Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:23:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818782.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_SRR1818782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:23:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,449,181
Mapped reads	1,409,232 / 97.24%
Unmapped reads	39,949 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,840 / 0.75%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	504,399 / 34.81%
Duplication rate	31.77%
Clipped reads	1,404,222 / 96.9%

2.2. ACGT Content

Number/percentage of A's	26,663,826 / 27.86%
Number/percentage of C's	20,749,164 / 21.68%
Number/percentage of T's	28,515,079 / 29.8%
Number/percentage of G's	19,757,655 / 20.65%
Number/percentage of N's	6,029 / 0.01%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.4055

2.4. Mapping Quality

Mean Mapping Quality	47.73

2.5. Mismatches and indels

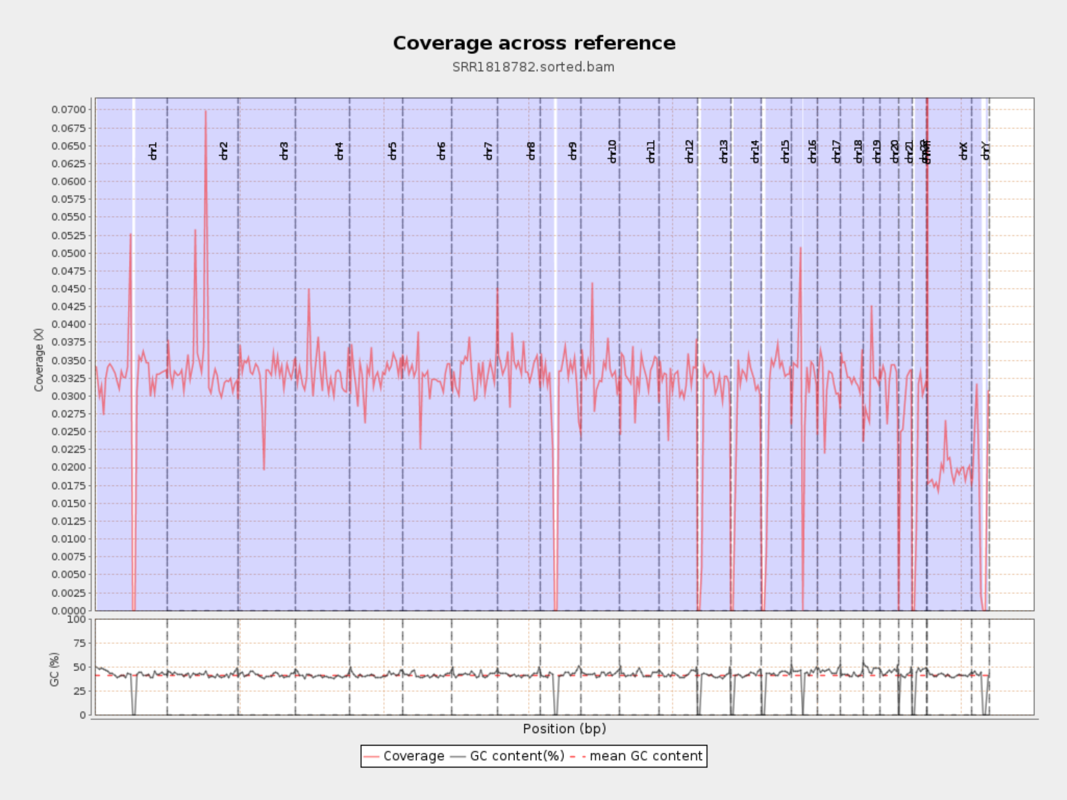
General error rate	0.55%
Mismatches	501,015
Insertions	12,190
Mapped reads with at least one insertion	0.85%
Deletions	24,675
Mapped reads with at least one deletion	1.73%
Homopolymer indels	42.1%

2.6. Chromosome stats

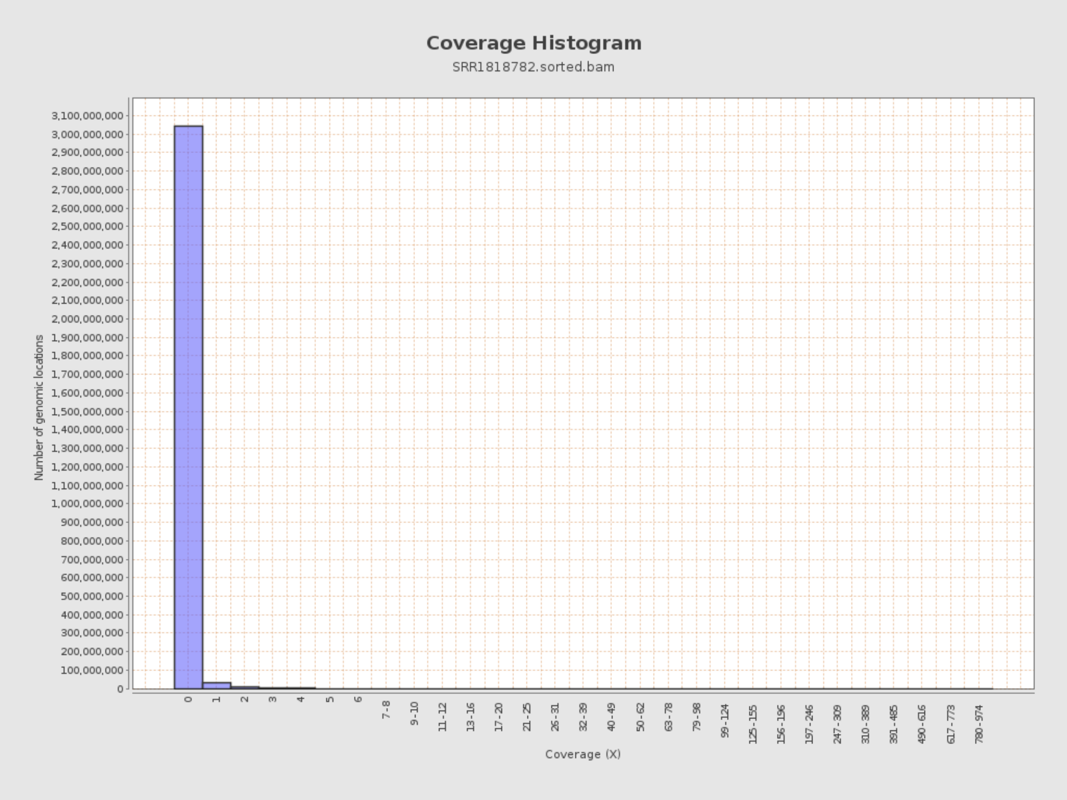
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7837087	0.0314	0.558
chr2	243199373	8437720	0.0347	0.7172
chr3	198022430	6554640	0.0331	0.2854
chr4	191154276	6366617	0.0333	0.3329
chr5	180915260	6017624	0.0333	0.2955
chr6	171115067	5611397	0.0328	0.3146
chr7	159138663	5292912	0.0333	0.3553

chr8	146364022	5012867	0.0342	0.3286
chr9	141213431	4106422	0.0291	0.3181
chr10	135534747	4586177	0.0338	0.405
chr11	135006516	4480845	0.0332	0.3283
chr12	133851895	4309482	0.0322	0.3054
chr13	115169878	3101498	0.0269	0.2584
chr14	107349540	2915452	0.0272	0.291
chr15	102531392	2806016	0.0274	0.2606
chr16	90354753	2805661	0.0311	0.478
chr17	81195210	2554166	0.0315	0.2943
chr18	78077248	2571821	0.0329	0.4067
chr19	59128983	1849727	0.0313	0.4741
chr20	63025520	2031300	0.0322	0.2993
chr21	48129895	1294762	0.0269	0.2724
chr22	51304566	1135427	0.0221	0.2608
chrMT	16571	76632	4.6245	4.5804
chrX	155270560	3021811	0.0195	0.2538
chrY	59373566	953471	0.0161	0.7751

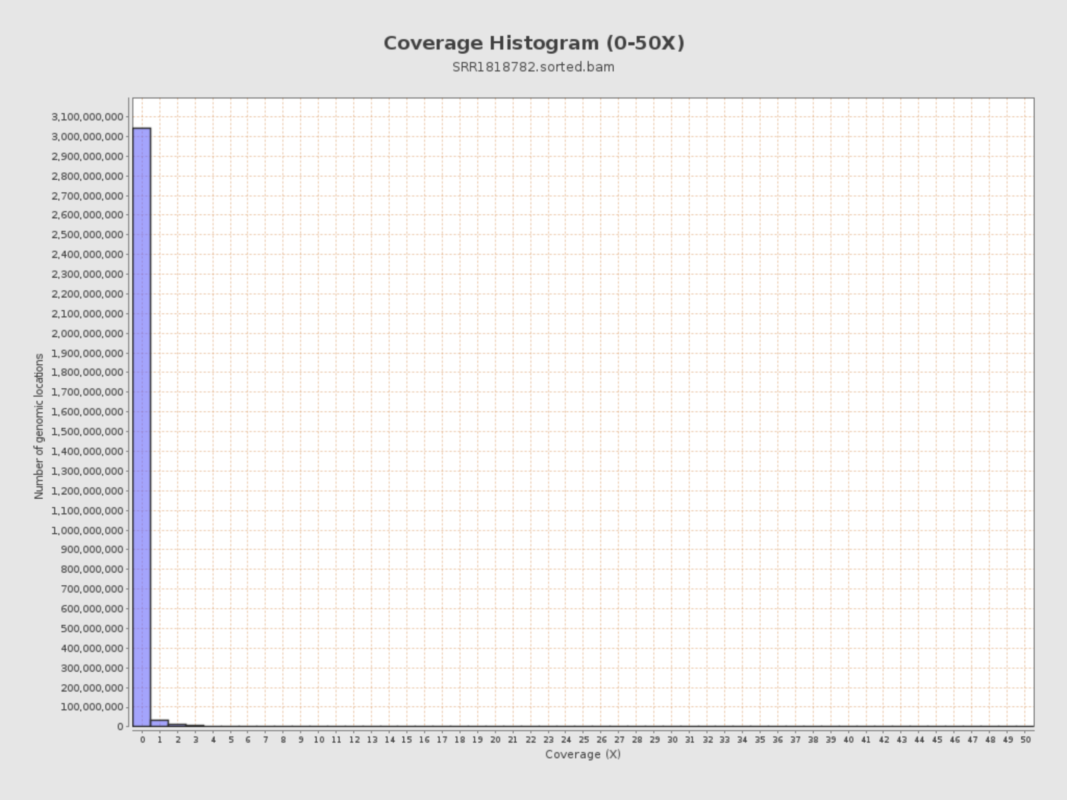
3. Results : Coverage across reference



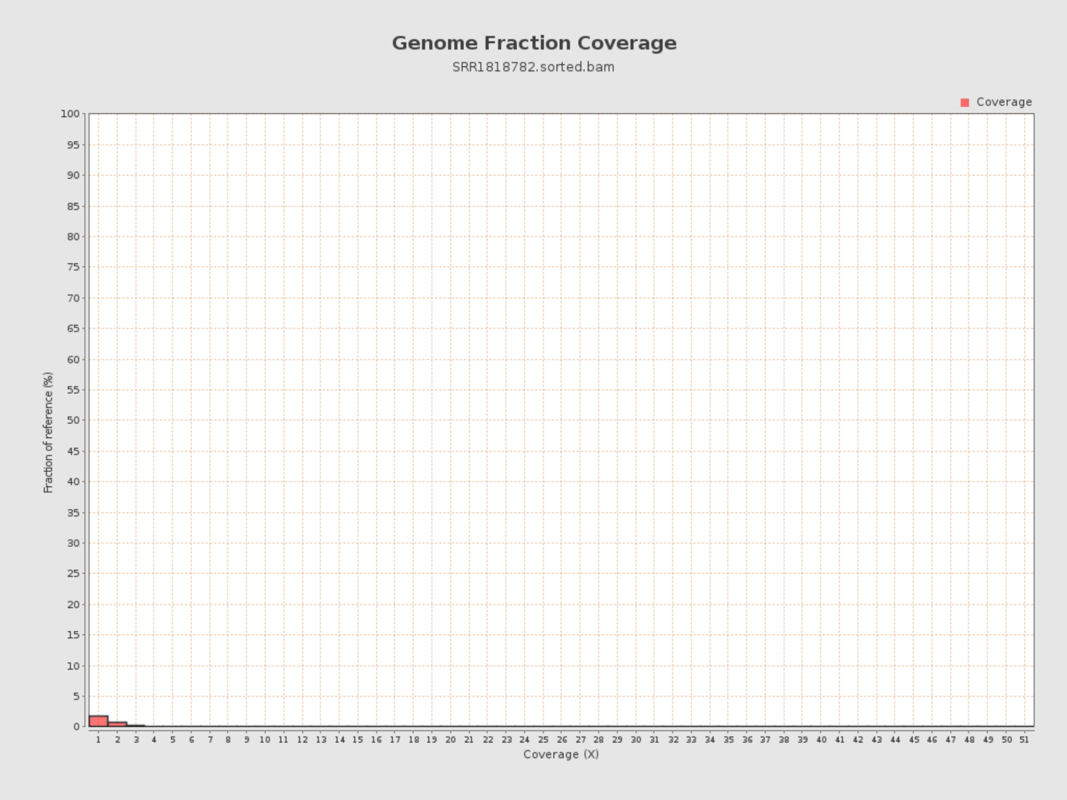
4. Results : Coverage Histogram



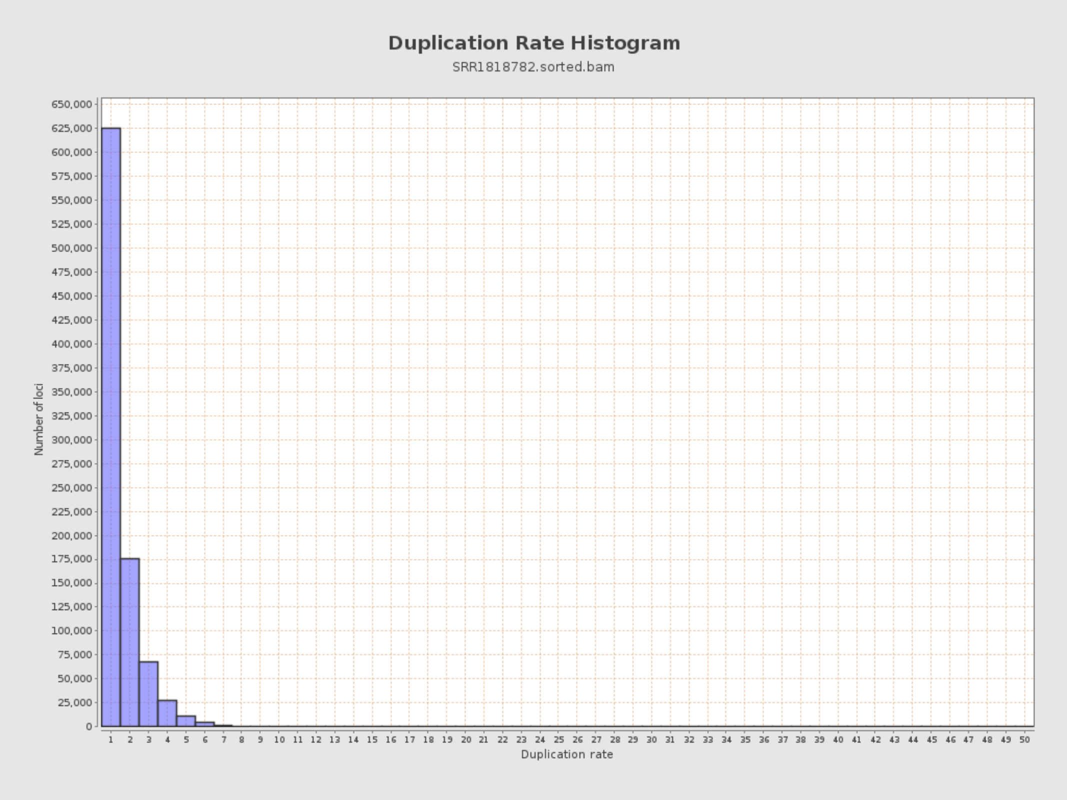
5. Results : Coverage Histogram (0-50X)



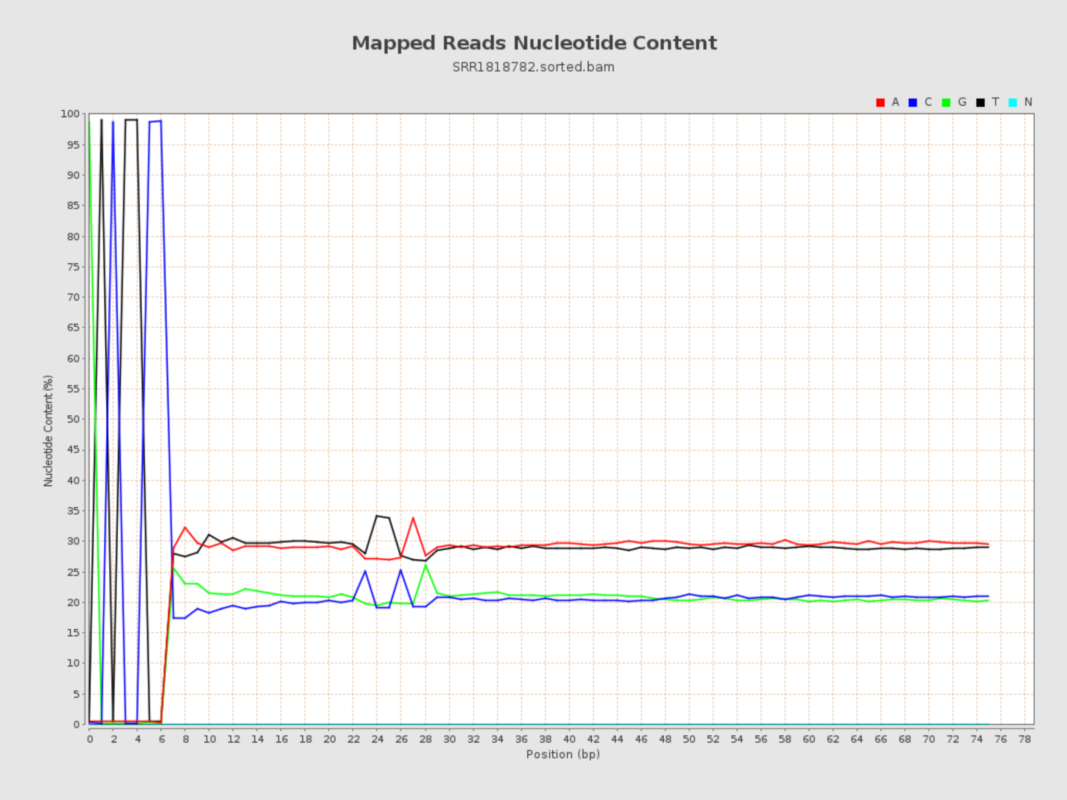
6. Results : Genome Fraction Coverage



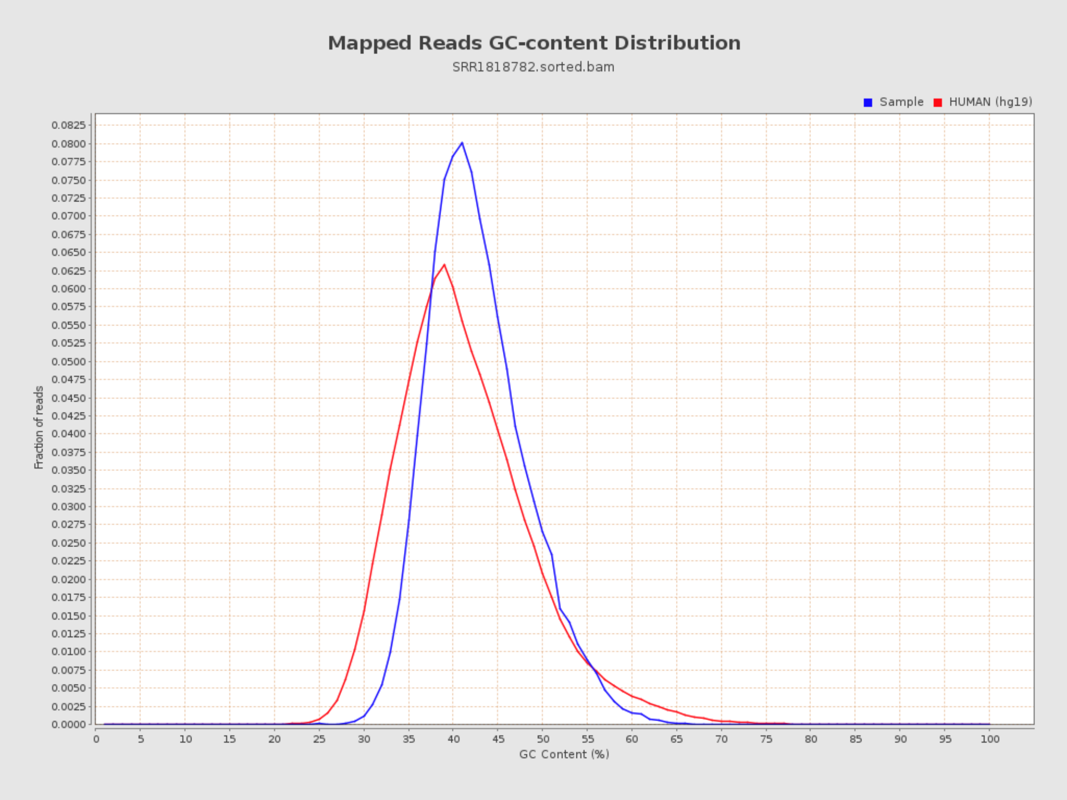
7. Results : Duplication Rate Histogram



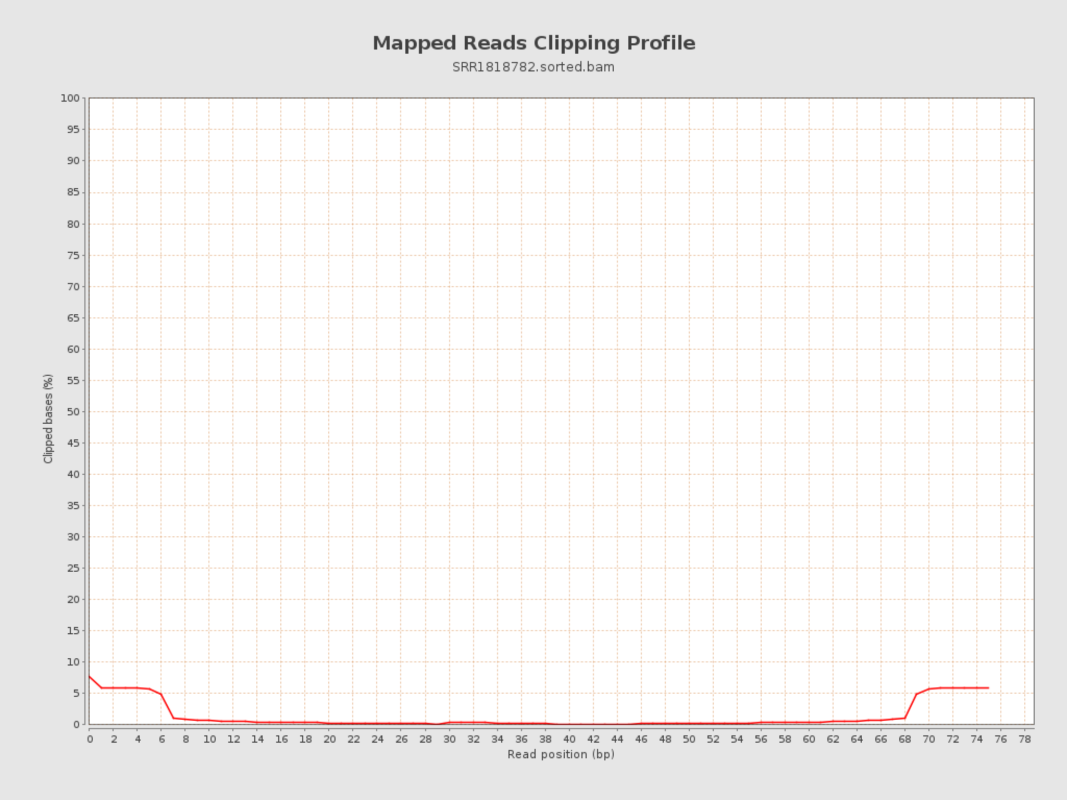
8. Results : Mapped Reads Nucleotide Content



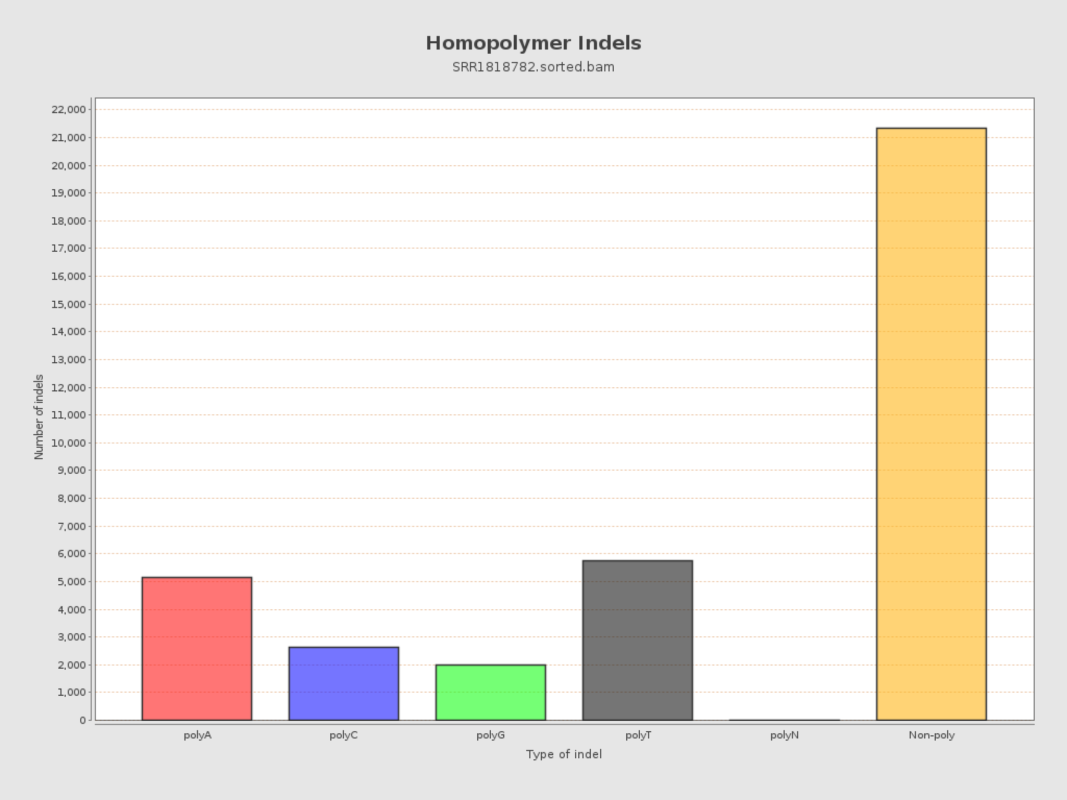
9. Results : Mapped Reads GC-content Distribution



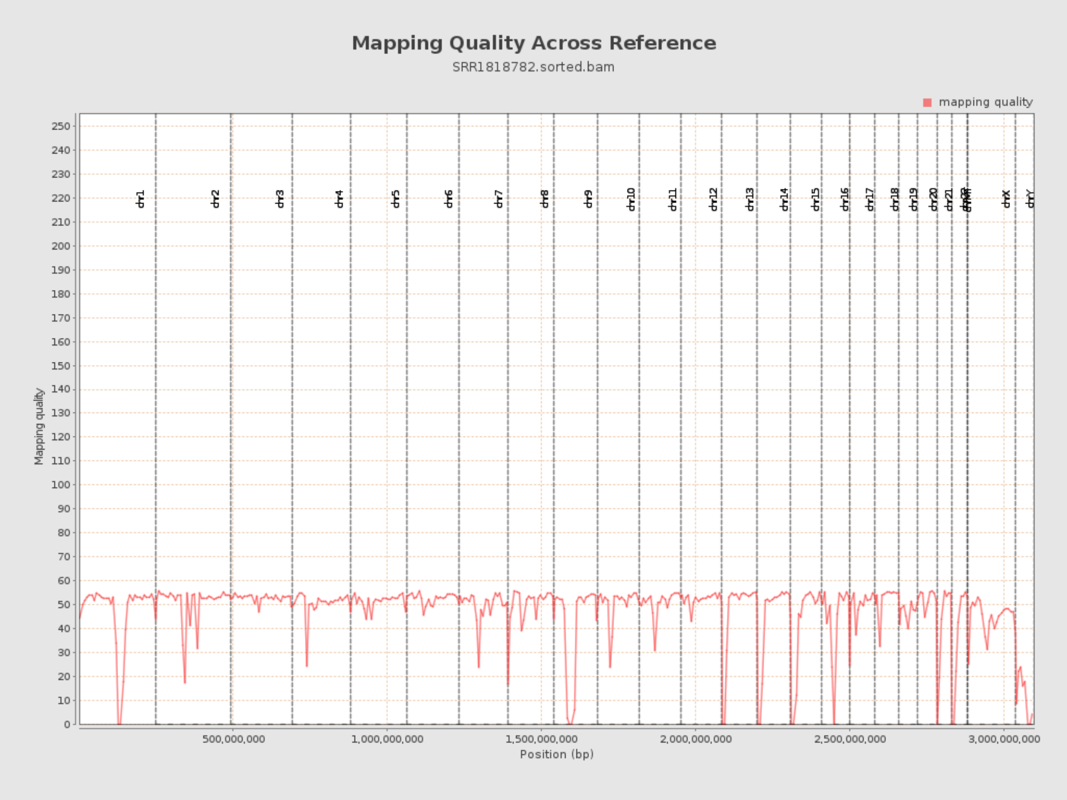
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram