Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:29:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068075.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_SRR6068075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:29:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,184,156
Mapped reads	4,895,382 / 94.43%
Unmapped reads	288,774 / 5.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,519 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	873,580 / 16.85%
Duplication rate	14.37%
Clipped reads	2,583,491 / 49.83%

2.2. ACGT Content

Number/percentage of A's	82,253,232 / 26.12%
Number/percentage of C's	56,522,645 / 17.95%
Number/percentage of T's	102,726,811 / 32.63%
Number/percentage of G's	73,328,437 / 23.29%
Number/percentage of N's	36,569 / 0.01%
GC Percentage	41.24%

2.3. Coverage

Mean	0.1018

Standard Deviation	1.1712

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

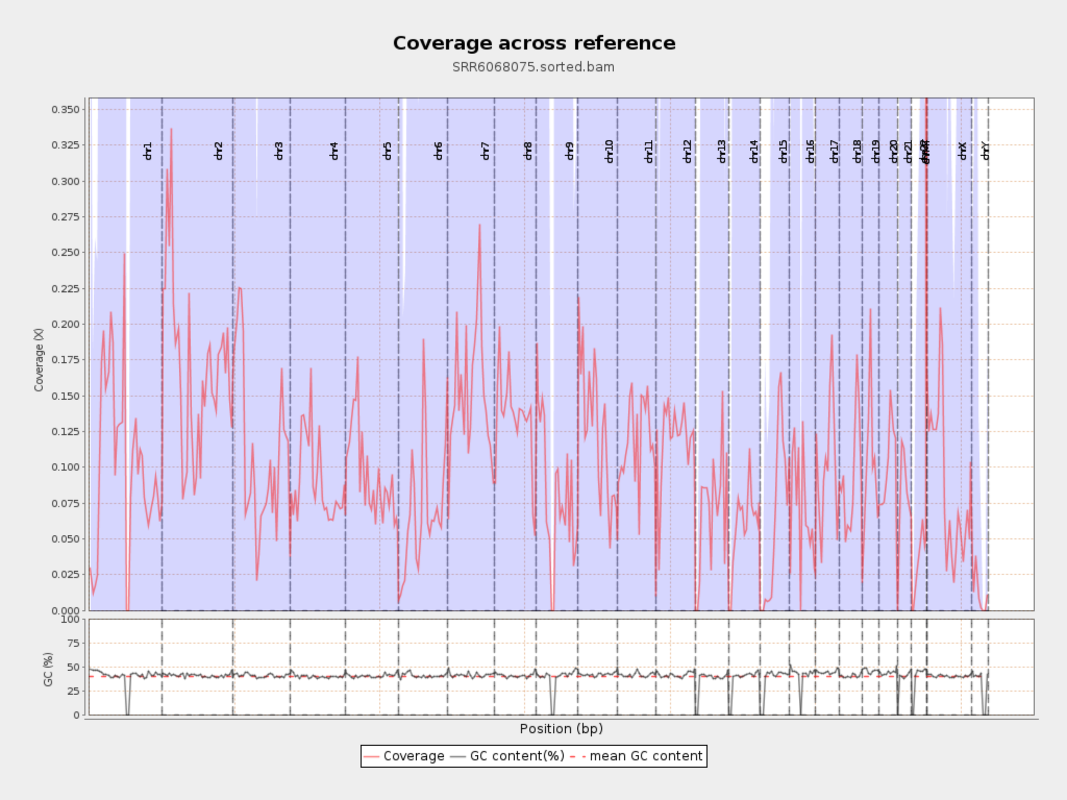
General error rate	0.56%
Mismatches	1,724,152
Insertions	19,415
Mapped reads with at least one insertion	0.39%
Deletions	73,709
Mapped reads with at least one deletion	1.49%
Homopolymer indels	44.67%

2.6. Chromosome stats

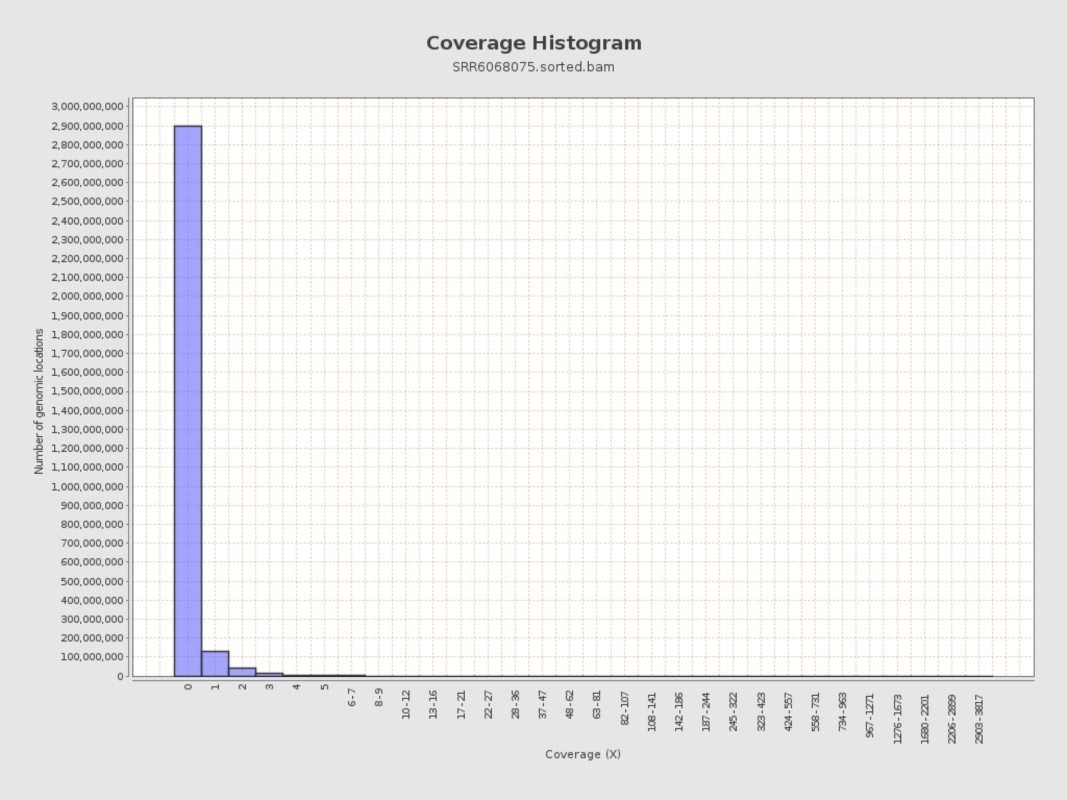
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25224142	0.1012	2.677
chr2	243199373	41269300	0.1697	1.8333
chr3	198022430	22175711	0.112	0.4981
chr4	191154276	17182770	0.0899	0.4625
chr5	180915260	17267989	0.0954	0.4679
chr6	171115067	11941786	0.0698	0.6212
chr7	159138663	24286173	0.1526	1.3805

chr8	146364022	19636880	0.1342	1.2904
chr9	141213431	11088216	0.0785	0.718
chr10	135534747	17039996	0.1257	0.8193
chr11	135006516	15837371	0.1173	1.0665
chr12	133851895	16066749	0.12	0.564
chr13	115169878	8002959	0.0695	0.4503
chr14	107349540	6319585	0.0589	0.4612
chr15	102531392	6231804	0.0608	0.4233
chr16	90354753	6402372	0.0709	0.4564
chr17	81195210	8264025	0.1018	0.5872
chr18	78077248	7464341	0.0956	1.3953
chr19	59128983	6156197	0.1041	1.6554
chr20	63025520	6336661	0.1005	0.4994
chr21	48129895	3808525	0.0791	0.4538
chr22	51304566	1670178	0.0326	0.2551
chrMT	16571	644810	38.912	20.6186
chrX	155270560	13956524	0.0899	0.542
chrY	59373566	720424	0.0121	0.2866

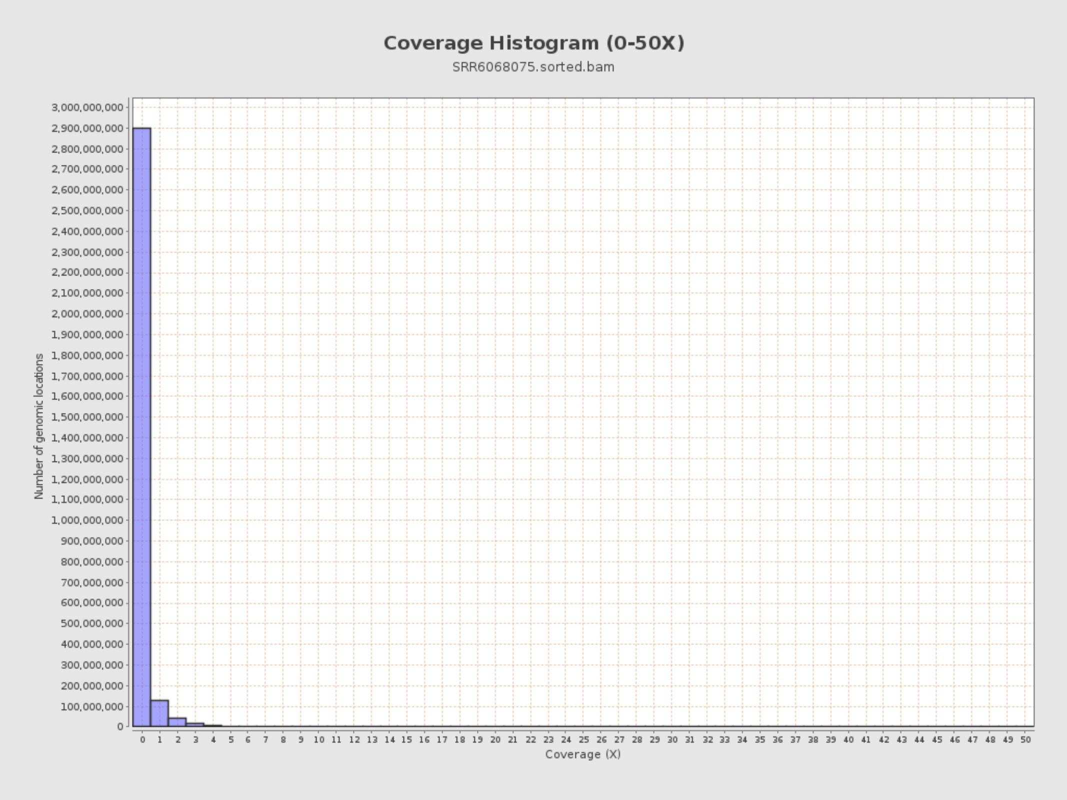
3. Results : Coverage across reference



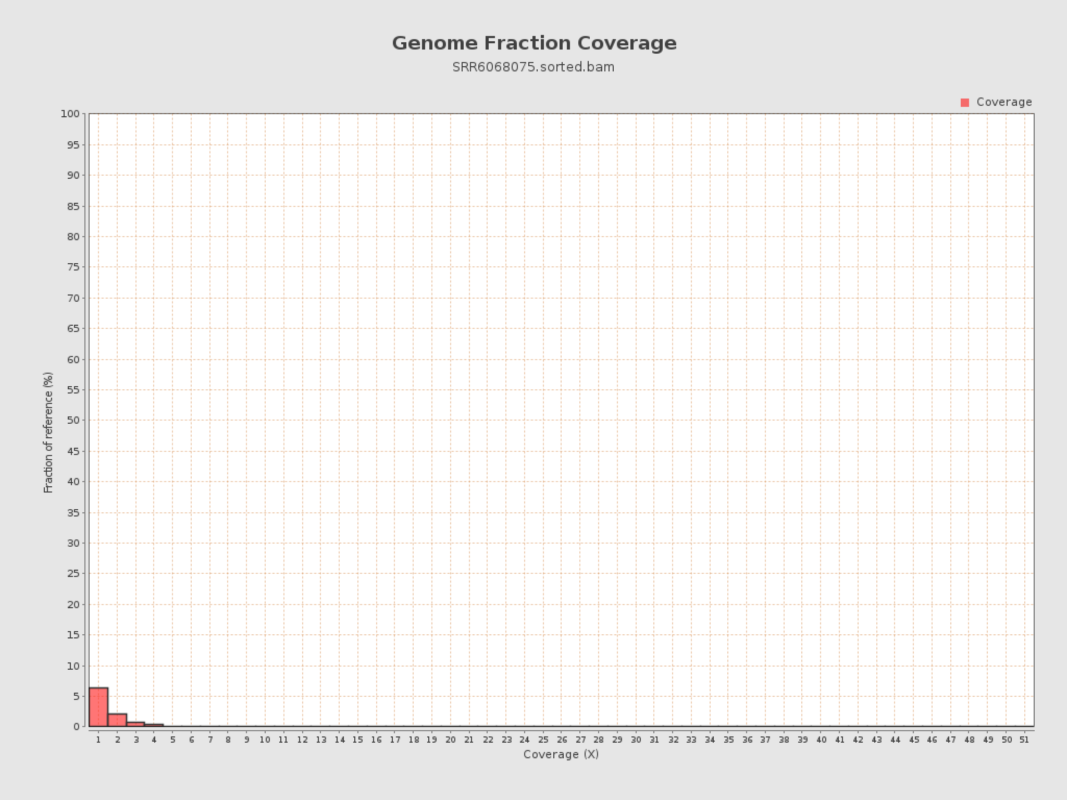
4. Results : Coverage Histogram



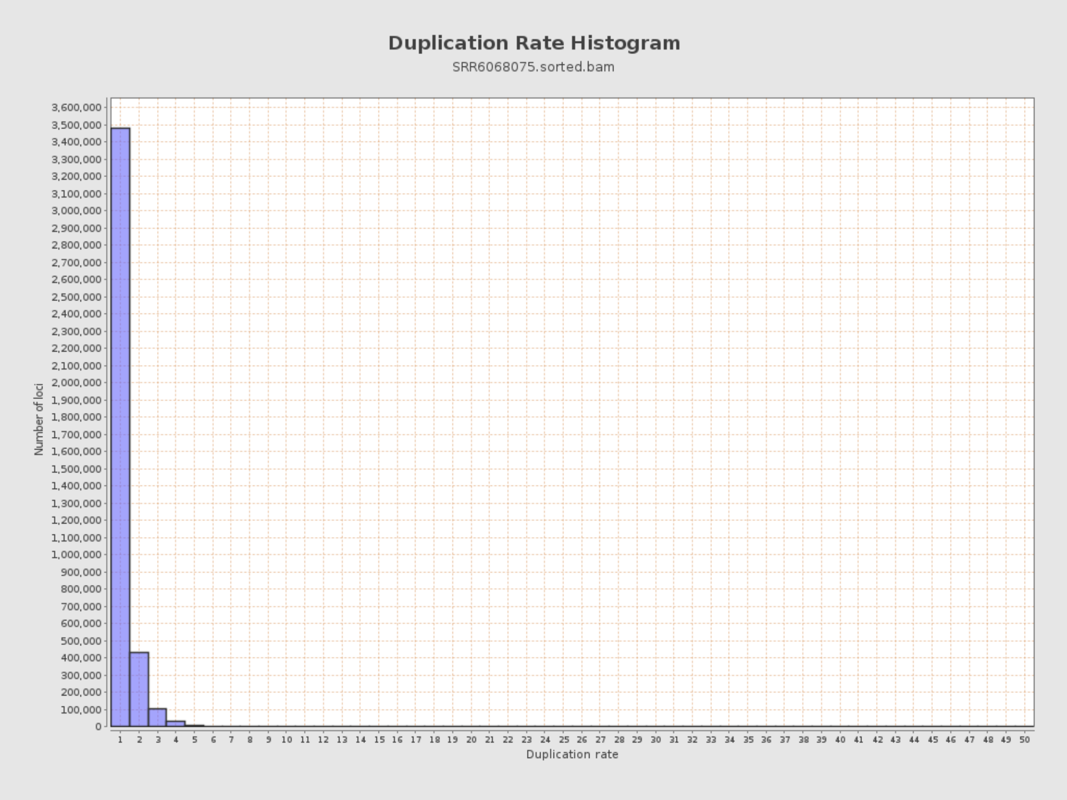
5. Results : Coverage Histogram (0-50X)



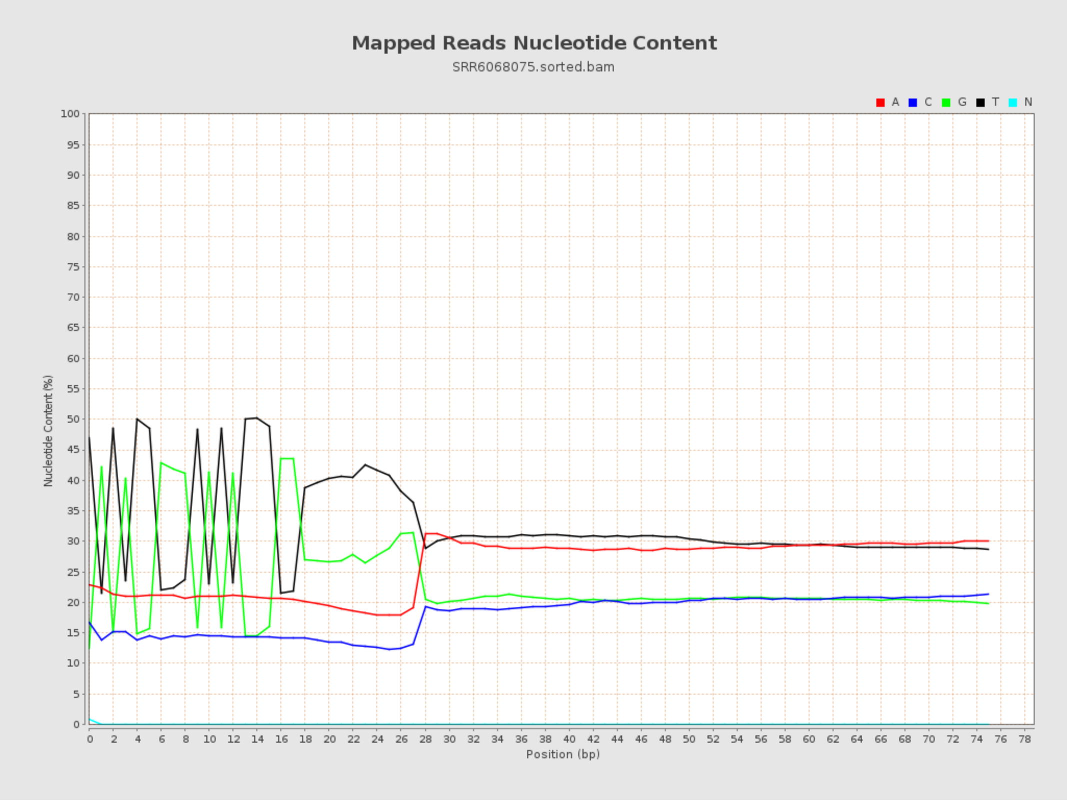
6. Results : Genome Fraction Coverage



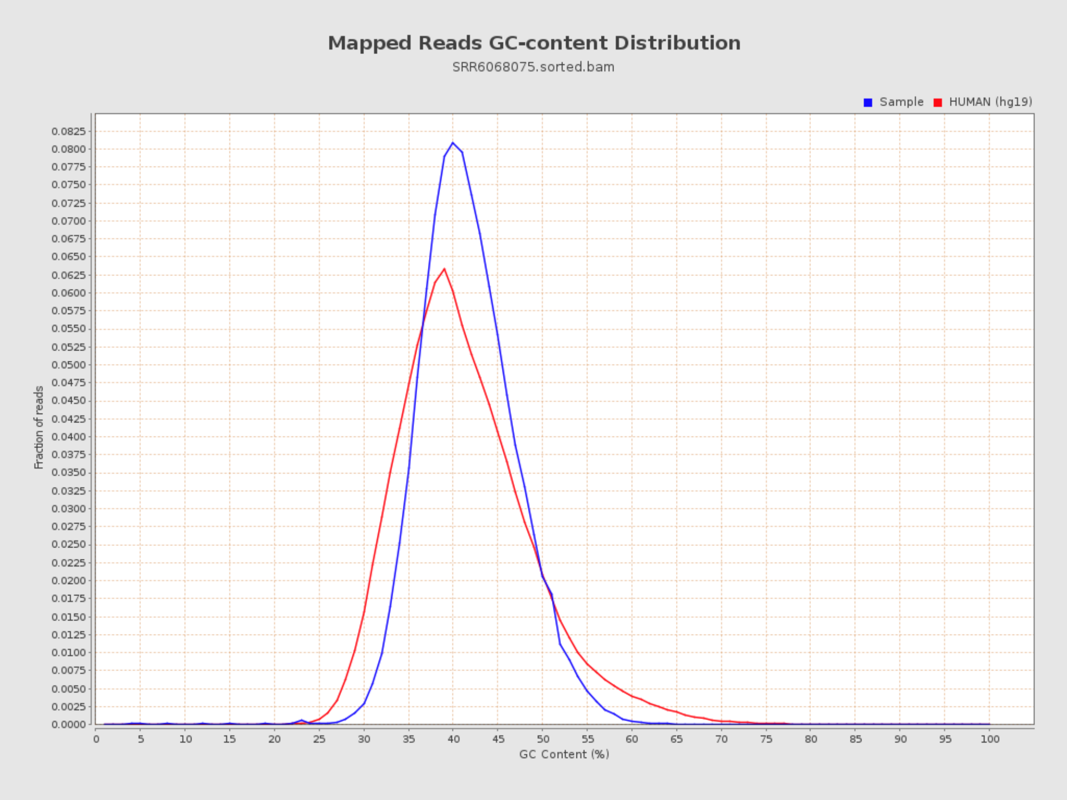
7. Results : Duplication Rate Histogram



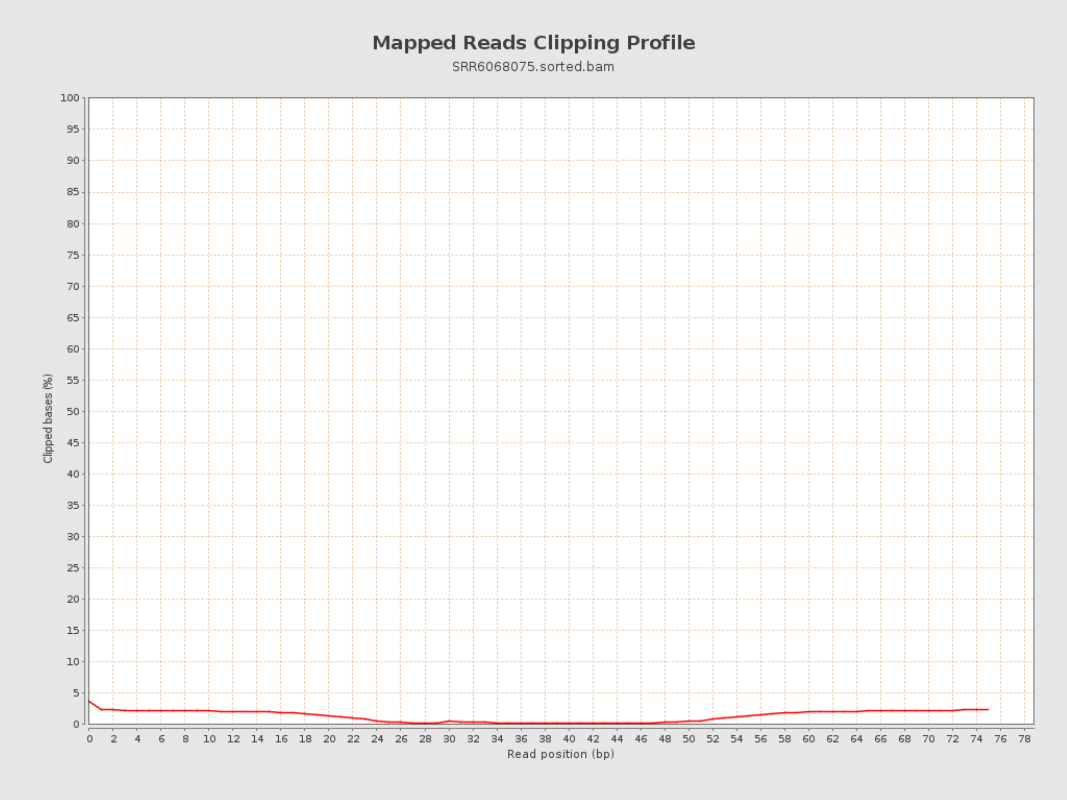
8. Results : Mapped Reads Nucleotide Content



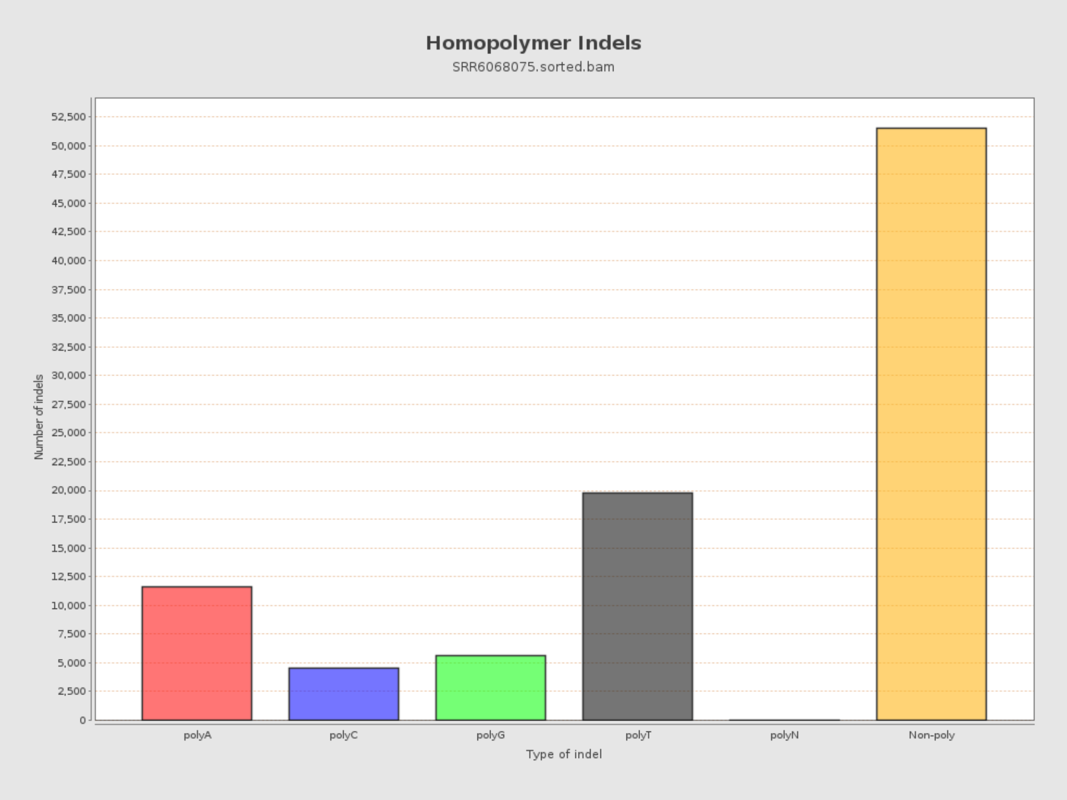
9. Results : Mapped Reads GC-content Distribution



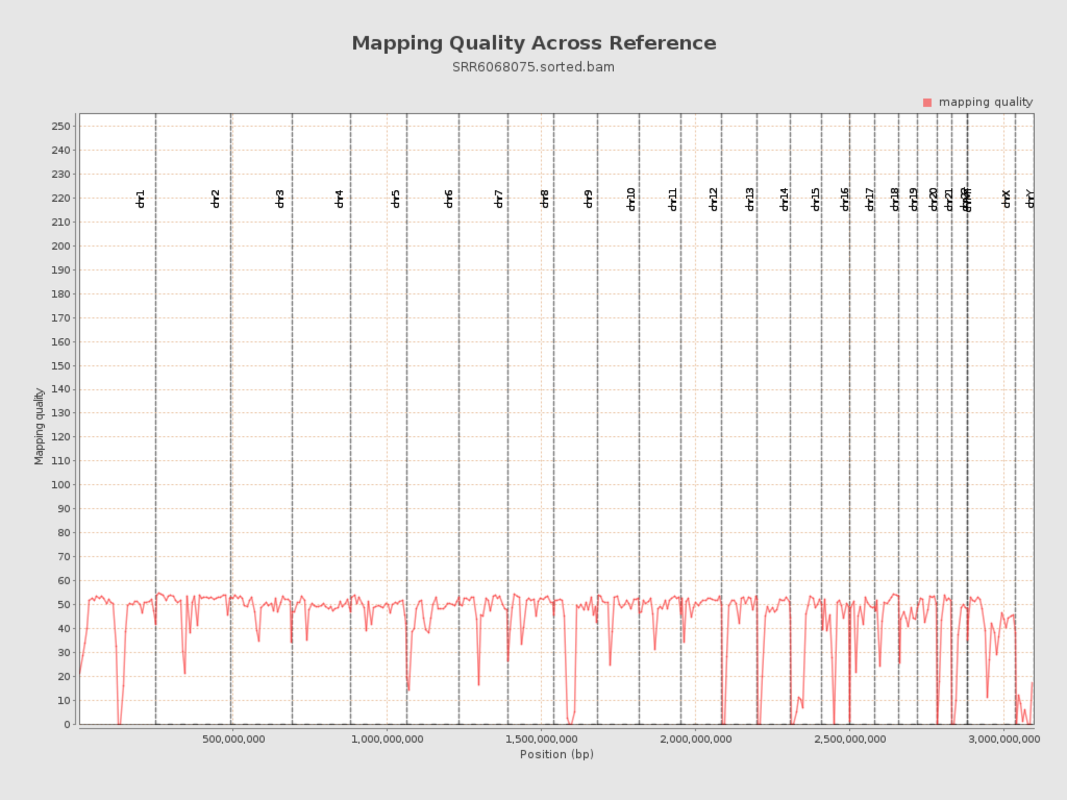
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram