



**Figure S1.** Summary of mapping of exome capture probes to the transcriptome design sequences and the switchgrass reference genome Release 0. A. A total of 904,693 probes used in the exome capture sequencing experiment were mapped to the original set of transcripts used to design the probe set using GMAP (version 2013-03-31) ([Wu and Watanabe 2005](#)) and alignments that passed the cutoff criteria of  $\geq 50\%$  coverage and  $\geq 90\%$  identity were sorted into bins based on how many times they mapped to the full transcript set. B. A total of 904,693 probes used in the exome capture sequencing experiment were mapped to the AP13 reference genome Release 0 (hard-masked, [http://www.phytozome.net/dataUsagePolicy.php?org=Org\\_Pvirgatum](http://www.phytozome.net/dataUsagePolicy.php?org=Org_Pvirgatum)) using GMAP (version 2013-03-31) ([Wu and Watanabe 2005](#)). Probes that passed the mapping quality cutoffs were further analyzed to assess the mapping frequency and location in the genome.