

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:09:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068162.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_SRR6068162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:09:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,843,764
Mapped reads	1,588,886 / 86.18%
Unmapped reads	254,878 / 13.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,405 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	183,608 / 9.96%
Duplication rate	9.15%
Clipped reads	702,687 / 38.11%

2.2. ACGT Content

Number/percentage of A's	30,236,116 / 28.42%
Number/percentage of C's	19,606,095 / 18.43%
Number/percentage of T's	33,749,677 / 31.73%
Number/percentage of G's	22,671,428 / 21.31%
Number/percentage of N's	115,856 / 0.11%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0344

Standard Deviation	0.3916
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2.4. Mapping Quality

Mean Mapping Quality	47.77
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2.5. Mismatches and indels

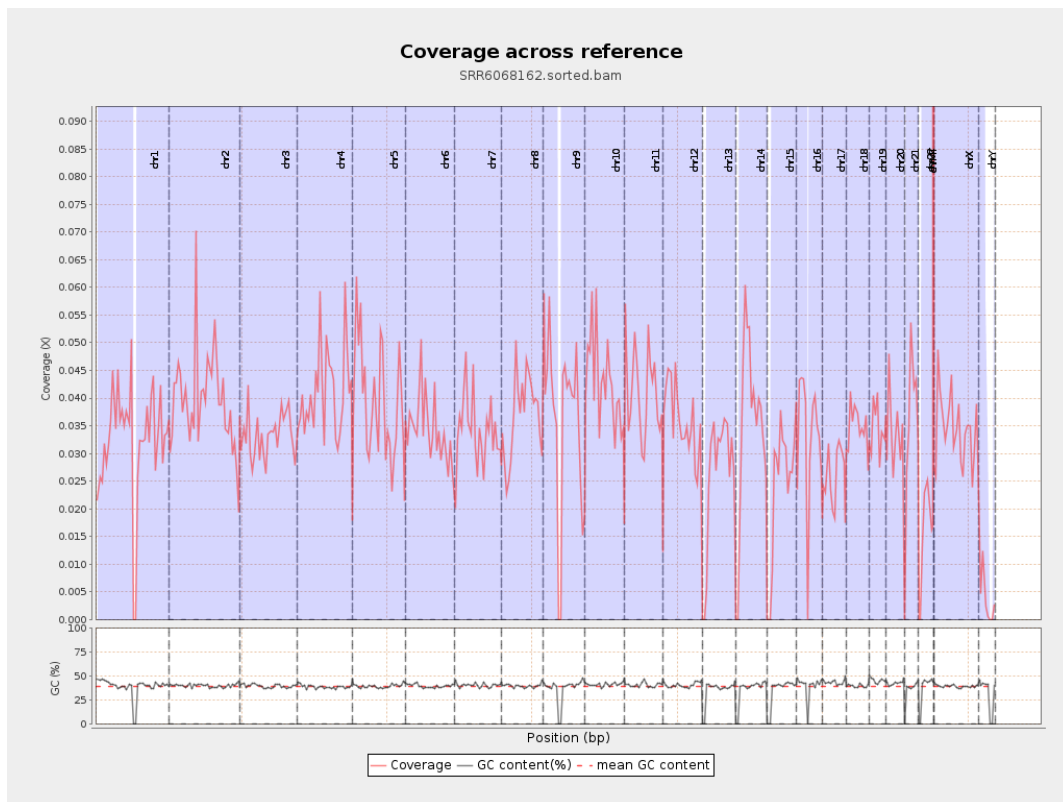
General error rate	0.86%
Mismatches	901,453
Insertions	7,258
Mapped reads with at least one insertion	0.45%
Deletions	25,262
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.79%

2.6. Chromosome stats

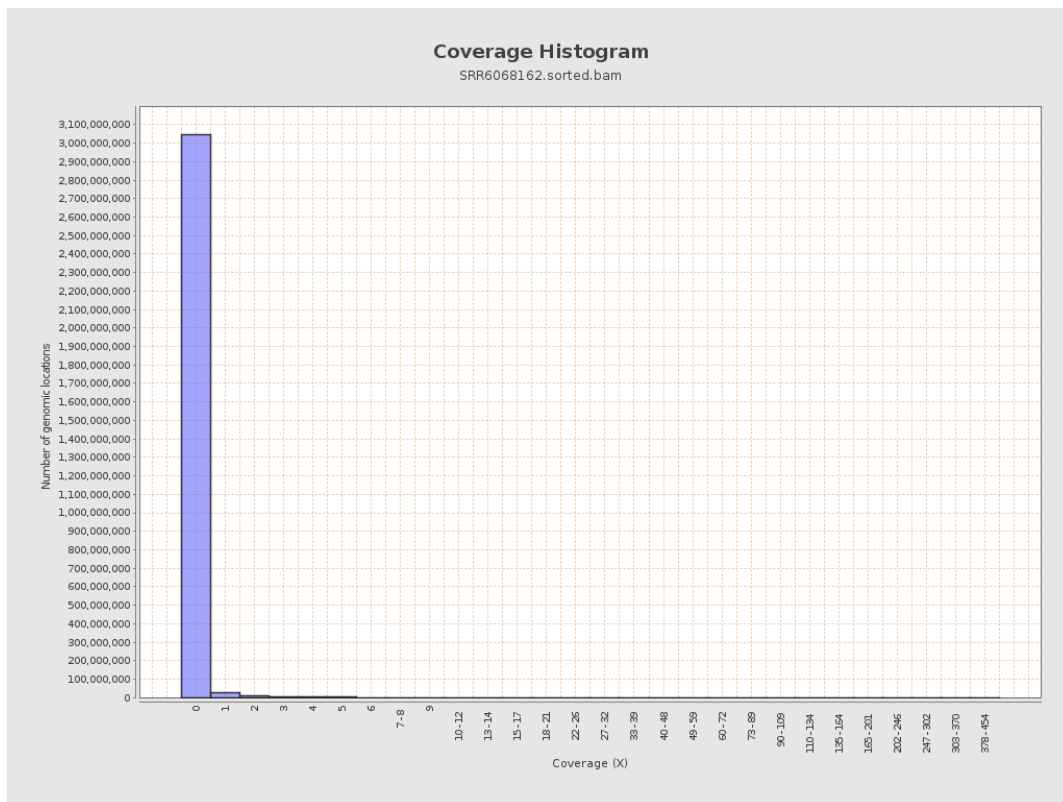
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8058559	0.0323	0.5193
chr2	243199373	9637683	0.0396	0.4403
chr3	198022430	6582370	0.0332	0.3334
chr4	191154276	7882831	0.0412	0.3776
chr5	180915260	7076883	0.0391	0.366
chr6	171115067	5852307	0.0342	0.3802
chr7	159138663	5473911	0.0344	0.432

chr8	146364022	5389751	0.0368	0.4456
chr9	141213431	5060534	0.0358	0.3996
chr10	135534747	5832085	0.043	0.4259
chr11	135006516	5490842	0.0407	0.4417
chr12	133851895	4796278	0.0358	0.34
chr13	115169878	2979373	0.0259	0.3022
chr14	107349540	3800412	0.0354	0.3609
chr15	102531392	2463234	0.024	0.2727
chr16	90354753	3004004	0.0332	0.3354
chr17	81195210	2088597	0.0257	0.2934
chr18	78077248	2729349	0.035	0.512
chr19	59128983	2042839	0.0345	0.424
chr20	63025520	2101861	0.0333	0.3312
chr21	48129895	1701492	0.0354	0.3397
chr22	51304566	792957	0.0155	0.21
chrMT	16571	13727	0.8284	1.3961
chrX	155270560	5324306	0.0343	0.3436
chrY	59373566	247111	0.0042	0.1126

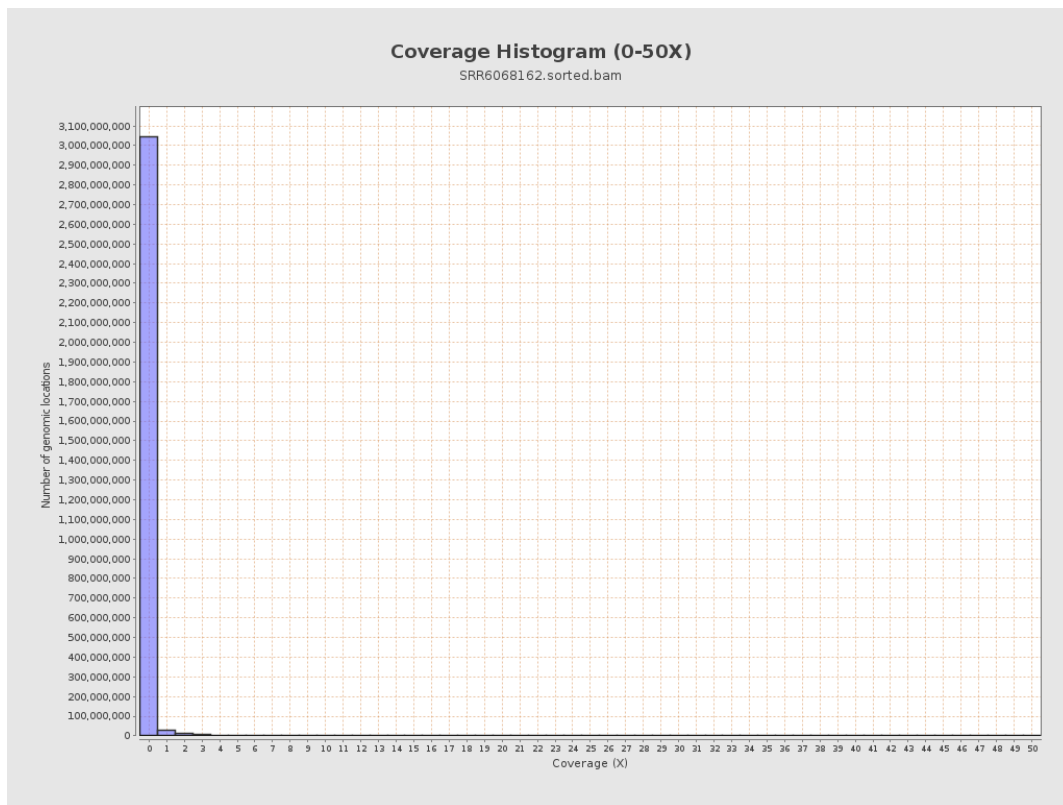
3. Results : Coverage across reference



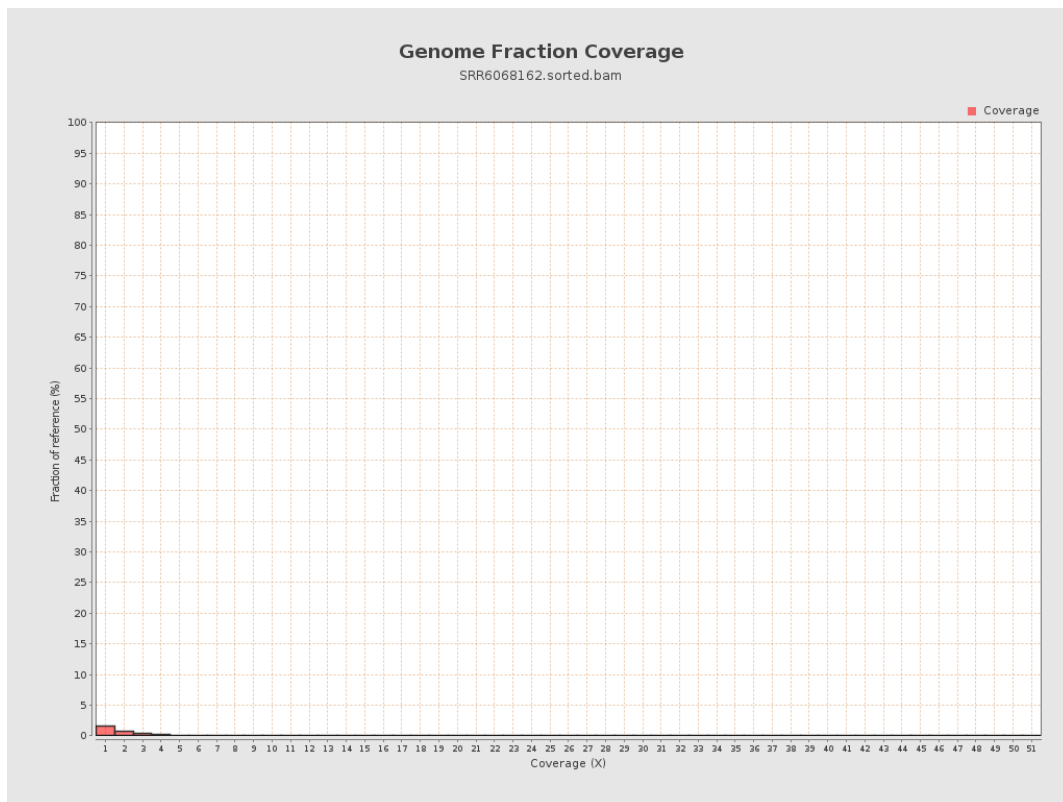
4. Results : Coverage Histogram



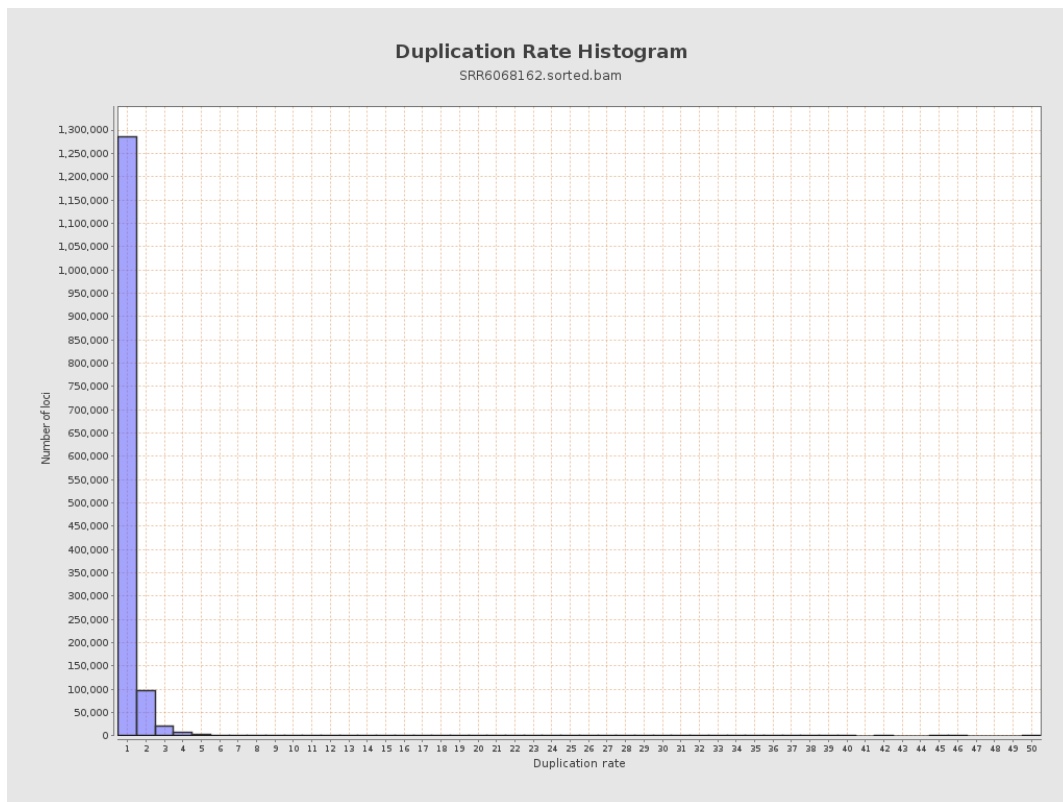
5. Results : Coverage Histogram (0-50X)



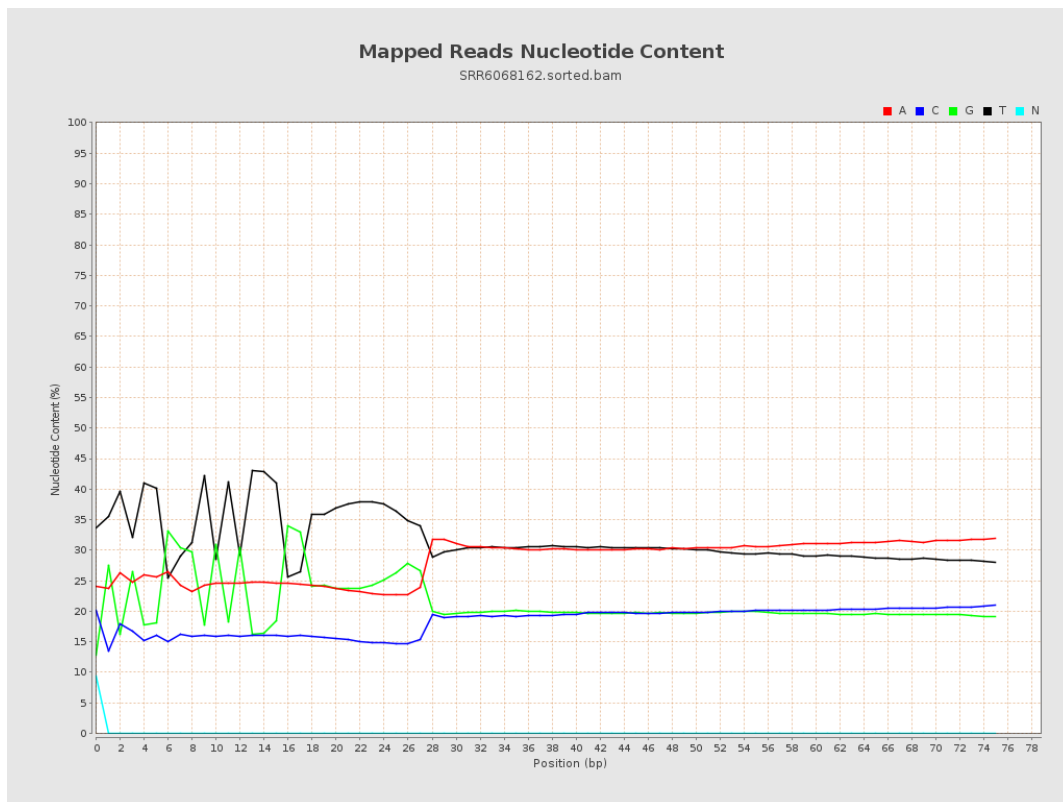
6. Results : Genome Fraction Coverage



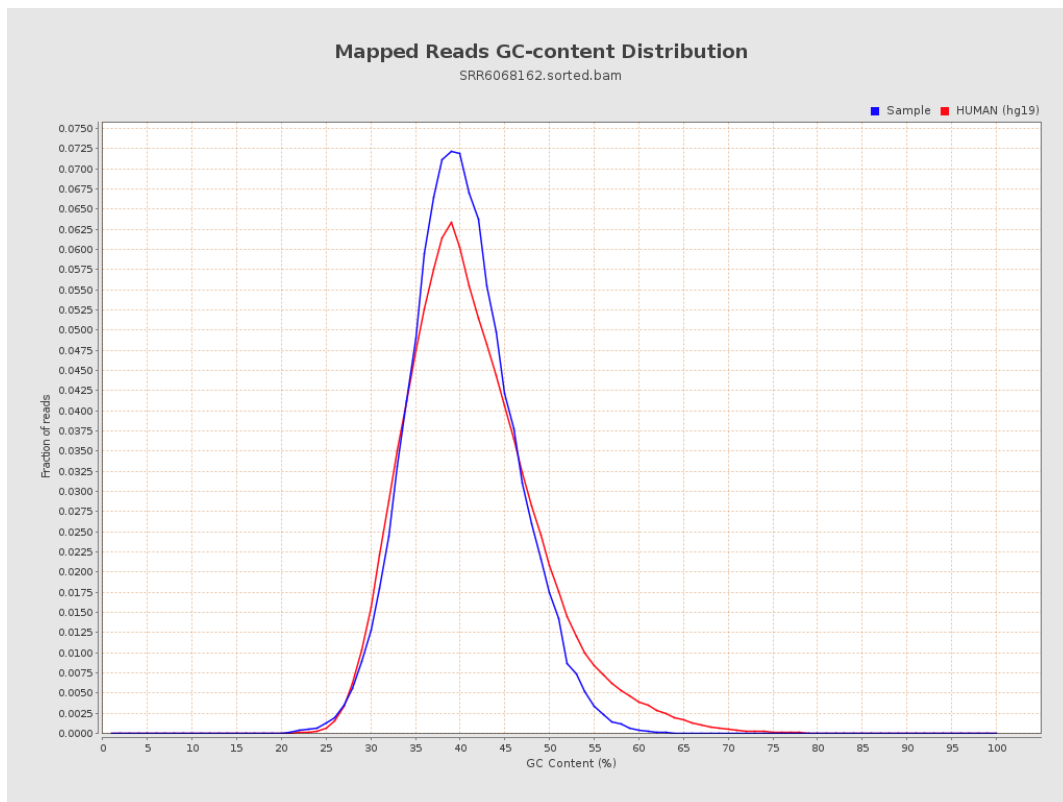
7. Results : Duplication Rate Histogram



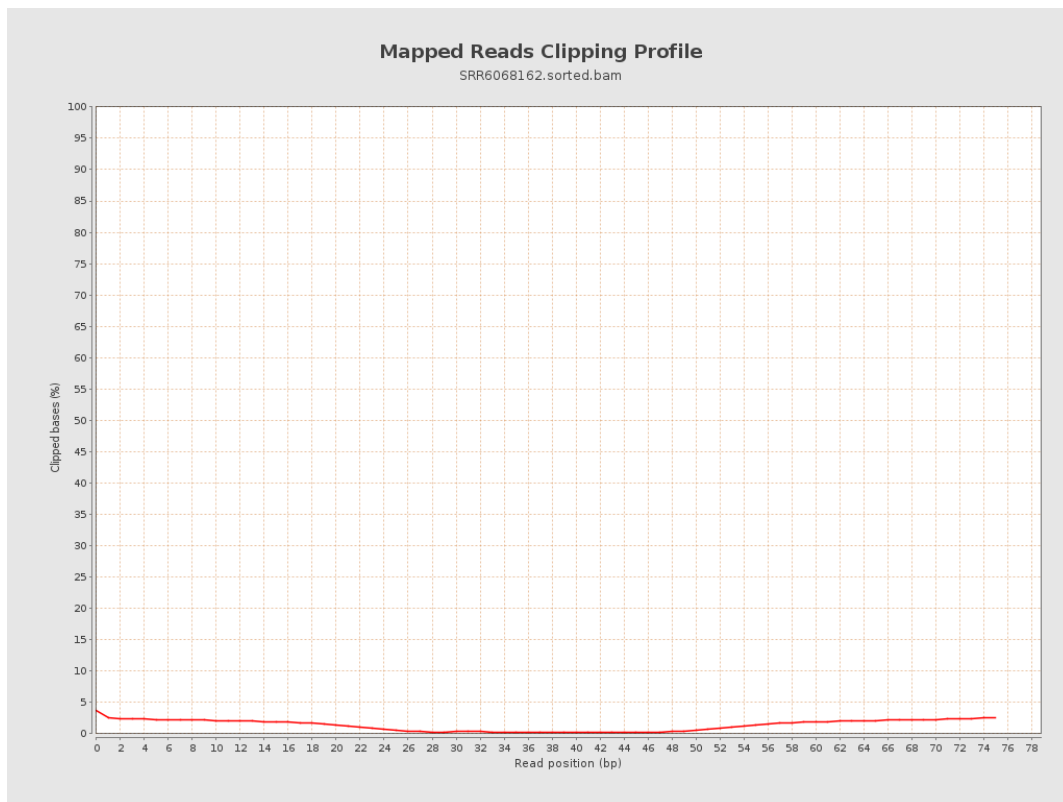
8. Results : Mapped Reads Nucleotide Content



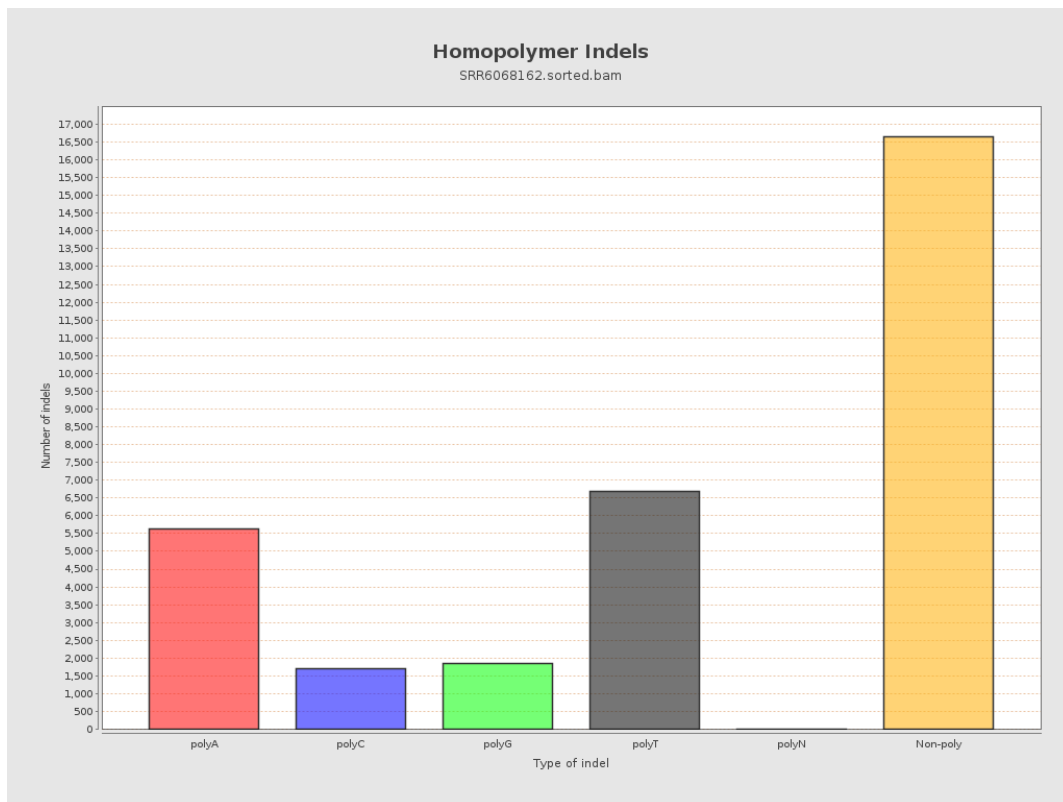
9. Results : Mapped Reads GC-content Distribution



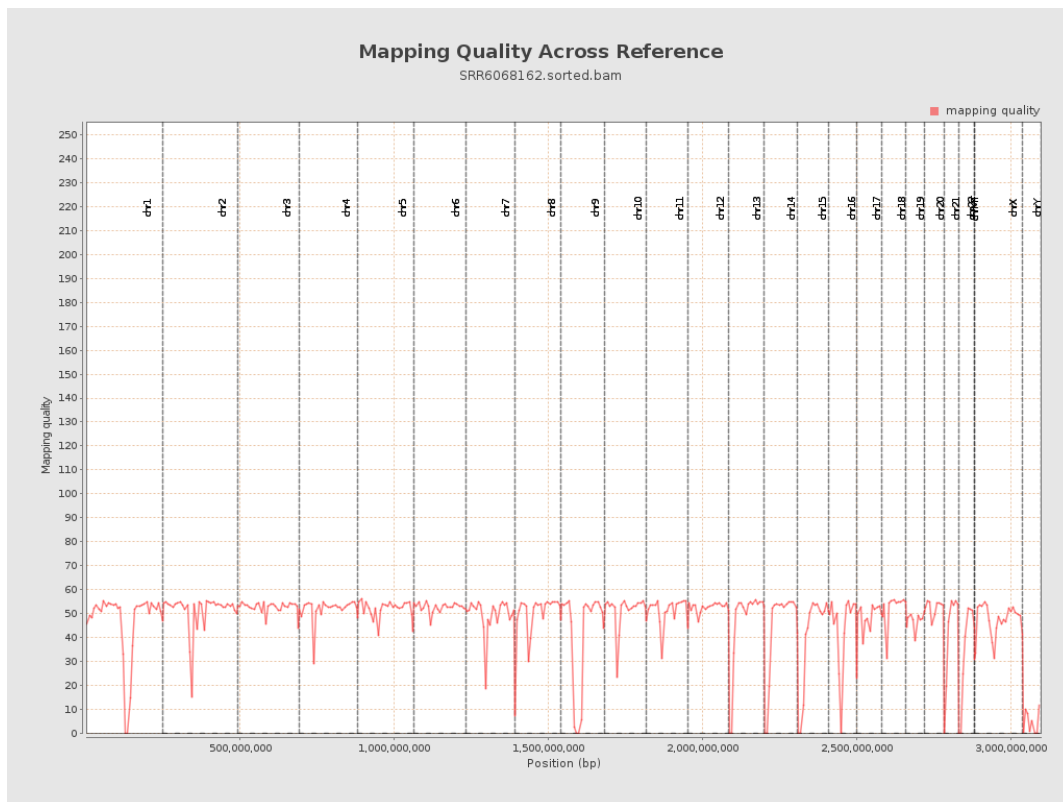
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

