Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:43:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013307.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_SRR6013307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:43:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,732,854
Mapped reads	1,545,344 / 89.18%
Unmapped reads	187,510 / 10.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,337 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	59,230 / 3.42%
Duplication rate	3.15%
Clipped reads	707,835 / 40.85%

2.2. ACGT Content

Number/percentage of A's	27,647,370 / 27.02%
Number/percentage of C's	19,324,004 / 18.88%
Number/percentage of T's	31,923,270 / 31.19%
Number/percentage of G's	23,417,638 / 22.88%
Number/percentage of N's	25,147 / 0.02%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.2787

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

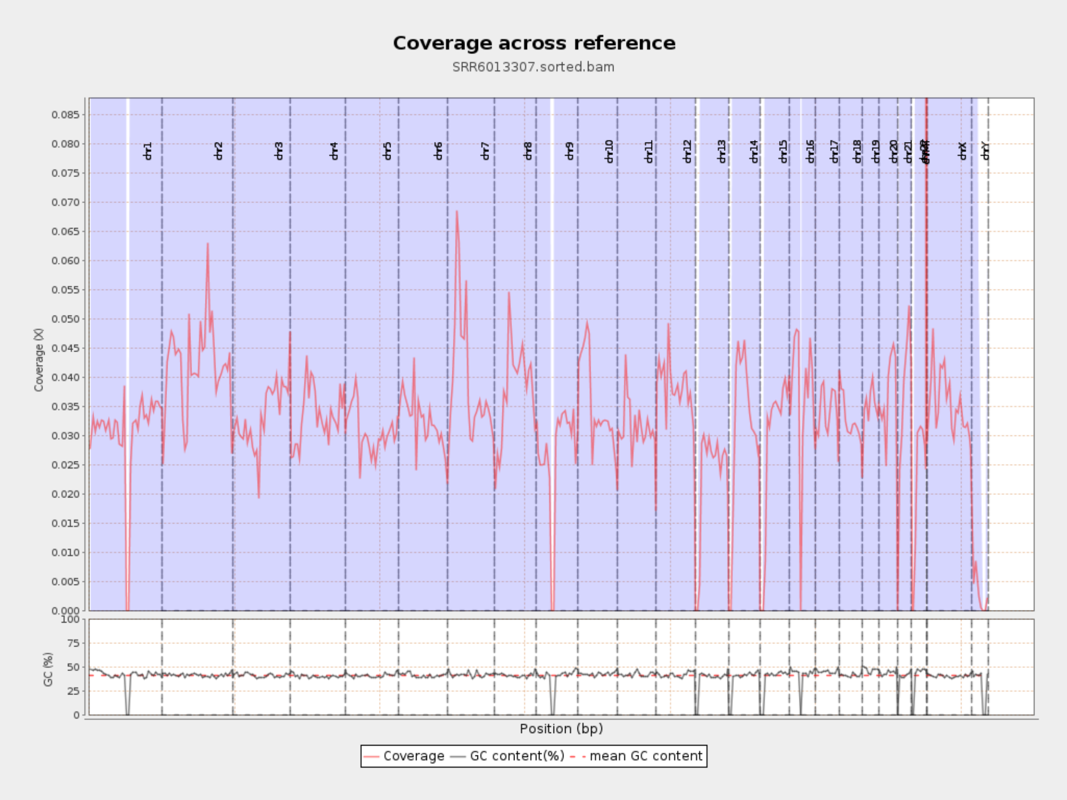
General error rate	0.79%
Mismatches	795,818
Insertions	6,784
Mapped reads with at least one insertion	0.44%
Deletions	24,605
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.95%

