

Table S1. Sequence reads and length generated for each RNA sample (paired end).

Tissue Used for RNA	Sequence Reads Per File	Average Read Length
Bulb	8,870,015	50
Flower	10,499,190	50
Leaf	8,811,375	50
Fall Rhizome	10,558,614	50
Spring Rhizome	11,237,164	50
Fall Roots	8,026,623	50
Green Shoots	10,021,063	50
White Shoots	10,563,408	50
Tissue Culture Week 1	9,946,944	50
Tissue Culture Week 2	12,413,973	50

Table S2. Transcriptome statistics provided by the NCGR.

Sequences	56994
Bases	41106915
Minimum length	100
Maximum length	16273
N50	1471
B1000*	64.4%
B2000**	35.9%

*B1000 is the percent of scaffolds greater than 1000 bases and **B2000 is the percent of scaffolds greater than 2000 bases.

Table S3. Selected top-scoring cytochrome P450 candidate cDNAs for the enzymatic conversion of cholesterol to cyclopamine.

Gene ID	Putative function
>medp_verca-20110208 2398	similar to CYP71D unknown function*
>medp_verca-20110208 31930	similar to CYP71D unknown function
>medp_verca-20110208 10041	similar to CYP728 taxane 13a-hydroxylase*
>medp_verca-20110208 13942	similar to CYP734 brassinolide C-26 hydroxylase*
>medp_verca-20110208 13284	similar to CYP90B1 steroid C-22 hydroxylase*+
>medp_verca-20110208 18017	similar to CYP90B1 steroid C-22 hydroxylase
>medp_verca-20110208 18580	similar to CYP90B1 steroid C-22 hydroxylase*+
>medp_verca-20110208 2646	similar to CYP90B1 steroid C-22 hydroxylase*
>medp_verca-20110208 32399	similar to CYP90B1 steroid C-22 hydroxylase
>medp_verca-20110208 12709	similar to CYP94D unknown function*

*indicates contigs that were successfully cloned and tested

+contigs are homologs, and exhibited the same function

Table S4. Selected top-scoring transaminases in the steroid alkaloid biosynthetic pathway to cyclopamine.

Gene ID	Putative function
>medp_verca-20110208 12217	aminotransferase ACS10
>medp_verca-20110208 12084	gamma aminobutyrate transaminase 1, mitochondrial-like*
>medp_verca-20110208 5285	1-aminocyclopropane-1-carboxylate synthase
>medp_verca-20110208 28717	aminotransferase ACS12-like*
>medp_verca-20110208 15871	histidinol-phosphate aminotransferase, chloroplastic-like*
>medp_verca-20110208 10159	cysteine desulfurase 1
>medp_verca-20110208 1461	methionine S-methyltransferase

*indicates contigs that were successfully cloned and tested.