Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:21:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818801.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_SRR1818801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:21:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,565,663
Mapped reads	1,512,824 / 96.63%
Unmapped reads	52,839 / 3.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,471 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	643,507 / 41.1%
Duplication rate	36.1%
Clipped reads	1,515,773 / 96.81%

2.2. ACGT Content

Number/percentage of A's	29,755,842 / 28.99%
Number/percentage of C's	21,839,234 / 21.28%
Number/percentage of T's	29,821,728 / 29.06%
Number/percentage of G's	21,211,215 / 20.67%
Number/percentage of N's	6,434 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.451

2.4. Mapping Quality

Mean Mapping Quality	47.7

2.5. Mismatches and indels

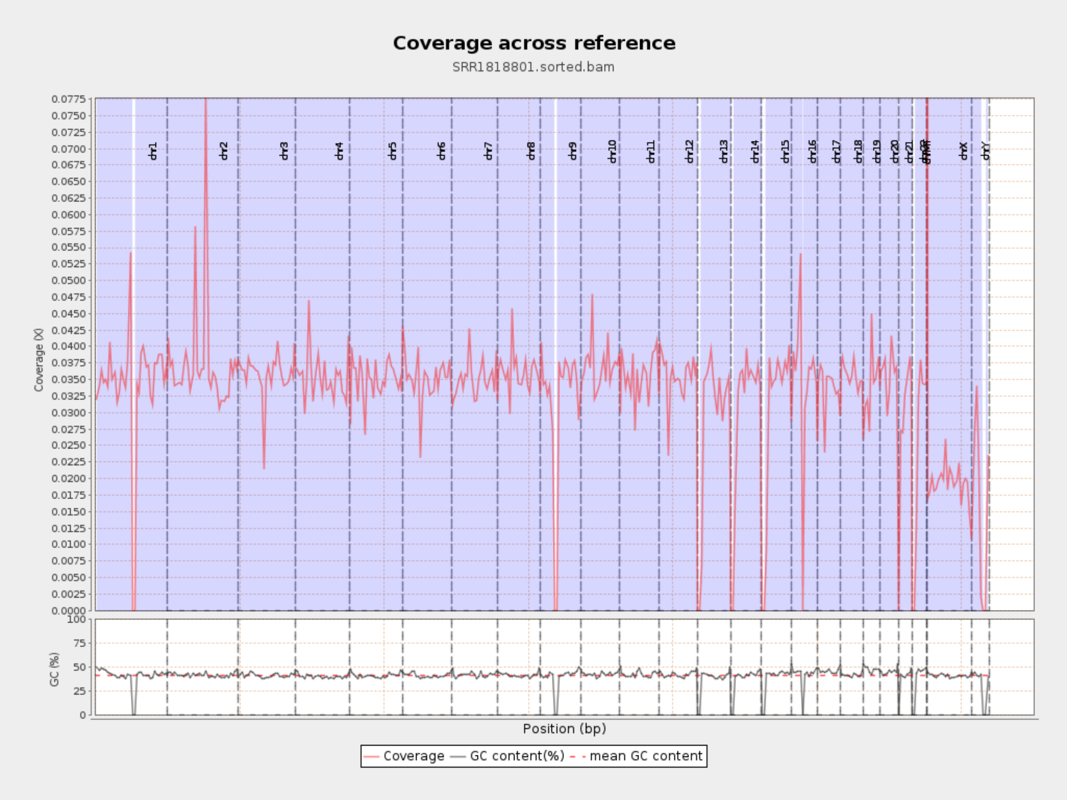
General error rate	0.54%
Mismatches	525,260
Insertions	12,884
Mapped reads with at least one insertion	0.84%
Deletions	26,378
Mapped reads with at least one deletion	1.72%
Homopolymer indels	39.97%

2.6. Chromosome stats

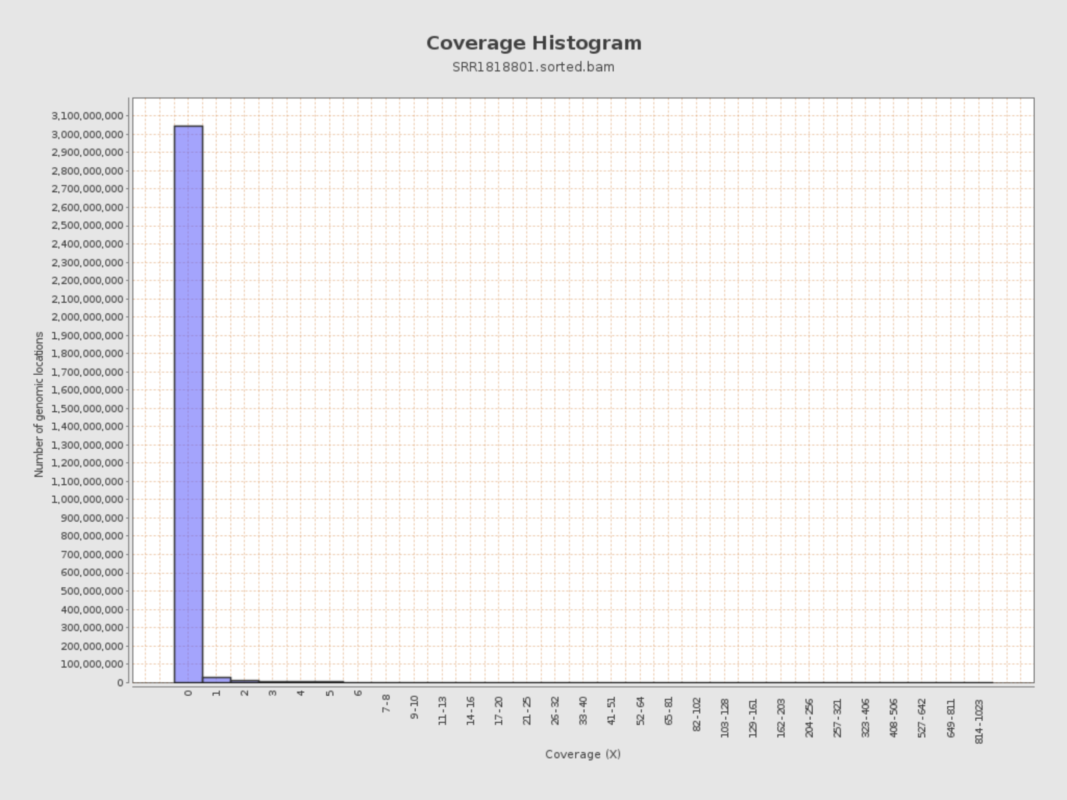
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8475637	0.034	0.5918
chr2	243199373	9118472	0.0375	0.8073
chr3	198022430	7070399	0.0357	0.3338
chr4	191154276	6771001	0.0354	0.369
chr5	180915260	6400060	0.0354	0.3414
chr6	171115067	6018634	0.0352	0.3695
chr7	159138663	5597291	0.0352	0.3883

chr8	146364022	5306520	0.0363	0.3729
chr9	141213431	4396712	0.0311	0.369
chr10	135534747	5033165	0.0371	0.4703
chr11	135006516	4807578	0.0356	0.3742
chr12	133851895	4746612	0.0355	0.362
chr13	115169878	3282835	0.0285	0.2985
chr14	107349540	3173676	0.0296	0.3375
chr15	102531392	3002979	0.0293	0.3053
chr16	90354753	3086528	0.0342	0.5445
chr17	81195210	2730462	0.0336	0.3463
chr18	78077248	2797357	0.0358	0.4555
chr19	59128983	2028981	0.0343	0.5302
chr20	63025520	2230614	0.0354	0.3582
chr21	48129895	1414453	0.0294	0.3172
chr22	51304566	1242868	0.0242	0.2986
chrMT	16571	16423	0.9911	1.9974
chrX	155270560	3001392	0.0193	0.2754
chrY	59373566	927331	0.0156	0.7183

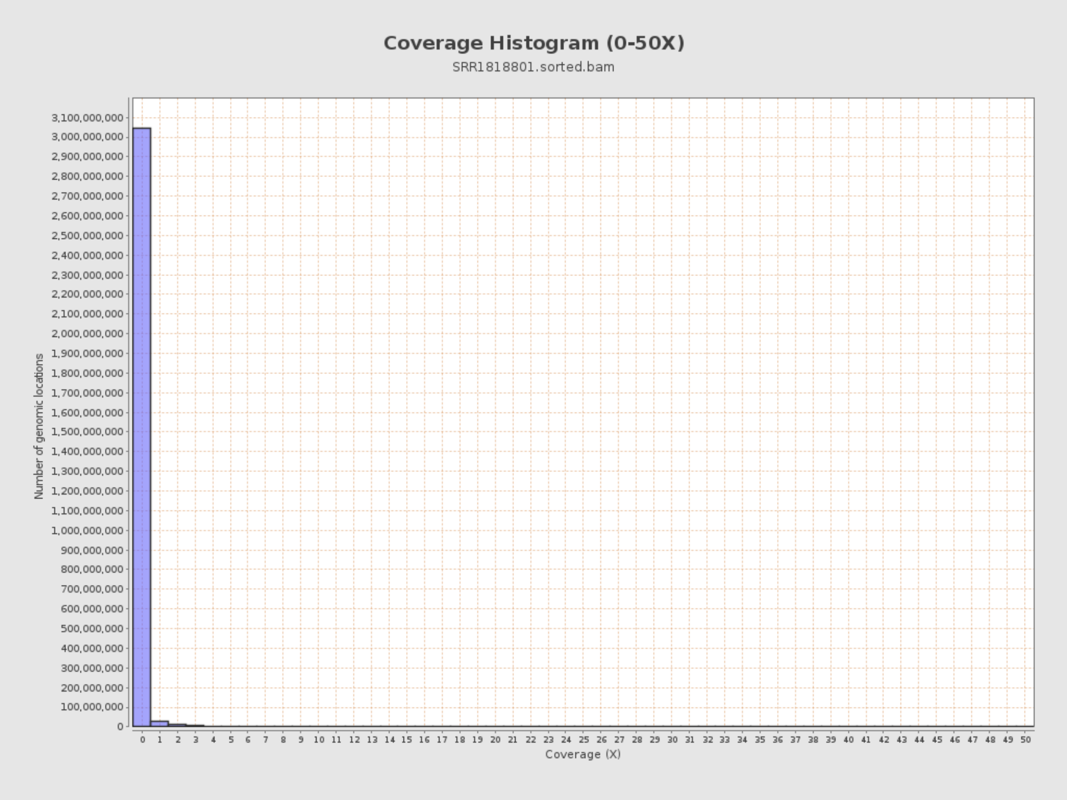
3. Results : Coverage across reference



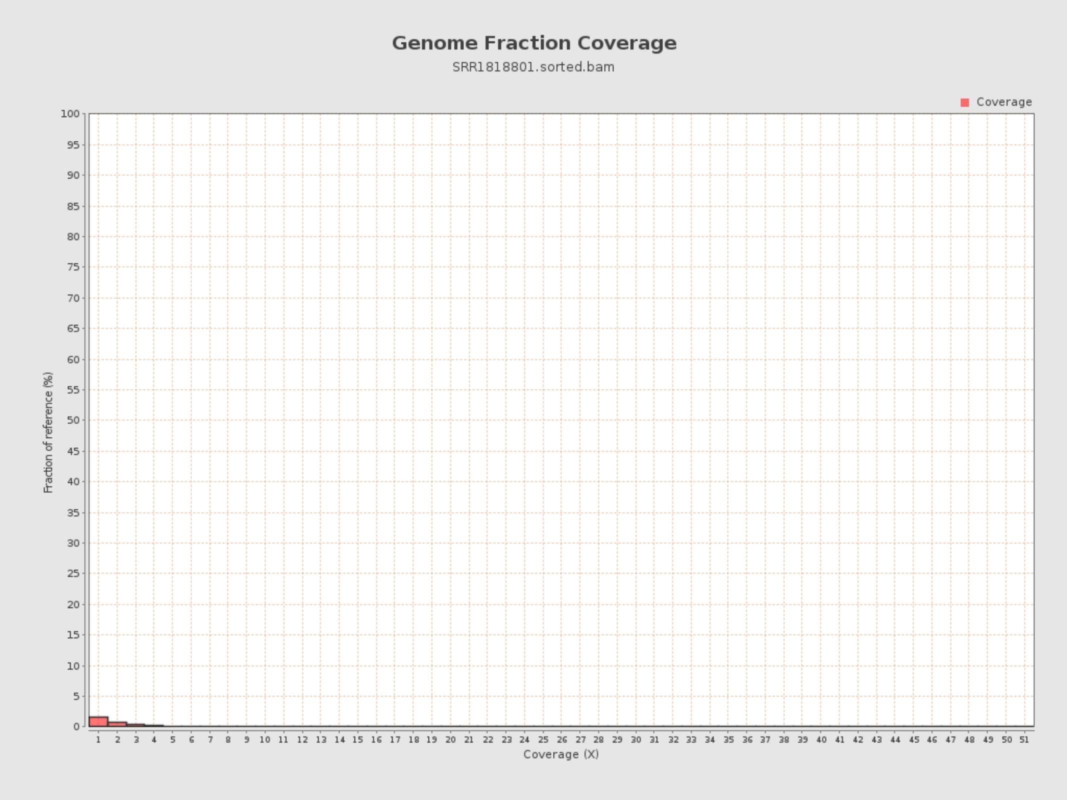
4. Results : Coverage Histogram



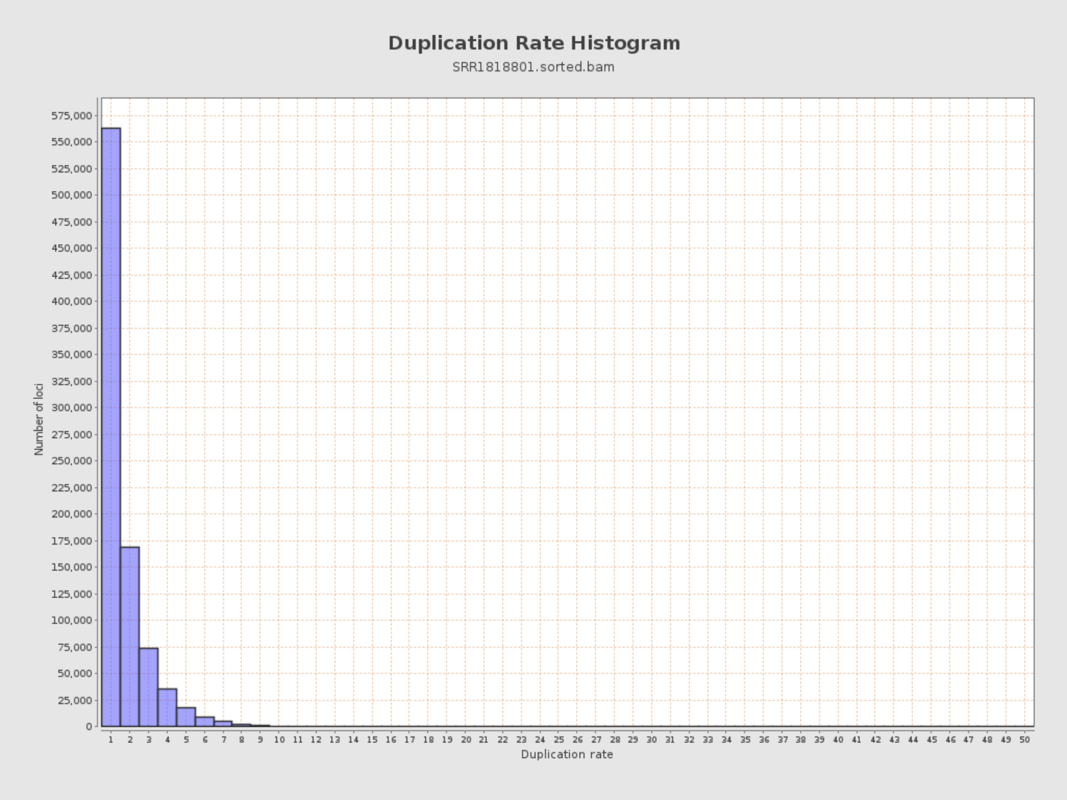
5. Results : Coverage Histogram (0-50X)



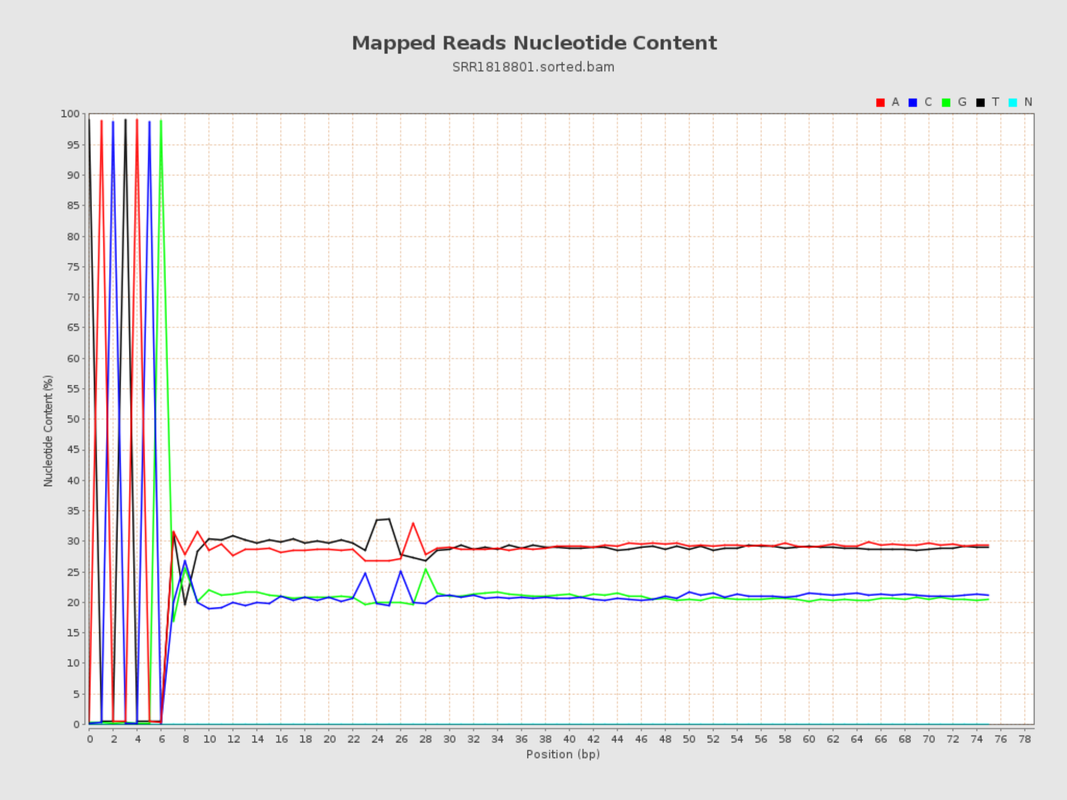
6. Results : Genome Fraction Coverage



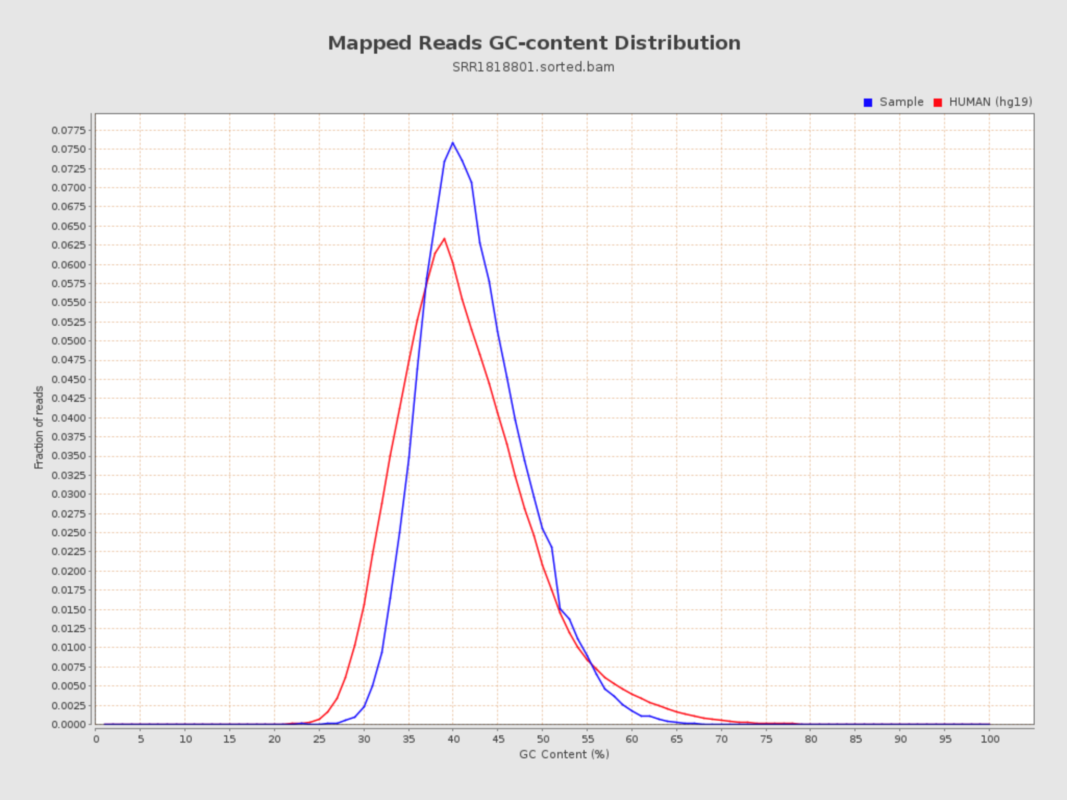
7. Results : Duplication Rate Histogram



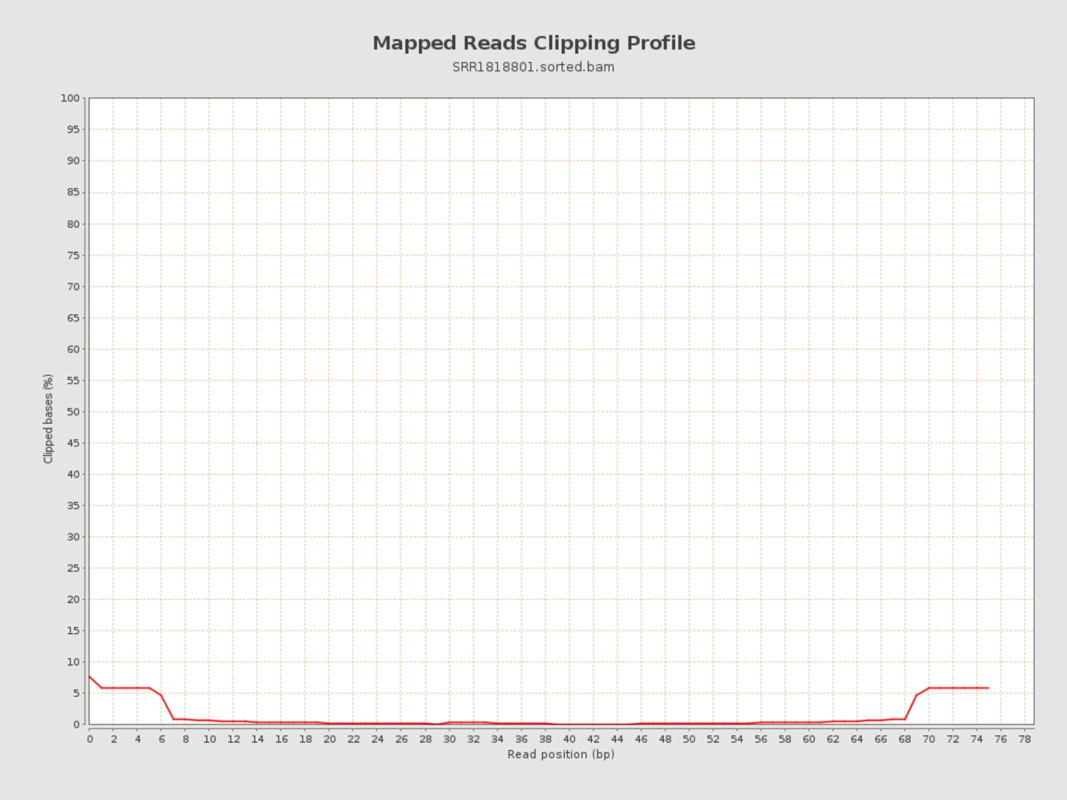
8. Results : Mapped Reads Nucleotide Content



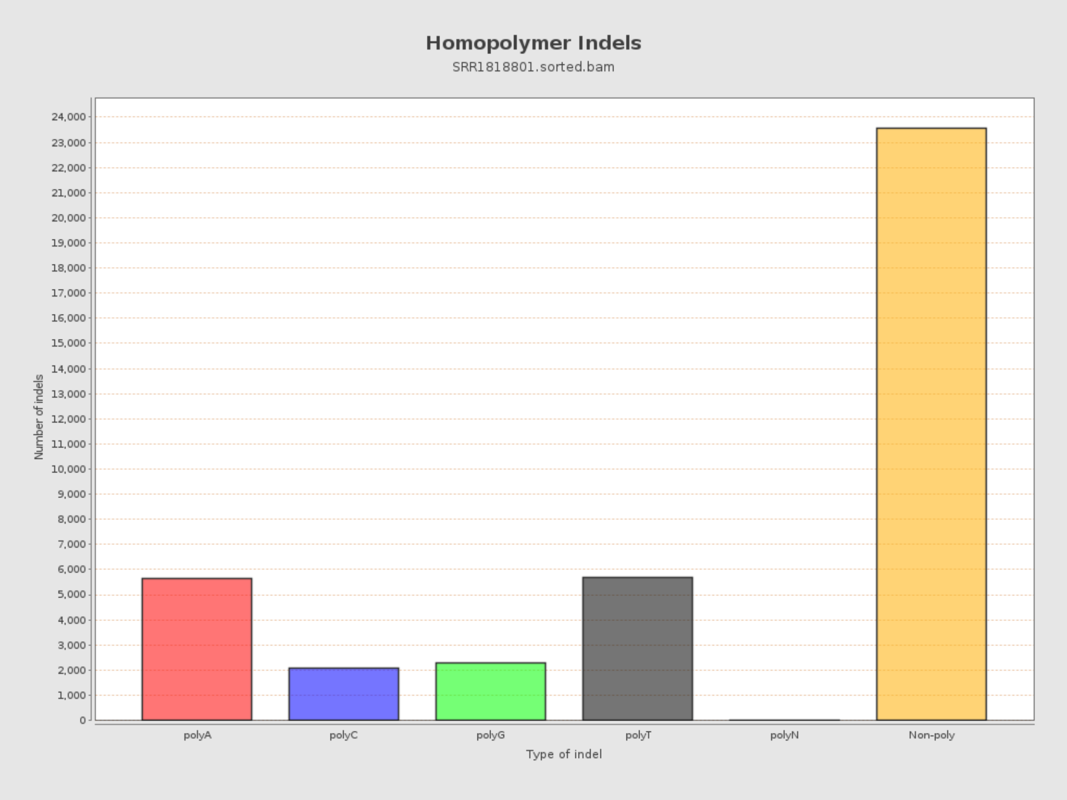
9. Results : Mapped Reads GC-content Distribution



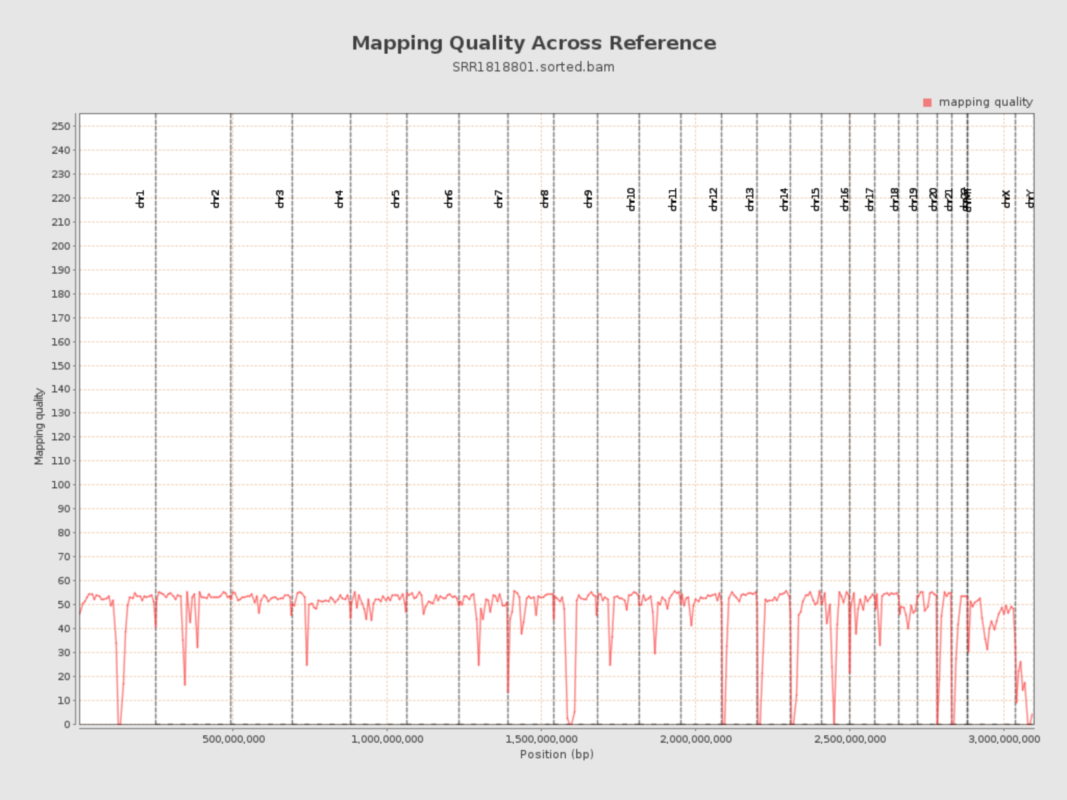
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram