Table S1. Mapping summary for switchgrass crown and rhizome samples analyzed by HTS

| Plant ID | Summer1 | Summer2 | Summer3 | Kanlow1 | Kanlow2 | Kanlow3 |
|---|---|---|---|---|---|---|
| Total Reads | 26,158,420 | 26,000,859 | 26,818,136 | 24,539,570 | 27,127,805 | 27,090,340 |
| Total Mapped to Genome | 20,032,371 | 20,879,066 | 20,548,960 | 20,463,917 | 22,290,859 | 21,847,400 |
| Percent of Total | 76.6 | 80.3 | 76.6 | 83.4 | 82.2 | 80.6 |
| Multi-Mapped Reads | 3,179,885 | 4,163,674 | 3,198,823 | 2,624,806 | 3,254,418 | 3,051,917 |
| Percent of Total | 12.2 | 16.0 | 11.9 | 10.7 | 12.0 | 11.3 |
| Uniquely Mapped Reads | | | | | | |
| In Annotated Genes | 14,573,318 | 14,674,977 | 14,936,660 | 15,198,819 | 16,141,080 | 16,024,441 |
| Percent of Total | 55.7 | 56.4 | 55.7 | 61.9 | 59.5 | 59.2 |
| In Unannotated Regions | 2,279,168 | 2,040,415 | 2,416,477 | 2,640,292 | 2,895,361 | 2,771,042 |
| Percent of Total | 8.7 | 7.8 | 9.0 | 10.8 | 10.7 | 10.2 |

Table S2. Annotation of all transcripts using Blast2GO

| | | | | |
|---|---|---|---|---|
| Total Transcripts | No Blastx Hit* | no GO Terms | not Annotated** | Annotated |
| 65,878 | 4,986 | 6,594 | 8,811 | 45,487 |
| Total EC Assigned | Transcripts with EC | Molecular Function | Biological Processes | |
| 15,507 | 13,406 | 35,438 | 28,115 | |
| KEGG Pathways | | | | |
| Enzymes in KEGG Paths | KEGG Paths Populated | | | |
| 1,347 | 138 | | | |

* at an e-value threshold of 1 x $10^{-7}$ or lower; ** at an e-value threshold of 1 x $10^{-15}$ or lower

Table S3. List of 124 KEGG Pathways populated by Blast2GO analysis of the switchgrass draft genome used for Gene Set Enrichment Analysis

| NAME | # Enzymes |
|---|---|
| PURINE METABOLISM | 52 |
| AMINO SUGAR AND NUCLEOTIDE SUGAR METABOLISM | 40 |
| ARGININE AND PROLINE METABOLISM | 40 |
| STARCH AND SUCROSE METABOLISM | 38 |
| PYRIMIDINE METABOLISM | 32 |
| CYSTEINE AND METHIONINE METABOLISM | 30 |
| GLYCOLYSIS / GLUCONEOGENESIS | 26 |
| ALANINE, ASPARTATE AND GLUTAMATE METABOLISM | 26 |
| GLYCEROPHOSPHOLIPID METABOLISM | 25 |
| GLYCINE, SERINE AND THREONINE METABOLISM | 25 |
| PORPHYRIN AND CHLOROPHYLL METABOLISM | 25 |
| METHANE METABOLISM | 24 |
| PYRUVATE METABOLISM | 23 |
| AMINOACYL-TRNA BIOSYNTHESIS | 22 |
| CARBON FIXATION IN PHOTOSYNTHETIC ORGANISMS | 21 |
| NITROGEN METABOLISM | 21 |
| INOSITOL PHOSPHATE METABOLISM | 21 |
| VALINE, LEUCINE AND ISOLEUCINE DEGRADATION | 20 |
| FRUCTOSE AND MANNOSE METABOLISM | 20 |
| GLYOXYLATE AND DICARBOXYLATE | 20 |

| | |
|---|---|
| METABOLISM | |
| TERPENOID BACKBONE BIOSYNTHESIS | 20 |
| PHENYLALANINE, TYROSINE AND TRYPTOPHAN BIOSYNTHESIS | 19 |
| GLUTATHIONE METABOLISM | 18 |
| GLYCEROLIPID METABOLISM | 18 |
| TYROSINE METABOLISM | 18 |
| GALACTOSE METABOLISM | 17 |
| PHOSPHATIDYLINOSITOL SIGNALING SYSTEM | 17 |
| BETA-ALANINE METABOLISM | 16 |
| CITRATE CYCLE (TCA CYCLE) | 16 |
| PROPANOATE METABOLISM | 16 |
| CARBON FIXATION PATHWAYS IN PROKARYOTES | 16 |
| PHENYLALANINE METABOLISM | 15 |
| PENTOSE PHOSPHATE PATHWAY | 15 |
| DRUG METABOLISM - OTHER ENZYMES | 15 |
| BUTANOATE METABOLISM | 15 |
| PANTOTHENATE AND COA BIOSYNTHESIS | 15 |
| PENTOSE AND GLUCURONATE INTERCONVERSIONS | 14 |
| FATTY ACID METABOLISM | 14 |
| DITERPENOID BIOSYNTHESIS | 14 |
| SULFUR METABOLISM | 13 |
| ONE CARBON POOL BY FOLATE | 13 |
| ASCORBATE AND ALDARATE METABOLISM | 12 |
| SPHINGOLIPID METABOLISM | 12 |
| N-GLYCAN BIOSYNTHESIS | 12 |
| LYSINE DEGRADATION | 11 |
| TRYPTOPHAN METABOLISM | 11 |
| CYANOAMINO ACID METABOLISM | 11 |
| UBIQUINONE AND OTHER TERPENOID-QUINONE | 11 |

| | |
|---|---|
| BIOSYNTHESIS | |
| HISTIDINE METABOLISM | 11 |
| ALPHA-LINOLENIC ACID METABOLISM | 10 |
| SELENOCOMPOUND METABOLISM | 10 |
| NICOTINATE AND NICOTINAMIDE METABOLISM | 10 |
| FLAVONOID BIOSYNTHESIS | 10 |
| STEROID BIOSYNTHESIS | 10 |
| AMINOBENZOATE DEGRADATION | 9 |
| RIBOFLAVIN METABOLISM | 9 |
| STEROID HORMONE BIOSYNTHESIS | 9 |
| FATTY ACID BIOSYNTHESIS | 9 |
| VALINE, LEUCINE AND ISOLEUCINE BIOSYNTHESIS | 9 |
| VARIOUS TYPES OF N-GLYCAN BIOSYNTHESIS | 9 |
| LYSINE BIOSYNTHESIS | 9 |
| STREPTOMYCIN BIOSYNTHESIS | 9 |
| PHENYLPROPANOID BIOSYNTHESIS | 8 |
| ARACHIDONIC ACID METABOLISM | 8 |
| BIOSYNTHESIS OF UNSATURATED FATTY ACIDS | 8 |
| FOLATE BIOSYNTHESIS | 8 |
| DRUG METABOLISM - CYTOCHROME P450 | 7 |
| THIAMINE METABOLISM | 7 |
| METABOLISM OF XENOBIOTICS BY CYTOCHROME P450 | 7 |
| OXIDATIVE PHOSPHORYLATION | 7 |
| OTHER GLYCAN DEGRADATION | 7 |
| RETINOL METABOLISM | 7 |
| TROPANE, PIPERIDINE AND PYRIDINE ALKALOID BIOSYNTHESIS | 7 |
| VITAMIN B6 METABOLISM | 7 |
| BENZOATE DEGRADATION | 6 |
| FATTY ACID ELONGATION | 6 |

| | |
|---|---|
| CAROTENOID BIOSYNTHESIS | 6 |
| ETHER LIPID METABOLISM | 5 |
| GLYCOSAMINOGLYCAN BIOSYNTHESIS - HEPARAN SULFATE | 5 |
| STYRENE DEGRADATION | 5 |
| LIPOPOLYSACCHARIDE BIOSYNTHESIS | 5 |
| LINOLEIC ACID METABOLISM | 4 |
| GLYCOSPHINGOLIPID BIOSYNTHESIS - GLOBO SERIES | 4 |
| ISOQUINOLINE ALKALOID BIOSYNTHESIS | 4 |
| TAURINE AND HYPOTAURINE METABOLISM | 4 |
| GERANIOL DEGRADATION | 4 |
| SYNTHESIS AND DEGRADATION OF KETONE BODIES | 4 |
| BIOTIN METABOLISM | 4 |
| GLYCOSAMINOGLYCAN BIOSYNTHESIS - CHONDROITIN SULFATE | 3 |
| GLYCOSAMINOGLYCAN DEGRADATION | 3 |
| INDOLE ALKALOID BIOSYNTHESIS | 3 |
| LIMONENE AND PINENE DEGRADATION | 3 |
| GLYCOSPHINGOLIPID BIOSYNTHESIS - GANGLIO SERIES | 3 |
| CHLOROALKANE AND CHLOROALKENE DEGRADATION | 3 |
| CAFFEINE METABOLISM | 3 |
| ZEATIN BIOSYNTHESIS | 3 |
| NOVOBIOCIN BIOSYNTHESIS | 3 |
| POLYKETIDE SUGAR UNIT BIOSYNTHESIS | 3 |
| CHLOROCYCLOHEXANE AND CHLOROBENZENE DEGRADATION | 3 |
| TOLUENE DEGRADATION | 3 |
| PHOSPHONATE AND PHOSPHINATE METABOLISM | 3 |

