FOR REVIEW PURPOSES ONLY

We have data on the SA content in 2 lines showing the same number of nodules as the WT (GI1.1 and GH3) and in 2 lines showing reduced nodule numbers (GK1.9 and GB3.13). We decided to focus on lines with a single T-DNA insertion, homozygous and with increased nodulation and, therefore, only 1 or 2 independent extractions were done on the other lines. However, as shown below, as suggested by the reviewer, the data are consistent with the fact that those plants showing lower or no effect on nodulation also showed little of no change in SA levels (compare data below to that in Table 1 of the manuscript). With the only exception of B3.13 roots, SA content could be quantified in the two different tissues of these lines showing values either similar, 2-, or a maximum of 3-fold lower than those shown by the WT.

Total SA content

Line	Letter assigned in Fig. 2	nahG copy#	Nod phenotype	Leaves (ng g^{-1} FW)	Roots (ng g^{-1} FW)
WT		0	+	824 ± 124	603 ± 132
GK1.9 T3	b	1	lower	317 ± 118	327 ± 99
GB3.13 T3	e	2	lower	356 ± 43	-[a]
GI1.1 T3	k	2	+	441 ± 48	194 ± 30
GH3 T2	g	4	+	520 ± 33	598 ± 29

[a] Not available