

**Table S1.** Primers used for qRT-PCR analyses

<b>Gene</b>	<b>Forward primer (5'→3')</b>	<b>Reverse primer (5'→3')</b>	<b>Efficiency (%)</b>
<i>LjUbiquitin</i>	TTCACCTTGTGCTCCGTCTTC	AACAACAGCACACACAGACAA	93.6
<i>LjATP synthase</i>	AACACCACTCTCGATCATTCTCTG	CAATGTCGCCAAGGCCCATGGTG	92.9
<i>LjelF4A</i>	AGAGGGTTTAAAGATCAAAT	ATGTCAATTCATCACGTTTT	92.1
<i>LjGlb1-1</i>	TTGAGGTTACAAAGTTTGCCTAC	TGCATTCTTCATCTCTGGTGAC	90.3
<i>LjGlb1-2</i>	CAGTGCCATCATAGCTGAAA	TATTGAAACTGAGAGCAAAGGG	99.3
<i>LjGlb2-1</i>	CTCAGCCCTTCAACTAAGAG	CTTTAAGCACCAGGAAATGGG	97.4
<i>LjGlb3-2</i>	GCAACAAGCATTAGACAGTACTC	TTCTTTAGCTCATTTCAGCC	97.6

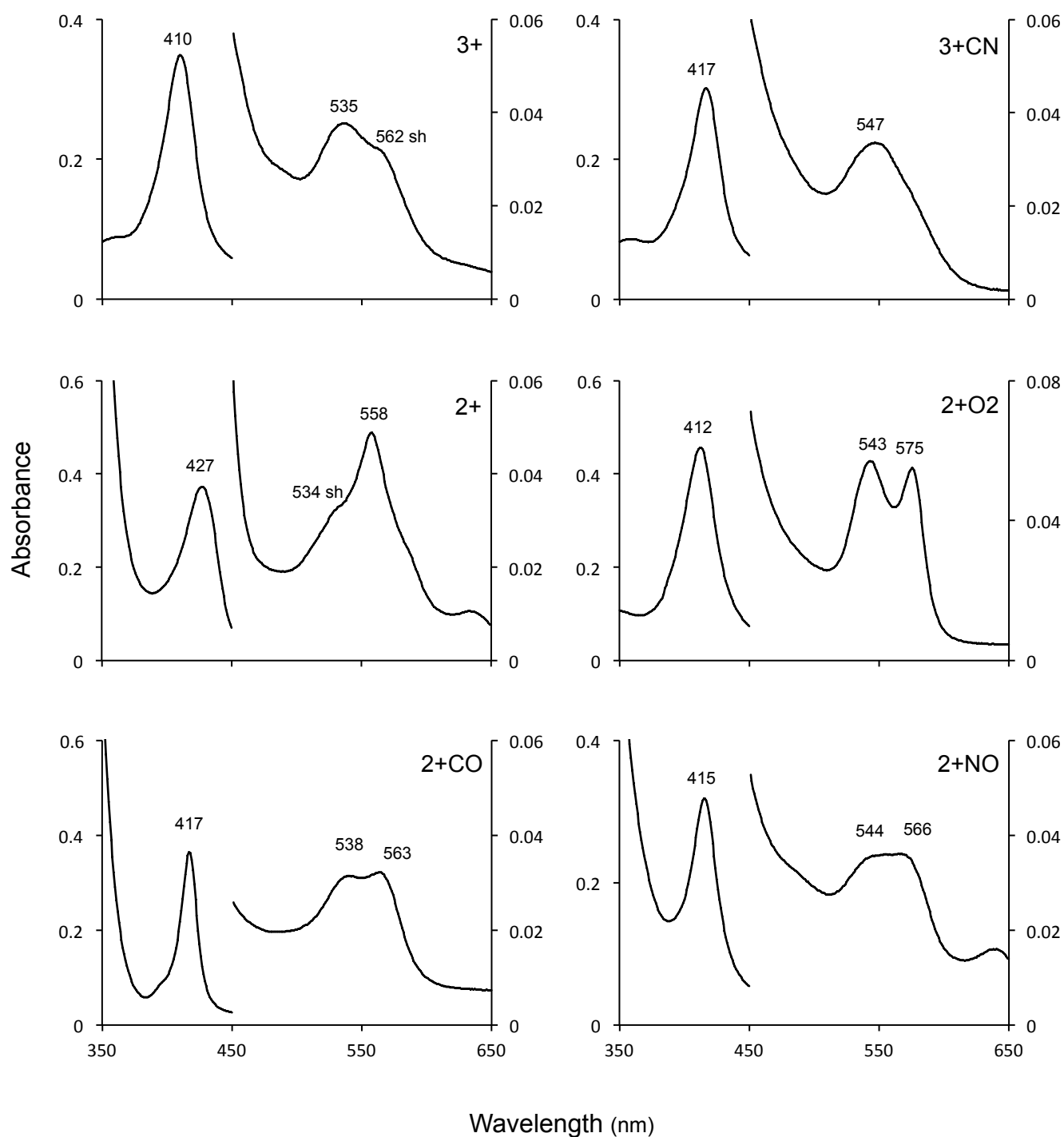
**Table S2** Details of the hemoglobin mutant lines used in the study

