Supplemental Table S2. Read coverage and single nucleotide polymorphisms determined by mapping reads from individual MDA sets to the *de novo* assembled contigs generated from MDA3. There were 3 SNPs shared in all MDAs limited to the 41% of the MDA3 contigs covered by MDA1 reads.

	% of Reference[a] Covered	# SNPs Within CDS	# of Genes with SNPs[a]	# of Missense	Shared SNPs		
					MDA1	MDA2	MDA3
MDA1	41	74	15	37	-	10	5
MDA2	94	39	16	14	10	-	6
MDA3	100	19	16	12	5	6	-

[a] Reference is the de novo assembled contigs from MDA3.
[b] the number of genes that had one or more SNPs.