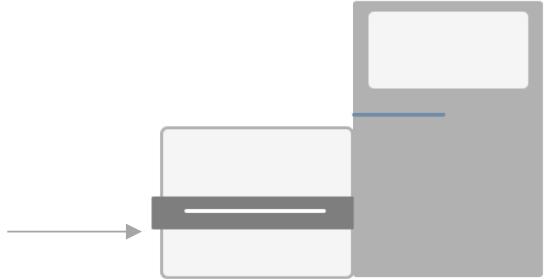
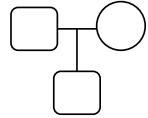


AJ Trio





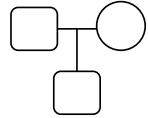
AJ Trio



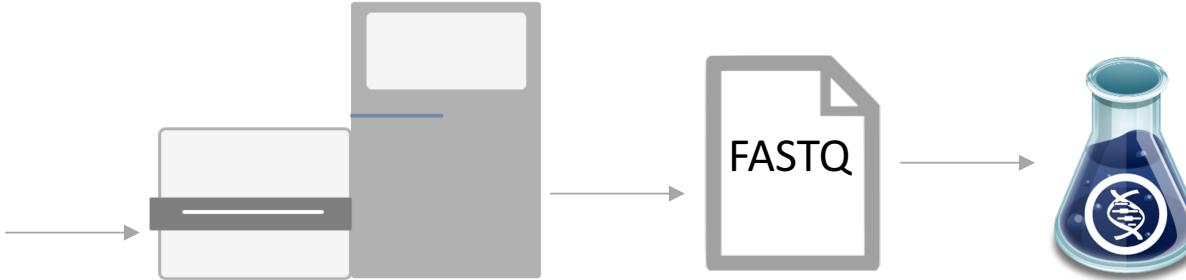
Technology	Lab	Library Type	Read Length [bp] (Mean)	Read Depth (Mean)
Illumina HiSeq 2500	NIST/Stanford	WGS Paired-End	2x148	296.83x
Illumina HiSeq 2500	NIST/Stanford	WGS Paired-End	2x250	40-50x
Illumina HiSeq 2500	NIST/Stanford	WGS mate-pair	2x100 [6000bp insert size]	13-14x
10X Genomics	10X Genomics	WGS Linked Reads	2x98	50x HG002 22x HG003 24x HG004
PacBio	NIST/ Mt. Sinai	WGS Single End	10-11Kb	69x HG002 30-32x HG003/HG004

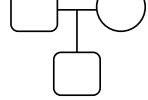


FASTQ

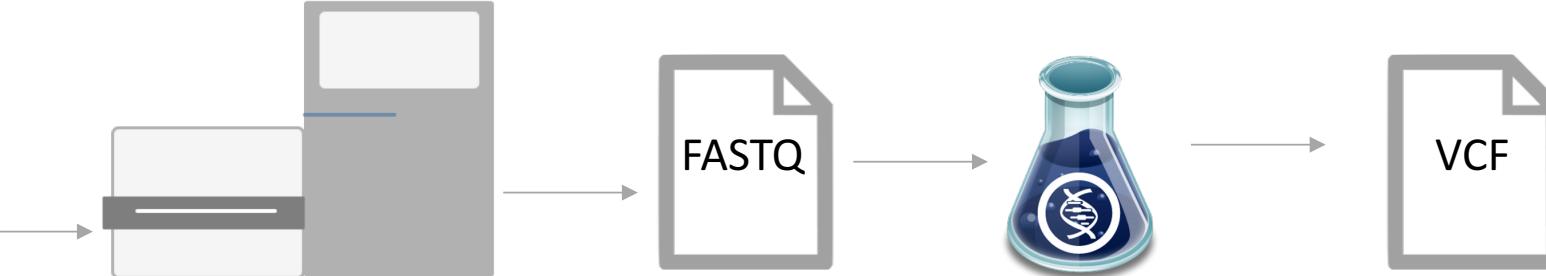


AJ Trio



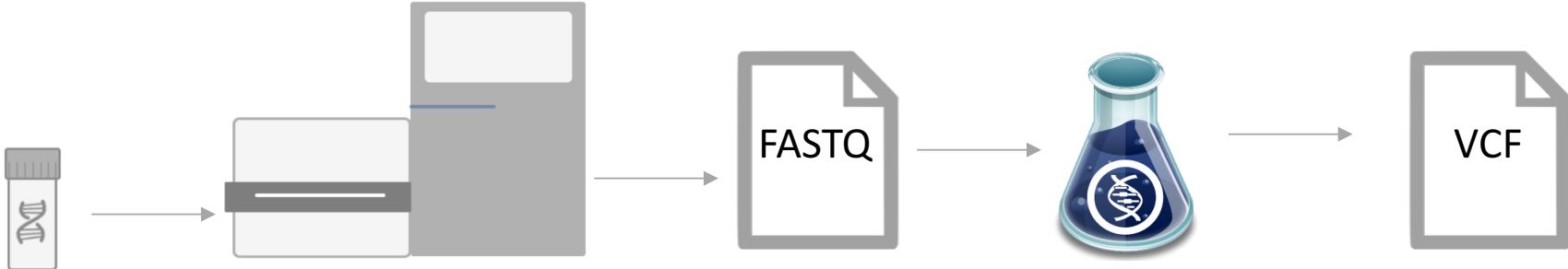
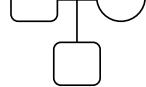


AJ Trio



30+ Variant Callers

Technology	Variant Caller
Illumina	<ul style="list-style-type: none">• Spiral• MetaSV• Fermikit
Complete Genomics	<ul style="list-style-type: none">• CG
PacBio	<ul style="list-style-type: none">• MSPacMon• Assemblytics
10X Genomics	<ul style="list-style-type: none">• Mapping based caller



AJ Trio



Sequence Resolved



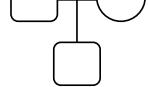
```
|10 81444005 HG2_Ill_GATKHC_20806 TGCAGATCATCTGCAACTTACGGAGGTACTTCCCCCACATGCCAGGAGGAGGCCCTGGCGGCAAGCAGGACCTGGACCC T 2696.73 . AC=1;AF=0.
5;AN=2;BaseQRankSum=-3.02;ClippingRankSum=1.51;DP=290;ExcessHet=3.0103;FS=2.819;MLEAC=1;MLEAF=0.5;MQ=69.38;MQRankSum=-1.108;QD=9.33;ReadPosRankSum=-3.2
75;SOR=0.608;SVTYPE=INS;END=81444088 GT:AD:DP:GQ:PGT:PID:PL 0/1:201,88:289:99:0|1:81443994_CCCGCAGAGG_C:2734,0,12765 83 1 DEL
```

Type	Size	Count
All	>=20bp	1,389,121
Sequence-resolved	>=20bp	1,183,270
Unique	>=20bp	509,452

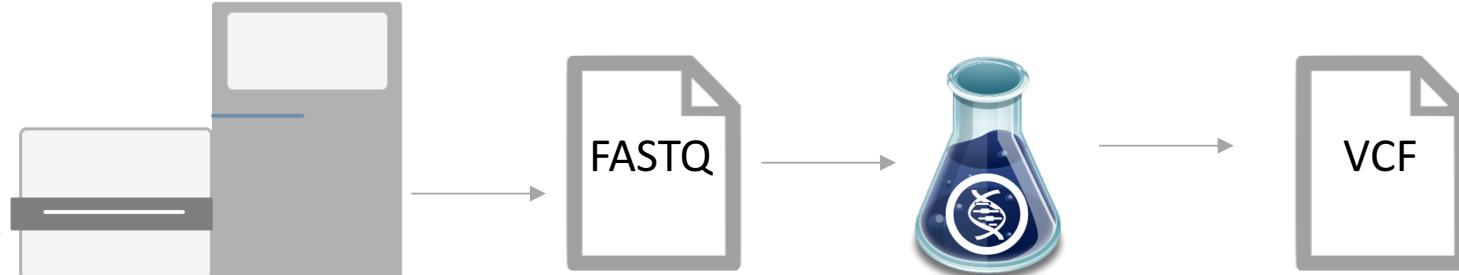
Non-Sequence Resolved



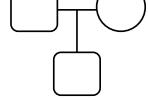
```
54 #CHROM POS ID REF ALT QUAL FILTER INFO FORMAT INTEGRATION
55 1 10105 . A C 5 allfilteredbutagree platforms=1;platform
me,SolidSE75bp;lowcov=CS HiSeqPE300xfreebayes_lowcov,CS_HiSeqPE300xG
```



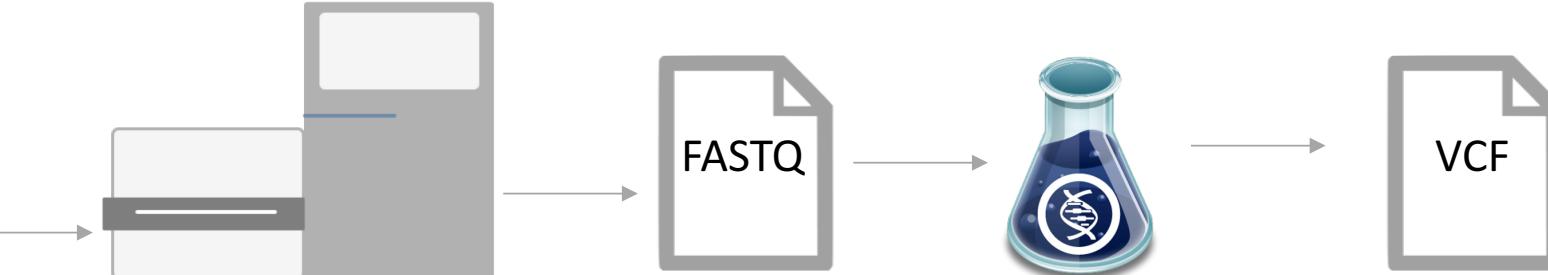
AJ Trio



Type	Size	Count
All	>=20bp	1,389,121
Sequence-resolved	>=20bp	1,183,270
Unique	>=20bp	509,452



AJ Trio



Type	Size	Count
All	>=20bp	1,389,121
Sequence-resolved	>=20bp	1,183,270
Unique	>=20bp	509,452

