

S1 Table. SRA data sets utilized for the identification of novel lncRNA sequences.

Species	SRA ID	Library type	Library size (bases)	Platform
<i>Arabidopsis thaliana</i>	ERR754084	PE*	3.6G	Illumina HiSeq 2000
<i>Brachypodium distachyon</i>	DRR048605	SE**	2.9G	Illumina HiSeq 2000
<i>Glycine max</i>	SRR3475914	PE	2.7G	Illumina HiSeq 2000
	SRR2079642	SE	9.7G	Illumina HiSeq 2000
	SRR1592302	PE	3.5G	Illumina HiSeq 2500
<i>Hordeum vulgare</i>	ERR674189	PE	3.4G	Illumina HiSeq 1000
<i>Medicago truncatula</i>	SRR1523070	PE	9.6G	Illumina HiSeq 2000
	SRR1523072	PE	9.5G	Illumina HiSeq 2000
	SRR1523077	PE	9.1G	Illumina HiSeq 2000
<i>Oryza sativa</i>	SRR952242	PE	3.2G	Illumina Genome Analyzer II
	ERR687857	PE	3.2G	Illumina HiSeq 2000
<i>Populus trichocarpa</i>	SRR1030352	PE	11.8G	Illumina HiSeq 2000
<i>Sorghum bicolor</i>	ERR886716	PE	4.7G	Illumina HiScanSQ

<i>Solanum lycopersicum</i>	SRR2923343	PE	5.9G	Illumina HiSeq 2000
	SRR3095793	PE	1.9G	Illumina HiSeq 2000
<i>Triticum aestivum</i>	SRR1542404	PE	16.3G	Illumina HiSeq 2000
	SRR1542405	PE	15.2G	Illumina HiSeq 2000
	SRR2306548	PE	5.5G	Illumina HiSeq 2500
	SRR1228254	PE	3.7G	Illumina HiSeq 2000
<i>Zea mays</i>	SRR2069900	PE	5.4G	Illumina HiSeq 2500
	SRR762350	SE	6.9G	Illumina Genome Analyzer IIx

*PE: Paired end, **SE: Single end