)
IGFBP2								
rs3770473	C	32.8	AA	36 (46.2)	73 (45.6)	1.0 (ref)	N/A[††]	
			AC	30 (38.5)	69 (43.1)	0.7 (0.4-1.3)		
			CC	12 (15.4)	18 (11.3)	1.2 (0.5-2.8)		
rs9341105	C	24.5	TT	43 (55.1)	88 (55.3)	1.0 (ref)	N/A	
			TC	28 (35.9)	64 (40.3)	0.9 (0.5-1.6)		
			CC	7 (9.0)	7 (4.4)	3.2 (0.9-11.2)		
rs9341130	G	9.4	AA	64 (83.1)	127 (81.9)	1.0 (ref)	N/A	
			AG	12 (15.6)	27 (17.4)	0.9 (0.4-2.0)		
			GG	1 (1.3)	1 (0.7)	2.0 (0.1-34.1)		
rs9341134	T	8.1	AA	72 (88.9)	134 (83.8)	1.0 (ref)	N/A	
			AT	8 (9.9)	26 (16.3)	0.7 (0.3-1.6)		
			TT	1 (1.2)	0	NC		
rs9341145	A	8.5	GG	68 (87.2)	133 (83.7)	1.0 (ref)	N/A	
			GA	8 (10.3)	25 (15.7)	0.6 (0.2-1.5)		
			AA	2 (2.6)	1 (0.6)	3.7 (0.3-42.2)		
rs9341156	A	5.3	GG	75 (94.9)	145 (89.5)	1.0 (ref)	N/A	
			GA	4 (5.1)	17 (10.5)	0.5 (0.2-1.5)		

			AA	0	0	NC	
rs9341193	T	2.2	CC	75 (96.2)	149 (95.5)	1.0 (ref)	N/A
			CT	3 (3.8)	7 (4.5)	0.6 (0.1-2.8)	
			TT	0	0	NC	
rs9341197	T	2.5	AA	78 (95.1)	153 (95.0)	1.0 (ref)	N/A
			AT	4 (4.9)	8 (5.0)	0.8 (0.2-3.0)	
			TT	0	0	NC	
rs2270360	C	30.9	AA	42 (53.2)	78 (48.8)	1.0 (ref)	N/A
			AC	32 (40.5)	65 (40.6)	1.0 (0.6-1.8)	
			CC	5 (6.3)	17 (10.6)	0.5 (0.1-1.5)	
IGF1R							
rs2229765	G	48.7	AA	15 (19.2)	32 (20.4)	1.0 (ref)	N/A
			AG	52 (66.7)	97 (61.8)	1.0 (0.5-1.9)	
			GG	11 (14.1)	28 (17.8)	0.7 (0.3-1.9)	
IRS1							
rs1801278 (G972R)	T	2.5	CC	69 (86.3)	153 (95.0)	1.0 (ref)	N/A
			CT	11 (13.8)	8 (5.0)	4.3 (1.5-12.1)	
			TT	0	0	NC	
rs17208470	A	7.8	CC	61 (77.2)	138 (85.7)	1.0 (ref)	N/A
			CA	18 (22.8)	21 (13.0)	2.2 (1.1-4.5)	

			AA	0	2 (1.2)	NC	
rs1801123	C	7.6	TT	63 (81.8)	133 (84.7)	1.0 (ref)	N/A
			TC	14 (18.2)	24 (15.3)	1.3 (0.6-2.7)	
			CC	0	0	NC	
IRS2							
rs913949	A	18.5	GG	57 (69.5)	109 (67.3)	1.0 (ref)	N/A
			GA	19 (23.2)	46 (23.4)	0.8 (0.4-1.5)	
			AA	6 (7.3)	7 (4.3)	2.3 (0.7-8.1)	
rs874016	A	33.1	GG	38 (47.5)	69 (43.1)	1.0 (ref)	N/A
			GA	32 (40.0)	76 (47.5)	0.7 (0.4-1.2)	
			AA	10 (12.5)	15 (9.4)	1.2 (0.5-3.1)	
rs12584136	A	5.9	CC	73 (91.3)	144 (88.9)	1.0 (ref)	N/A
			CA	6 (7.5)	17 (10.5)	0.5 (0.2-1.6)	
			AA	1 (1.3)	1 (0.6)	2.0 (0.1-32.7)	
rs9559646	C	48.1	TT	27 (33.8)	46 (29.1)	1.0 (ref)	N/A
			TC	32 (40.0)	72 (45.6)	0.7 (0.4-1.4)	
			CC	21 (26.3)	40 (25.3)	0.9 (0.4-1.9)	
rs2241745	C	13.9	TT	55 (70.5)	118 (74.7)	1.0 (ref)	N/A
			TC	20 (25.6)	36 (22.8)	1.1 (0.6-2.2)	
			CC	3 (3.8)	4 (2.5)	1.6 (0.3-7.3)	

rs7999797	G	44.7	AA	29 (35.8)	52 (32.3)	1.0 (ref)	N/A
			AG	33 (40.7)	74 (46.0)	0.9 (0.4-1.7)	
			GG	19 (23.5)	35 (21.7)	1.0 (0.5-2.2)	
rs4771646	T	32.1	CC	39 (48.1)	77 (47.5)	1.0 (ref)	N/A
			CT	29 (35.8)	66 (40.7)	0.9 (0.5-1.7)	
			TT	13 (16.0)	19 (11.7)	1.1 (0.5-2.8)	
rs12585507	C	7.6	TT	70 (88.6)	134 (85.4)	1.0 (ref)	N/A
			TC	9 (11.4)	22 (14.0)	0.9 (0.4-2.2)	
			CC	0	1 (0.6)	NC	
rs11618950	A	18.7	GG	51 (63.0)	110 (69.6)	1.0 (ref)	N/A
			GA	27 (33.3)	37 (23.4)	1.8 (1.0-3.4)	
			AA	3 (3.7)	11 (7.0)	0.9 (0.2-3.8)	
IL-6 signaling pathway genes							
IL6							
rs2069832	A	43.8	GG	20 (25.0)	50 (31.1)	1.0 (ref)	N/A
			GA	49 (61.3)	81 (50.3)	1.4 (0.7-2.7)	
			AA	11 (13.8)	30 (18.6)	0.8 (0.3-2.1)	
rs2069837	G	5.4	AA	70 (85.4)	141 (89.2)	1.0 (ref)	N/A
			AG	12 (14.6)	17 (10.8)	1.5 (0.6-3.4)	
			GG	0	0	NC	

rs2069840	G	32.2	CC	34 (43.0)	69 (43.1)	1.0 (ref)	N/A
			CG	38 (48.1)	79 (49.4)	1.1 (0.6-1.9)	
			GG	7 (8.9)	12 (7.5)	1.3 (0.4-3.9)	
rs1800795	C	42.6	GG	21 (27.3)	52 (32.1)	1.0 (ref)	N/A
(-174 G/C)			GC	46 (59.7)	82 (50.6)	1.2 (0.6-2.2)	
			CC	10 (13.0)	28 (17.3)	0.8 (0.3-1.9)	
rs1800796	C	5.7	GG	67 (88.2)	141 (88.9)	1.0 (ref)	N/A
(-572 G/C)			GC	8 (10.5)	18 (11.3)	1.1 (0.4-2.7)	
			CC	1 (1.3)	0	NC	
IL6R							
rs4845617	A	38.7	GG	30 (38.0)	61 (38.4)	1.0 (ref)	N/A
			GA	28 (35.4)	73 (45.9)	0.6 (0.3-1.1)	
			AA	21 (26.6)	25 (15.7)	1.4 (0.6-2.8)	
rs12083537	C	17.2	TT	50 (62.5)	109 (68.1)	1.0 (ref)	N/A
			TC	27 (33.8)	47 (29.4)	1.2 (0.6-2.2)	
			CC	3 (3.8)	4 (2.5)	1.7 (0.4-7.8)	
rs4075015	A	37.7	TT	32 (40.0)	63 (39.9)	1.0 (ref)	N/A
			TA	35 (43.8)	71 (44.9)	0.9 (0.5-1.7)	
			AA	13 (16.3)	24 (15.2)	1.2 (0.5-2.7)	
rs6684439	T	38.0	CC	21 (25.9)	58 (35.8)	1.0 (ref)	N/A
			CT	42 (51.9)	85 (52.5)	1.4 (0.7-2.8)	

			TT	18 (22.2)	19 (11.7)	2.9 (1.2-7.0)	
rs7529229	C	40.0	TT	21 (25.9)	51 (32.3)	1.0 (ref)	N/A
			TC	41 (50.6)	88 (55.7)	1.1 (0.6-2.2)	
			CC	19 (23.5)	19 (12.0)	2.5 (1.1-6.0)	
rs4845374	A	17.9	TT	53 (67.1)	108 (67.9)	1.0 (ref)	N/A
			TA	25 (31.7)	45 (28.3)	1.2 (0.6-2.2)	
			AA	1 (1.3)	6 (3.8)	0.3 (0.04-2.9)	
rs10752641	G	23.9	CC	56 (70.0)	94 (59.1)	1.0 (ref)	N/A
			CG	23 (28.8)	54 (34.0)	0.7 (0.4-1.4)**	
			GG	1 (1.3)	11 (6.9)	NC	
rs8192284 (*Ala*358*Asp,* D358A)	C	38.3	AA	24 (30.4)	54 (34.2)	1.0 (ref)	N/A
			AC	37 (46.8)	87 (55.1)	0.9 (0.5-1.7)	
			CC	18 (22.8)	17 (10.8)	2.5 (1.1-6.0)	
rs2229238	A	17.7	GG	65 (81.3)	108 (68.4)	1.0 (ref)	N/A
			GA	15 (18.8)	44 (27.9)	0.5 (0.3-1.1)**	
			AA	0	6 (3.8)	NC	
rs4845623	G	40.3	AA	18 (26.5)	48 (33.1)	1.0 (ref)	N/A
			AG	35 (51.5)	77 (53.1)	1.1 (0.6-2.0)	
			GG	15 (22.1)	20 (13.8)	1.6 (0.7-3.8)	

IL6ST (gp130)

rs1900173	T	9.3	AA	64 (81.1)	133 (82.6)	1.0 (ref)	N/A
			AT	14 (17.7)	26 (16.2)	1.0 (0.4-2.1)	
			TT	1 (1.3)	2 (1.2)	1.0 (0.1-11.9)	
rs11574780	C	5.3	TT	76 (96.2)	144 (89.4)	1.0 (ref)	N/A
			TC	3 (3.8)	17 (10.6)	0.4 (0.1-1.6)	
			CC	0	0	NC	
rs10940495	G	27.5	AA	51 (62.2)	82 (51.9)	1.0 (ref)	N/A
			AG	27 (32.9)	65 (41.1)	0.7 (0.4-1.2)	
			GG	4 (4.9)	11 (7.0)	0.7 (0.2-2.6)	
rs11744523	A	9.4	TT	51 (66.2)	129 (81.1)	1.0 (ref)	N/A
			TA	26 (33.8)	30 (18.9)	1.7 (0.9-3.3)	
			AA	0	0	NC	

Abbreviations: SNP, single nucleotide polymorphism; IGF, insulin-like growth factor; IL, interleukin; OR, odds ratio; CI, confidence interval; ref, reference category; IGFBP, IGF binding protein; NC, not computed; N/A, not available; IGF1R, IGF-1 receptor; IL6R, IL-6 receptor; IL6ST, IL-6 signal transducer.

[*] The N's may not sum to the column total due to the omission of undetermined genotypes; the %'s reflect the proportion of successfully genotyped samples and may not sum to 100% due to rounding.

[†] The ORs and 95% CIs are from unconditional logistic regression models controlling for study population (i.e., gender), age (months), and body mass index (kg/m^2).

[‡] The BPC3 characterized three haplotype blocks that overlap IGFBP1 and IGFBP3 (Cheng et al., 2006; reference 24), and thus the data for the corresponding tagging SNPs are tabulated in order prior to those for IGFBP2, which contains no haplotype blocks.

[§] Carriers of the homozygous wild type genotype comprise the reference category.

[‖] The OR was not computed due to one or more absent genotypes.

[**] The OR and 95% CI were based on the best estimate of the maximum likelihood in a logistic regression model that did not converge.

[††] Genotype data were not available for SNPs in IGFBP2, IGF1R, IRS1, IRS2, IL6, IL6R, or IL6ST in the supplemental controls.