| | |
|---|---|
| OTHER TYPES OF O-GLYCAN BIOSYNTHESIS | 3 |
| PEPTIDOGLYCAN BIOSYNTHESIS | 3 |
| T CELL RECEPTOR SIGNALING PATHWAY | 2 |
| GLYCOSPHINGOLIPID BIOSYNTHESIS - LACTO AND NEOLACTO SERIES | 2 |
| GLUCOSINOLATE BIOSYNTHESIS | 2 |
| CAPROLACTAM DEGRADATION | 2 |
| C5-BRANCHED DIBASIC ACID METABOLISM | 2 |
| STILBENOID, DIARYLHEPTANOID AND GINGEROL BIOSYNTHESIS | 2 |
| FLAVONE AND FLAVONOL BIOSYNTHESIS | 2 |
| LIPOIC ACID METABOLISM | 2 |
| BUTIROSIN AND NEOMYCIN BIOSYNTHESIS | 2 |
| FLUOROBENZOATE DEGRADATION | 2 |
| D-GLUTAMINE AND D-GLUTAMATE METABOLISM | 2 |
| ATRAZINE DEGRADATION | 2 |
| PRIMARY BILE ACID BIOSYNTHESIS | 2 |
| MTOR SIGNALING PATHWAY | 1 |
| NAPHTHALENE DEGRADATION | 1 |
| BIOSYNTHESIS OF VANCOMYCIN GROUP ANTIBIOTICS | 1 |
| ETHYLBENZENE DEGRADATION | 1 |
| PHOTOSYNTHESIS | 1 |
| GLYCOSYLPHOSPHATIDYLINOSITOL(GPI)-ANCHOR BIOSYNTHESIS | 1 |
| BIOSYNTHESIS OF TERPENOIDS AND STEROIDS | 1 |
| BETALAIN BIOSYNTHESIS | 1 |

Table S4: Gene Set Enrichment Analysis Results. KEGG pathways with an FDR <0.2 are shown. Transcript observed for individual enzymes in a given pathway are tabulated (enzymes).

**Up-regulated in Summer**

| Pathway | FDR | Enzymes |
|---|---|---|
| DITERPENOID BIOSYNTHESIS | 0.000 | 14 |
| VALINE, LEUCINE AND ISOLEUCINE DEGRADATION | 0.001 | 20 |
| DRUG METABOLISM - CYTOCHROME P450 | 0.012 | 7 |
| METABOLISM OF XENOBIOTICS BY CYTOCHROME P450 | 0.012 | 7 |
| FATTY ACID ELONGATION | 0.013 | 6 |
| BUTANOATE METABOLISM | 0.014 | 15 |
| GERANIOL DEGRADATION | 0.020 | 4 |
| VITAMIN B6 METABOLISM | 0.024 | 7 |
| BENZOATE DEGRADATION | 0.034 | 6 |
| STYRENE DEGRADATION | 0.039 | 5 |
| GLUTATHIONE METABOLISM | 0.051 | 18 |
| HISTIDINE METABOLISM | 0.058 | 11 |
| VALINE, LEUCINE AND ISOLEUCINE BIOSYNTHESIS | 0.063 | 9 |
| SYNTHESIS AND DEGRADATION OF KETONE BODIES | 0.066 | 4 |
| BETA-ALANINE METABOLISM | 0.067 | 16 |
| PROPANOATE METABOLISM | 0.073 | 16 |
| PYRUVATE METABOLISM | 0.079 | 23 |
| TRYPTOPHAN METABOLISM | 0.080 | 11 |
| PANTOTHENATE AND COA BIOSYNTHESIS | 0.188 | 15 |
| BIOSYNTHESIS OF UNSATURATED FATTY ACIDS | 0.193 | 8 |

**Up –regulated in Kanlow**

| Pathway | FDR | Enzymes |
|---|---|---|
| PHENYLPROPANOID BIOSYNTHESIS | 0.001 | 8 |

| | | |
|---|---|---|
| LINOLEIC ACID METABOLISM | 0.007 | 4 |
| STARCH AND SUCROSE METABOLISM | 0.007 | 38 |
| PHENYLALANINE METABOLISM | 0.017 | 15 |
| OTHER GLYCAN DEGRADATION | 0.020 | 7 |
| METHANE METABOLISM | 0.033 | 24 |
| PENTOSE AND GLUCURONATE INTERCONVERSIONS | 0.040 | 14 |
| CAROTENOID BIOSYNTHESIS | 0.047 | 6 |
| GLYCOSAMINOGLYCAN BIOSYNTHESIS - HEPARAN SULFATE | 0.050 | 5 |
| FLAVONOID BIOSYNTHESIS | 0.079 | 10 |
| STREPTOMYCIN BIOSYNTHESIS | 0.084 | 9 |
| SPHINGOLIPID METABOLISM | 0.089 | 12 |
| INOSITOL PHOSPHATE METABOLISM | 0.197 | 21 |

**Figure S1**. Temperature and rainfall at the field site prior to and post harvest.

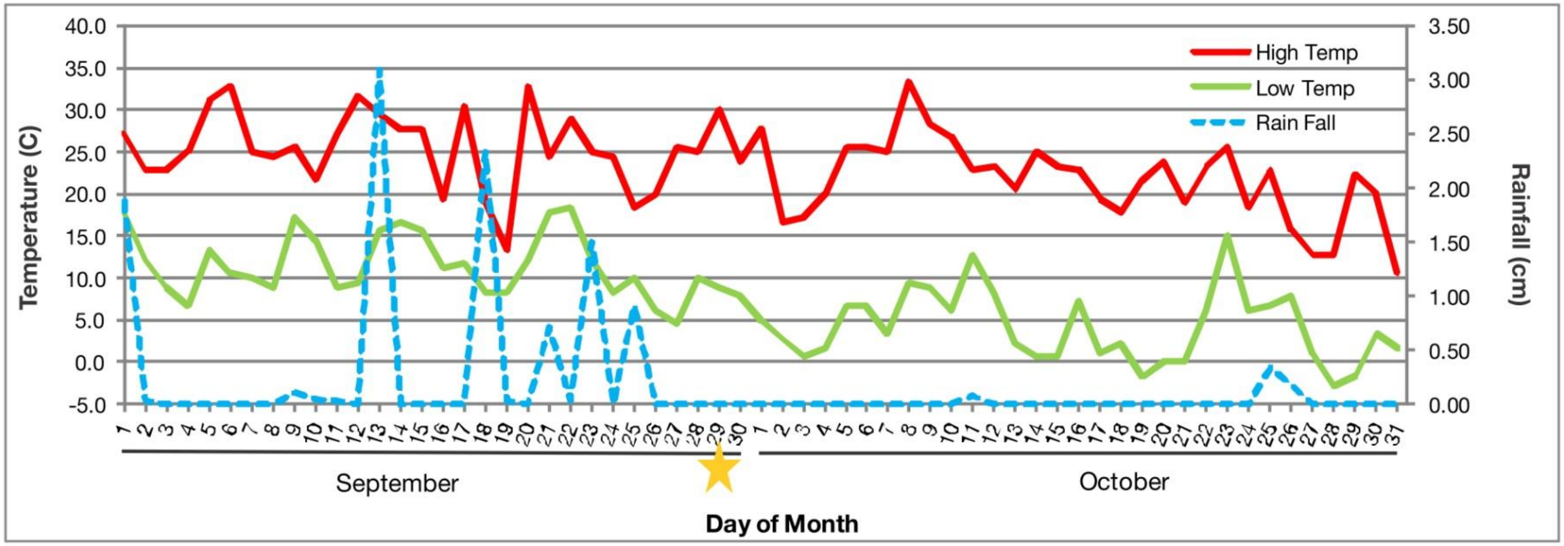

Figure S2. Two way heat map of all features observed by GCMS. Metabolites identified with higher degree of confidence are shown in Fig. 6 Red bar = Kanlow samples; Green bar = Summer samples. Yellow = high, black = low. Data from three independent extractions from each plant sample.