Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:44:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084287.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_SRR3084287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084287.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:44:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,676,256
Mapped reads	2,394,448 / 89.47%
Unmapped reads	281,808 / 10.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,311 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	80,800 / 3.02%
Duplication rate	2.72%
Clipped reads	1,219,662 / 45.57%

2.2. ACGT Content

Number/percentage of A's	44,054,882 / 28.01%
Number/percentage of C's	30,133,513 / 19.16%
Number/percentage of T's	48,019,836 / 30.53%
Number/percentage of G's	34,868,286 / 22.17%
Number/percentage of N's	201,515 / 0.13%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.3574

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

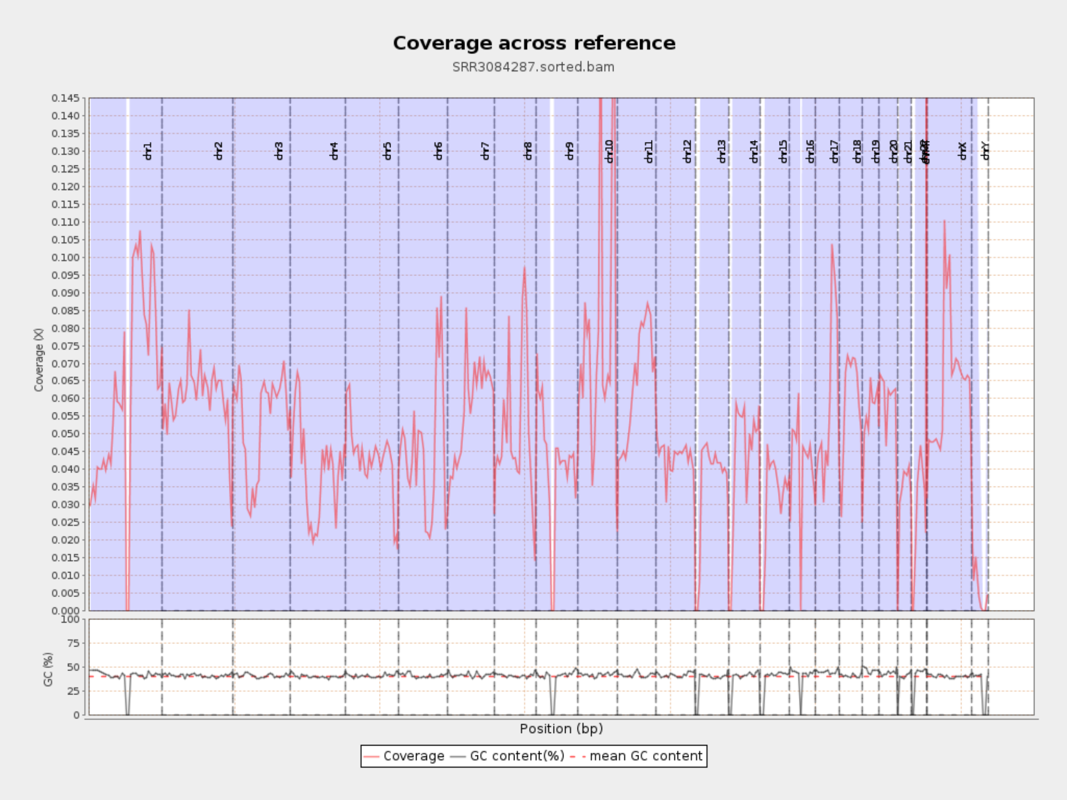
General error rate	1.06%
Mismatches	1,648,932
Insertions	12,001
Mapped reads with at least one insertion	0.5%
Deletions	33,768
Mapped reads with at least one deletion	1.4%
Homopolymer indels	45.94%

2.6. Chromosome stats

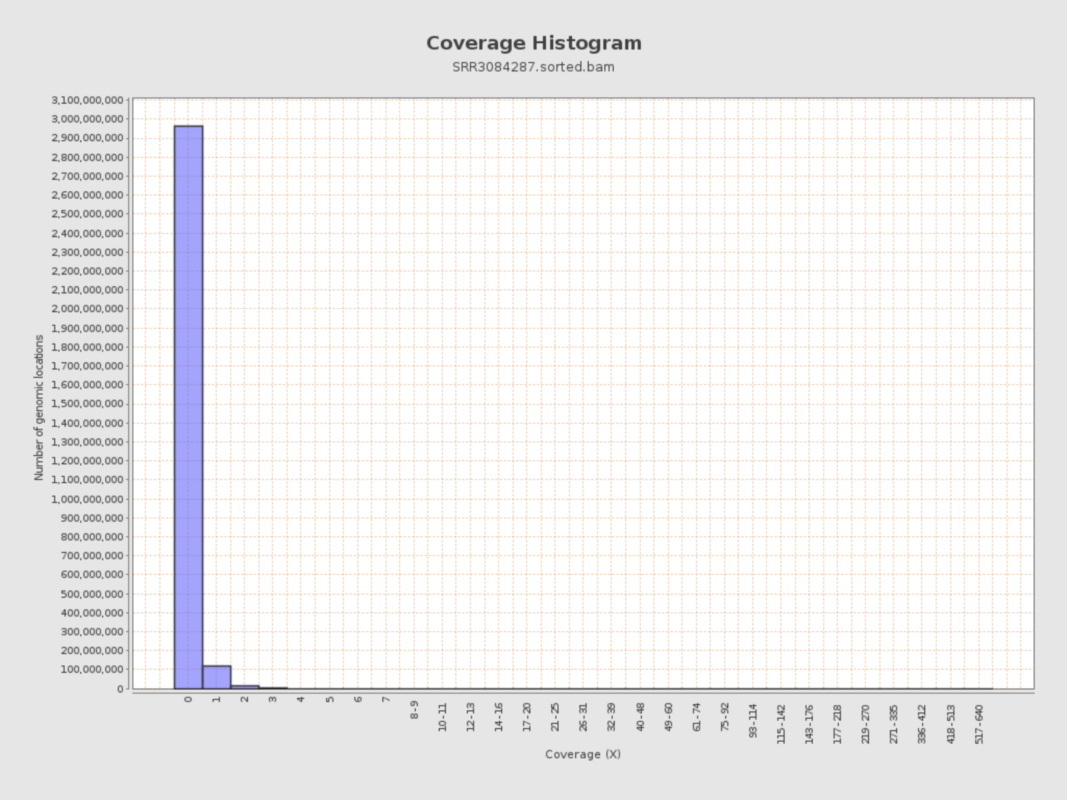
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15427885	0.0619	0.6197
chr2	243199373	14766809	0.0607	0.4277
chr3	198022430	10702173	0.054	0.2657
chr4	191154276	7602047	0.0398	0.2358
chr5	180915260	7796763	0.0431	0.2342
chr6	171115067	7693515	0.045	0.2745
chr7	159138663	9183754	0.0577	0.4804

chr8	146364022	7495355	0.0512	0.3426
chr9	141213431	5766286	0.0408	0.2973
chr10	135534747	11122519	0.0821	0.4819
chr11	135006516	8621894	0.0639	0.3467
chr12	133851895	5794249	0.0433	0.2365
chr13	115169878	4091424	0.0355	0.2123
chr14	107349540	4581210	0.0427	0.2409
chr15	102531392	3153733	0.0308	0.2075
chr16	90354753	3746141	0.0415	0.2552
chr17	81195210	4766152	0.0587	0.2937
chr18	78077248	4645513	0.0595	0.4972
chr19	59128983	3303553	0.0559	0.4588
chr20	63025520	3786932	0.0601	0.2789
chr21	48129895	1575241	0.0327	0.2138
chr22	51304566	1386514	0.027	0.1848
chrMT	16571	5773	0.3484	0.6422
chrX	155270560	9968012	0.0642	0.3154
chrY	59373566	348802	0.0059	0.1164

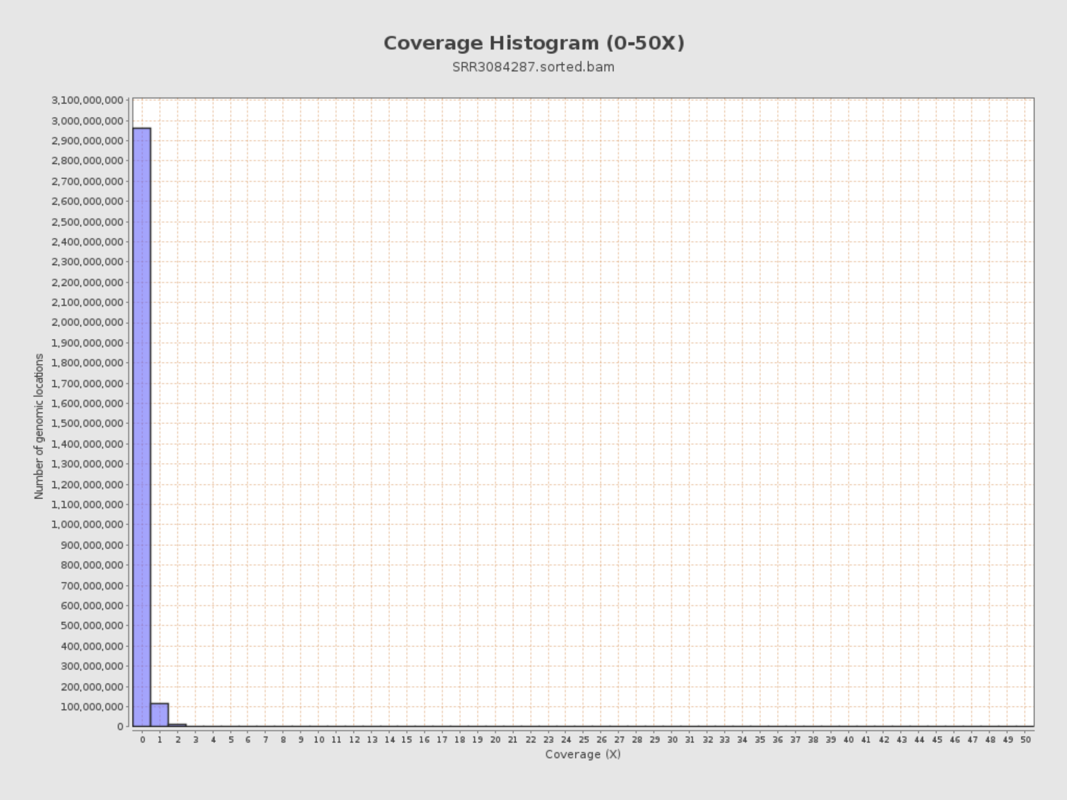
3. Results : Coverage across reference



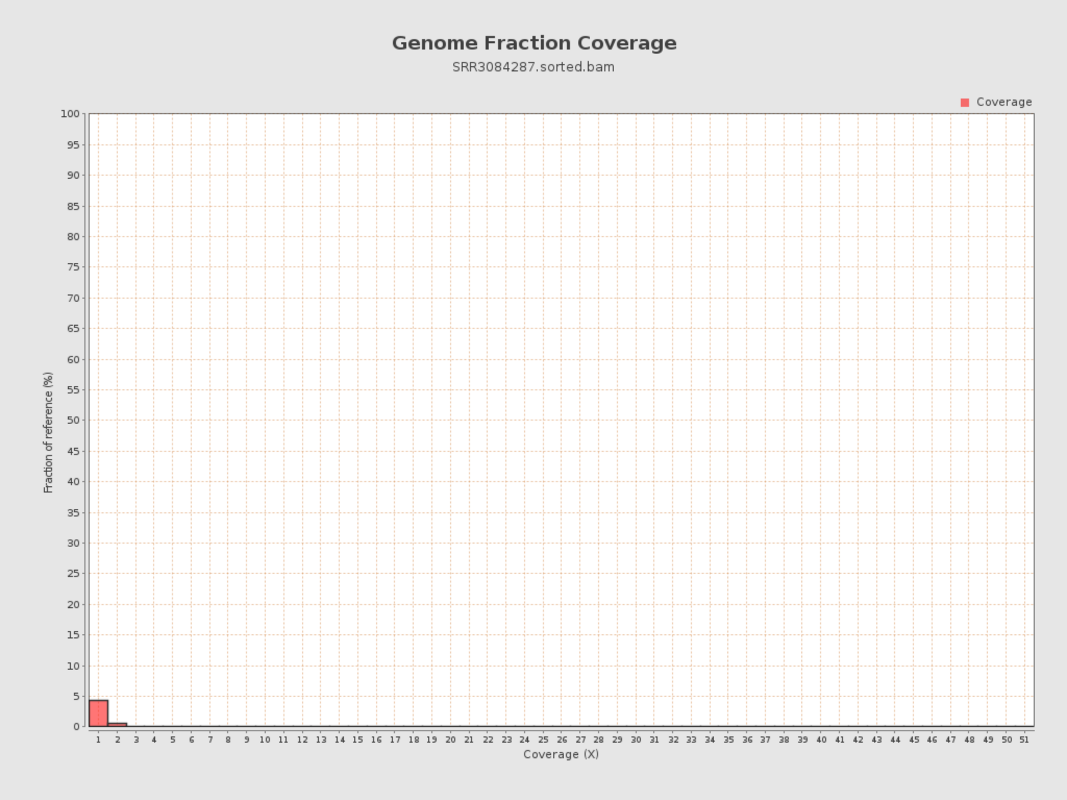
4. Results : Coverage Histogram



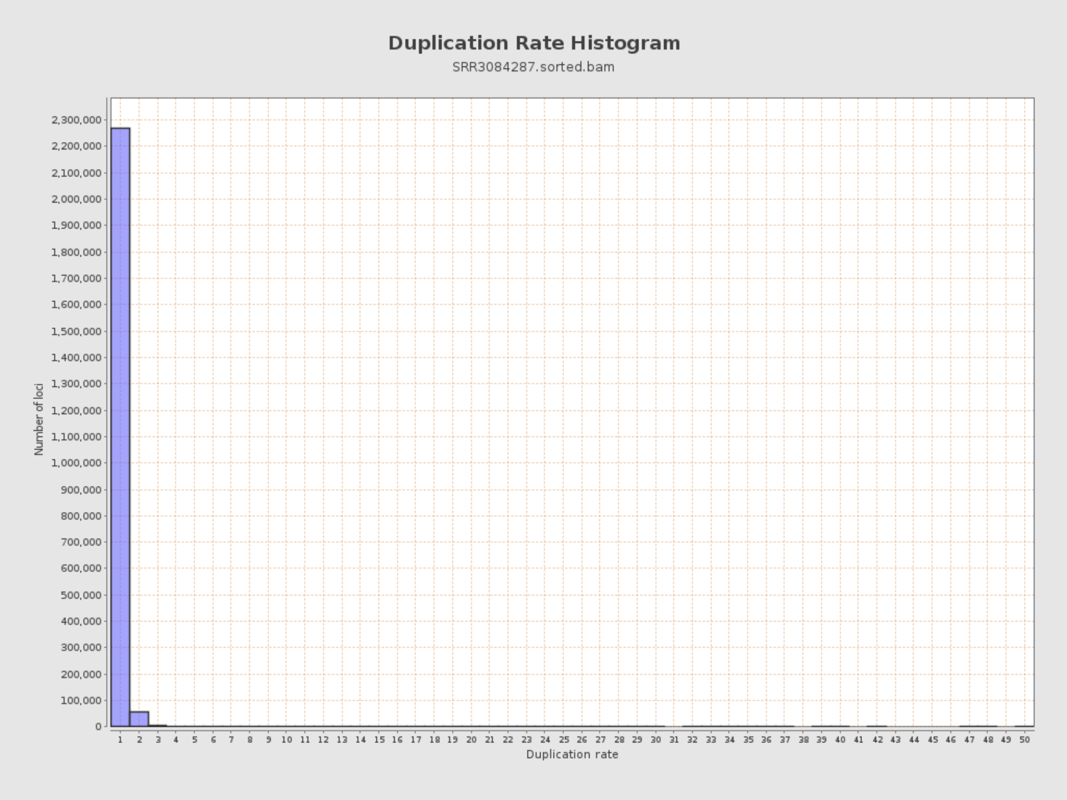
5. Results : Coverage Histogram (0-50X)



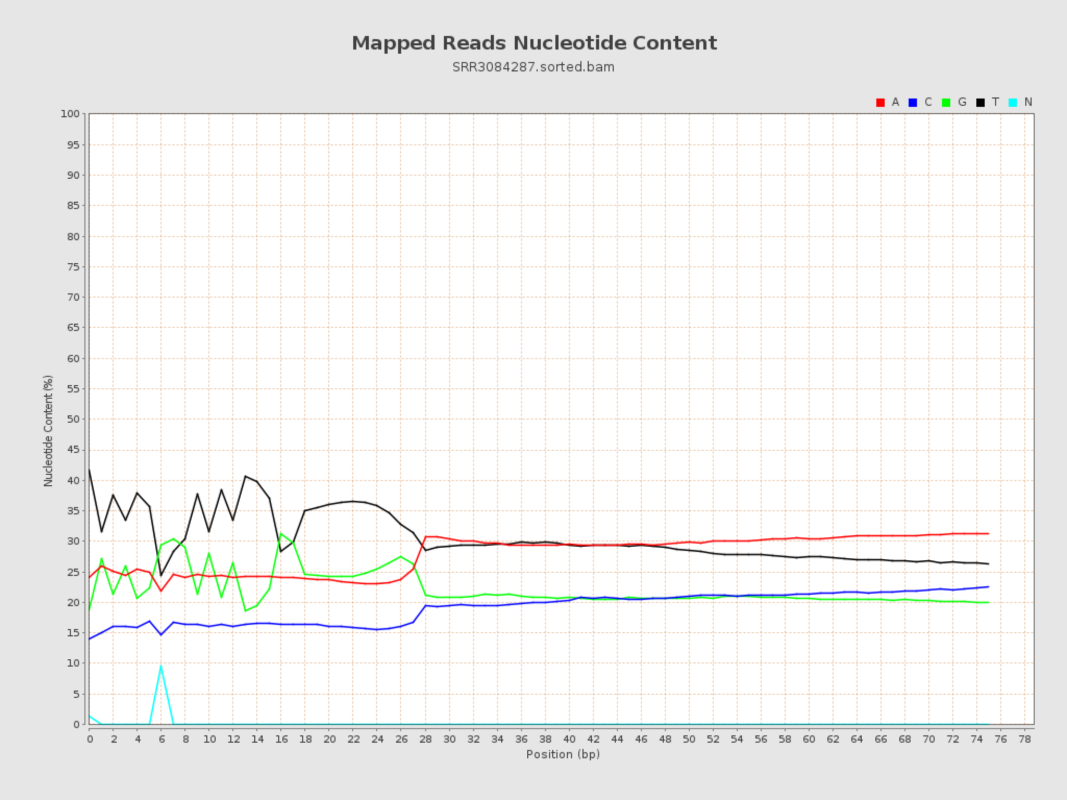
6. Results : Genome Fraction Coverage



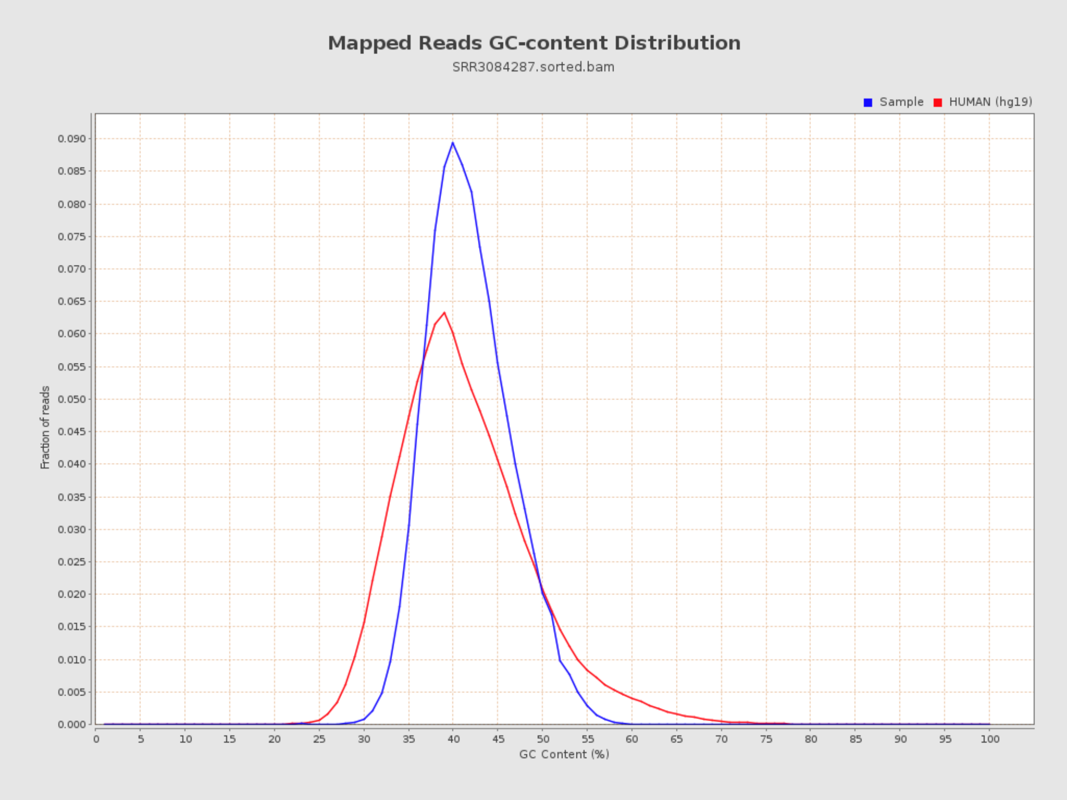
7. Results : Duplication Rate Histogram



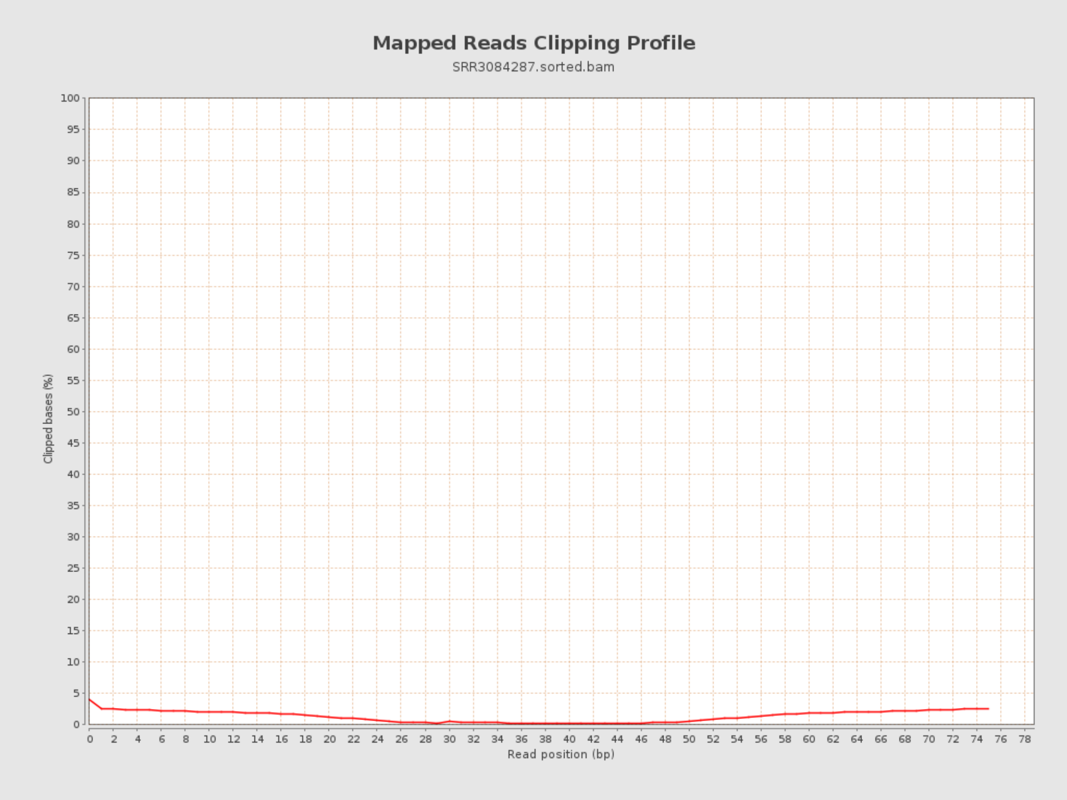
8. Results : Mapped Reads Nucleotide Content



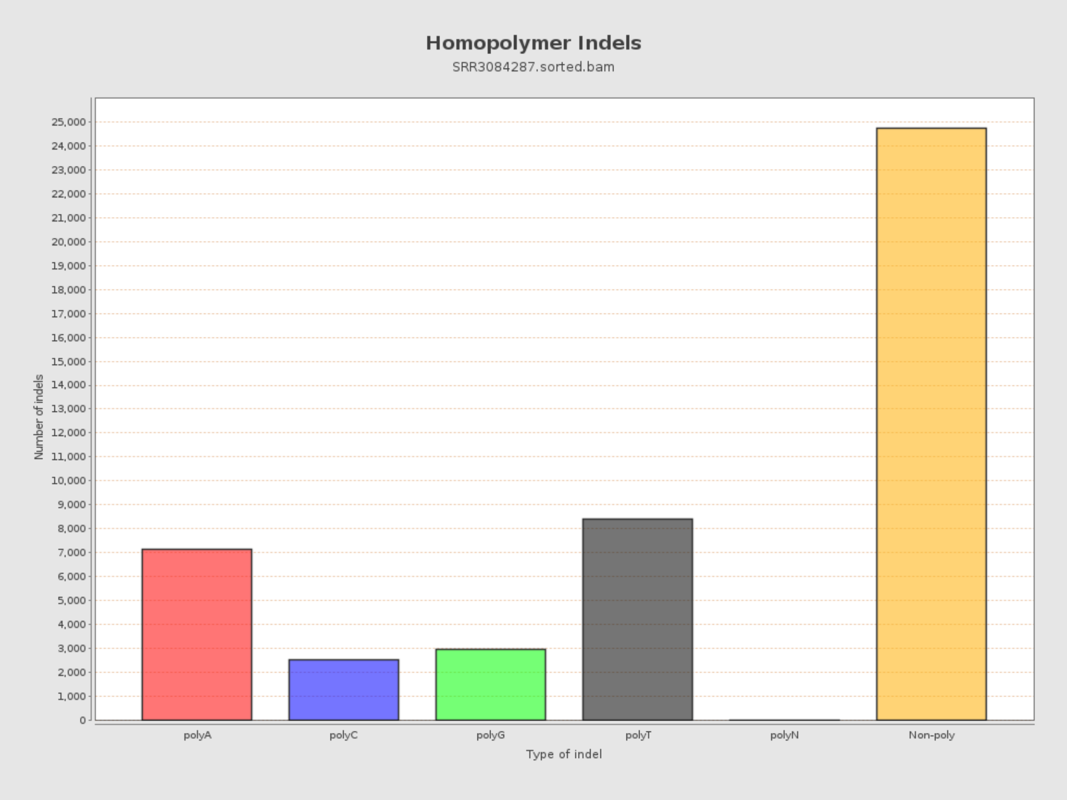
9. Results : Mapped Reads GC-content Distribution



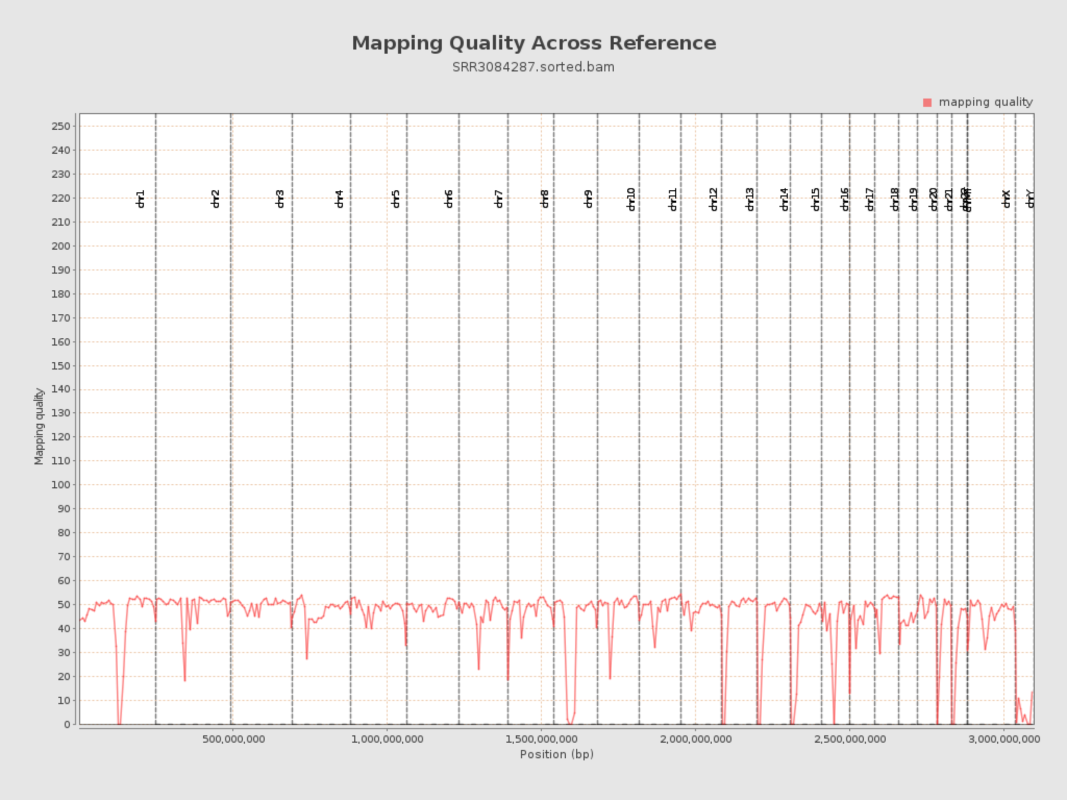
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram