SUPPLEMENTARY FIGURES
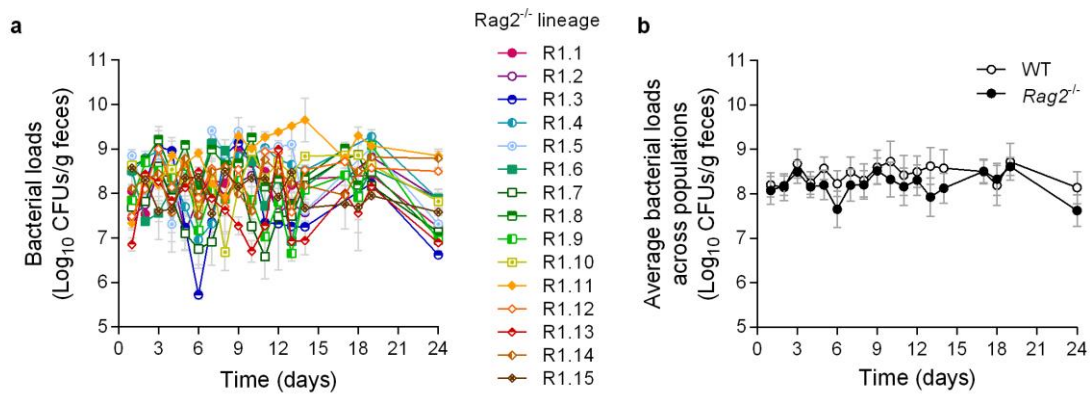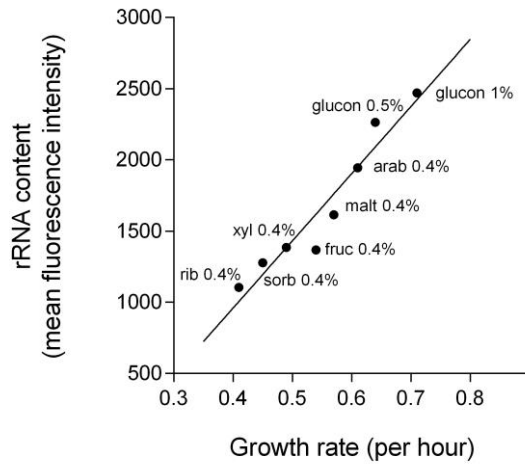
3   **Supplementary Figure 1. Similar *E. coli* load in WT and *Rag2*^{-/-} mice during the**

4   **evolution experiments**

5   **a)** *Escherichia coli* colonization of the gut of *Rag2*^{-/-} mice. Bacterial loads per gram of

6   feces (±2 s.e.m) during 24 days of adaptation of *E. coli* to the mouse gut (populations

7   R1.1 to R1.15). **b)** Average bacterial loads (±2 s.e.m) over time in WT (white circles) or

8   *Rag2*^{-/-} (black circles) populations. The host genotype does not influence the temporal

9   dynamics of bacterial loads over time (interaction host genotype and time, ANOVA

10   χ^2_{17}=18.64, *p* = 0.35) nor the bacterial loads (host genotype, ANOVA χ^2_1=3.35, *p* =

11   0.07).

12

Supplementary Figure 2. Dynamics of the *gat*-negative phenotype

Emergence and expansion of beneficial mutations in the *gat* operon in *Rag2*^{-/-} (upper panels) and WT (lower panels) mice, which cause the increase in frequency of a *gat*-negative phenotype. Each plot displays a group of 5 *Rag2*^{-/-} (upper panels) or WT (lower panels) mice, corresponding to 3 independent experimental blocks.

21

Supplementary Figure 3. Cellular content of ribosomes (cy3 intensity per cell) inferred by whole-cell hybridization

E. coli MG1655 strain DM09-CFP (ancestral) was grown in M9 minimal medium supplemented with (from left to right): ribose 0.4%, sorbitol 0.4%, xylose 0.4%, fructose 0.4%, maltose 0.4%, arabinose 0.4%, gluconate 0.5% and gluconate 1%. Circles represent the average of two hybridization measurements and four growth rates estimates (±2 s.e.m.)

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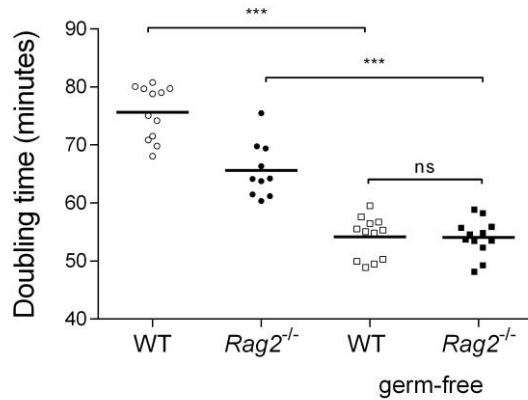
Supplementary Figure 4. Higher growth rate of *E. coli* in GF mice

The doubling time of *E. coli* colonizing the gut of WT or *Rag2*^{-/-} is estimated by the amount of rRNA (see Fig. S3). Each symbol corresponds to an average of 2 independent quantifications made for each mouse (n=6) during day 1 and 3 of colonization. The growth rate is significantly higher in GF compared to microbiota-harboring animals (WT vs WT GF, Mann-Whitney U test with Benjamini and Hochberg correction, $W=$ 144, $P<10^{-3}$ and *Rag2*^{-/-} vs *Rag2*^{-/-} GF, Mann-Whitney U test with Benjamini and Hochberg correction, $W=120$, $P<10^{-3}$).

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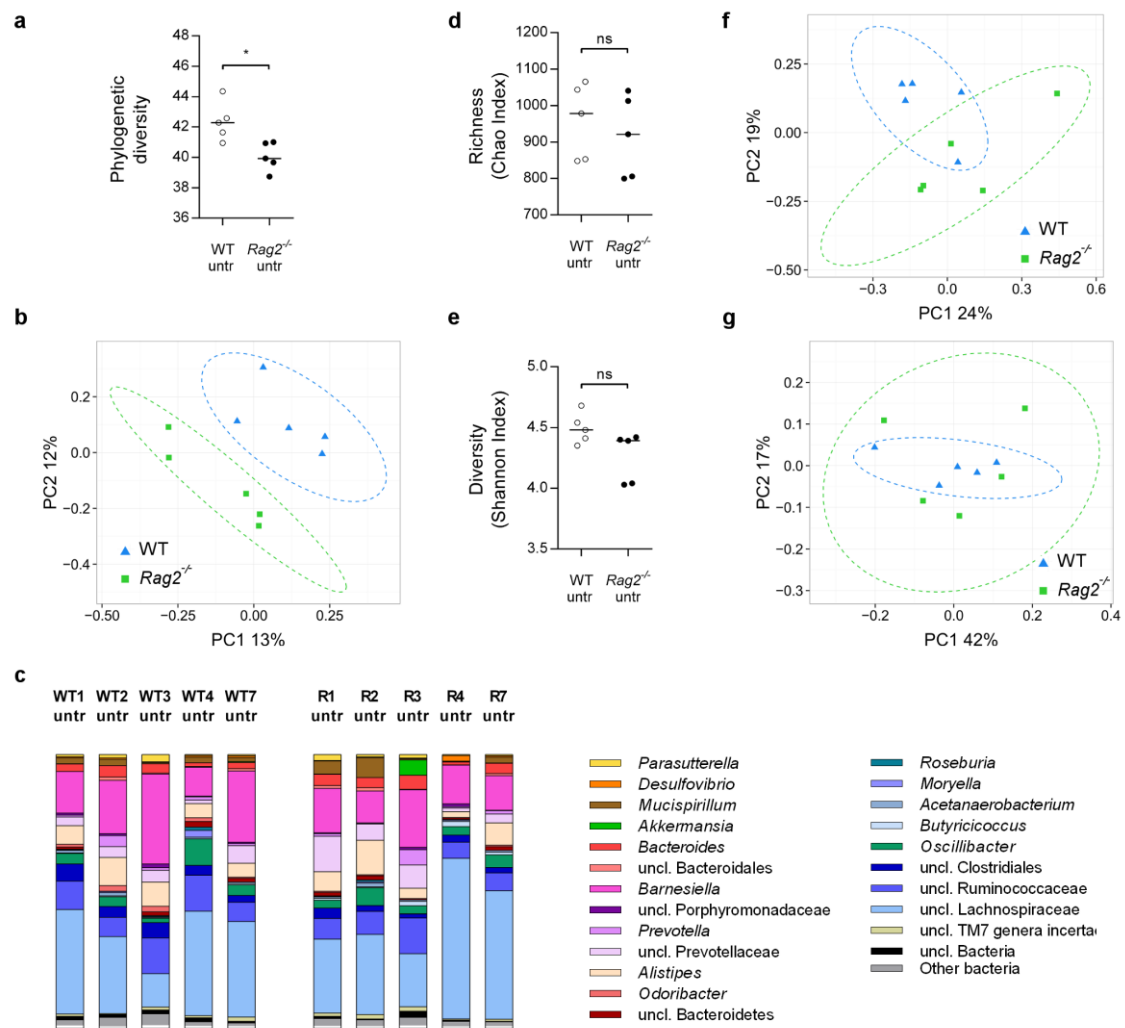
Supplementary Figure 5. Microbiota composition of naïve (unmanipulated) WT

and *Rag2*-/- mice.

a) Alpha diversity estimates of microbiota community phylogenetic diversity in WT

and *Rag2*-/- animals. Phylogenetic diversity was increased in the WT mice (Mann–

Whitney U test, *W*=23.5, *P*=0.03). *$P < 0.05$.

b) Principal coordinates analysis (PCoA) of the unweighted UniFrac distance matrices

of faecal microbiota of WT and *Rag2*-/- mice. The first two coordinates are shown.

Ellipses centered on the averages of the metric distances with a 90% confidence interval

for the first two coordinates were drawn on the associated PCoA.

c) Microbiota composition at the genus level of 5 WT and 5 *Rag2*-/- mice before

streptomycin treatment and *E. coli* colonization. Genera with a relative abundance

53   larger than 1% are displayed. The colored segments represent the relative abundance of

54   each genus.

55   Alpha diversity estimates of microbiota community richness (**d**) and OTU-based

56   diversity (**e**). Both parameters were similar in *Rag2*$^{-/-}$ and WT animals (Mann–Whitney

57   U test, *W*=17, *P*=0.4 and *W*=21, *P*=0.1, respectively). Ns (not significant,) *P* > 0.05.

58   Principal coordinates analysis (PCoA) of the weighted UniFrac (**f**) or Bray Curtis (**g**)

59   distance matrices of faecal microbiota of WT and *Rag2*$^{-/-}$ mice. The first two

60   coordinates are shown. Ellipses centered on the averages of the metric distances with a

61   90% confidence interval for the first two coordinates were drawn on the associated

62   PCoA.

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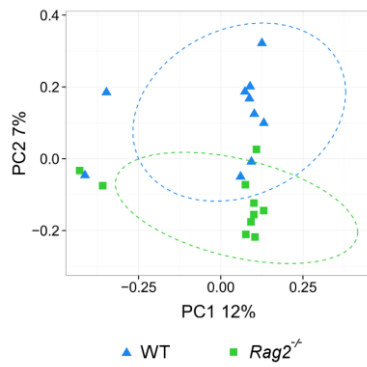
Supplementary Figure 6. Analysis of the phylogenetic membership of WT and

***Rag2^{-/-}* mice from the day 3 of the evolution experiment (streptomycin-treated and**

colonized with *E. coli*).

Principal coordinates analysis (PCoA) of the unweighted UniFrac distance matrices of

faecal microbiota of WT and *Rag2^{-/-}* mice. The first two coordinates are shown. Ellipses

centered on the averages of the metric distances with a 90% confidence interval for the

first two coordinates were drawn on the associated PCoA.

77

78   **Supplementary Table 1. In vivo competitions between a *gatZ* mutant and the**

79   **ancestral strain in WT and *Rag2^{-/-}* mice.**

Mice		Time (hours)				*s*
		0	24	48	72	
WT	1	-0.23	2.32	2.87	4.28	**0.066**
	2	-0.23	1.49	2.32	3.47	**0.053**
	3	-0.07	1.23	2.23	3.19	**0.047**
	4	-0.07	1.31	3.04	3.63	**0.056**
	5	-0.62	1.89	2.58	4.63	**0.073**
	6	-0.62	2.17	3.30	3.70	**0.070**
	7	-0.62	1.66	2.72	4.37	**0.071**
	8	-1.02	1.61	3.26	3.97	**0.078**
	9	-1.02	0.22	3.96	4.93	**0.087**
	10	-1.02	2.28	3.79	4.05	**0.084**
Rag2^{-/-}	1	-0.23	0.83	2.26	3.67	**0.053**
	2	-0.23	1.96	2.58	2.43	**0.047**
	3	-0.07	1.55	3.02	2.80	**0.049**
	4	-0.07	-0.97	-0.90	-0.80	**-0.014**
	5	-0.62	1.23	2.13	2.66	**0.051**
	6	-0.62	-0.53	-0.76	0.08	**0.006**
	7	-0.62	1.34	1.48	1.59	**0.038**
	8	-1.02	-0.31	0.09	0.28	**0.020**
	9	-1.02	-0.49	0.76	0.99	**0.030**
	10	-1.02	-0.26	-0.52	-0.55	**0.009**

80

81   Table displaying the change in ln(*gatZ*/anc), i.e., the natural logarithm of the ratio

82   between the frequencies of the *gatZ* mutant and the ancestral strain, over 3 days (72

83   hours) of competition in WT and *Rag2^{-/-}* mice (see also Fig. 2c). *s* represents the

84   selective advantage of *gatZ* along the three days of competition, inferred from the slope

85   of the linear regression of ln(*gatZ*/anc).

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87

88 **Supplementary Table 2. In vivo competitions between a *gatZ* mutant and the**

89 **ancestral strain in WT and *Rag2^-/-* co-housed mice.**

Mice		Time (hours)				*s*
		0	**24**	**48**	**72**	
WT co-housed	**1**	-0.05	0.50	0.81	2.06	**0.026**
	2	-0.05	0.79	2.04	1.06	**0.025**
	3	-0.60	1.29	2.87	3.73	**0.065**
	4	-0.60	0.87	3.37	4.26	**0.071**
	5	-0.60	0.77	1.97	2.82	**0.050**
	6	-0.60	0.69	2.31	3.73	**0.060**
	7	-0.60	1.20	3.82	0.86	**0.045**
	8	-0.65	1.02	2.37	3.17	**0.057**
	9	-0.54	1.75	3.16	3.65	**0.066**
	10	-0.45	1.24	1.78	2.75	**0.047**
	11	-0.52	1.57	4.40	4.14	**0.077**
Rag2^-/- co-housed	**1**	-0.05	0.84	2.00	2.45	**0.037**
	2	-0.05	0.73	1.78	0.67	**0.020**
	3	-0.60	1.46	2.45	2.90	**0.056**
	4	-0.60	0.84	2.81	1.01	**0.039**
	5	-0.60	-0.13	1.38	2.39	**0.040**
	6	-0.60	1.02	2.45	2.93	**0.054**
	7	-0.60	0.94	2.21	3.38	**0.057**
	8	-0.65	1.79	3.55	4.20	**0.076**
	9	-0.54	2.03	2.83	3.35	**0.062**
	10	-0.45	1.74	3.49	1.21	**0.045**
	11	-0.52	2.14	2.79	3.41	**0.063**

90

91 Table displaying the change in ln(*gatZ*/anc), i.e., the natural logarithm of the ratio

92 between the frequencies of the *gatZ* mutant and the ancestral strain, over 3 days (72

93 hours) of competition in WT and *Rag2^-/-* co-housed mice (see also Fig. 3a). *s* represents

94 the selective advantage of *gatZ* along the three days of competition, inferred from the

95 slope of the linear regression of ln(*gatZ*/anc).

96

97

98 **Supplementary Table 3. In vivo competitions between a *gatZ* mutant and the**

99 **ancestral strain in WT and *Rag2*^{-/-} germ-free mice.**

Mice		Time (hours)				*s*
		0	**24**	**48**	**72**	
WT germ-free	**1**	-0.61	0.46	0.92	1.27	**0.029**
	2	-0.61	0.43	1.17	1.76	**0.035**
	3	-0.20	0.71	1.32	1.79	**0.030**
	4	-0.20	0.56	0.87	1.92	**0.028**
	5	-0.54	0.24	0.41	0.83	**0.020**
	6	-0.54	0.43	0.99	1.25	**0.028**
	7	-0.54	0.19	0.51	0.88	**0.021**
Rag2^{-/-} germ-free	**1**	-0.77	0.55	1.08	1.28	**0.033**
	2	-0.77	0.52	1.00	1.18	**0.032**
	3	-0.77	0.20	0.95	1.25	**0.031**
	4	-0.54	0.06	0.76	1.48	**0.028**
	5	-0.54	-0.11	0.56	1.19	**0.023**
	6	-0.54	-0.27	0.53	1.13	**0.022**
	7	-0.54	-0.09	0.49	0.83	**0.020**

100

101 Table displaying the change in ln(*gatZ*/anc), i.e., the natural logarithm of the ratio

102 between the frequencies of the *gatZ* mutant and the ancestral strain, over 3 days (72

103 hours) of competition in WT and *Rag2*^{-/-} germ-free mice (see also Fig. 3b). *s* represents

104 the selective advantage of *gatZ* along the three days of competition, inferred from the

105 slope of the linear regression of ln(*gatZ*/anc).

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107

108 **Supplementary Table 4. In vivo competitions between two *gat* mutants (*gatZ* and**

109 ***gatC*) in WT and *Rag2^-/-^* mice.**

Mice		Time (hours)				*s*
		0	**24**	**48**	**72**	
WT	**1**	-0.64	-0.54	-0.51	0.25	**0.009**
	2	-0.64	-0.87	-0.24	-0.21	**0.006**
	3	-0.64	0.69	0.45	0.42	**0.020**
	4	-0.64	-0.11	0.08	0.71	**0.018**
	5	-0.64	0.12	-0.32	0.14	**0.011**
	6	-0.70	0.30	0.20	0.41	**0.018**
	7	-0.70	-0.48	0.05	0.06	**0.012**
	8	-0.70	-0.15	0.34	0.37	**0.017**
*Rag2^-/-^*	**1**	-0.64	-0.71	-0.77	-1.50	**-0.009**
	2	-0.64	-0.54	-1.09	0.01	**0.003**
	3	-0.64	-2.71	-4.42	-6.42	**-0.080**
	4	-0.64	-0.45	-1.69	-2.88	**-0.026**
	5	-0.64	-1.13	-1.36	-1.52	**-0.014**
	6	-0.70	-0.07	-0.32	-2.48	**-0.012**
	7	-0.70	0.08	-2.15	-3.90	**-0.035**
	8	-0.70	-1.37	-1.55	-3.45	**-0.032**

110

111 Table displaying the change in $\ln(gatZ/gatC)$, i.e., the natural logarithm of the ratio

112 between the frequencies of the *gatZ* and *gatC* mutants, over 3 days (72 hours) of

113 competition in WT and *Rag2^-/-^* mice (see also Fig. 4a). *s* represents the selective

114 advantage of *gatZ* along the three days of competition, inferred from the slope of the

115 linear regression of $\ln(gatZ/anc)$.

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117

118 **Supplementary Table 5. In vivo competitions between two *gat* mutants (*gatZ* and**

119 ***gatC*) in WT and *Rag2*$^{-/-}$ co-housed mice.**

Mice		Time (hours)				*s*
		0	24	48	72	
WT co-housed	1	-0.35	-0.17	1.36	0.97	**0.023**
	2	-0.35	-0.10	2.04	1.96	**0.038**
	3	-0.35	-0.37	0.18	0.90	**0.018**
	4	-0.35	0.11	0.84	0.71	**0.016**
	5	-0.35	-0.21	0.51	0.58	**0.015**
	6	-0.08	0.10	0.25	0.31	**0.006**
	7	-0.08	-0.30	0.48	0.50	**0.011**
	8	-0.40	0.61	0.54	0.67	**0.013**
	9	-0.72	0.55	0.95	0.83	**0.021**
	10	-0.59	0.43	0.53	0.44	**0.013**
Rag2$^{-/-}$ co-housed	1	-0.35	-0.06	0.21	0.71	**0.014**
	2	-0.35	-0.20	0.04	-1.51	**-0.008**
	3	-0.35	0.06	0.57	0.32	**0.013**
	4	-0.35	0.50	1.00	0.70	**0.020**
	5	-0.08	1.49	2.69	2.95	**0.048**
	6	-0.08	-0.42	0.34	0.64	**0.008**
	7	-0.40	0.37	1.35	-0.01	**0.016**
	8	-0.72	0.39	0.26	-1.08	**0.006**
	9	-0.59	0.42	1.23	1.48	**0.032**

120

121 Table displaying the change in ln(*gatZ*/*gatC*), i.e., the natural logarithm of the ratio

122 between the frequencies of the *gatZ* and *gatC* mutants, over 3 days (72 hours) of

123 competition in WT and *Rag2*$^{-/-}$ co-housed mice (see also Fig. 4b). *s* represents the

124 selective advantage of *gatZ* along the three days of competition, inferred from the slope

125 of the linear regression of ln(*gatZ*/anc).

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128

129 **Supplementary Table 6. The number and nature of adaptive events across**

130 **independently evolved populations of _E. coli_ after 24 days of adaptation in WT**

131 **mice**

Population	Genome position	Gene	Mutation	Frequency	
1.1	4346885	_dcuB / dcuR_	IS5 +4 bp	77%	
	2173581	_gatZ_	IS1 +9 bp	77%	
	2173490	_gatZ_	IS1 +8 bp	36%	
	3527427	_hslR_	del/dupl 56 bp	6%	*
	4035239	_ileT / ileT/alaT_	del/dupl 11 bp	5%	*
	1269768	_ldrC / chaA_	G→T	7%	
	3873556	_yidX_	T→G	8%	
	4601137	_yjjP / yjjQ_	IS5	5%	¤
	3214187	_yqjH_	del/dupl 82 bp	6%	*
1.2	921810	_cspD_	C→T	6%	
	4346885	_dcuB / dcuR_	IS5 +4 bp	48%	
	2172866	_gatA_	IS5 +4 bp	5%	
	2175295	_gatY / fbaB_	IS1 +9 bp	60%	
	2173751	_gatZ_	IS1 +9 bp	30%	
	2173522	_gatZ_	IS1 +9 bp	7%	
	968583	_lpxK/ycaQ / ycaQ_	del/dupl 42 bp	6%	*
	3996061	_uvrD_	del/dupl 39 bp	5%	*
	2180108	_yegW_	IS3	24%	¤
	4601256	_yjjP / yjjQ_	IS5 +4 bp	28%	
1.3	4346885	_dcuB / dcuR_	IS5 +4 bp	28%	
	2172866	_gatA_	IS5 +4 bp	7%	
	2175234	_gatY / fbaB_	IS1 +9 bp	13%	
	2175282	_gatY / fbaB_	IS5 +4 bp	5%	
	2173544	_gatZ_	IS1	27%	
	2173511	_gatZ_	IS1	6%	¤
	2173225	_gatZ_	IS1 +9 bp	7%	
	1847931	_sppA_	C→T	8%	
	2711851	_srmB_	del/dupl 79 bp	7%	*
	4601140	_yjjP / yjjQ_	IS5 +12 bp	25%	
	4601120	_yjjP / yjjQ_	IS2 +5 bp	10%	
1.4	4346885	_dcuB / dcuR_	IS5 +4 bp	12%	
	2172869	_gatA_	IS5	10%	¤
	2175284	_gatY / fbaB_	IS1 +9 bp	24%	
	2175250	_gatY / fbaB_	IS1 +9 bp	22%	
	2175266	_gatY / fbaB_	IS1	8%	¤
	2173522	_gatZ_	IS1 +9 bp	16%	
	2174014	_gatZ_	IS1 +9 bp	7%	
	2827379	_srlR_	IS1	7%	¤
	285098	_yagG_	del/dupl 22 bp	5%	*
	2143874	_yegE / yehD/yehE_	del/dupl 46 kb	5%	*
	3214187	_yqjH_	del/dupl 82 bp	5%	*
1.5	446451	_cyoE_	del/dupl 39 bp	6%	*

	4346885	*dcuB / dcuR*	IS5 +4 bp	31%	
	2172866	*gatA*	IS5 +4 bp	44%	
	2174422	*gatY*	IS1 +9 bp	45%	
	695730	*glnV*	Δ112 bp	6%	
	1907559	*kdgR*	G→A	8%	
	2827493	*srlR*	G→C	39%	
	4601137	*yjjP / yjjQ*	IS5	5%	¤
1.6	4346885	*dcuB / dcuR*	IS5 +4 bp	60%	
	3379861	*degQ*	del/dupl 30 bp	6%	*
	2566222	*eutH / eutG*	Δ100 bp	6%	
	2172784	*gatA*	IS1 +9 bp	14%	
	2172866	*gatA*	IS5 +4 bp	7%	
	2172489	*gatB*	IS1 +9 bp	8%	
	2172260	*gatC*	Δ1 bp	27%	
	2175282	*gatY/fbaB*	IS1	5%	¤
	2173533	*gatZ*	IS5 +4 bp	6%	
	2174345	*gatZ / gatY*	IS1 +8 bp	27%	
	1510987	*ydcT*	del/dupl 65 bp	5%	*
1.7	953901	*focA / ycaO*	IS5 +4 bp	68%	
	3269213	*garK*	C→T	12%	
	2172535	*gatB*	IS1	10%	¤
	2172265	*gatC*	IS1 +9 bp	7%	
	2175290	*gatY / fbaB*	IS1 +9 bp	66%	
	1907949	*kdgR*	IS5 +4 bp	8%	
	1908116	*kdgR*	IS5 +4 bp	6%	
	1902230	*manZ / kdgR*	Δ 5452 bp	72%	*
	1573764	*yddB*	IS5	7%	¤
1.8	2172866	*gatA*	IS5 +4 bp	6%	
	2172221	*gatC*	IS5 +4 bp	49%	
	2172265	*gatC*	IS1 +9 bp	15%	
	2173970	*gatZ*	IS1	10%	¤
	2174027	*gatZ*	IS1 +8 bp	7%	
	2440543	*mnmC*	del/dupl 103 bp	7%	*
	2827492	*srlR*	G→A	28%	
	3634862	*yhiN*	del/dupl 14 bp	7%	*
1.9	2880256	*casB*	del/dupl 18 bp	6%	*
	3379861	*degQ*	del/dupl 30 bp	8%	*
	2172633	*gatA*	IS5 +4 bp	29%	
	2172265	*gatC*	IS1 +9 bp	9%	
	2175296	*gatY / fbaB*	IS1 +9 bp	11%	
	2173104	*gatZ*	IS1 +9 bp	25%	
	1434252	*ompN*	del/dupl 16 bp	5%	*
	2827073	*srlR*	A→T	24%	
	1877853	*yeaR*	Δ1 :: IS186 +6 bp :: Δ1	10%	
	2763434	*yfjL / yfjM*	Δ8 bp	8%	
	4601117	*yjjP / yjjQ*	IS5 +4 bp	27%	
	4601148	*yjjP / yjjQ*	IS5 +4 bp	16%	
	4601266	*yjjP / yjjQ*	IS5 +4 bp	6%	
	4601006	*yjjP / yjjQ*	IS2	9%	¤
1.10	3379861	*degQ*	del/dupl 30 bp	6%	*
	953892	*focA / ycaO*	IS5 +13 bp	66%	

	2171086	*gatC*	IS1 +8 bp	47%	
	2172265	*gatC*	IS1 +9 bp	15%	
	2174223	*gatZ*	Δ2 bp	33%	
	4601134	*yjjP / yjjQ*	IS5 +4 bp	5%	
1.11	2172866	*gatA*	IS5 +4 bp	83%	
	2174150	*gatZ / gatY/fbaB*	Δ1111 bp	14%	*
	2827172	*srlR*	C→A	16%	
	1691840	*uidB*	del/dupl 20 bp	5%	*
	4601110	*yjjP / yjjQ*	IS5 +4 bp	72%	
	4601256	*yjjP / yjjQ*	IS5 +4 bp	7%	
1.12	953901	*focA / ycaO*	IS5 +4 bp	20%	
	2172079	*gatC*	.→C	97%	
	2827234	*srlR*	G→A	36%	
	2827117	*srlR*	C→T	6%	
	12154	*yaaI / dnaK*	IS4	47%	¤
1.13	4637714	*arcA*	G→T	87%	
	2171150	*gatC*	IS5 +4 bp	93%	
	3265169	*tdcA / tdcR*	IS5 +4 bp	11%	
	572125	*ybcN*	IS2 +5 bp	6%	
1.14	4346885	*dcuB / dcuR*	IS5 +4 bp	70%	
	953892	*focA / ycaO*	IS5 +4 bp	58%	
	2172912	*gatA*	IS5 +4 bp	15%	
	2175256	*gatY / fbaB*	IS1 +9 bp	81%	
	2827117	*srlR*	C→T	13%	
	1877853	*yeaR*	IS186 +6 bp	66%	
	4601151	*yjjP / yjjQ*	IS5	7%	¤

132

133 Mutations found in *E. coli* populations after adaptation to the gut of WT mice. For

134 intergenic mutations the two flanking genes are listed, otherwise the mutation occurred

135 in the gene coding region. SNPs are represented by an arrow between the ancestral and

136 the evolved nucleotide. The symbol Δ means a deletion event and a + symbol represents

137 an insertion of the nucleotide that follows the symbol. The initials IS denote the

138 abbreviation of insertion sequence element at the indicated position. del/dup indicates

139 that either a deletion or a duplication of the indicated size occurred but it is not possible

140 to distinguish between the two. * indicates that the mutation corresponds to a supported

141 unassigned new junction whereas ¤ denotes a IS insertion where only one new junction

142 was identified.

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144

Supplementary Table 7. The number and nature of adaptive events across independently evolved populations of *E. coli* after 24 days of adaptation in *Rag2*^{-/-} mice

Population	Genome position	Gene	Mutation	Frequency	
R1.1	3925453	*asnA*	inv 15 bp	6%	
	953892	*focA / ycaO*	IS5 +4 bp	56%	
	2172791	*gatA*	IS1 +9 bp	8%	
	2172073	*gatC*	IS1 +9 bp	80%	
	2827355	*srlR*	T→C	59%	
	2827528	*srlR*	G→A	13%	
	2827712	*srlR*	+CCCCAA	9%	
	2827388	*srlR*	Δ1 bp	5%	
	3634862	*yhiN*	del/dupl 14 bp	5%	*
	4601143	*yjjP / yjjQ*	IS5	5%	¤
R1.2	3925441	*asnA*	del/dupl 39 b	7%	*
	2172008	*gatC*	Δ 7508 bp	90%	
	2827081	*srlR*	C→T	83%	
	3214187	*yqjH*	del/dupl 82 bp	8%	*
R1.3	3350864	*arcB*	+AAA	37%	
	3925441	*asnA*	del/dupl 39 b	5%	*
	3502248	*frlR*	IS5 +4 bp	29%	
	3502642	*frlR*	Δ1 bp	7%	
	2172835	*gatA*	IS1 +9 bp	29%	
	2175289	*gatY / fbaB*	IS1	62%	
	2173225	*gatZ*	IS1 +9 bp	8%	
	156651	*yadN*	IS5 +4 bp	10%	
	4592986	*yjjM*	IS1 +9 bp	7%	
	4601157	*yjjP / yjjQ*	IS1 +8 bp	5%	
	2039432	*zinT*	IS5 +4 bp	14%	
R1.4	2173491	*gatZ*	IS5 +4 bp	94%	
	2827492	*srlR*	G→A	87%	
R1.5	2172972	*gatA*	IS1 +9 bp	84%	
	2752245	*ratB*	del/dupl 23 bp	5%	*
	2827793	*srlR*	T→G	85%	
	3634862	*yhiN*	del/dupl 14 bp	6%	*
R1.6	2172774	*gatA*	IS1	6%	¤
	2173014	*gatA*	IS5	5%	¤
	2175284	*gatY / fbaB*	IS1 +9 bp	81%	
	4035239	*ileT / ileT/alaT*	del/dupl 21 bp	7%	*
	932176	*lrp*	G→T	8%	
R1.7	3925441	*asnA*	del/dupl 39 b	5%	*
	3496103	*cysG*	del/dupl 5 bp	5%	*
	251816	*dinB*	del/dupl 48 bp	5%	*
	2172211	*gatC*	IS1 Δ4 bp	22%	
	2175244	*gatY / fbaB*	IS1 +9 bp	71%	
	2827492	*srlR*	G→A	43%	

	2891617	*ygcN / gcvP*	del/dupl 153 kb	63%	*
R1.8	3925441	*asnA*	del/dupl 39 b	5%	*
	953892	*focA / ycaO*	IS5 +4 bp	63%	
	3502032	*frlD / frlR*	IS4 +12 bp	7%	
	2172866	*gatA*	IS5 +4 bp	51%	
	2175266	*gatY / fbaB*	IS1 +9 bp	16%	
	2173571	*gatZ*	IS1 +9 bp	9%	
	1125212	*rimJ*	IS5 +4 bp	15%	
	761046	*sucB*	del/dupl 67 bp	7%	*
	931615	*trxB / lrp*	IS5 +4 bp	5%	
	3240783	*uxaA*	del/dupl 26 bp	5%	*
	3856228	*yidJ*	del/dupl 23 bp	5%	*
	3152375	*yqhC*	del/dupl 13 bp	6%	*
R1.9	4359175	*cadC*	A→T	8%	
	2173093	*gatA*	IS1 +8 bp	5%	
	2173093	*gatZ*	IS1 +9 bp	38%	
	2174199	*gatZ*	G→A	37%	
	1907809	*kdgR*	Δ2 bp	26%	
	2827627	*srlR*	G→A	26%	
	1221585	*ymgD*	C→T	25%	
R1.10	3379861	*degQ*	del/dupl 30 bp	5%	*
	628178	*entA*	del/dupl 97 bp	6%	*
	2172912	*gatA*	IS5 +4 bp	45%	
	2172866	*gatA*	IS5 +4 bp	13%	
	2175244	*gatY / fbaB*	IS1 +9 bp	35%	
	1907971	*kdgR*	IS1	12%	¤
	4197319	*nfi*	del/dupl 40 bp	5%	*
	298917	*paoC*	del/dupl 53 bp	7%	*
	3878678	*recF*	del/dupl 62 bp	7%	*
	1125212	*rimJ*	IS5 +4 bp	12%	
	2827490	*srlR*	C→T	21%	
	2030708	*yedJ*	del/dupl 50 bp	6%	*
R1.11	2173028	*gatA*	IS1 +9 bp	76%	
	2172073	*gatC*	IS1 +9 bp	6%	
	2173584	gatZ	IS1	*6%*	¤
	2173160	*gatZ*	IS1 +9 bp	6%	
	3325215	*rlmE*	del/dupl 37 bp	5%	*
	2827712	*srlR*	G→A	50%	
	2827492	*srlR*	G→A	13%	
R1.12	953901	*focA / ycaO*	IS5 (+) +4 bp	85%	
	1985465	*ftnB / yecJ*	del/dupl 9 bp	5%	*
	2172866	*gatA*	IS5 (+) +4 bp	97%	
	2827184	*srlR*	A→G	36%	
R1.13	3350023	*arcB*	T→C	33%	
	953919	*focA / ycaO*	IS1	7%	¤
	2172153	*gatC*	IS1 +9 bp	5%	
	2173559	*gatZ*	IS1 +9 bp	47%	
	3353621	*gltB*	del/dupl 52 bp	5%	*
	1482153	*hrpA*	del/dupl 35 bp	6%	*
	4035239	*ileT / ileT/alaT*	del/dupl 21 bp	6%	*
	2373853	*menC*	IS186	7%	¤

	2317269	*rcsC*	del/dupl 17 bp	5%	*
	2066430	*yoeH*	del/dupl 5 bp	5%	*
R1.14	953901	*focA / ycaO*	IS5 +4 bp	87%	
	2172650	*gatA*	IS1 +8 bp	83%	
	2171899	*gatC*	IS1	8%	¤
	1632600	*tfaQ*	del/dupl 72 bp	6%	*
	4368228	*yjeH*	del/dupl 111 bp	7%	*
R1.15	3925441	*asnA*	del/dupl 39 b	9%	*
	953901	*focA / ycaO*	IS5 +4 bp	75%	
	2172889	*gatA*	IS1 +8 bp	30%	
	2173012	*gatA*	IS1 +9 bp	10%	
	2171613	*gatC*	IS1 +9 bp	26%	
	3527427	*hslR*	del/dupl 56 bp	8%	*
	2620189	*purM*	G→T	30%	
	4470157	*pyrB*	del/dupl 49 bp	5%	*
	4383948	*yjeO*	Δ1 bp	5%	

148

149 Mutations found in *E. coli* populations after adaptation to the gut of *Rag2*$^{-/-}$ mice. See

150 Supplementary Table 1 legend for further details.

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