Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:19:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819015.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_SRR1819015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:19:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,628,667
Mapped reads	1,442,524 / 54.88%
Unmapped reads	1,186,143 / 45.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,590 / 0.75%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	453,867 / 17.27%
Duplication rate	25.52%
Clipped reads	1,452,511 / 55.26%

2.2. ACGT Content

Number/percentage of A's	38,832,495 / 29.1%
Number/percentage of C's	29,021,584 / 21.75%
Number/percentage of T's	37,429,349 / 28.05%
Number/percentage of G's	28,136,631 / 21.09%
Number/percentage of N's	6,804 / 0.01%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0431

Standard Deviation	0.535

2.4. Mapping Quality

Mean Mapping Quality	49.12

2.5. Mismatches and indels

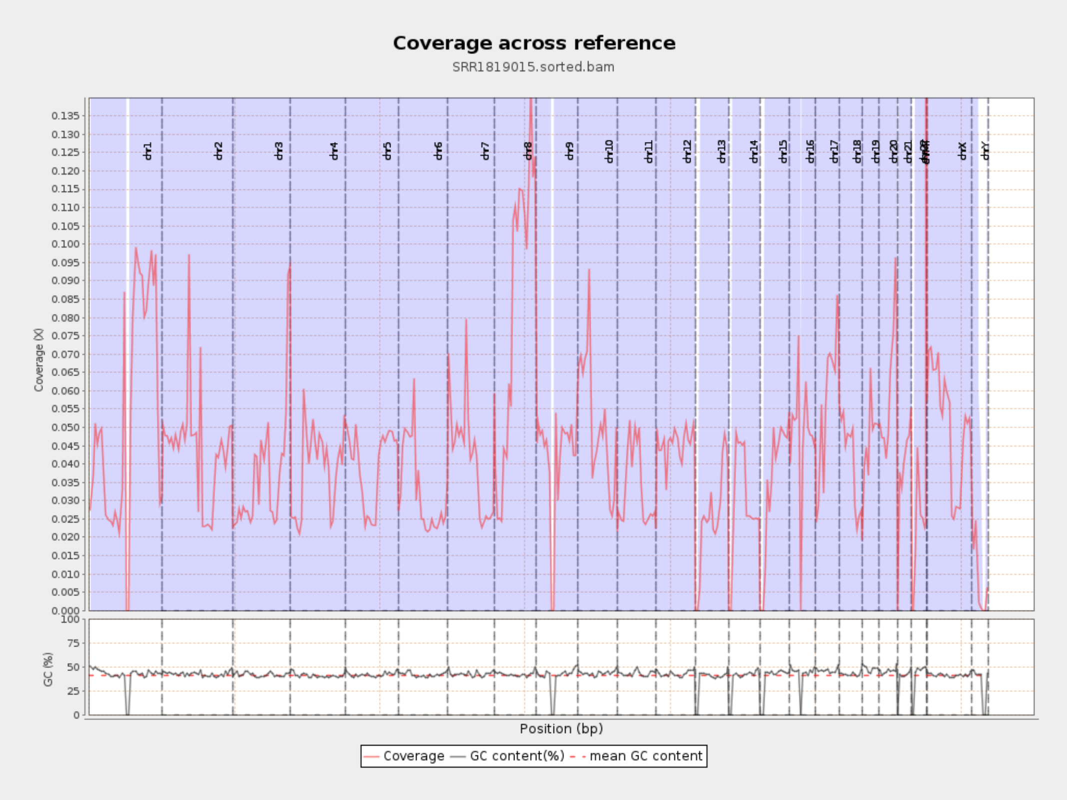
General error rate	0.67%
Mismatches	845,928
Insertions	21,341
Mapped reads with at least one insertion	1.43%
Deletions	42,406
Mapped reads with at least one deletion	2.88%
Homopolymer indels	42.06%

2.6. Chromosome stats

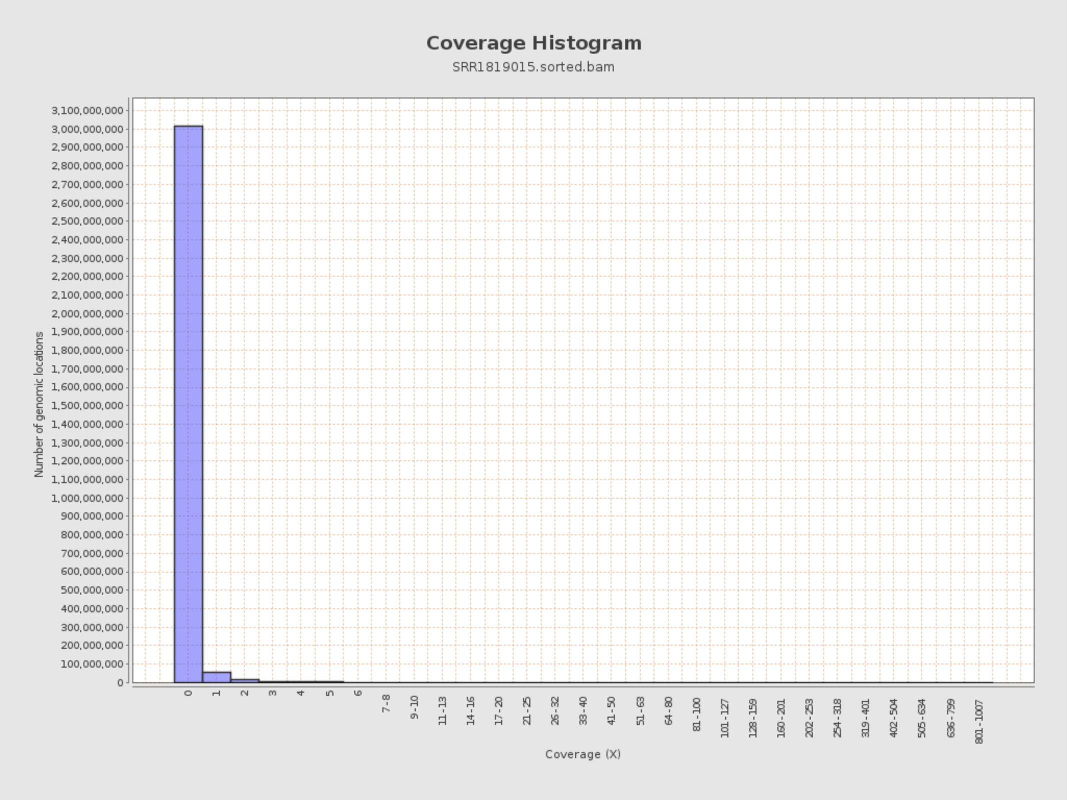
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13373629	0.0537	0.9139
chr2	243199373	10765248	0.0443	0.7871
chr3	198022430	7215538	0.0364	0.2904
chr4	191154276	7344929	0.0384	0.349
chr5	180915260	7169052	0.0396	0.3207
chr6	171115067	5582213	0.0326	0.3492
chr7	159138663	6669870	0.0419	0.6715

chr8	146364022	12104042	0.0827	0.4993
chr9	141213431	5772898	0.0409	0.5171
chr10	135534747	6966080	0.0514	0.6635
chr11	135006516	4553952	0.0337	0.3351
chr12	133851895	6114001	0.0457	0.3346
chr13	115169878	2935128	0.0255	0.2436
chr14	107349540	3143229	0.0293	0.2799
chr15	102531392	3563240	0.0348	0.2907
chr16	90354753	4321040	0.0478	0.623
chr17	81195210	4641051	0.0572	0.4316
chr18	78077248	3213886	0.0412	0.6128
chr19	59128983	2779751	0.047	0.8267
chr20	63025520	3820011	0.0606	0.413
chr21	48129895	1865280	0.0388	0.3454
chr22	51304566	1083402	0.0211	0.2542
chrMT	16571	38164	2.3031	2.5431
chrX	155270560	7967247	0.0513	0.4339
chrY	59373566	503513	0.0085	0.5563

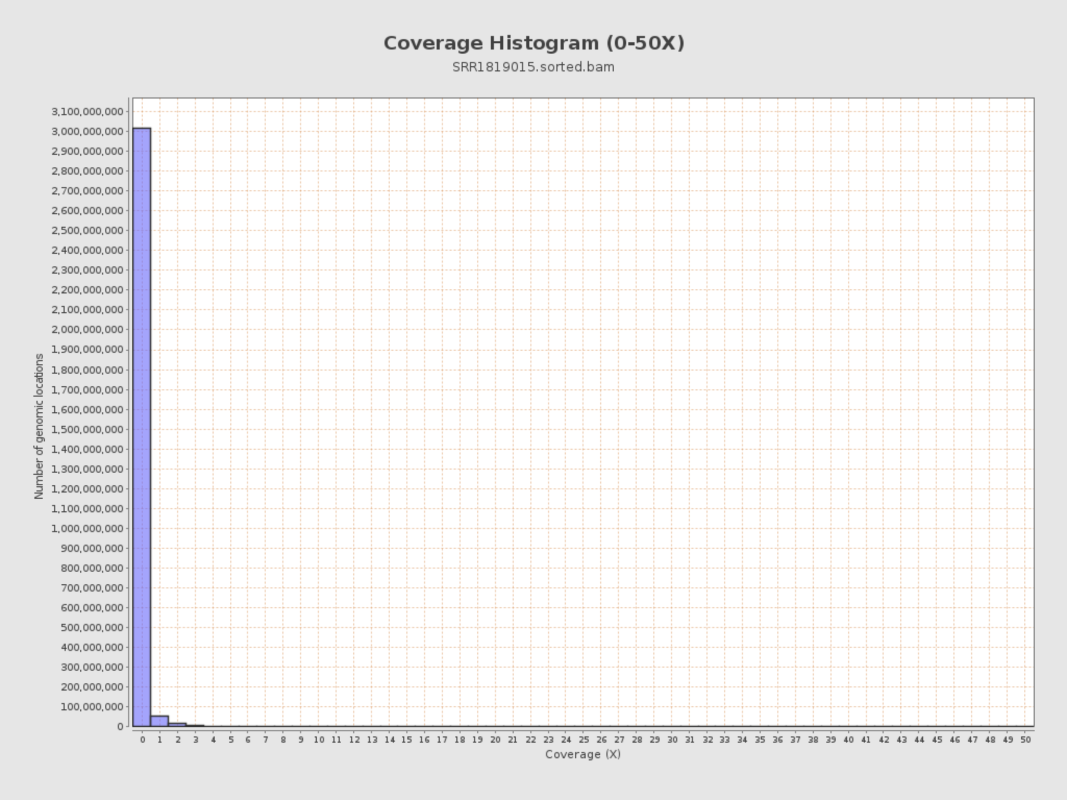
3. Results : Coverage across reference



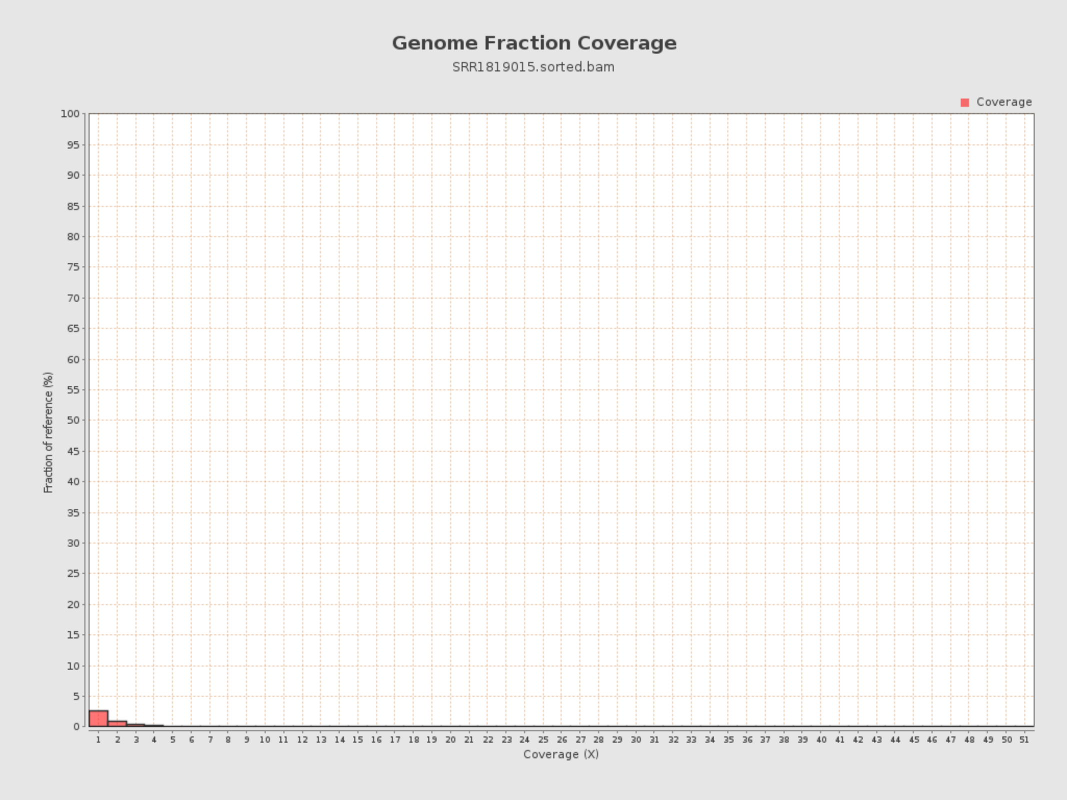
4. Results : Coverage Histogram



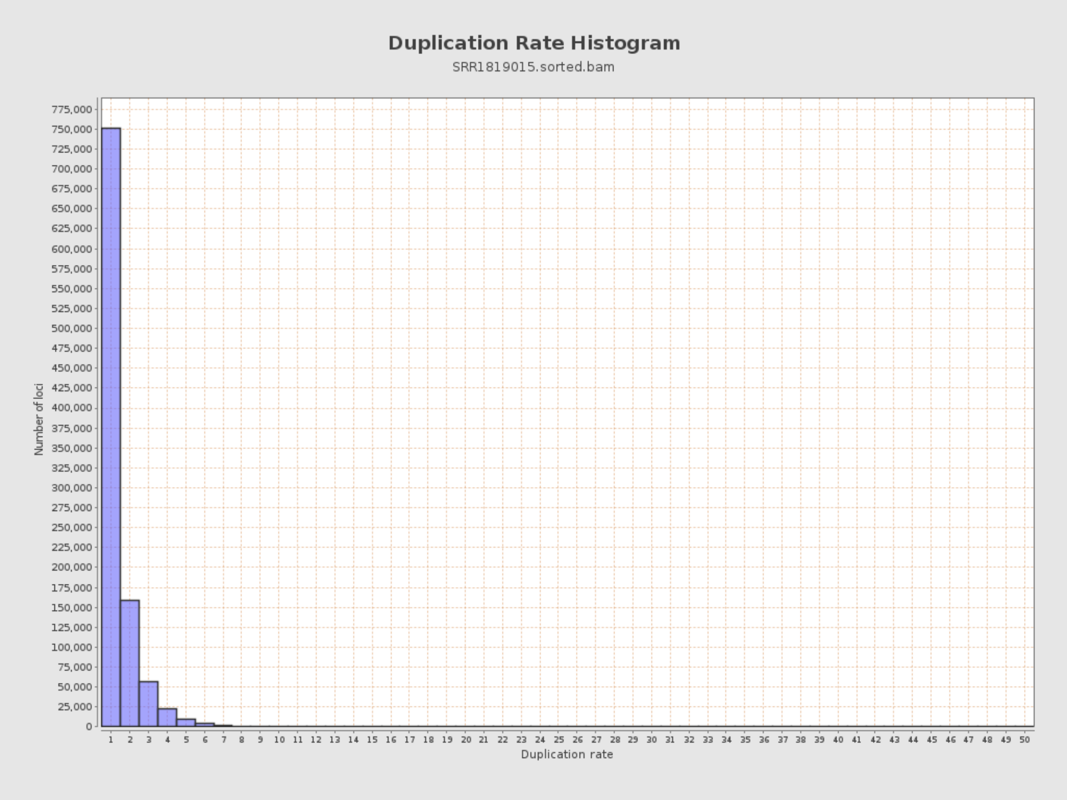
5. Results : Coverage Histogram (0-50X)



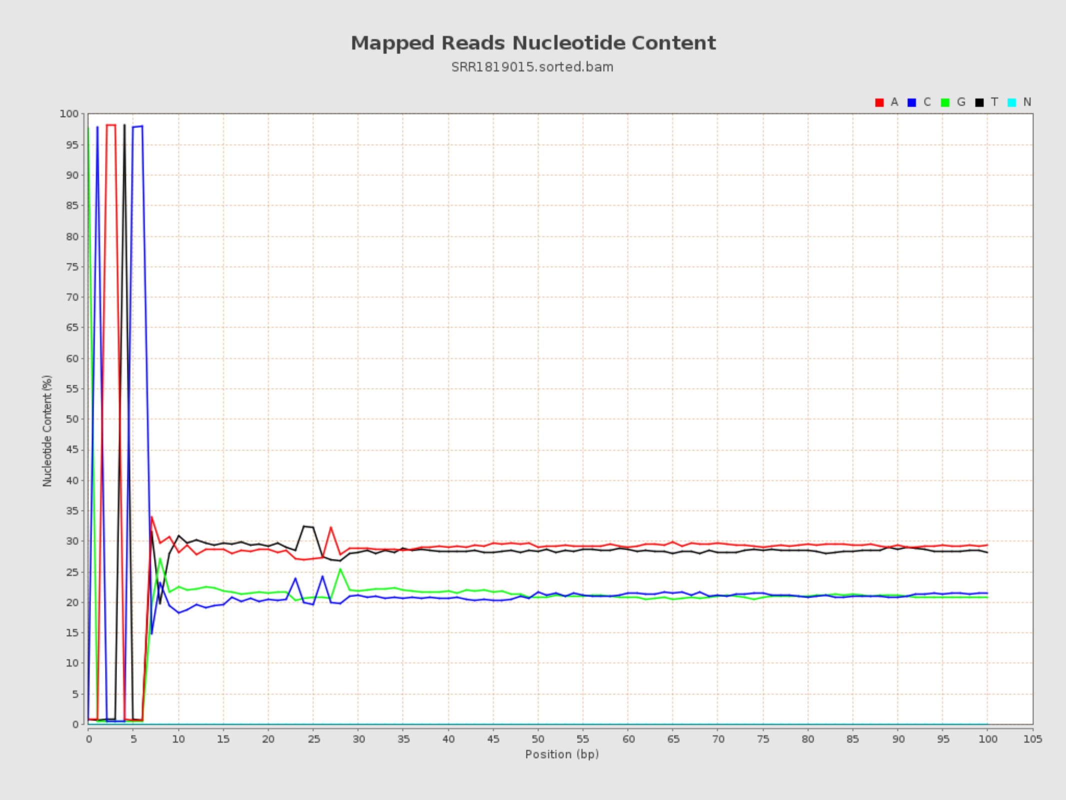
6. Results : Genome Fraction Coverage



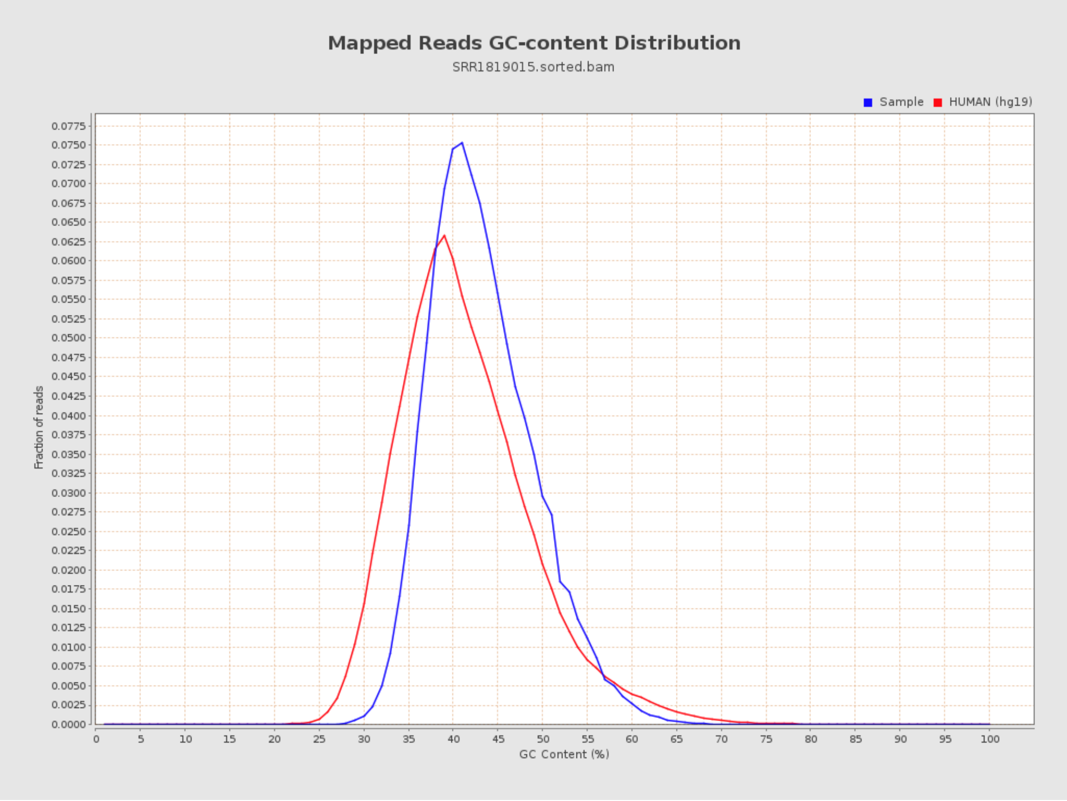
7. Results : Duplication Rate Histogram



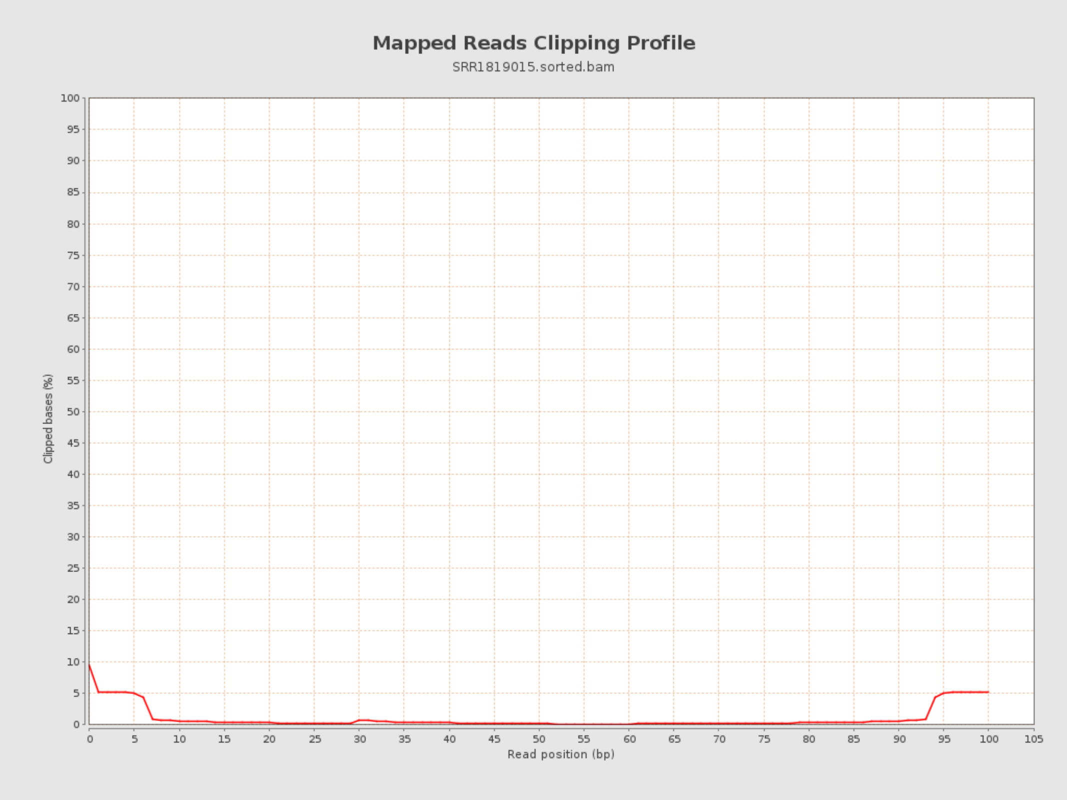
8. Results : Mapped Reads Nucleotide Content



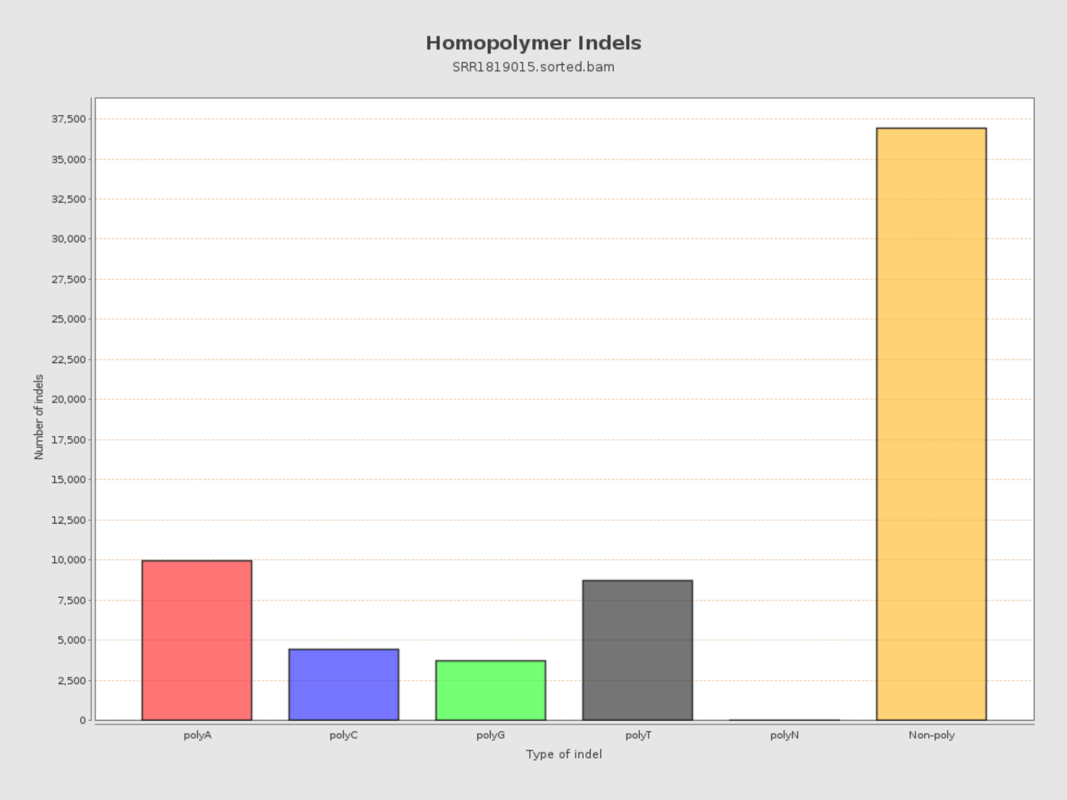
9. Results : Mapped Reads GC-content Distribution



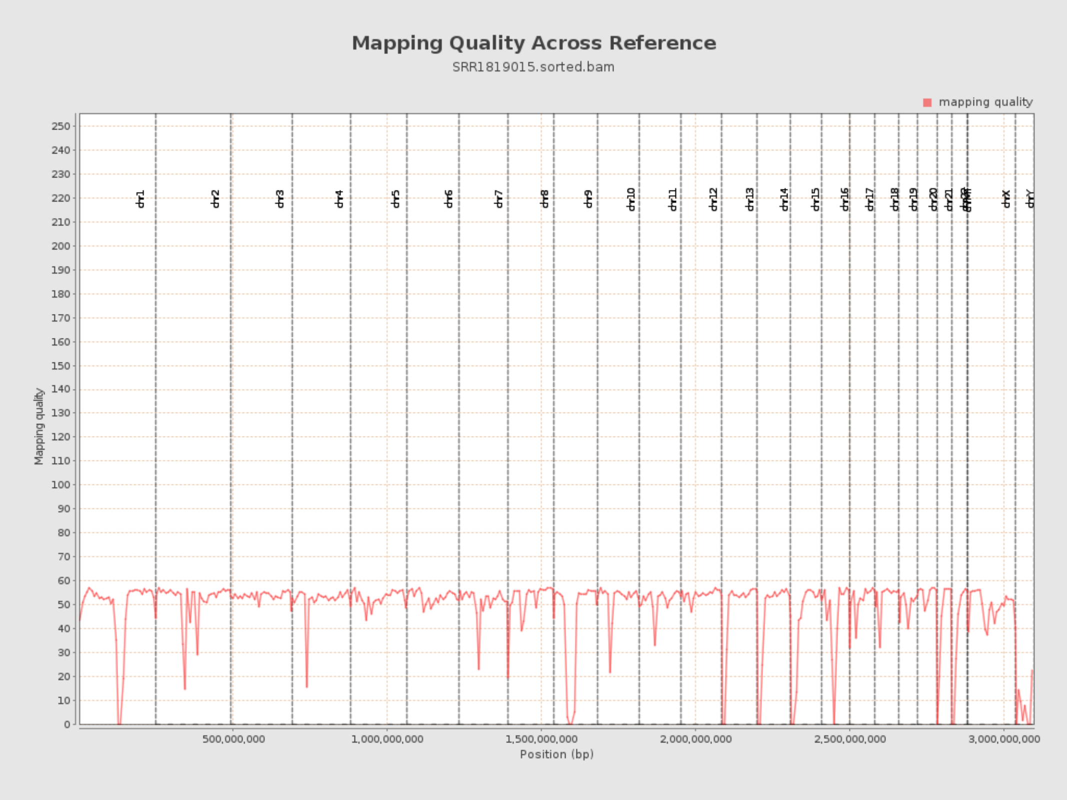
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram