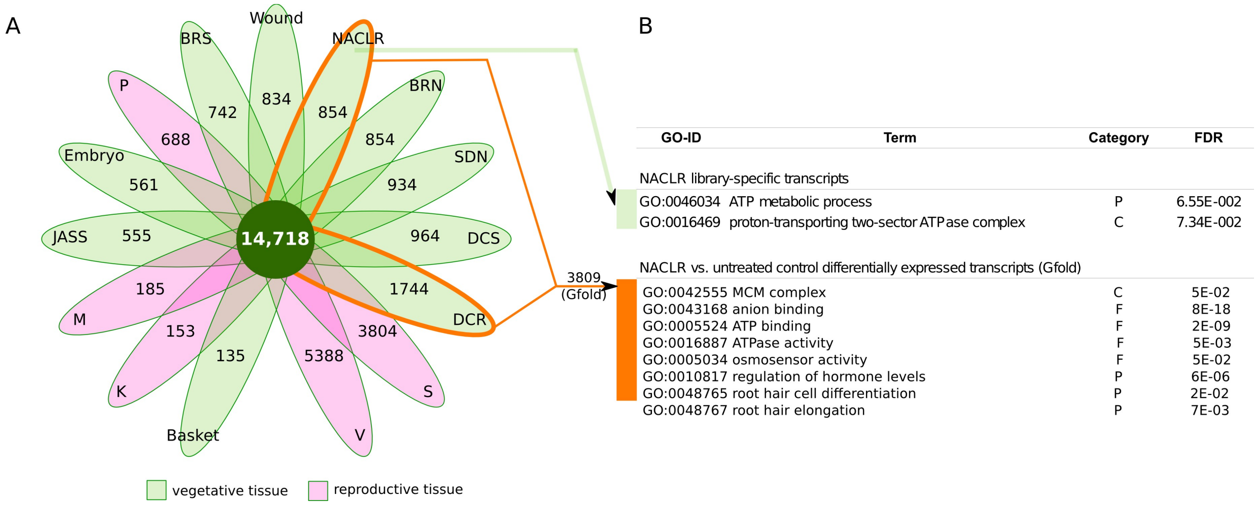

GO-ID	Term	Category	FDR
NACLR library-specific transcripts			
GO:0046034	ATP metabolic process	P	6.55E-002
GO:0016469	proton-transporting two-sector ATPase complex	C	7.34E-002
NACLR vs. untreated control differentially expressed transcripts (Gfold)			
GO:0042555	MCM complex	C	5E-02
GO:0043168	anion binding	F	8E-18
GO:0005524	ATP binding	F	2E-09
GO:0016887	ATPase activity	F	5E-03
GO:0005034	osmosensor activity	F	5E-02
GO:0010817	regulation of hormone levels	P	6E-06
GO:0048765	root hair cell differentiation	P	2E-02
GO:0048767	root hair elongation	P	7E-03

Figure S8. Treatment-specific *P. lambertiana* transcripts analysis. (A) Number of treatment-specific transcripts for each analyzed tissue (green background): K (pollen), M (early female cones (2 weeks) before pollination), P (pollen cones), E1 (seed), Basket (root), stem and needles), SDN (needle), BRS (stem), WS (stem), NACLR (root), JAS (stem), S (2 cm female cones), V (female cones at time of pollination), DCR (root), DCS (stem), BRN (needle). (B) Gene Ontology (GO) terms overrepresented in the library-specific NACLR transcripts (green), and differentially expressed transcripts in NaCl treated samples (NACLR) compared to the root healthy control (DCR) (orange), identified with Gfold.