

**Supplementary Table S1. QUAST statistics about AAI genome.** In the table are indicated information about AAI genome assembly characteristics that include number of contigs, GC percentage, genome size, N50-75, L50-75. The sequencing coverage has been calculated as follows: coverage (reads nr. \* reads length)/genome size).

<b>AAI assembly characteristics</b>	
Coverage	383
contigs ( $\geq 0$ bp)	58
contigs ( $\geq 1000$ bp)	46
contigs ( $\geq 5000$ bp)	40
contigs ( $\geq 10000$ bp)	37
contigs ( $\geq 25000$ bp)	27
contigs ( $\geq 50000$ bp)	22
Total length ( $\geq 0$ bp)	4101808
Total length ( $\geq 1000$ bp)	4095819
Total length ( $\geq 5000$ bp)	4082350
Total length ( $\geq 10000$ bp)	4060871
Total length ( $\geq 25000$ bp)	3904567
Total length ( $\geq 50000$ bp)	3713911
Contigs nr. ( $> 500$ bp)	53
Largest contig	519866
Total length	4100139
GC (%)	64.99
N50	168583
N75	103839
L50	7
L75	14