Gene	Gene ID <sup>a</sup>	Line	Insertion	mRNA (%) <sup>b</sup>
<i>LjGlb1-1</i>	LotjaGi3g1v0504500	30096642	Exon 1 (5'-UTR)	0.9
<i>LjGlb1-2</i>	LotjaGi3g1v0504600	P0494	Exon 4	7.4
<i>LjGlb2-1</i>	LotjaGi5g1v0253250	30015049	Exon 2	6.6
<i>LjGlb3-2</i>	LotjaGi1g1v0172000	30086451	Exon 1	1.7
		30108411	Exon 2	1.5

<sup>a</sup>Gene IDs are given according to the *Lotus japonicus* Gifu genome sequence (Kamal *et al.*, 2020).

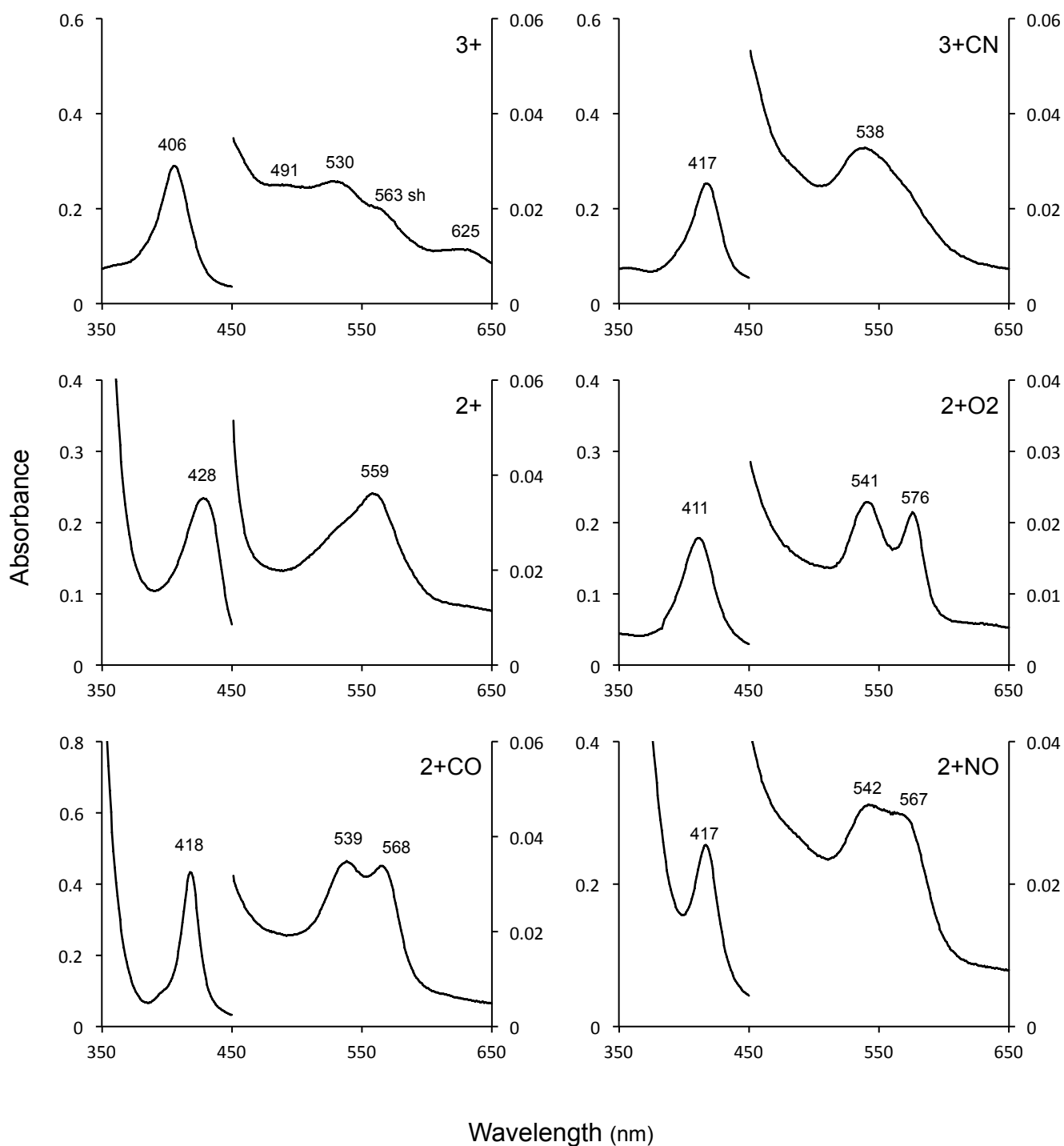
<sup>b</sup>Transcript levels were normalized using *LjUbiquitin* as the reference gene and are expressed as percent of those of the wild type.

## LjGlb2-1



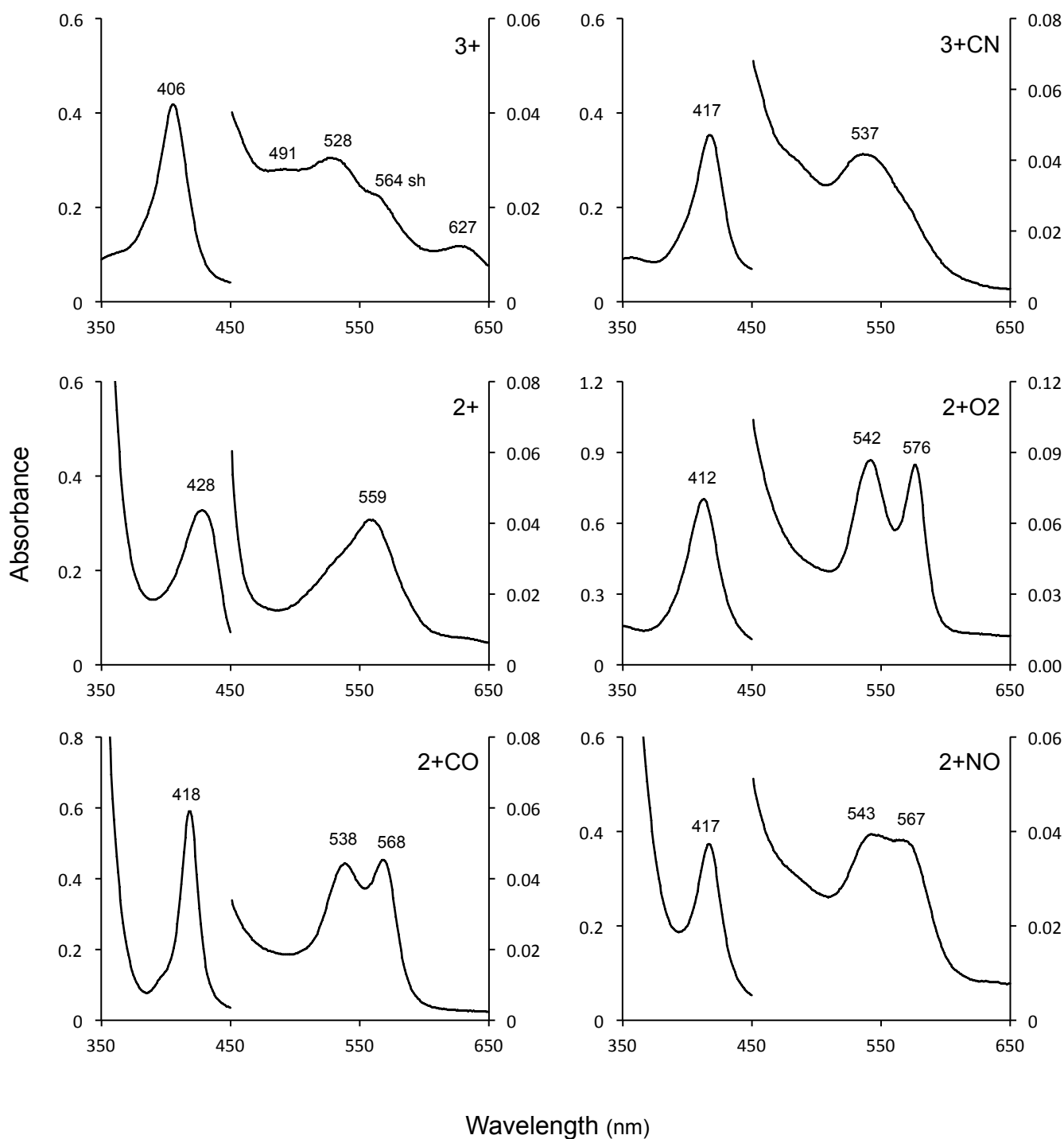
**Fig. S1.** UV-visible spectra of the 3+ and 2+ forms of LjGlb2-1 and their representative complexes. Spectra were taken with 24  $\mu\text{M}$  protein in 50 mM potassium phosphate buffer (pH 7.0).

# MtLb3

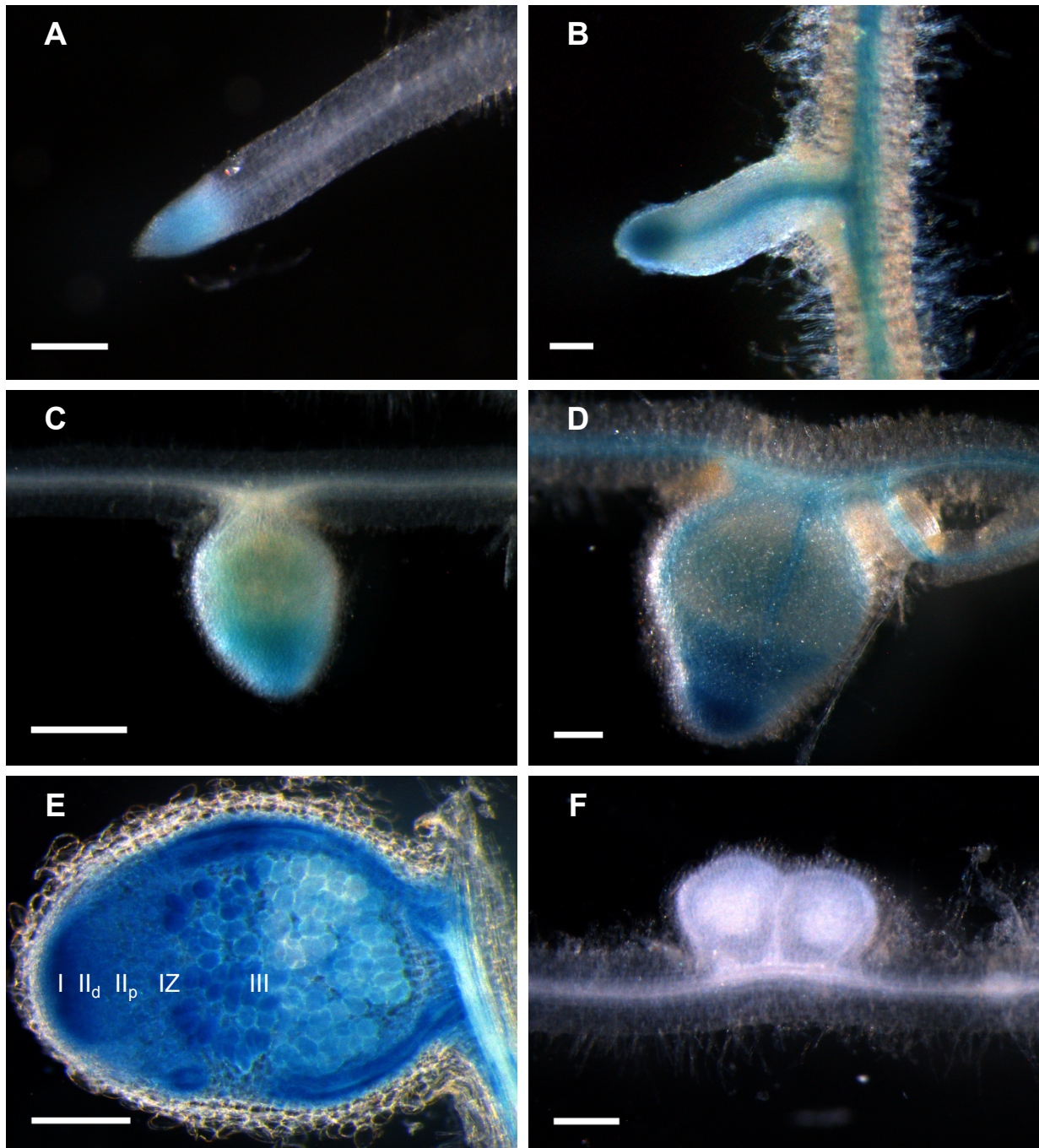


**Fig. S2.** UV-visible spectra of the 3+ and 2+ forms of MtLb3 and their representative complexes. Spectra were taken with 19  $\mu\text{M}$  protein in 50 mM potassium phosphate buffer (pH 7.0).

## MtLb3-C135S



**Fig. S3.** UV-visible spectra of the 3+ and 2+ forms of MtLb3-C135S and their representative complexes. Spectra were taken with 28  $\mu$ M protein in 50 mM potassium phosphate buffer (pH 7.0).



**Fig. S4.** Localization of promoter activity of *MtLb3* in *Medicago truncatula* using a *GUS* reporter gene. Expression was detected using X-Gluc and tissues were observed in a stereomicroscope using transmitted light. (A, B) GUS activity is observed in the apex and vascular bundles of the primary root and lateral roots. (C) In young nodules, ~2 weeks post-inoculation (wpi), the gene is predominantly expressed in the apex, encompassing zones I and II. (D, E) At later stages (4 wpi), expression is mainly visible in the apex, zones I and II, and vascular bundles, and to a lower extent, in zone III. The following zones are marked in this nodule for reference: zone I (meristem); zone II (infection), distal (d) and proximal (p); IZ (interzone); and zone III (fixation). (F) Nodulated roots of plants (2 wpi) transformed with the empty vector pBGWFS7 were used as a negative control. Images are representative of nodules from at least five plants with similar localization results. Scale bars, 200  $\mu$ m.