Supplementary Material:

Supplementary Methods:

Creation of an MHC-defined rhesus macaque model of transplantation: We have performed an immunogenetic analysis on >350 animals from the Yerkes National Primate Research Center and >800 animals from the NIAID-sponsored colony at Yemassee, SC, including family tree and MHC haplotype determination via DNA microsatellite testing. To accomplish this, we employed a two-part strategy based on microsatellite genotypes. DNA was first purified from 1cc of citrate-anticoagulated blood, and eight multiplexed PCR reactions were then performed to obtain genotype data for 41 markers, 15 of which spanned the MHC region. Details of markers, primers and multiplex groups are summarized in Supplementary Table 1. PCR reactions were combined as described in Supplementary Table 1 for separation by capillary electrophoresis on ABI 3730 instruments (Applied Biosystems, Foster City, CA). Pedigrees were then established based on analysis of the inheritance patterns of 26 microsatellite markers. (17, 23) Once animals were placed in a pedigree, MHC sharing was determined between full and half-siblings by comparing the inheritance of parental MHC haplotypes based on high-density microsatellite analysis of the MHC region from the rhesus chromosome 4. This process allowed us to unambiguously assign macaque offspring to a family tree and to assign them two unique MHC haplotype codes. A typical family pedigree display is shown in Supplementary Figure 1a. As demonstrated in this Figure, rhesus pedigrees contain a large number of full and half-sibling pairs that share either one or two MHC haplotypes. It is from this large pool of potential MHC-matched and -mismatched transplant pairs that our experimental cohorts were chosen. Figures 1b and 1c show a detailed view of the microsatellite haplotypes in each of the transplant pairs that were studied.

454-Sequencing of MHC Haplotypes: To define the MHC class I alleles transcribed on each of the MHC haplotypes, 454 pyrosequencing was performed as previously described. (24, 25) Briefly, a diagnostic amplicon of 367 b.p spanning the highly polymorphic peptide binding domain encoded by exons 2 and 3 was amplified from total RNA by cDNA-PCR. Pooled amplicons were pyrosequenced on a Roche/454 GS FLX instrument (Branford, CT) using FLX chemistry. After image processing the resultant transcript sequences were identified by comparison to a custom library of previously described rhesus macaque MHC class I alleles using NCBI blastn.

Supplementary Results:

MHC disparity predicts the degree of pre-transplant alloreactivity in a pedigreed, MHC-defined rhesus macaque colony. Having established a system to determine the degree of MHC disparity between transplant pairs, we were able to rigorously determine the degree to which MHC sharing impacted alloproliferation. We performed an analysis of alloproliferation as measured by CFSE-MLR, and compared four cohorts: (1) two MHC-haplotype matched pairs (n= 8), (2) one MHC-haplotype-matched pairs (n = 48), (3) autologous controls (with responder and stimulator cells derived from the same animal, n = 61) and (4) a cohort of animals for whom haplotype information was not available at the time of the CFSE MLR (n=99). Examples of representative CFSE MLR assays for each of the groups are shown in Supplementary Figure 2a. Supplementary Figure 2b shows that pairs matched at both MHC haplotypes displayed minimal pre-transplant alloproliferation (1.1% $\pm$1%), not statistically different than autologous controls (1.3% $\pm$ 1.5%). As expected, pairs matched at just one MHC haplotype displayed significantly more alloproliferation (8.4% + 8.5%) than either the two MHC haplotype-matched pairs or the autologous controls ($p<0.01$). The percentage of cells that had proliferated in the MLR cohort with unknown MHC disparity (17% $\pm$ 14.9%) was higher than for either the one MHC-haplotype- or two MHC-haplotype-matched pairs ($p<0.01$). However, the

proliferation measured in this untyped cohort was not uniform, with these MLR pairs displaying a high standard deviation around the mean (Supplementary Figure 2b), with many animals demonstrating surprisingly low levels of alloproliferation. These examples of low levels of alloproliferation in the cohort that had not been pedigreed or MHC typed led us to hypothesize that some pairs included in this group serendipitously possessed significant degrees of relatedness or MHC similarity.

To test this hypothesis, we determined the profiles of MHC class I allele transcripts in a subset of donor/recipient animal pairs by pyrosequencing (24, 25) This analysis allowed us to (1) confirm the results of the microsatellite-based MHC analysis shown in Supplementary Figure 1 and (2) determine if serendipitous MHC similarity could accompany low alloproliferation by CFSE MLR. As shown in Supplementary Figure 2c, the degree of MHC identity predicted by microsatellite analysis for RDe9/RNs9 or DK5P/DL74 (both two MHC haplotype-matched pairs) as well as RWk10/RMn10 (one MHC haplotype-matched) was confirmed by pyrosequencing. This comprehensive analysis of expressed alleles also confirmed that high degrees of MHC similarity could be found in the untyped cohort. Thus, CX6X and CX2A, who showed significant allo-proliferation as measured by MLR (22.4%), were found to have totally disparate MHC haplotypes (Figure 2c). In contrast, pyrosequencing analysis of CX3M and RMn10, led to a significantly different outcome. Although these two animals had no known familial relationship, and were derived from two different primate colonies (RMn10 from the Yerkes National Primate Research Center and CX3M from NIAID-sponsored colony at Yemassee, SC), they demonstrated low levels of alloproliferation by CFSE MLR (1.2%). Pyrosequencing analysis detected a shared MHC haplotype between these animals, and a resultant high degree of MHC similarity (Supplementary Figure 2c). These results confirm the utility of rapid microsatellite-based MHC typing to determine the degree of MHC disparity *within a pedigreed colony* and, perhaps most

importantly, point to a significant potential confounder in transplant analysis of untyped and unpedigreed animals: serendipitously high levels of MHC similarity, even between animals from different colonies, might significant impact alloreactivity and potentially, transplant outcome.

Locus [a]	Mmu # [b]	Dye	Multiplex[c]	Forward Primer (5'-3')	Reverse Primer (5'-3')[d]	µM in PCR	Size Range [e]
D1S548	1	NED	C1	GAACTCATTGGCAAAAGGAA	gttcttGCCTCTTTGTTGCAGTGATT	0.09	190-210
D2S1333	12	NED	C1	CTTTGTCTCCCCAGTTGCTA	TCTGTCATAAACCGTCTGCA	0.18	269-341
D3S1768	2	FAM	A2	GGTTGCTGCCAAAGATTAGA	CACTGTGATTTGCTGTTGGA	0.08	181-233
D4S2365	5	FAM	A2	AGTAATTCTTCAACTGCATCACC	ATGCCAAGGATGGTGAGTTA	0.16	117-151
D4S413	5	VIC	C2	TCTGAATATAGTGCTCCAGAAA	CAATCAGTGGGTTTTTGAA	0.31	271-307
D5S1457	6	NED	A2	TAGGTTCTGGGCATGTCTGT	gttcttTGCTTGGCACACTTCAGG	0.09	112-148
D6S501	4	NED	B2	GCTGGAAACTGATAAGGGCT	GCCACCCTGGCTAAGTTACT	0.06	160-196
D7S513	3	VIC	A1	AGTGTTTTGAAGGTTGTAGGTTAAT	ATATCTTTCAGGGGAGCAGG	0.13	185-249
D7S794	3	FAM	A1	ACCATACTCCTCAGCCTCCA	GTGTTCGGGTTCTCCAAAGA	0.09	108-140
D8S1106	8	FAM	C1	GCGGCATGTTTTCCTACTTT	TTCTCAGAATTGCTCATAGTGC	0.08	132-188
D9S921	15	PET	C1	CCTGGAGAATCTTGTGATGC	gttcttTCTTTCATGTTGGCTCCTGT	0.10	167-203
D10S1412	9	VIC	B2	TGCCTTAGCTCCTGCATACTGA	GGGACAGTTCTTCTCCCTCCA	0.06	154-166
D11S2002	14	VIC	B2	AGTAGTAGGAGGCCCCAAGG	CAAGCAATCCTCCCACCTTA	0.11	244-272
D11S925	14	VIC	A1	GCTCCTCCAGTAATTCTGTC	TTAGACCATTATGGGGGCAA	0.25	298-348
D12S364	11	FAM	B2	TTGGGAAAGTCGTTTTGCAT	TGAGACTCAAATCCCCTGGA	0.22	264-296
D12S67	11	PET	B2	GCAACAGTTTATGCTAAAGC	GCCTATGCAGTTCAAATCTA	0.47	105-244
D13S765	17	NED	A2	TGTAACTTACTTCAAATGGCTCA	TTGAAACTTACAGACAGCTTGC	0.12	196-272
D15S823	7	VIC	C1	GGCTTTGCATCCAGAATTTA	gtttcttCACTTCCAACACTGAGGATC	0.13	317-385
D16S403	20	PET	A1	GTTTTCTCCCTGGGACATTT	TATTCATTTGTGTGGGCATG	0.56	140-182
D17S1300	16	PET	A2	TAGTGTGTATATATGTATGCATGCA	ggataacaatttcacacaggTGCAGATATCTGTCTTTTGGC	0.22	224-328
D18S537	18	VIC	C1	TCCATCTATCTTTGATGTATCTATG	gttcttAGTTAGCAGACTATGTTAATCAGGA	0.14	162-178
D18S72	18	NED	B1	GCTAGATGACCCAGTTCCC	CTGCAGAAAGGTTACATATTCCA	0.18	302-344
D22S685	10	PET	C2	TTCTCAGTGGGGGAGGGAT	TGGAGTTTGATGTTTTTGAGAGAC	0.25	223-267
DXS2506	X	VIC	C1	GGAGAAATGGGGAGTAACTG	gttcttACACATGGCTGGCTAGCTT	0.09	258-296
MFGT21	8	FAM	B1	AACTTCAGTAAGATAAGGACC	CCTGAGGTCTGGACTTTAT	0.20	93-133
MFGT22	?	VIC	B1	CAACATAGAGAGATTCCATCTC	CGTTAAGTATGATGTTAGCTAG	0.25	94-128
MHC-linked							
D6S291	4	VIC	B1	CTCAGAGGATGCCATGTCTAAAATA	GGGGATGACGAATTATTCACTAACT	0.16	177-231
D6S2741	4	VIC	D	AGACTAGATGTAGGGCTAGC	CTGCACTTGGCTATCTCAAC	0.03	247-297
D6S2876	4	FAM	D	GGTAAAATTCCTGACTGGCC	GACAGCTCTTCTTAACCTGC	0.04	194-252
9P06	4	NED	E	CACTAACGATAGCTGATGAGCTTAAA	TGCACATCCCTGTATATCAAGC	0.11	175-191
D6S2883	4	NED	D	TGGAATCTCATCAAGGTCAG	TTGAAATTGATACTTTCCCAGTTCTC	0.03	112-152
MICA	4	NED	D	CCTTTTTTTCAGGGAAAGTGC	CCTTACCATCTCCAGAAACTGC	0.03	185-209
246K06	4	NED	E	GCCCAATAGCAAGCCAAGAA	TGGTGAGGGGATTTCTCTGAA	0.05	271-287
162B17A	4	VIC	E	ACAGCCTCACCAACACCTGA	CCCCTTCTCTCCCCAAAGAT	0.15	238-252
162B17B	4	FAM	E	GAAGATGTGCCCATTTCCAGA	TTTCCACCACTGCCTTCTCA	0.22	281-317
151L13	4	PET	E	AGGGCATCTCAGGCATTCAT	GGGGGAGGGATAGCATTAGG	0.03	300-326
MOG-CA	4	FAM	D	GAAATGTGAGAATAAAGGAGA	GATAAAGGGGAACTACTACA	0.19	107-137
268P23	4	FAM	E	TCAGAAATGTGAGAATAAAGGAGACA	TGAAGCATTGGAAGGCAAAA	0.09	148-156
222I18	4	VIC	E	GGAGGGAGGGAGAGAAAGTCA	GCCTCGGCACTCACACATTA	0.03	161-177
D6S276	4	NED	B1	TTCCAGTGTATACATCAATCAAATCA	GGGTGCAACTTGTTCCTCCT	0.28	195-245
D6S1691	4	FAM	B1	AGGACAGAATTTTGCCTC	GCTGCTCCTGTATAAGTAATAAAC	0.22	196-222

Supplementary Table 1. Microsatellite marker panels used to establish pedigrees and MHC haplotypes. [a]: Names with D prefix correspond to human nomenclature for markers; [b]: Rhesus macaque chromosome number in Jan 2006 MSGC Merged 1.0/rheMac2 draft assembly (http://genome.ucsc.edu/cgi-bin/hgGateway); [c]: Multiplexes with same group letter (e.g. A1 and A2) were combined for electrophoresis; [d]: bases in lower case are tails added to primers; [e]: allele size range does not include tails.

Supplementary Figure Legends:

Supplementary Figure 1: Creation of a pedigreed and MHC-defined rhesus macaque transplant model.

Supplementary Figure 1a: Pedigree and MHC Inheritance Map for N5K, his mating pairs and his offspring. The sire, N5K, is depicted at the center of the circular pedigree. Each dam with whom he mated is depicted on the edge of the circle, with a linear connection to N5K. Offspring from each of the mating pairs are depicted emanating from these connections. Circles indicate female offspring and dams. Squares indicate male offspring and sires. MHC haplotypes are indicated by color coded bars associated with each animal. N5K's MHC haplotypes are indicated as either a red or a black bar. MHC haplotypes for each of the dams are indicated by unique color-coded bars. The inheritance of an MHC haplotype from the sire or dam is indicated by the color of the bars for each of the offspring.

Supplementary Figure 1b: Detailed view of the DNA microsatellite-based MHC haplotypes for the two MHC haplotype-matched transplant pairs. Animals were analyzed using 8-15 microsatellites that spanned the MHC and haplotypes were derived from their inheritance between parents and offspring. Individual MHC haplotypes are color-coded.

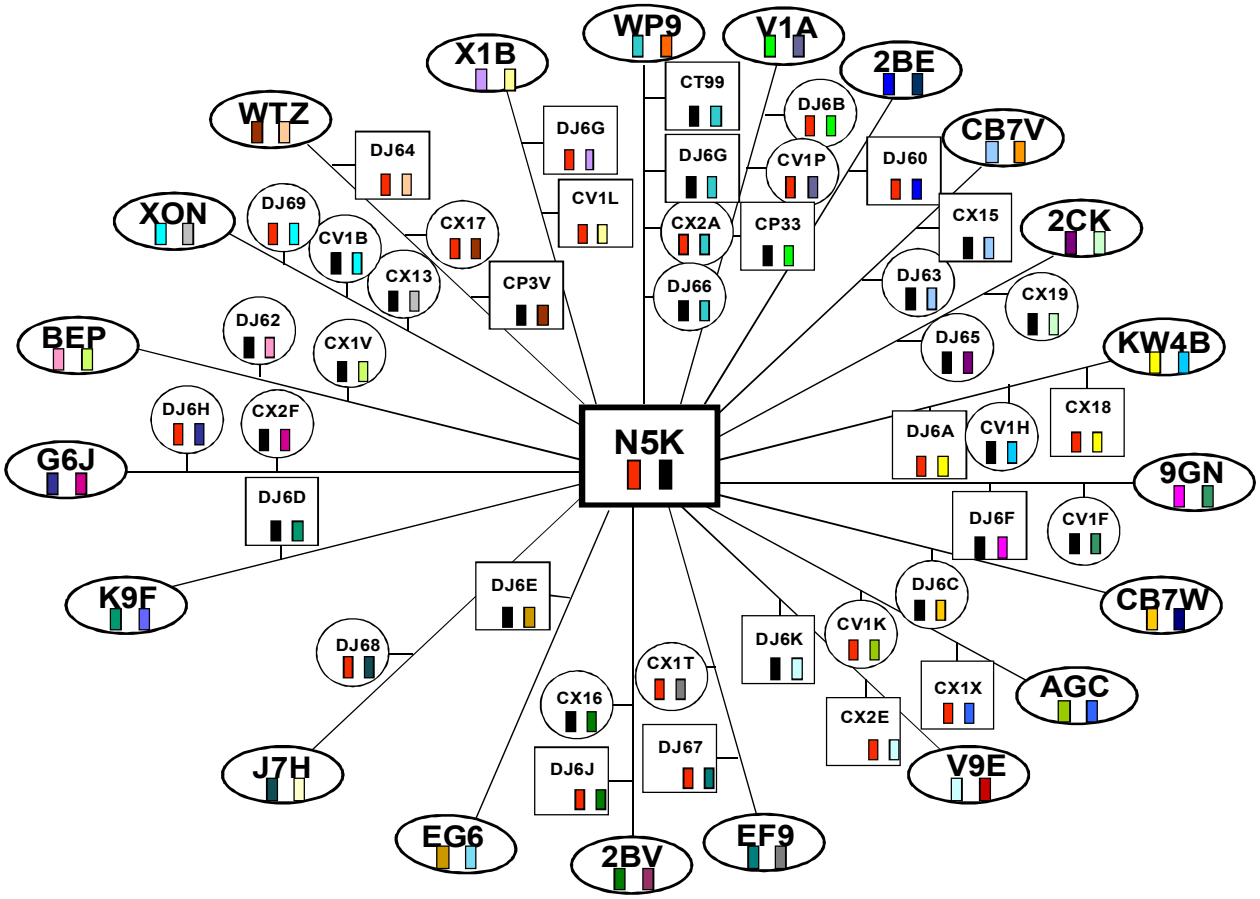
Supplementary Figure 1c: Detailed view of the DNA microsatellite-based MHC haplotypes for the one MHC-haploptye-matched transplant pairs. Animals were analyzed using 8-15 microsatellites that spanned the MHC and haplotypes were derived from their inheritance between parents and offspring. Individual MHC haplotypes are color-coded.

Supplementary Figure 2: MHC disparity predicts alloproliferation as measured by CFSE MLR.

Supplementary Figure 2a. CFSE MLR analysis reveals increasing alloproliferation with increasing MHC disparity. This figure shows CFSE fluorescence for both CD4+ and CD8+ cells after a 5 day MLR culture. Shown (left to right, top row) are a representative autologous control, a two MHC-haplotype matched pair, and a one MHC-haplotype matched pair. The bottom row shows a representative pair with unknown MHC disparity and high proliferation (left) and a representative pair with unknown MHC disparity and low proliferation (right).

Supplementary Figure 2b. The amount of CD8+ T cell alloproliferation correlated with the degree of MHC disparity. CFSE MLR analysis was performed on two-MHC haplotype matched pairs (n= 8), one MHC-haplotype-matched pairs (n=48), autologous controls (n=61), and animals for whom MHC disparity Information was not available (n=99). The percent of CD8+ T cells remaining at the end of the five day MLR incubation period that had undergone at least one round of cell division (% proliferation) was then determined using the FloJo flow cytometry analysis program. Shown are the average % proliferation and the standard deviation for all four groups. Statistical significance was determined by ANOVA analysis of the log-transformed data followed by a post-hoc Tukey HST test to determine significant differences for pair-wise comparisons.

Supplementary Figure 2c: Class I transcript profiles for animals with varying degrees of MHC disparity. MHC class I genotypes were determined by pyrosequencing of cDNA-PCR amplicons for representative pairs of animals used in the CFSE-MLR assays. The number of sequence reads identified for specific MHC class I alleles or closely related allele lineages are indicated for each animal. MHC haplotypes shared between animals are highlighted with open boxes.



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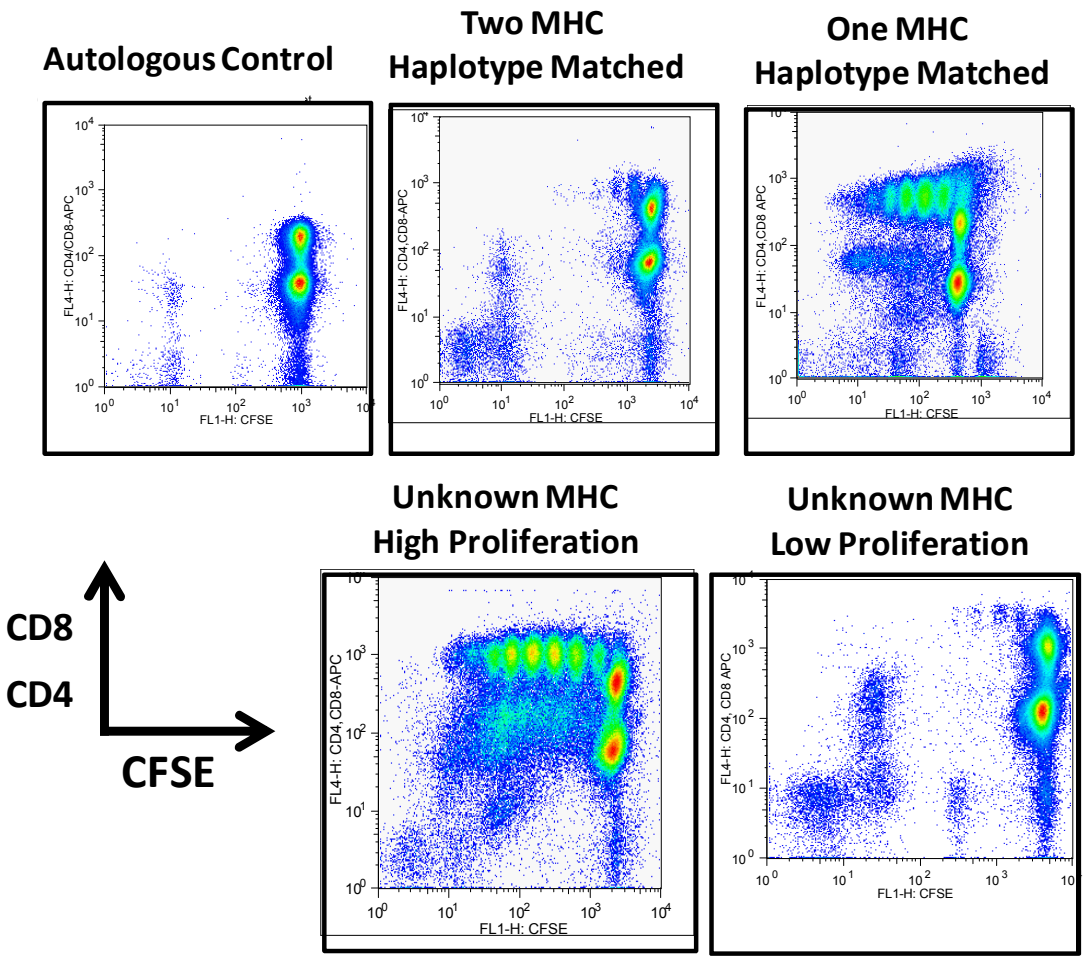
Two MHC-Haplotype Matched Pairs			Microsatellites														
ID	Sire	Dam	D6S291	G25641	G51152	9P06	DRA	MICA	246K06	162B17A	162B17B	151L13	MOGCA	268P23	222I18	D6S276	D6S1691
CW7A	GJF	AW44	197	279	209	183	136	200	279	240	295	309	123	150	168	233	208
CW7A	GJF	AW44	209	261	215	175	126	200	279	240	295	299	121	148	173	225	208
CW7E	GJF	AW4E	197	279	209	183	136	200	279	240	295	309	123	150	168	233	208
CW7E	GJF	AW4E	209	261	215	175	126	200	279	240	295	299	121	148	173	225	208
DJ63	N5K	CB7V	197	281	210	177	134	200	283	250	309	303	123	150	161	215	206
DJ63	N5K	CB7V	205	271	219	191	112	200	279	240	297	309	123	150	168	233	214
CX15	N5K	CB7V	197	281	210	177	134	200	283	250	309	303	123	150	161	215	206
CX15	N5K	CB7V	205	271	219	191	112	200	279	240	297	309	123	150	168	233	214
DJ66	N5K	WP9	206	281	210	177	134	200	283	250	309	303	123	150	161	215	197
DJ66	N5K	WP9	216	259	208	165	114	200	283	240	293	305	127	154	173	215	197
CT99	N5K	WP9	206	281	210	177	134	200	283	250	309	303	123	150	161	215	197
CT99	N5K	WP9	216	259	208	165	114	200	283	240	293	305	127	154	173	215	197
DK8B	AV58	CC53	212	265	208	ND	114	200	ND	ND	ND	ND	127	ND	ND	225	203
DK8B	AV58	CC53	208	269	208	ND	138	191	ND	ND	ND	ND	119	ND	ND	211	216
CW5R	AV58	CC53	212	265	208	187	114	200	279	242	309	305	127	154	165	225	203
CW5R	AV58	CC53	208	269	208	185	138	191	285	244	293	301	119	146	165	211	216
RCh9	unknown	RKf5	216	281	195	ND	132	200	ND	ND	ND	ND	125	ND	ND	225	197
RCh9	unknown	RKf5	208	273	219	ND	128	194	ND	ND	ND	ND	123	ND	ND	233	197
RJt7	unknown	RKf5	216	281	195	ND	132	200	ND	ND	ND	ND	125	ND	ND	225	197
RJt7	unknown	RKf5	208	273	219	ND	128	194	ND	ND	ND	ND	123	ND	ND	233	197
RCq7	RMc4	RQg5	214	259	219	ND	112	203	ND	ND	ND	ND	123	ND	ND	225	197
RCq7	RMc4	RQg5	206	261	210	ND	134	200	ND	ND	ND	ND	123	ND	ND	225	217
RAi9	RMc4	RQg5	214	259	219	ND	110	203	ND	ND	ND	ND	123	ND	ND	225	197
RAi9	RMc4	RQg5	206	261	210	ND	134	200	ND	ND	ND	ND	123	ND	ND	225	217
RDe9	RMc4	RHe5	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RDe9	RMc4	RHe5	216	261	203	ND	120	200	ND	ND	ND	ND	121	ND	ND	225	199
RNs9	RMc4	RHe5	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RNs9	RMc4	RHe5	216	261	203	ND	120	200	ND	ND	ND	ND	121	ND	ND	225	199
RFo9	RMc4	RKg7	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RFo9	RMc4	RKg7	216	269	195	ND	132	200	ND	ND	ND	ND	125	ND	ND	221	207
RIi8	RMc4	RUn5	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RIi8	RMc4	RUn5	216	269	195	ND	132	200	ND	ND	ND	ND	125	ND	ND	221	207
RQq9	RMc4	RUn5	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RQq9	RMc4	RUn5	216	269	195	ND	132	200	ND	ND	ND	ND	125	ND	ND	221	207
RKg7	RMc4	RUn5	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RKg7	RMc4	RUn5	216	269	195	ND	132	200	ND	ND	ND	ND	125	ND	ND	221	207

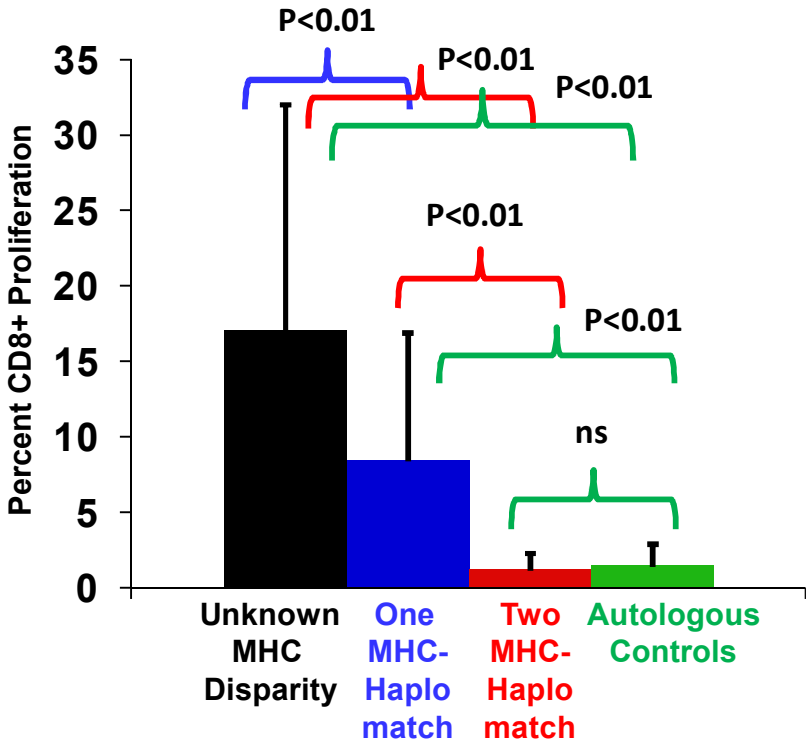
Supplementary Figure 1b: Detailed view of the DNA microsatellite-based MHC haplotypes for the two MHC haplotype-matched transplant pairs. Animals were analyzed using 8-15 microsatellites that spanned the MHC and haplotypes were derived from their inheritance between parents and offspring. Individual MHC haplotypes are color-coded.

One MHC-Haplotype Matched Pairs			Microsatellites														
ID	Sire	Dam	D6S291	G25641	G51152	9P06	DRA	MICA	246K06	162B17A	162B17B	151L13	MOGCA	268P23	222I18	D6S276	D6S1691
CW54	AW9W	CC52	197	277	215	185	124	200	279	242	309	303	123	150	168	225	208
CW54	AW9W	CC52	205	261	209	191	136	200	279	240	297	309	123	150	168	233	208
CW5X	AW9W	AV60	197	277	215	185	124	200	279	242	309	303	123	150	168	225	208
CW5X	AW9W	AV60	209	261	203	185	114	200	289	246	292	309	127	154	167	211	216
CW55	AV58	CC5R	203	265	208	187	114	200	279	242	309	305	127	154	165	225	212
CW55	AV58	CC5R	205	281	208	165	136	200	285	242	293	317	125	152	167	233	208
CW5P	AV58	CC5D	203	265	208	187	114	200	279	242	309	305	127	154	165	225	212
CW5P	AV58	CC5D	197	269	219	189	128	200	275	240	311	309	123	150	168	227	206
RPh9	RMc4	RHl5	214	259	219	ND	112	203	ND	ND	ND	ND	123	ND	ND	225	197
RPh9	RMc4	RHl5	208	259	219	ND	112	200	ND	ND	ND	ND	127	ND	ND	225	197
RMc4	N770	N740	208	261	210	ND	134	191	ND	ND	ND	ND	127	ND	ND	215	211
RMc4	N770	N740	214	259	219	ND	112	203	ND	ND	ND	ND	123	ND	ND	225	197

Supplementary Figure 1c: Detailed view of the DNA microsatellite-based MHC haplotypes for the one MHC-haploptye-matched transplant pairs. Animals were analyzed using 8-15 microsatellites that spanned the MHC and haplotypes were derived from their inheritance between parents and offspring. Individual MHC haplotypes are color-coded.



Supplementary Figure 2a. CFSE MLR analysis reveals increasing alloproliferation with increasing MHC disparity. This figure shows CFSE fluorescence for both CD4+ and CD8+ cells after a 5 day MLR culture. Shown (left to right, top row) are a representative autologous control, a two MHC-haplotype matched pair, and a one MHC-haplotype matched pair. The bottom row shows a representative pair with unknown MHC disparity and high proliferation (left) and a representative pair with unknown MHC disparity and low proliferation (right).



Supplementary Figure 2b. The amount of CD8+ T cell alloproliferation correlated with the degree of MHC disparity. CFSE MLR analysis was performed on two-MHC haplotype matched pairs (n= 8), one MHC-haplotype-matched pairs (n=48), autologous controls (n=61), and animals for whom MHC disparity Information was not available (n=99). The percent of CD8+ T cells remaining at the end of the five day MLR incubation period that had undergone at least one round of cell division (% proliferation) was then determined using the FloJo flow cytometry analysis program. Shown are the average % proliferation and the standard deviation for all four groups. Statistical significance was determined by ANOVA analysis of the log-transformed data followed by a post-hoc Tukey HST test to determine significant differences for pair-wise comparisons.

	Two Haplotype Match				One Haplotype Match			No Match	
Animal ID	DK5P	DL74	RNS-9	RDe9	RWK10	RMN10	CX3M	CX6X	CX2A
# Reads Identified	1340	1368	1328	1194	1413	533	1561	1262	456
# Alleles Identified	15	16	18	18	14	15	13	15	11
Mamu-A									
A1*00101			162	296	504	95	610		207
A1*0040102/0201/0202/0203/08/09						86		580	
A1*0080101	253	270							
A1*01101/03/04			74	222					
A1*02301/02	333	299							
A2*050203			34	16					
A2*050402/40			11	6	8		6		2
A3*1303/11	58	42							
A4*140301/0301like2/0302/05/09	43	36				10		122	
Mamu-B									
B*0010101			72	78		46	115		48
B*00702/03			242	78		46	125		50
B*01201								108	
B*01701							91		
B*01901			53	102	137	45			39
B*02201								52	
B*02401			210	136	184	41			29
B*02601;B*05702			124	66	38	18			13
B*02602	46	24							
B*0290101/0102/02							308		
B*03001/0301/0302/0303/04	73	87						35	
B*03002/05			30	41		27	67		16
B*03103	54	88							
B*04101	48	65							
B*04301	82	60							
B*0460101/09/15			22	3	16	13		27	
B*04801	209	236							
B*05002								29	
B*05102						10	13		
B*05104			21	7	6	4		3	
B*05201					205				
B*05501					124				
B*05701								2	
B*05802					86				
B*06001			14	31					
B*06002							30		
B*06101							23		
B*06301					4				
B*06501								86	
B*06901								192	
B*07201/02	23	36	195	34	34	61	159	6	22
B*07301	105	97							
B*07401/02								4	
B*08202			43	67	62	24			28
B*09201like	6	15							
B*09601	5	2							
B*09701			5	2					
B*09801								12	
Mm-B*nov037							5		
Mamu-I									
B*009/0903;Mm-I*nov011	2	8	11	4				4	
I*010201;I*02012		3					9		
I*012002;I*03012;Mm-I*nov010			5	5	5	7			2

Supplementary Figure 2c: Class I transcript profiles for animals with varying degrees of MHC disparity. MHC class I genotypes were determined by pyrosequencing of cDNA-PCR amplicons for representative pairs of animals used in the CFSE-MLR assays. The number of sequence reads identified for specific MHC class I alleles or closely related allele lineages are indicated for each animal. MHC haplotypes shared between animals are highlighted with open boxes.