Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:42:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080907.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_SRR3080907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:42:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,657,881
Mapped reads	3,255,938 / 89.01%
Unmapped reads	401,943 / 10.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,309 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	142,316 / 3.89%
Duplication rate	3.56%
Clipped reads	1,140,600 / 31.18%

2.2. ACGT Content

Number/percentage of A's	65,019,671 / 29.02%
Number/percentage of C's	39,601,289 / 17.68%
Number/percentage of T's	71,727,434 / 32.01%
Number/percentage of G's	46,623,430 / 20.81%
Number/percentage of N's	1,071,746 / 0.48%
GC Percentage	38.49%

2.3. Coverage

Mean	0.0724

Standard Deviation	0.4645

2.4. Mapping Quality

Mean Mapping Quality	48.03

2.5. Mismatches and indels

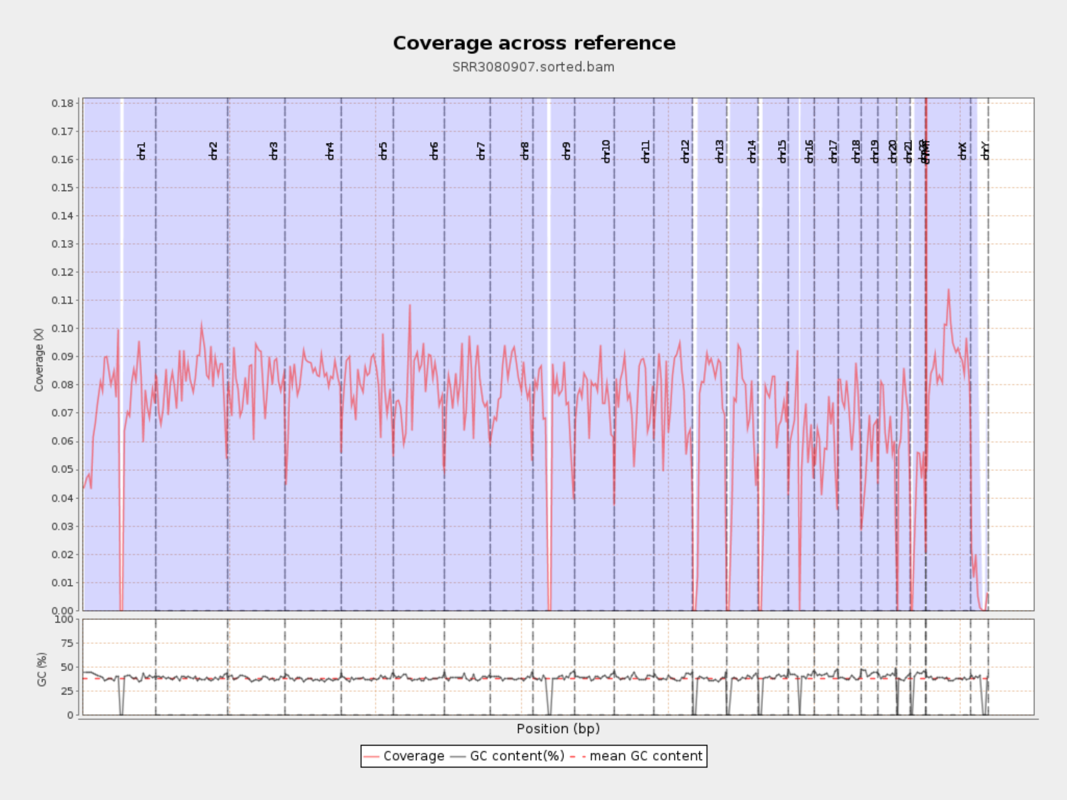
General error rate	1.13%
Mismatches	2,510,824
Insertions	16,880
Mapped reads with at least one insertion	0.51%
Deletions	49,348
Mapped reads with at least one deletion	1.5%
Homopolymer indels	49.85%

2.6. Chromosome stats

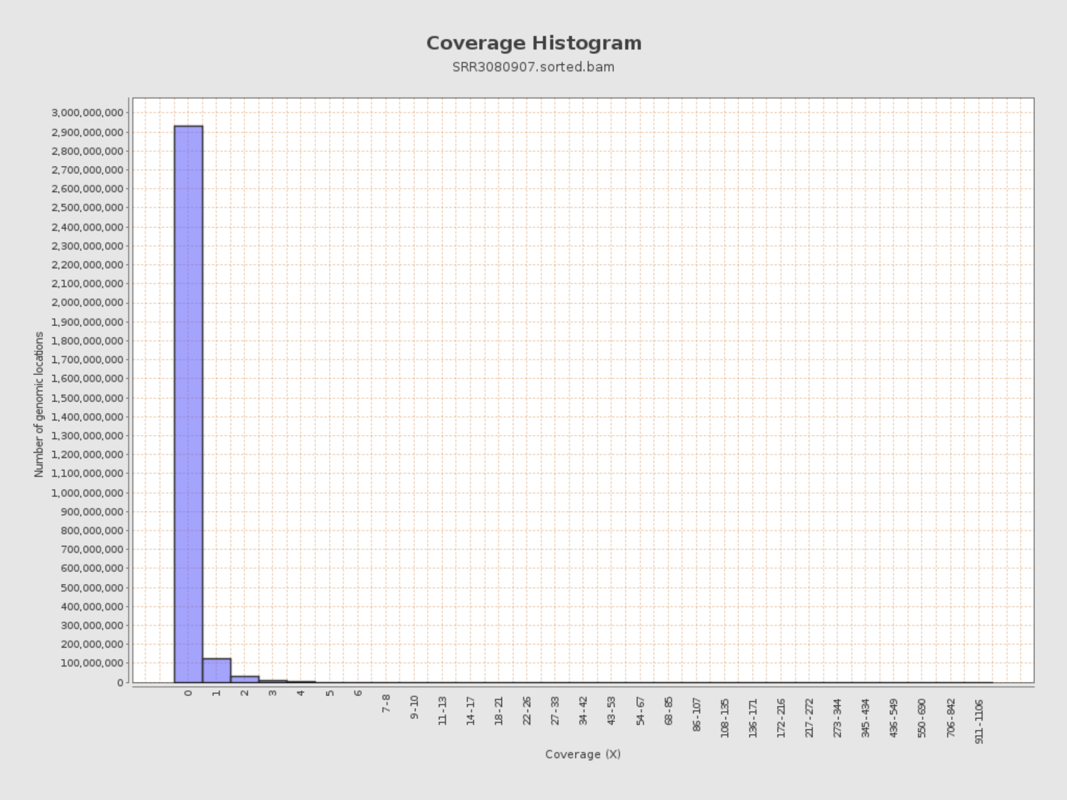
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17233503	0.0691	0.6801
chr2	243199373	19985168	0.0822	0.4638
chr3	198022430	16043926	0.081	0.3662
chr4	191154276	15739884	0.0823	0.3754
chr5	180915260	14388095	0.0795	0.3643
chr6	171115067	13760218	0.0804	0.4282
chr7	159138663	12323793	0.0774	0.5507

chr8	146364022	11647191	0.0796	0.7623
chr9	141213431	9440310	0.0669	0.4796
chr10	135534747	10331768	0.0762	0.43
chr11	135006516	10277567	0.0761	0.4232
chr12	133851895	10116866	0.0756	0.3598
chr13	115169878	7853761	0.0682	0.336
chr14	107349540	6667830	0.0621	0.3483
chr15	102531392	6108836	0.0596	0.3133
chr16	90354753	5163784	0.0572	0.3354
chr17	81195210	4772787	0.0588	0.3396
chr18	78077248	5794936	0.0742	0.7461
chr19	59128983	3234803	0.0547	0.4871
chr20	63025520	4024858	0.0639	0.3293
chr21	48129895	2912728	0.0605	0.3482
chr22	51304566	1884700	0.0367	0.2435
chrMT	16571	200749	12.1145	6.206
chrX	155270560	13763303	0.0886	0.4067
chrY	59373566	452927	0.0076	0.1378

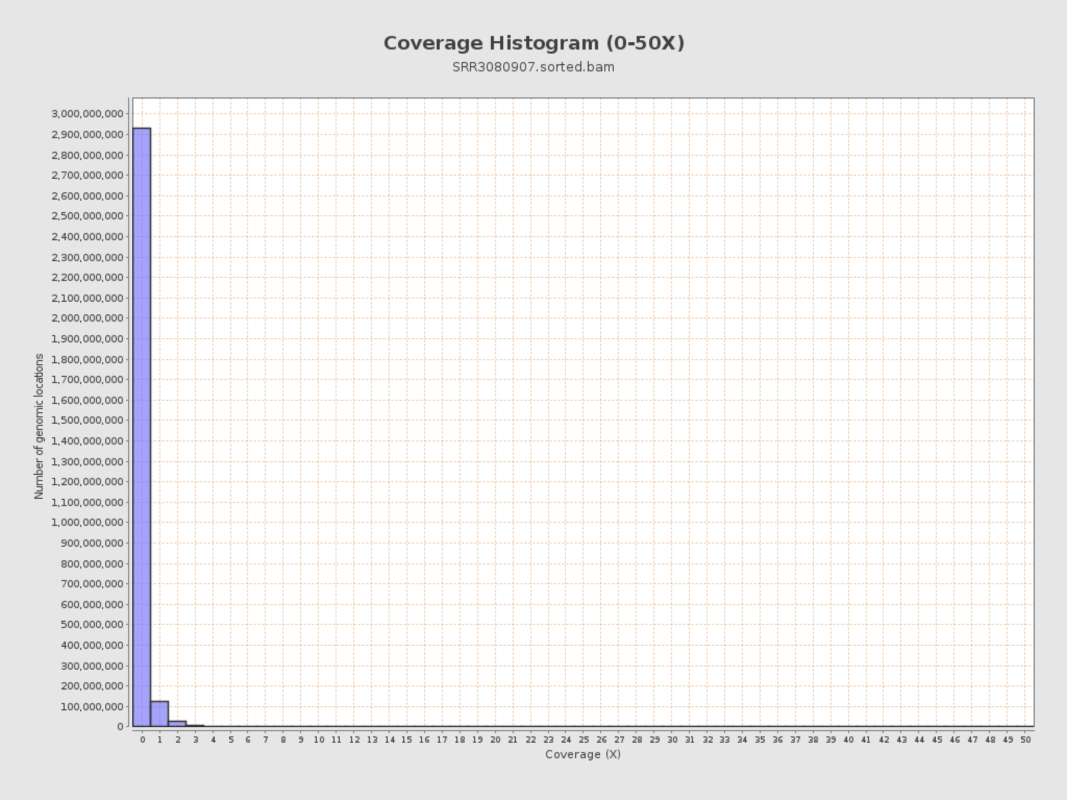
3. Results : Coverage across reference



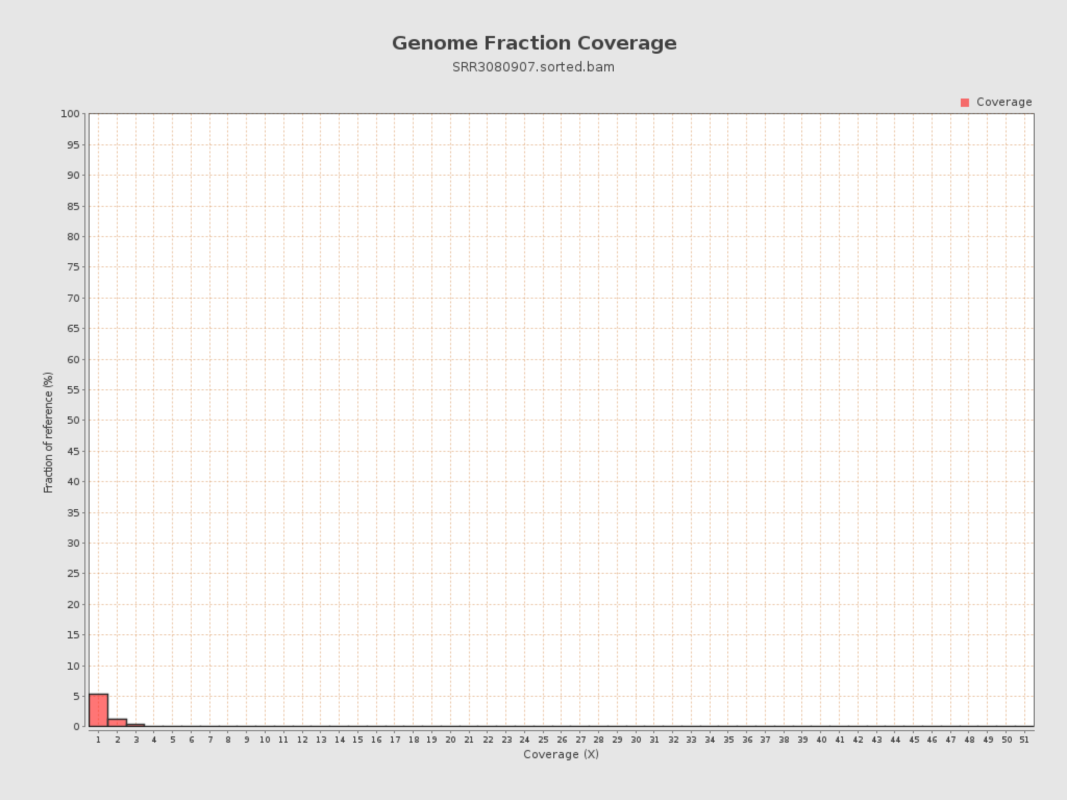
4. Results : Coverage Histogram



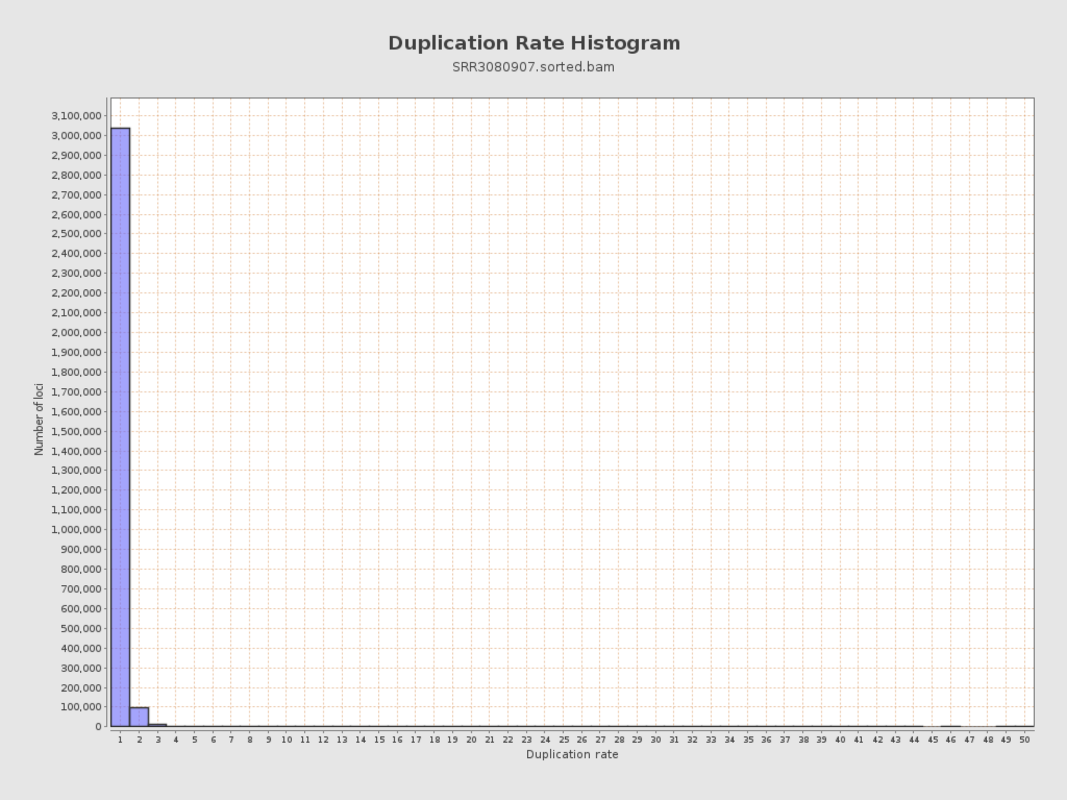
5. Results : Coverage Histogram (0-50X)



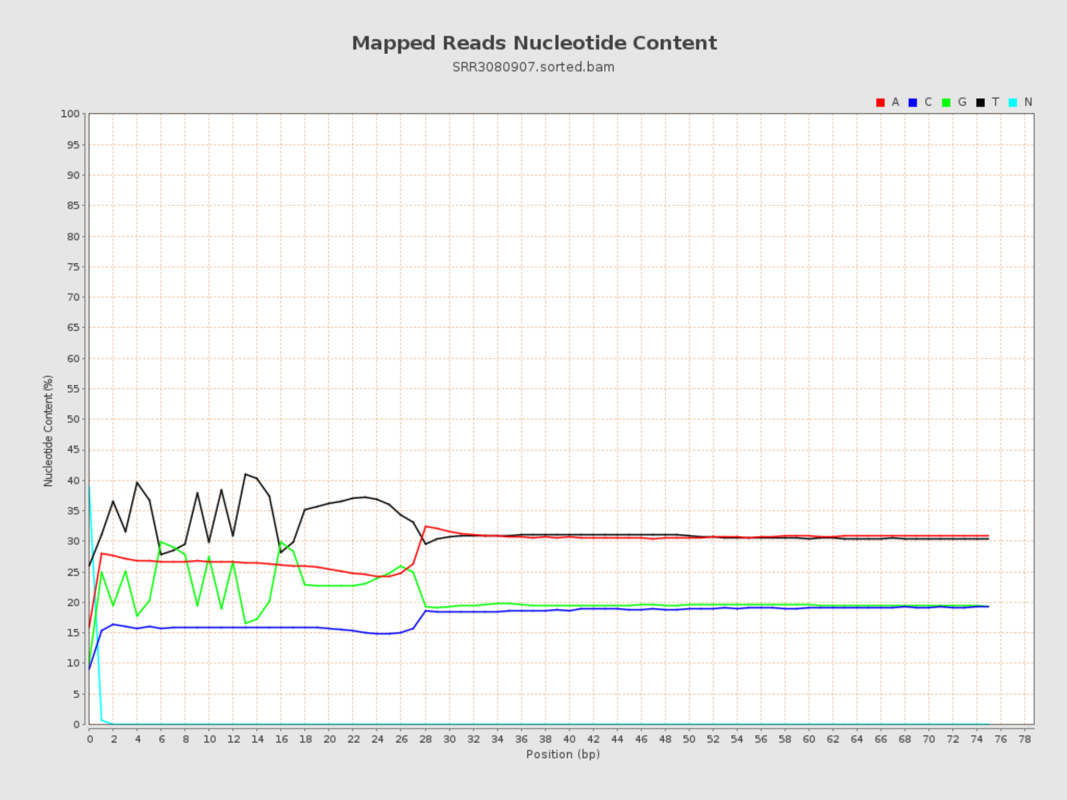
6. Results : Genome Fraction Coverage



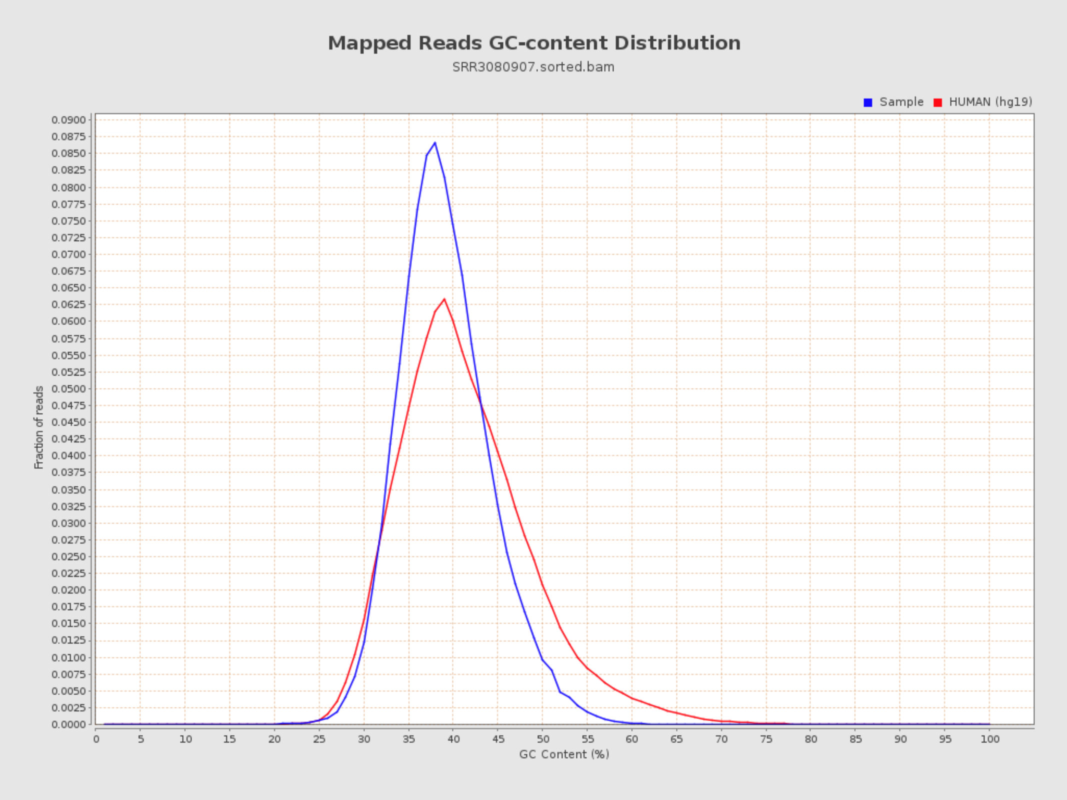
7. Results : Duplication Rate Histogram



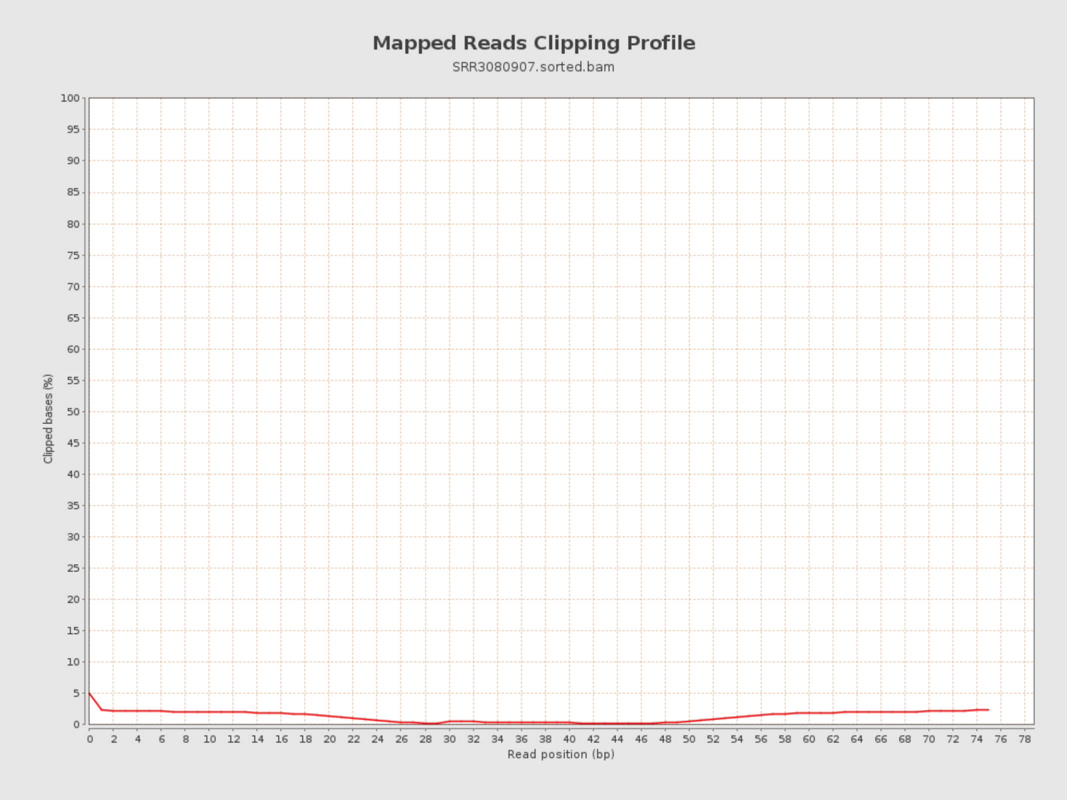
8. Results : Mapped Reads Nucleotide Content



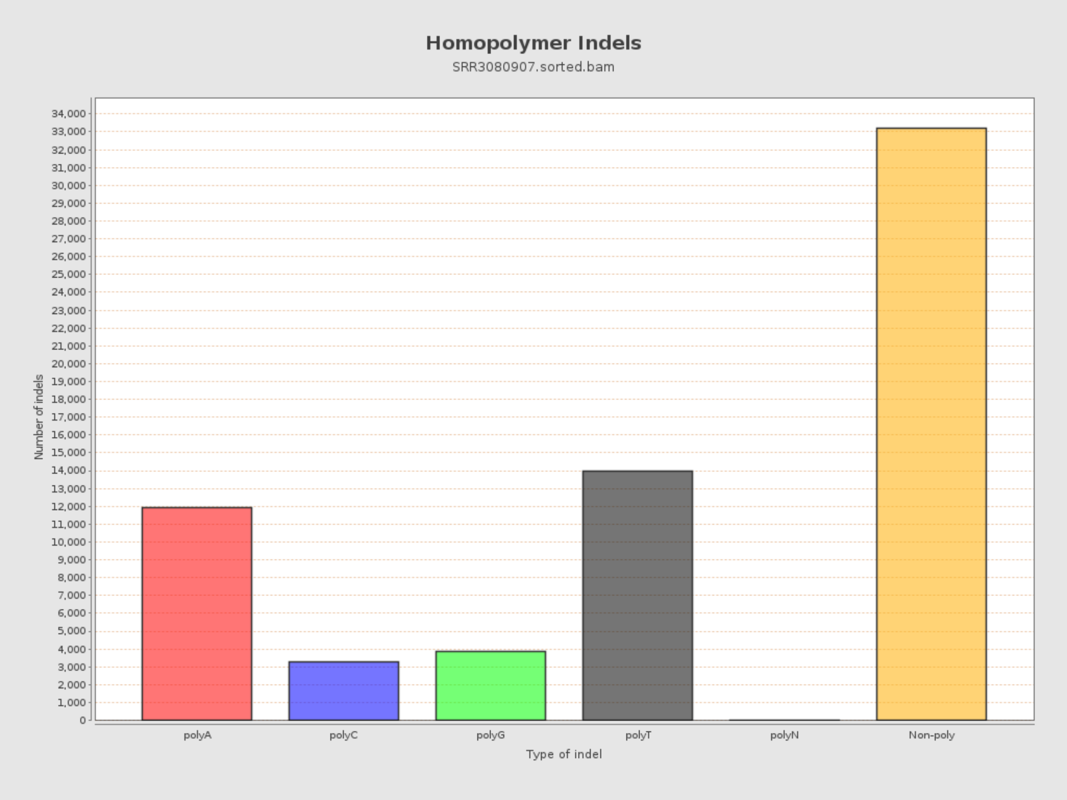
9. Results : Mapped Reads GC-content Distribution



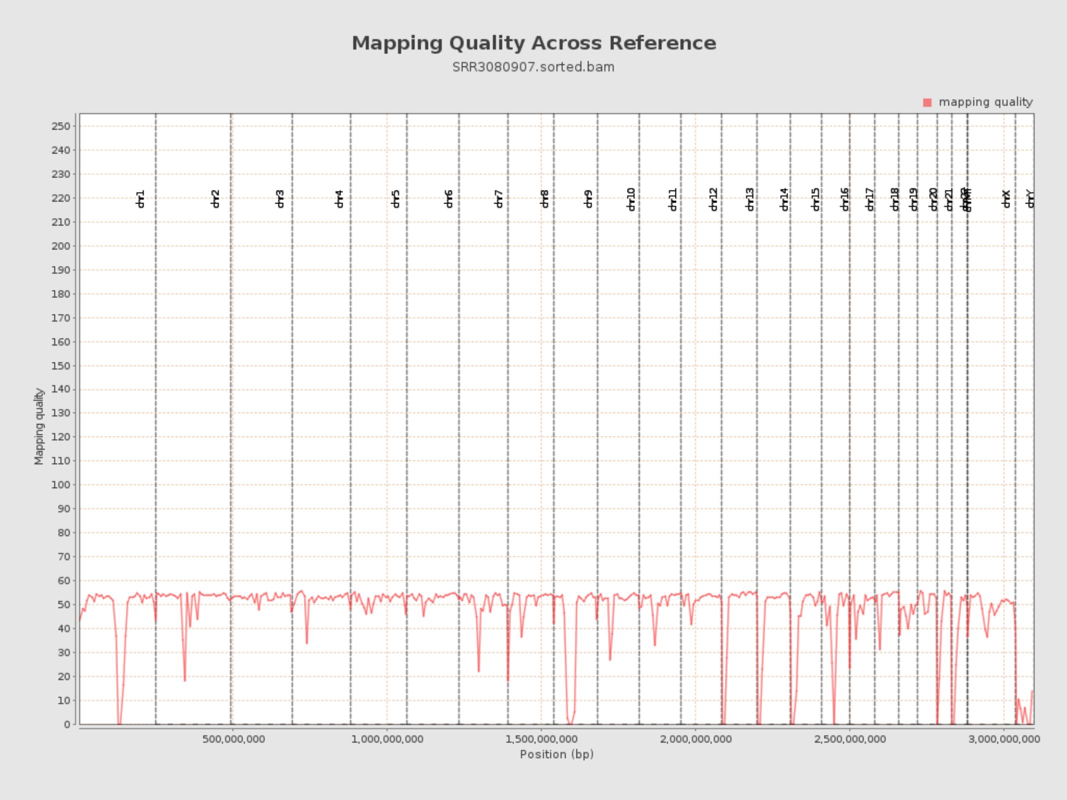
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram