

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013179.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:30:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,385,631
Mapped reads	2,136,822 / 89.57%
Unmapped reads	248,809 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,035 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	79,979 / 3.35%
Duplication rate	2.83%
Clipped reads	1,072,148 / 44.94%

2.2. ACGT Content

Number/percentage of A's	38,073,480 / 27.26%
Number/percentage of C's	26,602,984 / 19.05%
Number/percentage of T's	43,107,933 / 30.87%
Number/percentage of G's	31,840,636 / 22.8%
Number/percentage of N's	32,941 / 0.02%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.389
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2.4. Mapping Quality

Mean Mapping Quality	45.16
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2.5. Mismatches and indels

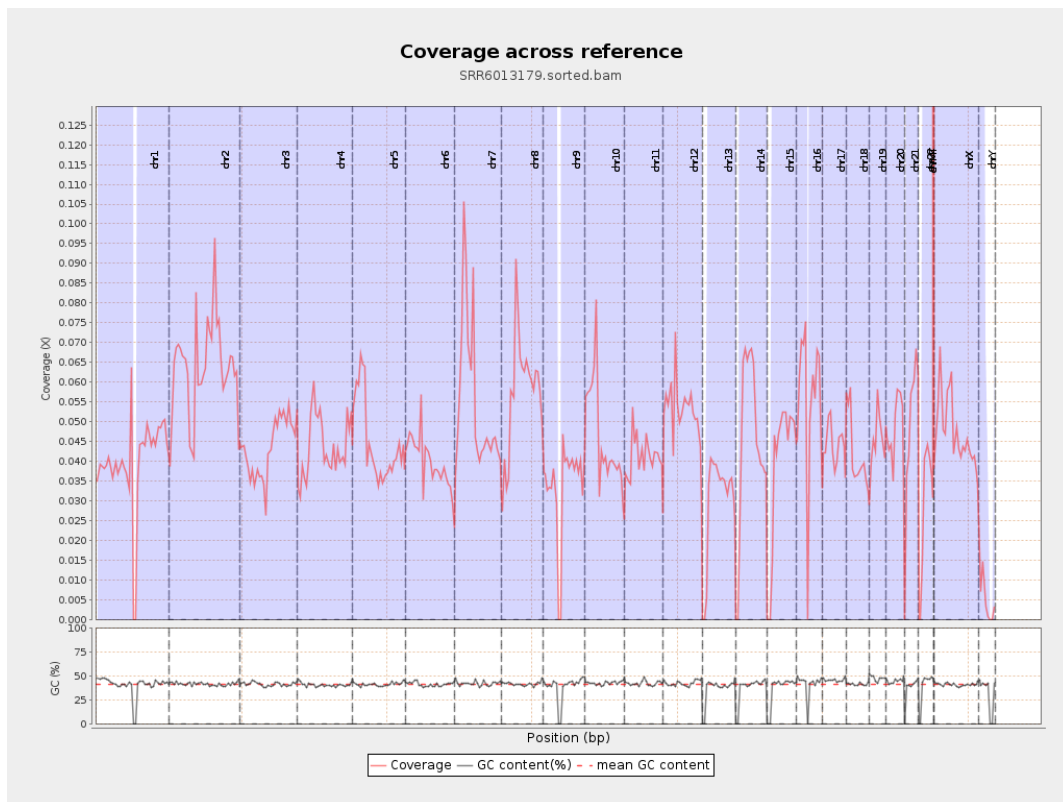
General error rate	0.86%
Mismatches	1,184,172
Insertions	9,479
Mapped reads with at least one insertion	0.44%
Deletions	44,284
Mapped reads with at least one deletion	2.04%
Homopolymer indels	43.81%

2.6. Chromosome stats

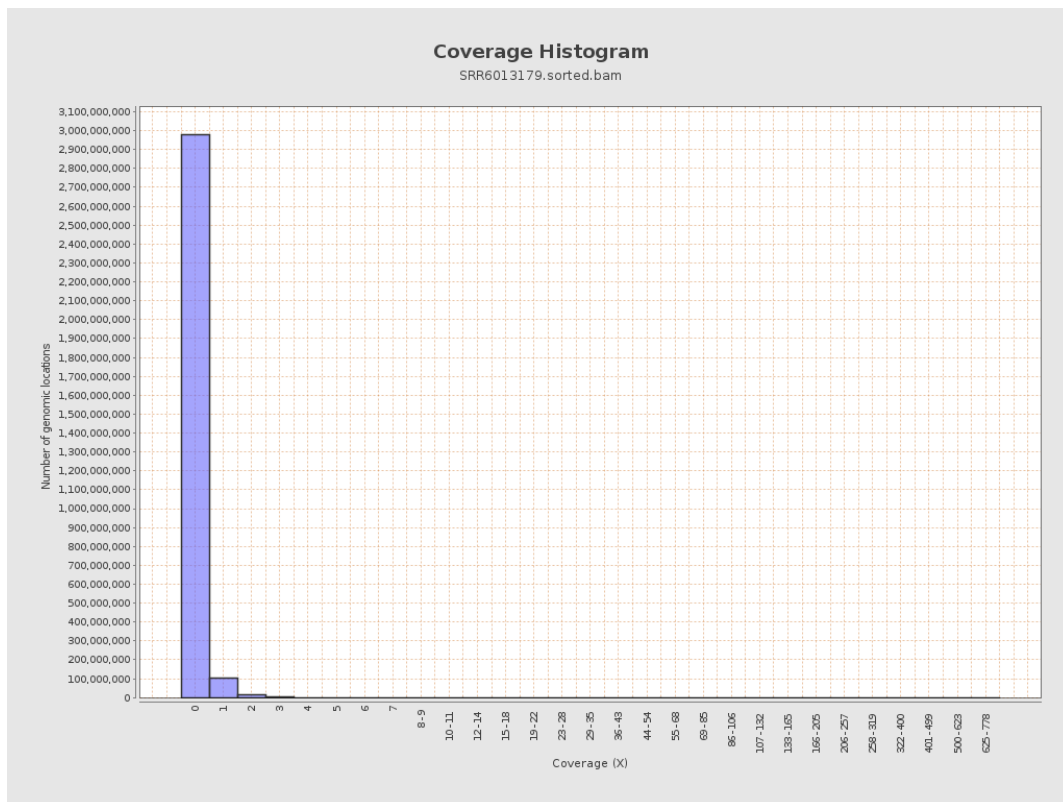
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9918531	0.0398	0.6593
chr2	243199373	15481029	0.0637	0.4678
chr3	198022430	8584609	0.0434	0.2356
chr4	191154276	8326608	0.0436	0.2465
chr5	180915260	8113465	0.0448	0.2401
chr6	171115067	6789528	0.0397	0.2884
chr7	159138663	8807207	0.0553	0.691

chr8	146364022	8410440	0.0575	0.3894
chr9	141213431	4700081	0.0333	0.3072
chr10	135534747	6273516	0.0463	0.4184
chr11	135006516	5540786	0.041	0.2961
chr12	133851895	7117546	0.0532	0.2636
chr13	115169878	3415019	0.0297	0.1962
chr14	107349540	4895740	0.0456	0.2627
chr15	102531392	4006092	0.0391	0.2234
chr16	90354753	5048771	0.0559	0.3003
chr17	81195210	3572519	0.044	0.2717
chr18	78077248	3260633	0.0418	0.5732
chr19	59128983	2702143	0.0457	0.5424
chr20	63025520	3029968	0.0481	0.2537
chr21	48129895	2343868	0.0487	0.2635
chr22	51304566	1434765	0.028	0.1859
chrMT	16571	300477	18.1327	10.5657
chrX	155270560	7348081	0.0473	0.2737
chrY	59373566	313927	0.0053	0.1126

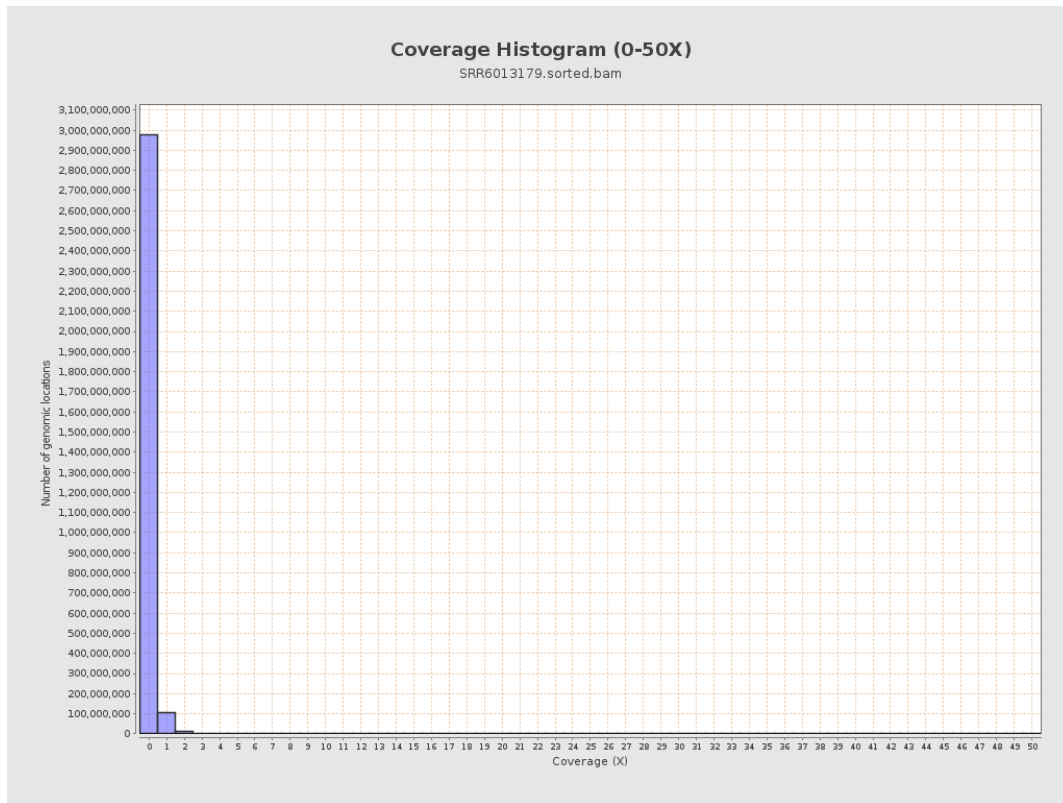
3. Results : Coverage across reference



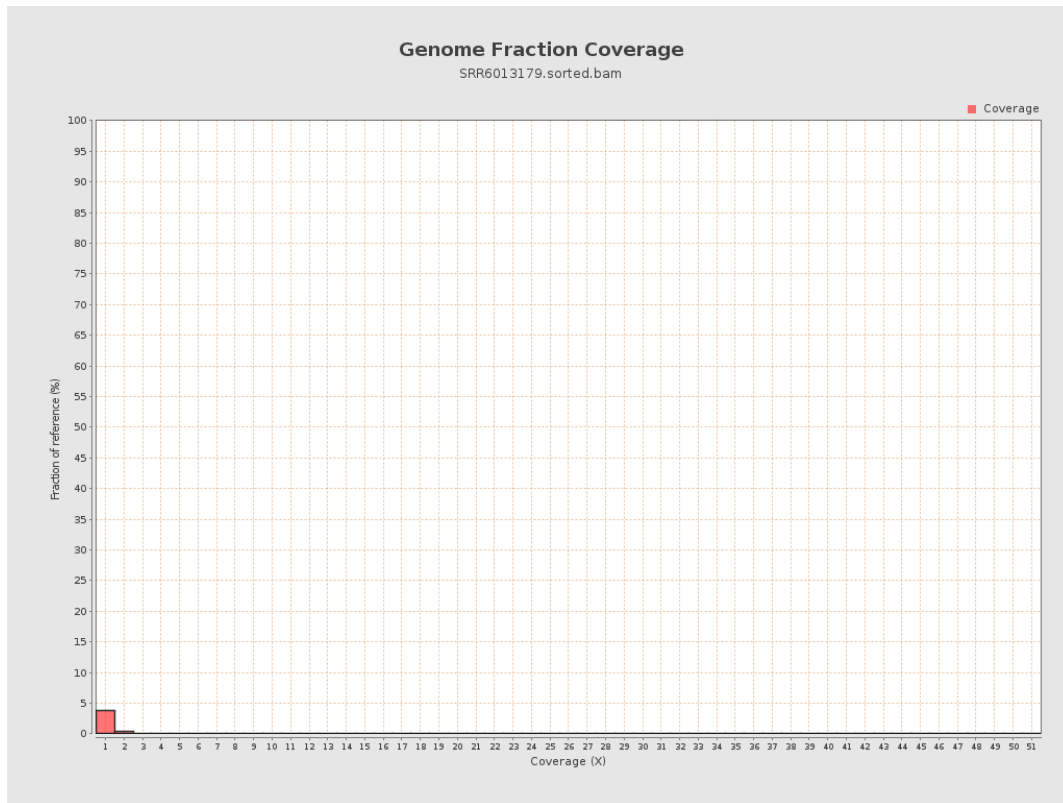
4. Results : Coverage Histogram



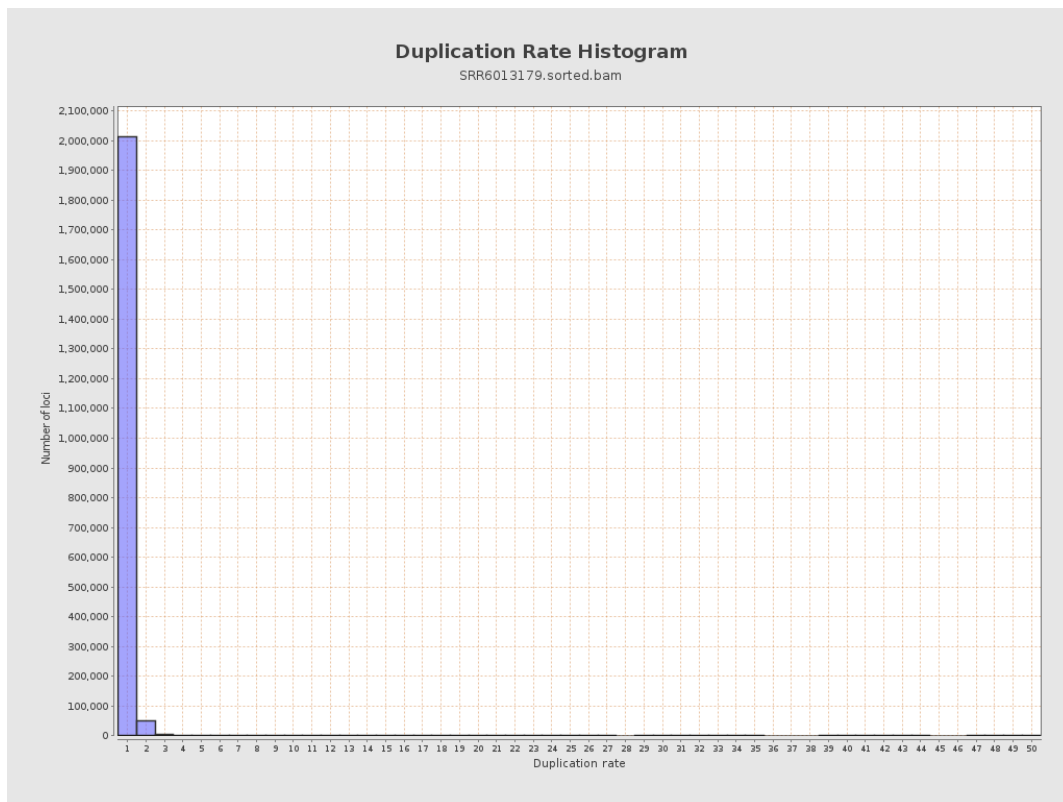
5. Results : Coverage Histogram (0-50X)



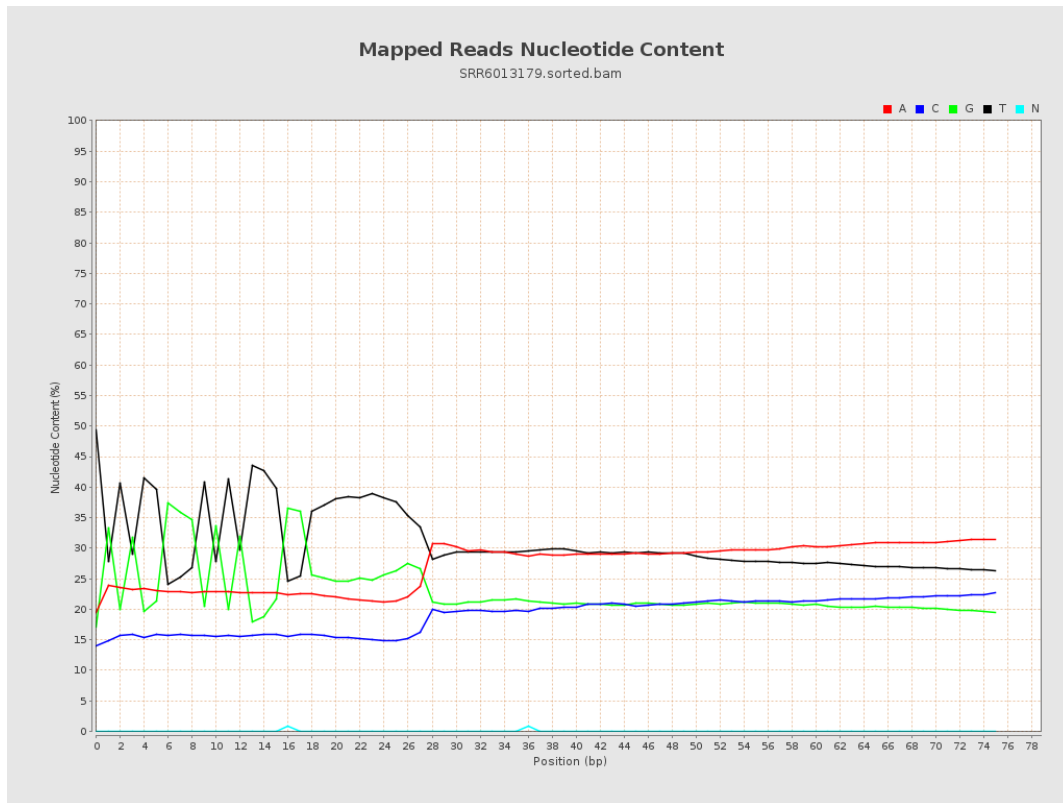
6. Results : Genome Fraction Coverage



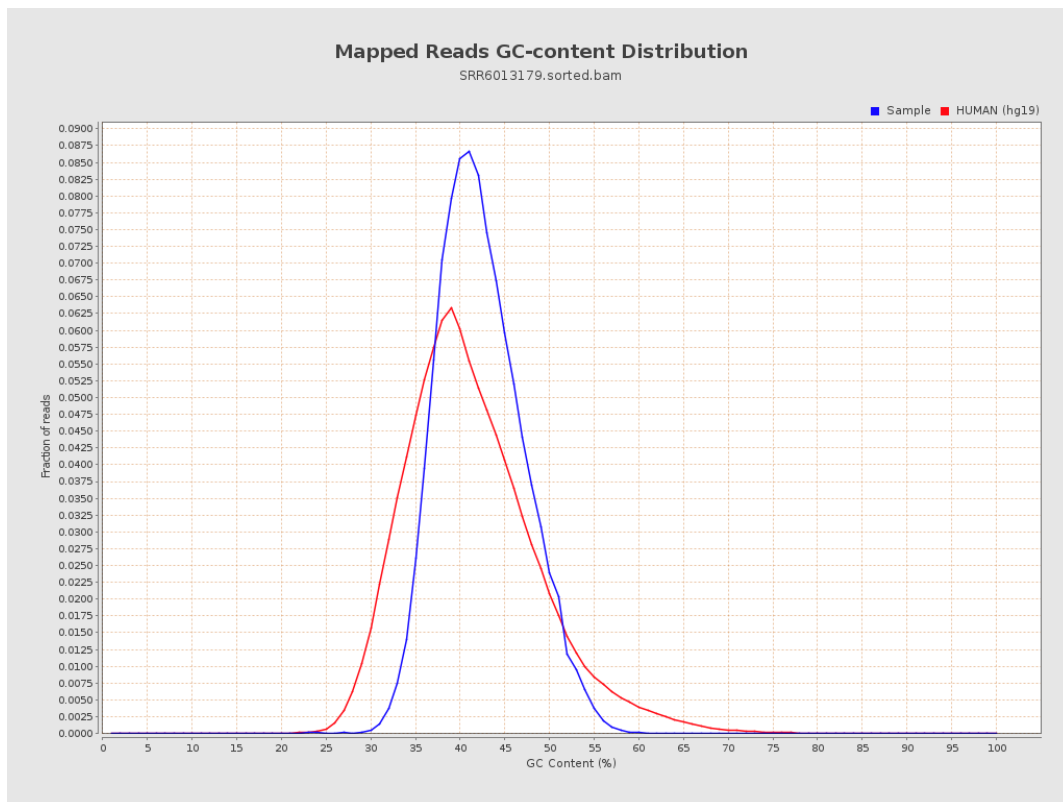
7. Results : Duplication Rate Histogram



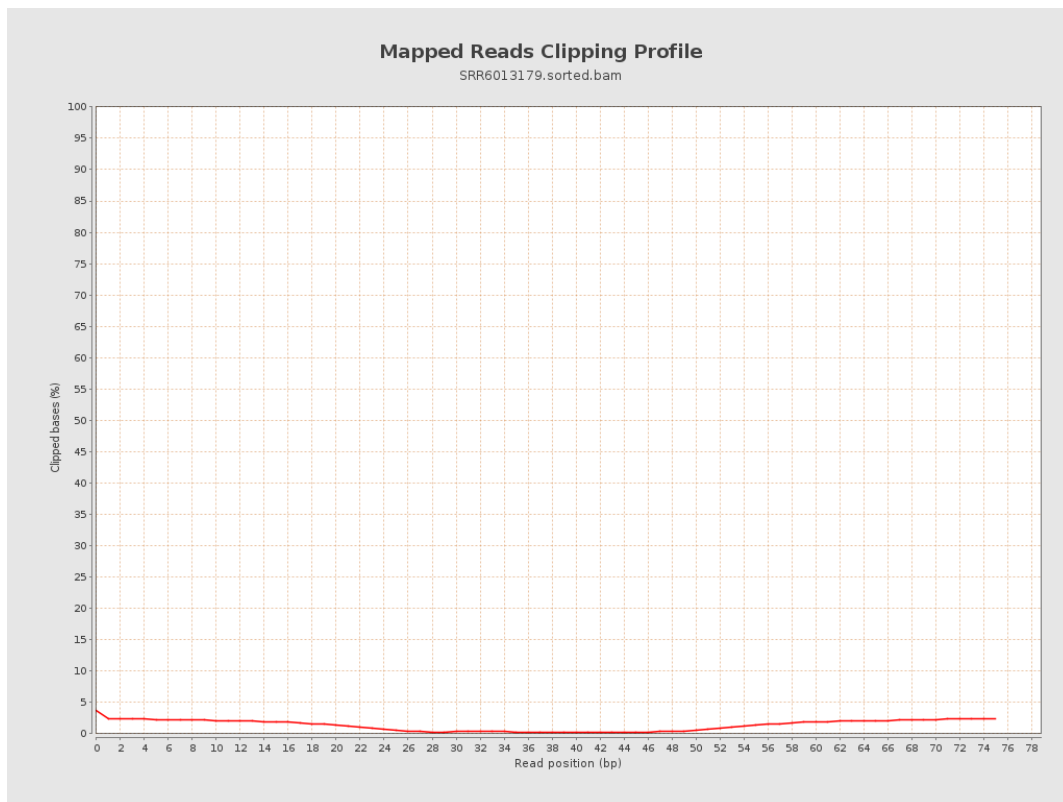
8. Results : Mapped Reads Nucleotide Content



