

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:54:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013167.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_SRR6013167 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013167.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:54:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,195,999
Mapped reads	1,501,780 / 68.39%
Unmapped reads	694,219 / 31.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,369 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	425,406 / 19.37%
Duplication rate	16.54%
Clipped reads	930,486 / 42.37%

2.2. ACGT Content

Number/percentage of A's	24,941,788 / 26.69%
Number/percentage of C's	16,860,894 / 18.04%
Number/percentage of T's	29,903,256 / 32%
Number/percentage of G's	21,603,217 / 23.12%
Number/percentage of N's	137,617 / 0.15%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.4906
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2.4. Mapping Quality

Mean Mapping Quality	45.17
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2.5. Mismatches and indels

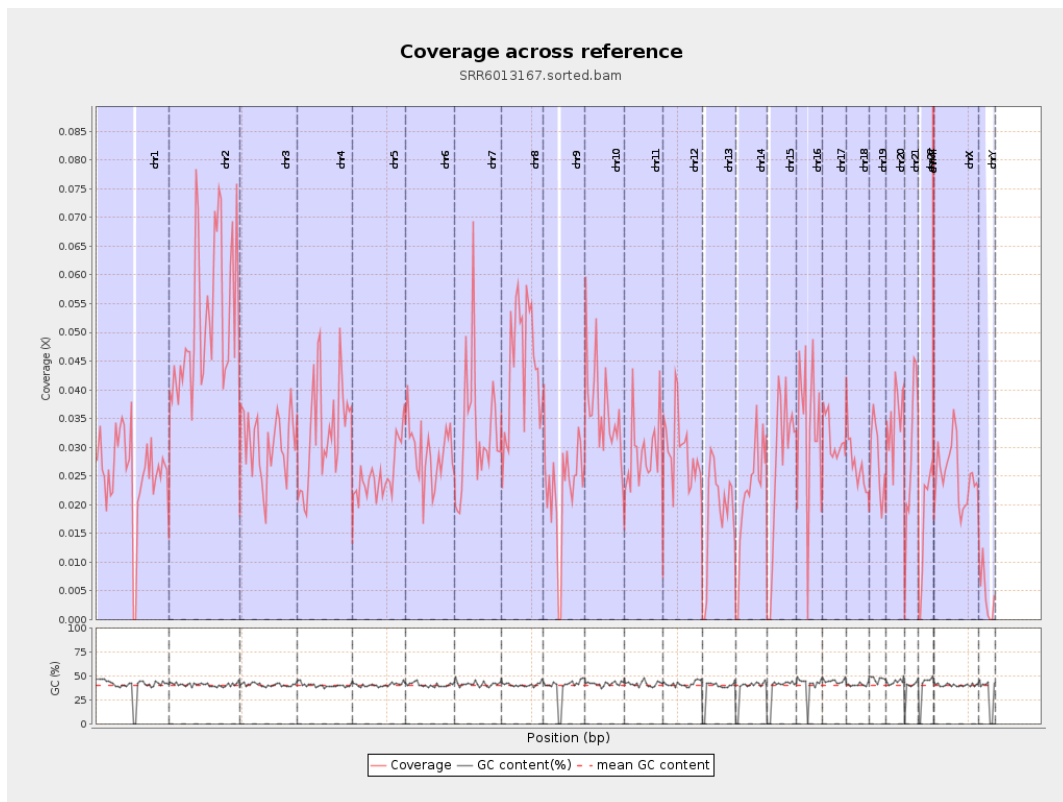
General error rate	1.02%
Mismatches	943,631
Insertions	6,494
Mapped reads with at least one insertion	0.43%
Deletions	37,835
Mapped reads with at least one deletion	2.48%
Homopolymer indels	43.68%

2.6. Chromosome stats

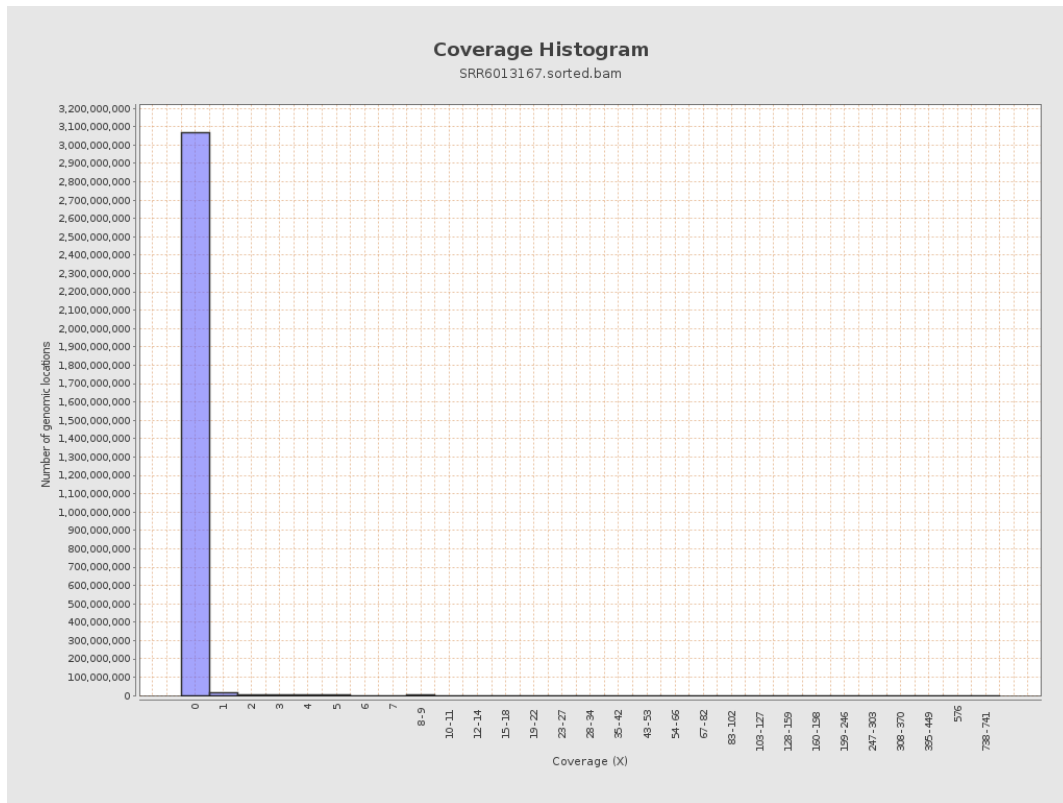
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6363601	0.0255	0.5088
chr2	243199373	12665415	0.0521	0.6869
chr3	198022430	6018925	0.0304	0.4682
chr4	191154276	6210671	0.0325	0.4654
chr5	180915260	4565722	0.0252	0.4194
chr6	171115067	4938313	0.0289	0.4687
chr7	159138663	5223944	0.0328	0.6157

chr8	146364022	6433664	0.044	0.572
chr9	141213431	3154147	0.0223	0.4161
chr10	135534747	4950521	0.0365	0.531
chr11	135006516	3901718	0.0289	0.4607
chr12	133851895	3940642	0.0294	0.4492
chr13	115169878	2115442	0.0184	0.3594
chr14	107349540	2328709	0.0217	0.3835
chr15	102531392	2740152	0.0267	0.4451
chr16	90354753	2980818	0.033	0.4917
chr17	81195210	2553874	0.0315	0.4647
chr18	78077248	2109020	0.027	0.5275
chr19	59128983	1654162	0.028	0.4788
chr20	63025520	2220525	0.0352	0.4967
chr21	48129895	1380548	0.0287	0.4393
chr22	51304566	874535	0.017	0.3386
chrMT	16571	66986	4.0424	5.632
chrX	155270560	3873704	0.0249	0.4113
chrY	59373566	246421	0.0042	0.1462

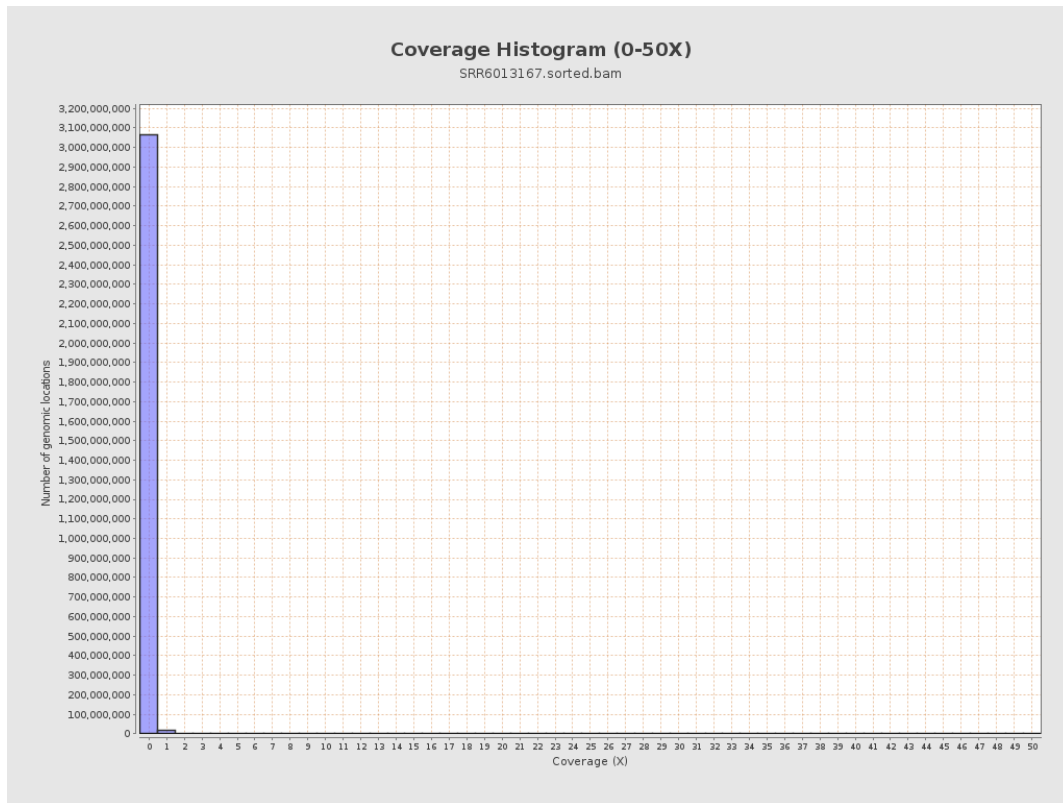
3. Results : Coverage across reference



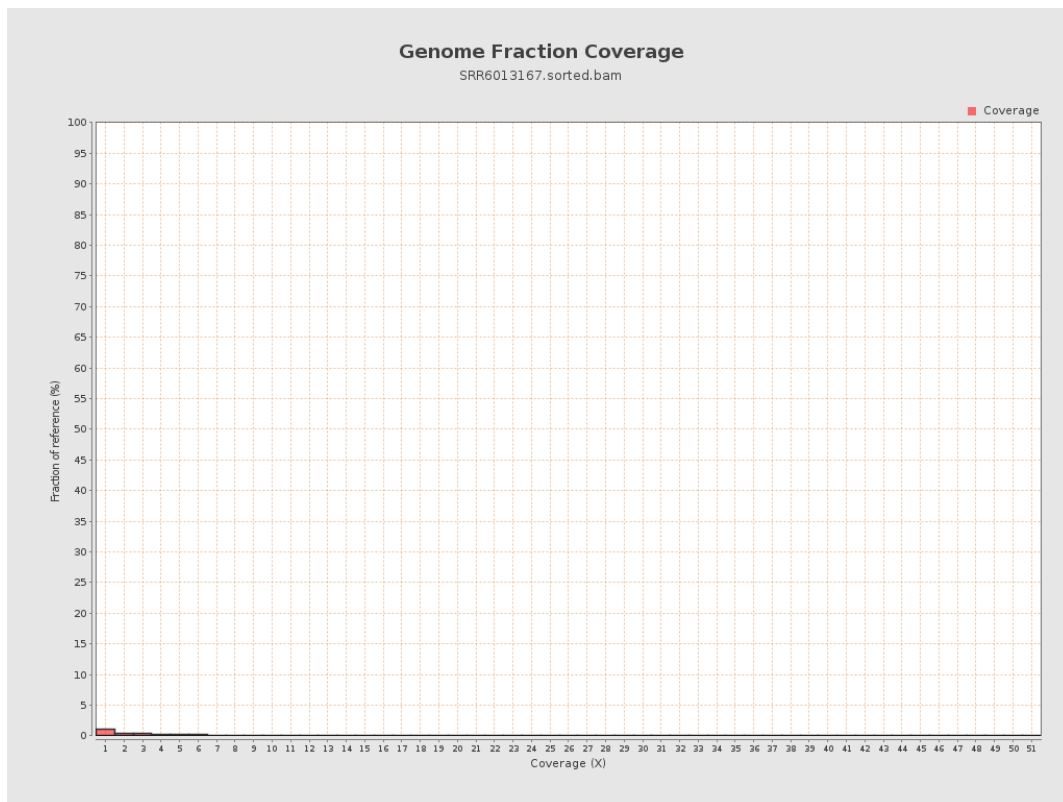
4. Results : Coverage Histogram



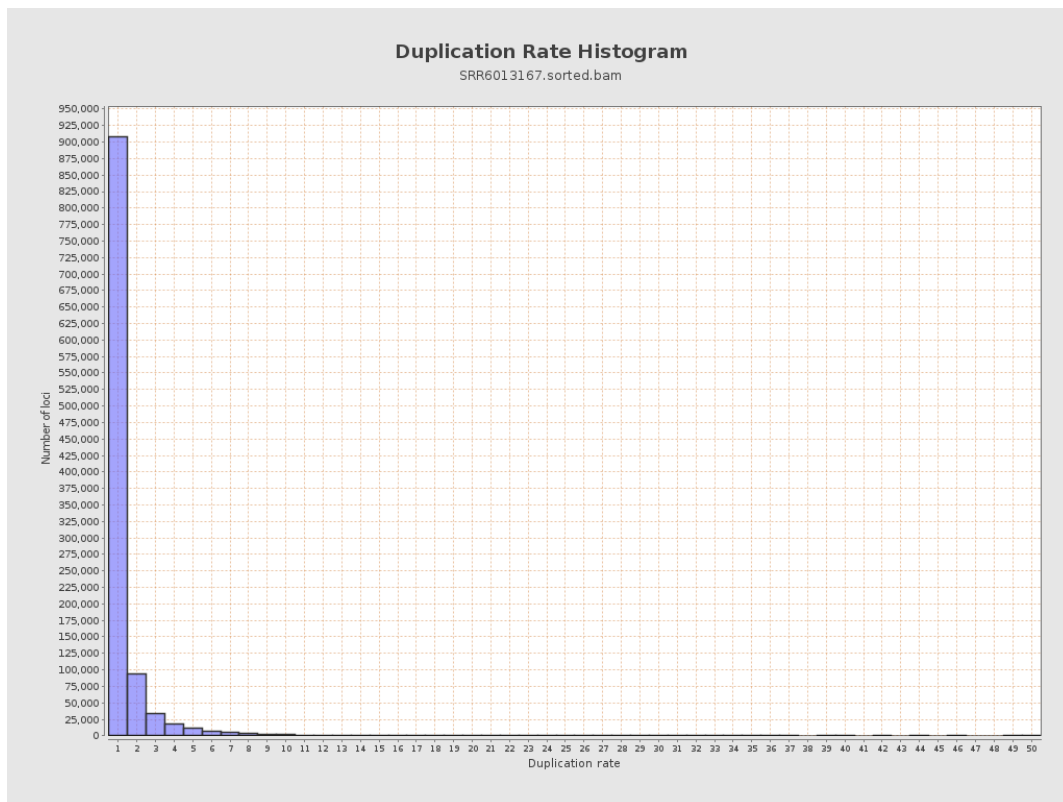
5. Results : Coverage Histogram (0-50X)



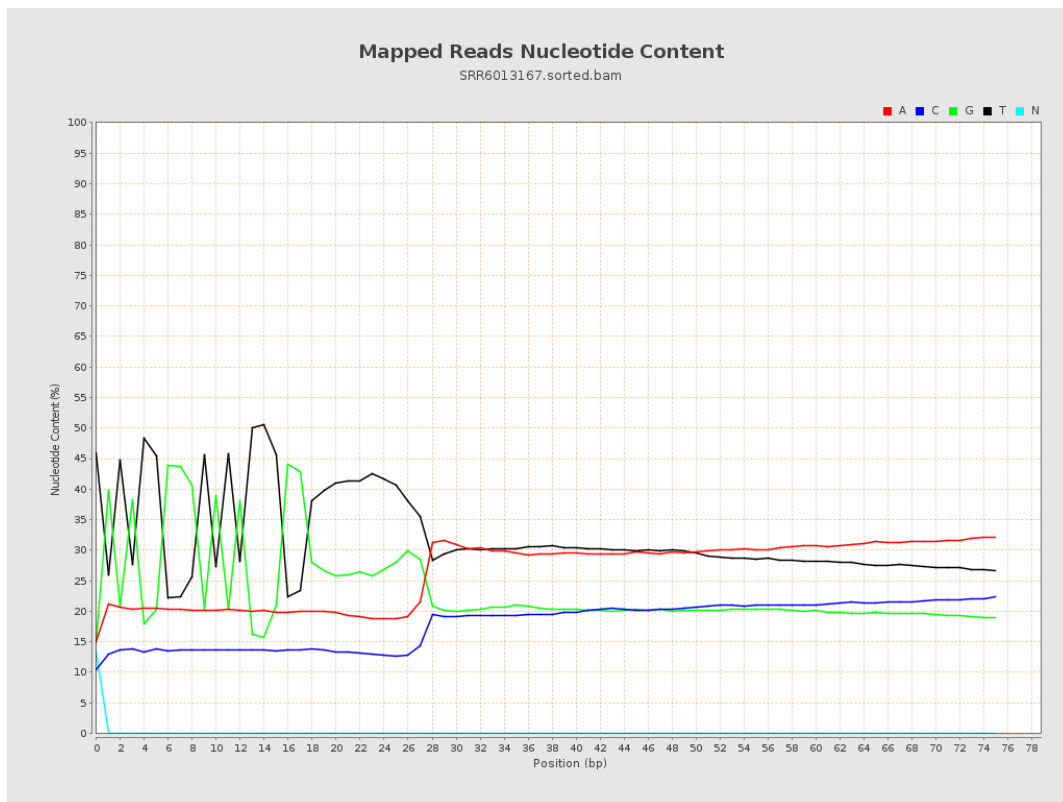
6. Results : Genome Fraction Coverage



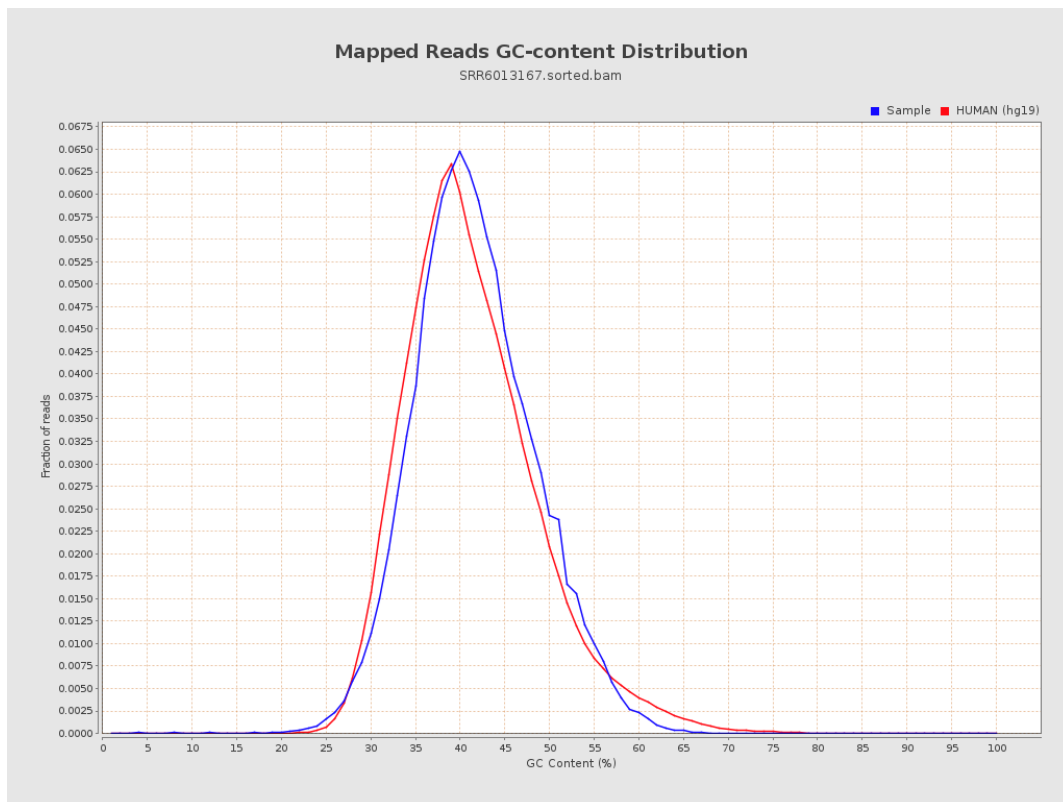
7. Results : Duplication Rate Histogram



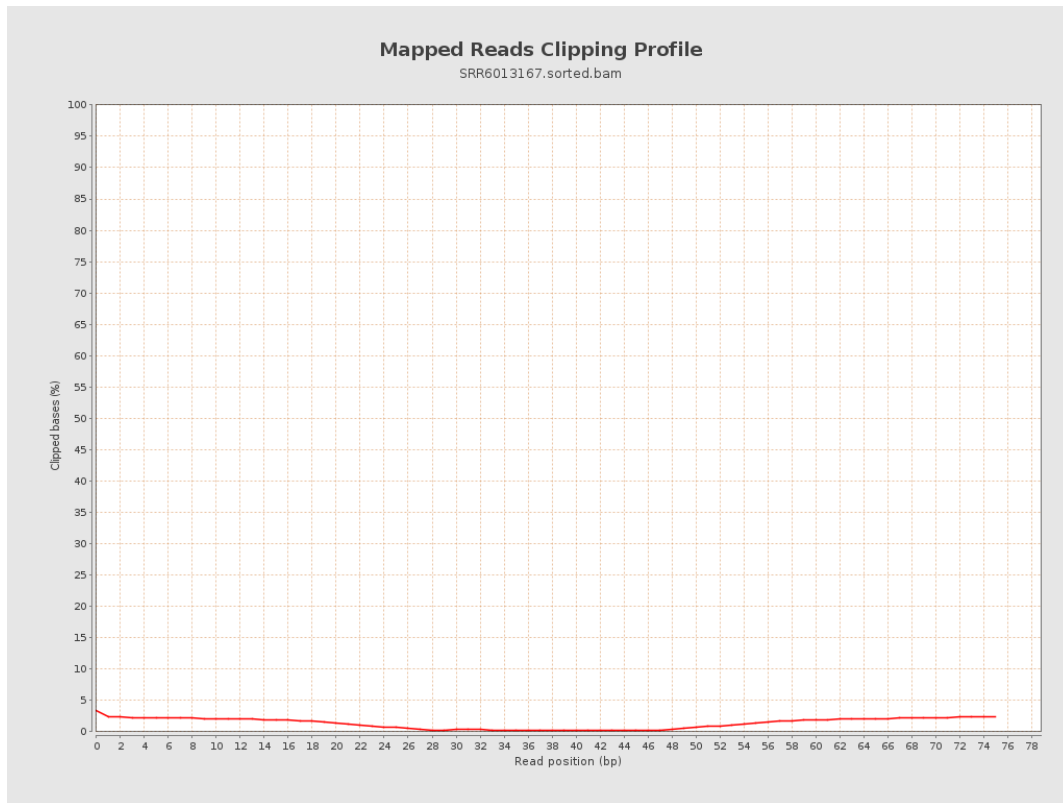
8. Results : Mapped Reads Nucleotide Content



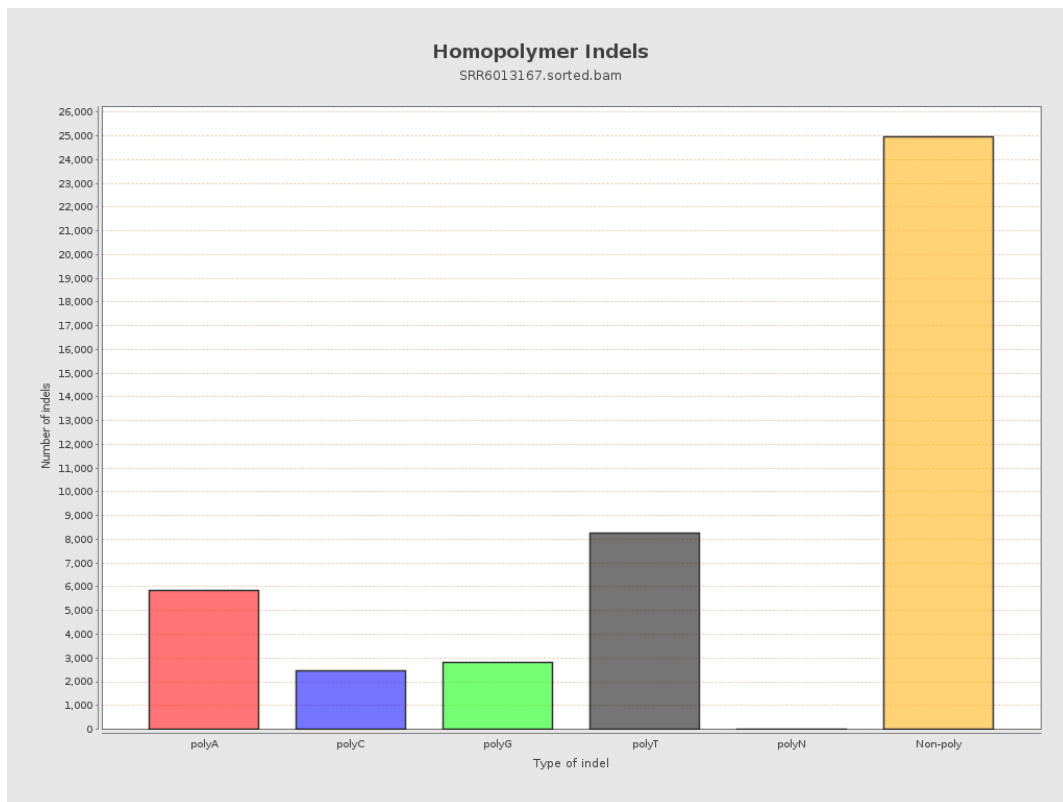
9. Results : Mapped Reads GC-content Distribution



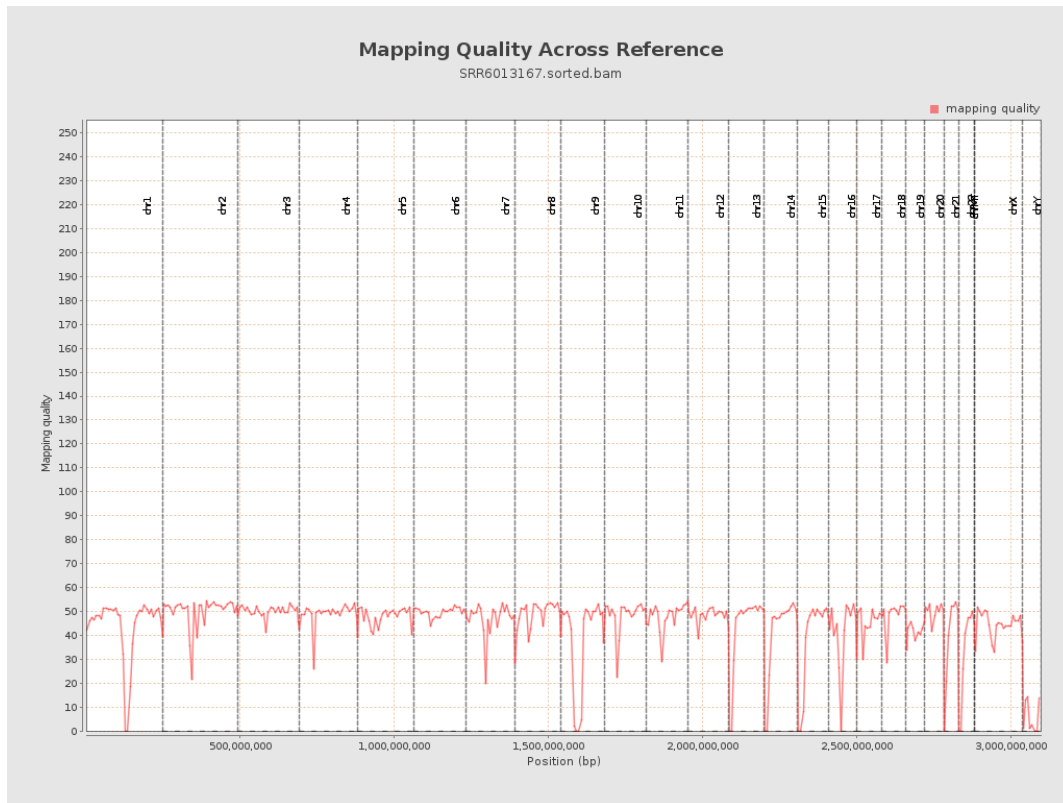
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

