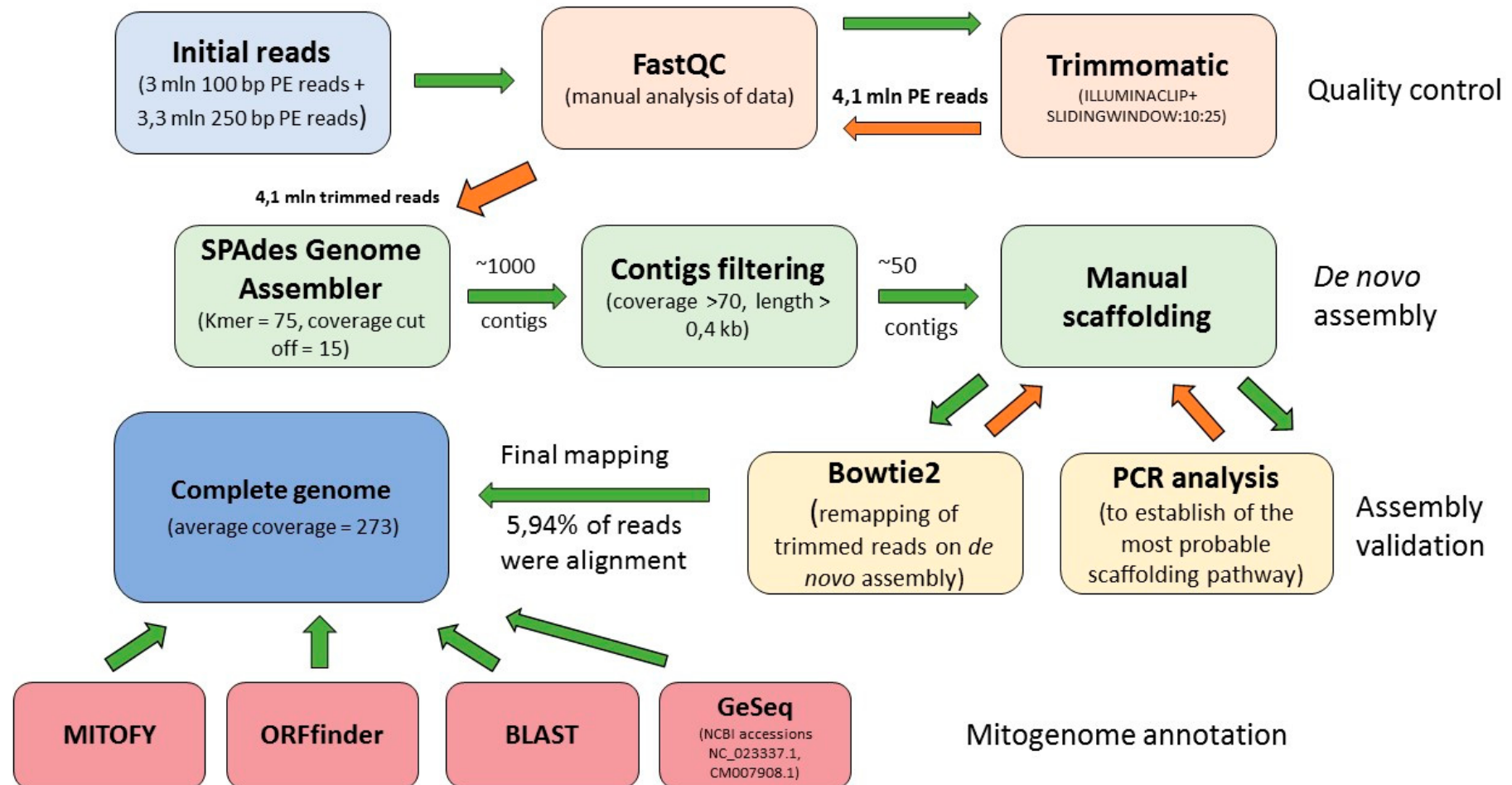


Suppl Figure 1. Bioinformatic pipeline for mitochondrial genome analysis. Trimmed reads are available at <https://doi.org/10.6084/m9.figshare.8945084.v1>.



Suppl Table 1. The primers sets used for transcription activity analysis.

Gene	Forward Primer Sequence (5'-3')	Reverse Primer Sequence (5'-3')	The Amplicon Size (bp) in HA89 Male-Fertile Line	The Amplicon Size (bp) in HA89(ANN2) Male-Sterile Line
<i>orf324</i>	GAACCACCTTTTCGCTAACCT	CATCGACTTGAGAATTTGCCTC	-	101
<i>orf327</i>	GGGGATCAGTACAAGACGGC	GCAAGCATTAAAGCCGTCGAA	-	114
<i>orf345</i>	GCTTTTGCCCATGCCATGAA	TCCCGGTAATTCCTTCCCCT	-	135
<i>orf558</i>	CCCGAATCGCTCGGTAAGAG	TTTCACTGCTACGCCAGCTT	-	134
5'	ACTTCTTCGTGAATCTCCGCT	TTCCCATCCCAGTCTTTTCGC	163	163
<i>nad6/orf891</i>				
3' <i>nad6</i>	CAAGCCTGGACCCGCTATAC	TGGGAGGTCGGGGTATTCAA	94	-
3' <i>orf891</i>	CAAGCCTGGACCCGCTATAC	TGGAGAGTTTCCGTGTAGAAGA	-	_*
<i>orf933</i>	AGCACTTTGGGCATTCCGT	ACAAGGGTTGGACCATCAGG	-	126
<i>orf1197</i>	AGTGGGCTAGGTACCACCAT	AAGCTTGACTCTATGCGCCA	-	140
<i>atp1</i>	CCCATGGCACAGCCAGAATA	CAGAAACGCTCAACTGTGGC	140	140

*151 bp amplicon was expected.

Suppl Table 2. The protein coding genes annotated in HA89(ANN2) mitochondrial genome.

Gene Name	Gene Features	Position in HA89(ANN2) Mitogenome	Orientation
	Complex I		
<i>nad1</i>	Encoding NADH-ubiquinone oxidoreductase chain 1. Trans-spliced gene, counting 4 exons	exon1 277278..277664	Plus

		exon2 41187..41267	Minus
		exon3 40142..40399	Minus
		exon4 109446..109697	Minus
		exon 1 130673..130876	Plus
<i>nad2</i>	Encoding NADH-ubiquinone oxidoreductase chain 2. Trans-spliced gene, counting 4 exons	exon 2 132080..132430	Plus
		exon 3 4997..5158	Minus
		exon 4 2049..2693	Minus
<i>nad3</i>	Encoding NADH-ubiquinone oxidoreductase chain 3	114556..114912	Plus
<i>nad4</i>	Encoding NADH-ubiquinone oxidoreductase chain 4. Gene consists of 2 exons	exon 1 226998..228021	Minus
<i>nad4L</i>	Encoding NADH-ubiquinone oxidoreductase chain 4L	exon 2 229483..229943	Minus
		28690..28962	Minus
		exon1 104046..104243	Minus
<i>nad5</i>	Encoding NADH-ubiquinone oxidoreductase chain 5. Trans-spliced gene, counting 4 exons	exon 2 105116..105511	Minus
		exon 3 293119..294333	Minus
		exon4 295182..295409	Minus
		exon1 198509..198677	Plus
<i>nad7</i>	Encoding NADH-ubiquinone oxidoreductase chain 7. Gene consists of 4 exons	exon2 201101..201542	Plus
		exon3 202607..202853	Plus
		exon4 204591..204905	Plus
<i>nad9</i>	Encoding NADH-ubiquinone oxidoreductase chain 9	120750..121322	Plus
	Complex III		
<i>cob</i>	Encoding cytochrome <i>b</i>	172018..173211	Minus
	Complex IV		
<i>cox1</i>	Encoding cytochrome <i>c</i> oxidase subunit 1	287502..289196	Plus
<i>cox2</i>	Encoding cytochrome <i>c</i> oxidase subunit 2. Gene consists of 2 exons	exon1 156440..156873	Plus
<i>cox3</i>	Encoding cytochrome <i>c</i> oxidase subunit 3	exon2 158160..158604	Plus
	Complex V	218657..219454	Plus
<i>atp1</i>	Encoding ATP synthase subunit 1	215911..217443	Plus
<i>atp4</i>	Encoding ATP synthase subunit 4	27935..28510	Minus
<i>atp8</i>	Encoding ATP synthase subunit 8	217608..218087	Plus
<i>atp9</i>	Encoding ATP synthase subunit 9	76854..77153	Plus

Cytochrome c biogenesis			
<i>ccmB</i>	Encoding cytochrome <i>c</i> biogenesis B	247143..247763	Plus
<i>ccmC</i>	Encoding cytochrome <i>c</i> biogenesis C	15296..16039	Plus
<i>ccmFC</i>	Encoding cytochrome <i>c</i> biogenesis FC. Gene consists of 2 exons	exon1 168065..168833	Minus
		exon2 169479..170329	Minus
<i>ccmFN</i>	Encoding cytochrome <i>c</i> biogenesis FN	205193..206911	Plus
Ribosomal protein			
<i>rpl5</i>	Encoding ribosomal protein L5	223773..224336	Minus
<i>rpl10</i>	Encoding ribosomal protein L10	248071..248559	Minus
<i>rpl16</i>	Encoding ribosomal protein L16	90552..91067	Plus
<i>rps3</i>	Encoding ribosomal protein S3	88985..90661	Plus
<i>rps4</i>	Encoding ribosomal protein S4	68382..69377	Minus
<i>rps11</i>	Encoding ribosomal protein S11	289608..290027	Plus
<i>rps12</i>	Encoding ribosomal protein S12	114964..115341	Plus
<i>rps13</i>	Encoding ribosomal protein S13	42094..42444	Minus
Gene with other functions and conservative ORFs with unknown function			
<i>mttB</i>	Encoding protein translocase component TatC. Gene consists of 2 exons	exon1 182524..183276	Minus
		exon2 183749..183784	Minus
<i>matR</i>	Encoding intron maturase	110473..112440	Minus
<i>orf873</i>	Conservative ORF with unknown function. *According to genomic data has premature codon resulted in shorter transcript (orf618). However RNA editing may be involved, resulting in normal transcript	170474..171094*	Minus
Newly detected ORFs			
<i>orf324</i>	ORF with unknown function	77915..78241	Minus
<i>orf327</i>	ORF with unknown function	84497..84826	Minus
<i>orf345</i>	ORF with unknown function	149669..150016	Minus
<i>orf558</i>	<i>cox2</i> -chimeric gene, encoding protein with transmembrane domain	295955..296515	Minus
<i>orf891</i>	<i>nad6</i> -chimeric gene, encoding protein with transmembrane domains	192053..192946	Plus
<i>orf933</i>	ORF with unknown function, encoding protein with transmembrane domains	82591..83526	Minus
<i>orf1197</i>	<i>atp6</i> -chimeric gene, encoding protein with transmembrane domains	146967..148166	Minus