

# Genetic variations in T-cell activation and effector pathways modulate alloimmune responses after allogeneic hematopoietic stem cell transplantation in patients with hematologic malignancies

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Online Supplementary Table S1. Primer sequences used in the SNaPshot reaction.

Mutation position	Polymerase chain reaction amplification primers	Extension primers
For CD28 -594 A/G (rs35593994)	F TCGGCTCATAGCAGCCTCCA R1 GGGTGCTTGAATCCAGCAGAG R2 GGGTGCTTGAATCCAGCAGAGA	F TTTTTTTTTTTTTTCCACCTCCTGGGTTCAAGC
For ICOS -693 A/G (rs11883722)	F TGGTCACCATTGGGATGATTAAGA R TTTAAAAGCCTGCCGTGGTCTC	R TTTTAGCCTGCCGTGGTCTCCC
For CTLA-4 -1722 A/G (rs733618) +49 A/G (rs231775) CT60 A/G (rs3087243)	F GCCAGACTGGGCAACAGAGGT R TGAACCACTGGCTTCTGCTCCT F CCTGAACACCGCTCCATAAAG R TCCTCCATCTTCATGCTCCAAA F CAGCTTTGCACCAGCCATTACC R AGGGACGTGGTTGCCAACATT	R TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTATCATGATCATGGGTTTAGCTG F TTTTTTTTTTTTTTTTTTTTTTTTTTTGGCTCAGCTGAACCTGGCT R TTTTTTTTTTTTTTTTTTTTTTTTTTTGACTGTTATGTCTGTGTTAACCCA
For Granzyme B +55 A/G (rs8192917) -295 C/T (rs7144366)	F GGAGATCATCGGGGACATGA R CAGGAGGGTGTGGGCTGTTTT F TGACGTCTCTGGGTGCTTGT R GGCATTGGCGGTTCTATCACTG	R TTTTTTTTTTTTTTGGCTGTCAGCACGAAGTCGTCT R TTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGGCTGATACCACATCTACA
For Fas -1377 A/G (rs2234767) -670 C/T (rs1800682)	F TCCTTCCCTCACACCCCTTTTC R GGCTTGTCTCTGTTCCACCTTTCA F GAAAGACTTGCGGGGCATTTG R GAGCCCTATGGCGCAACATCT	R TTTTTTTTTTCCATGAGGAAGACCCTGGG F TTTTTTTTTTTTTTTCATGAGAGGCTCACAGACGTT
For FasL -844 C/T (rs763110)	F TGCTTGAGCCCAGGAGTTTGA R GCAAACCACTGGAACCCACAGA	F TTTTTTTTTTTTTTTTTTTTTTTTTTTTGGCAAACAATGAAATGAAAACATTG

**Online Supplementary Table S2.** Frequency of gene polymorphisms and association with phenotype in the donors and patients in the unrelated and sibling donor transplantation cohorts.

Genotype	Associated phenotype	Donor type, n. (%)			Patient type, n. (%)		
		Unrelated cohort	Sibling cohort	P value	Unrelated cohort	Sibling cohort	P value
CD28 (-594)				0.958			0.204
GG	Not applicable	81 (58.7)	60 (58.8)		95 (68.8)	59 (57.8)	
GA	Not applicable	50 (36.2)	36 (35.3)		39 (28.2)	36 (35.3)	
AA	Not applicable	7 (5.1)	6 (5.9)		6 (4.3)	7 (6.9)	
ICOS (-693)				0.658			0.926
AA	Not applicable	31 (22.5)	27 (26.5)		27 (19.6)	22 (21.6)	
AG	Not applicable	64 (46.4)	48 (47.1)		70 (50.7)	51 (50.0)	
GG	Not applicable	43 (31.2)	27 (26.5)		41 (29.7)	29 (28.4)	
CTLA-4 (-1722)				0.995			0.990
AA	Not applicable	57 (41.3)	42 (41.2)		44 (31.8)	32 (31.4)	
AG	Not applicable	60 (43.5)	44 (43.1)		65 (47.1)	49 (48)	
GG	Not applicable	21 (15.2)	16 (15.7)		29 (21.0)	21 (20.6)	
CTLA-4 (+49)				0.576			0.972
AA	Higher production	16 (11.6)	8 (7.8)		12 (8.7)	8 (7.8)	
AG	-	62 (44.9)	45 (44.1)		56 (40.6)	42 (41.2)	
GG	Lower production	60 (43.5)	49 (48.0)		70 (50.7)	52 (51.0)	
CTLA-4 (CT60)				0.459			0.798
AA	Higher production	18 (13.0)	9 (8.8)		14 (10.1)	9 (8.8)	
AG	-	39 (28.3)	26 (25.5)		34(24.6)	30 (29.4)	
GG	Lower production	81 (58.7)	67 (65.7)		90 (65.2)	63 (61.8)	
Granzyme B (+55)				0.718			0.766
AA	-	62 (44.9)	42 (41.2)		66 (47.8)	49 (48.0)	
AG	Incapable of inducing apoptosis	55 (39.9)	46 (45.1)		53 (38.4)	42 (41.2)	
GG		21 (15.2)	14 (13.7)		19 (13.8)	11 (10.8)	
Granzyme B (-295)				0.240			0.781
CC	Not applicable	25 (18.1)	24 (23.5)		32 (23.2)	21 (20.6)	
CT	Not applicable	76 (55.1)	45 (44.1)		68 (49.3)	48 (48.0)	
TT	Not applicable	37 (26.8)	33 (32.4)		38 (27.5)	32 (31.4)	
Fas (-1377)				0.514			0.734
GG	-	47 (34.1)	39 (38.2)		44 (31.9)	34 (33.3)	
GA	Reduced ability to bind the transcription factor SP1	63 (45.6)	48 (47.1)		70 (50.7)	47 (46.1)	
AA		28 (20.3)	15 (14.7)		24 (17.4)	21 (20.6)	
Fas (-670)				0.641			0.257
CC	Higher production	24 (17.4)	14 (13.7)		16 (11.6)	19 (18.6)	
TC	-	63 (45.7)	52 (51.0)		73 (52.9)	46 (45.1)	
TT	Lower production	51 (37.0)	36 (35.3)		49 (35.5)	37 (36.3)	
FasL (-844)				0.275			0.402
CC	Higher production	69 (50.0)	49 (48.0)		70 (50.7)	45 (44.1)	
CT	-	52 (37.7)	46 (45.1)		53 (38.4)	48 (47.1)	
TT	Lower production	17 (12.3)	7 (6.9)		15 (10.9)	9 (8.8)	