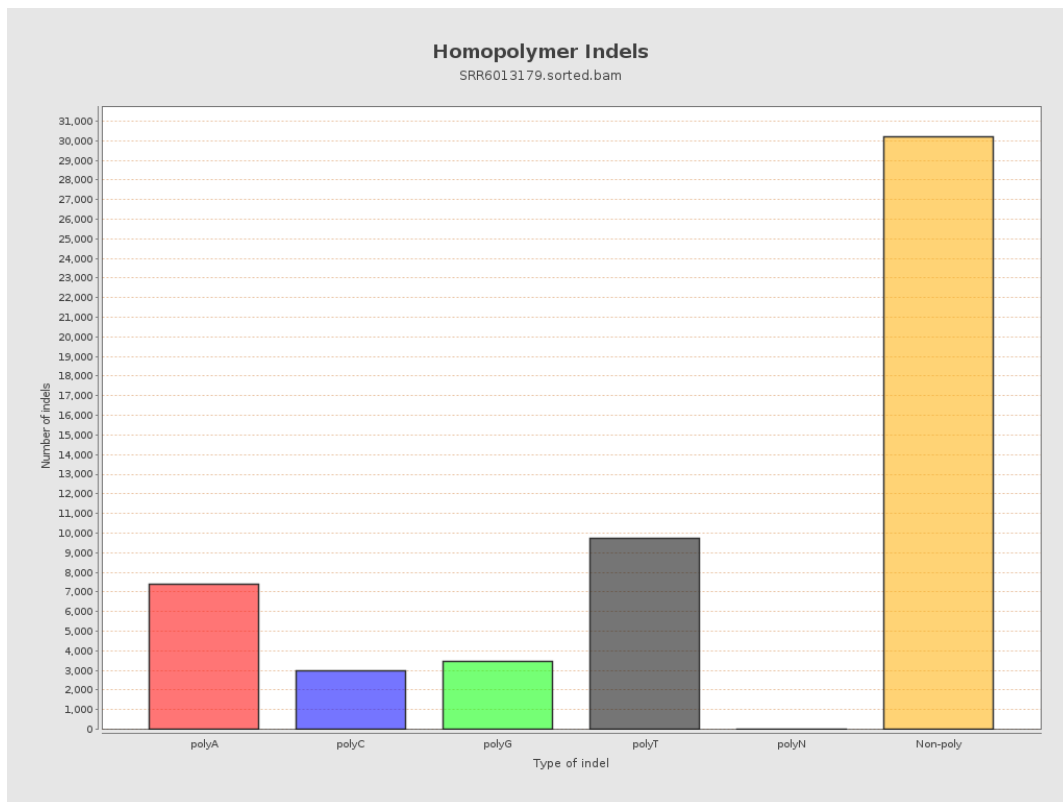
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

