Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:09:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013337.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_SRR6013337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:09:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,254,521
Mapped reads	1,875,104 / 83.17%
Unmapped reads	379,417 / 16.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,087 / 1.29%
Read min/max/mean length	30 / 76 / 76.45
Duplicated reads (estimated)	225,357 / 10%
Duplication rate	9.45%
Clipped reads	1,090,689 / 48.38%

2.2. ACGT Content

Number/percentage of A's	32,592,144 / 27.27%
Number/percentage of C's	21,963,890 / 18.38%
Number/percentage of T's	38,018,420 / 31.81%
Number/percentage of G's	26,914,354 / 22.52%
Number/percentage of N's	12,849 / 0.01%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3958

2.4. Mapping Quality

Mean Mapping Quality	43.48

2.5. Mismatches and indels

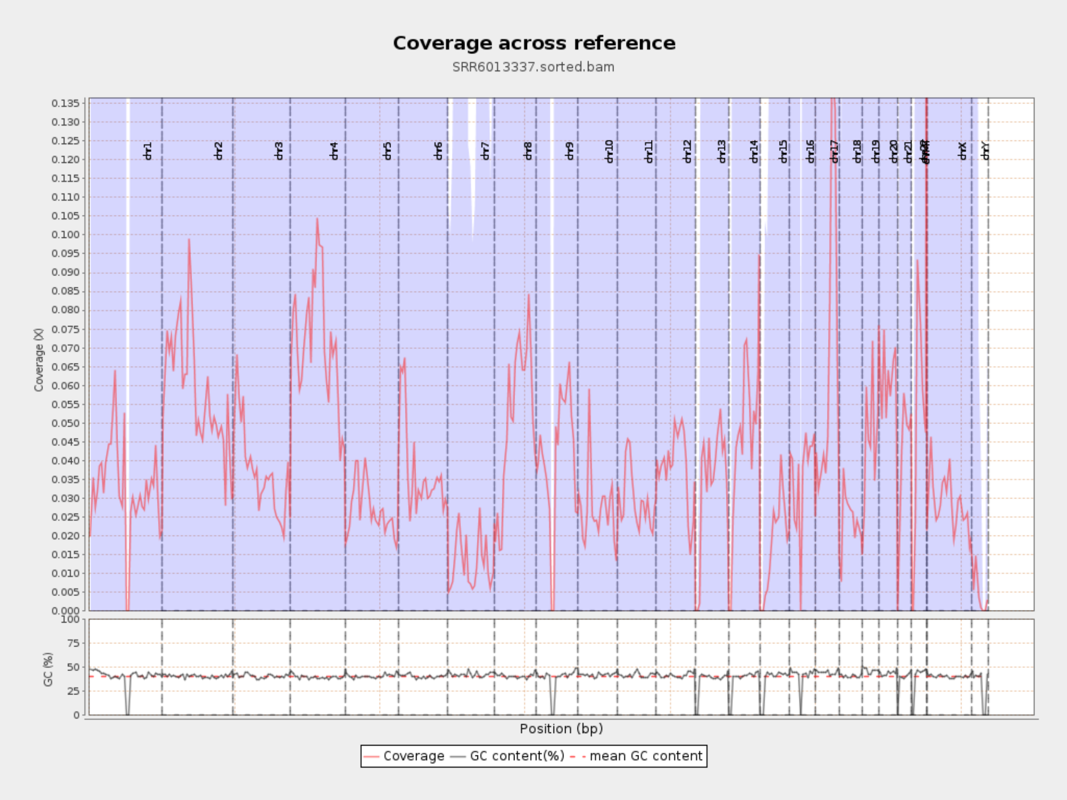
General error rate	0.88%
Mismatches	1,037,387
Insertions	8,567
Mapped reads with at least one insertion	0.45%
Deletions	45,718
Mapped reads with at least one deletion	2.4%
Homopolymer indels	43.56%

2.6. Chromosome stats

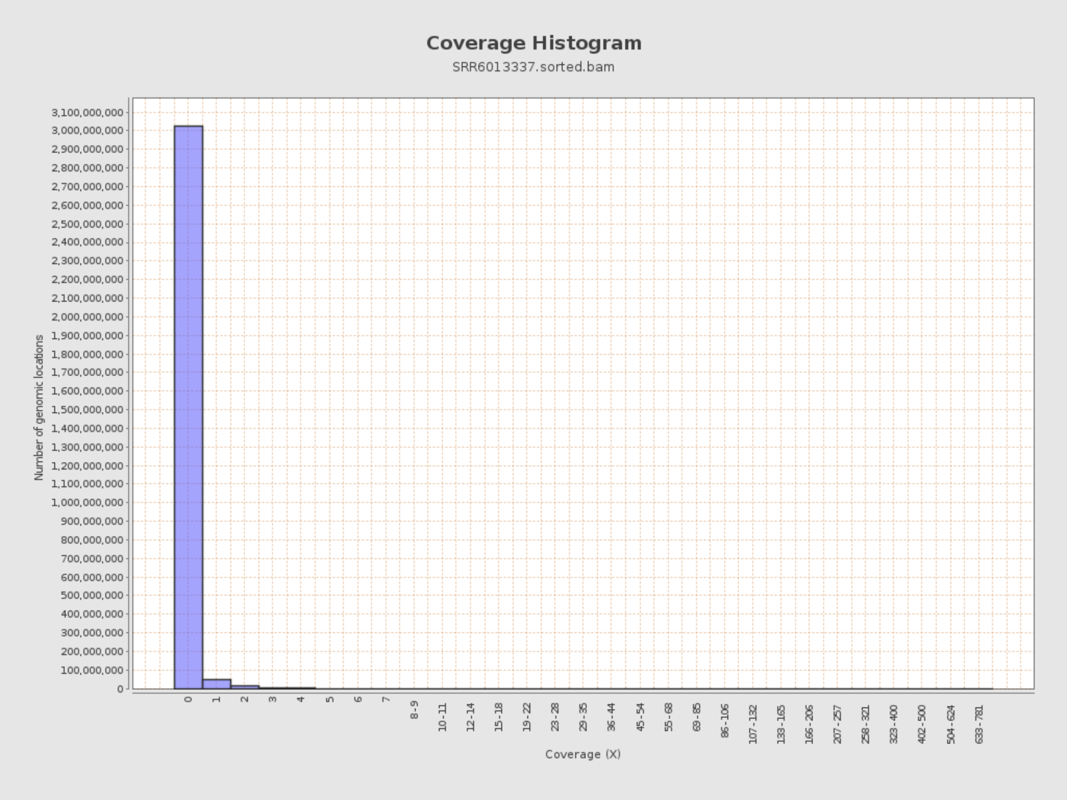
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8126584	0.0326	0.4752
chr2	243199373	14319280	0.0589	0.5694
chr3	198022430	7349587	0.0371	0.2877
chr4	191154276	13633085	0.0713	0.4204
chr5	180915260	4882813	0.027	0.2425
chr6	171115067	6315697	0.0369	0.3423
chr7	159138663	2040939	0.0128	0.2216

chr8	146364022	7567746	0.0517	0.5619
chr9	141213431	5829505	0.0413	0.4344
chr10	135534747	3649267	0.0269	0.379
chr11	135006516	3989708	0.0296	0.3514
chr12	133851895	5143001	0.0384	0.302
chr13	115169878	3872879	0.0336	0.2775
chr14	107349540	4802809	0.0447	0.3506
chr15	102531392	1855636	0.0181	0.2
chr16	90354753	3200734	0.0354	0.3004
chr17	81195210	5355270	0.066	0.4086
chr18	78077248	1874377	0.024	0.7901
chr19	59128983	2782189	0.0471	0.4136
chr20	63025520	3879922	0.0616	0.3871
chr21	48129895	1954347	0.0406	0.3173
chr22	51304566	2433343	0.0474	0.3295
chrMT	16571	8591	0.5184	0.8513
chrX	155270560	4440683	0.0286	0.2719
chrY	59373566	272208	0.0046	0.1356

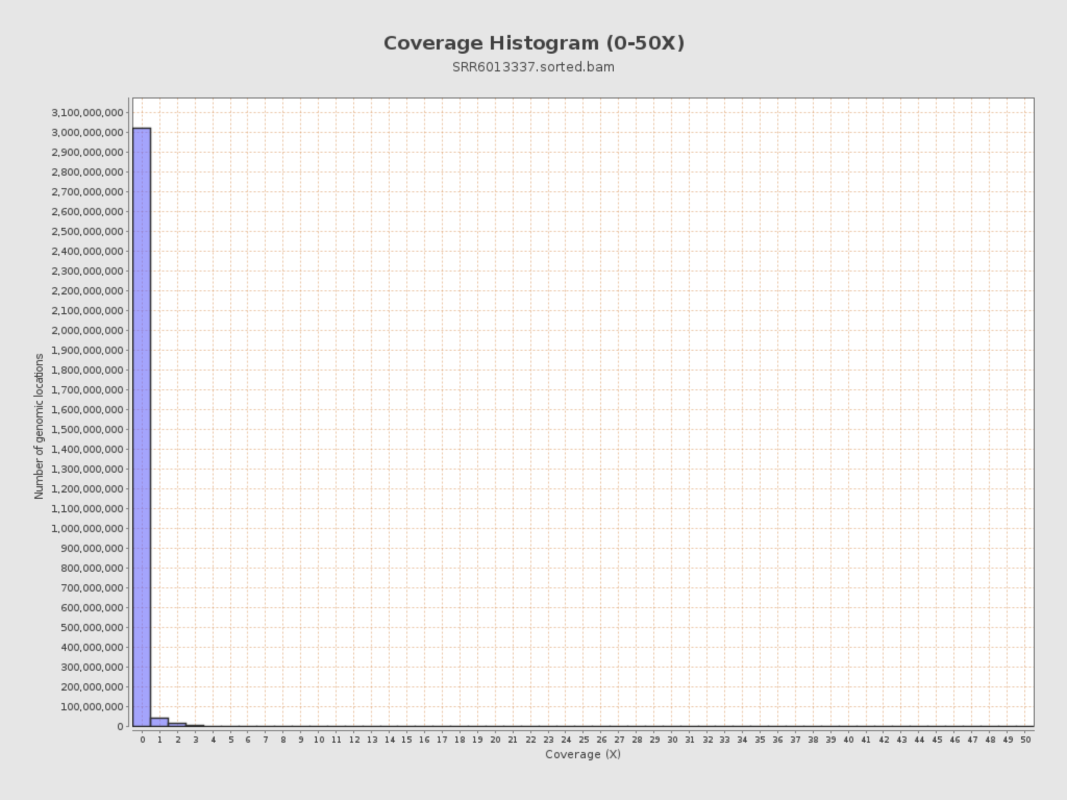
3. Results : Coverage across reference



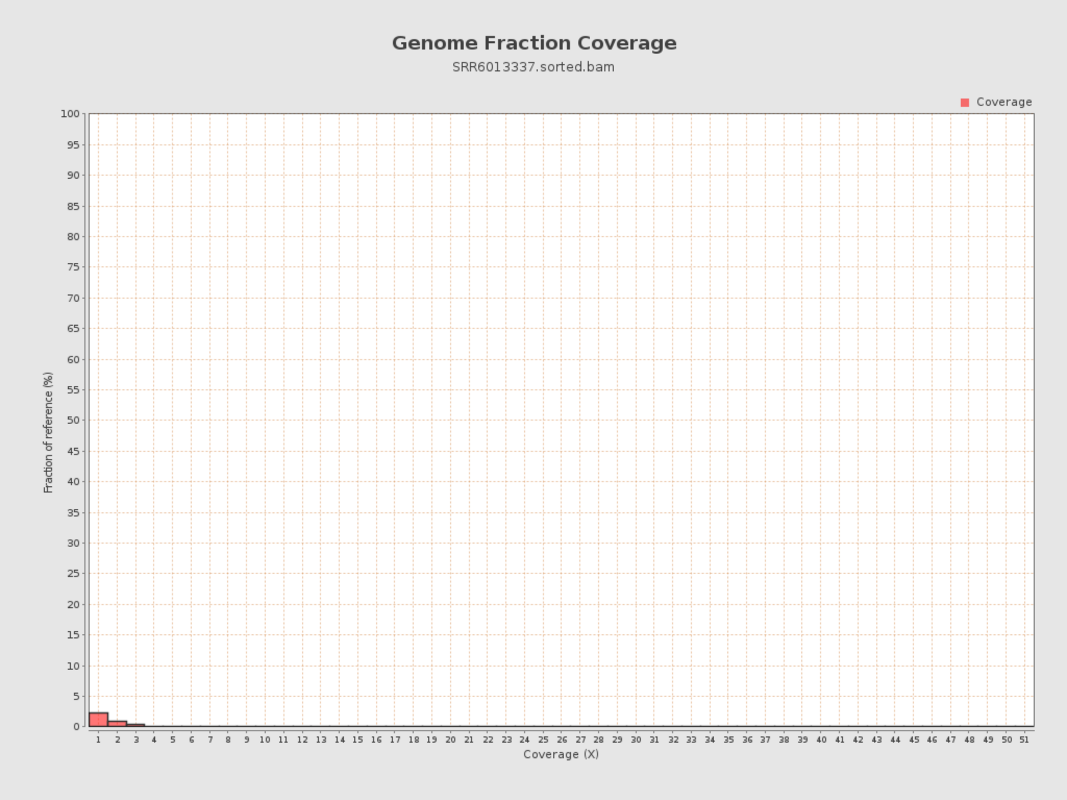
4. Results : Coverage Histogram



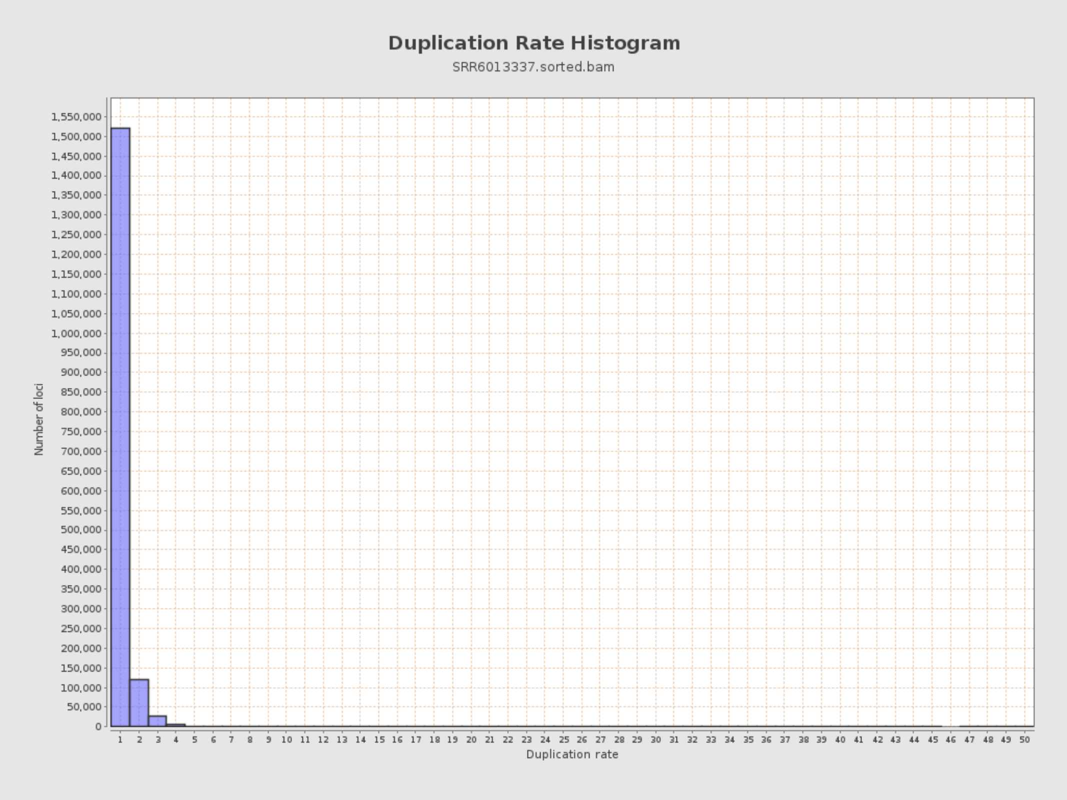
5. Results : Coverage Histogram (0-50X)



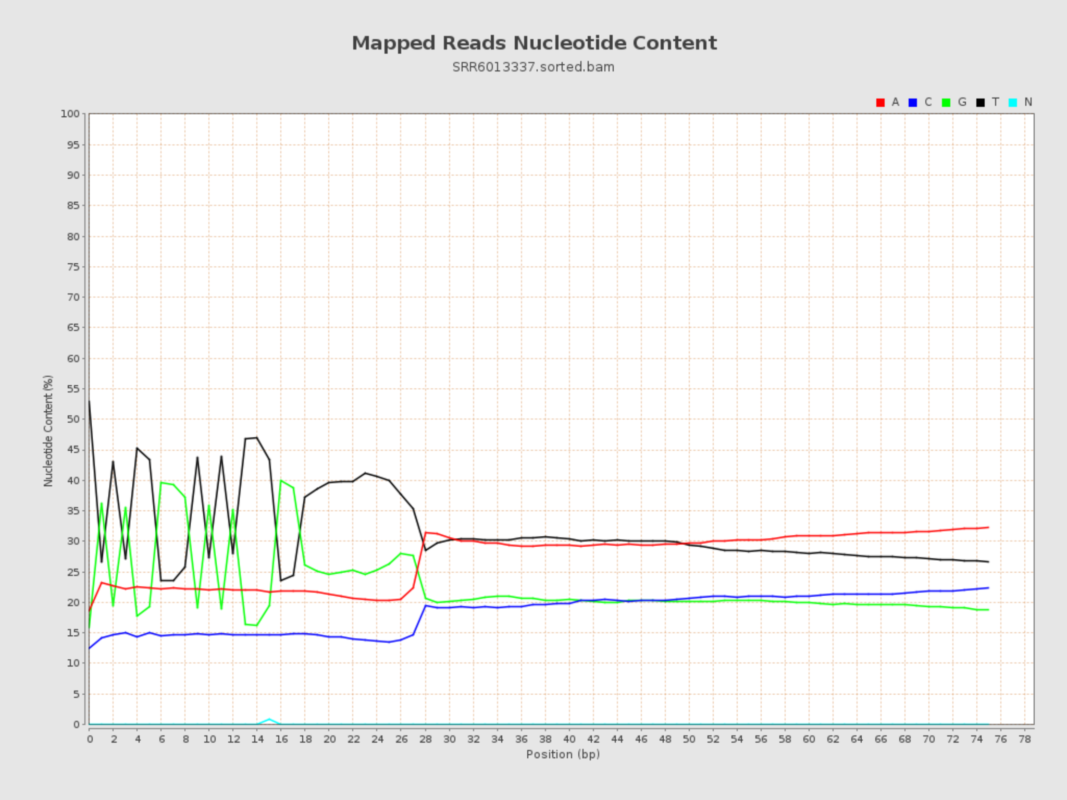
6. Results : Genome Fraction Coverage



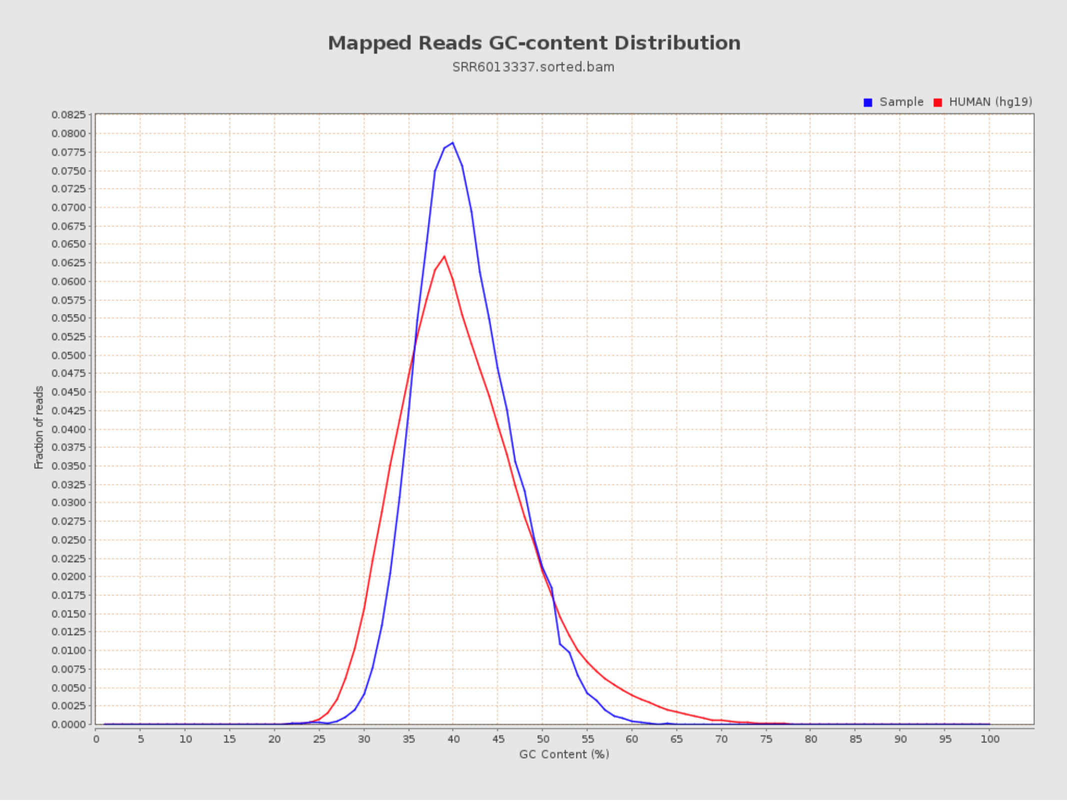
7. Results : Duplication Rate Histogram



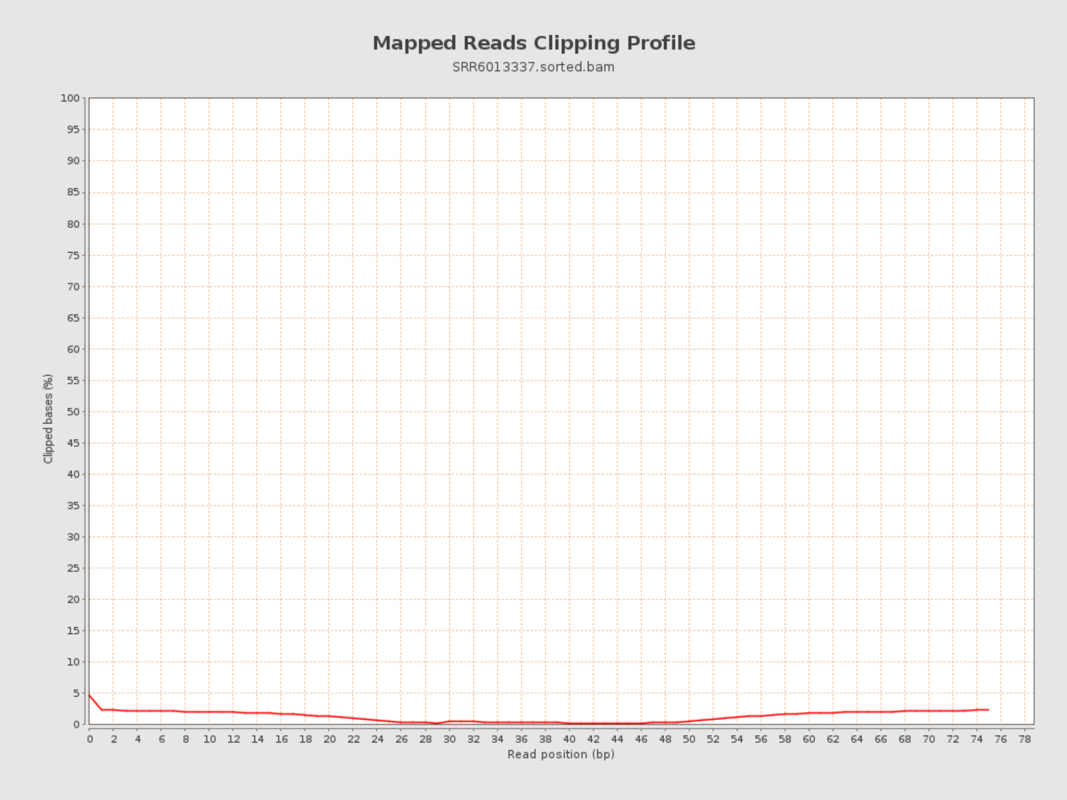
8. Results : Mapped Reads Nucleotide Content



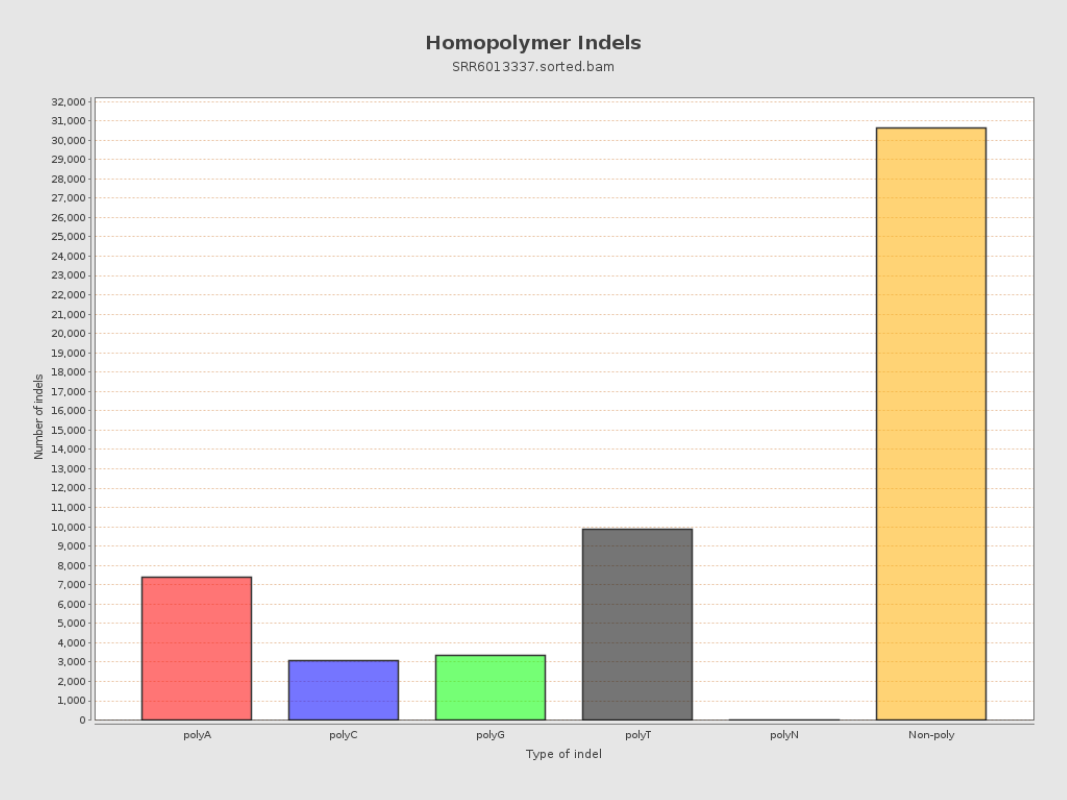
9. Results : Mapped Reads GC-content Distribution



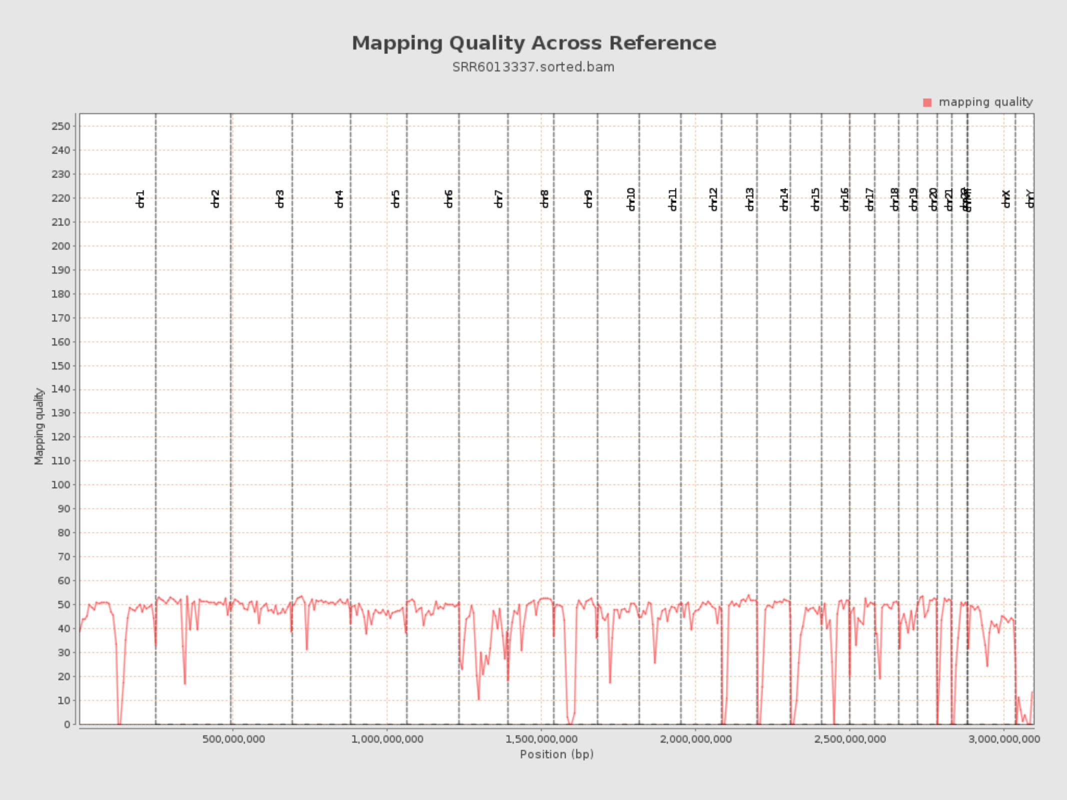
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram