

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:59:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013169.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_SRR6013169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:59:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,999,952
Mapped reads	1,418,027 / 70.9%
Unmapped reads	581,925 / 29.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,771 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	223,091 / 11.15%
Duplication rate	11.83%
Clipped reads	912,119 / 45.61%

2.2. ACGT Content

Number/percentage of A's	23,335,924 / 26.74%
Number/percentage of C's	15,515,675 / 17.78%
Number/percentage of T's	28,153,100 / 32.26%
Number/percentage of G's	20,126,661 / 23.06%
Number/percentage of N's	133,306 / 0.15%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.3495
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2.4. Mapping Quality

Mean Mapping Quality	43.8
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2.5. Mismatches and indels

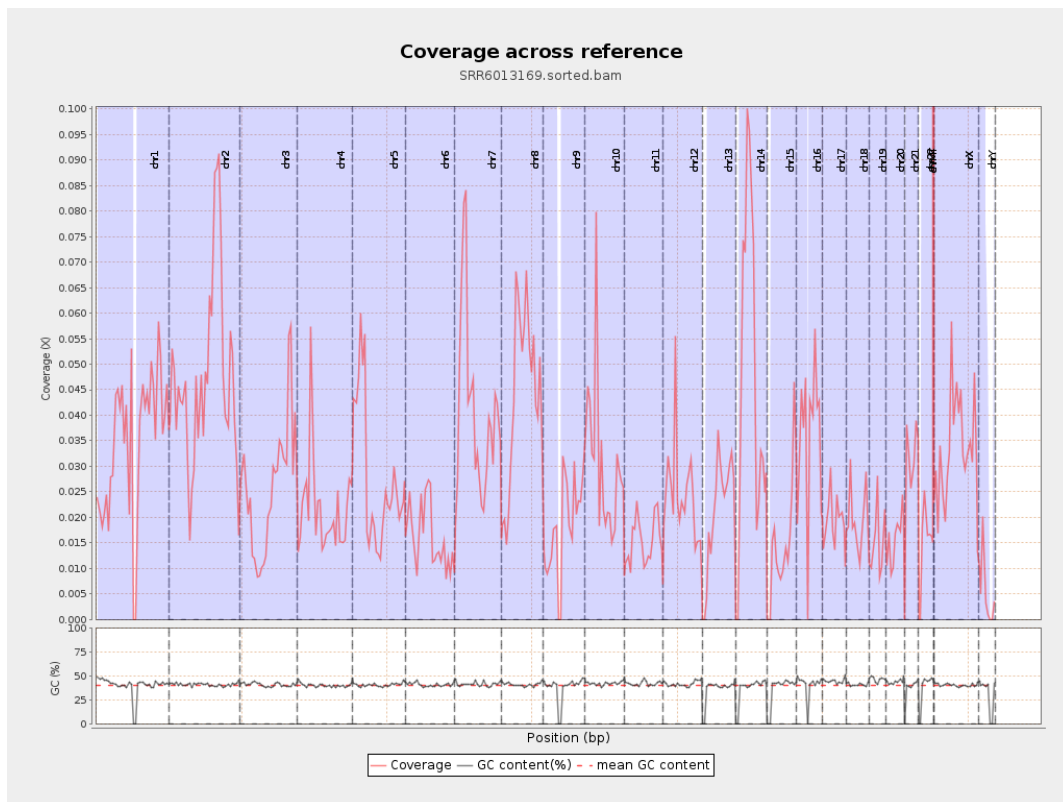
General error rate	1.16%
Mismatches	997,230
Insertions	6,077
Mapped reads with at least one insertion	0.43%
Deletions	52,166
Mapped reads with at least one deletion	3.6%
Homopolymer indels	41.21%

2.6. Chromosome stats

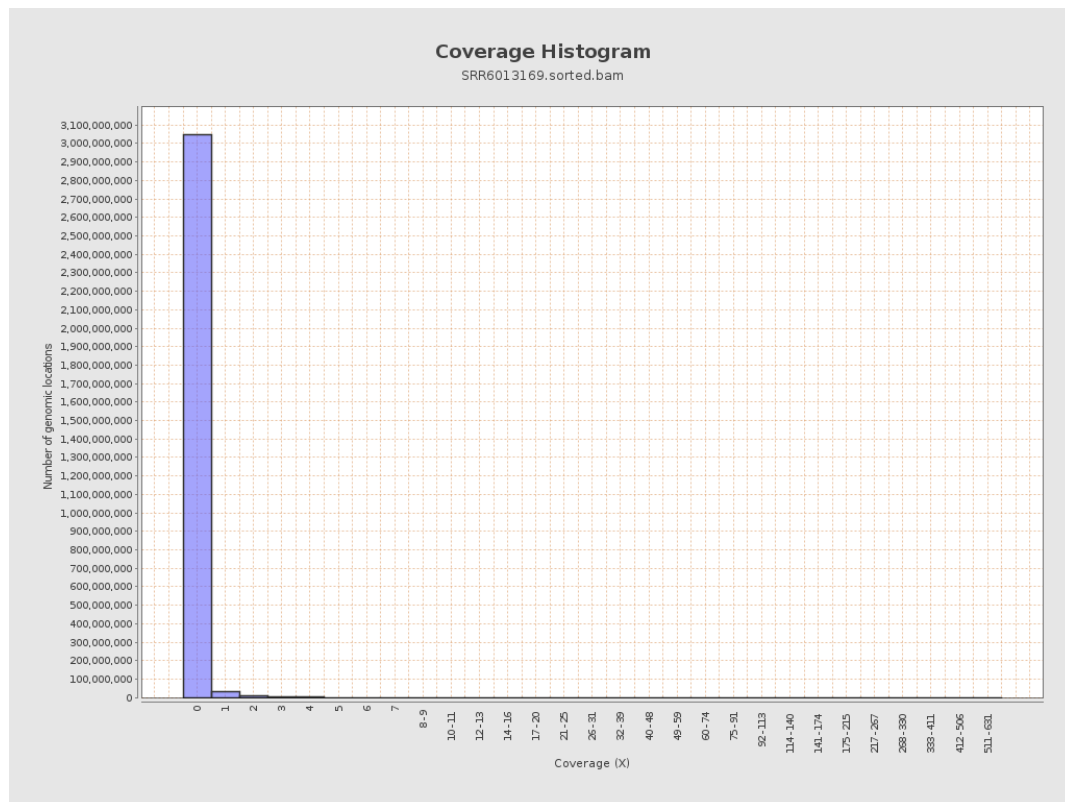
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8618011	0.0346	0.5298
chr2	243199373	11516753	0.0474	0.4705
chr3	198022430	5127518	0.0259	0.2638
chr4	191154276	4114038	0.0215	0.256
chr5	180915260	5016964	0.0277	0.2703
chr6	171115067	2749082	0.0161	0.2419
chr7	159138663	6568774	0.0413	0.4306

chr8	146364022	6473075	0.0442	0.3921
chr9	141213431	2561948	0.0181	0.2723
chr10	135534747	4163405	0.0307	0.4745
chr11	135006516	2054435	0.0152	0.2269
chr12	133851895	3265545	0.0244	0.2506
chr13	115169878	2489519	0.0216	0.2377
chr14	107349540	5118963	0.0477	0.3735
chr15	102531392	1528209	0.0149	0.1998
chr16	90354753	3245272	0.0359	0.3405
chr17	81195210	1565399	0.0193	0.2344
chr18	78077248	1527034	0.0196	0.5107
chr19	59128983	912301	0.0154	0.3943
chr20	63025520	1001364	0.0159	0.2167
chr21	48129895	1457309	0.0303	0.306
chr22	51304566	751354	0.0146	0.1941
chrMT	16571	21880	1.3204	1.6465
chrX	155270560	5201618	0.0335	0.3074
chrY	59373566	306669	0.0052	0.1721

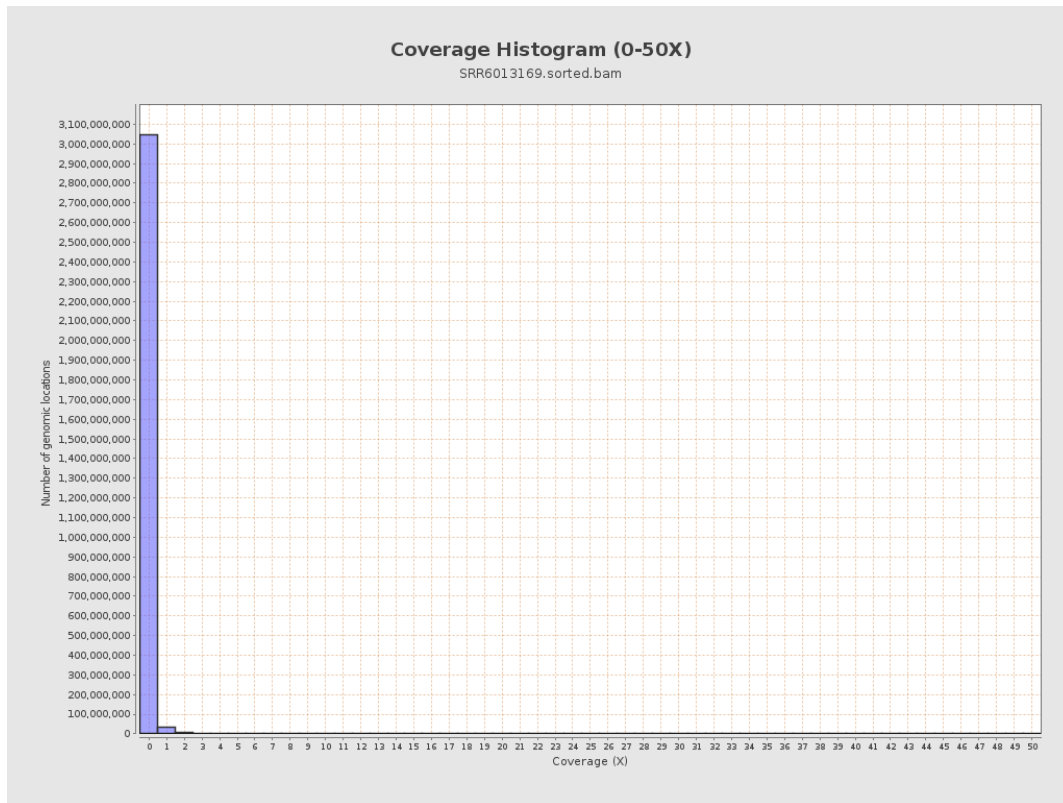
3. Results : Coverage across reference



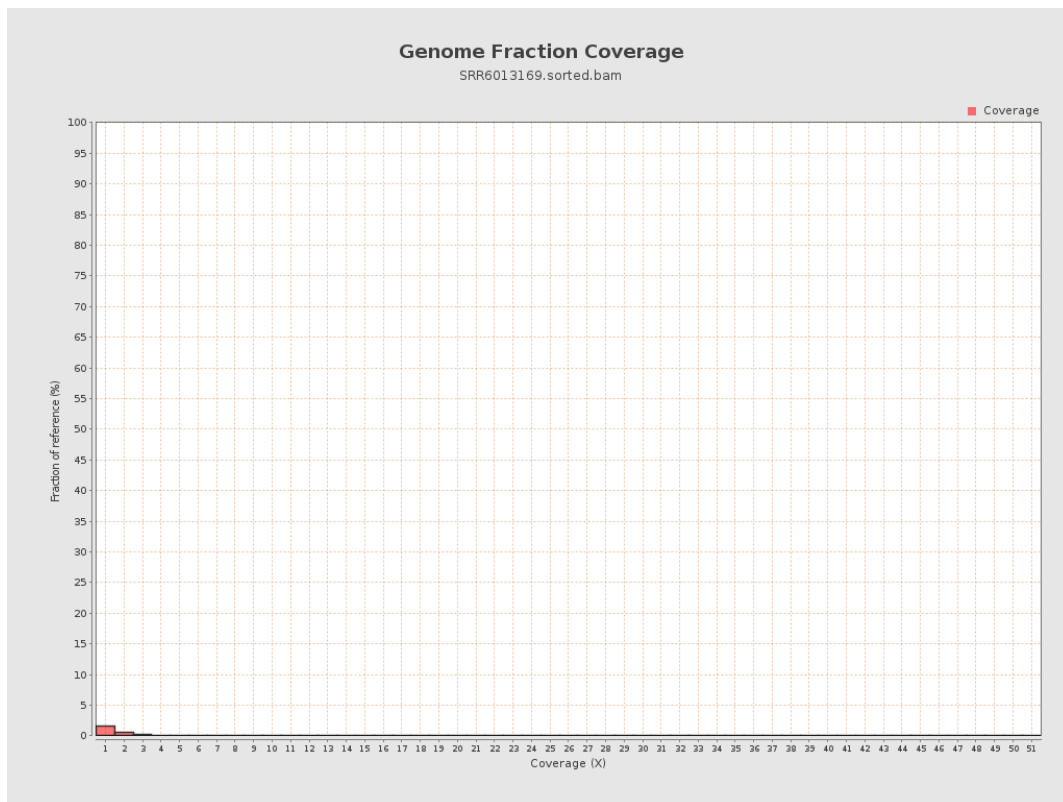
4. Results : Coverage Histogram



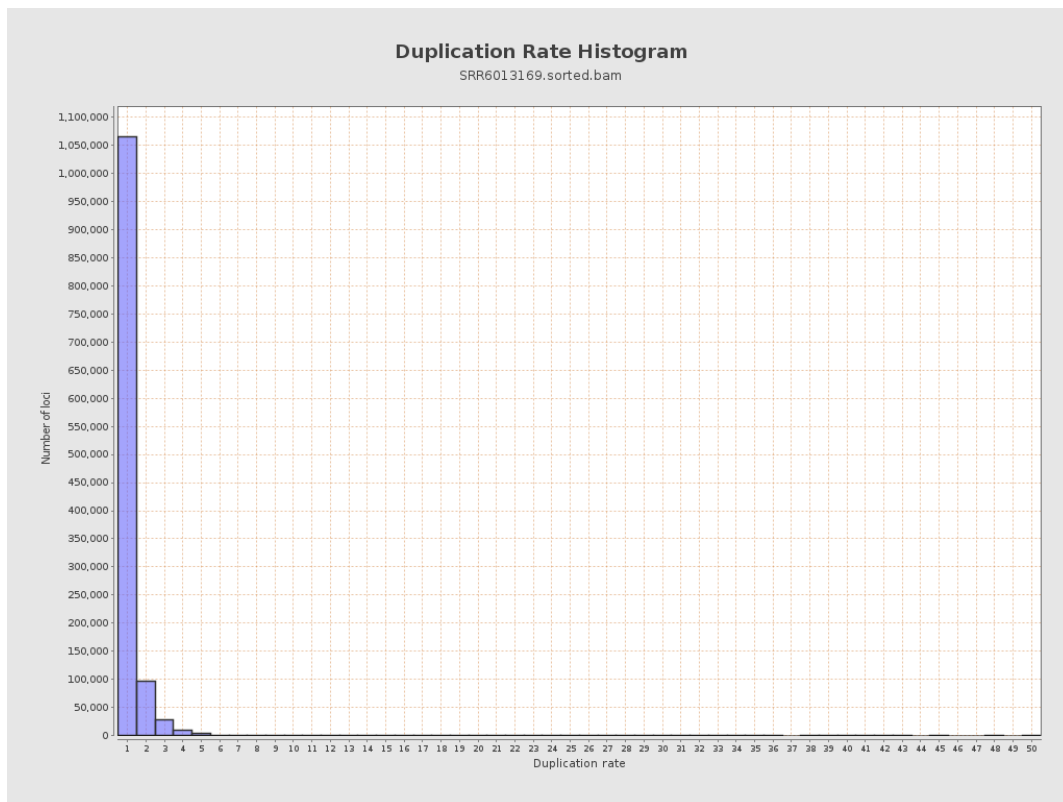
5. Results : Coverage Histogram (0-50X)



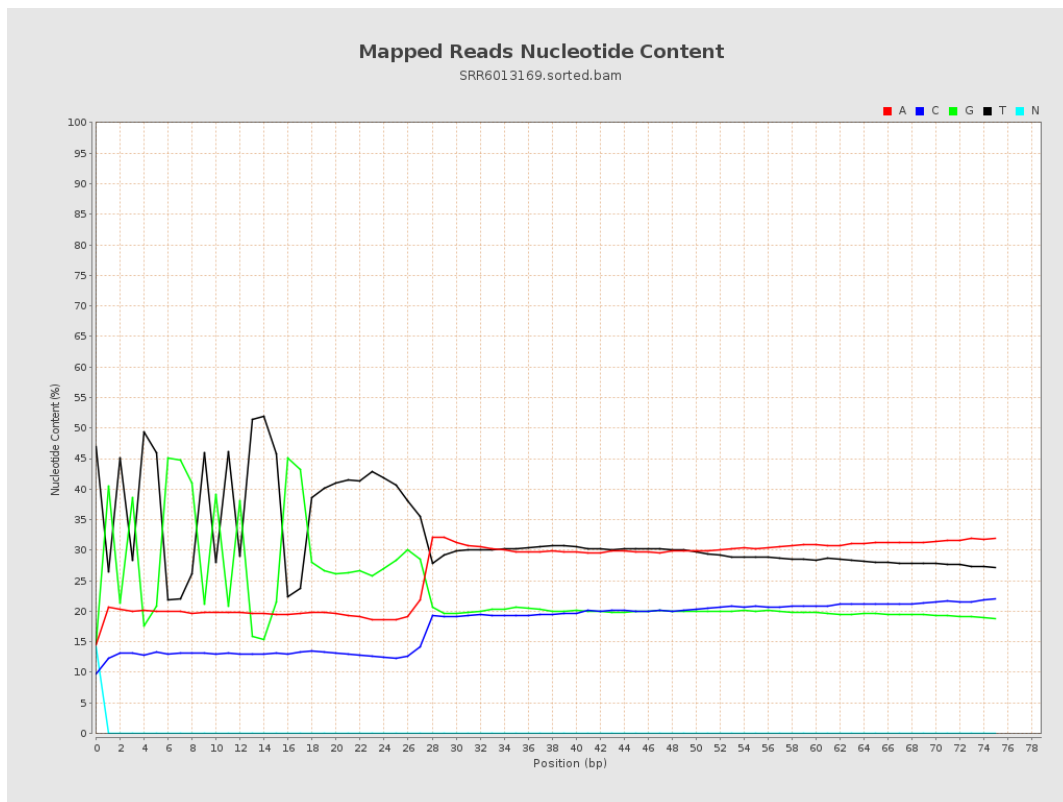
6. Results : Genome Fraction Coverage



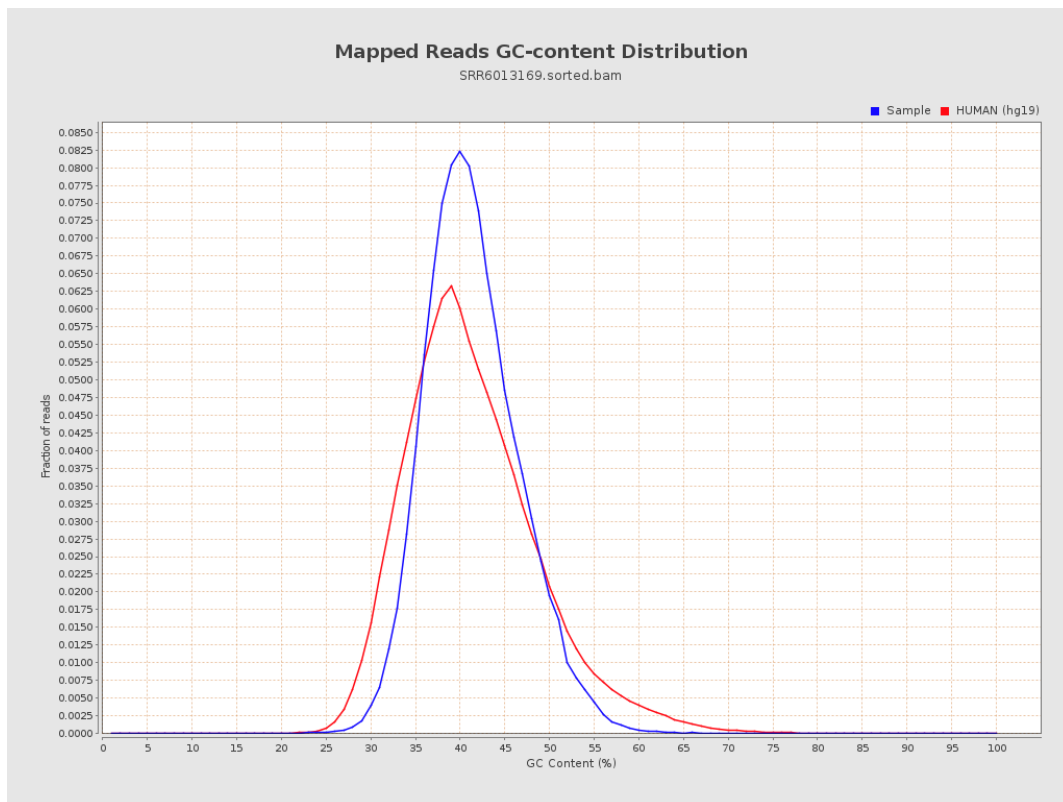
7. Results : Duplication Rate Histogram



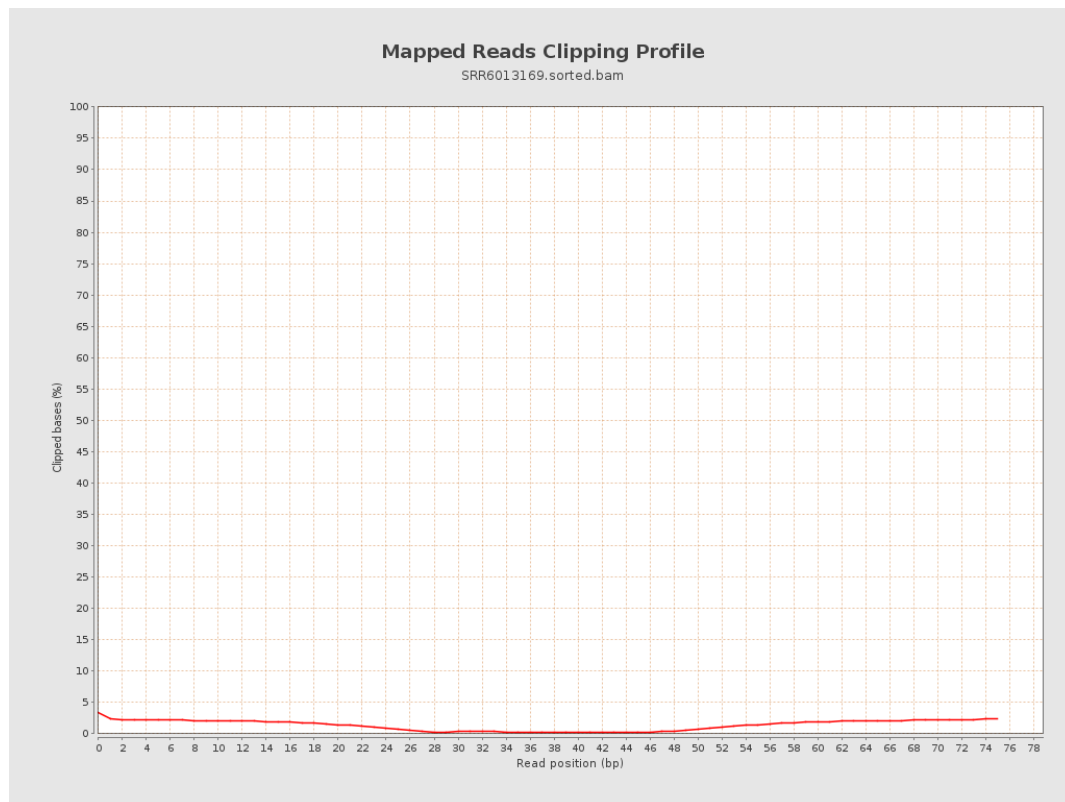
8. Results : Mapped Reads Nucleotide Content



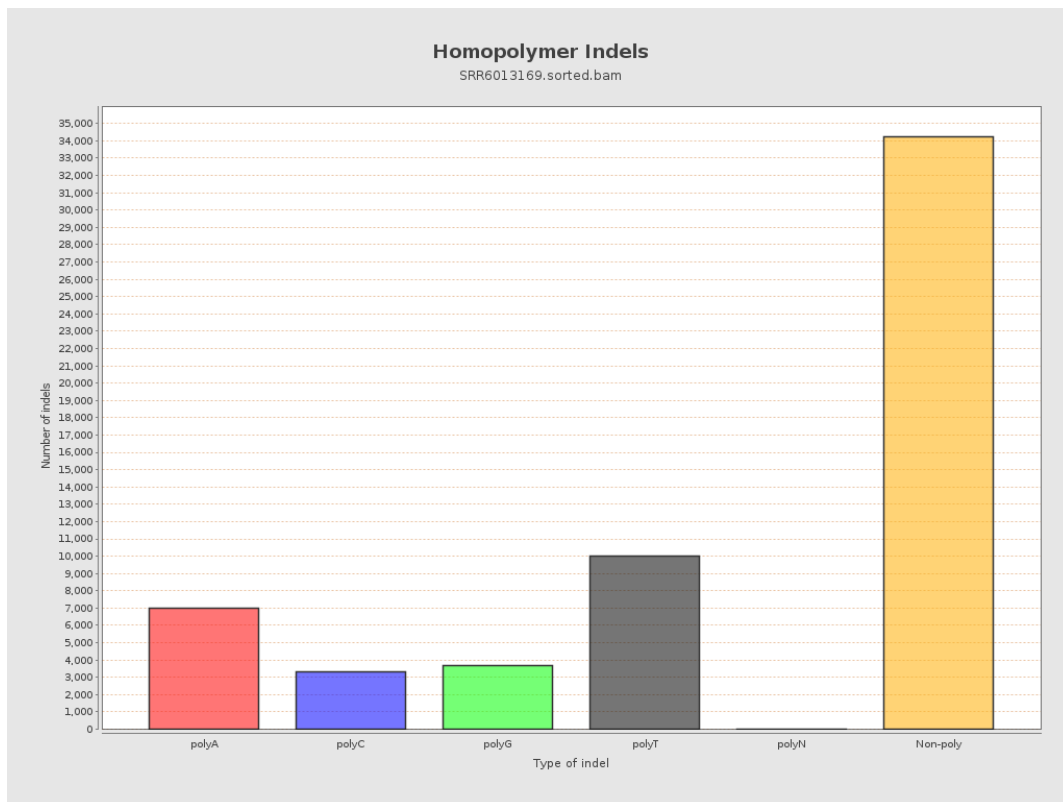
9. Results : Mapped Reads GC-content Distribution



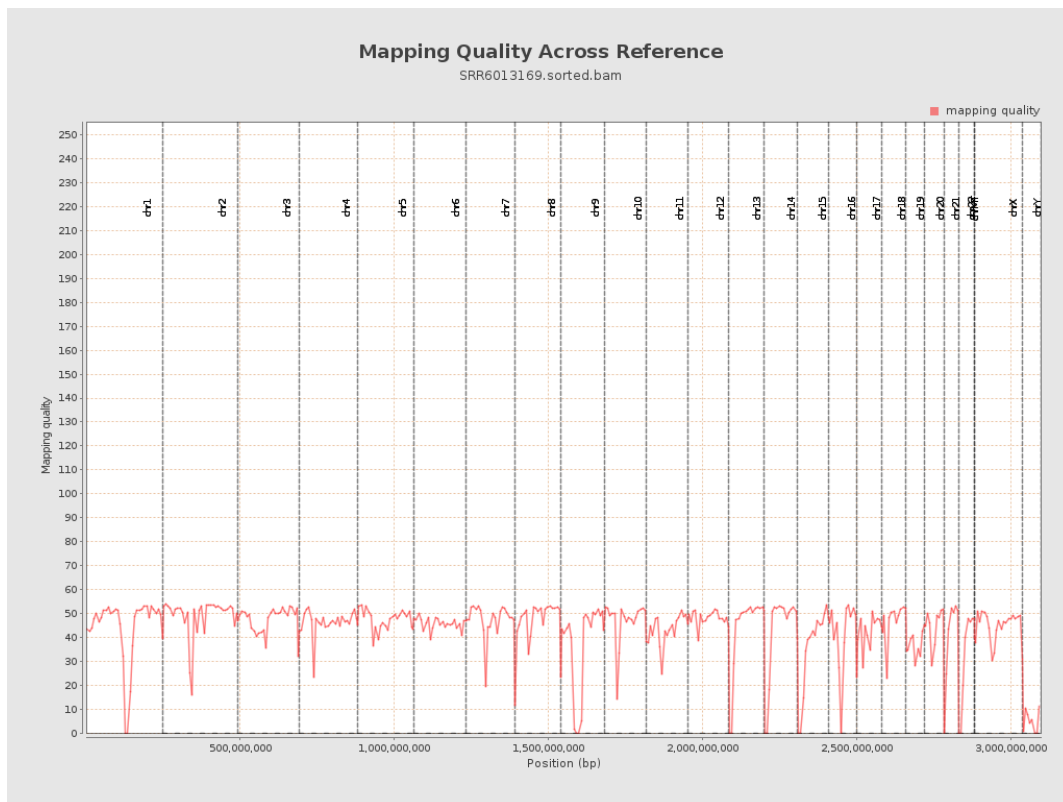
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

