Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:26:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013197.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_SRR6013197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013197.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:26:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,984,531
Mapped reads	1,582,963 / 79.77%
Unmapped reads	401,568 / 20.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,821 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	66,242 / 3.34%
Duplication rate	3.1%
Clipped reads	921,032 / 46.41%

2.2. ACGT Content

Number/percentage of A's	29,783,300 / 29.78%
Number/percentage of C's	18,171,597 / 18.17%
Number/percentage of T's	29,896,045 / 29.89%
Number/percentage of G's	22,174,941 / 22.17%
Number/percentage of N's	772 / 0%
GC Percentage	40.34%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.5757

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

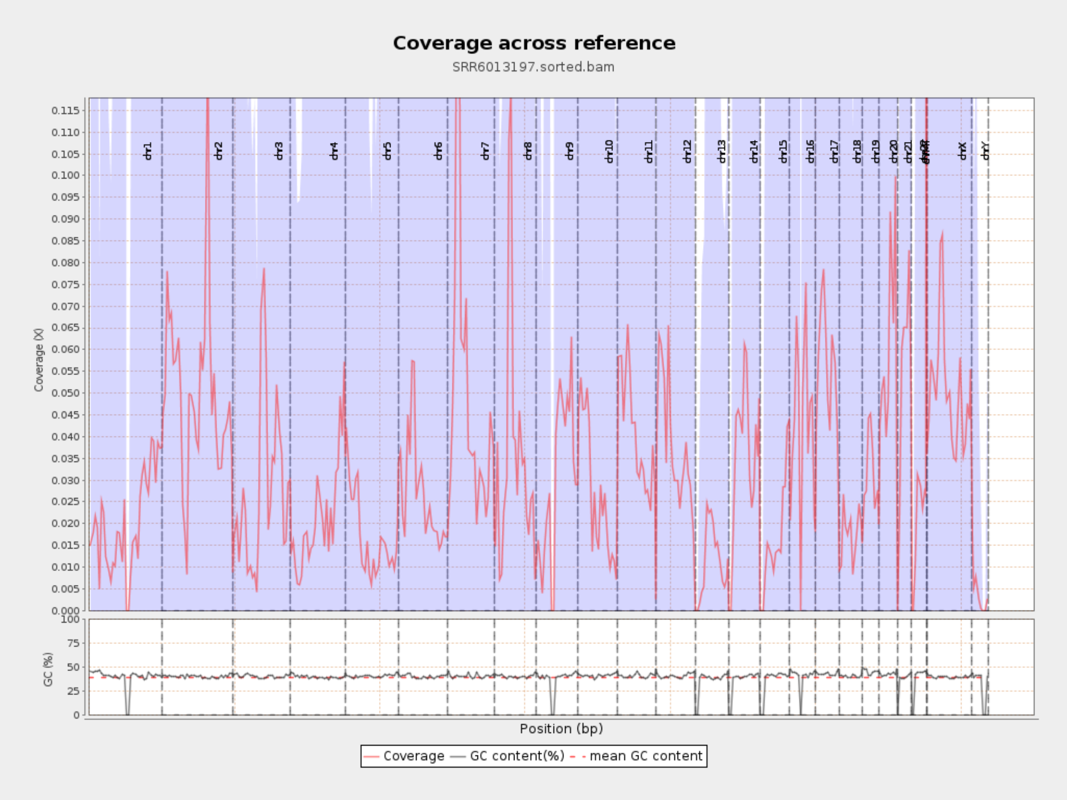
General error rate	0.88%
Mismatches	866,704
Insertions	7,244
Mapped reads with at least one insertion	0.45%
Deletions	30,901
Mapped reads with at least one deletion	1.93%
Homopolymer indels	47.47%

2.6. Chromosome stats

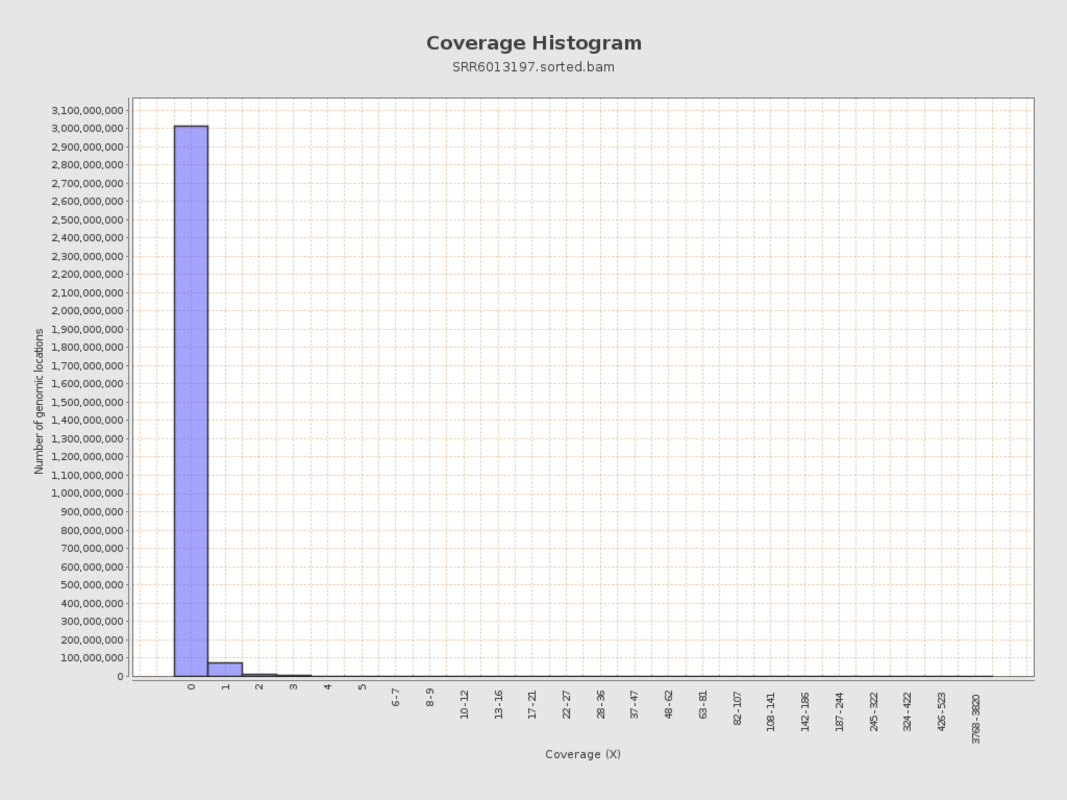
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4973991	0.02	0.371
chr2	243199373	12207056	0.0502	0.3447
chr3	198022430	5414571	0.0273	0.1943
chr4	191154276	4111537	0.0215	0.1731
chr5	180915260	3084845	0.0171	0.154
chr6	171115067	4648230	0.0272	0.2541
chr7	159138663	8126101	0.0511	0.5827

chr8	146364022	5180589	0.0354	2.2982
chr9	141213431	4269943	0.0302	0.2669
chr10	135534747	3748375	0.0277	0.2669
chr11	135006516	5483409	0.0406	0.3336
chr12	133851895	5081245	0.038	0.2302
chr13	115169878	1283049	0.0111	0.1218
chr14	107349540	3710068	0.0346	0.2298
chr15	102531392	1677313	0.0164	0.1507
chr16	90354753	3839487	0.0425	0.2553
chr17	81195210	4527334	0.0558	0.3501
chr18	78077248	1366309	0.0175	0.3491
chr19	59128983	1880531	0.0318	0.3115
chr20	63025520	3848435	0.0611	0.2996
chr21	48129895	2538328	0.0527	0.2809
chr22	51304566	1001697	0.0195	0.1606
chrMT	16571	8101	0.4889	0.8017
chrX	155270560	7844873	0.0505	0.2858
chrY	59373566	223606	0.0038	0.0748

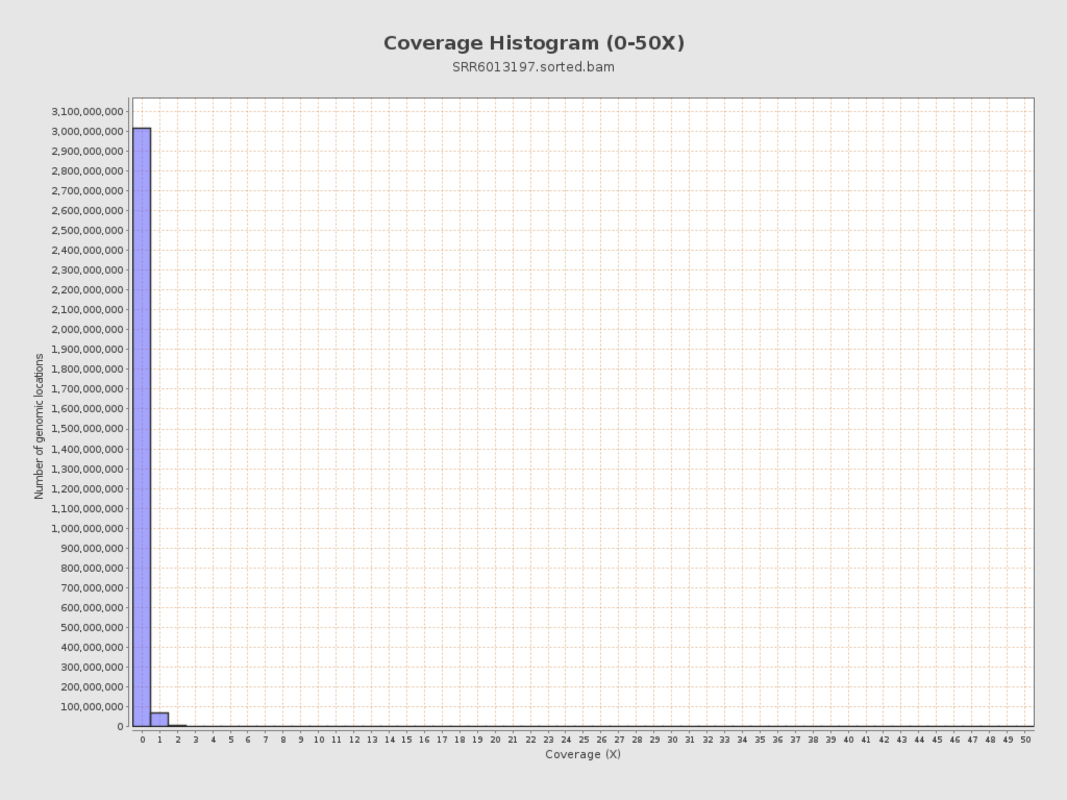
3. Results : Coverage across reference



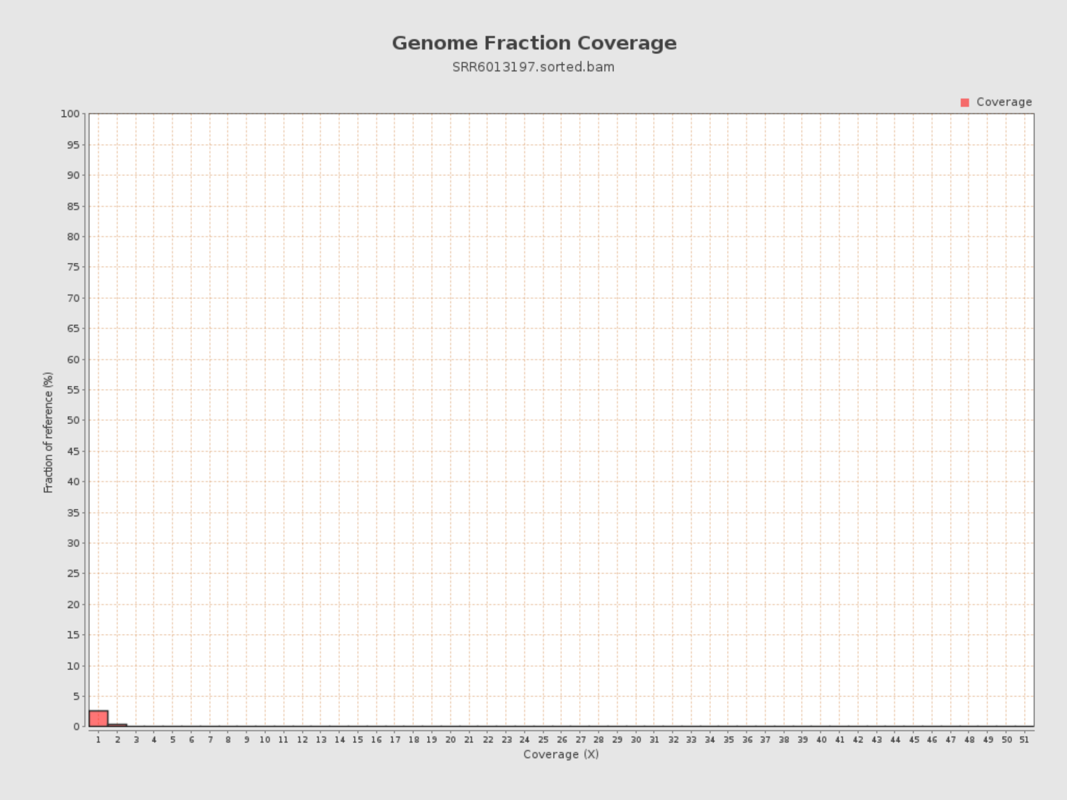
4. Results : Coverage Histogram



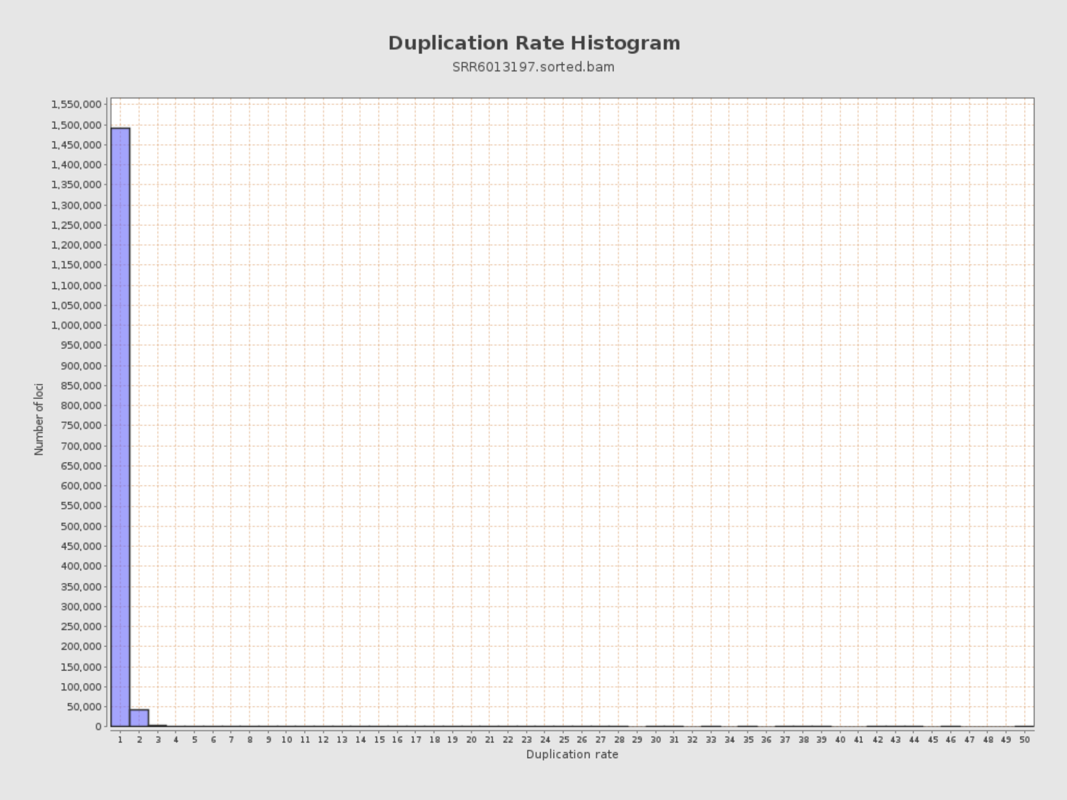
5. Results : Coverage Histogram (0-50X)



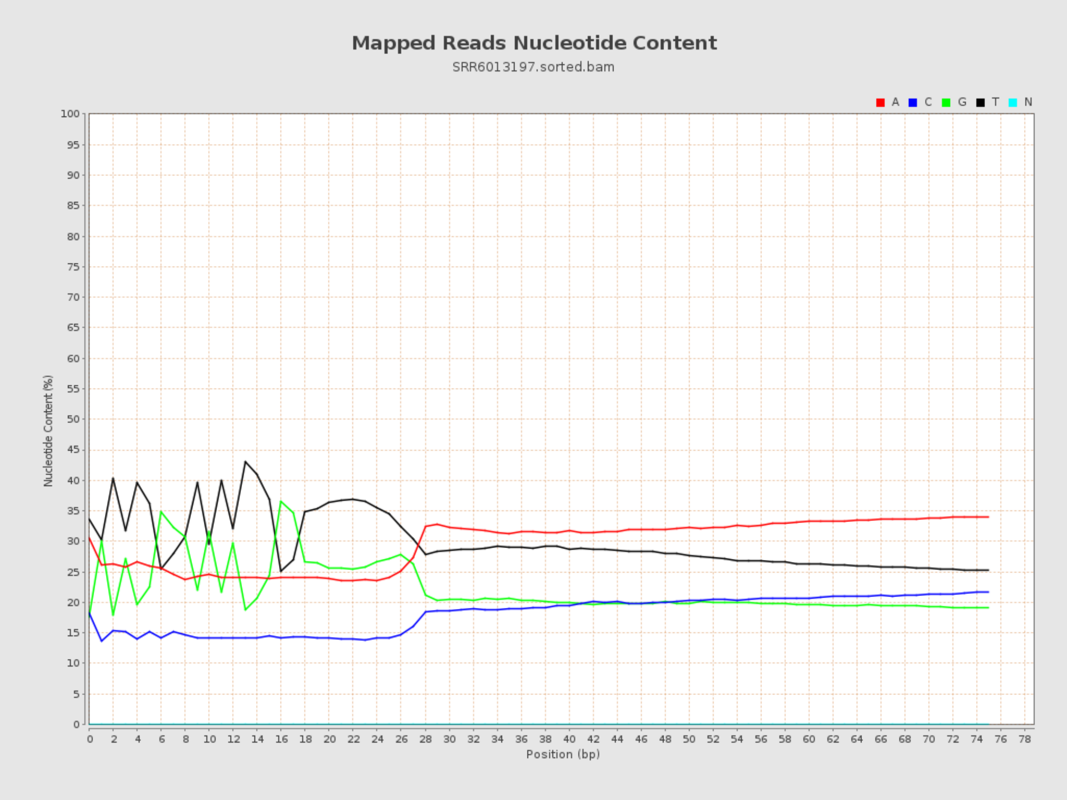
6. Results : Genome Fraction Coverage



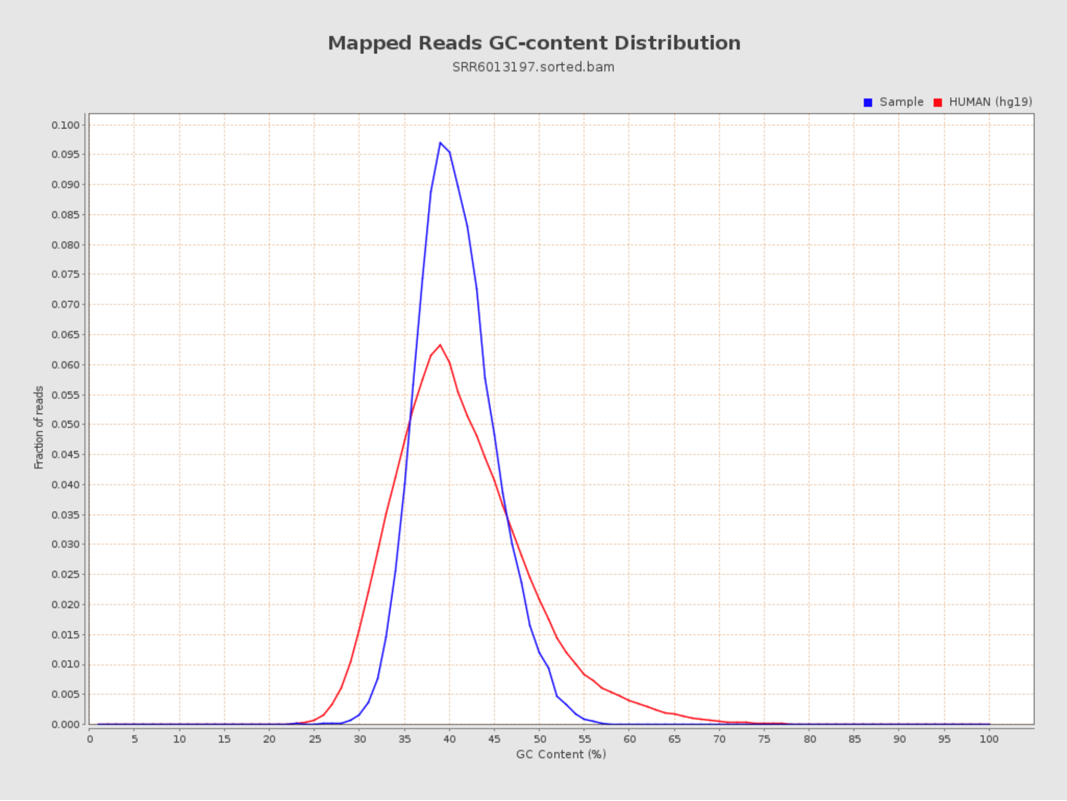
7. Results : Duplication Rate Histogram



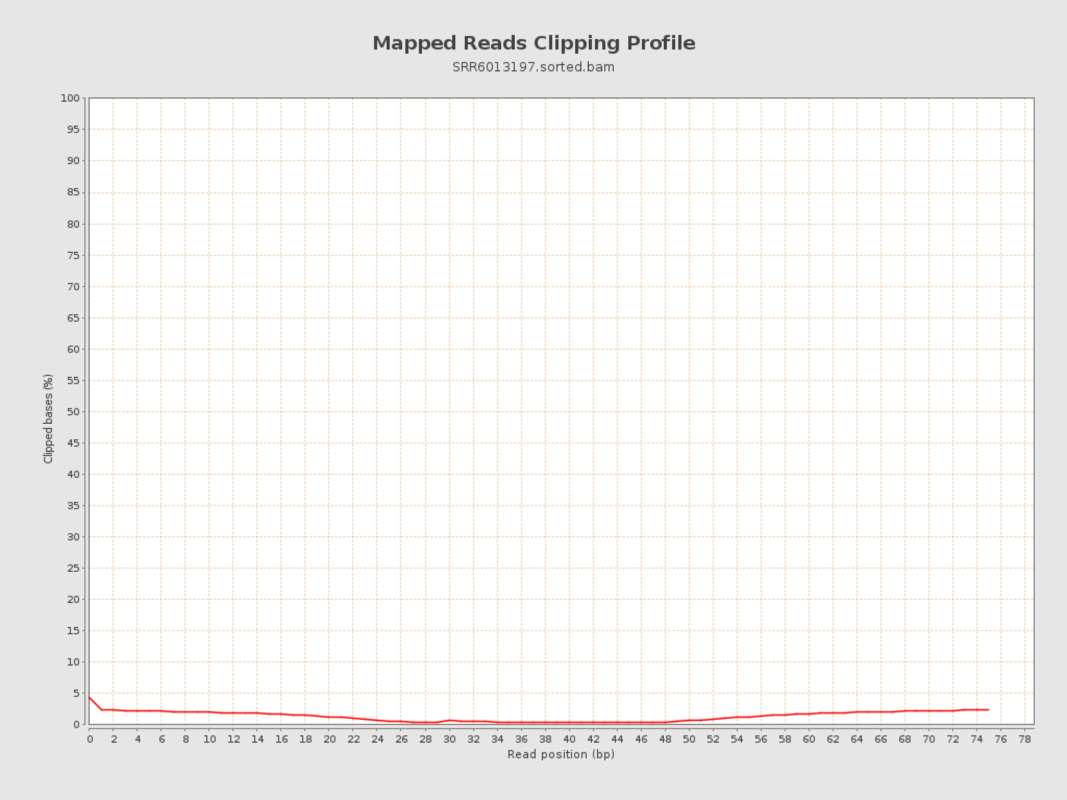
8. Results : Mapped Reads Nucleotide Content



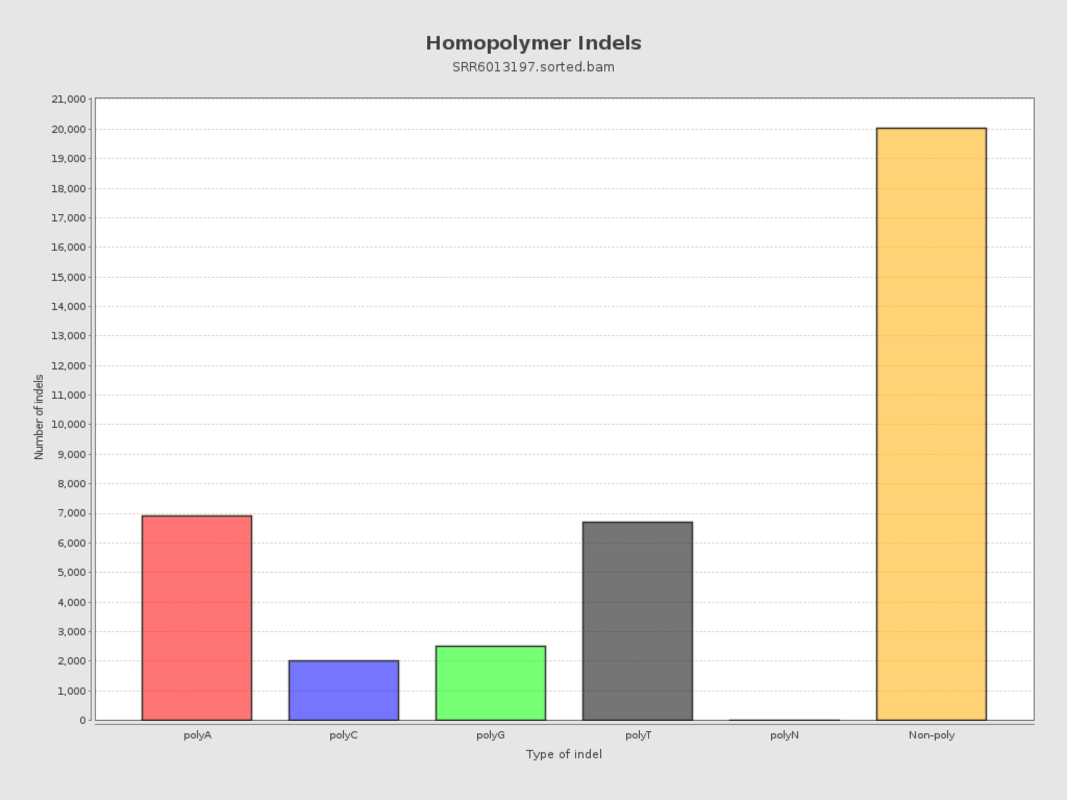
9. Results : Mapped Reads GC-content Distribution



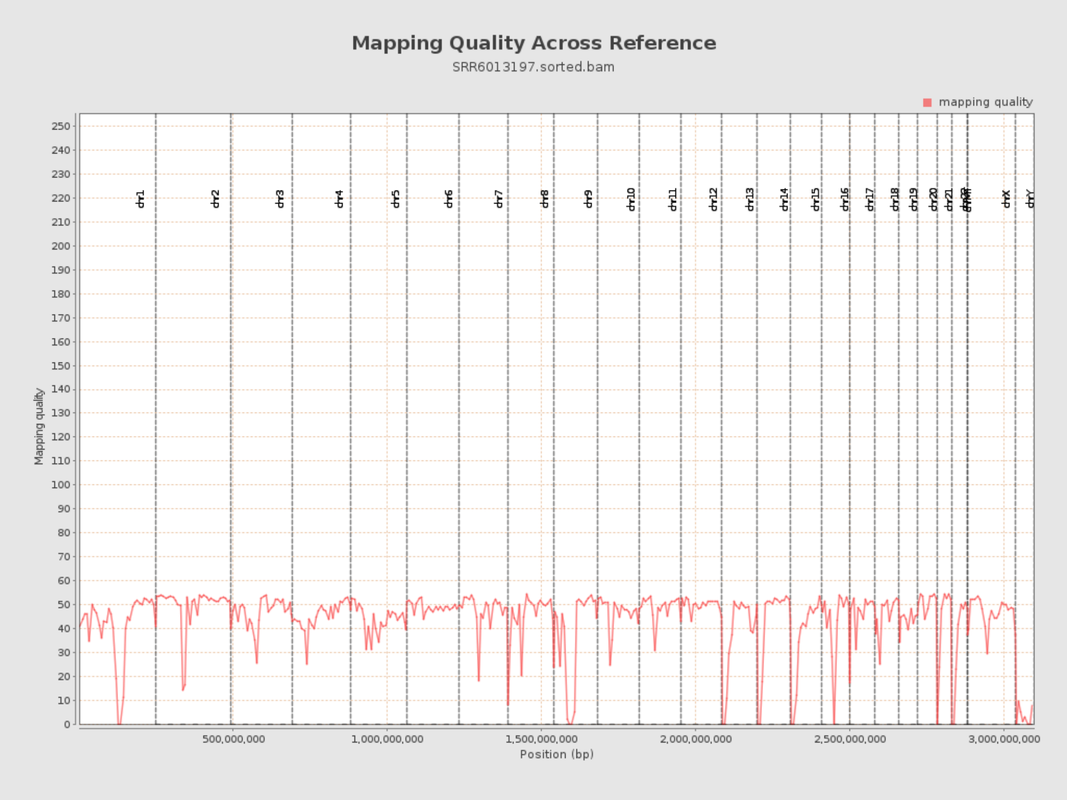
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram