Table S2A. Summary of filtering & sorting of exome sequencing data (SNVs).

	SNVs	
	FL donor	**FL recipient**
called variants	52349	46043
excluding non-coding and synonymous variants, and known polymorphisms[1]	887	867
excluding probable germline variations[2]	543	548
QC filtering[3] and excluding reads mapping to Y chromosome and HLA variations	251	263
final selection[4]	46	50

Table S2B. Summary of filtering & sorting of exome sequencing data (InDels).

	InDels	
	FL donor	**FL recipient**
called variants	3794	4776
excluding non-coding and synonymous variants and known polymorphisms[1]	3645	4637
excluding probable germline variations[2]	3491	4514
sorted for high composite score[5] and selection of top ranked	32	28

[1] based on dbSNP release 130

[2] variants detected in DLI (>2 reads in DLI, Phred score >20, %variant > 10%

[3] filtered for high quality reads based on Phred scores (>30), number of different start sites (>2), reads' orientation diversely distributed, sufficient covera

[4] ranked and selected based on combination of favorable QCs (high Phred score, high number of variant reads, high number of different start sites, reads

[5] Score = (Consensus Quality + SNP Quality) * Variant Coverage / (Total Coverage)^2

ıge >5 reads)

ş' orientation distribution close to 50%) and visualization by IGV