

Supplemental Table 1. Input microbiota, cohort structure and mouse numbers in the current study.

Cohort	Source of microbiota	G0 strains	G1 F	M	Total number of mice per group per experiment
1	B6 UC (JAX)	B61F	2	1	11
		B61F	4	4	
		BALB/cJ1F	0	10	10
		BALB.H-2 ^j 1F	7	5	12
		C3H/HeN1F	4	5	9
2	B6 TAC	BALB/cJ Rag1 ^{-/-} 1F	1	2	5
		BALB/cJ Rag1 ^{-/-} 1F	1	1	
		C57BL/6J1F	1	1	4
		C57BL/6J1F	2	0	
		BALB.H-2 ^j 1F	0	4	7
		BALB.H-2 ^j 1F	3	0	
		BALB/cJ1F	2	3	12
		BALB/cJ1F	5	2	
		I/LnJ1F	1	2	12
		I/LnJ1F	1	4	
		I/LnJ1F	2	2	
		C3H/HeN1F	1	1	4
		C3H/HeN1F	2	0	
		BALB.H-2 ^b 1F	2	2	8
		BALB.H-2 ^b 1F	2	2	
3	B6 TAC	I/LnJ.H-2 ^k 1F	0	4	8
		I/LnJ.H-2 ^k 1F	0	4	
		BALB/cJ1F	2	4	10
		BALB/cJ1F	1	3	
		I/LnJ1F	2	3	8
		I/LnJ1F	2	1	
		B61F	2	2	8
		B61F	2	2	
4	B6 JAX	B61F	3	2	16
		B61F	2	2	
		B61F	5	2	

Sources of microbiota for GF mice repopulation: Cohort 1 - B6 (UC) JAX originated from The Jackson Laboratory, but were bred and housed at the University of Chicago for several generations; Cohorts 2 and 3 – donors arrived straight from Taconic; B6 JAX – donors arrived straight from The Jackson Laboratory.

Each line shows the size and gender break of the progeny of a particular G0 female.

Last column summarizes mouse numbers used for statistical analysis in each experiment (cohort).