2.6. Chromosome stats

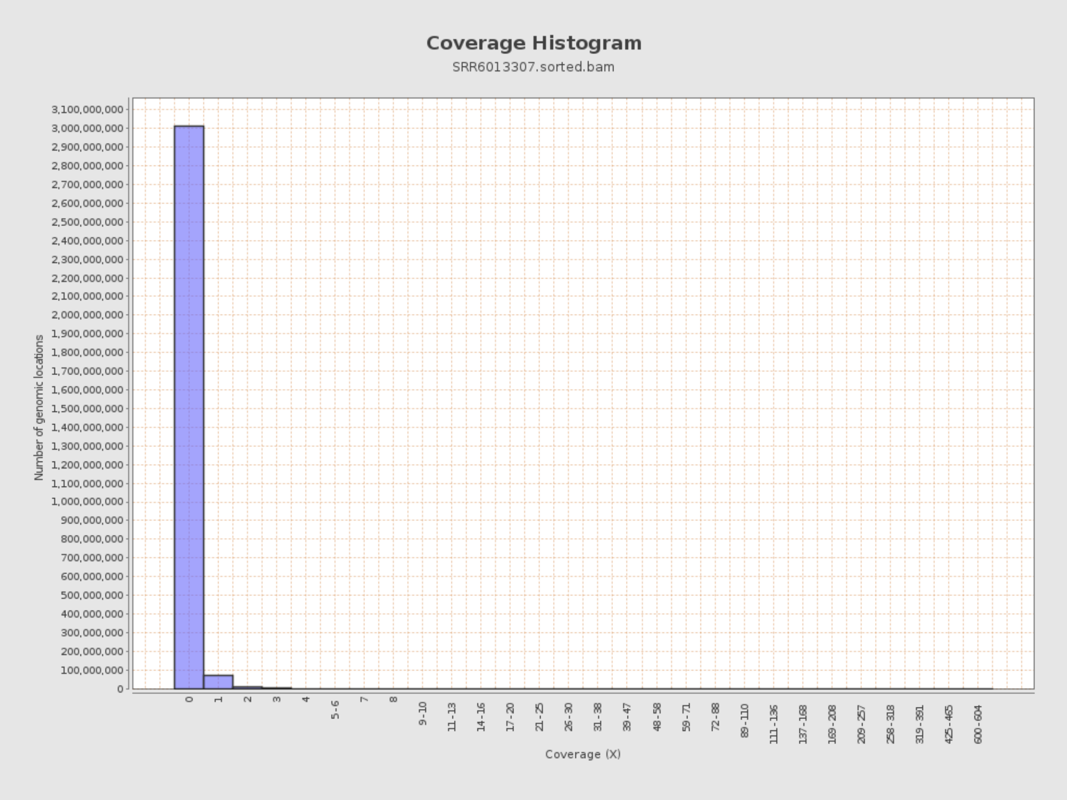
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7583769	0.0304	0.3715
chr2	243199373	10227458	0.0421	0.371
chr3	198022430	6569573	0.0332	0.2115
chr4	191154276	6391035	0.0334	0.2142
chr5	180915260	5549085	0.0307	0.2029
chr6	171115067	5561823	0.0325	0.2449
chr7	159138663	6319583	0.0397	0.4646

chr8	146364022	5549460	0.0379	0.2843
chr9	141213431	3702368	0.0262	0.2246
chr10	135534747	4844385	0.0357	0.2819
chr11	135006516	4257522	0.0315	0.2258
chr12	133851895	5137537	0.0384	0.2306
chr13	115169878	2620658	0.0228	0.1796
chr14	107349540	3357163	0.0313	0.2126
chr15	102531392	2921437	0.0285	0.1975
chr16	90354753	3347770	0.0371	0.2336
chr17	81195210	2749767	0.0339	0.2246
chr18	78077248	2568106	0.0329	0.3631
chr19	59128983	2073317	0.0351	0.309
chr20	63025520	2330035	0.037	0.2265
chr21	48129895	1698595	0.0353	0.2246
chr22	51304566	1076082	0.021	0.1681
chrMT	16571	250782	15.1338	11.7844
chrX	155270560	5485947	0.0353	0.2274
chrY	59373566	206583	0.0035	0.0769

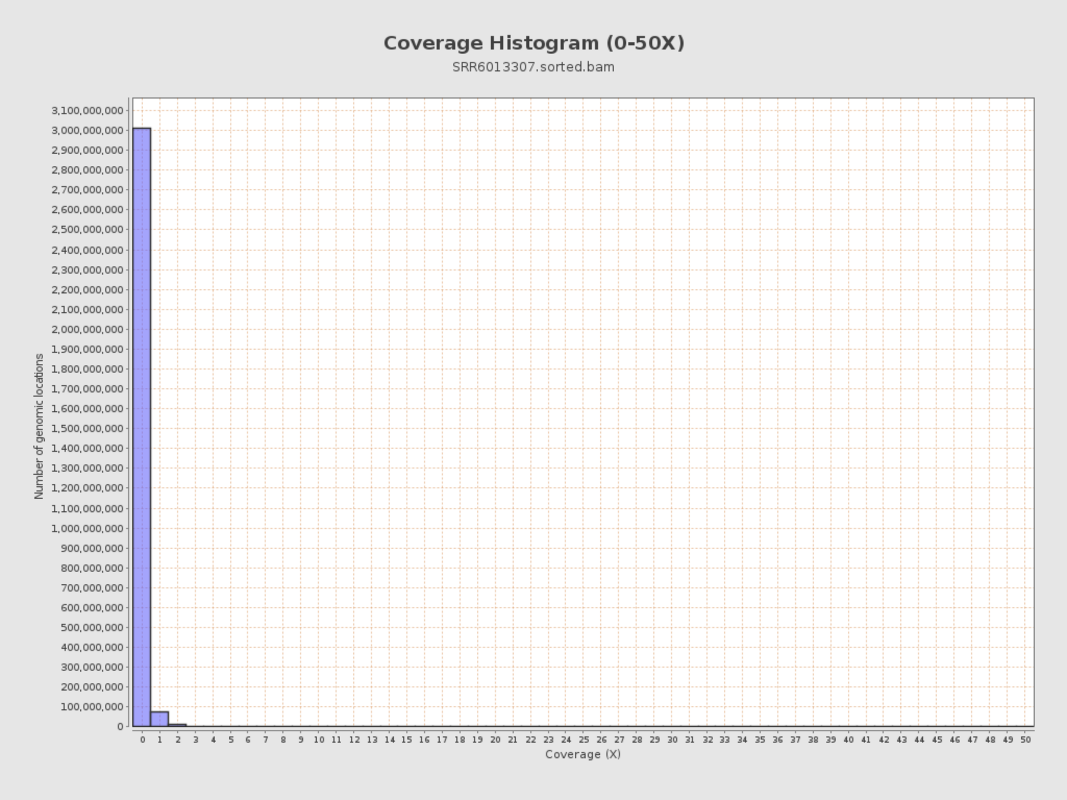
3. Results : Coverage across reference



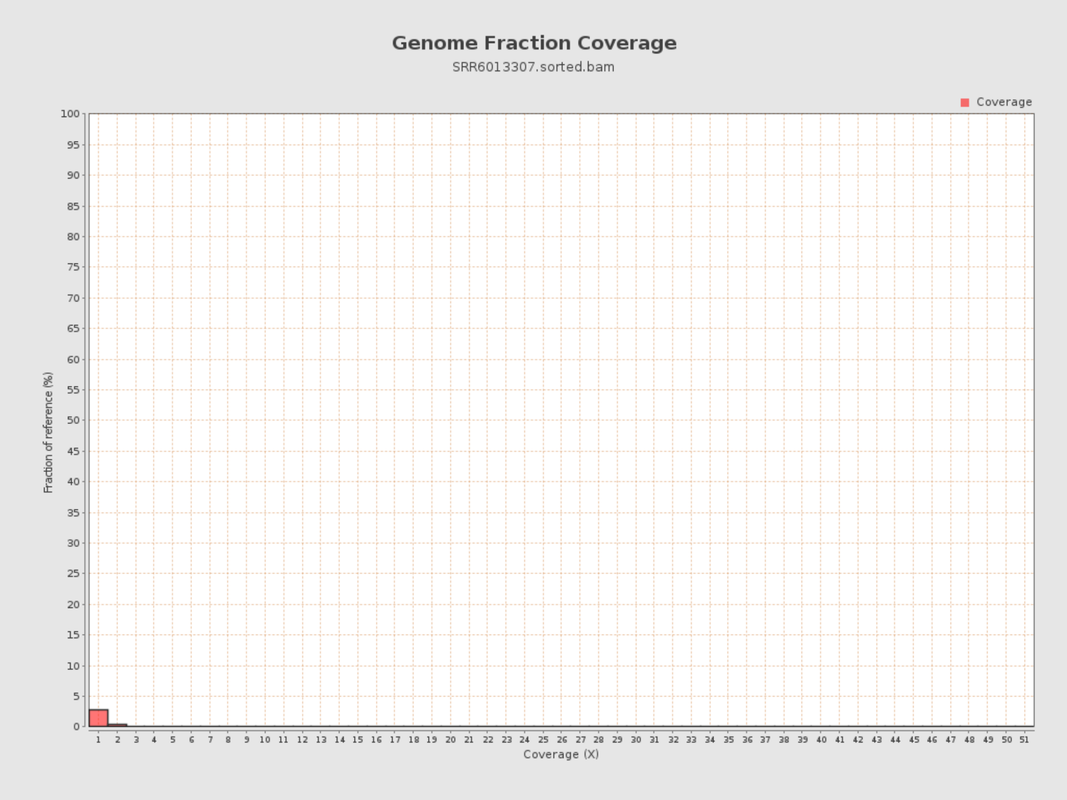
4. Results : Coverage Histogram



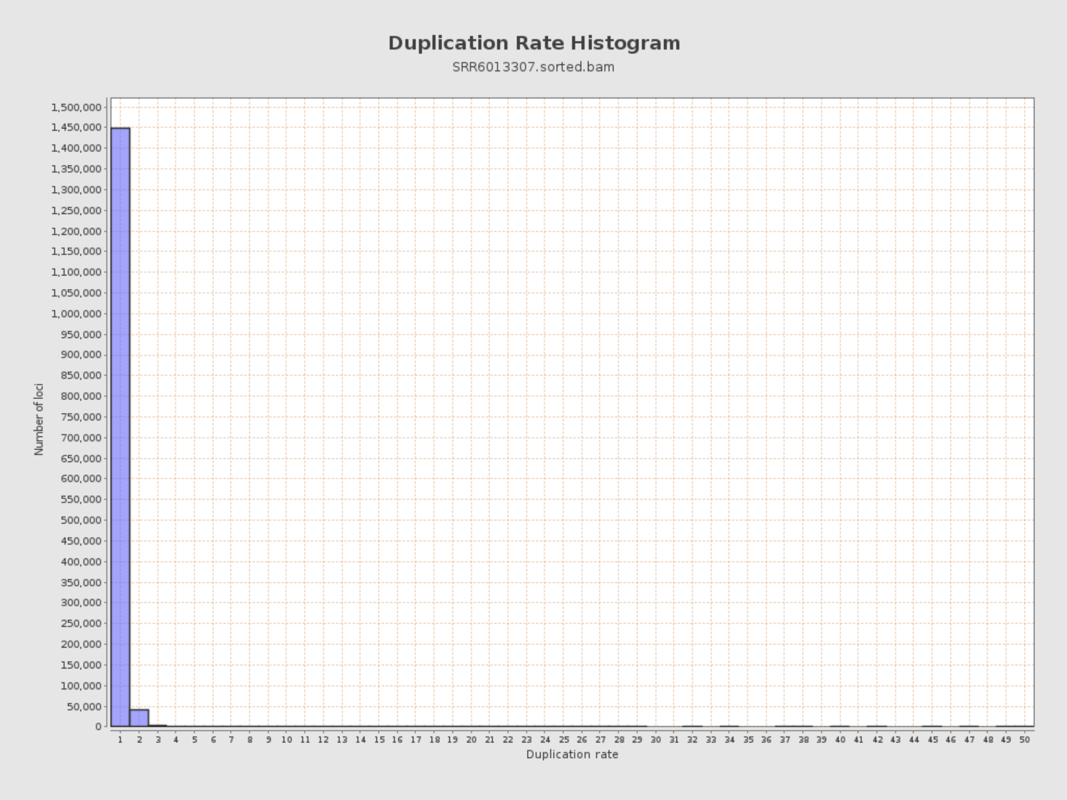
5. Results : Coverage Histogram (0-50X)



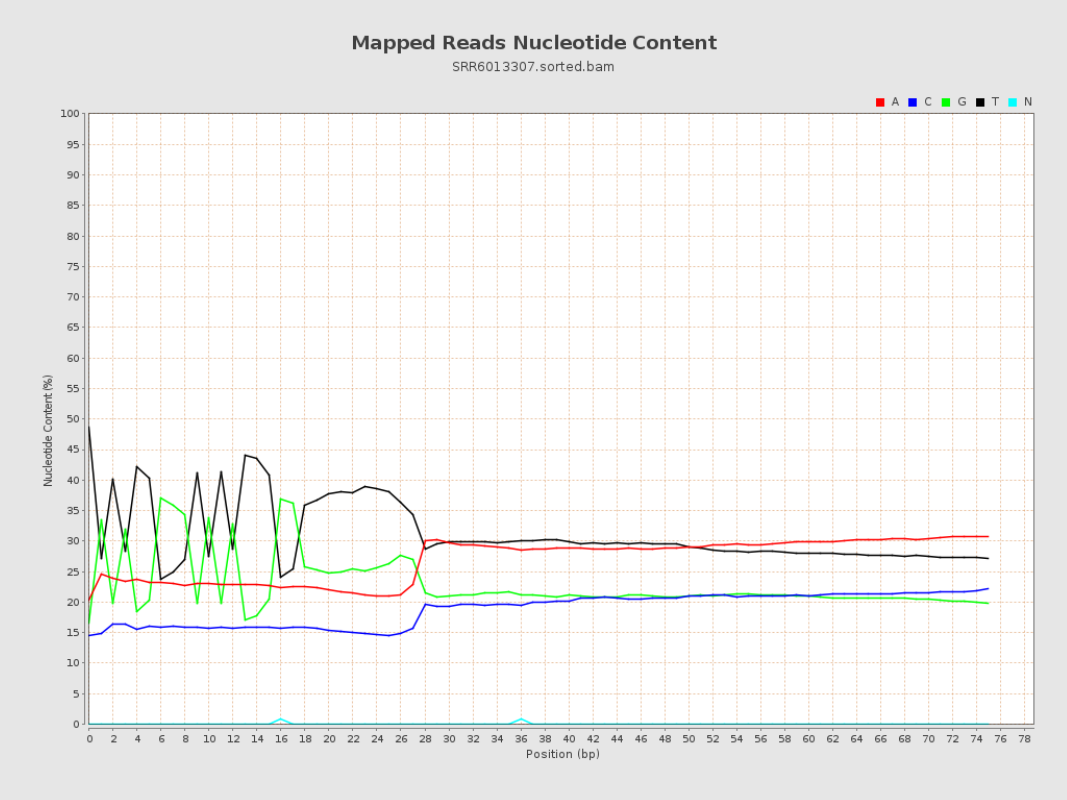
6. Results : Genome Fraction Coverage



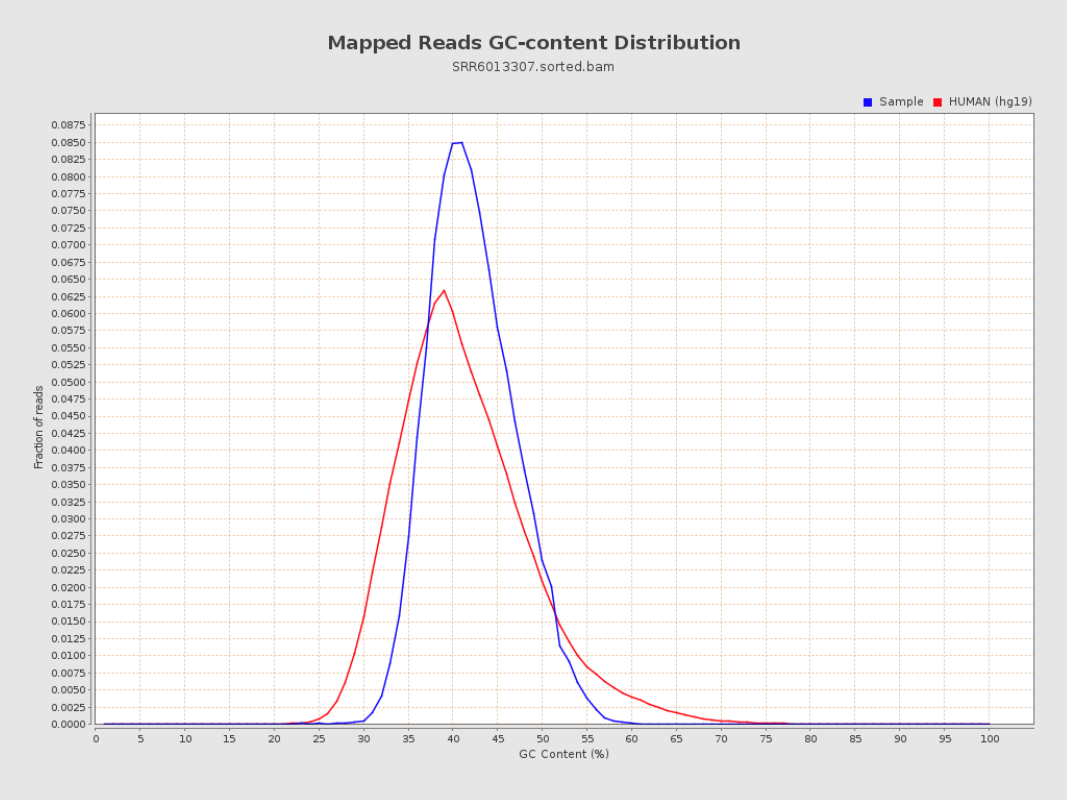
7. Results : Duplication Rate Histogram



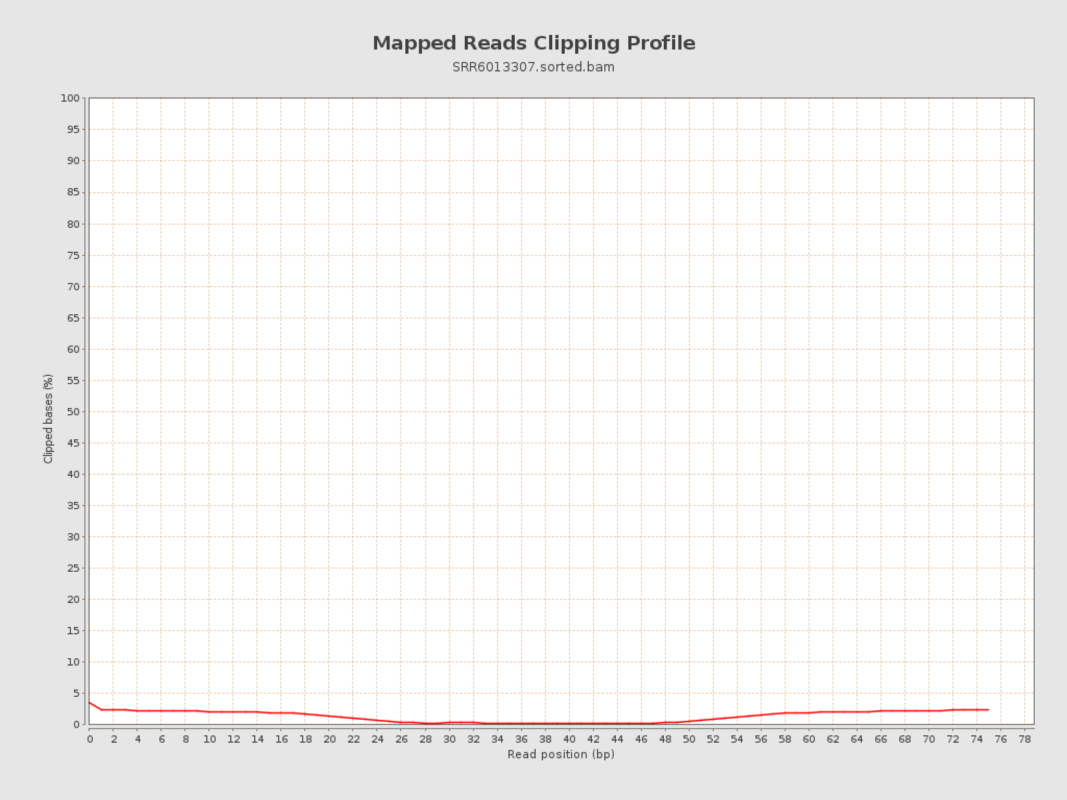
8. Results : Mapped Reads Nucleotide Content



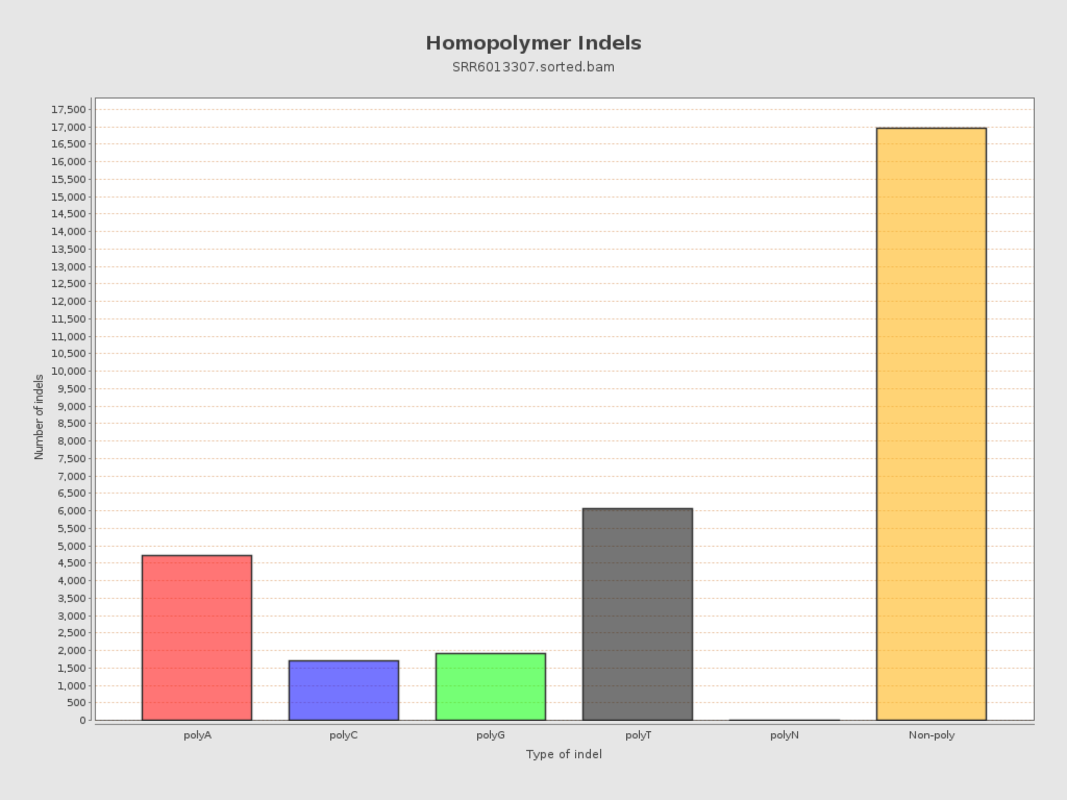
9. Results : Mapped Reads GC-content Distribution



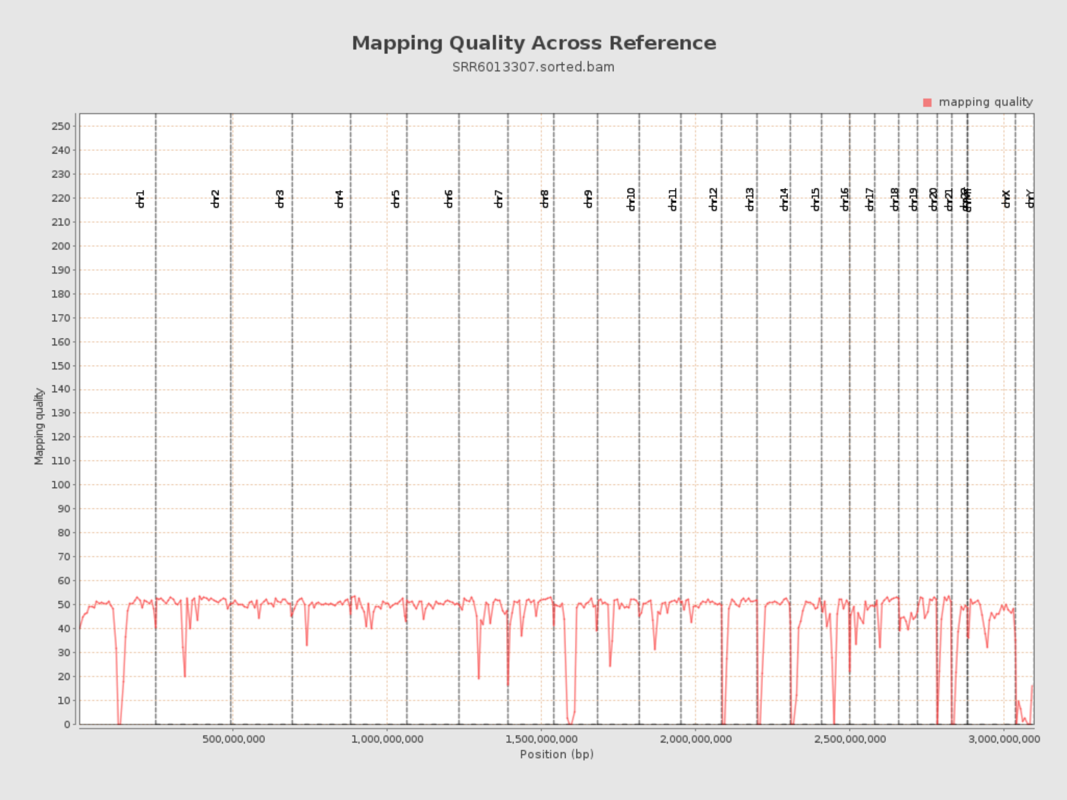
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram