

Supplementary Materials

Supplementary Table S1: P2X7 primer sequences

SNP_ID	PCR Primer 1	PCR Primer 2	Extension Primer
rs28360445	ACGTTGGATGACTCCAGGTCCCCTCCTTAC	ACGTTGGATGGGAACTCTTTCTTCGTGATG	CCTCGGGACACAACC
rs28360447	ACGTTGGATGTTCTACGATGCTTTGACCCC	ACGTTGGATGCAGAGACTTCACAGGTCTTC	CCCTATAGGAATTCAGACC
rs28360451	ACGTTGGATGCAGGCCTGCTCTCTTGAAC	ACGTTGGATGCTTACGTGGTGTAGTTGTGG	CCTGCTCTCTTGAACAGTGCC
rs28360452	ACGTTGGATGGCACTTACGTGGTGTAGTTG	ACGTTGGATGTGAACAGTGCCGAAAAC TTC	AGTCGATATTGTTCTTGATG
rs7958311	ACGTTGGATGGTCGTC AAGGCGAAGGAAAC	ACGTTGGATGTTGAGATCTACTGGGACTGC	IGGAAACTGTATTGGGA
rs7958316	ACGTTGGATGAGGGTACAAGGACACGTTGG	ACGTTGGATGTAGACCGTTGGTTCCATCAC	TCTTGTCGTCAAGGCGA
rs28360457	ACGTTGGATGCTTCCTACAGATACGCCAAG	ACGTTGGATGTCAAAACGGATCCCGAAGAC	ACGGAAAACAATGTTGAGAAAC
rs3751143	ACGTTGGATGAACAGCTCTGAGGTGGTGAT	ACGTTGGATGATCTCAACTCCCTGAGAGCC	TTCCGGCAGCACAGC
rs1653624	ACGTTGGATGACTGTGCCTACAGGTGCTAC	ACGTTGGATGTCTTTCCGGATCCTCCAGC	TGGCTGACTTTGCCA
rs35933842	ACGTTGGATGTTTCTGTGCTGTCGGCCACT	ACGTTGGATGGGTTCTTCCACGTGATCATC	CCCCAGATCCCACTTA
rs17525809	ACGTTGGATGTCATCAGTTCTGTGCACACC	ACGTTGGATGCACTGTGCACCAACTTCTTC	AGGTGAAAGAGGAGATCG
rs2230911	ACGTTGGATGCTGTGTTTCATCGACTTCCTC	ACGTTGGATGGGGATAAATATGGGAGCGAC	CGACTTCCTCATCGACA
rs2230912	ACGTTGGATGTATCCCTGGATCTAGGAGTC	ACGTTGGATGTCCATGACACACCCCCGATT	CCTCCTTTCTAAGCAGC
rs2230913	ACGTTGGATGTTGGTGGAATCCACATCCAG	ACGTTGGATGAGCTGTT CAGGAAGCTGGTC	GAGGAACTGCAGGAC
rs208294	ACGTTGGATGCAGAGACTTCACAGGTCTTC	ACGTTGGATGTTCTACGATGCTTTGACCCC	CTTCTGGTTCCCTTCAT
rs1718119	ACGTTGGATGTGTCGATGAGGAAGTCGATG	ACGTTGGATGGAGAAGGAAGTGACTAACGC	GAGGAAGTCGATGAACACAG

Supplementary Table S2: MAF correlation to aGVHD grade

Recipient

Polymorphism	MAF		P value	RR	95% CI	MAF		P value	RR	95% CI
	grade 0	grade 1-4				grade 0-1	grade 2-4			
Gly150Arg	0.01	0.02	0.388	1.008	0.9894-1.027	0.02	0.01	0.7432	0.9937	0.9769-1.011
Arg270His	0.24	0.29	0.1415	1.066	0.9790-1.161	0.25	0.29	0.2661	1.058	0.9591-1.168
Arg276His	0.02	0.02	0.799	0.9952	0.9766-1.014	0.02	0.00	0.1416	0.981	0.6991-0.9961
Arg307Gln	0.02	0.01	1	0.9974	0.9810-1.014	0.02	0.01	0.7431	0.9935	0.9769-1.01
Glu496Ala	0.18	0.17	0.5796	0.981	0.9201-1.046	0.19	0.13	0.0457	0.9267	0.8683-0.989
Ile568Asn	0.01	0.04	0.0173	1.027	1.003-1.051	0.02	0.03	0.2454	1.014	0.9878-1.041
Val76Ala	0.07	0.09	0.2763	1.023	0.9811-1.066	0.07	0.10	0.1634	1.033	0.9827-1.086
Thr357Ser	0.10	0.09	0.7177	0.9885	0.9456-1.033	0.09	0.10	0.6826	1.012	0.9599-1.067
Gln460Arg	0.17	0.14	0.2449	0.9622	0.9077-1.02	0.17	0.12	0.1256	0.9471	0.8901-1.008
His155Tyr	0.45	0.46	0.7746	1.022	0.8980-1.162	0.47	0.43	0.2582	0.916	0.7971-1.053
Ala348Thr	0.40	0.38	0.4658	0.9621	0.8727-1.061	0.39	0.40	0.804	1.021	0.8970-1.163

Donor

Polymorphism	MAF		P value	RR	95% CI	MAF		P value	RR	95% CI
	grade 0	grade 1-4				grade 0-1	grade 2-4			
Gly150Arg	0.02	0.02	1	0.9973	0.9790-1.016	0.02	0.02	0.7691	1.002	0.9802-1.025
Arg270His	0.28	0.29	0.7534	1.016	0.9297-1.11	0.28	0.29	1	1.003	0.9080-1.108
Arg276His	0.03	0.03	1	0.9982	0.9740-1.023	0.03	0.02	0.8161	0.992	0.9666-1.018
Arg307Gln	0.02	0.02	1	1.001	0.9811-1.02	0.02	0.02	1	1.001	0.9785-1.023
Glu496Ala	0.18	0.18	0.8543	0.9914	0.9289-1.058	0.19	0.16	0.4682	0.9707	0.9042-1.042
Ile568Asn	0.02	0.02	0.785	1.004	0.9852-1.024	0.01	0.03	0.1235	1.017	0.9911-1.044
Val76Ala	0.08	0.10	0.2064	1.028	0.9833-1.075	0.08	0.11	0.114	1.042	0.9869-1.1
Thr357Ser	0.08	0.08	1	1.001	0.9600-1.044	0.08	0.10	0.4645	1.018	0.9687-1.071
Gln460Arg	0.15	0.13	0.3645	0.9733	0.9209-1.029	0.15	0.13	0.5677	0.9779	0.9195-1.040
His155Tyr	0.47	0.40	0.0635	0.8875	0.7872-1.001	0.46	0.40	0.1702	0.9039	0.7917-1.032
Ala348Thr	0.36	0.37	0.8238	1.015	0.9120-1.129	0.36	0.37	0.8673	1.013	0.8982-1.144

RR = Relative Risk, CI = Confidence Interval

Supplementary Table S3: P2X7 SNP correlation to RFS

Recipient

Polymorphism	P value	Hazard Ratio	95% CI
Gly150Arg	0.0958	2.236	0.8673-5.764
Arg270His*	0.7383		
Arg276His	0.6932	0.8369	0.3455-2.057
Arg307Gln	0.4300	0.6531	0.2267-1.881
Glu496Ala*	0.5178		
Ile568Asn	0.8231	1.114	0.4329-2.866
Val76Ala	0.4364	0.8232	0.5044-1.344
Thr357Ser*	0.4972		
Gln460Arg*	0.1942		
His155Tyr*	0.2926		
Ala348Thr*	0.4755		

*Analysis of 3 groups (common homozygote, heterozygote and rare homozygote). Hazard ratio and 95% CI unable to be calculated.

Donor

Polymorphism	P value	Hazard Ratio	95% CI
Gly150Arg	0.8160	0.8944	0.3494-2.290
Arg270His*	0.7584		
Arg276His	0.7054	0.8634	0.4032-1.849
Arg307Gln	0.6313	0.8024	0.3266-1.972
Glu496Ala*	0.4417		
Ile568Asn	0.8172	1.135	0.3874-3.326
Val76Ala	0.6779	1.099	0.7041-1.715
Thr357Ser*	0.6009		
Gln460Arg*	0.1961		
His155Tyr*	0.6454		
Ala348Thr*	0.2194		

*Analysis of 3 groups (common homozygote, heterozygote and rare homozygote). Hazard ratio and 95% CI unable to be calculated.

Supplementary Table S4: P2X7 SNP correlation to OS

Recipient

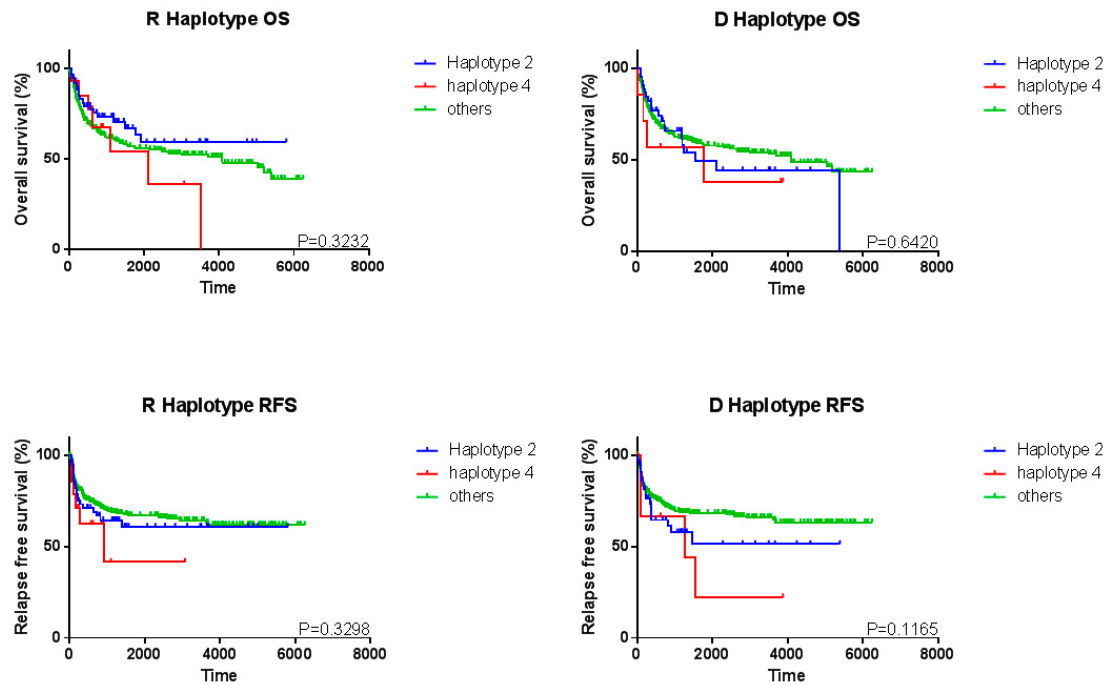
Polymorphism	P value	Hazard Ratio	95% CI
Gly150Arg	0.4569	1.371	0.5971-3.147
Arg270His*	0.7105		
Arg276His	0.3761	3.039	1.606-5.751
Arg307Gln	0.1206	0.9980	0.4103-2.428
Glu496Ala*	0.0207		
Ile568Asn	0.0979	2.331	1.267-4.289
Val76Ala	0.9610	0.9993	0.6633-1.505
Thr357Ser*	0.8168		
Gln460Arg*	0.7960		
His155Tyr*	0.7497		
Ala348Thr*	0.5088		

*Analysis of 3 groups (common homozygote, heterozygote and rare homozygote). Hazard ratio and 95% CI unable to be calculated.

Donor

Polymorphism	P value	Hazard Ratio	95% CI
Gly150Arg	0.3724	4.919	2.422-9.993
Arg270His*	0.1517		
Arg276His	0.8939	1.046	0.5419-2.018
Arg307Gln	0.4111	0.9993	0.5113-1.953
Glu496Ala*	0.0525		
Ile568Asn	0.6353	2.329	1.032-5.256
Val76Ala	0.8184	0.7871	0.5398-1.148
Thr357Ser*	0.4657		
Gln460Arg*	0.3545		
His155Tyr*	0.6456		
Ala348Thr*	0.7037		

*Analysis of 3 groups (common homozygote, heterozygote and rare homozygote). Hazard ratio and 95% CI unable to be calculated.



Supplementary Figure S1: Association between recipient (R) and donor (D) haplotype and overall survival (OS) and relapse free survival (RFS). Patients were classified as haplotype 2 (homozygous Ala348Thr), haplotype 4 (homozygous Gln460Arg and Ala348Thr) or other. Proportions of OS and RFS were calculated using Kaplan-Meier method.

Supplementary Table S5: Correlation of aGVHD grade to haplotype

	Haplotype 2		Haplotype 4		Others		P value*
	Grade 0	Grade 1-4	Grade 0	Grade 1-4	Grade 0	Grade 1-4	
Recipient	41	18	10	3	234	129	0.5118
Donor	27	17	6	1	245	133	0.4561

	Haplotype 2		Haplotype 4		Others		P value*
	Grade 0-1	Grade 2-4	Grade 0-1	Grade 2-4	Grade 0-1	Grade 2-4	
Recipient	45	14	11	2	280	83	0.8041
Donor	31	13	6	1	291	87	0.5293

*analysed using Chi square test. Any patients who relapsed prior to aGVHD or had an undetermined aGVHD grade were excluded from analysis.