Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:02:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013189.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_SRR6013189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:02:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,437,019
Mapped reads	2,172,953 / 89.16%
Unmapped reads	264,066 / 10.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,123 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	68,043 / 2.79%
Duplication rate	1.71%
Clipped reads	1,207,296 / 49.54%

2.2. ACGT Content

Number/percentage of A's	37,387,609 / 26.89%
Number/percentage of C's	26,906,875 / 19.35%
Number/percentage of T's	41,763,796 / 30.03%
Number/percentage of G's	32,982,139 / 23.72%
Number/percentage of N's	15,594 / 0.01%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0449

Standard Deviation	0.4909

2.4. Mapping Quality

Mean Mapping Quality	41.79

2.5. Mismatches and indels

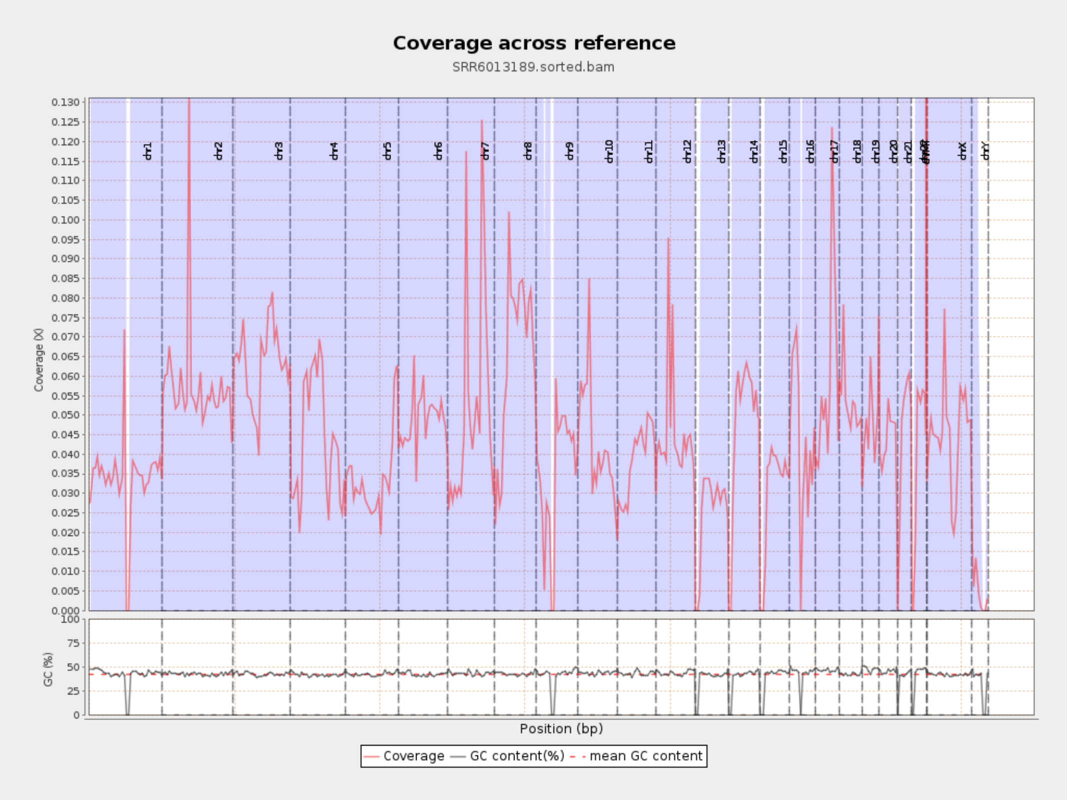
General error rate	0.8%
Mismatches	1,090,762
Insertions	10,559
Mapped reads with at least one insertion	0.48%
Deletions	34,093
Mapped reads with at least one deletion	1.55%
Homopolymer indels	43.65%

2.6. Chromosome stats

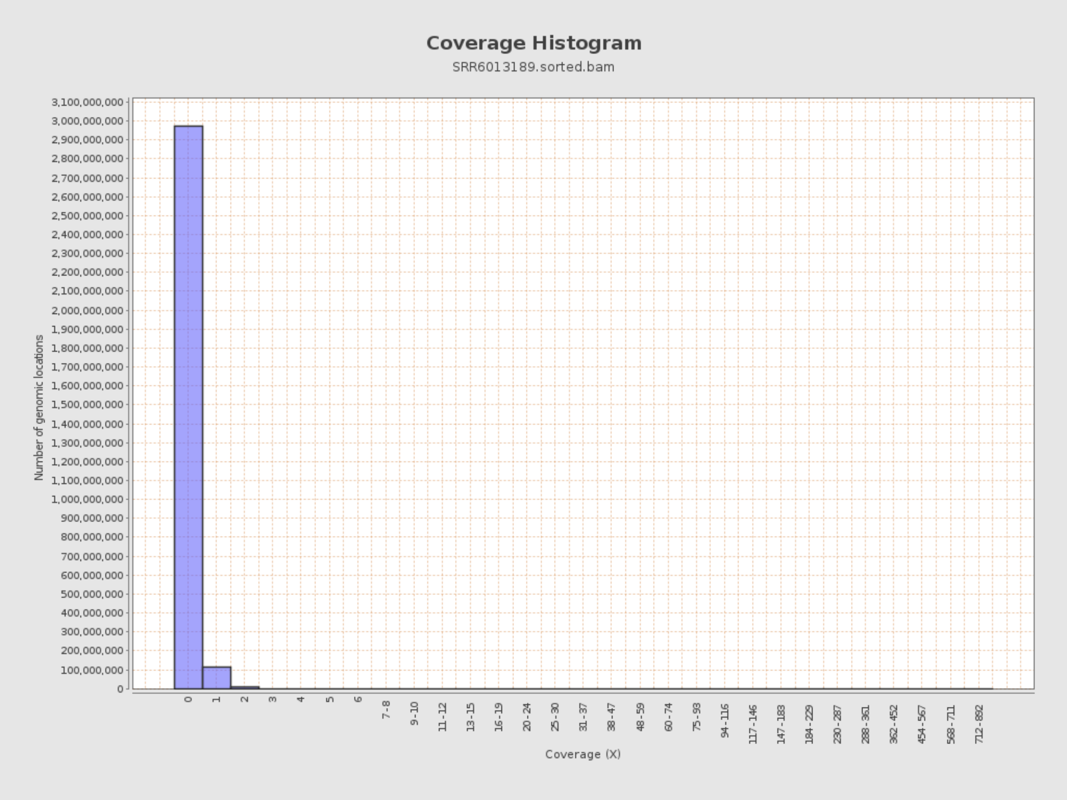
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8403664	0.0337	0.7703
chr2	243199373	14102254	0.058	0.6968
chr3	198022430	12530904	0.0633	0.2703
chr4	191154276	8274778	0.0433	0.2393
chr5	180915260	6075135	0.0336	0.2033
chr6	171115067	8367963	0.0489	0.3388
chr7	159138663	8440734	0.053	0.9743

chr8	146364022	9600417	0.0656	0.4655
chr9	141213431	4867490	0.0345	0.4944
chr10	135534747	5889826	0.0435	0.4762
chr11	135006516	5154065	0.0382	0.3603
chr12	133851895	6187356	0.0462	0.2441
chr13	115169878	2887950	0.0251	0.1677
chr14	107349540	5138042	0.0479	0.277
chr15	102531392	3088697	0.0301	0.2191
chr16	90354753	3968641	0.0439	0.2823
chr17	81195210	4812341	0.0593	0.3106
chr18	78077248	4210708	0.0539	0.9803
chr19	59128983	2871132	0.0486	0.6137
chr20	63025520	2757996	0.0438	0.2429
chr21	48129895	2149130	0.0447	0.2467
chr22	51304566	1945965	0.0379	0.2088
chrMT	16571	134734	8.1307	5.2935
chrX	155270560	6971738	0.0449	0.2967
chrY	59373566	282423	0.0048	0.1142

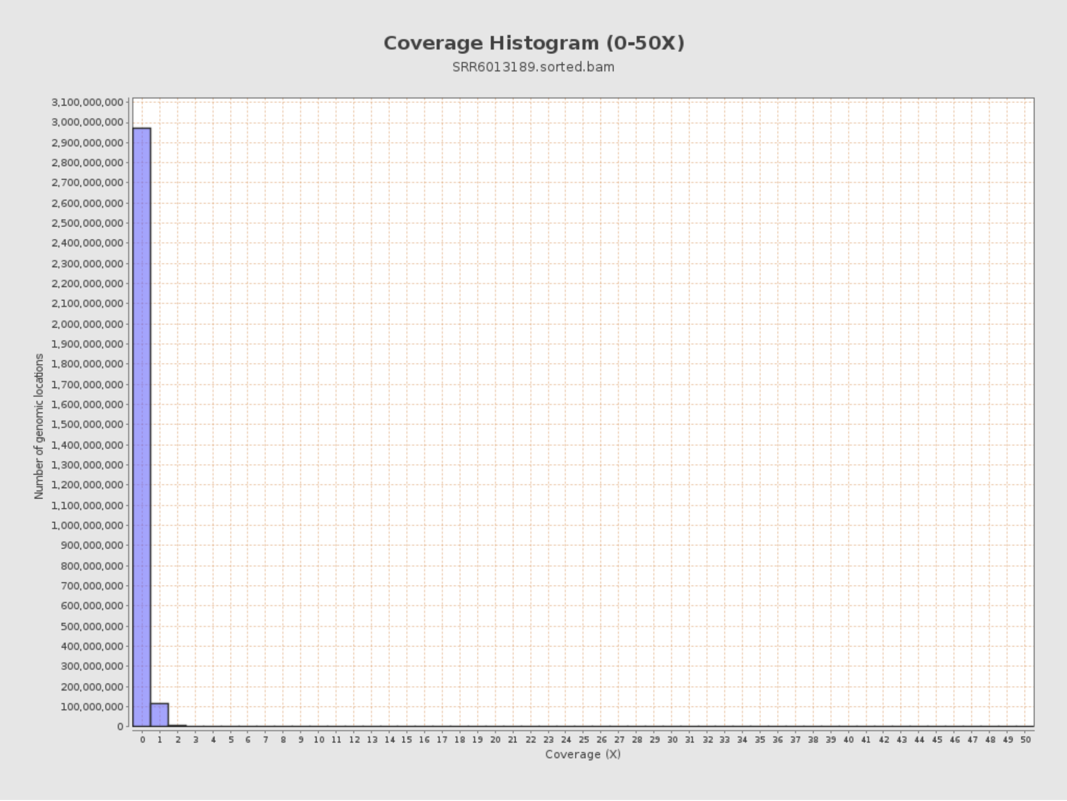
3. Results : Coverage across reference



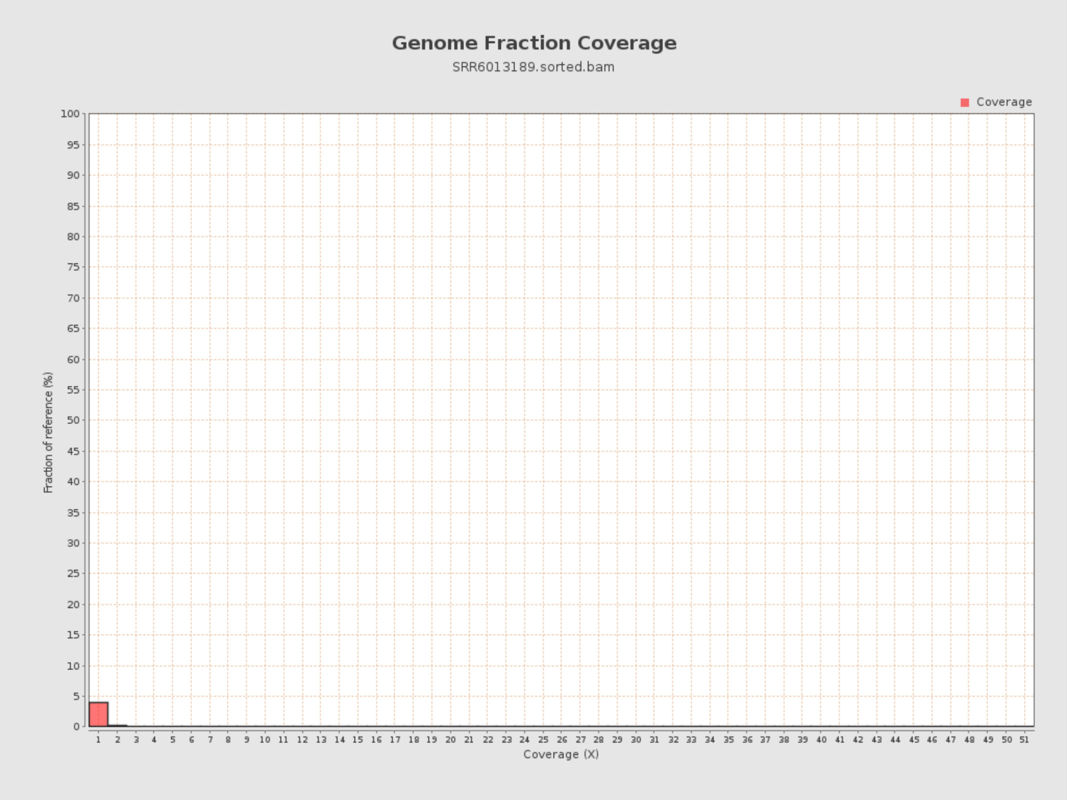
4. Results : Coverage Histogram



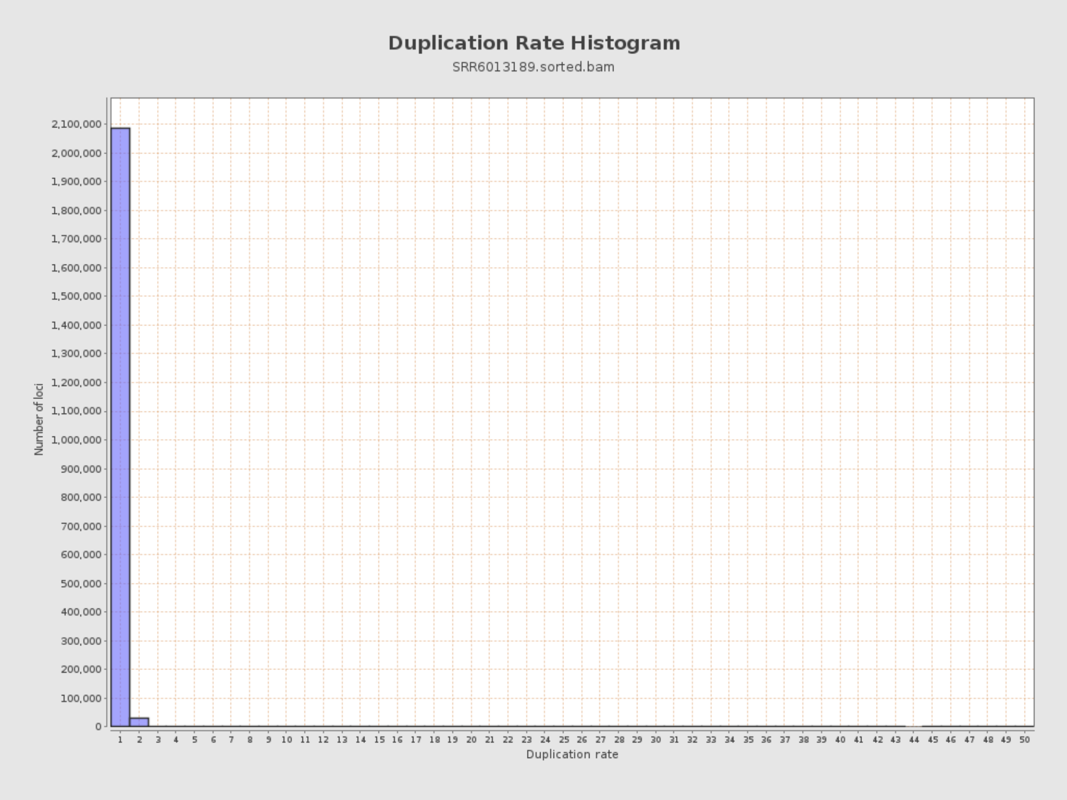
5. Results : Coverage Histogram (0-50X)



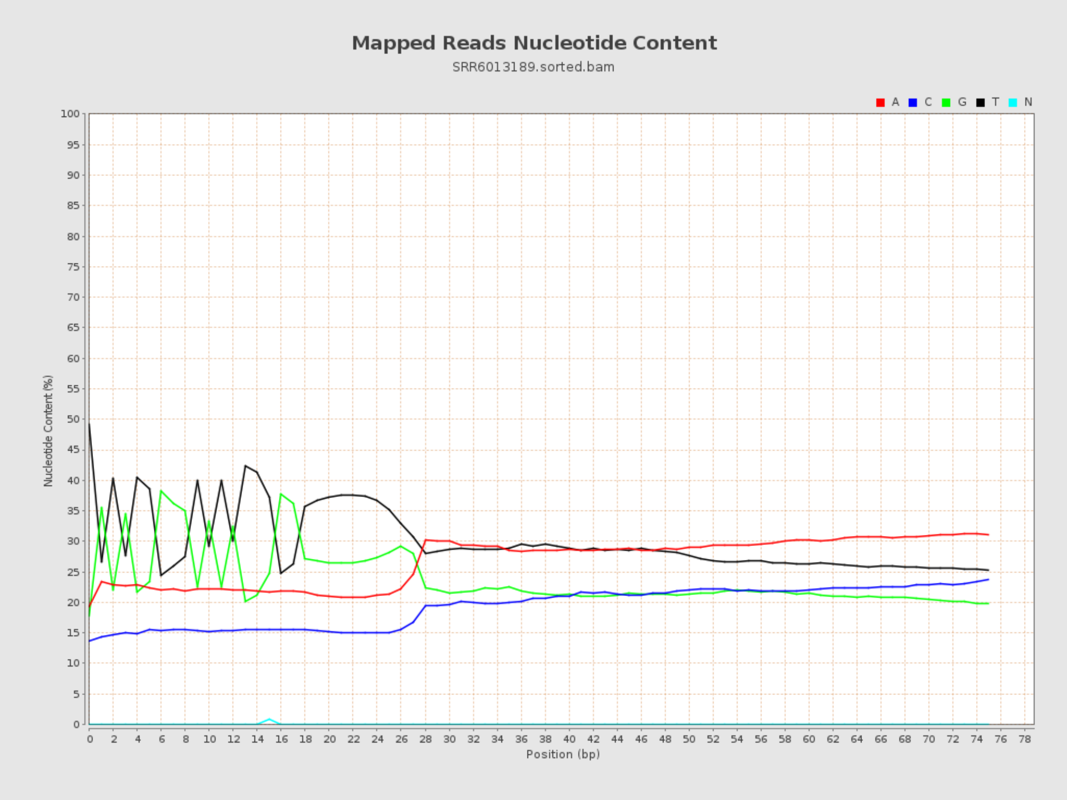
6. Results : Genome Fraction Coverage



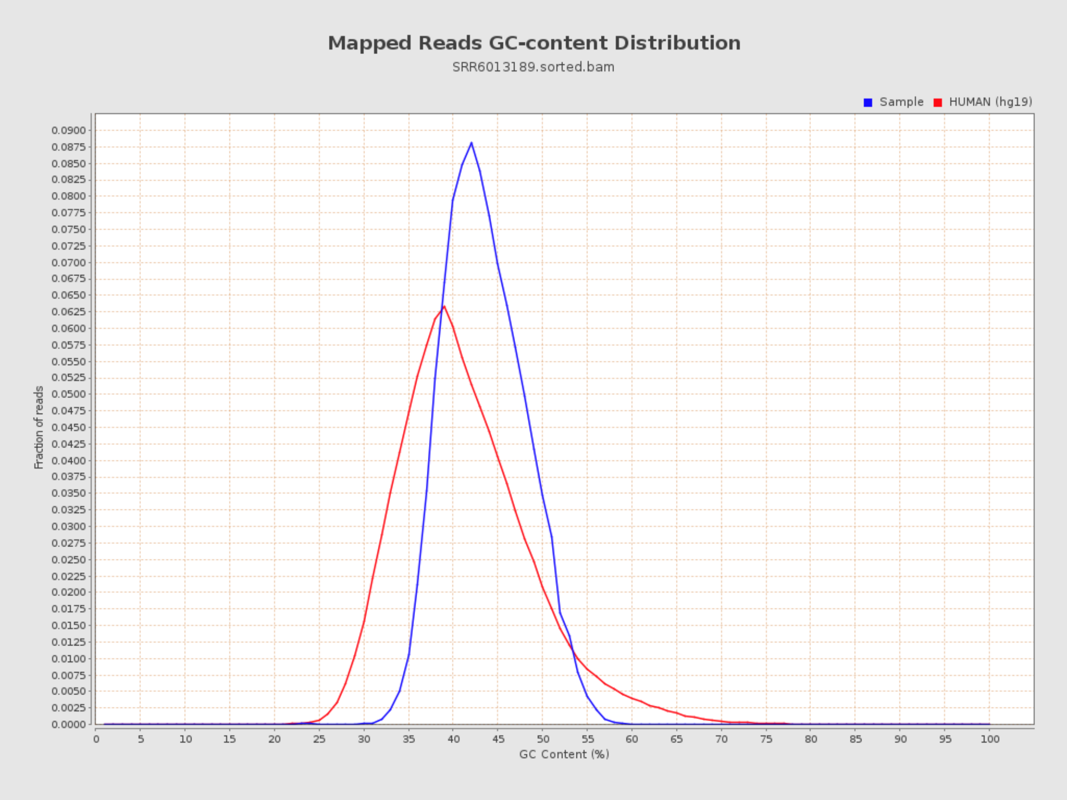
7. Results : Duplication Rate Histogram



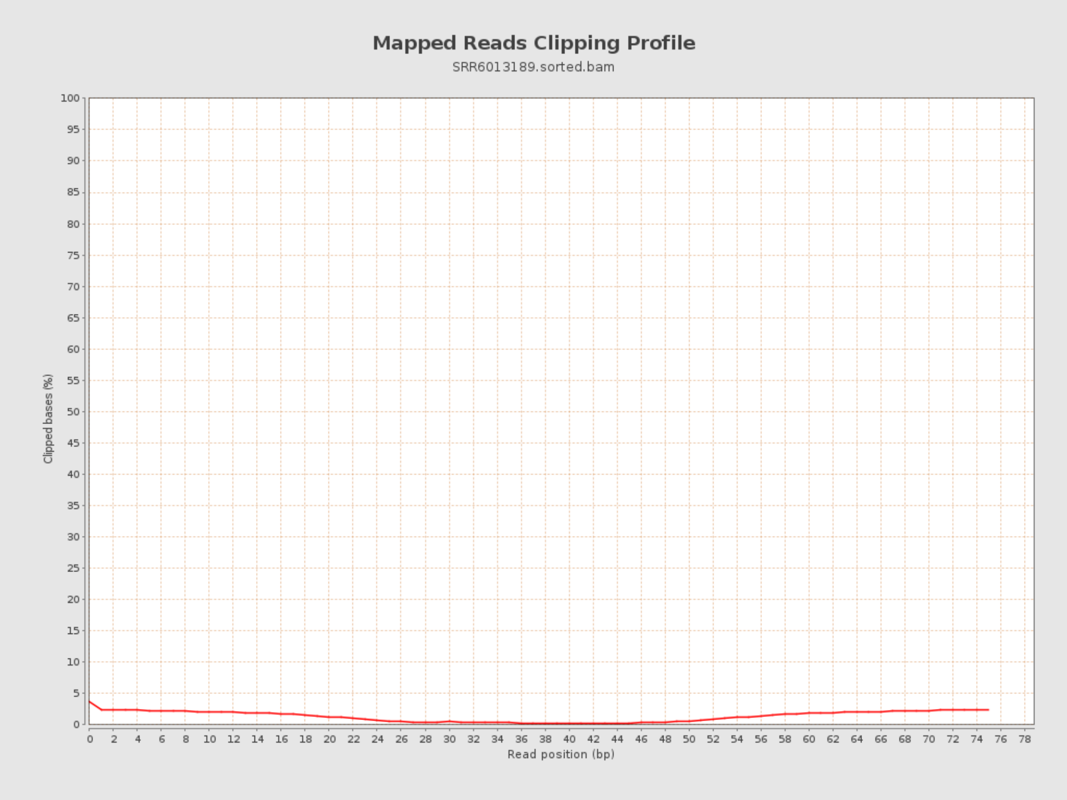
8. Results : Mapped Reads Nucleotide Content



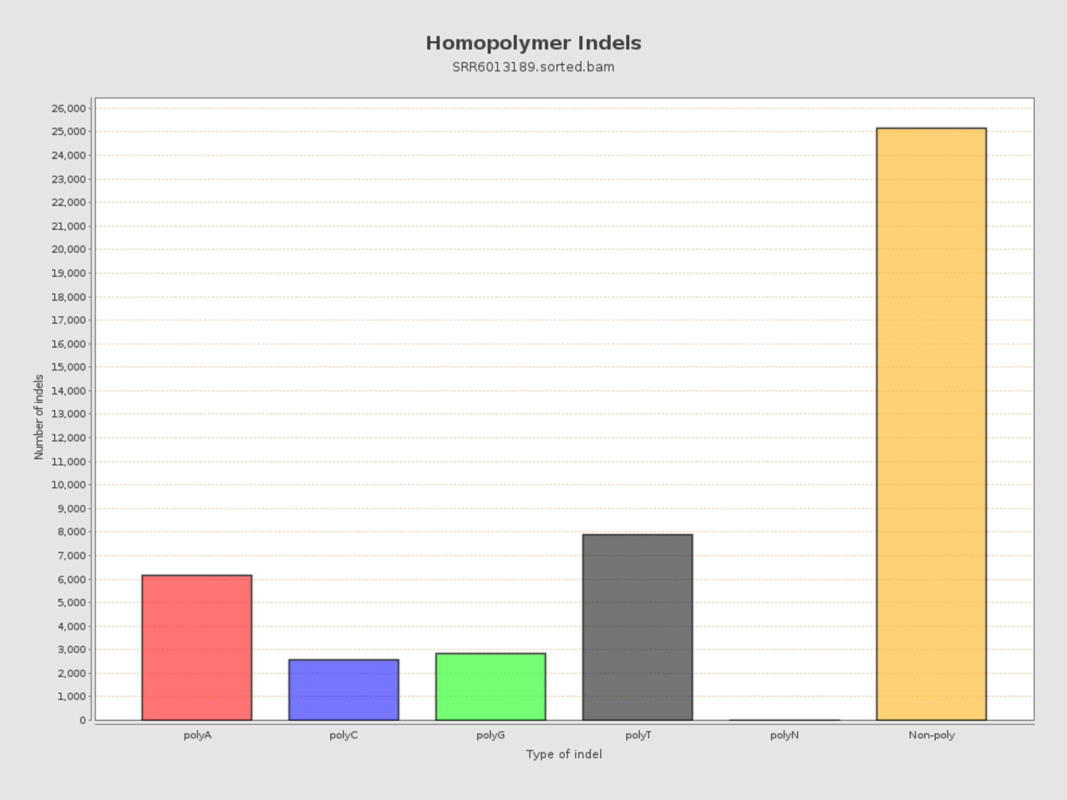
9. Results : Mapped Reads GC-content Distribution



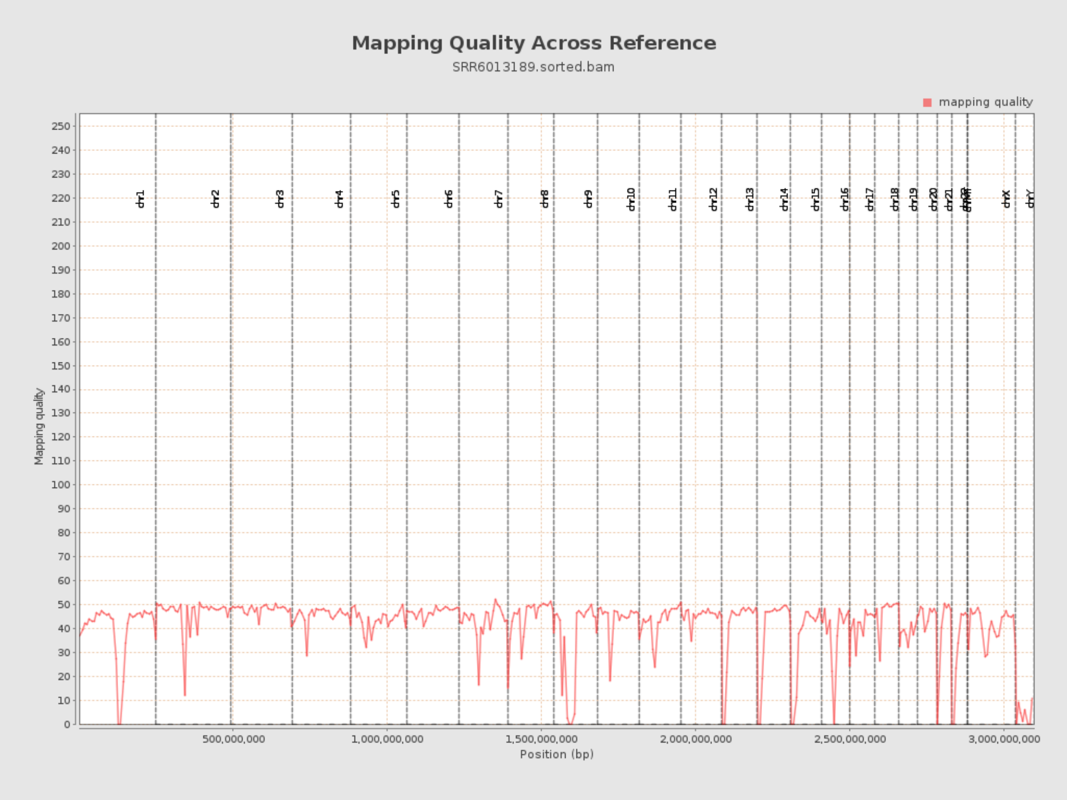
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram