Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:24:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080615.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_SRR3080615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:24:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,877,311
Mapped reads	4,043,344 / 82.9%
Unmapped reads	833,967 / 17.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,679 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	182,214 / 3.74%
Duplication rate	3.32%
Clipped reads	1,993,358 / 40.87%

2.2. ACGT Content

Number/percentage of A's	73,184,046 / 27.24%
Number/percentage of C's	48,155,158 / 17.93%
Number/percentage of T's	86,503,907 / 32.2%
Number/percentage of G's	60,566,458 / 22.55%
Number/percentage of N's	217,474 / 0.08%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0868

Standard Deviation	0.7017

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

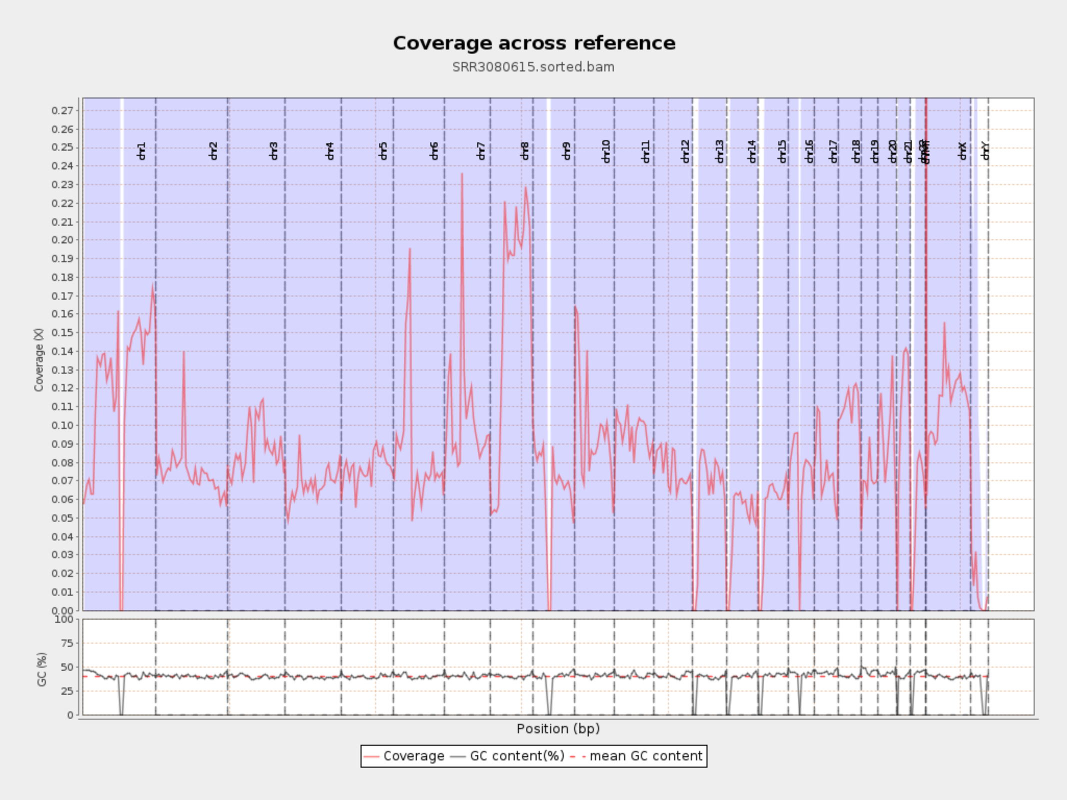
General error rate	0.94%
Mismatches	2,474,997
Insertions	23,986
Mapped reads with at least one insertion	0.59%
Deletions	66,983
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.46%

2.6. Chromosome stats

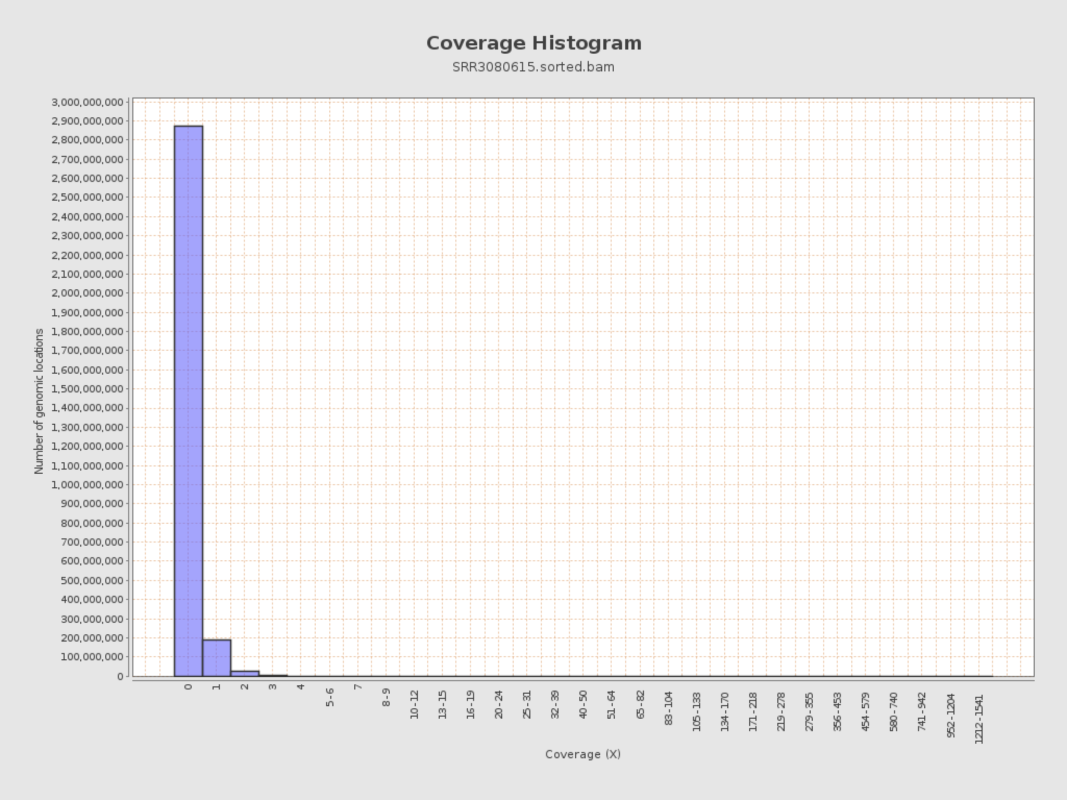
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29738547	0.1193	0.9856
chr2	243199373	18242087	0.075	0.6881
chr3	198022430	17413469	0.0879	0.3422
chr4	191154276	13067034	0.0684	0.341
chr5	180915260	13880193	0.0767	0.3194
chr6	171115067	14918210	0.0872	0.5763
chr7	159138663	16814785	0.1057	1.8785

chr8	146364022	23663903	0.1617	0.8822
chr9	141213431	9231885	0.0654	0.5328
chr10	135534747	13357793	0.0986	0.6595
chr11	135006516	12956606	0.096	0.5382
chr12	133851895	10138456	0.0757	0.3238
chr13	115169878	7081796	0.0615	0.2806
chr14	107349540	5164602	0.0481	0.3126
chr15	102531392	5338538	0.0521	0.2621
chr16	90354753	6469952	0.0716	0.3672
chr17	81195210	6263961	0.0771	0.4173
chr18	78077248	8677964	0.1111	0.9659
chr19	59128983	4196333	0.071	0.7049
chr20	63025520	6105673	0.0969	0.3982
chr21	48129895	5039905	0.1047	0.4217
chr22	51304566	2769540	0.054	0.2648
chrMT	16571	98141	5.9225	6.0141
chrX	155270560	17466544	0.1125	0.4759
chrY	59373566	640400	0.0108	0.2203

