Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:51:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818751.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_SRR1818751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:51:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,028,686
Mapped reads	1,969,445 / 97.08%
Unmapped reads	59,241 / 2.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,062 / 0.89%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	1,074,123 / 52.95%
Duplication rate	45.67%
Clipped reads	1,972,079 / 97.21%

2.2. ACGT Content

Number/percentage of A's	38,088,547 / 28.51%
Number/percentage of C's	29,164,002 / 21.83%
Number/percentage of T's	39,789,607 / 29.78%
Number/percentage of G's	26,554,607 / 19.88%
Number/percentage of N's	8,446 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.5616

2.4. Mapping Quality

Mean Mapping Quality	47.93

2.5. Mismatches and indels

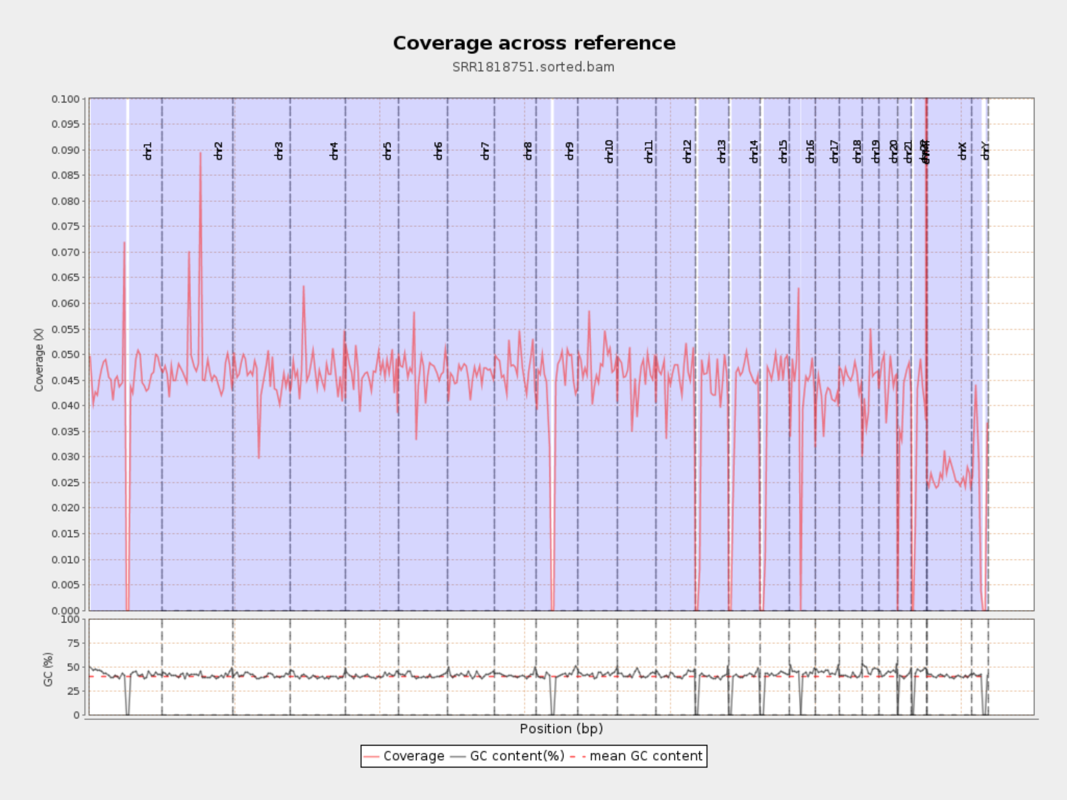
General error rate	0.55%
Mismatches	697,455
Insertions	15,934
Mapped reads with at least one insertion	0.8%
Deletions	34,835
Mapped reads with at least one deletion	1.75%
Homopolymer indels	41.35%

2.6. Chromosome stats

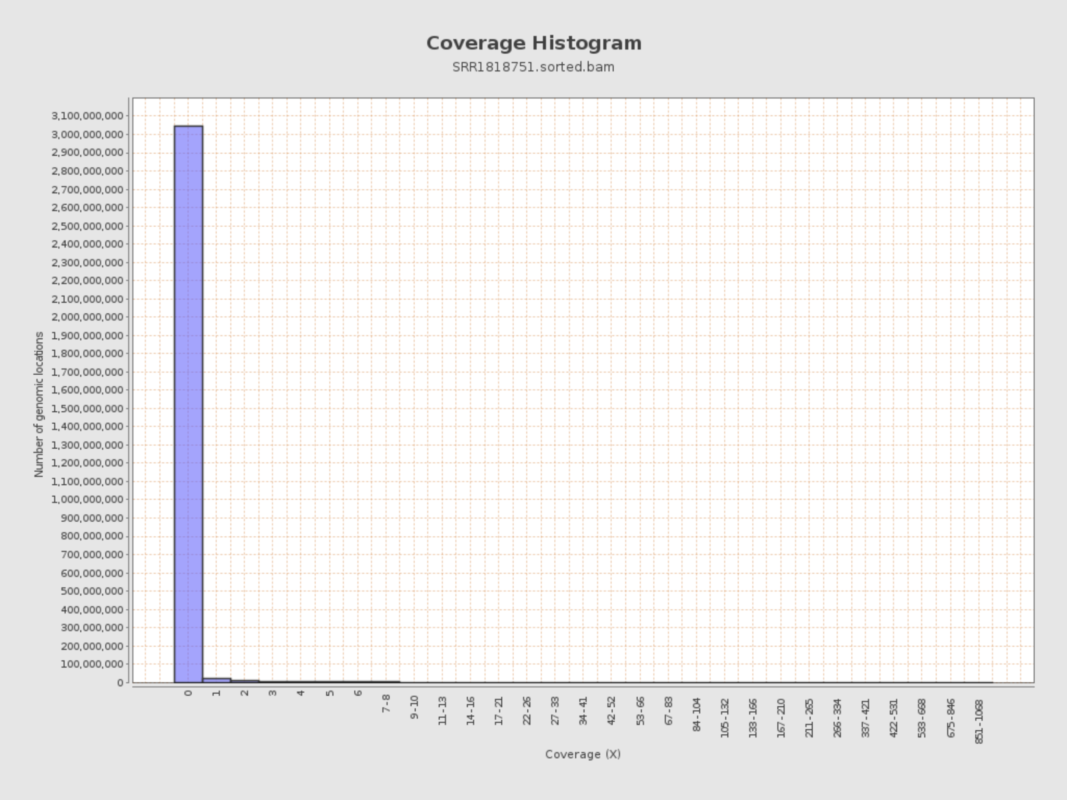
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10901893	0.0437	0.78
chr2	243199373	11767820	0.0484	0.8562
chr3	198022430	9016913	0.0455	0.4513
chr4	191154276	8962481	0.0469	0.5129
chr5	180915260	8442347	0.0467	0.4664
chr6	171115067	8036856	0.047	0.4865
chr7	159138663	7320033	0.046	0.5152

chr8	146364022	6975991	0.0477	0.5139
chr9	141213431	5812943	0.0412	0.4766
chr10	135534747	6517424	0.0481	0.5713
chr11	135006516	6194210	0.0459	0.4863
chr12	133851895	6163148	0.046	0.4757
chr13	115169878	4376188	0.038	0.4085
chr14	107349540	4165068	0.0388	0.4395
chr15	102531392	3890557	0.0379	0.4108
chr16	90354753	3848832	0.0426	0.599
chr17	81195210	3372427	0.0415	0.4441
chr18	78077248	3588206	0.046	0.5773
chr19	59128983	2573770	0.0435	0.6497
chr20	63025520	2859814	0.0454	0.4739
chr21	48129895	1822273	0.0379	0.4281
chr22	51304566	1565593	0.0305	0.4079
chrMT	16571	138014	8.3286	8.5791
chrX	155270560	4074131	0.0262	0.3578
chrY	59373566	1273642	0.0215	0.8792

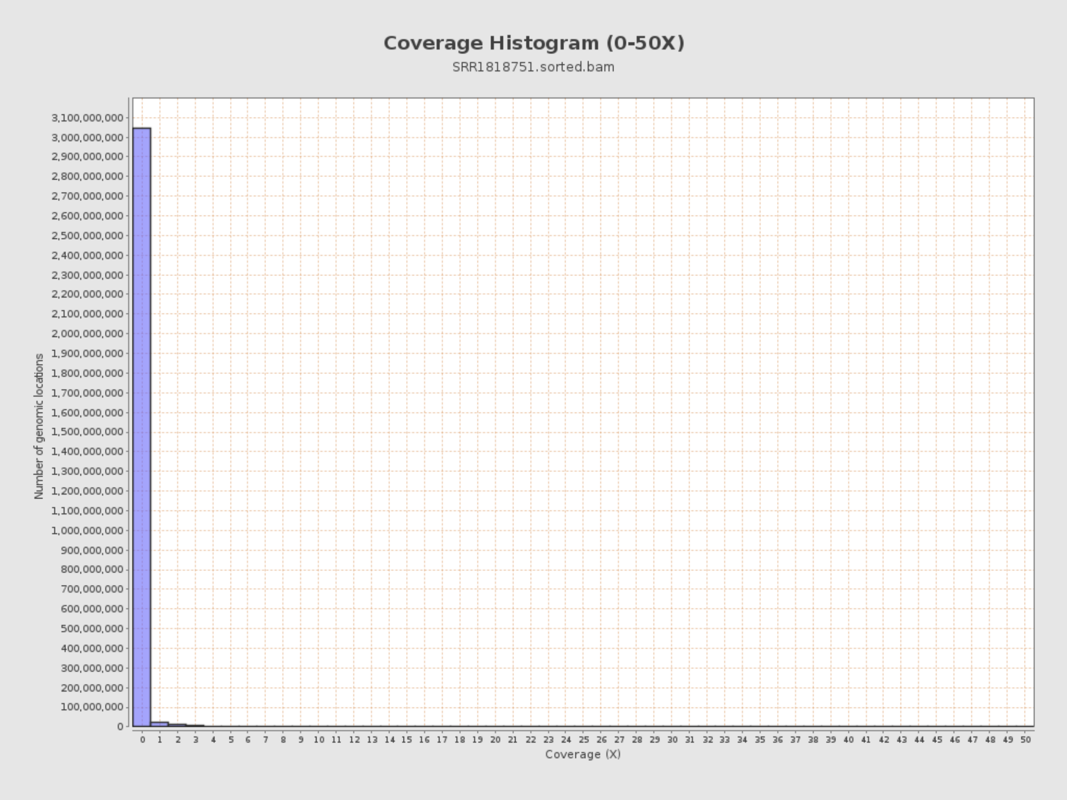
3. Results : Coverage across reference



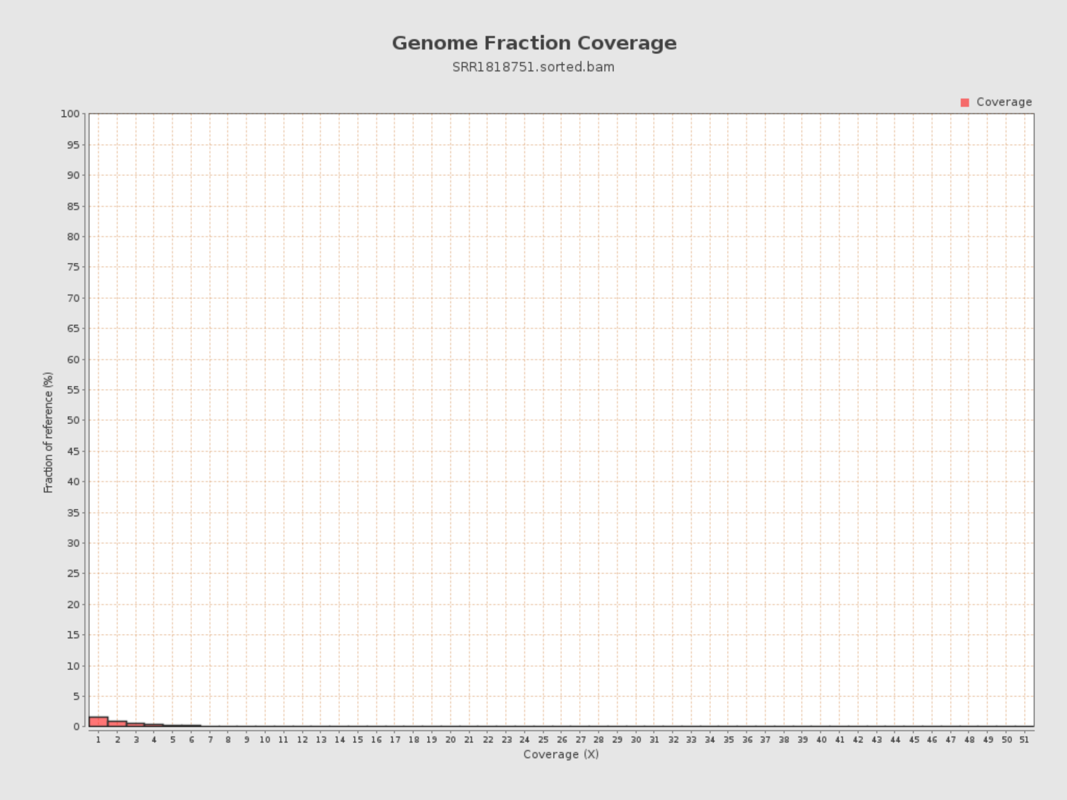
4. Results : Coverage Histogram



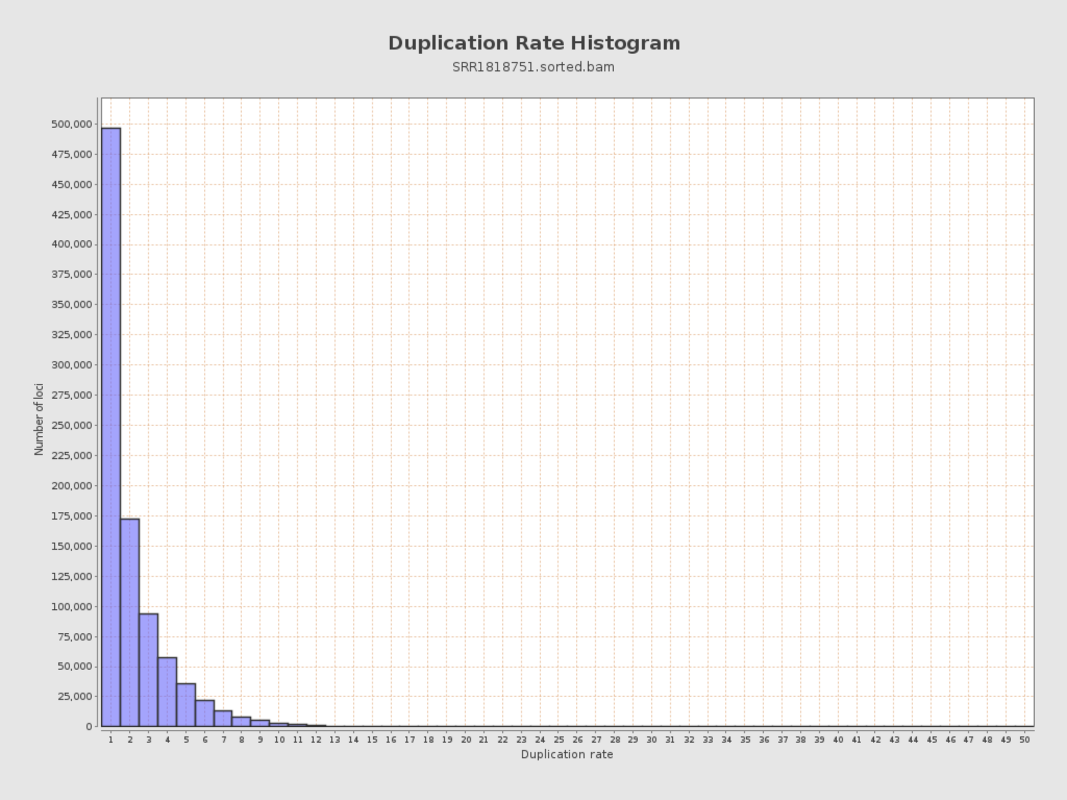
5. Results : Coverage Histogram (0-50X)



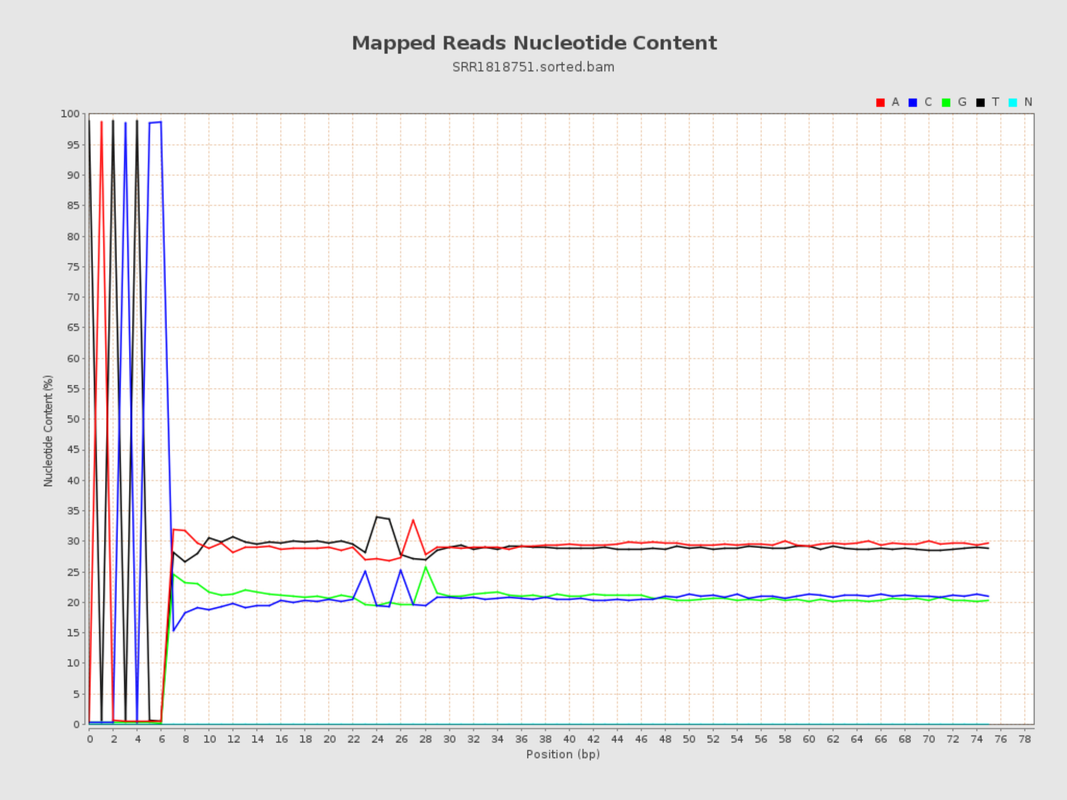
6. Results : Genome Fraction Coverage



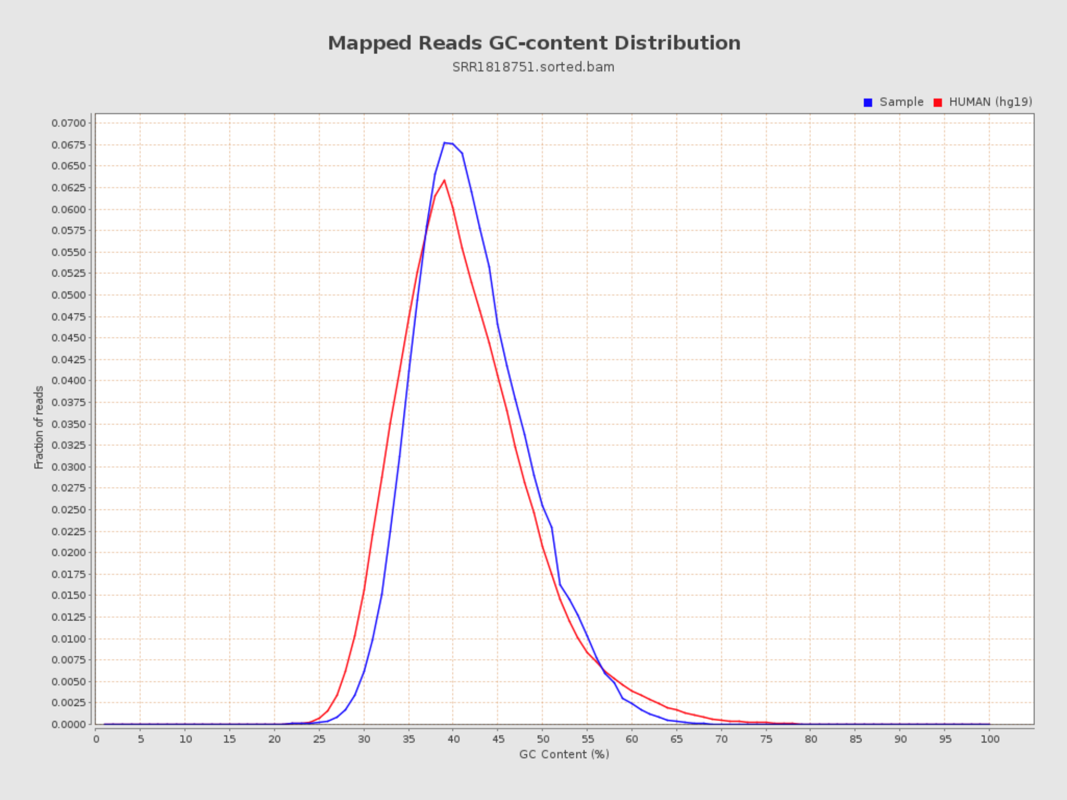
7. Results : Duplication Rate Histogram



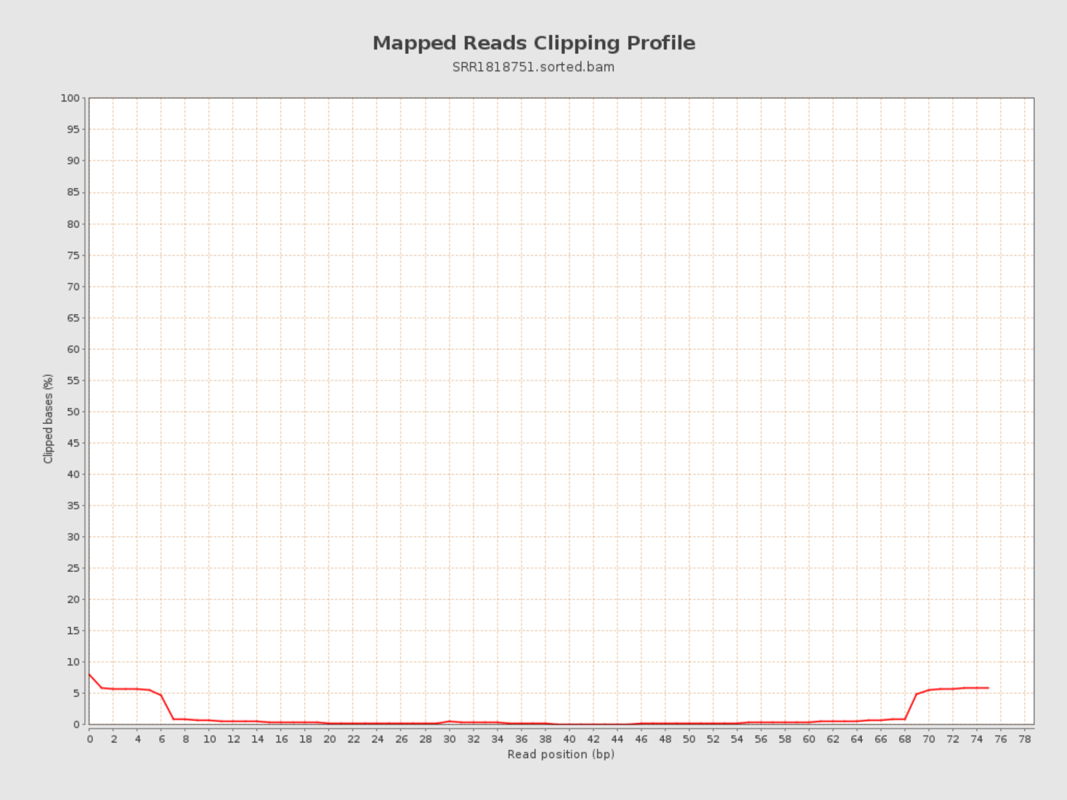
8. Results : Mapped Reads Nucleotide Content



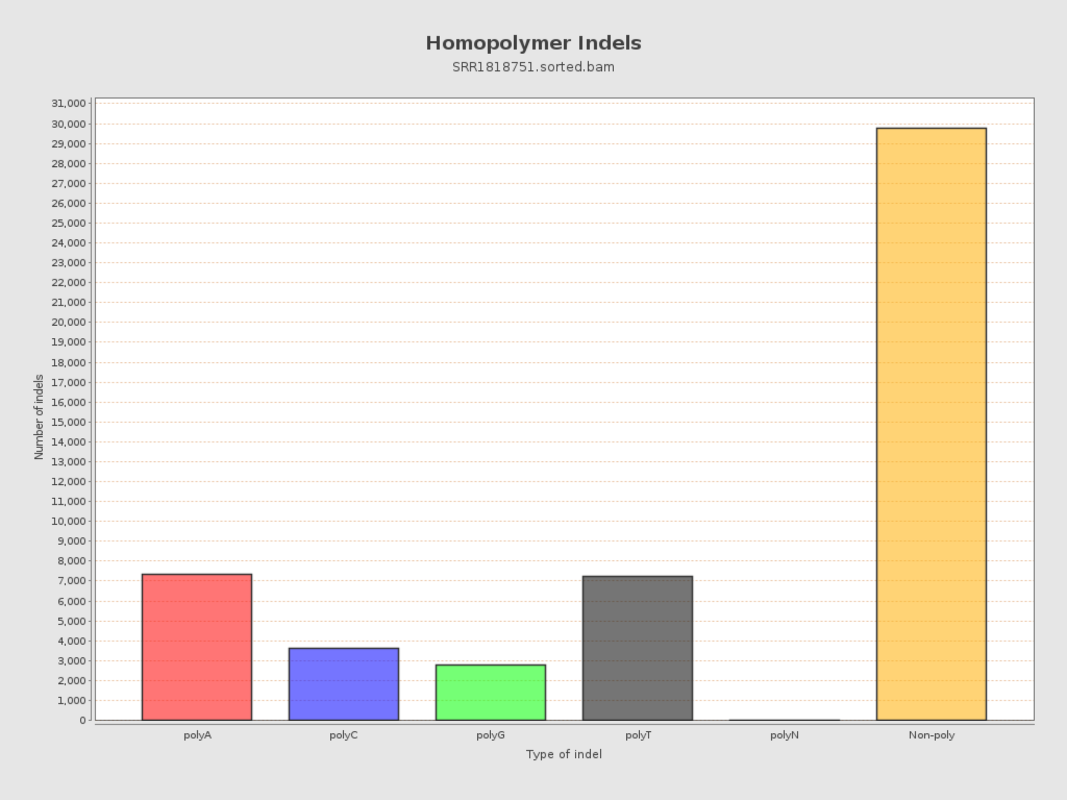
9. Results : Mapped Reads GC-content Distribution



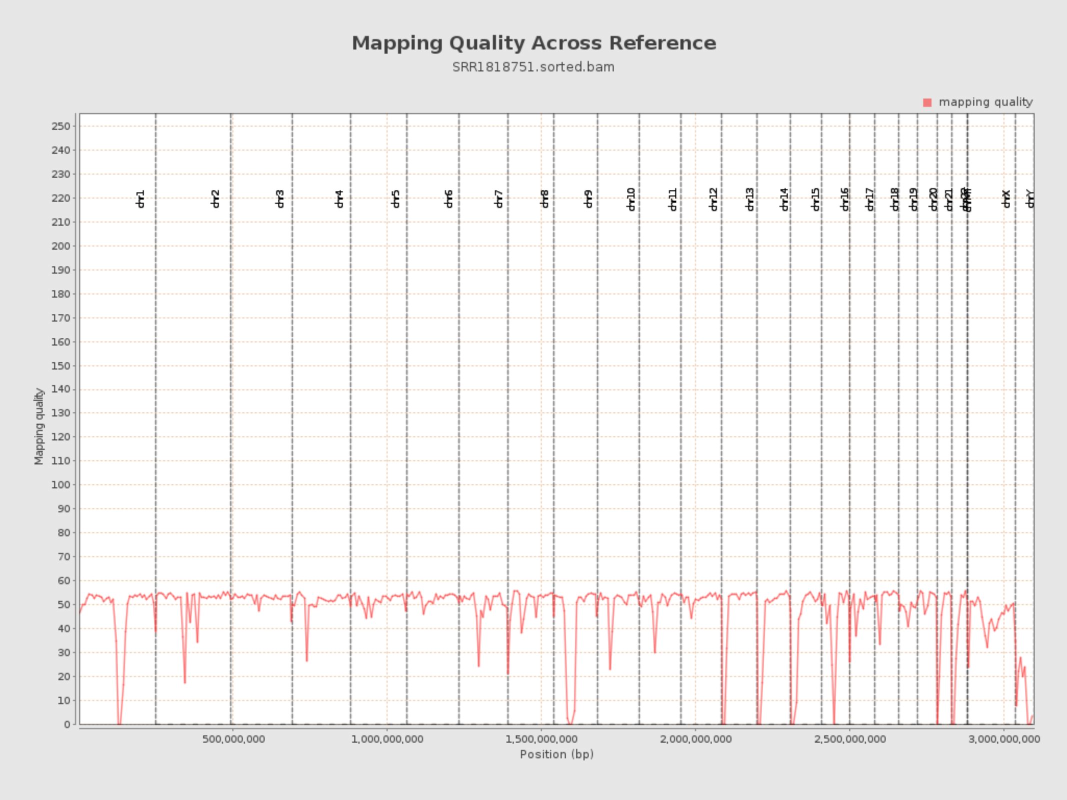
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram