

# The transcriptome of *A.crassus*: Evaluating a method of combining assemblies

Emanuel Heitlinger

## 1 Overview

The pre-processed *A. crassus* data-set consisting of 100491819 bases in 353055 reads (58617 generated using “FLX-chemistry”, 294438 using “Titanium-chemistry”) was assembled following an approach proposed by [1]: two assemblies were generated, one using Newbler v2.6 [2], the other using Mira v3.2.1 [3]. The resulting assemblies (referred to as first-order assemblies) were merged with Cap3 [4] into a combined assembly (referred to as second-order assembly).

## 2 The Newbler first-order assembly

During transcriptome-assembly (with options `-cdna -urt`) Newbler can split individual reads spanning the breakpoints of alternate isoforms, to assemble e.g. the first portion of the reads in one contig, the second portion in two different contigs. Later multiple so called isotigs would be constructed and reported, one for each putative transcript-variant. While this approach could be helpful for the detection of alternate isoforms, it also produces short contigs (especially at error-prone edges of high-coverage transcripts) when the building of isotigs fails. The read-status report and the assembly output in ace-format the program provides are including short contigs only used during the assembly-process, but not reported in the contigs-file used in transcriptome-assembly projects (454Isotigs.fna). Therefore to get all reads not included in contigs (i.e. a consistent definition of “singleton”) it was necessary to add all reads appearing only in contigs not reported in the fasta-file to the reported singletons. The number of singletons increased in this step from the 26211 reported to 109052. We later also address the usefulness of Newbler’s report vs. the expanded singleton-category, but for the meantime we define singletons as all reads not present in a given assembly.

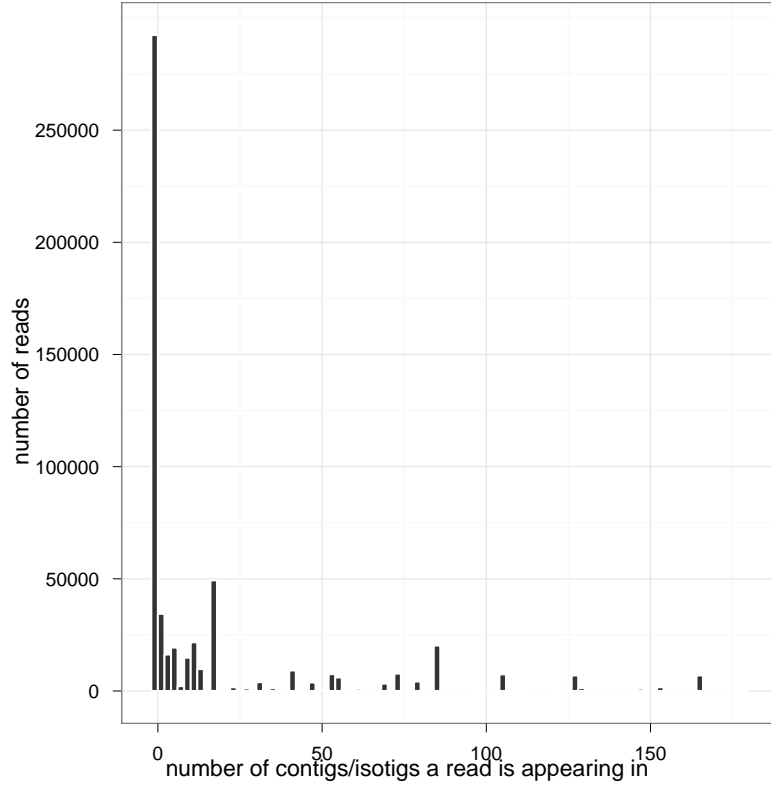


Figure 1: A histogram of the number of contigs/isotigs Newbler splitted one read into.

As mentioned above, the splitting of reads in the Newbler assembly can give useful information on possible isoforms, however, the number of contigs **Newbler** split one read into (in some cases more than 100 contigs) seems artificially inflated (see figure 1). If information would correspond to real isoforms it should be about an order of magnitude lower. This fact emphasises the need for further processing of the contigs. The maximum number of read-splits in a given contig and its usefulness will be discussed later in greater detail.

### 3 The Mira-assembly and the second-order assembly

The Mira assembly (with options `-job=denovo,est,accurate,454`) provided a second estimate of the transcriptome. In this assembly individual reads are

not split. The number of reads not used in the Mira-assembly was 65368.

To combine the two assemblies Cap3 was used with default parameters and including the quality information from first-order assemblies. The remainder of this text deals with the exploratory analysis of how information from both estimates of the transcriptome are integrated into the final second-order assembly.

	Newbler	Mira	Second-order(MN)
Max length	6300	6352	6377
Number of contigs	15934	22596	14064
Number of Bases	8085922	12010349	8139143
N50	579	579	662
Number of contigs in N50	4301	6749	3899
non ATGC bases	375	29962	5245
Mean length	508	532	579

Table 1: Basic statistics for the first-order assemblies and the second-order assembly (for which only the most reliable category of contigs is shown efsec:data-categ-second)

Table 1 gives basic summary-statistics of the different assemblies. Mira clearly produced the biggest assembly, both in terms of number of contigs and bases), the second-order assembly is slightly smaller size than the Newbler assembly. The second-order assembly had on average longer contigs than both first-order assemblies and a higher weighted median contig size (N50).

## 4 Data-categories in the second-order assembly

Three main categories of assembled sequence data can be distinguished in the second-order assembly, each one with different reliability and purpose in downstream applications:

The first category of data obtained are the singletons of the final second-order assembly. It comprises raw sequencing reads that neither of the first-order assemblers used. It is therefore the intersecion of the Newbler-singletons (as defined in 2) and the Mira-singletons. 47669 reads fell in this category. A second category of sequence contains the first-order contigs, that could not be assembled in the second-order assembly (the singletons in the Cap3-assembly; M\_1 and N\_1 in table 2). Furthermore second-order contigs in which first-order contigs from only one assembler are combined (M\_n and N\_n in table 2) also have to be included in this category. Sequences in this category should be considered only moderately reliable as they are supported by only one assembly algorithm.

Finally the category of contigs considered most reliable contains all second-order contigs with contribution from both first-order assemblies (MN in table 2).

	M_1	M_n	MN	N_n	N_1
Snd.o.con		164	13887	13	
Fst.o.con	2347	897	mira=19352/Newbler=14410	40	1484
reads	42172	21153	one=269868/both=193308	1538	13100

Table 2: **Number of reads, first-order contigs (Fst.o.con) and second-order contigs (Snd.o.con) for different categories of contigs (M\_1 and N\_1 = first-order contigs not assembled in second-order assembly, from mira and newbler respectively; M\_n and N\_n = assembled in second-order contigs only with contigs from the same first-order assembly; MN = assembled in second-order contigs with first order contigs from both first order assemblies**

For this last, most reliable (MN) category, reads contained in the assembly can be categorised depending on whether they entered the assembly via both or only via one first-order assembly.

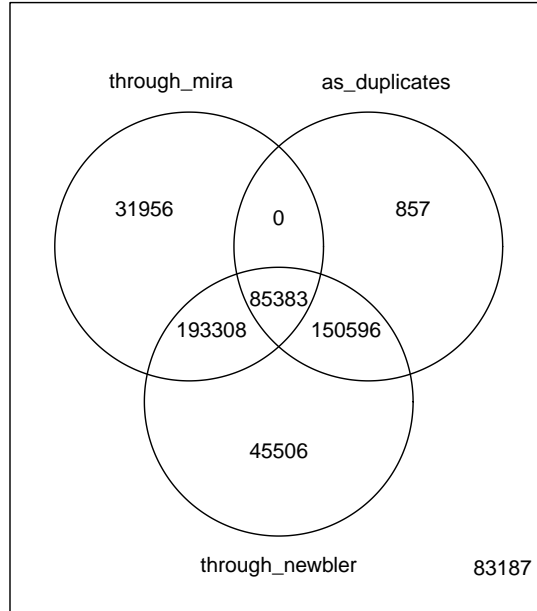


Figure 2: The way of reads into the most reliable (MN) assembly-category

Figure 2 gives a more detailed view of the fate of the reads Newbler splited during first-order assembly. Interestingly most reads Newbler splited ended in the high-quality category of the second order assembly.

## 5 Contribution of first-order assemblies to second-order contigs

Looking at the contribution of contigs from each of the assemblies to one second-order contig in figure 3a it becomes clear, that the Mira-assembly had a high number of redundant contigs. These were assembled into the same contig by Newbler and finally also in one second-order contig by Cap3.

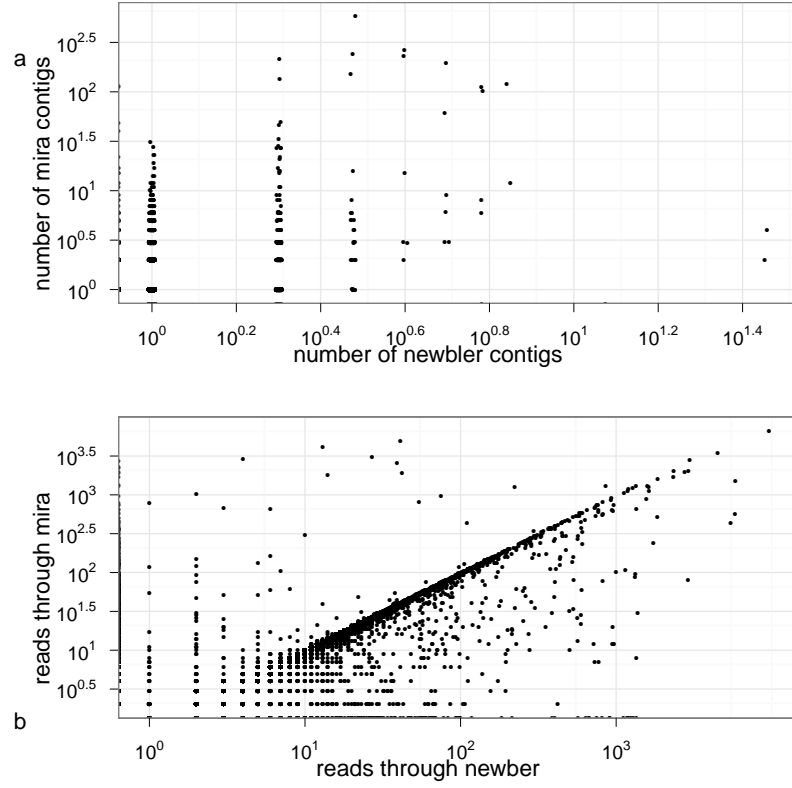


Figure 3: Number of first-order contigs from both first-order assemblies for each second order contig (a) number of reads through Newbler and Mira for each second-order contig (b)

A different picture emerges from the contribution of reads through each of the first-order assemblies (figure 3b). Here, for most second-order contigs many more reads are contributed through Newbler-contigs. This is because Newbler has more reads summed over all contigs caused by the duplication due to the splitting of reads.

## 6 Evaluation of the assemblies

To further compare assemblies (Mira or Newbler first-order assemblies including or excluding their singletons) and the second-order assembly (including different contigs-categories and singletons) we evaluated the number of bases or proteins their contigs and singletons (partially) cover in the related model-nematodes, *Caenorhabditis elegans* and *Brugia malayi*. To this purpose we used Blast (blastx e-value cut-off 1e-5) and a custom perl-script provided by S. Kumar.

In addition, the size of the assembly can give an indication of redundancy or artificially assembled data. If it increases without improving the reference-coverage the dataset is likely to contain more redundant or artificial information, a more parsimonious assembly should be preferred.

The database-coverage for the two reference species can then be plotted against the size of the assembly-dataset to estimate the completeness conditional to the size of the assembly (figures 4, 5, 6).

From the assemblies excluding singletons (in the lower left corner with lower size and database-coverage) the highly reliable contig-category of the second-order assembly produced the highest per-base coverage in both reference-species, with the Newbler assembly on a second place and Mira producing the lowest reference-coverage. When adding the contigs considered lower quality supported by only one assembler to the second-order assembly the reference-coverage increased moderately.

Including singletons the Mira and Newbler assemblies were of increased size. A comparison of the Newbler's reported singletons with all singletons added to the Newbler-assembly shows, that the reported singletons increased reference-coverage to the same amount than all singletons, while the non-reported singletons only increased the size of the assembly. It can be concluded, that the latter contain hardly any additional information but only error-prone or variant reads.

The second-order assembly including the intersection of first-order singletons performed similar to the Newbler assembly for the number of bases covered, but was larger in size. Adding the less reliable set of one-assembler supported second-order-contigs the assembly covered the most bases in both references. When not the singleton of the second-order assembly (as defined in 2) but the intersection of Newbler's "reported singletons" and Mira's singletons were considered a very parsimonious assembly with high reference-coverage (termed fullest assembly; and labeled FU in the plots above) was obtained.

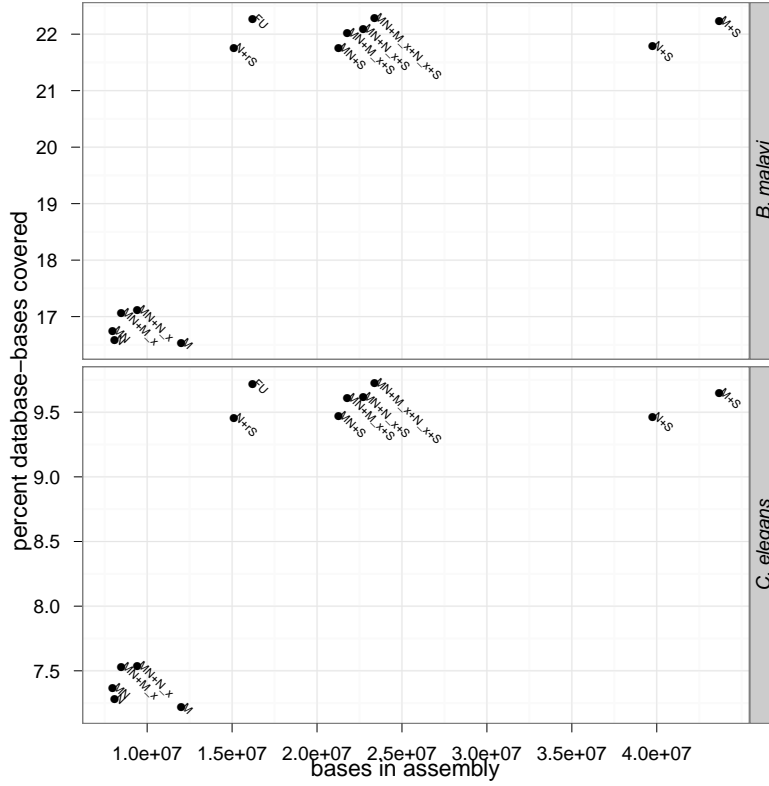


Figure 4: Base-content and reference-transcriptome coverage (in bases) for different assemblies and assembly-combinations (M = Mira; N = Newbler;  $M + S$  = Mira + singletons;  $N + S$  = Newbler plus singletons;  $N + Sr$  = Newbler plus singletons reported in readstatus.txt; MN = second-order contigs supported by both first-order;  $MN + N_x$  = second-order MN plus contigs only supported by Newbler ( $N_x = N_n$  and  $N_1$ );  $MN + M_x$  = same for Mira-first-order-contigs;  $MN + M_x + S$  and  $MN + N_x + S$  same with singletons; FU = second-order contigs supported by both or one assembler plus the intersection of Newbler reported singletons and Mira-singletons = the basis for the “fullest assembly” used in later analyses)





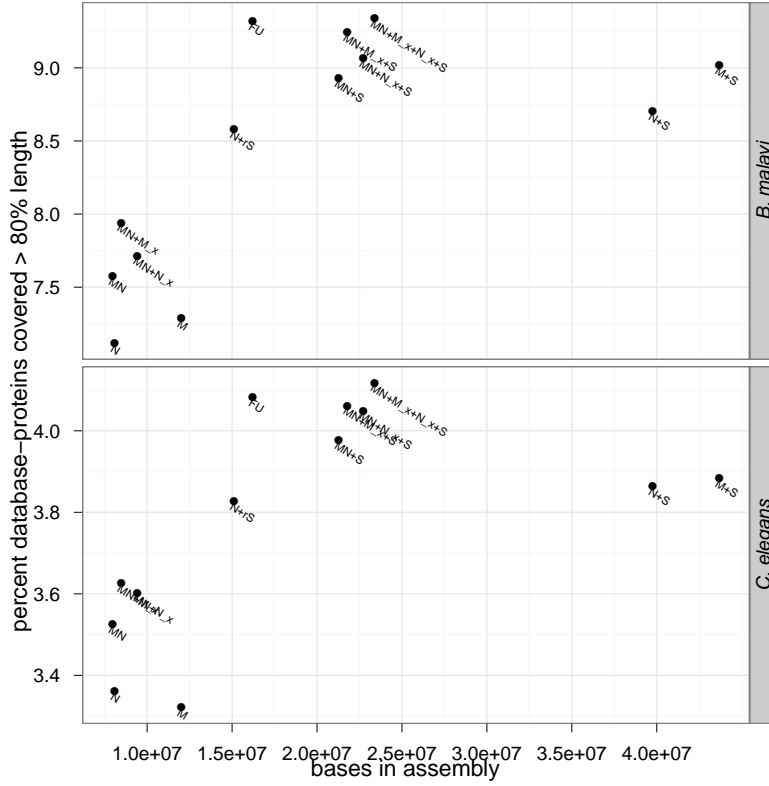


Figure 6: Base-content and reference-transcriptome coverage in percent of proteins covered to at least 80% of their length for different assemblies and assembly-combinations (for category-abbreviations see Figure 4)

When database-proteins covered for at least to 80% of their length are considered the second-order assembly showed its superiority: Both ex- and including singletons the second-order assembly outperformed the first-order assemblies. Moderate gains in reference coverage were made again for the addition of dubious single-assembler supported second-order contigs. We give most weight in our analysis to these results as in average longer correct contigs will allow finding the highest number of putative full-length genes.

Given this evaluation we defined a “minimal adequate” assembly as the subset of contigs of the second-order assembly supported by both assemblers (labeled MN above). Given the performance of the singletons **Newbler** reported. We defined a “fullest-assembly” as all second-order contigs (including those supported by only one assembler) plus the intersection of reported **Newbler**-singletons and **Mira** singletons.

## 7 Measurments on second-order assembly

Based on the tracking of reads through the complicated assembly process, we calculated the following statistics for each contig in the second-order assembly.

- number of Mira and Newbler first-order contigs
- number of reads through Mira and reads through Newbler
- number of reads being split by Newbler in first-order assembly
- number of read-split events in the first-order assembly (equals the sum of reads multiplied by number of contigs a read has been split into)
- maximal number of first-order contigs a read in the contig has been split into during Newbler-assembly
- the number of reads same-read-paires from the Newbler and Mira first order-assembly merged in a second order contig
- cluster-id of the contig: All contigs “connected” by sharing reads (similar to the graph clustering reported in [5]).
- number of other second order contigs containing the same read (size of the cluster)

### 7.1 Contig coverage

```
null device
      1
```

```
null device
      1
```

As well defined coverage-information is not readily available from the output of this combined assembly approach (although we followed individual reads through the process) we inferred coverage by mapping the reads used for assembly against the fullest assembly using ssaha2 [6] with parameters (-kmer 13 -skip 3 -seeds 6 -score 100 -cmatch 10 -ckmer 6 -output sam -best 1):

- mean per base coverage

- mean unique per base coverage

The ratio of mean per base coverage and unique per base coverage (the standard for assessing coverage) can be used as to asses the redundancy of a contig.

## 7.2 Example use of the contig-measurements

Based on these measurements the emergence of a given contig from the assembly process can be reconstructed. Table 3 gives an excerpt of the contig-measurements reported in additional-file contig-data.csv. The example contigs are all from large contig-clusters (cluster.size), where interpretation of the assembly history is complicated, but not impossible:

	Contig1047	Contig10719	Contig104	Contig13672
reads_through_Newbler	16	1351	0	14
reads_through_Mira	26	651	135	0
Newbler_contigs	1	5	0	2
Mira_contigs	1	9	4	0
category	MN	MN	M_n	N_n
num.new.split	8	1314	0	0
sum.new.split	16	2628	0	0
max.new.split	2	2	0	0
num.SndO.pair	13	644	0	0
cluster.id	CL62	CL6	CL176	CL235
cluster.size	24	18	5	5
coverage	4.200342	267.495458	41.003369	2.920755
uniq_coverage	4.248960	7.425507	2.568000	1.196078

Table 3: example table for assembly-measurements on contigs (as given in contig-data.csv)

**Contig1047** is in the well trusted MN category of contigs. It consists of only one contig from each first-order assembly (newbler\_contigs and mira\_contigs), each containing a set of reads of moderate size: 16 from Newbler (reads\_through\_newbler) 26 from Mira (reads\_through\_mira). 8 of the 16 reads Newbler used in its one assembled contig were also assembled to a differnt Newbler-contig (num.new.split). That each of the 8 reads was only appearing in one other Newbler-contig is visible from the fact, that the number of split events is 16 (sum.new.split) and the maximal number of splits for

one read is 2 (max.new.split). 13 (num.SndO.pair) same-read-pairs from the two different first-order assemblies were merged in this second-order contig, leaving 3 (16-13) reads in Newbler-contigs and 13 (26-13) reads in Mira contigs, which all could potentially have ended up in other contigs. The contig is in a cluster (CL62), which contains in total 24 contigs (cluster.size). It has to be admitted that the whole graph-structure linking this 24 contigs can't be reconstructed from this contig summary data. On the other hand the summary data makes clear, from what source the links for cluster-affiliation have resulted: In this case from 3 and 13 unlinked read-pairs from both first-order assemblies and 8 split-reads from Newbler-first order contigs.

A comprehensive interpretation of the other example-contigs depicted is left to the reader. It should just be remarked, that in case of one-assembler supported contigs, all reads in that contig could potentially be represented in other contigs, making average cluster-size in these contigs bigger than in MN category.

One of the most interesting measurement calculated for each contig is the cluster-membership and cluster-size. Such clusters can represent close paralogs, duplicated genes, isoforms from alternative splicing or allelic variants.

These measurements can be used in later analysis to e.g. reevaluate the likelihood of misassembly in a given set of biologically relevant contigs. All gene-sets mentioned later (in chapter the main text) were thus, as a matter of routine, controlled for unusual patterns in the contig meta-data.

## 8 Finalising the fullest assembly set

In order to minimize the amount of sequence with artificially inferred isoform-breakpoints we used the unique-mapping-information described above to detect contigs and singletons not supported by any raw data (reads). Table 4 gives a summary of these unsupported data by contig-category. For all downstream-analysis we removed the all well trusted MN-category-contigs no coverage and the contigs (and singletons) from other categories having no unique coverage.

Thereby we reduced our dataset to 40,187 tentative unique genes (TUGs), redefining the “fullest assembly” dataset. Based on the above evaluation we decided to treat the MN-category of contigs as high credibility assembly (highCA) and to subsume the M\_n, N\_n, M\_1, N\_1 and **Newbler's** reported singletons as additional low credibility assembly (lowCA).

	singletons	M_1	M_n	MN	N_1	N_n
coverage == 0	546	34	2	36	158	0
unique coverage == 0	584	48	2	42	210	3

Table 4: number of contigs with a coverage and unique-coverage of zero, inferred from mapping of raw reads, listed by contig-category

## References

- [1] Kumar S, Blaxter ML: **Comparing de novo assemblers for 454 transcriptome data**. *BMC Genomics* 2010, **11**:571, [<http://dx.doi.org/10.1186/1471-2164-11-571>].
- [2] Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM: **Genome sequencing in microfabricated high-density picolitre reactors**. *Nature* 2005, **437**:376–380, [<http://dx.doi.org/10.1038/nature03959>].
- [3] Chevreux B, Pfisterer T, Drescher B, Driesel AJ, Muller WE, Wetter T, Suhai S: **Using the miraEST assembler for reliable and automated mRNA transcript assembly and SNP detection in sequenced ESTs**. *Genome Res.* 2004, **14**:1147–1159, [<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC419793>].
- [4] Huang X, Madan A: **CAP3: A DNA sequence assembly program**. *Genome Res.* 1999, **9**:868–877, [<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC310812>].
- [5] Schwartz TS, Tae H, Yang Y, Mockaitis K, Van Hemert JL, Proulx SR, Choi JH, Bronikowski AM: **A garter snake transcriptome: pyrosequencing, de novo assembly, and sex-specific differences**. *BMC Genomics* 2010, **11**:694, [<http://www.ncbi.nlm.nih.gov/pubmed/21138572>].

- [6] Ning Z, Cox AJ, Mullikin JC: **SSAHA: a fast search method for large DNA databases**. *Genome Res.* 2001, **11**:1725–1729, [<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC311141>].