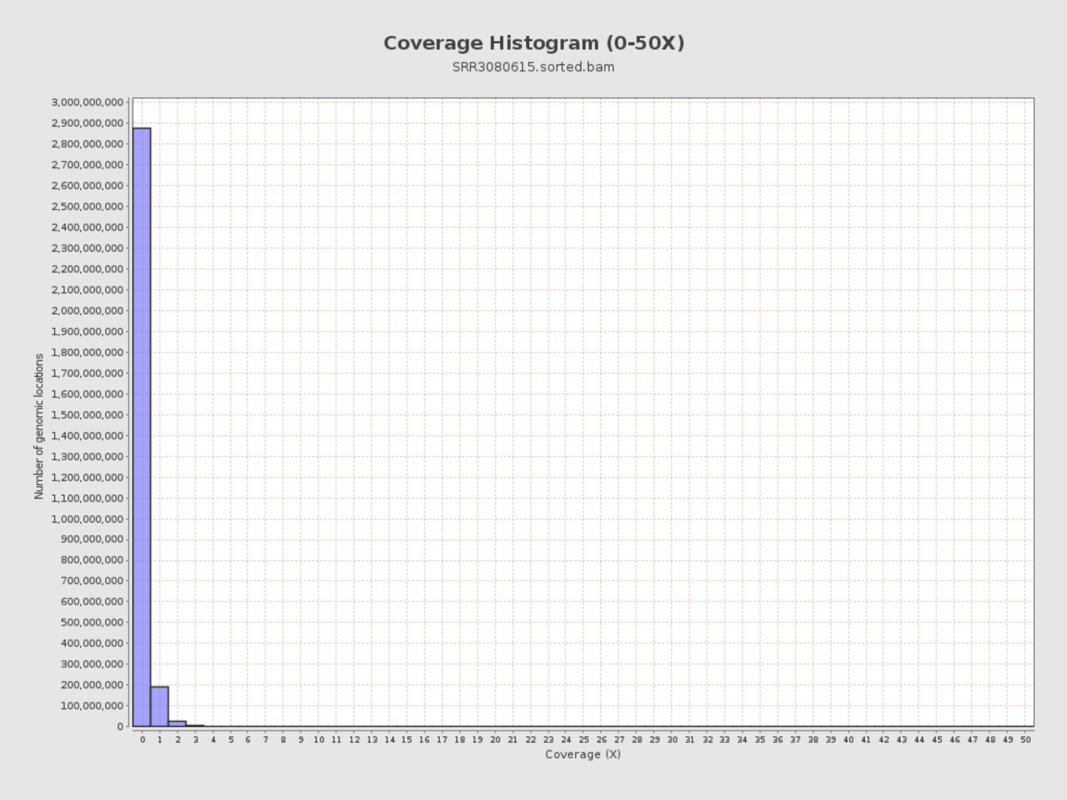
3. Results : Coverage across reference



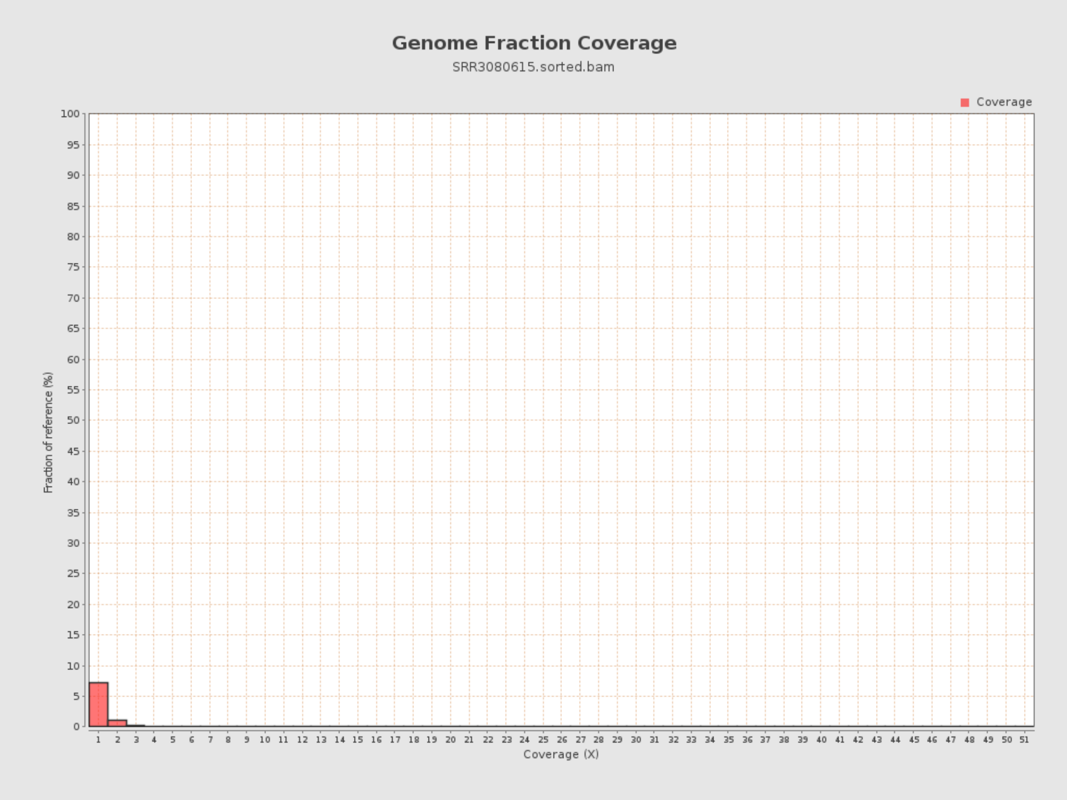
4. Results : Coverage Histogram



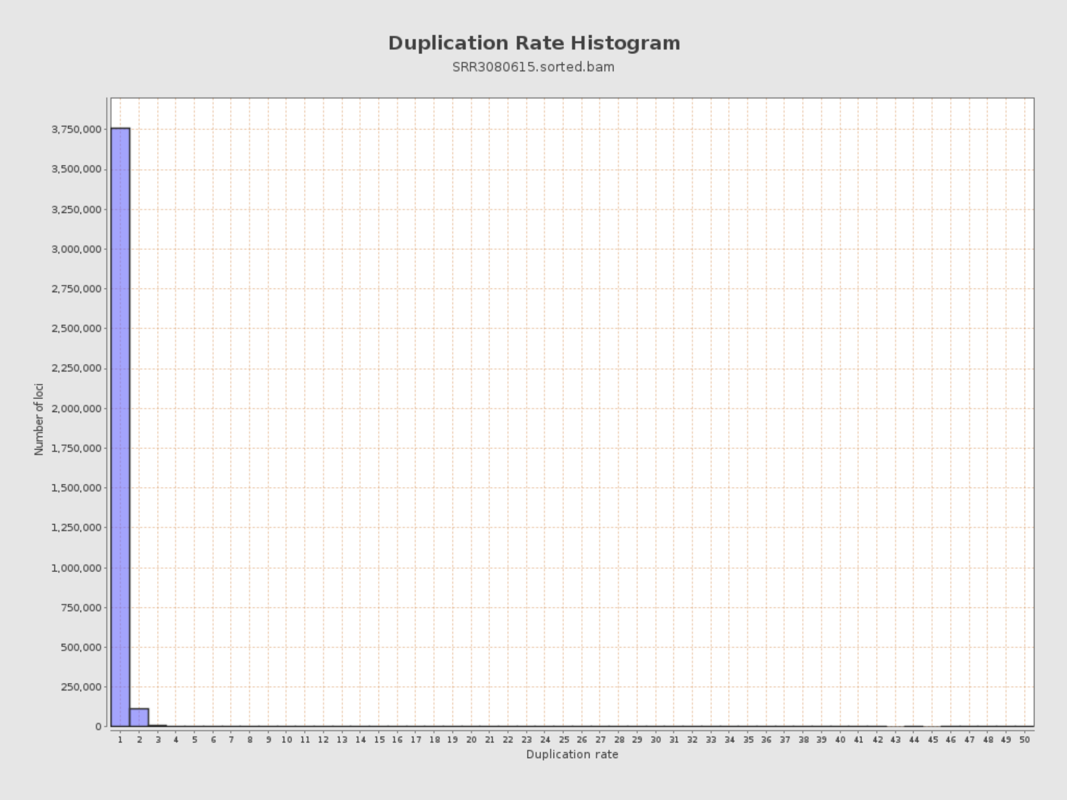
5. Results : Coverage Histogram (0-50X)



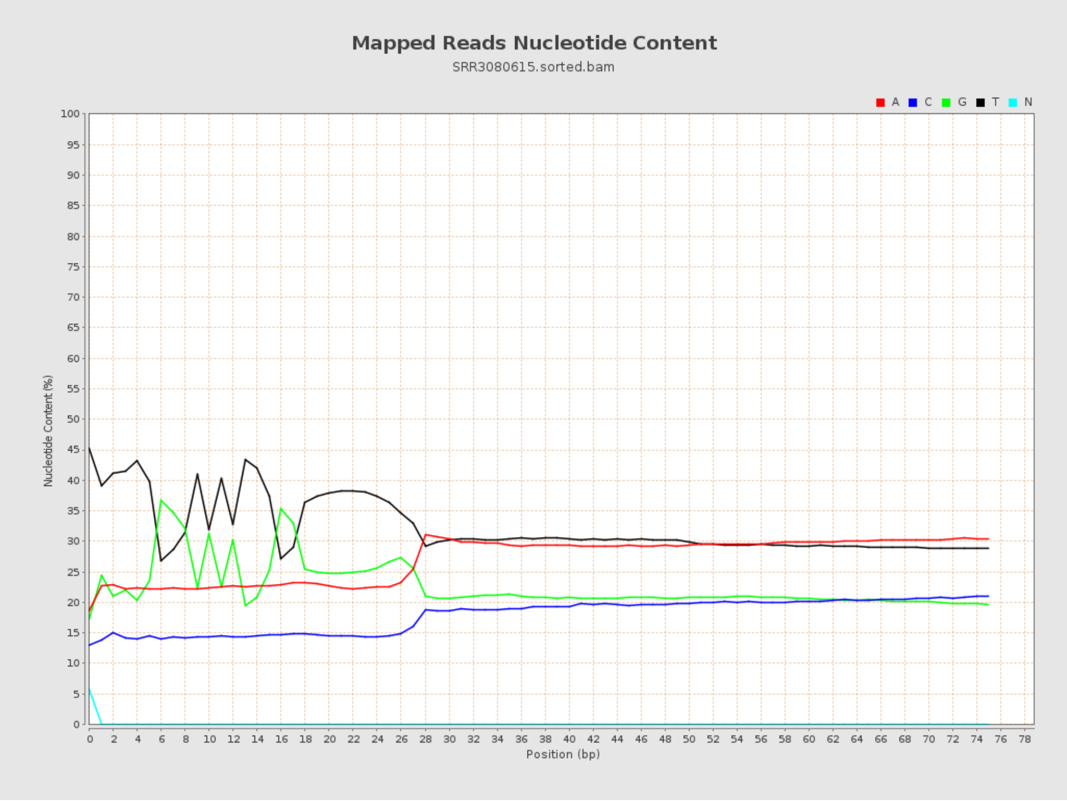
6. Results : Genome Fraction Coverage



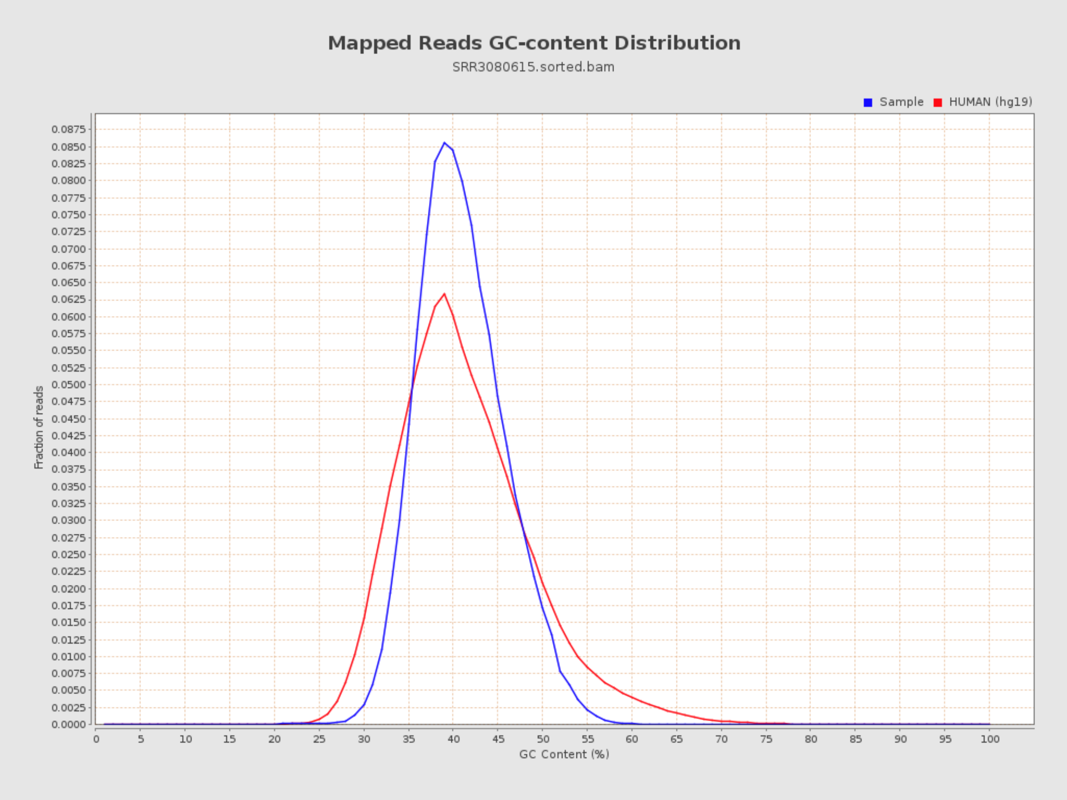
7. Results : Duplication Rate Histogram



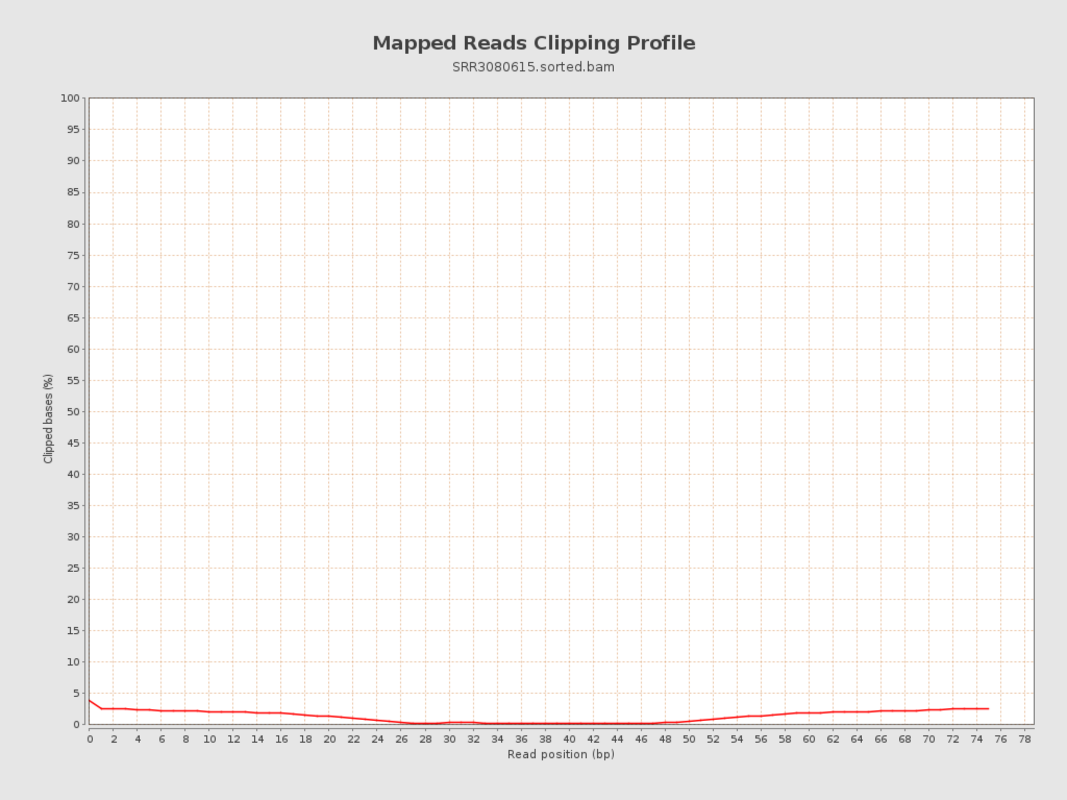
8. Results : Mapped Reads Nucleotide Content



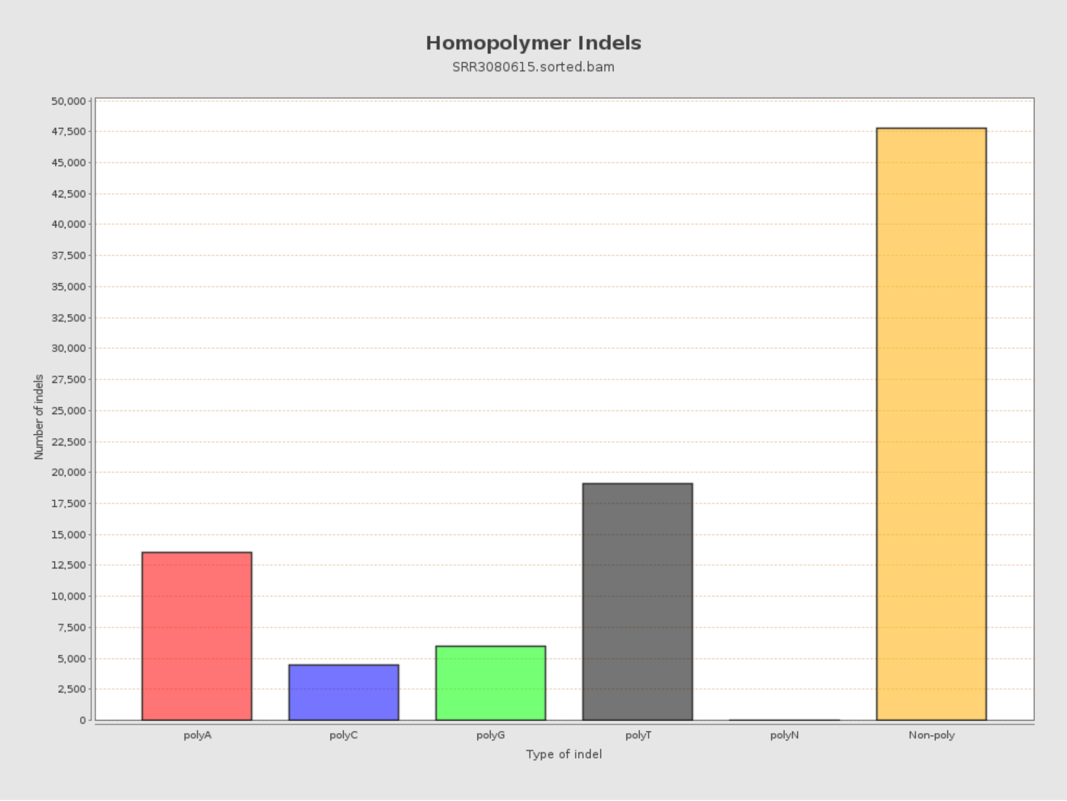
9. Results : Mapped Reads GC-content Distribution



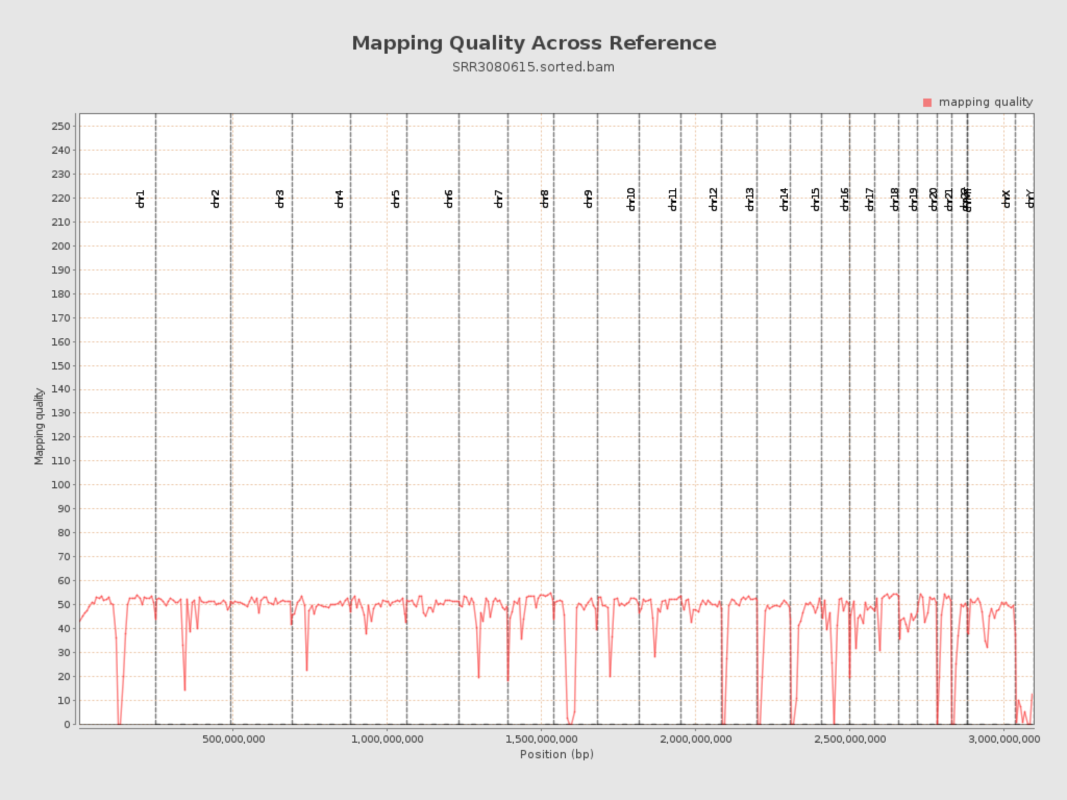
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram