

S2 Table. Reference genome assemblies utilized for short read mapping and alignment statistics associated with the transcriptome libraries.

Reference Assembly	SRA ID	Number of input reads	Average input read length	Mapped reads %
<i>A. thaliana</i> - TAIR10	ERR754084	17789212	202	79.16
<i>B. distachyon</i> - v1.0	DRR048605	29269012	202	91.11
<i>G. max</i> - V1.0	SRR3475914	17397088	202	94.07
	SRR2079642	30643459	100	91.53
	SRR1592302	26749369	100	95.16
<i>H. vulgare</i> - ASM32608v1	ERR674189	16791756	200	64.67
<i>M. truncatula</i> - MedtrA17_4.0	SRR1523070	47999588	200	86.38
	SRR1523072	47434133	200	88.18
	SRR1523077	45585568	200	88.72
<i>Oryza sativa</i> - IRGSP-1.0	SRR952242	15874767	202	95.98

	ERR687857	15781946	202	82.51
<i>P. trichocarpa</i> - JGI2.0	SRR1030352	65442430	180	96.45
<i>S. bicolor</i> - Sorbi1	ERR886716	23431944	202	94.83
<i>S. lycopersicum</i> - SL2.50	SRR2923343	29643874	200	84.47
	SRR3095793	18881356	100	98.03
<i>T. aestivum</i> - IWGSC1+popseq	SRR1542404	18110600	202	90.96
	SRR1542405	81331219	200	91.34
	SRR2306548	76134375	200	93.70
	SRR1228254	27518448	200	86.36
<i>Z. mays</i> - AGPv3	SRR2069900	59966193	35	68.80
	SRR762350	26544807	202	96.13