Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:59:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068083.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_SRR6068083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:59:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,191,394
Mapped reads	2,858,615 / 89.57%
Unmapped reads	332,779 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,925 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	203,854 / 6.39%
Duplication rate	5.36%
Clipped reads	1,262,015 / 39.54%

2.2. ACGT Content

Number/percentage of A's	54,075,360 / 28.23%
Number/percentage of C's	35,541,576 / 18.56%
Number/percentage of T's	60,625,113 / 31.65%
Number/percentage of G's	41,299,739 / 21.56%
Number/percentage of N's	4,021 / 0%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0619

Standard Deviation	0.7008

2.4. Mapping Quality

Mean Mapping Quality	43.18

2.5. Mismatches and indels

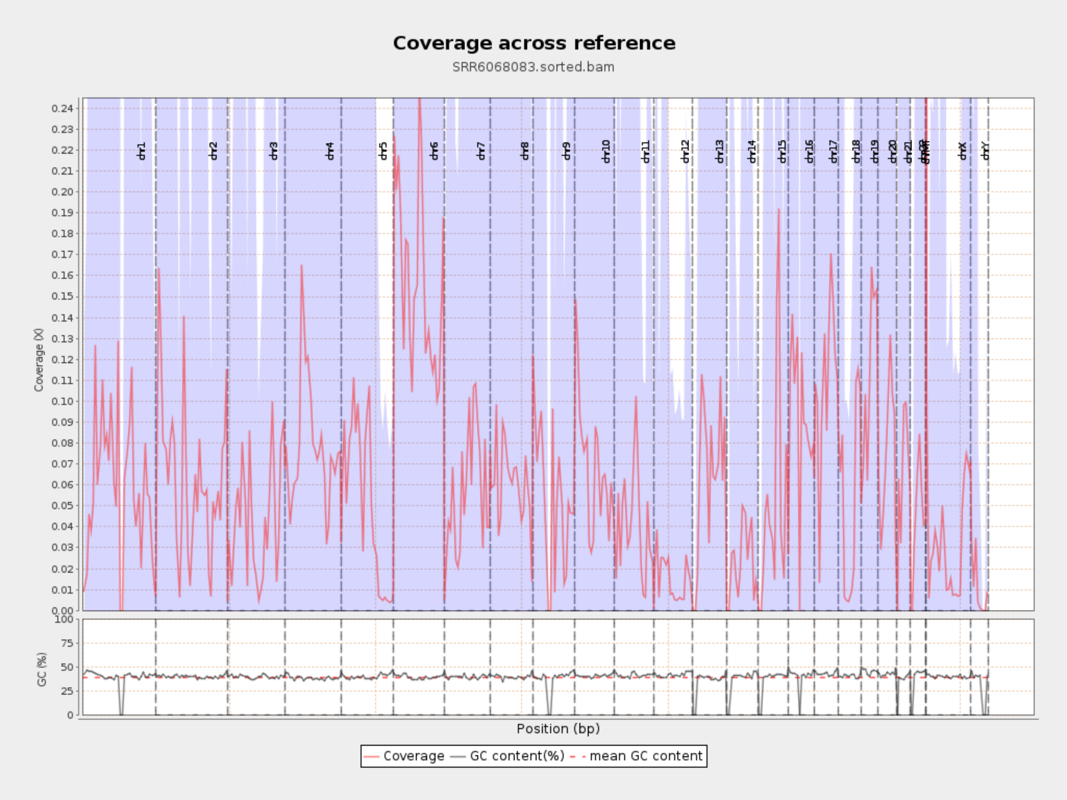
General error rate	0.82%
Mismatches	1,547,657
Insertions	15,935
Mapped reads with at least one insertion	0.55%
Deletions	54,523
Mapped reads with at least one deletion	1.89%
Homopolymer indels	46.74%

2.6. Chromosome stats

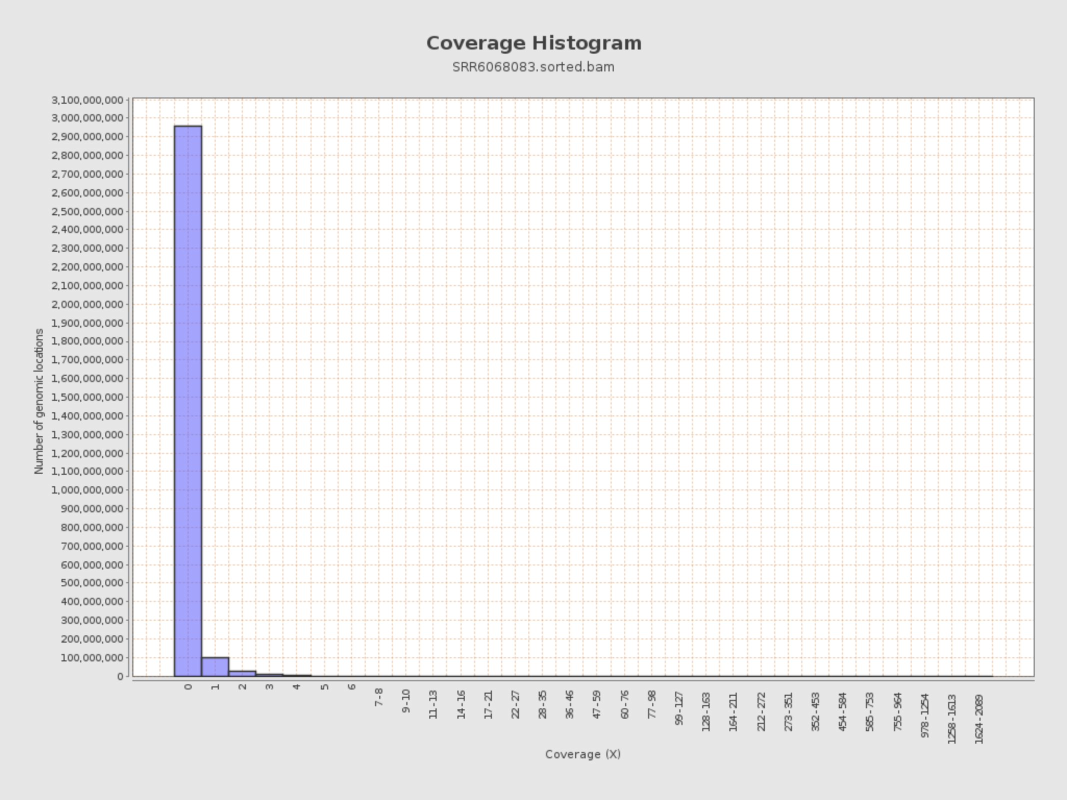
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14753602	0.0592	1.4948
chr2	243199373	15609825	0.0642	0.7167
chr3	198022430	8482889	0.0428	0.2782
chr4	191154276	15097388	0.079	0.3782
chr5	180915260	9368089	0.0518	0.309
chr6	171115067	27019296	0.1579	0.5652
chr7	159138663	9032731	0.0568	0.4592

chr8	146364022	8889298	0.0607	1.2568
chr9	141213431	7263072	0.0514	0.7229
chr10	135534747	9372792	0.0692	0.4475
chr11	135006516	5437589	0.0403	0.3485
chr12	133851895	2075854	0.0155	0.2467
chr13	115169878	7569142	0.0657	0.3333
chr14	107349540	2474861	0.0231	0.3286
chr15	102531392	5494393	0.0536	0.3066
chr16	90354753	8152647	0.0902	0.4649
chr17	81195210	8983066	0.1106	0.4438
chr18	78077248	4075208	0.0522	1.2964
chr19	59128983	6597917	0.1116	1.2221
chr20	63025520	4739920	0.0752	0.4052
chr21	48129895	3156435	0.0656	0.3718
chr22	51304566	2264782	0.0441	0.2691
chrMT	16571	87748	5.2953	4.6809
chrX	155270560	4997119	0.0322	0.2963
chrY	59373566	639394	0.0108	0.3283

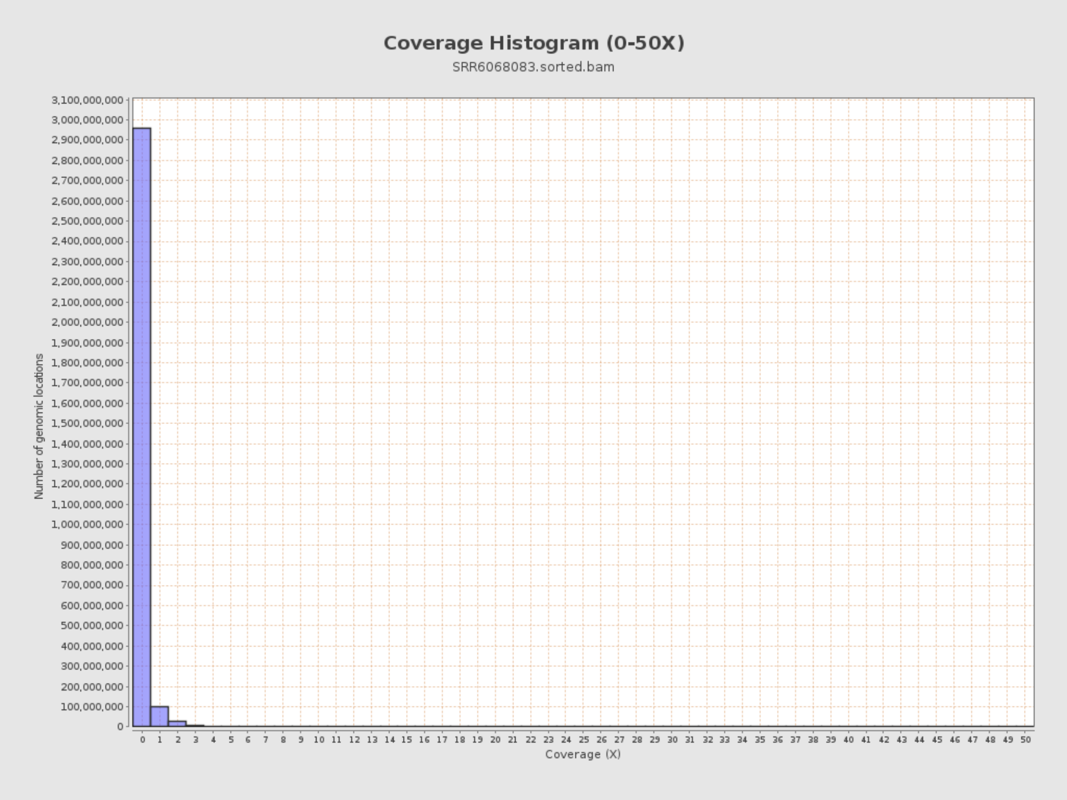
3. Results : Coverage across reference



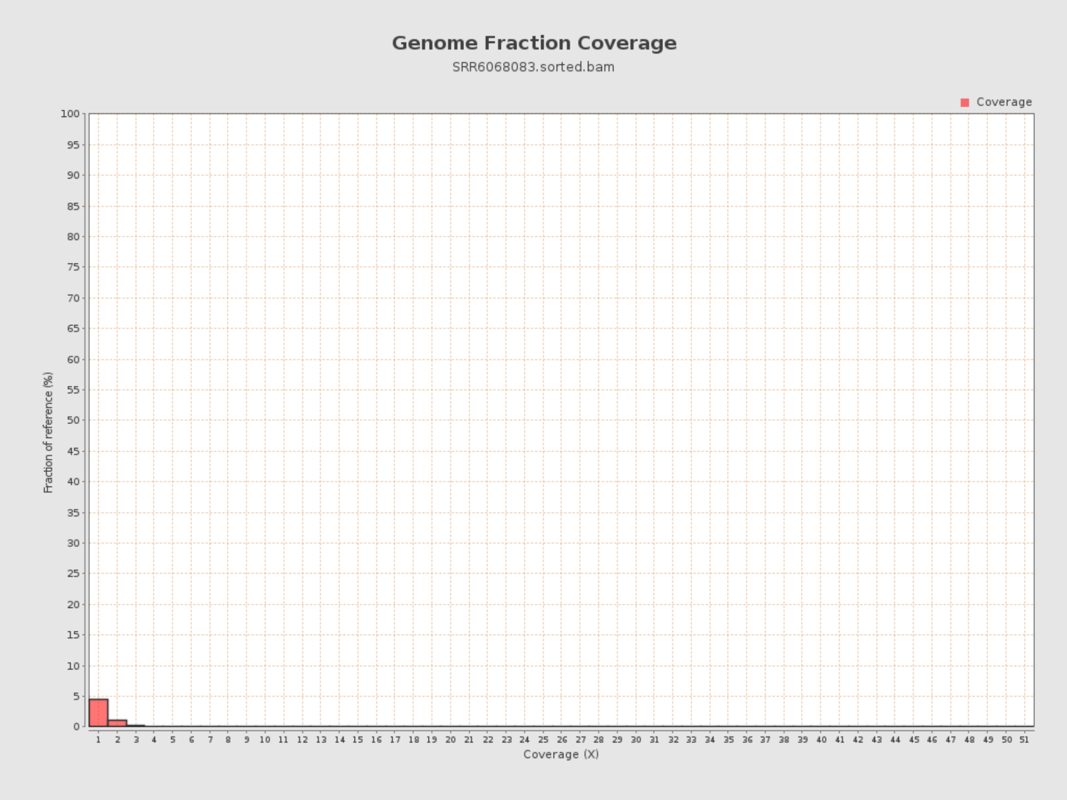
4. Results : Coverage Histogram



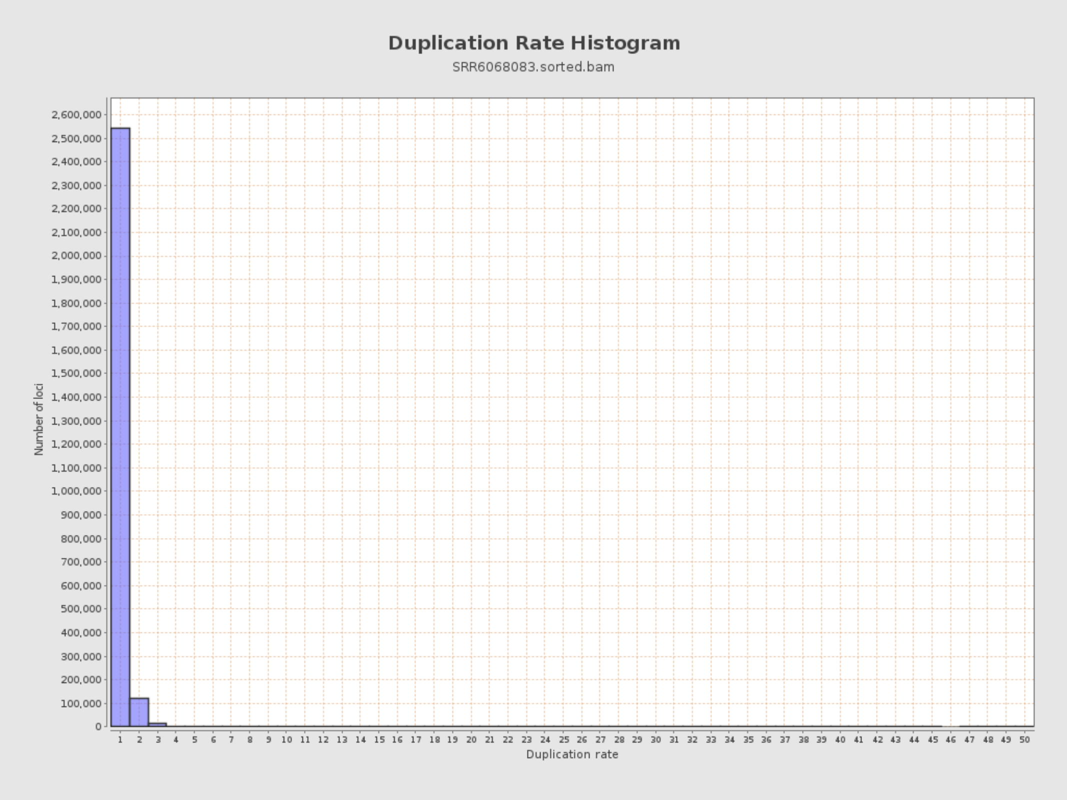
5. Results : Coverage Histogram (0-50X)



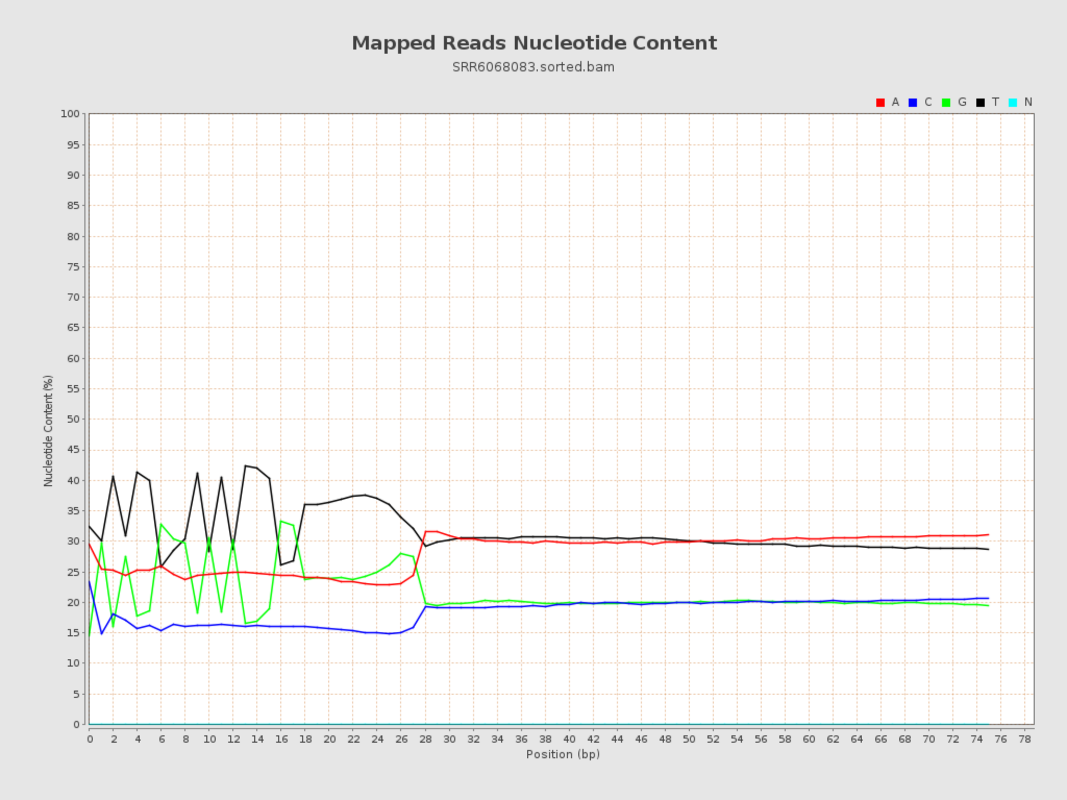
6. Results : Genome Fraction Coverage



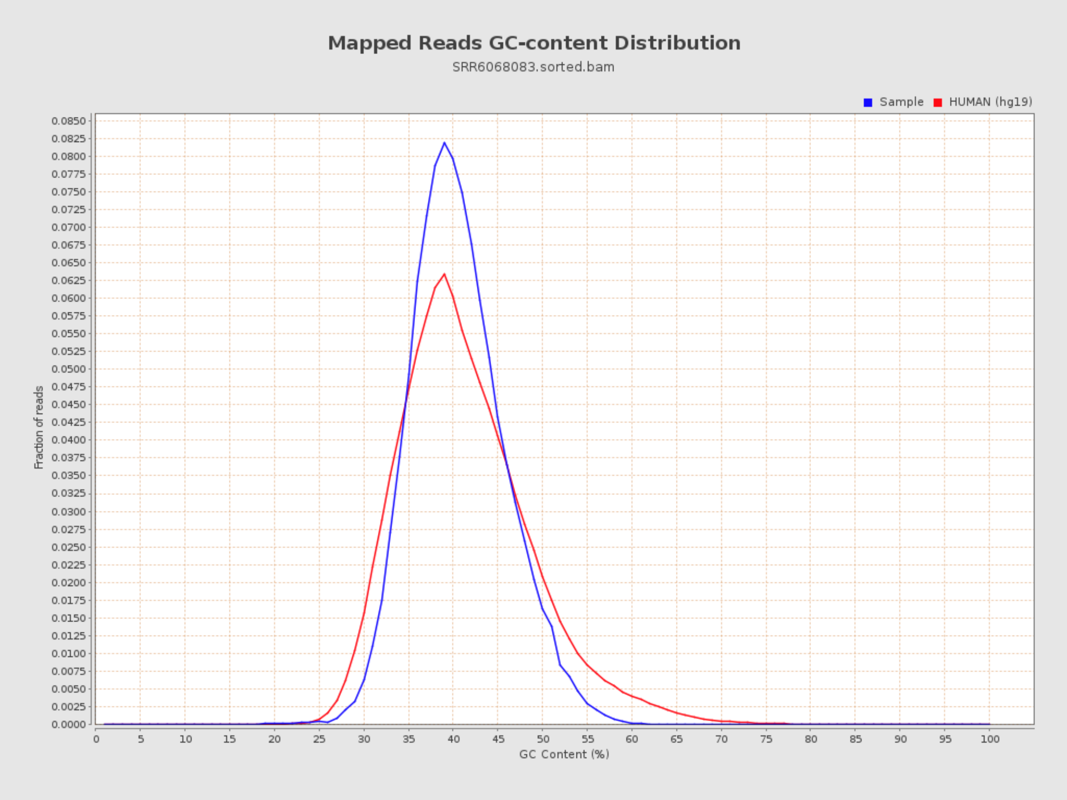
7. Results : Duplication Rate Histogram



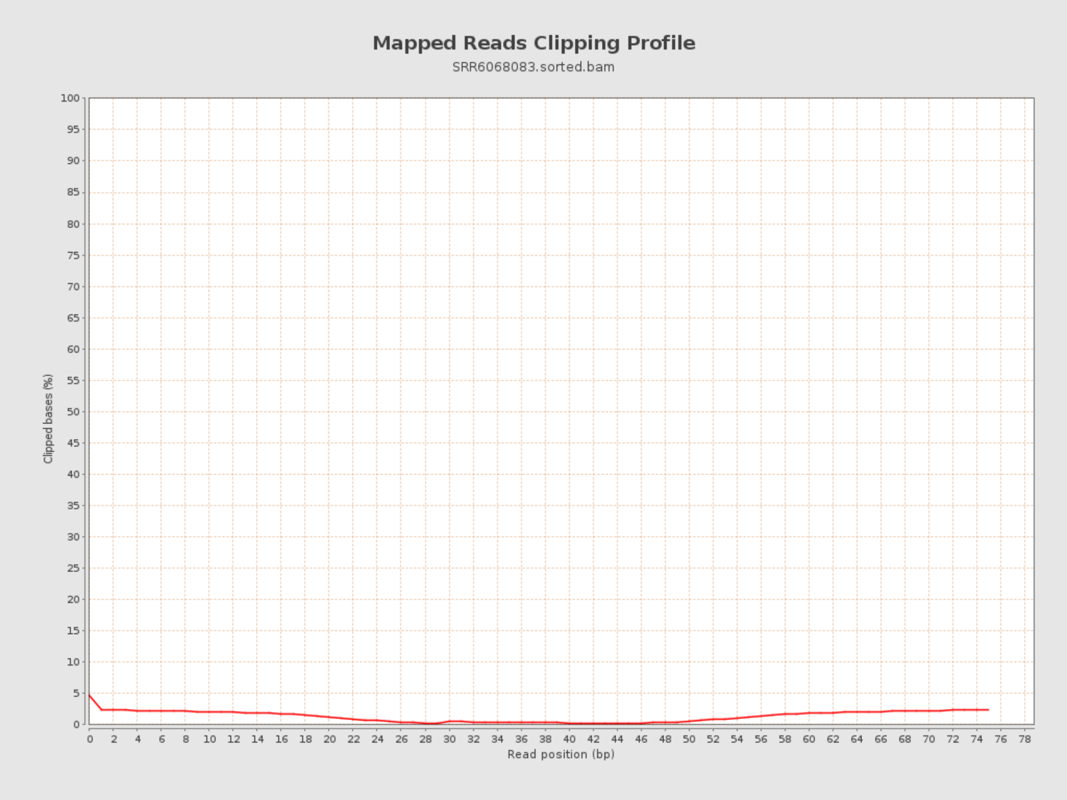
8. Results : Mapped Reads Nucleotide Content



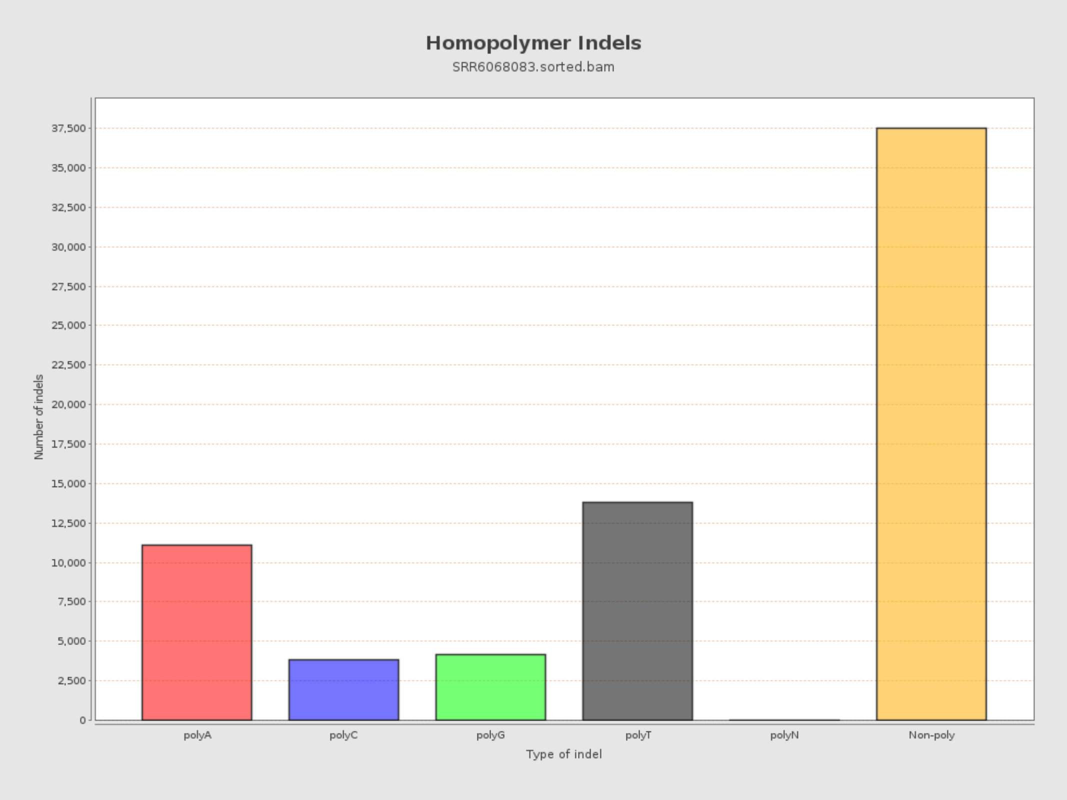
9. Results : Mapped Reads GC-content Distribution



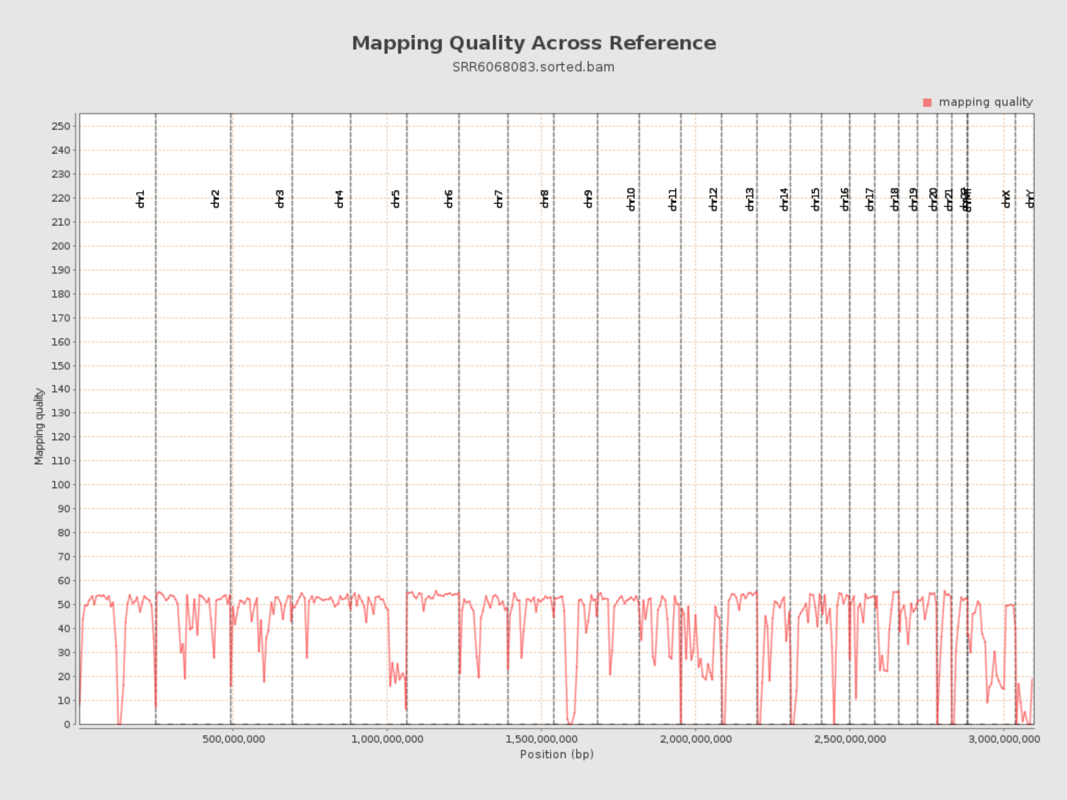
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram