Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:37:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013201.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_SRR6013201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:37:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,279,733
Mapped reads	2,073,799 / 90.97%
Unmapped reads	205,934 / 9.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,234 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	91,840 / 4.03%
Duplication rate	3.39%
Clipped reads	741,804 / 32.54%

2.2. ACGT Content

Number/percentage of A's	40,735,468 / 28.54%
Number/percentage of C's	26,729,066 / 18.73%
Number/percentage of T's	45,034,432 / 31.55%
Number/percentage of G's	30,203,328 / 21.16%
Number/percentage of N's	31,058 / 0.02%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.4321

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Mismatches and indels

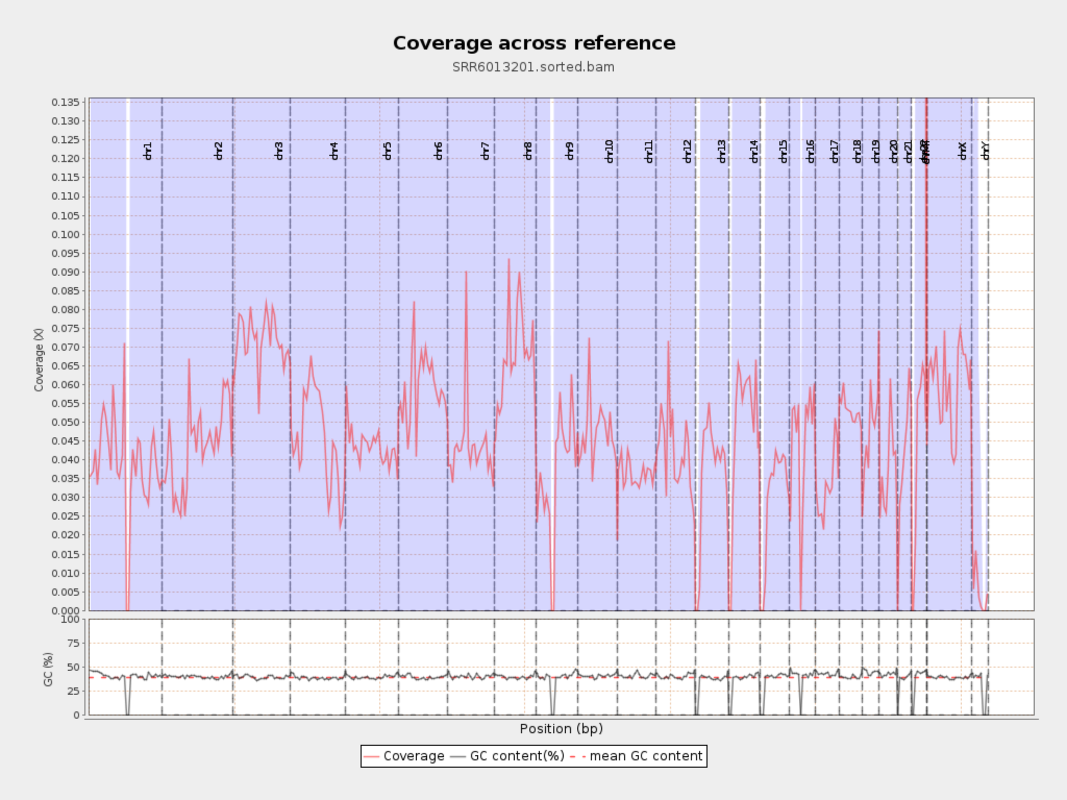
General error rate	0.78%
Mismatches	1,098,000
Insertions	10,617
Mapped reads with at least one insertion	0.51%
Deletions	37,614
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.95%

2.6. Chromosome stats

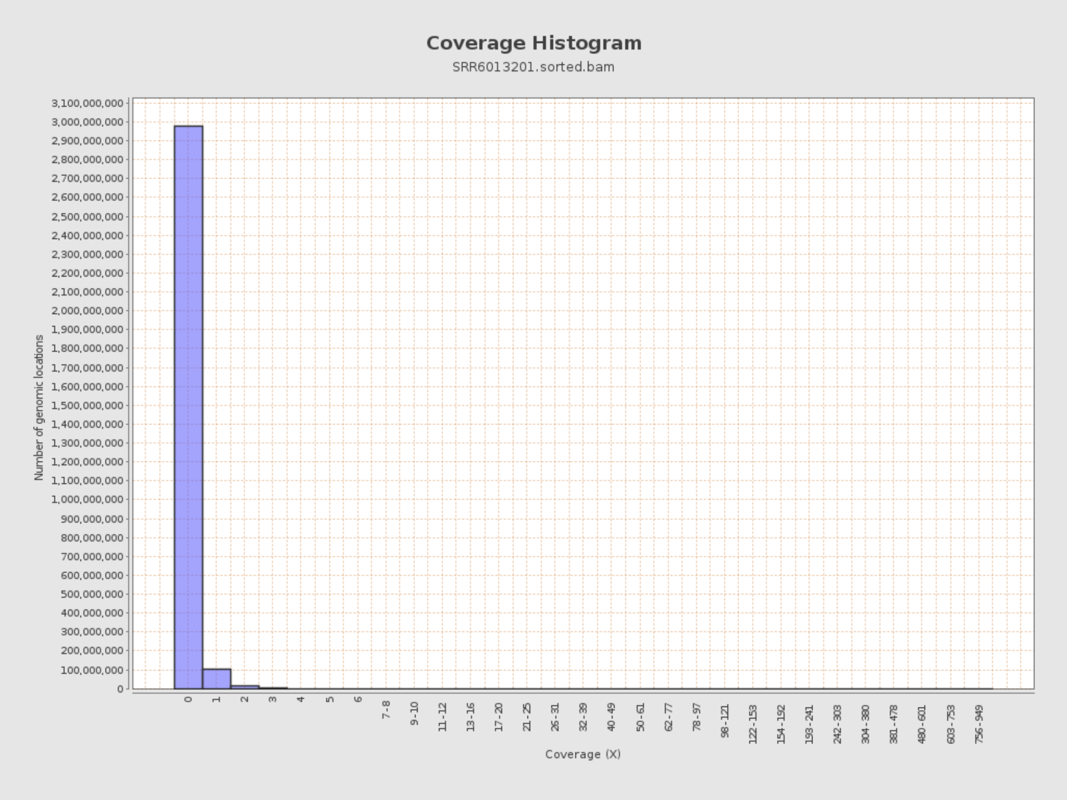
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9699321	0.0389	0.8072
chr2	243199373	10607114	0.0436	0.4136
chr3	198022430	14245158	0.0719	0.3048
chr4	191154276	8686281	0.0454	0.2702
chr5	180915260	7905189	0.0437	0.2381
chr6	171115067	10158977	0.0594	0.3388
chr7	159138663	6974500	0.0438	0.6991

chr8	146364022	9871785	0.0674	0.5941
chr9	141213431	5154024	0.0365	0.3321
chr10	135534747	6414433	0.0473	0.4412
chr11	135006516	4872294	0.0361	0.2918
chr12	133851895	5703548	0.0426	0.2439
chr13	115169878	4105820	0.0357	0.2154
chr14	107349540	5193800	0.0484	0.2622
chr15	102531392	3037478	0.0296	0.1941
chr16	90354753	4089893	0.0453	0.266
chr17	81195210	2706039	0.0333	0.2172
chr18	78077248	4160624	0.0533	0.6814
chr19	59128983	2838587	0.048	0.56
chr20	63025520	2343262	0.0372	0.2345
chr21	48129895	1952156	0.0406	0.2489
chr22	51304566	2119009	0.0413	0.2305
chrMT	16571	419759	25.3309	13.8496
chrX	155270560	9221175	0.0594	0.3068
chrY	59373566	318216	0.0054	0.1428

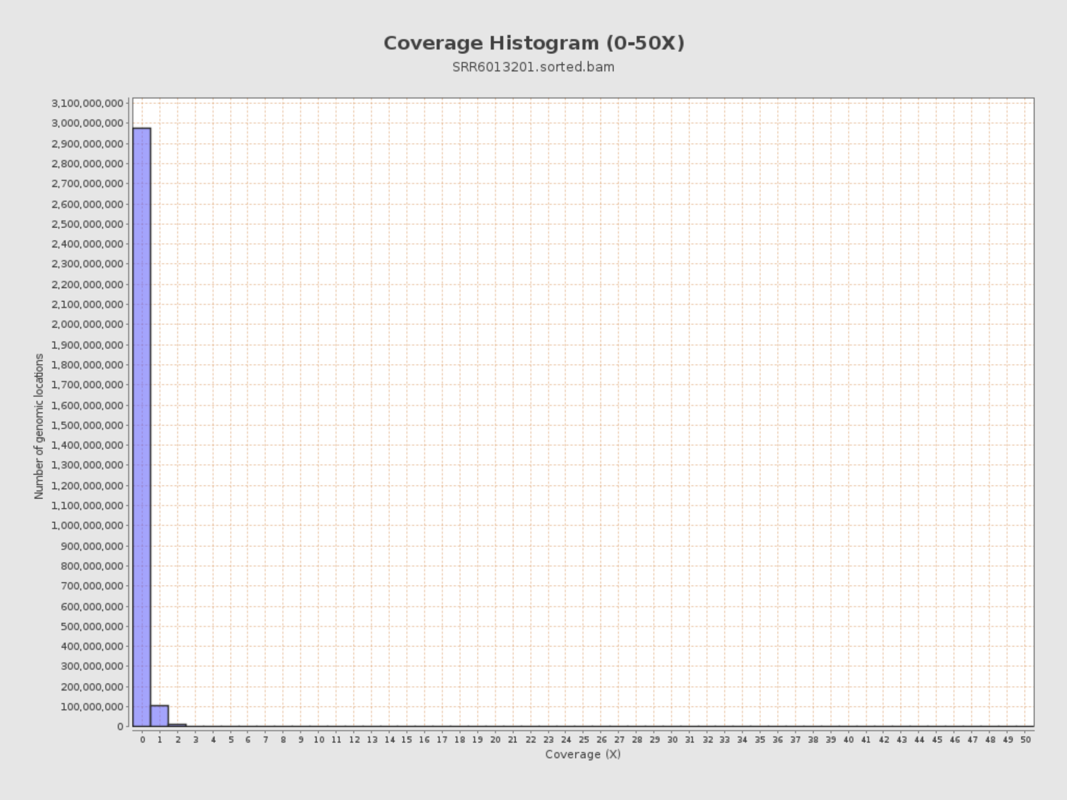
3. Results : Coverage across reference



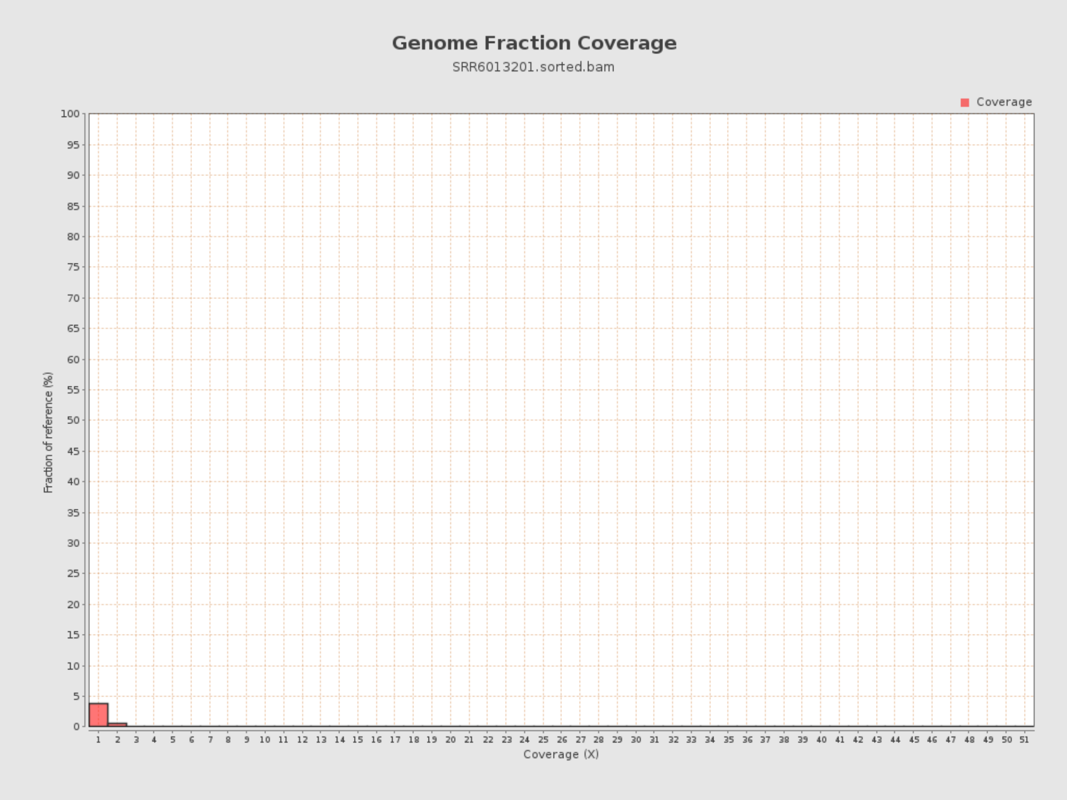
4. Results : Coverage Histogram



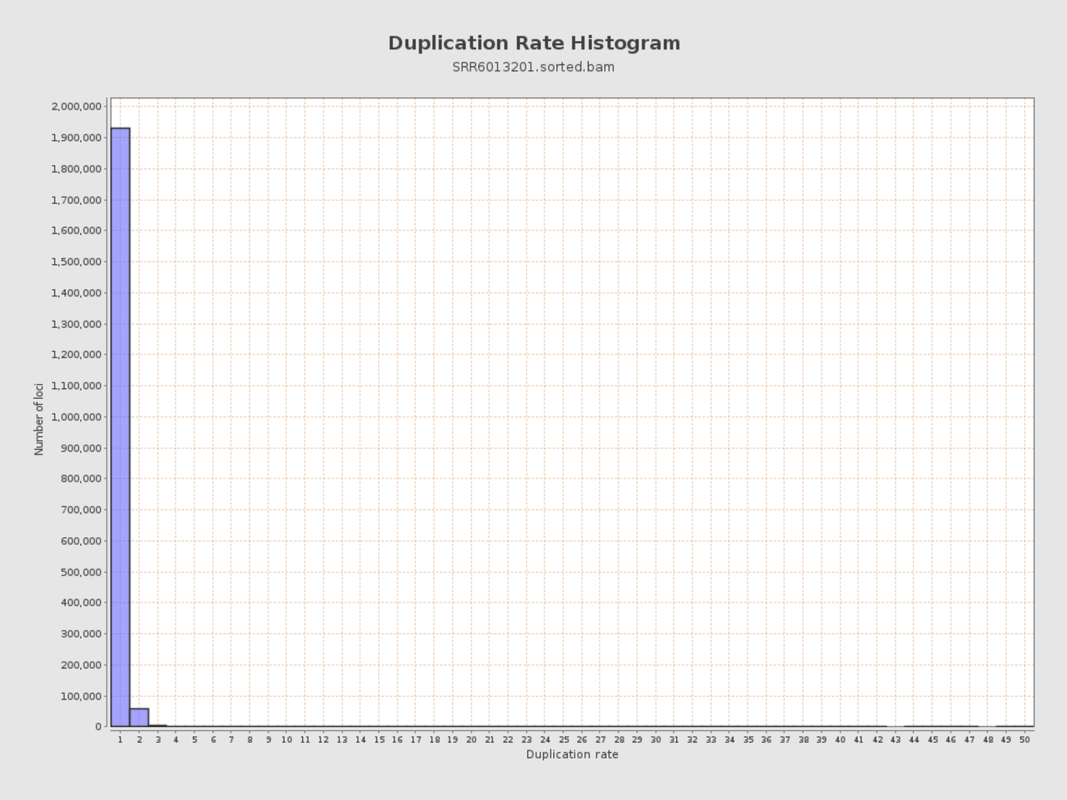
5. Results : Coverage Histogram (0-50X)



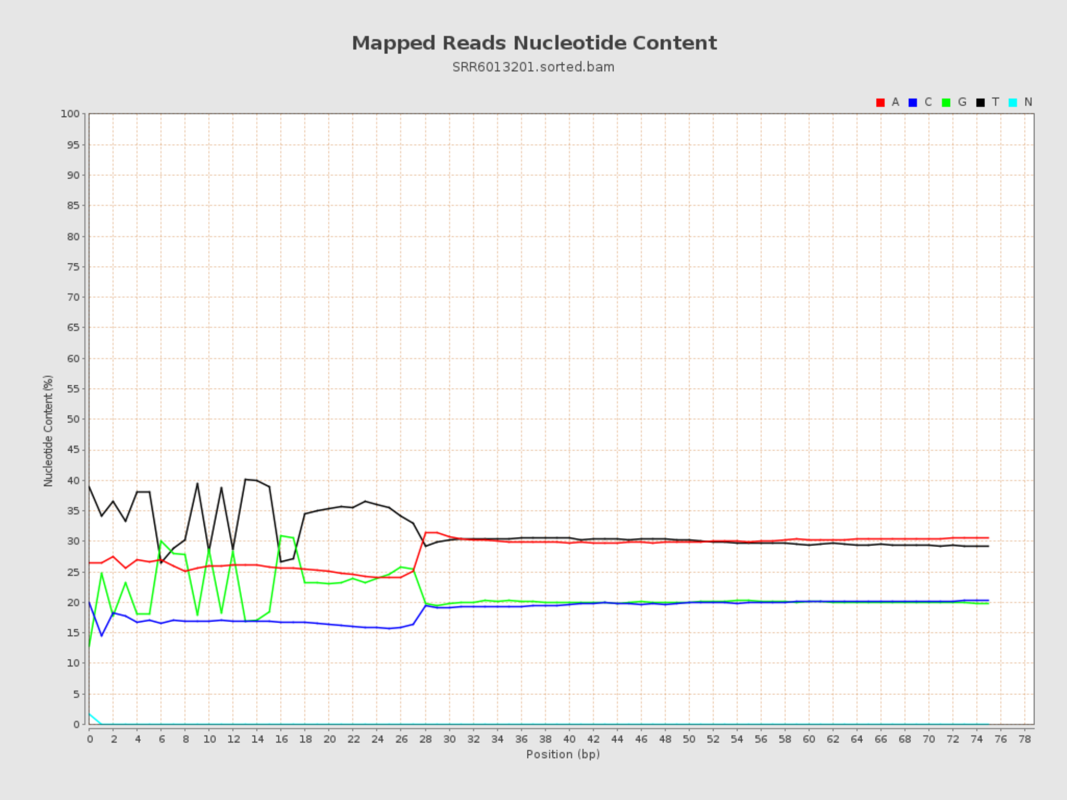
6. Results : Genome Fraction Coverage



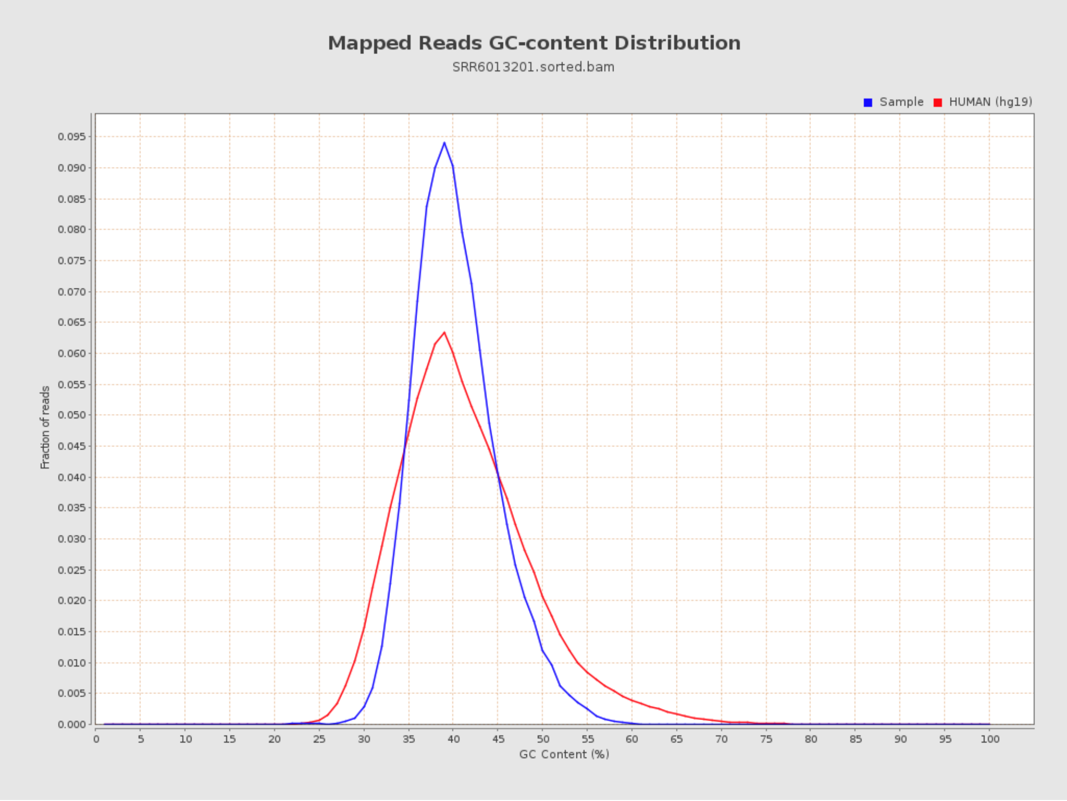
7. Results : Duplication Rate Histogram



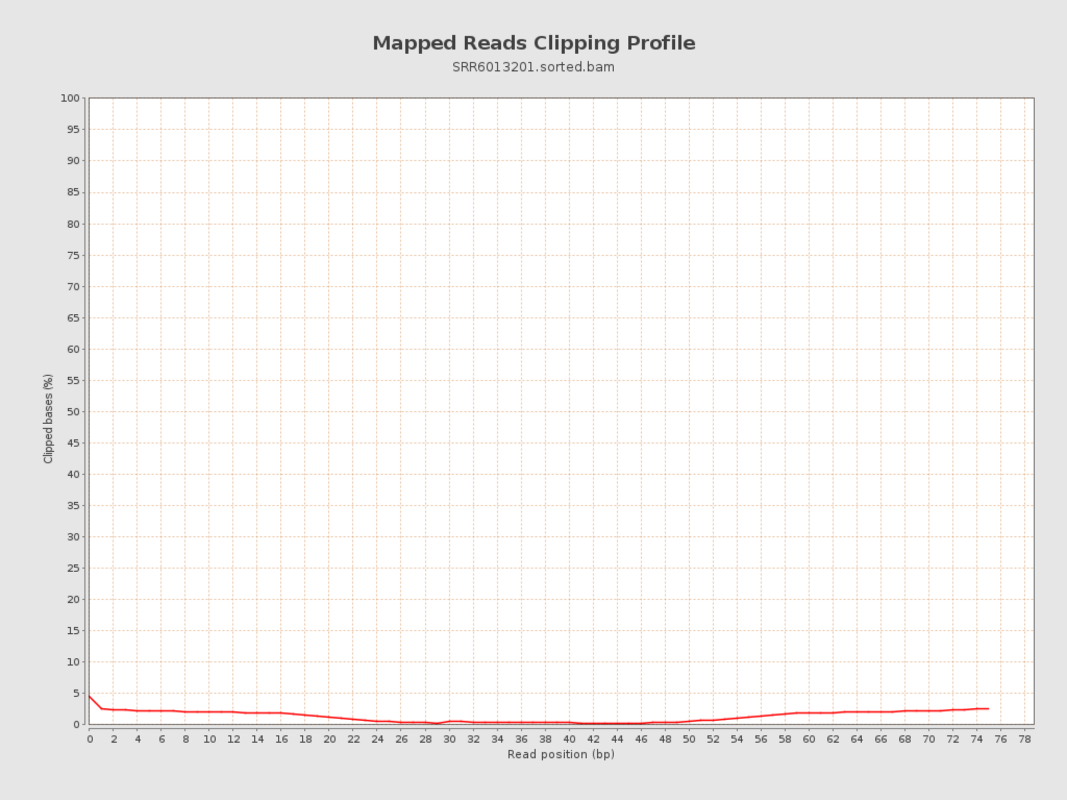
8. Results : Mapped Reads Nucleotide Content



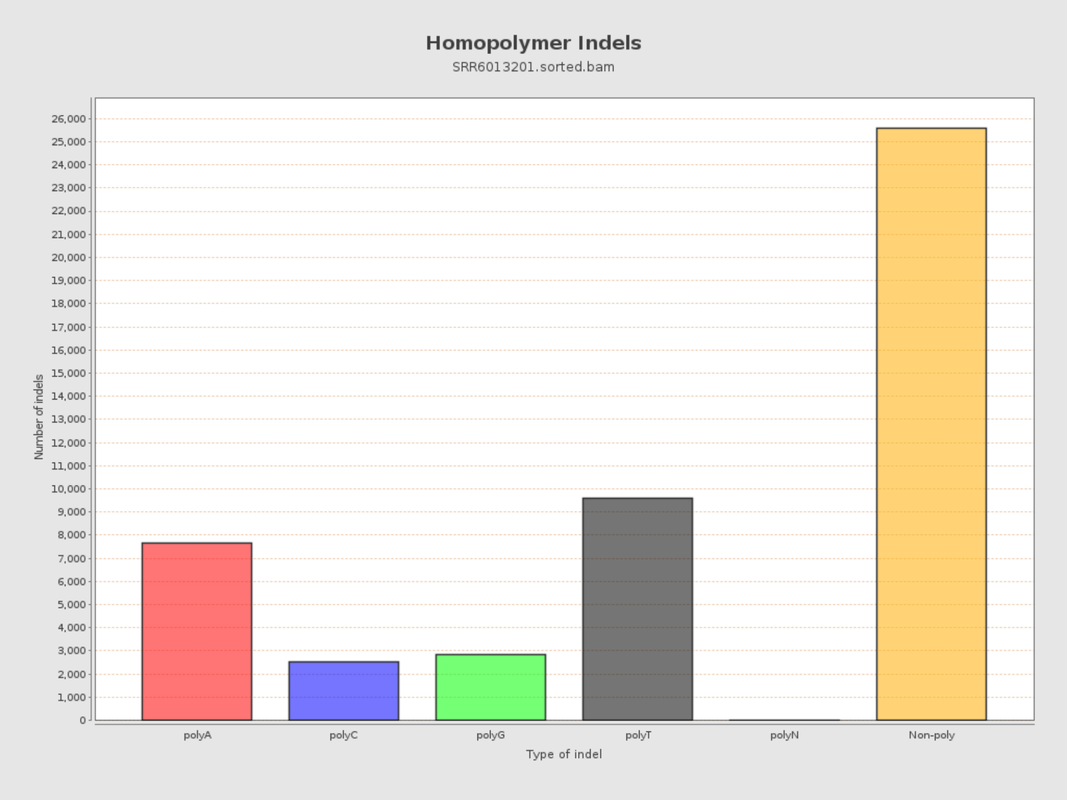
9. Results : Mapped Reads GC-content Distribution



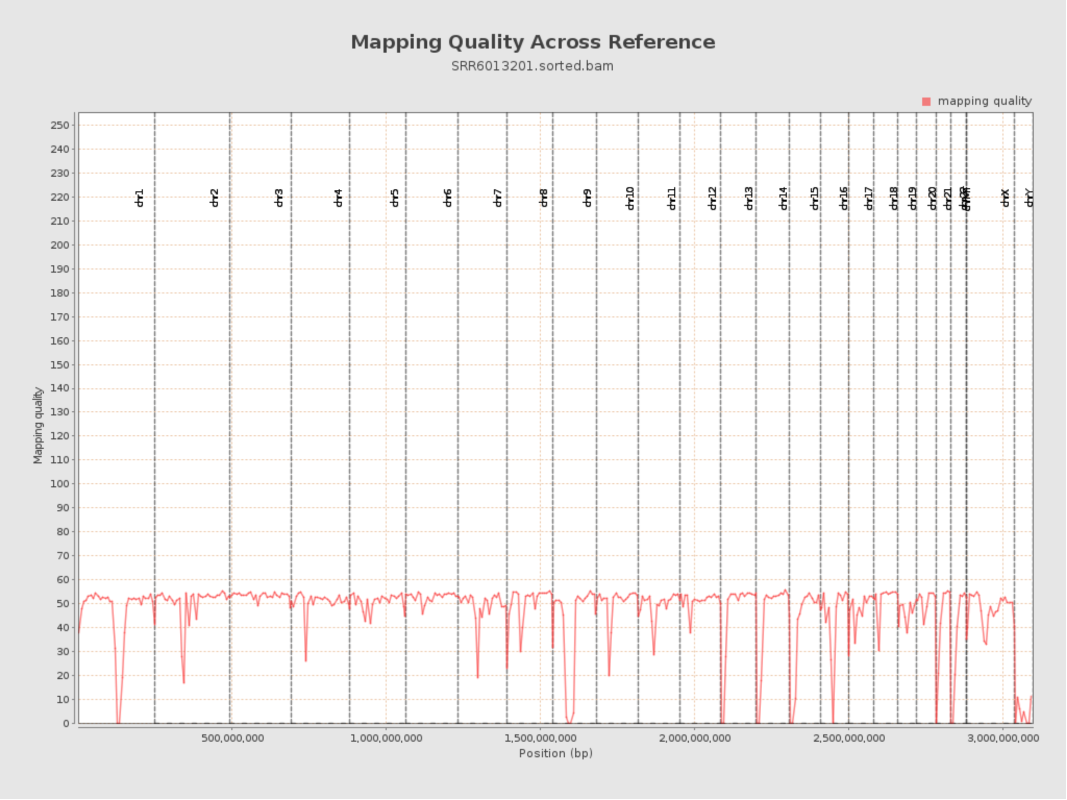
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram