Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:24:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068168.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_SRR6068168 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068168.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:24:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,444,384
Mapped reads	1,313,982 / 90.97%
Unmapped reads	130,402 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,108 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	40,355 / 2.79%
Duplication rate	2.53%
Clipped reads	458,509 / 31.74%

2.2. ACGT Content

Number/percentage of A's	26,296,073 / 28.99%
Number/percentage of C's	17,152,144 / 18.91%
Number/percentage of T's	28,168,082 / 31.05%
Number/percentage of G's	19,002,511 / 20.95%
Number/percentage of N's	93,233 / 0.1%
GC Percentage	39.86%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.271

2.4. Mapping Quality

Mean Mapping Quality	48.03

2.5. Mismatches and indels

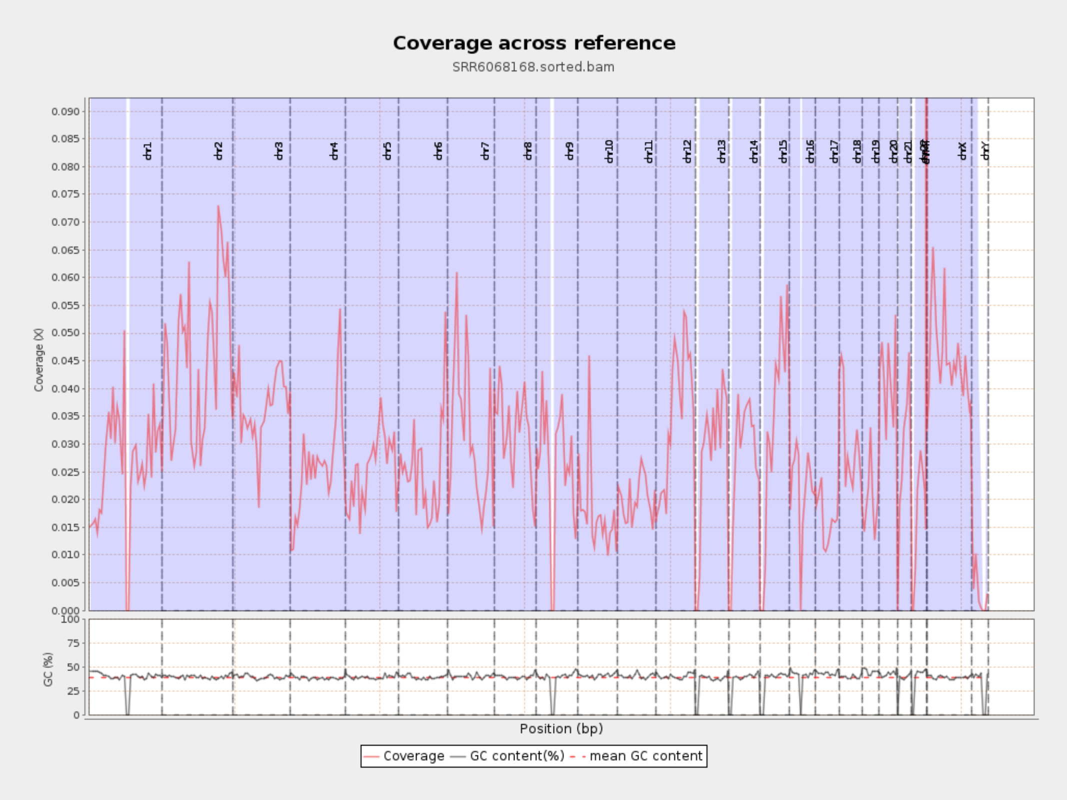
General error rate	0.83%
Mismatches	738,491
Insertions	6,130
Mapped reads with at least one insertion	0.46%
Deletions	22,777
Mapped reads with at least one deletion	1.71%
Homopolymer indels	47.96%

2.6. Chromosome stats

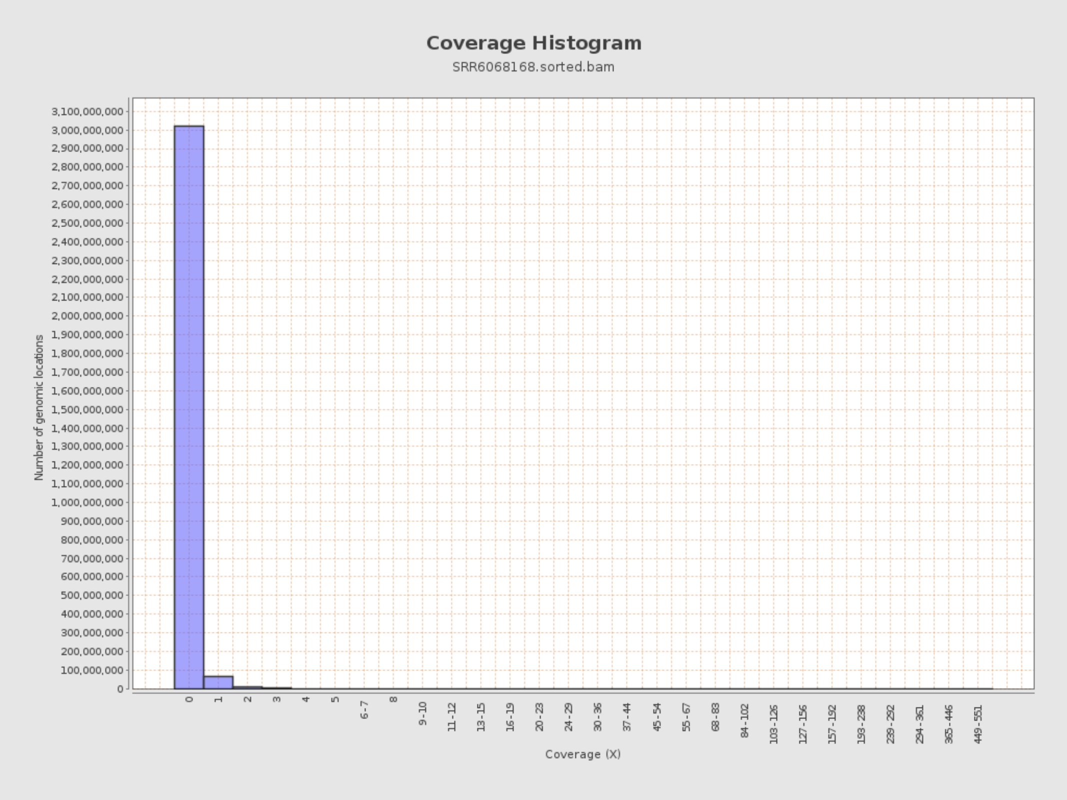
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6472920	0.026	0.477
chr2	243199373	11140673	0.0458	0.3137
chr3	198022430	7265366	0.0367	0.2223
chr4	191154276	5036671	0.0263	0.1904
chr5	180915260	4656432	0.0257	0.1821
chr6	171115067	4368917	0.0255	0.2037
chr7	159138663	5048996	0.0317	0.373

chr8	146364022	4718866	0.0322	0.3146
chr9	141213431	3614761	0.0256	0.2229
chr10	135534747	2388750	0.0176	0.2964
chr11	135006516	2725941	0.0202	0.1793
chr12	133851895	4724522	0.0353	0.2128
chr13	115169878	3252651	0.0282	0.1904
chr14	107349540	2916061	0.0272	0.1902
chr15	102531392	3388977	0.0331	0.2054
chr16	90354753	2009797	0.0222	0.18
chr17	81195210	1321899	0.0163	0.15
chr18	78077248	2394670	0.0307	0.3683
chr19	59128983	1200017	0.0203	0.3039
chr20	63025520	2644805	0.042	0.2349
chr21	48129895	1339879	0.0278	0.193
chr22	51304566	844355	0.0165	0.1449
chrMT	16571	13364	0.8065	0.9738
chrX	155270560	7053634	0.0454	0.2619
chrY	59373566	209474	0.0035	0.0849

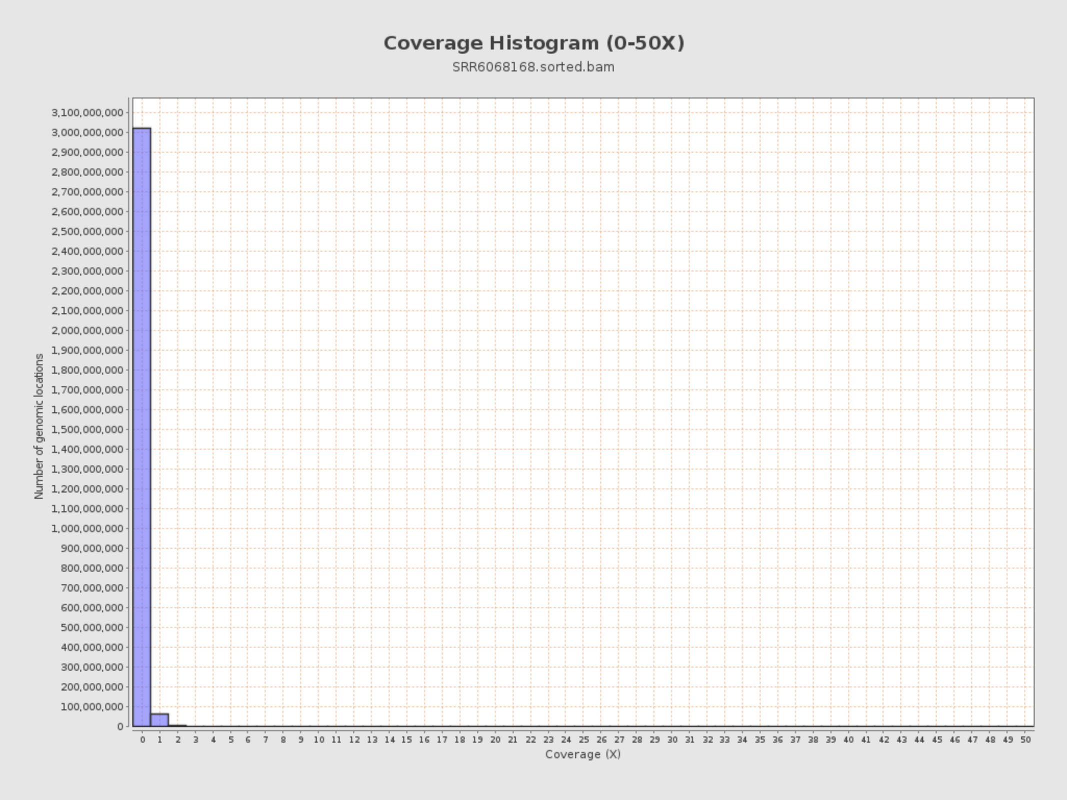
3. Results : Coverage across reference



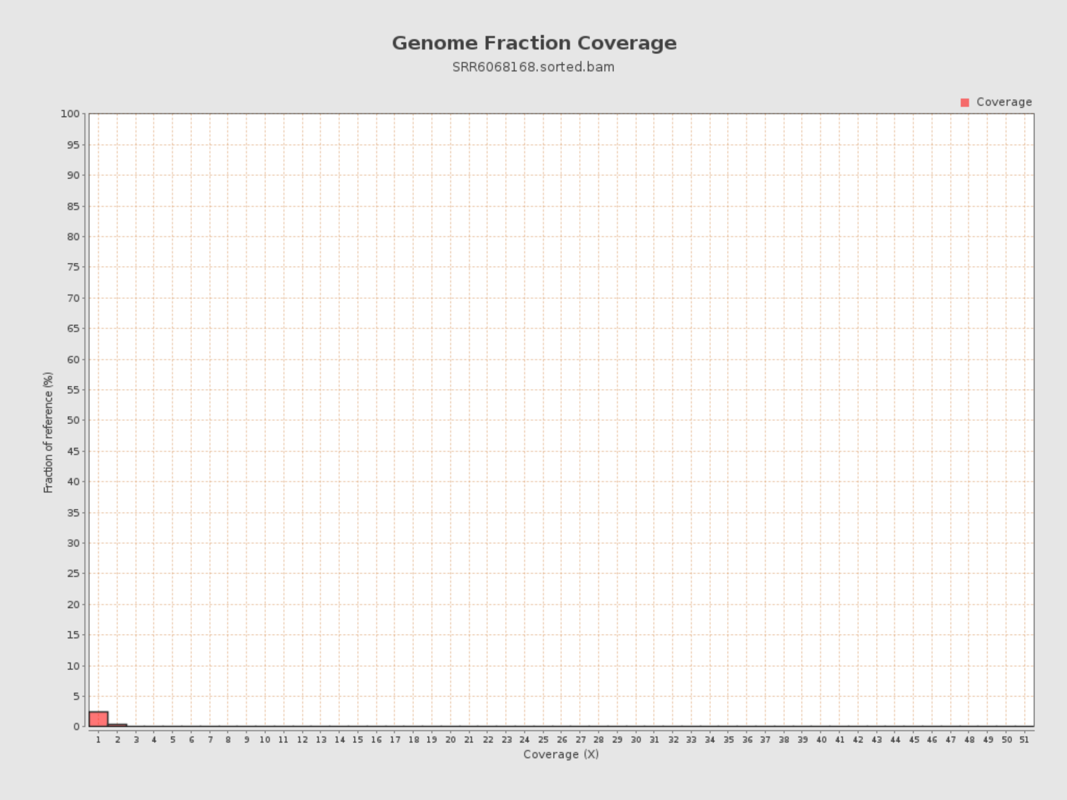
4. Results : Coverage Histogram



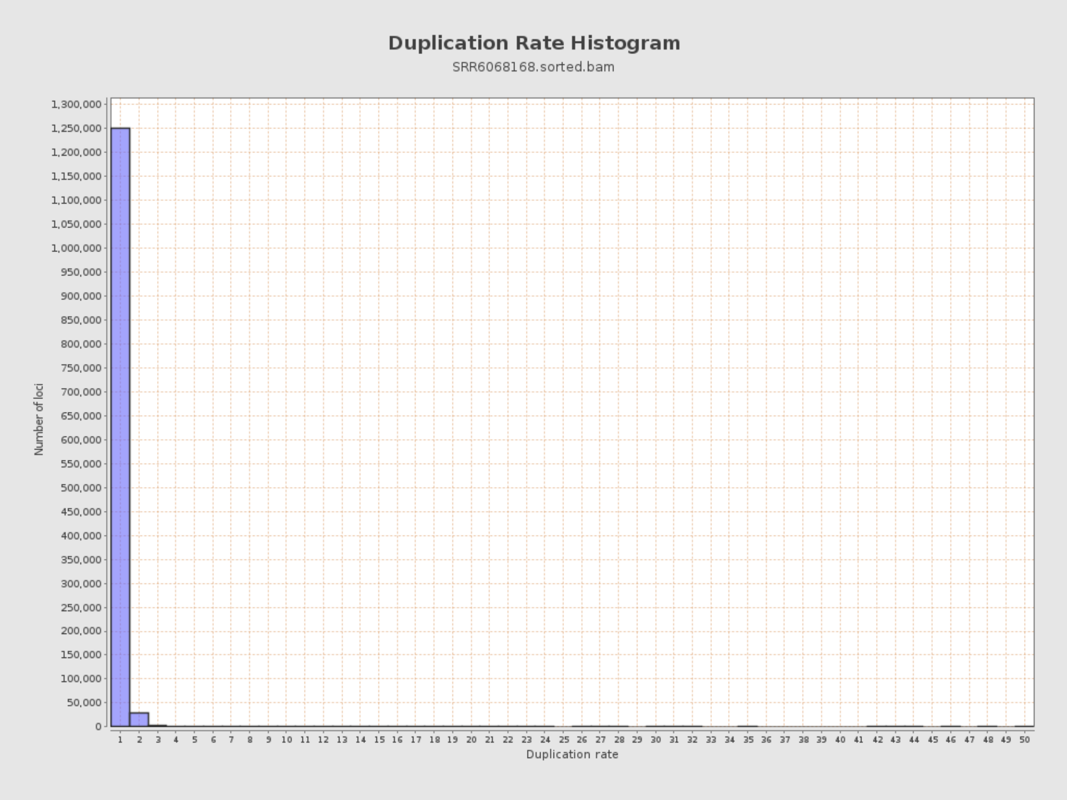
5. Results : Coverage Histogram (0-50X)



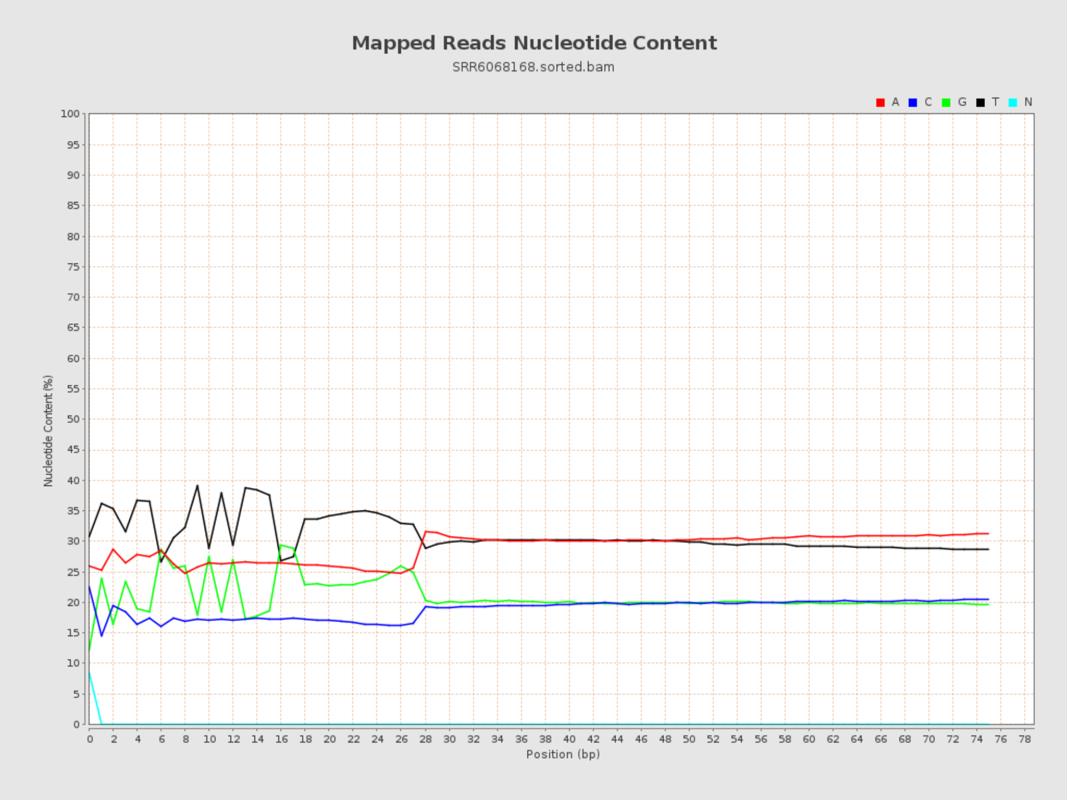
6. Results : Genome Fraction Coverage



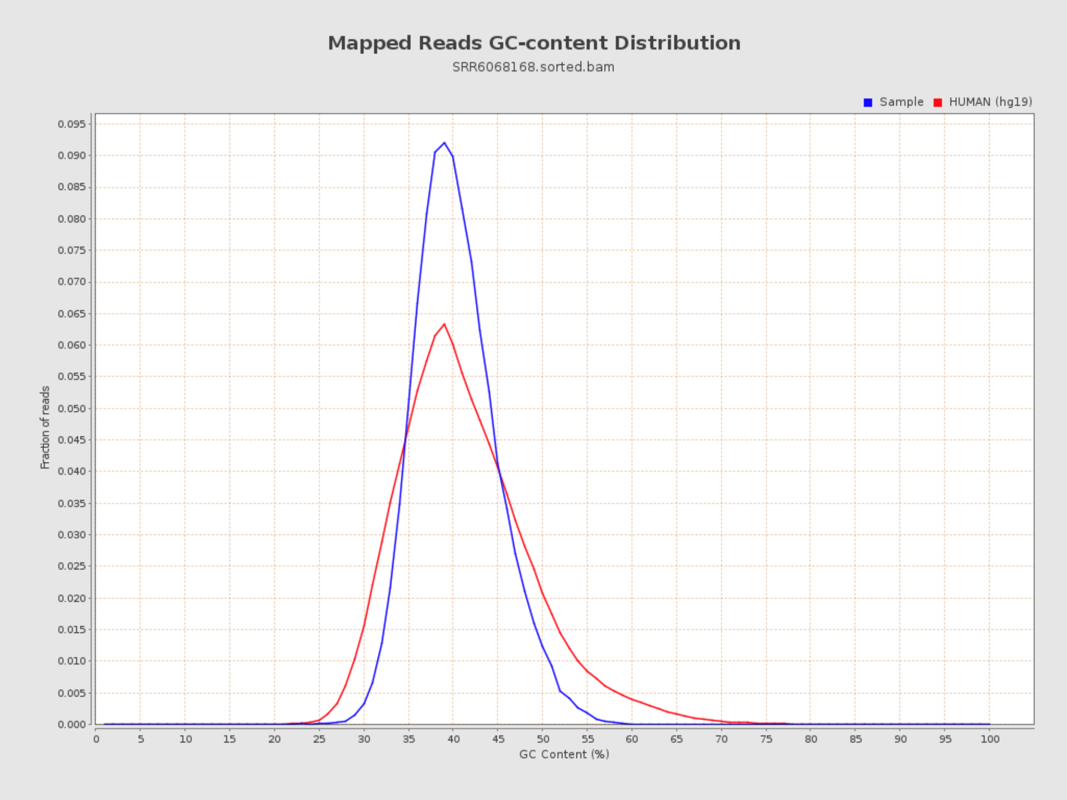
7. Results : Duplication Rate Histogram



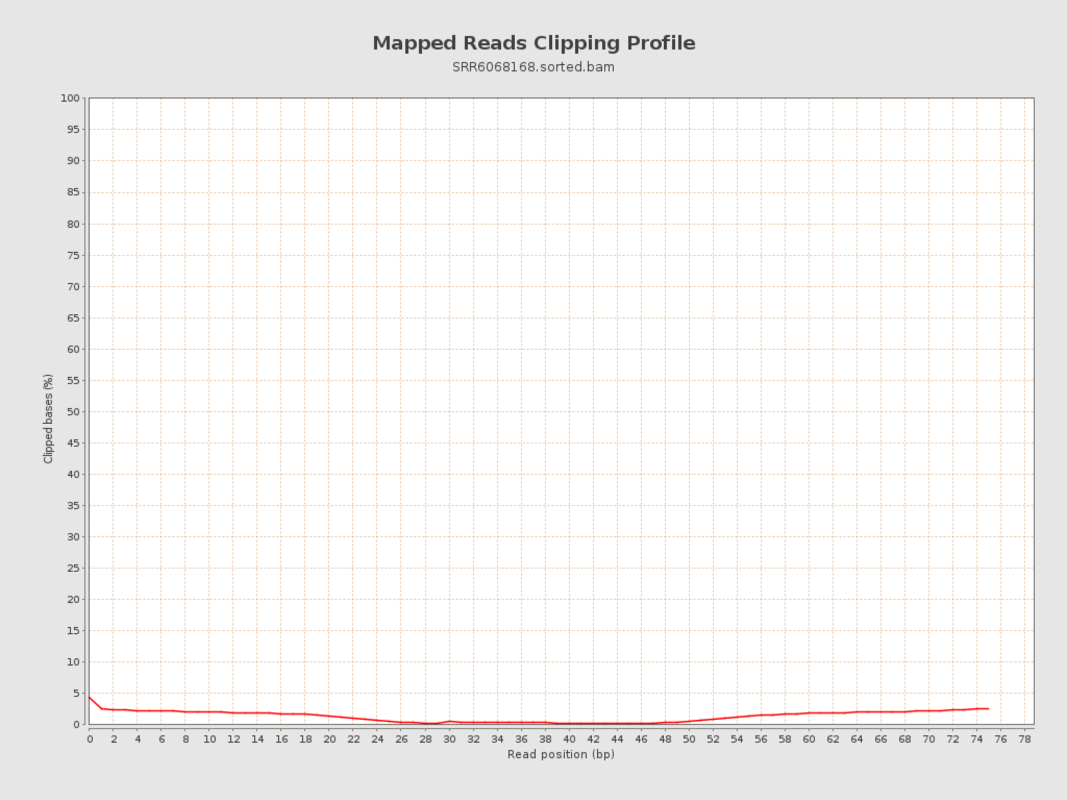
8. Results : Mapped Reads Nucleotide Content



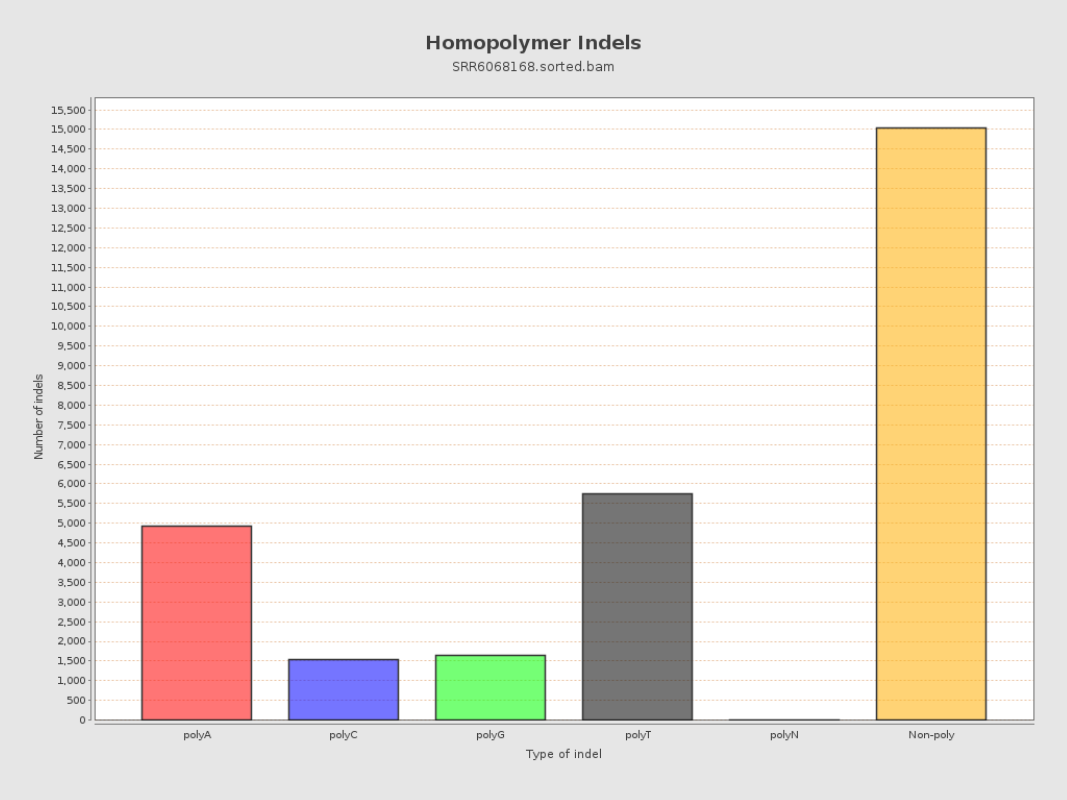
9. Results : Mapped Reads GC-content Distribution



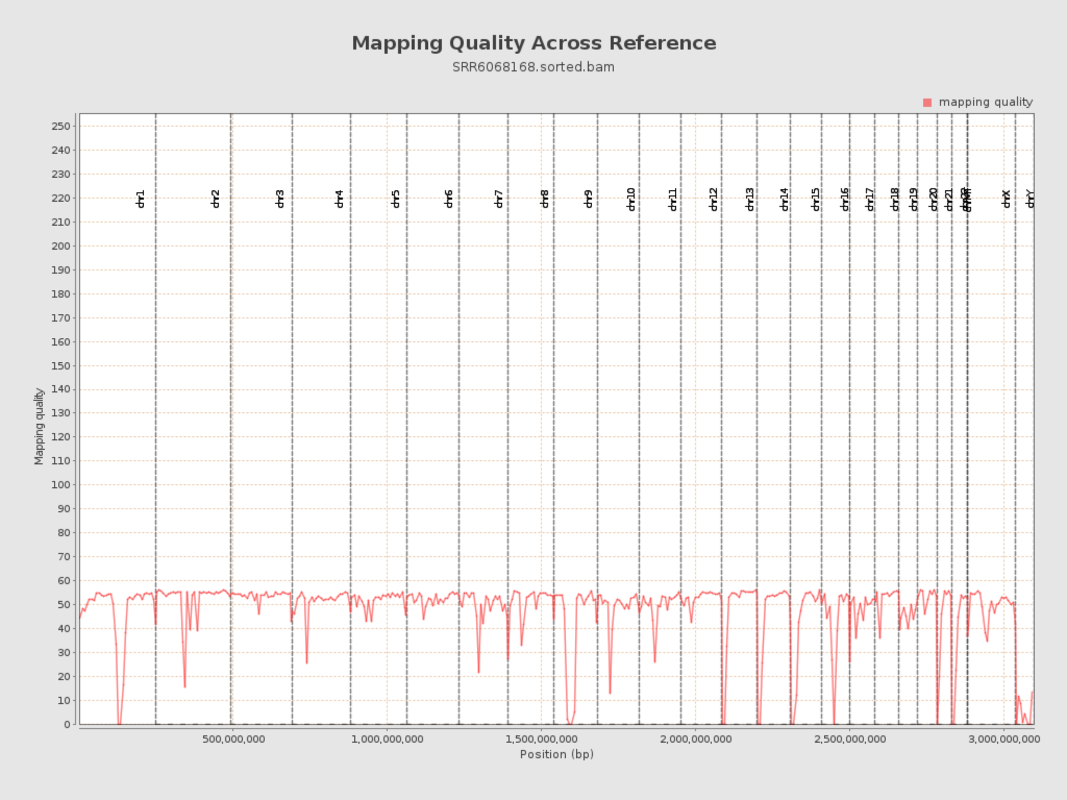
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram