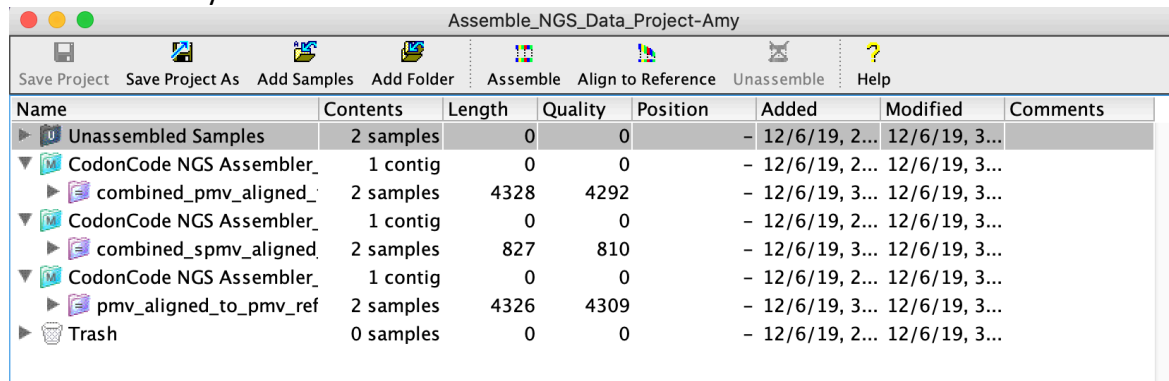


CodonCodeAligner How-To:

1. Download & install CodonCode Aligner:
<https://www.codoncode.com/aligner/download.htm>
2. Open a new Project: File > New Project
3. Upload fastq files by clicking on the 'Add Samples' button and selecting files through file browser.
4. Assemble by Tools > Assemble NGS Data > CodonCode NGS Assembler



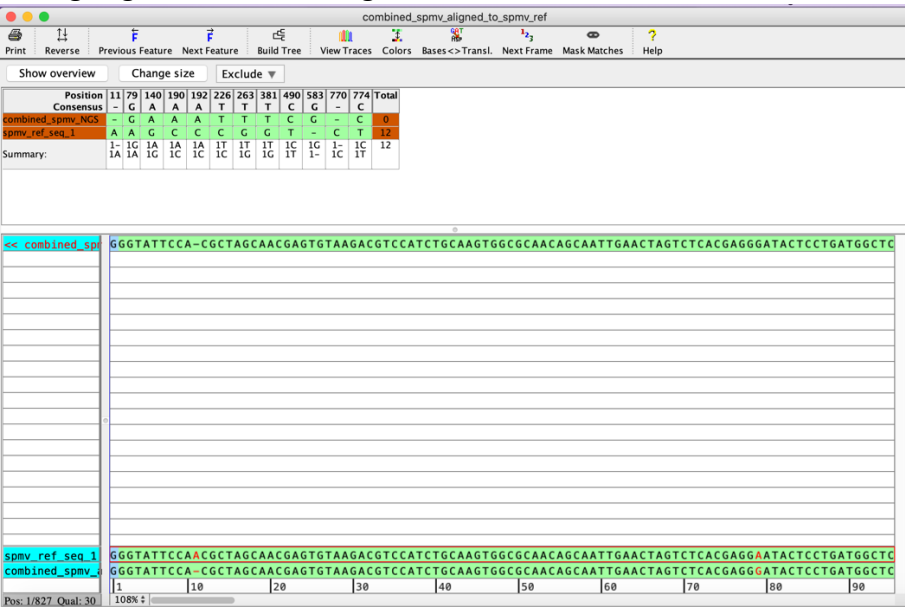
Name	Contents	Length	Quality	Position	Added	Modified	Comments
Unassembled Samples	2 samples	0	0	-	12/6/19, 2...	12/6/19, 3...	
CodonCode NGS Assembler_	1 contig	0	0	-	12/6/19, 2...	12/6/19, 3...	
combined_pmv_aligned_	2 samples	4328	4292	-	12/6/19, 3...	12/6/19, 3...	
CodonCode NGS Assembler_	1 contig	0	0	-	12/6/19, 2...	12/6/19, 3...	
combined_spmv_aligned_	2 samples	827	810	-	12/6/19, 3...	12/6/19, 3...	
CodonCode NGS Assembler_	1 contig	0	0	-	12/6/19, 2...	12/6/19, 3...	
pmv_aligned_to_pmv_ref	2 samples	4326	4309	-	12/6/19, 3...	12/6/19, 3...	
Trash	0 samples	0	0	-	12/6/19, 2...	12/6/19, 3...	

5. View Contigs by double clicking on the file.

Contig:

1	GGGTATTCCA	ACGCTAGCAA	CGAGTGTAAG	ACGTCCATCT	GCAAGTGGCG	CAACAGCAAT
61	TGAAGTAGTC	TACAGAGGAA	TACTCCTGAT	GGCTCCTAAG	CGTTCCAGGC	GATCTAATCG
		SmaI		BstXI		
121	TCGGGCGGGC	TCCCGGGCTG	CTGCCACATC	ACTGGGTGAC	GATACGTGCT	ACGTCACCTT
181	GACGGAGCGC	GCTACTACCT	CTTTTCAGAG	GCAGAGTTTC	CCGACCTCA	AGGGGATGGG
241	GGACCGTGCA	TTCCAGGTTG	TCGCGTTTAC	AATCCAGGGG	GTGTCAGCAG	CCCCCCTGAT
		SmaI				
301	GTATAACGCG	CGCCTGTATA	ACCCGGGCGA	CACAGACTCT	GTCCATGCCA	CCGGGGTACA
361	GTTGATGGGC	ACAGTCCCTA	GGACCGTTTC	GCTCACCCTT	AGGGTGGGCC	AGAACAACCTG
					XmiI	
421	GTTCTTTGGT	AACACTGAAG	AAGCCGAGAC	CATTTTGGCC	ATCGACGGAC	TCGTGTCTAC
481	CAAGGGTGCT	AACGCCCCCA	GCAATACCGT	CATTGTTACG	GGTTGCTTTA	GGCTGGCGCC
541	TAGCGAGCTT	CAGTCTTCAT	AAAGTATCCC	CCTCTTATGG	GG-TGTCGCC	GTACACACCG
601	TTAGTCCCGC	GCCTCTACCG	GCTGTCGGAC	TCCTACCATG	CCCTCCGGTG	GATGTTGAGG
661	AAGTGGGGGA	ATCAGGAGGC	TACGAAGCCG	TCGCAGCAAA	GGCGACCGTG	TGTACAACCA
721	ACCCGGCCAG	AAATATACCC	CGAAAGGGGG	GGTCCTGCGG	CTGGGTCCCC	TTTCAATGG
		BstXI				
781	CAATGCCATT	TTCTTGGGGG	GAGATGCGTC	TCCCCCTCCT	AGGACCC	

Contig aligned to reference genome:



6. Export contigs to FASTA file: File > Export > Samples>Selected sample > FASTA format > Export