

## Supplementary Material to: “Genome-wide analysis of the transcriptional response to drought stress in root and leaf of common bean”

**Table S2** Information of raw sequence derived from each library sequenced on the Illumina HiSeq and Illumina Genome Analyzer II platforms including the total number of reads, and the paired-end (2x150bp) and single-end total resulting reads after the quality control (QC) data.

Library	Genotype	Tissue	Physiol. treatment	N° of raw paired-end reads	Total of reads	Paired-end reads remaining	% of paired-end reads remaining	Single-end reads remaining	Total of reads remaining	% of reads remaining (Total)	Discarded reads	% of discarded reads
<b>Illumina Genome Analyzer II</b>												
Lib01	BAT 477	root	0 min	14347428	11621328	11186032	80.71%	2666004	10330824	87.51%	3697682	3.73%
Lib02	BAT 477	root	75 min	4168237	17475314	3318208	79.96%	721361	15473837	87.26%	3656788	4.50%
Lib03	BAT 477	root	150 min	17394311	20910150	13754688	78.49%	3039320	18309586	88.63%	2773852	17.92%
Lib04	BAT 477	leaf	0 min	17505097	8336474	13709575	79.61%	3218579	7357777	88.55%	2001477	20.93%
Lib05	BAT 477	leaf	75 min	12202546	35010194	9781481	78.32%	2068278	30637729	88.26%	978697	24.01%
Lib06	BAT 477	leaf	150 min	8336865	16673730	2357296	28.28%	5033085	9747677	58.46%	6926053	41.54%
Lib07	Pérola	root	0 min	6499354	12998708	5110795	78.64%	1163963	11385553	87.59%	1613155	12.41%
Lib08	Pérola	root	75 min	5810664	29610270	4689510	78.52%	951804	25912588	88.82%	1103664	42.94%
Lib09	Pérola	root	150 min	14805135	9874980	11625580	80.40%	2661428	8771316	87.81%	4239926	7.48%
Lib10	Pérola	leaf	0 min	8737657	28694856	6986533	77.97%	1500771	25038068	88.90%	1290504	31.82%
Lib11	Pérola	leaf	75 min	4937490	34788622	3969802	79.08%	831712	30548696	87.56%	2600564	13.27%
Lib12	Pérola	leaf	150 min	10455075	24405092	8205859	80.16%	1897868	21631240	87.51%	4372465	2.80%
<b>Total:</b>				<b>125199859</b>	<b>250399718</b>	<b>94695359</b>	<b>75.64%</b>	<b>25754173</b>	<b>215144891</b>	<b>85.92%</b>	<b>35254827</b>	<b>14.08%</b>
<b>Illumina HiSeq</b>												
Lib01	BAT 477	root	0 min	12122950	26664506	7924229	63.56%	2084395	19404767	74.01%	6034821	40.90%
Lib02	BAT 477	root	75 min	14135389	24817868	9179107	60.24%	2516610	17441307	73.96%	6313047	29.94%
Lib03	BAT 477	root	150 min	12891083	28393246	8665937	67.51%	2192479	21577525	72.47%	5937525	36.34%
Lib04	BAT 477	leaf	0 min	14398137	28270778	9189312	64.94%	2580275	20874824	70.28%	7376561	25.44%
Lib05	BAT 477	leaf	75 min	10782705	28796274	6804553	63.82%	2018779	20958899	73.84%	7395954	26.09%
Lib06	BAT 477	leaf	150 min	12263336	24526672	8271060	67.45%	2062933	18605053	75.86%	5921619	24.14%
Lib07	Pérola	root	0 min	17787446	35574892	11612045	65.28%	3108273	26332363	74.02%	9242529	25.98%
Lib08	Pérola	root	75 min	13332253	23220140	8474461	64.88%	2455845	17185319	74.29%	9497030	16.94%
Lib09	Pérola	root	150 min	11610070	36933750	7532519	65.47%	2120281	27436720	75.73%	6257813	26.44%
Lib10	Pérola	leaf	0 min	12408934	24245900	7474747	65.37%	2491813	17932853	72.77%	7259739	22.63%
Lib11	Pérola	leaf	75 min	18466875	25782166	12090958	67.22%	3254804	19524353	76.00%	6815721	20.91%
Lib12	Pérola	leaf	150 min	14196623	21565410	9583566	63.11%	2410393	15627885	72.78%	7837375	25.68%
<b>Total:</b>				<b>164395801</b>	<b>328791602</b>	<b>106802494</b>	<b>64.97%</b>	<b>29296880</b>	<b>242901868</b>	<b>73.88%</b>	<b>85889734</b>	<b>26.12%</b>