

**Table S1. Quantification of genetic interactions with  $\Delta elsL$ .**

	sgRNA:				
	control	<i>ldtAb</i>	<i>RS13190</i>	<i>blhA</i>	<i>miaF</i>
Growth phenotype of single CRISPRi strain (A) <sup>1</sup>	1.00 (n = 20)	1.00 (n = 12)	0.8 (n = 10)	1.03 (n = 9)	0.83 (n = 7)
Growth phenotype of single $\Delta elsL$ strain (B) <sup>2</sup>	0.87 (n = 16)	–	–	–	–
Expected growth phenotype of double lesion strain (A*B)	–	0.87	0.69	0.90	0.73
Observed growth phenotype of double lesion strain <sup>3</sup>	–	0.28* (n = 8)	n.d.	0.56* (n = 5)	0.47* (n = 5)

<sup>1</sup>Mean colony diameter, relative to WT control, of single CRISPRi lesion (sgRNA in WT background)

<sup>2</sup>Mean colony diameter, relative to WT control, of single  $\Delta elsL$  lesion (control sgRNA in  $\Delta elsL$  background)

<sup>3</sup>Mean colony diameter, relative to WT control, of double lesion (sgRNA in  $\Delta elsL$  background)

n, number of measured colonies

–, not applicable

n.d., colonies not detected

\*, p < 0.001 in one sample t test using the expected growth phenotype as reference value.