



**Table S1.** Summary of the ATAC-seq data for the three groups of *S. latifolia*.

| Item               | D1                    | D2                   | L1                    | L2                    | P1                    | P2                    |
|--------------------|-----------------------|----------------------|-----------------------|-----------------------|-----------------------|-----------------------|
| All                | 1.09×10 <sup>8</sup>  | 7.00×10 <sup>7</sup> | 1.23×10 <sup>8</sup>  | 1.18×10 <sup>8</sup>  | 1.27×10 <sup>8</sup>  | 1.26×10 <sup>8</sup>  |
| UnMapped           | 2.60×10 <sup>7</sup>  | 1.52×10 <sup>7</sup> | 3.12×10 <sup>7</sup>  | 2.85×10 <sup>7</sup>  | 5.54×10 <sup>7</sup>  | 5.55×10 <sup>7</sup>  |
| Mapped             | 8.28×10 <sup>7</sup>  | 5.48×10 <sup>7</sup> | 9.18×10 <sup>7</sup>  | 8.91×10 <sup>7</sup>  | 7.19×10 <sup>7</sup>  | 7.01×10 <sup>7</sup>  |
| MappedRate         | 0.76                  | 0.78                 | 0.75                  | 0.76                  | 0.57                  | 0.56                  |
| Unique Mapped      | 7.80×10 <sup>7</sup>  | 5.17×10 <sup>7</sup> | 8.61×10 <sup>7</sup>  | 8.38×10 <sup>7</sup>  | 6.81×10 <sup>7</sup>  | 6.64×10 <sup>7</sup>  |
| Unique Mapped Rate | 0.72                  | 0.74                 | 0.70                  | 0.71                  | 0.54                  | 0.53                  |
| Repeat Mapped      | 4.86×10 <sup>6</sup>  | 3.04×10 <sup>6</sup> | 5.74×10 <sup>6</sup>  | 5.24×10 <sup>6</sup>  | 3.83×10 <sup>6</sup>  | 3.75×10 <sup>6</sup>  |
| All Base           | 1.21×10 <sup>10</sup> | 8.40×10 <sup>9</sup> | 1.26×10 <sup>10</sup> | 1.27×10 <sup>10</sup> | 1.39×10 <sup>10</sup> | 1.37×10 <sup>10</sup> |
| UnMapped Base      | 2.57×10 <sup>9</sup>  | 1.69×10 <sup>9</sup> | 2.96×10 <sup>9</sup>  | 2.79×10 <sup>9</sup>  | 5.63×10 <sup>9</sup>  | 5.64×10 <sup>9</sup>  |
| Mapped Base        | 9.52×10 <sup>9</sup>  | 6.71×10 <sup>9</sup> | 9.61×10 <sup>9</sup>  | 9.91×10 <sup>9</sup>  | 8.25×10 <sup>9</sup>  | 8.02×10 <sup>9</sup>  |
| Unique Mapped Base | 9.04×10 <sup>9</sup>  | 6.40×10 <sup>9</sup> | 9.10×10 <sup>9</sup>  | 9.41×10 <sup>9</sup>  | 7.87×10 <sup>9</sup>  | 7.65×10 <sup>9</sup>  |
| Repeat Mapped Base | 4.81×10 <sup>8</sup>  | 3.18×10 <sup>8</sup> | 5.09×10 <sup>8</sup>  | 4.98×10 <sup>8</sup>  | 3.80×10 <sup>8</sup>  | 3.71×10 <sup>8</sup>  |
| Peak Calling       | 9.40×10 <sup>3</sup>  | 7.72×10 <sup>3</sup> | 1.13×10 <sup>4</sup>  | 1.08×10 <sup>4</sup>  | 8.51×10 <sup>3</sup>  | 8.35×10 <sup>3</sup>  |

**Table S2.** Differential accessible peaks statistics.

| Sample  | P vs. D |      | L vs. D |     |
|---------|---------|------|---------|-----|
|         | down    | up   | down    | up  |
| PeakNum | 1912    | 1768 | 273     | 234 |

**Table S3.** Summary of the clean transcriptome sequencing data for the three groups of *S. latifolia*.

| Statistics         | D1                   | D2                    | D3                   | L1                    | L2                    | L3                   | P1                   | P2                    | P3                   |
|--------------------|----------------------|-----------------------|----------------------|-----------------------|-----------------------|----------------------|----------------------|-----------------------|----------------------|
| All                | 6.18×10 <sup>7</sup> | 7.13×10 <sup>7</sup>  | 6.54×10 <sup>7</sup> | 7.05×10 <sup>7</sup>  | 6.83×10 <sup>7</sup>  | 6.10×10 <sup>7</sup> | 5.78×10 <sup>7</sup> | 6.79×10 <sup>7</sup>  | 6.40×10 <sup>7</sup> |
| UnMapped           | 7.41×10 <sup>6</sup> | 8.15×10 <sup>6</sup>  | 8.07×10 <sup>6</sup> | 8.61×10 <sup>6</sup>  | 9.93×10 <sup>6</sup>  | 7.93×10 <sup>6</sup> | 9.64×10 <sup>6</sup> | 1.48×10 <sup>7</sup>  | 1.01×10 <sup>7</sup> |
| Mapped             | 5.44×10 <sup>7</sup> | 6.31×10 <sup>7</sup>  | 5.73×10 <sup>7</sup> | 6.19×10 <sup>7</sup>  | 5.84×10 <sup>7</sup>  | 5.31×10 <sup>7</sup> | 4.81×10 <sup>7</sup> | 5.31×10 <sup>7</sup>  | 5.39×10 <sup>7</sup> |
| Mapped Rate        | 0.88                 | 0.89                  | 0.88                 | 0.88                  | 0.86                  | 0.87                 | 0.83                 | 0.78                  | 0.84                 |
| Unique Mapped      | 5.37×10 <sup>7</sup> | 6.24×10 <sup>7</sup>  | 5.66×10 <sup>7</sup> | 6.10×10 <sup>7</sup>  | 5.77×10 <sup>7</sup>  | 5.24×10 <sup>7</sup> | 4.75×10 <sup>7</sup> | 5.26×10 <sup>7</sup>  | 5.31×10 <sup>7</sup> |
| Unique Mapped Rate | 0.87                 | 0.88                  | 0.87                 | 0.87                  | 0.85                  | 0.86                 | 0.82                 | 0.77                  | 0.83                 |
| Repeat Mapped      | 6.87×10 <sup>5</sup> | 7.85×10 <sup>5</sup>  | 6.41×10 <sup>5</sup> | 8.66×10 <sup>5</sup>  | 6.52×10 <sup>5</sup>  | 6.93×10 <sup>5</sup> | 5.66×10 <sup>5</sup> | 5.73×10 <sup>5</sup>  | 7.65×10 <sup>5</sup> |
| Junction All       | 2.21×10 <sup>7</sup> | 2.63×10 <sup>7</sup>  | 2.30×10 <sup>7</sup> | 2.45×10 <sup>7</sup>  | 2.30×10 <sup>7</sup>  | 2.10×10 <sup>7</sup> | 1.91×10 <sup>7</sup> | 2.10×10 <sup>7</sup>  | 2.15×10 <sup>7</sup> |
| Mapped             | 2.21×10 <sup>7</sup> | 2.63×10 <sup>7</sup>  | 2.30×10 <sup>7</sup> | 2.45×10 <sup>7</sup>  | 2.30×10 <sup>7</sup>  | 2.10×10 <sup>7</sup> | 1.91×10 <sup>7</sup> | 2.10×10 <sup>7</sup>  | 2.15×10 <sup>7</sup> |
| Junction Unique    | 2.18×10 <sup>7</sup> | 2.59×10 <sup>7</sup>  | 2.28×10 <sup>7</sup> | 2.42×10 <sup>7</sup>  | 2.27×10 <sup>7</sup>  | 2.07×10 <sup>7</sup> | 1.89×10 <sup>7</sup> | 2.08×10 <sup>7</sup>  | 2.11×10 <sup>7</sup> |
| Mapped             | 2.18×10 <sup>7</sup> | 2.59×10 <sup>7</sup>  | 2.28×10 <sup>7</sup> | 2.42×10 <sup>7</sup>  | 2.27×10 <sup>7</sup>  | 2.07×10 <sup>7</sup> | 1.89×10 <sup>7</sup> | 2.08×10 <sup>7</sup>  | 2.11×10 <sup>7</sup> |
| All Base           | 9.27×10 <sup>9</sup> | 1.07×10 <sup>10</sup> | 9.80×10 <sup>9</sup> | 1.06×10 <sup>10</sup> | 1.02×10 <sup>10</sup> | 9.16×10 <sup>9</sup> | 8.66×10 <sup>9</sup> | 1.02×10 <sup>10</sup> | 9.61×10 <sup>9</sup> |
| UnMapped Base      | 1.11×10 <sup>9</sup> | 1.22×10 <sup>9</sup>  | 1.21×10 <sup>9</sup> | 1.29×10 <sup>9</sup>  | 1.49×10 <sup>9</sup>  | 1.19×10 <sup>9</sup> | 1.45×10 <sup>9</sup> | 2.22×10 <sup>9</sup>  | 1.52×10 <sup>9</sup> |
| MappedBase         | 8.16×10 <sup>9</sup> | 9.47×10 <sup>9</sup>  | 8.59×10 <sup>9</sup> | 9.28×10 <sup>9</sup>  | 8.76×10 <sup>9</sup>  | 7.97×10 <sup>9</sup> | 7.22×10 <sup>9</sup> | 7.97×10 <sup>9</sup>  | 8.08×10 <sup>9</sup> |
| Unique Mapped Base | 8.05×10 <sup>9</sup> | 9.35×10 <sup>9</sup>  | 8.50×10 <sup>9</sup> | 9.15×10 <sup>9</sup>  | 8.66×10 <sup>9</sup>  | 7.86×10 <sup>9</sup> | 7.13×10 <sup>9</sup> | 7.89×10 <sup>9</sup>  | 7.97×10 <sup>9</sup> |
| Repeat Mapped Base | 1.03×10 <sup>8</sup> | 1.18×10 <sup>8</sup>  | 9.61×10 <sup>7</sup> | 1.30×10 <sup>8</sup>  | 9.78×10 <sup>7</sup>  | 1.04×10 <sup>8</sup> | 8.49×10 <sup>7</sup> | 8.59×10 <sup>7</sup>  | 1.15×10 <sup>8</sup> |
| InsertSize         | 679.00               | 665.00                | 631.00               | 760.00                | 609.00                | 649.00               | 645.00               | 613.00                | 595.00               |

**Table S4.** Summary of the DEGs in integration of ATAC-seq with RNA-seq.

| Genes | Code         | GenBank No. | Primer pairs (5'→3')                             | Descriptions                                 |
|-------|--------------|-------------|--------------------------------------------------|----------------------------------------------|
| D1    | Gglean000619 | MK972849    | F:CGCTGTCTGGCCGGTATATT<br>D:AAAGCGAATCCACTGAGGCA | MFS general substrate transporter            |
| D2    | Gglean000957 | MK972850    | F:CCAGGAGCGACCTTGGTATT<br>D:CAAGAACGGGGTATCTCCGA | Delta (12) fatty acid desaturase             |
| D3    | Gglean001542 | MK972851    | F:TCAAGATGCTCGGTGGTGAC<br>D:CAATGAGCATGCACGTCGAG | Putative glycine dehydrogenase               |
| D4    | Gglean001940 | MK972852    | F:GTACGGACACAACCTGCTCA<br>D:CGGATATCCCGGTCCACAAG | Phenol 2-monooxygenase                       |
| D5    | Gglean003676 | MK972853    | F:GCCCCCGAGAAGAACATGAA                           | cofactor-independent phosphoglycerate mutase |

|       |              |          |                                                                            |                                                                       |
|-------|--------------|----------|----------------------------------------------------------------------------|-----------------------------------------------------------------------|
| D6    | Gglean005508 | MK972854 | D:CCTCGTCGCCATTGACGATA<br>F:ACGCGAGTTAGCTATGGAGC<br>D:CCAAGCAATGACAACGCCAA | Uncharacterized transporter                                           |
| D7    | Gglean006573 | MK972855 | F:GGTTCATCCACCATGCAGA<br>D:CTACGCCGGAGATGAAGTCC                            | Alpha/beta hydrolase                                                  |
| D8    | Gglean008033 | MK972856 | F:AGCACTTTCGTTCCGGGTGAT<br>D:CGCTGTCTGCTTTCCAGTA                           | Meiosis-specific protein hop1                                         |
| D9    | Gglean009036 | MK972857 | F:GGATGGCCTCAAGAGGATCG<br>D:CAAGAGGGACTCCATACCGC                           | Aldo-keto reductase yakc [NADP(+)]                                    |
| D10   | Gglean009487 | MK972858 | F:AGCTCGAAGAACTGCACGA<br>D:TCTCGTCCCCAGCCTTGATA                            | lactate 2-monooxygenase                                               |
| D11   | Gglean010344 | MK972859 | F:ACTCCAACCTCACGTTCTGTC<br>D:CTGATCCGGCGTGAGCTTAT                          | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase |
| D12   | Gglean011299 | MK972860 | F:TTCGGTAGAGAACCCCCGAT<br>D:CATGTGGGGCTCAACTGCTA                           | O-methylsterigmatocystin oxidoreductase                               |
| D13   | Gglean011958 | MK972861 | F:ACGATTTTCGACCCCTCAAC<br>D:TAACCACCTGTGATGGCGAC                           | Uncharacterized trans-sulfuration enzyme YHR112C                      |
| U1    | Gglean000572 | MK972862 | F:GCCGTCCGACTATGACGAAT<br>D:CGAGTCAGGTATGCGGTCTC                           | Dehydrogenase patE                                                    |
| U2    | Gglean002577 | MK972863 | F:CGTCACATCGATGAACACGC<br>D:AACCTCGAACGGGAACCTCAC                          | hypothetical protein 1                                                |
| U3    | Gglean002700 | MK972864 | F:CGTCACATCGATGAACACGC<br>D:AACCTCGAACGGGAACCTCAC                          | Iron-sulfur clusters transporter ATM1                                 |
| U4    | Gglean002720 | MK972865 | F:TTTCGCTGGGTGCTTATCGT<br>D:GGAACCCTAACTTCAACCGCA                          | hypothetical protein 2                                                |
| U5    | Gglean002890 | MK972866 | F:AGATGATGAGCGTCTTCCGC<br>D:AACCTCGACCATGATGGGCTC                          | hypothetical protein 3                                                |
| U6    | Gglean003085 | MK972867 | F:CCAATGCAGTGAAGCGGACT<br>D:ATGTCTGAAGTGGGAAGCCG                           | Pre-mRNA-splicing factor CWC22                                        |
| U7    | Gglean003249 | MK972868 | F:TGCGTCCAAGATATCGTCCG<br>D:GAACAATCGCGATGAGCCAC                           | hypothetical protein 4                                                |
| U8    | Gglean003319 | MK972869 | F:TTCACGAGGACCACAAGCTC<br>D:CTGCTTCCCAAACCTCGTCT                           | Phospholipid methyltransferase                                        |
| U9    | Gglean005067 | MK972870 | F:CGACGATGATTGACACCGC<br>D:CTCTCCGGACTGCGATTCTC                            | SH3 domain-containing protein                                         |
| U10   | Gglean005727 | MK972871 | F:CCATCACCGTCATCGGAGTT<br>D:AACCAAGTTGCCGTAGCTGT                           | Fruiting body protein SC4 (Precursor)                                 |
| U11   | Gglean007619 | MK972872 | F:CCCCTCAGCGTCGATAGTTC<br>D:GAGGTTAGAGGCGACATCGG                           | Gluconate transport inducer 1                                         |
| U12   | Gglean008695 | MK972873 | F:CGCGATTGCAAAAAGGAGCTG<br>D:AGGATGGAGAGGACGAGCTT                          | LON peptidase N-terminal domain and RING finger protein               |
| U13   | Gglean008796 | MK972874 | F:TATATGCGCGCAAAGCACAC<br>D:CGAGTAAGATCACCGTCCCG                           | hypothetical protein 5                                                |
| U14   | Gglean008871 | MK972875 | F:TGAAGAGCAGACGACTACCG<br>D:ATTTCAGTTCCGCGATGGA                            | Putative methyltransferase-like protein C27D7.08c                     |
| U15   | Gglean010591 | KX671998 | F:CCAGCATCACCAACTACAAGAA<br>D:CCTCTGCGGGAGTATTATTGAC                       | White collar 1 protein                                                |
| U16   | Gglean010678 | MK972876 | F:CCGATACCACCTTCCTCGTG<br>D:AGCCAAGTTCTTGAGGGTCG                           | Cysteine proteinase 1                                                 |
| U17   | Gglean012354 | MK972877 | F:GTACCACCGGACTCACCTTC<br>D:TACTGCTTTTCGAGACCTGG                           | Dehydrogenase citC                                                    |
| GAPDH | Gglean007906 | MF975750 | F:TCATTACCGCACCTCTTCC<br>D:CCACCACGCCAGTCTTTATG                            | Glyceraldehyde-3-phosphate dehydrogenase                              |

Table S5. Gene ontology and pathway enrichment analysis of the DEGs.

| Categories         | Term ID    | Term                         | Symbol       | P-    |       |            |
|--------------------|------------|------------------------------|--------------|-------|-------|------------|
|                    |            |                              |              | Value | FDR   | Enrichment |
| biological process | GO:0042820 | vitamin B6 catabolic process | Gglean009036 | 0.006 | 0.035 | 160.56     |
|                    | GO:0006544 | glycine metabolic process    | Gglean001542 | 0.006 | 0.035 | 160.56     |

|           |            |                                              |              |       |       |        |
|-----------|------------|----------------------------------------------|--------------|-------|-------|--------|
|           |            | glycine decarboxylation via glycine cleavage |              |       |       |        |
|           | GO:0019464 | system                                       | Gglean001542 | 0.006 | 0.035 | 160.56 |
|           | GO:0006546 | glycine catabolic process                    | Gglean001542 | 0.010 | 0.035 | 96.33  |
|           | GO:0071266 | 'de novo' L-methionine biosynthetic process  | Gglean011958 | 0.010 | 0.035 | 96.33  |
|           |            | cysteine biosynthetic process via            |              |       |       |        |
|           | GO:0019343 | cystathionine                                | Gglean011958 | 0.014 | 0.040 | 68.81  |
|           | GO:0019346 | transsulfuration                             | Gglean011958 | 0.017 | 0.040 | 60.21  |
|           | GO:0006730 | one-carbon metabolic process                 | Gglean001542 | 0.027 | 0.051 | 37.05  |
|           | GO:0006790 | sulfur compound metabolic process            | Gglean011958 | 0.031 | 0.051 | 32.11  |
|           | GO:1903222 | quinolinic acid transmembrane transport      | Gglean005508 | 0.031 | 0.051 | 32.11  |
|           | GO:0046942 | carboxylic acid transport                    | Gglean005508 | 0.033 | 0.051 | 30.10  |
|           | GO:0008150 | biological_process                           | Gglean009036 | 0.047 | 0.067 | 5.47   |
|           | GO:0008150 | biological_process                           | Gglean000619 | 0.047 | 0.067 | 5.47   |
| <hr/>     |            |                                              |              |       |       |        |
| cellular  |            |                                              |              |       |       |        |
| component | GO:0005960 | glycine cleavage complex                     | Gglean001542 | 0.010 | 0.145 | 96.27  |
| <hr/>     |            |                                              |              |       |       |        |
|           |            | 5-methyltetrahydropteroyltriglutamate-       |              |       |       |        |
|           | GO:0003871 | homocysteine S-methyltransferase activity    | Gglean010344 | 0.002 | 0.015 | 480.83 |
|           | GO:0016594 | glycine binding                              | Gglean001542 | 0.002 | 0.015 | 480.83 |
|           | GO:0030170 | pyridoxal phosphate binding                  | Gglean011958 | 0.002 | 0.015 | 25.99  |
|           | GO:0030170 | pyridoxal phosphate binding                  | Gglean001542 | 0.002 | 0.015 | 25.99  |
|           | GO:0050236 | pyridoxine:NADP 4-dehydrogenase activity     | Gglean009036 | 0.006 | 0.028 | 160.28 |
|           | GO:0004121 | cystathionine beta-lyase activity            | Gglean011958 | 0.008 | 0.028 | 120.21 |
|           |            | glycine dehydrogenase (decarboxylating)      |              |       |       |        |
|           | GO:0004375 | activity                                     | Gglean001542 | 0.010 | 0.028 | 96.17  |
|           | GO:0004123 | cystathionine gamma-lyase activity           | Gglean011958 | 0.010 | 0.028 | 96.17  |
|           | GO:0003962 | cystathionine gamma-synthase activity        | Gglean011958 | 0.012 | 0.030 | 80.14  |
|           |            | carboxylic acid transmembrane transporter    |              |       |       |        |
|           | GO:0046943 | activity                                     | Gglean005508 | 0.033 | 0.069 | 30.05  |
| <hr/>     |            |                                              |              |       |       |        |
|           | PATH:00750 | Vitamin B6 metabolism                        | Gglean009036 | 0.011 | 0.030 | 91.37  |
|           | PATH:00450 | Selenocompound metabolism                    | Gglean010344 | 0.012 | 0.030 | 82.23  |
| KEGG      | PATH:00270 | Cysteine and methionine metabolism           | Gglean010344 | 0.040 | 0.046 | 24.92  |
|           | PATH:00260 | Glycine, serine and threonine metabolism     | Gglean001542 | 0.044 | 0.046 | 22.23  |
|           | PATH:00630 | Glyoxylate and dicarboxylate metabolism      | Gglean001542 | 0.046 | 0.046 | 21.64  |

Table S6. Information of peaks enriched near these DEGs.

| Gene | PeakID    | Peak Score | Annotation | Distance to TSS | Nearest PromoterID |
|------|-----------|------------|------------|-----------------|--------------------|
| D1   | peaks616  | 4.17       | TTS        | 2340            | Gglean000619       |
| D2   | peaks688  | 11.11      | promoter   | -646            | Gglean000957       |
| D3   | peaks4313 | 2.86       | exon       | 2542            | Gglean001542       |
| D3   | peaks4312 | 10.82      | promoter   | -185            | Gglean001542       |
| D4   | peaks3981 | 6.07       | TTS        | 744             | Gglean001940       |

|     |            |        |            |        |              |
|-----|------------|--------|------------|--------|--------------|
| D5  | peaks5312  | 6.87   | promoter   | -785   | Gglean003676 |
| D6  | peaks6386  | 9.21   | promoter   | -871   | Gglean005508 |
| D7  | peaks6891  | 5.41   | promoter   | -276   | Gglean006573 |
| D8  | peaks2007  | 21.15  | exon       | 842    | Gglean008033 |
| D9  | peaks8706  | 15.25  | promoter   | -161   | Gglean009036 |
| D10 | peaks2432  | 15.54  | exon       | 741    | Gglean009487 |
| D11 | peaks2601  | 17.31  | TTS        | 2444   | Gglean010344 |
| D12 | peaks10056 | 19.80  | promoter   | -871   | Gglean011299 |
| D13 | peaks10409 | 317.64 | Intergenic | -32526 | Gglean011958 |
| D13 | peaks10408 | 68.56  | Intergenic | -26507 | Gglean011958 |
| D13 | peaks10406 | 3.06   | Intergenic | -8245  | Gglean011958 |
| D13 | peaks10405 | 2.79   | Intergenic | -7116  | Gglean011958 |
| D13 | peaks10407 | 2.53   | Intergenic | -25360 | Gglean011958 |
| U1  | peaks519   | 4.08   | exon       | 2648   | Gglean000572 |
| U2  | peaks5074  | 6.03   | intron     | 376    | Gglean002577 |
| U3  | peaks12468 | 11.23  | exon       | 755    | Gglean002700 |
| U4  | peaks5484  | 6.92   | TTS        | 462    | Gglean002720 |
| U4  | peaks5485  | 4.07   | Intergenic | -2537  | Gglean002720 |
| U5  | peaks5486  | 16.79  | Intergenic | -1301  | Gglean002890 |
| U6  | peaks5650  | 13.42  | exon       | 758    | Gglean003085 |
| U6  | peaks5649  | 2.54   | exon       | 212    | Gglean003085 |
| U7  | peaks5701  | 2.32   | TTS        | 2161   | Gglean003249 |
| U8  | peaks5820  | 2.52   | intron     | 2154   | Gglean003319 |
| U9  | peaks7234  | 7.79   | exon       | 484    | Gglean005067 |
| U10 | peaks7634  | 8.92   | promoter   | -822   | Gglean005727 |
| U11 | peaks9215  | 9.63   | Intergenic | -1149  | Gglean007619 |
| U12 | peaks9759  | 9.20   | promoter   | -794   | Gglean008695 |
| U13 | peaks9814  | 17.10  | promoter   | -171   | Gglean008796 |
| U14 | peaks9893  | 5.76   | promoter   | -685   | Gglean008871 |
| U15 | peaks11140 | 2.81   | exon       | 1830   | Gglean010591 |
| U15 | peaks11141 | 15.52  | promoter   | -340   | Gglean010591 |
| U16 | peaks11214 | 2.67   | TTS        | 365    | Gglean010678 |
| U17 | peaks4041  | 2.52   | TTS        | -2047  | Gglean012354 |