Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 07:49:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083787.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_SRR3083787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 07:49:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,520,377
Mapped reads	1,923,249 / 76.31%
Unmapped reads	597,128 / 23.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,903 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	67,705 / 2.69%
Duplication rate	2.9%
Clipped reads	1,052,288 / 41.75%

2.2. ACGT Content

Number/percentage of A's	34,397,520 / 27.96%
Number/percentage of C's	23,578,664 / 19.17%
Number/percentage of T's	37,275,237 / 30.3%
Number/percentage of G's	27,751,231 / 22.56%
Number/percentage of N's	1,415 / 0%
GC Percentage	41.73%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.2857

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

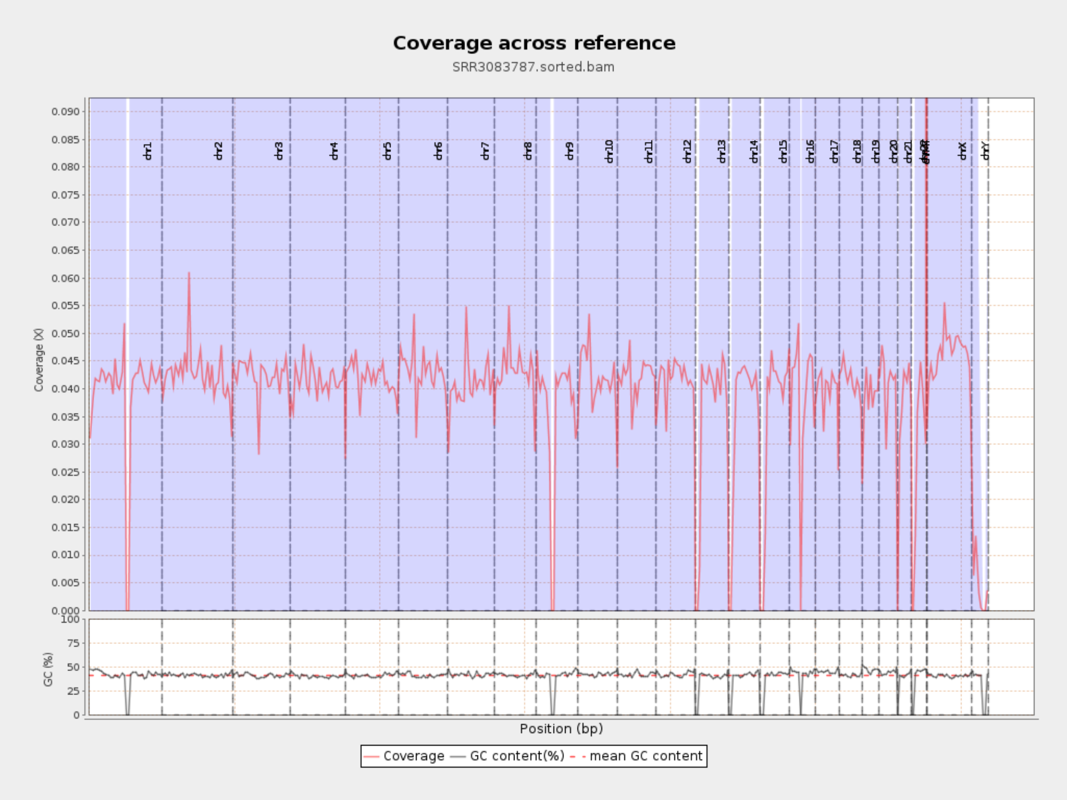
General error rate	0.84%
Mismatches	1,022,512
Insertions	9,298
Mapped reads with at least one insertion	0.48%
Deletions	25,960
Mapped reads with at least one deletion	1.34%
Homopolymer indels	45.83%

2.6. Chromosome stats

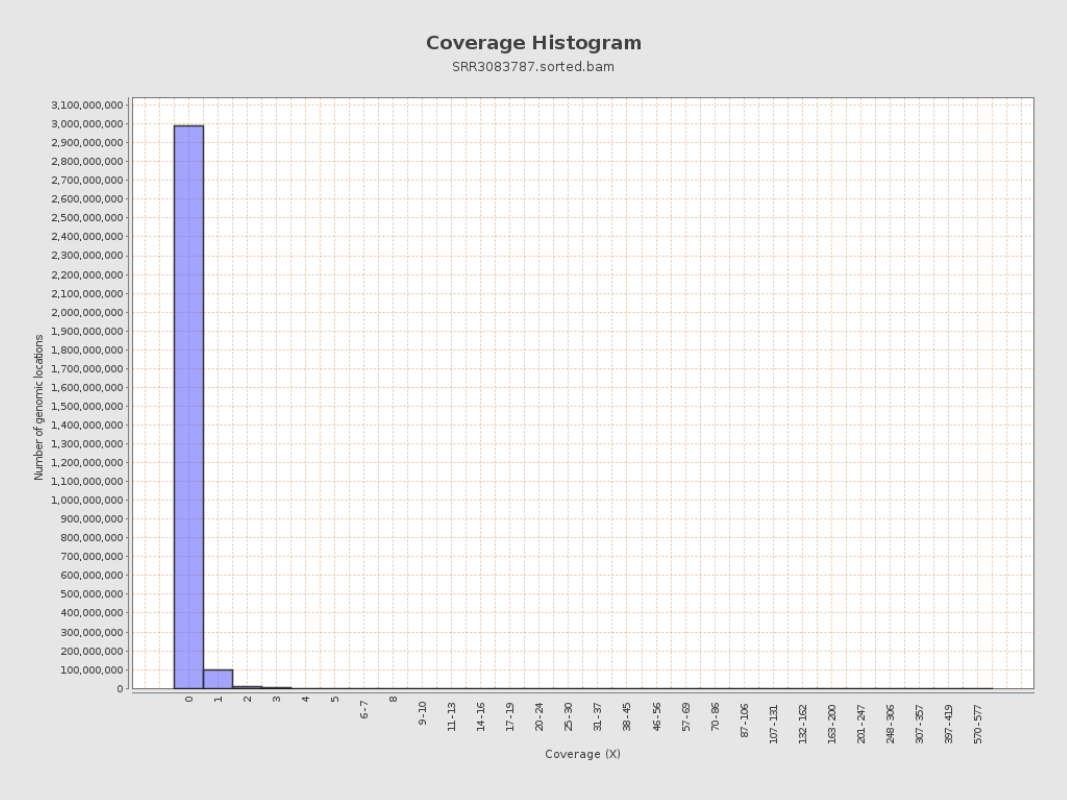
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9778969	0.0392	0.3644
chr2	243199373	10392463	0.0427	0.3852
chr3	198022430	8389177	0.0424	0.228
chr4	191154276	7946134	0.0416	0.2327
chr5	180915260	7604423	0.042	0.2283
chr6	171115067	7393627	0.0432	0.2638
chr7	159138663	6551149	0.0412	0.331

chr8	146364022	6308543	0.0431	0.3043
chr9	141213431	5000929	0.0354	0.28
chr10	135534747	5747437	0.0424	0.2778
chr11	135006516	5662400	0.0419	0.2685
chr12	133851895	5570002	0.0416	0.2288
chr13	115169878	4005662	0.0348	0.209
chr14	107349540	3749047	0.0349	0.2189
chr15	102531392	3504900	0.0342	0.2135
chr16	90354753	3455570	0.0382	0.2351
chr17	81195210	3204343	0.0395	0.2371
chr18	78077248	3260719	0.0418	0.5284
chr19	59128983	2292408	0.0388	0.3153
chr20	63025520	2561395	0.0406	0.2298
chr21	48129895	1700968	0.0353	0.2189
chr22	51304566	1362086	0.0265	0.1798
chrMT	16571	143443	8.6563	5.6619
chrX	155270560	7165840	0.0462	0.2592
chrY	59373566	294269	0.005	0.0996

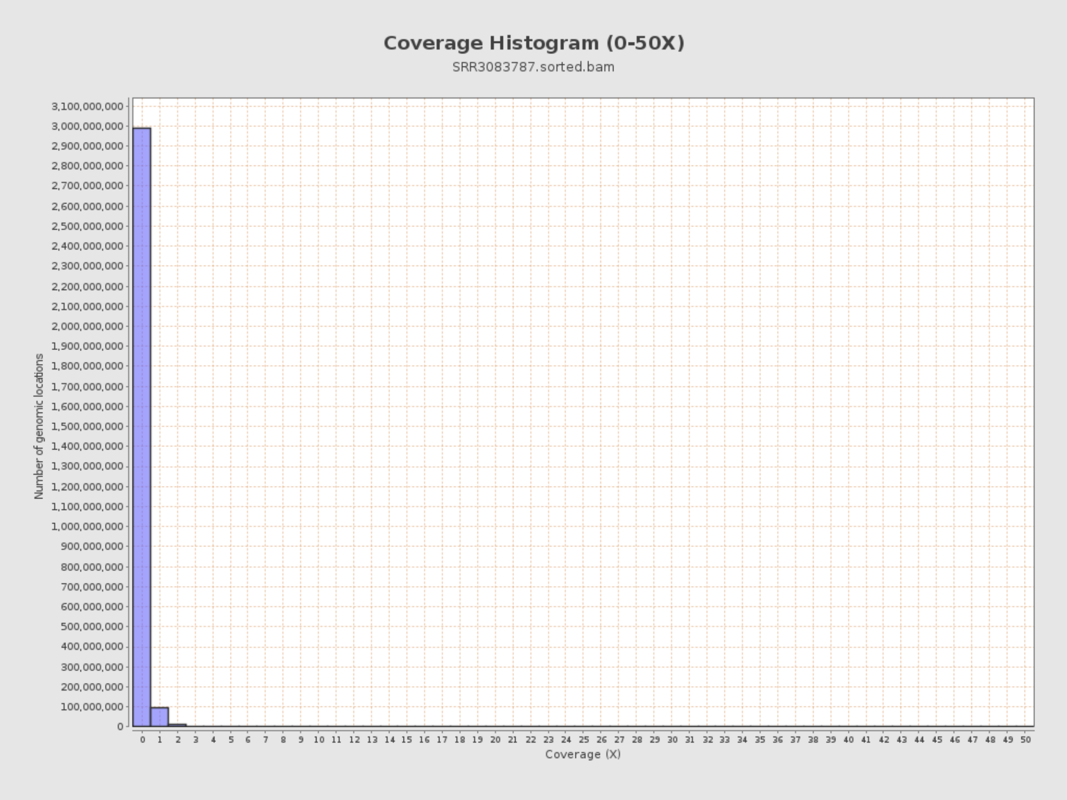
3. Results : Coverage across reference



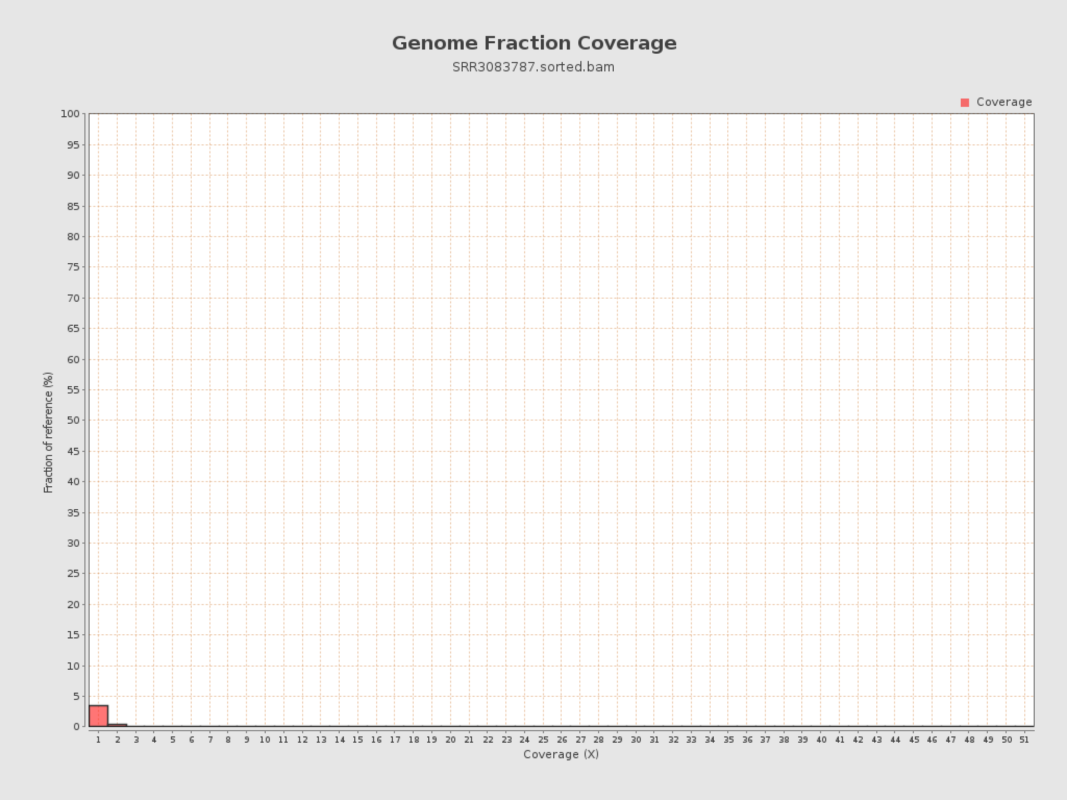
4. Results : Coverage Histogram



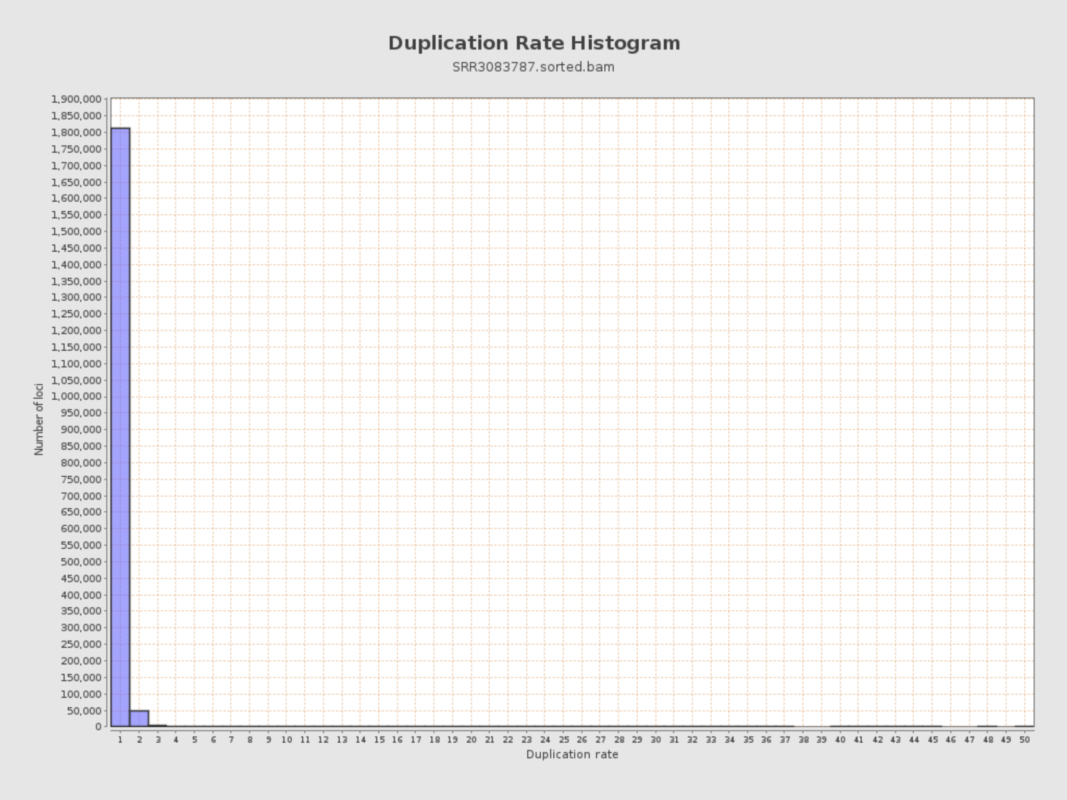
5. Results : Coverage Histogram (0-50X)



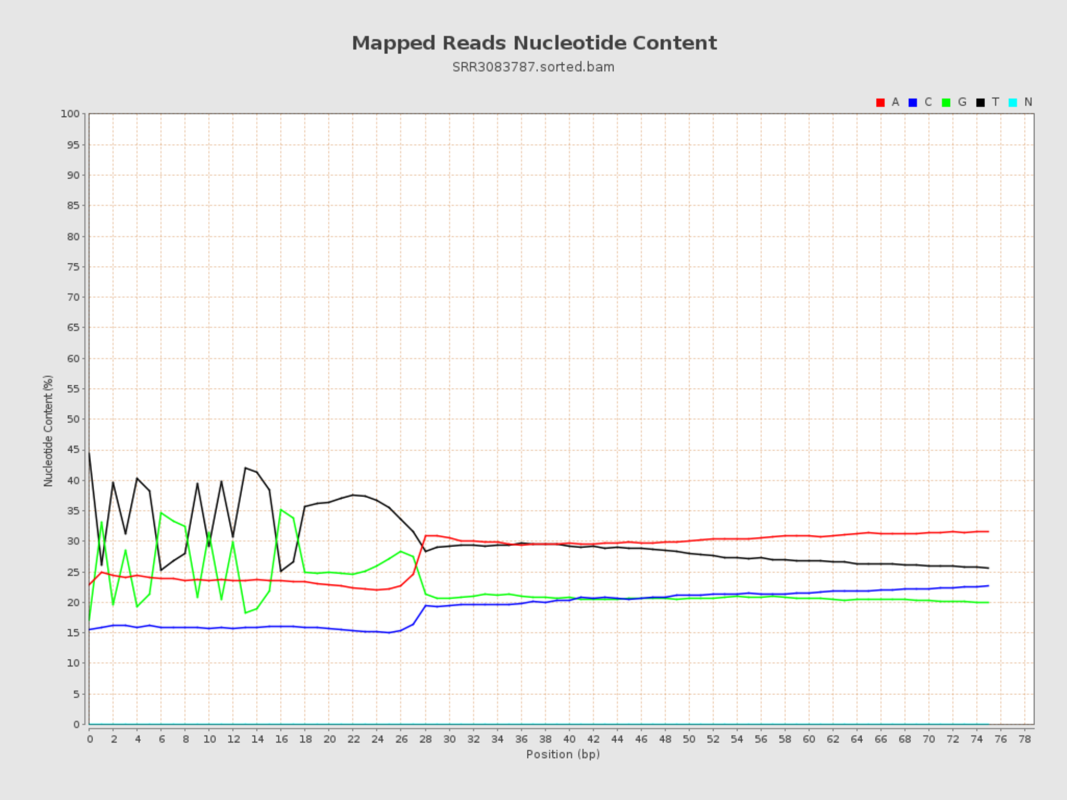
6. Results : Genome Fraction Coverage



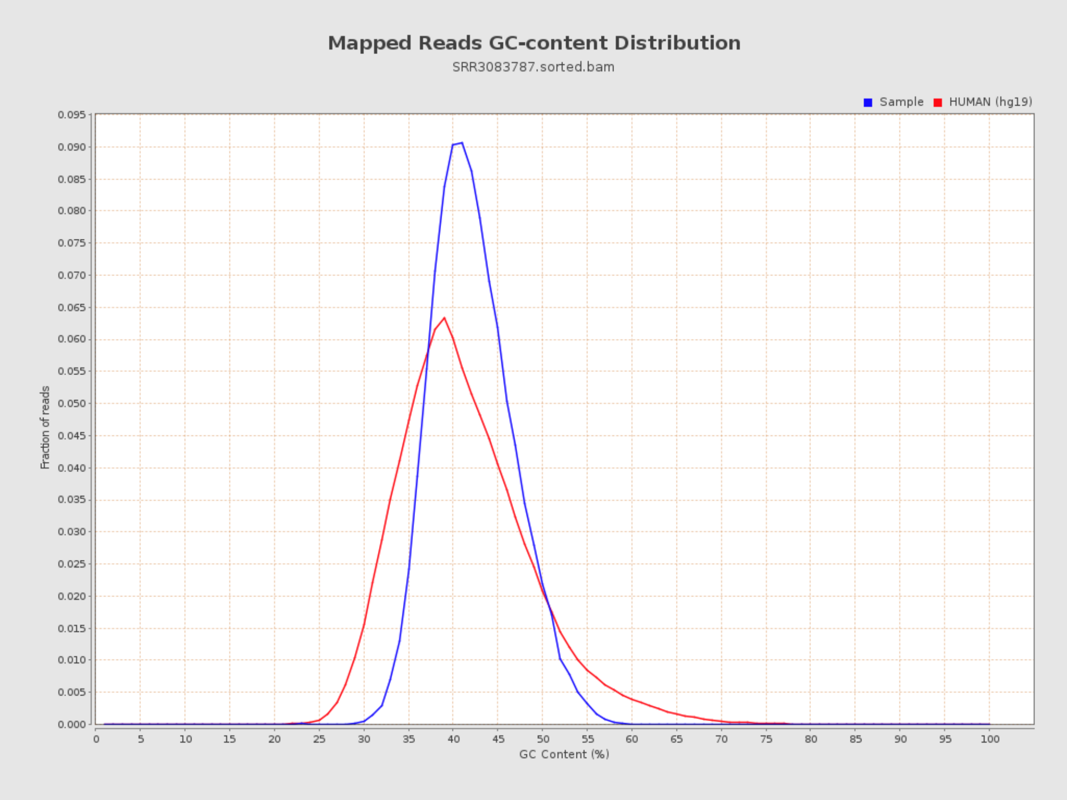
7. Results : Duplication Rate Histogram



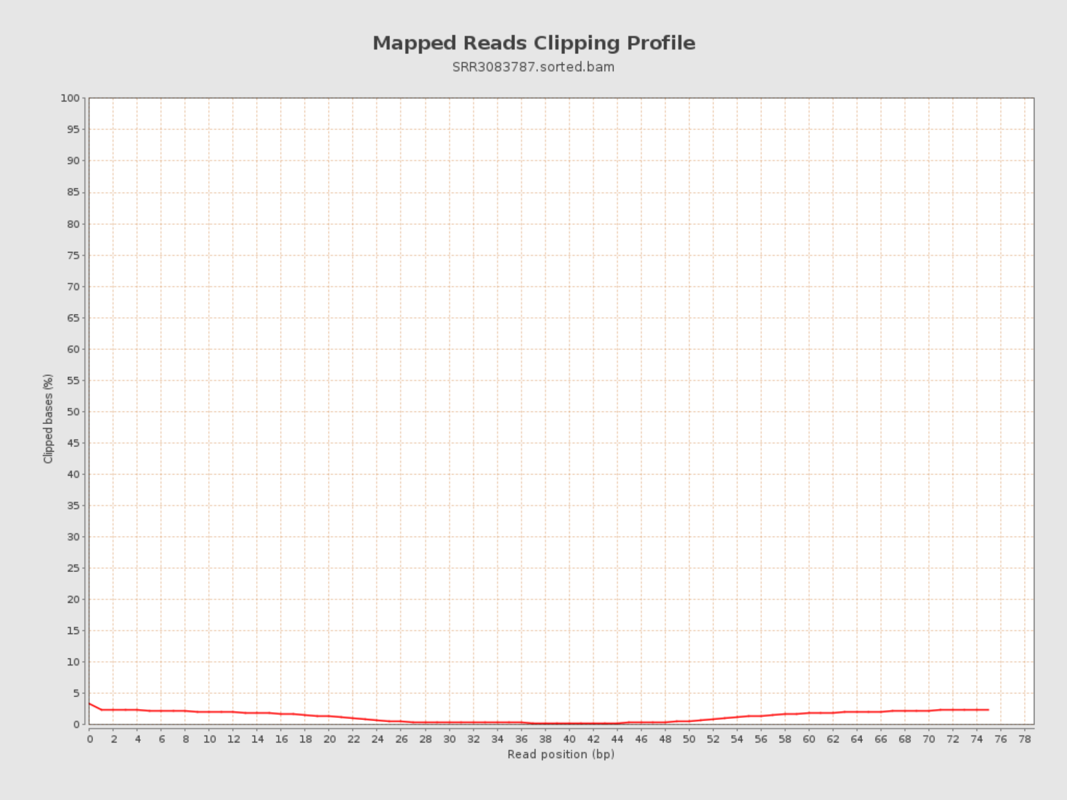
8. Results : Mapped Reads Nucleotide Content



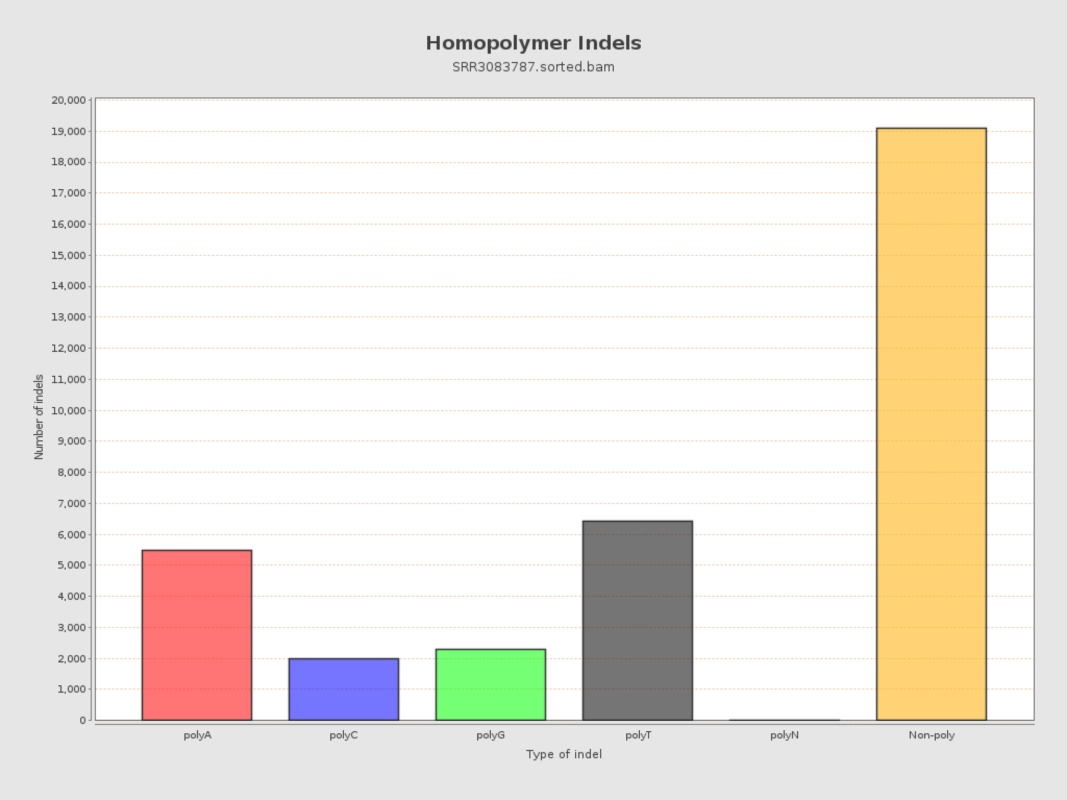
9. Results : Mapped Reads GC-content Distribution



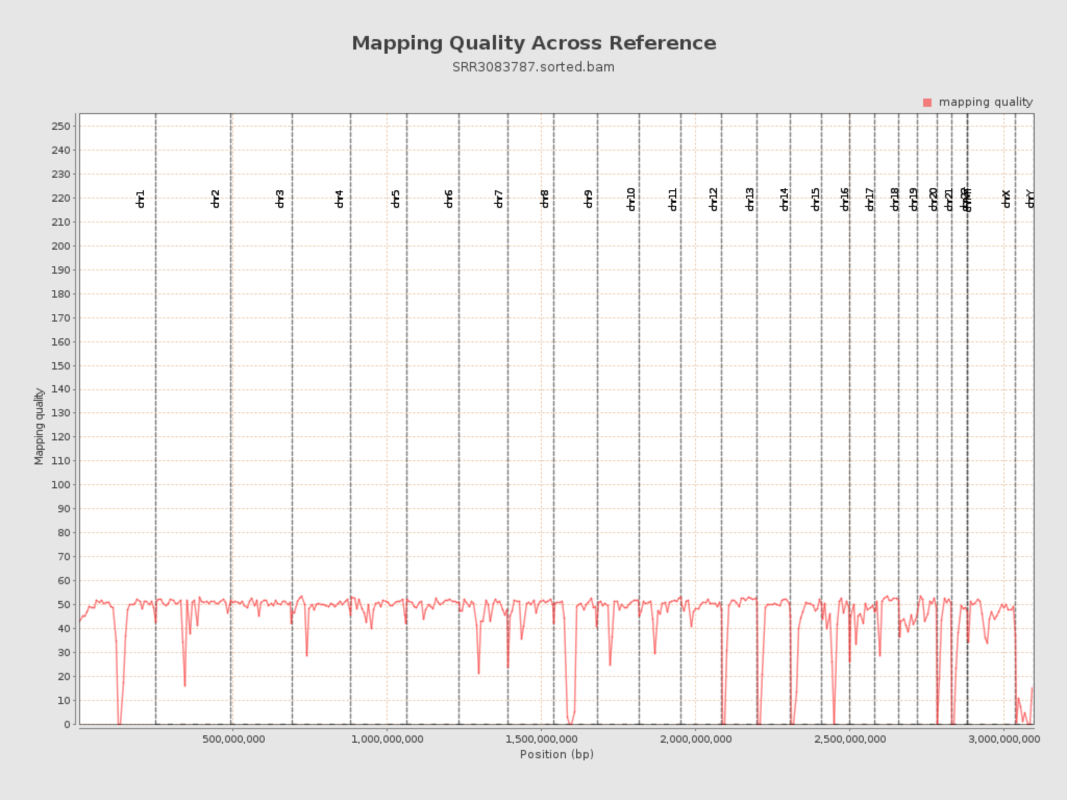
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram