Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:29:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818789.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_SRR1818789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:29:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,387,569
Mapped reads	1,351,323 / 97.39%
Unmapped reads	36,246 / 2.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,315 / 0.74%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	615,334 / 44.35%
Duplication rate	38.25%
Clipped reads	1,340,725 / 96.62%

2.2. ACGT Content

Number/percentage of A's	26,045,662 / 28.36%
Number/percentage of C's	18,685,073 / 20.34%
Number/percentage of T's	27,151,731 / 29.56%
Number/percentage of G's	19,956,666 / 21.73%
Number/percentage of N's	5,609 / 0.01%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.3884

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

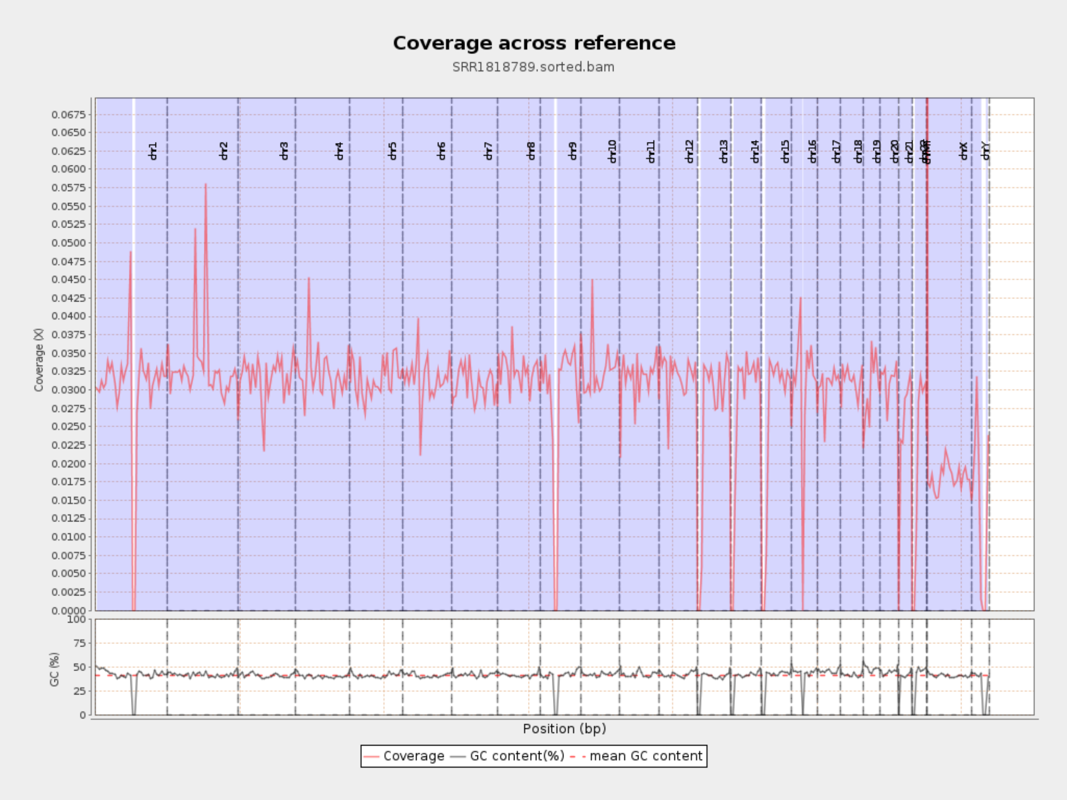
General error rate	0.54%
Mismatches	476,693
Insertions	12,027
Mapped reads with at least one insertion	0.88%
Deletions	23,084
Mapped reads with at least one deletion	1.69%
Homopolymer indels	39.83%

2.6. Chromosome stats

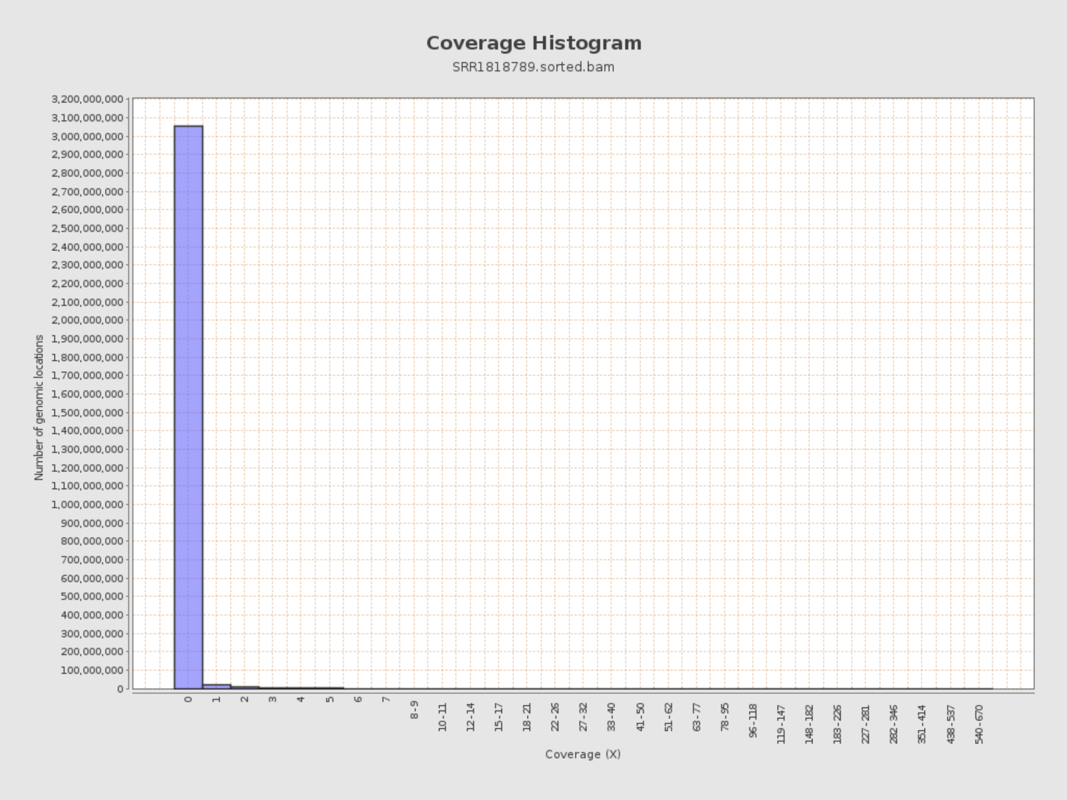
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7512610	0.0301	0.527
chr2	243199373	8107159	0.0333	0.5522
chr3	198022430	6273971	0.0317	0.3291
chr4	191154276	6176319	0.0323	0.3562
chr5	180915260	5716850	0.0316	0.3386
chr6	171115067	5387185	0.0315	0.3516
chr7	159138663	4902985	0.0308	0.3656

chr8	146364022	4767712	0.0326	0.3674
chr9	141213431	4043041	0.0286	0.3582
chr10	135534747	4438842	0.0328	0.4091
chr11	135006516	4302691	0.0319	0.3581
chr12	133851895	4284033	0.032	0.3432
chr13	115169878	3016253	0.0262	0.3
chr14	107349540	2904189	0.0271	0.3256
chr15	102531392	2661676	0.026	0.3024
chr16	90354753	2719931	0.0301	0.3948
chr17	81195210	2486016	0.0306	0.3446
chr18	78077248	2444418	0.0313	0.4244
chr19	59128983	1792376	0.0303	0.4681
chr20	63025520	1971408	0.0313	0.3442
chr21	48129895	1205796	0.0251	0.3007
chr22	51304566	1069724	0.0209	0.2952
chrMT	16571	30054	1.8137	2.9291
chrX	155270560	2816128	0.0181	0.2605
chrY	59373566	850407	0.0143	0.4525

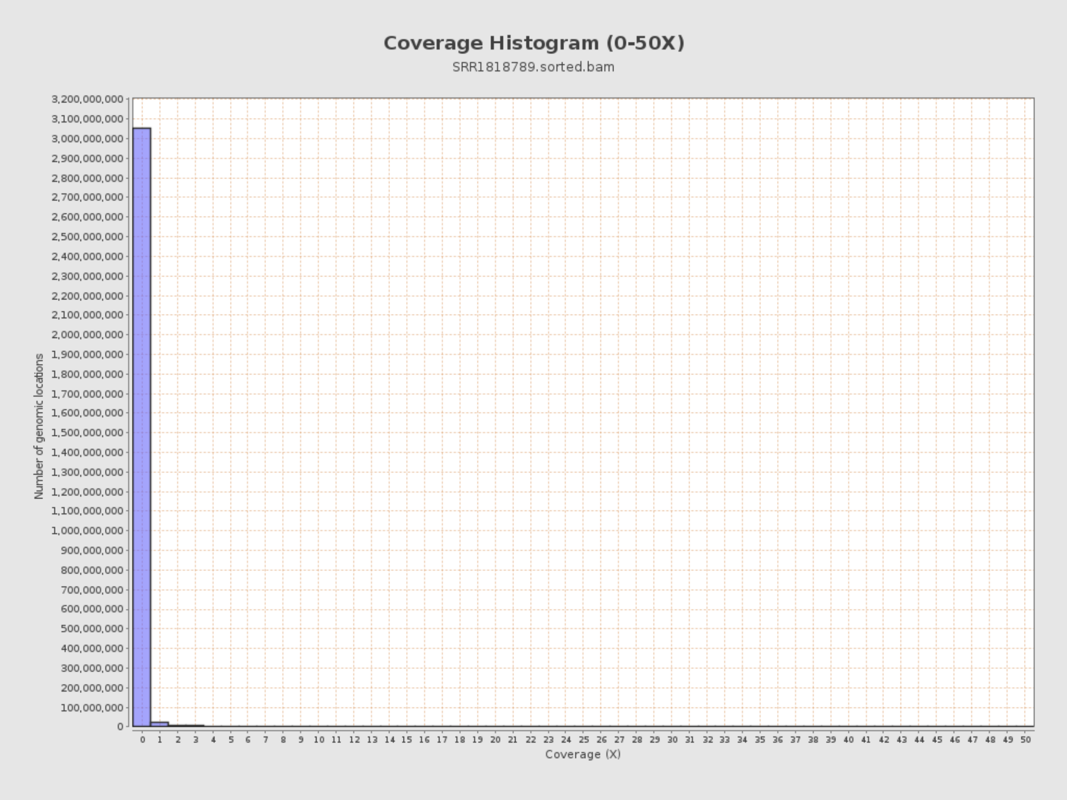
3. Results : Coverage across reference



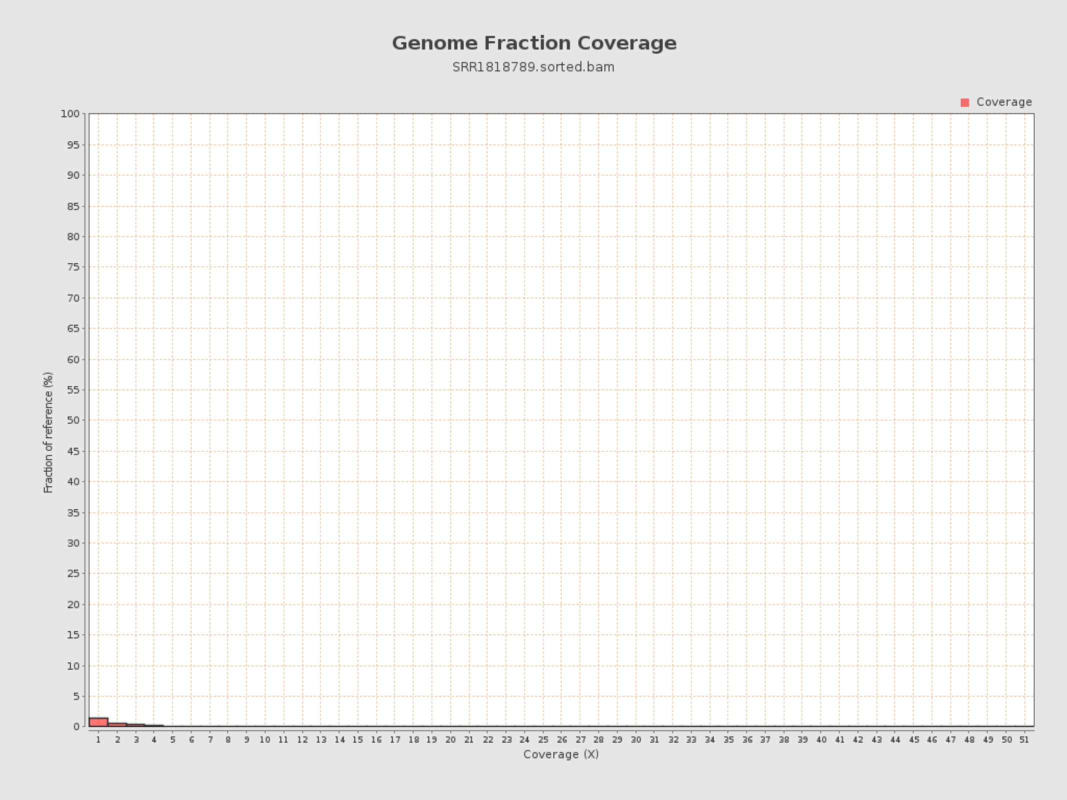
4. Results : Coverage Histogram



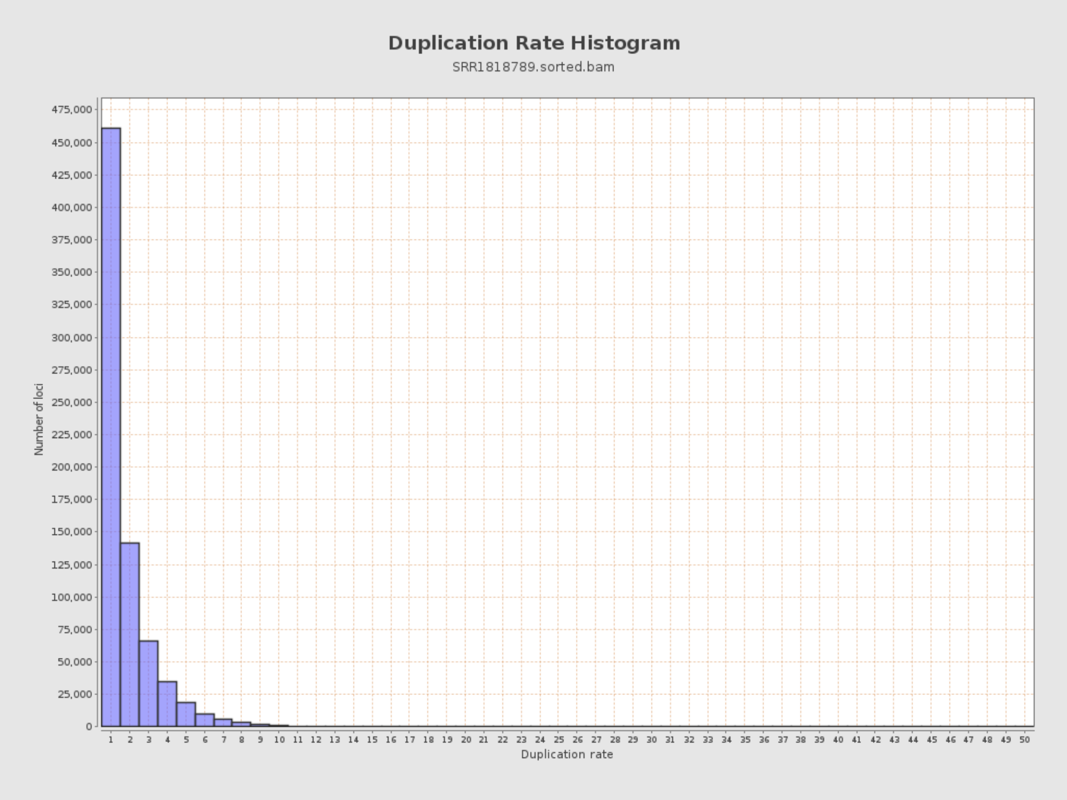
5. Results : Coverage Histogram (0-50X)



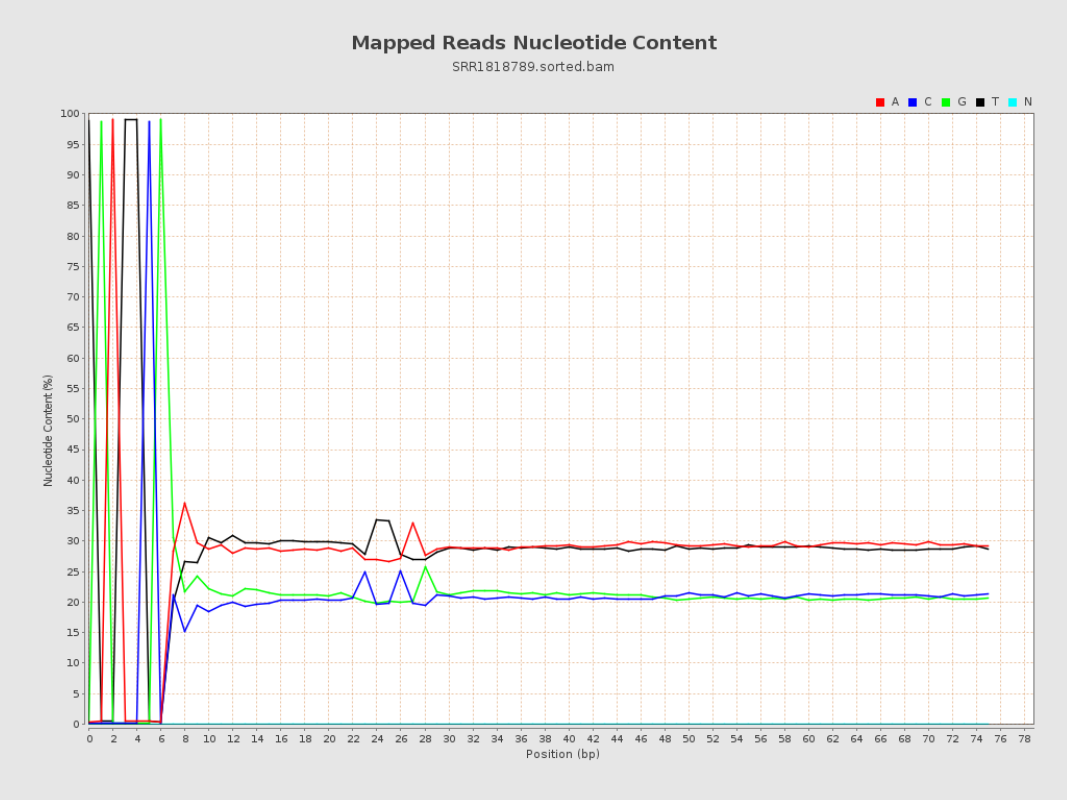
6. Results : Genome Fraction Coverage



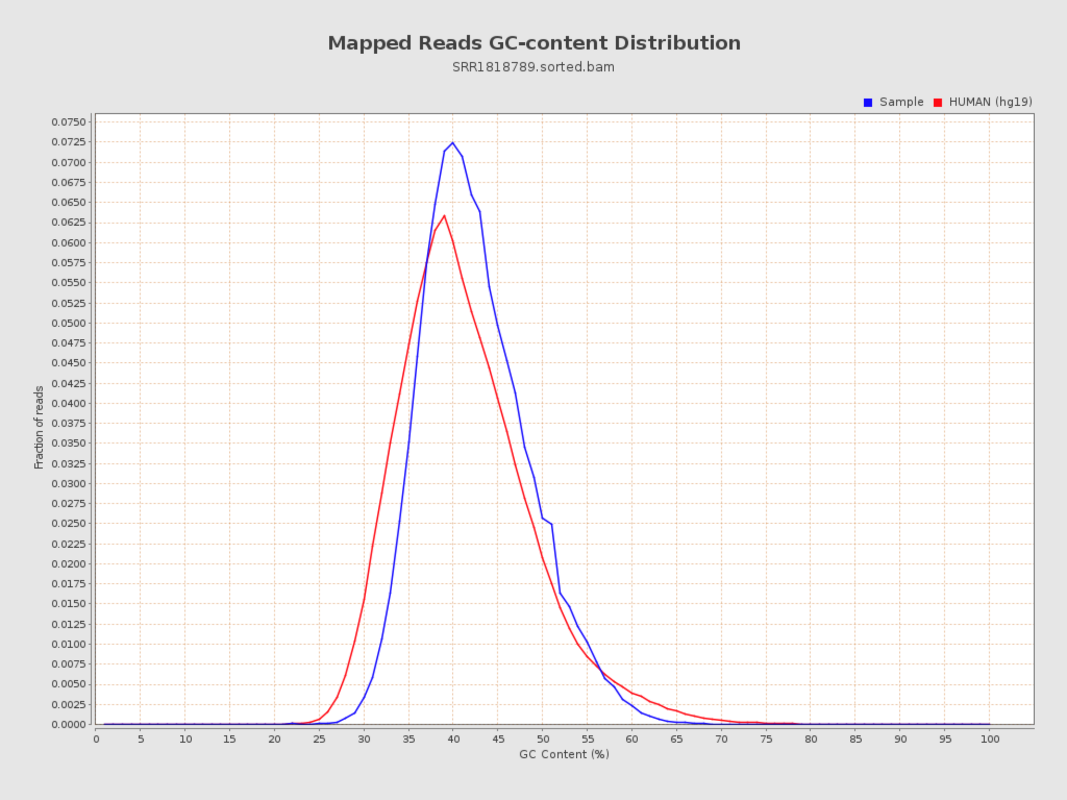
7. Results : Duplication Rate Histogram



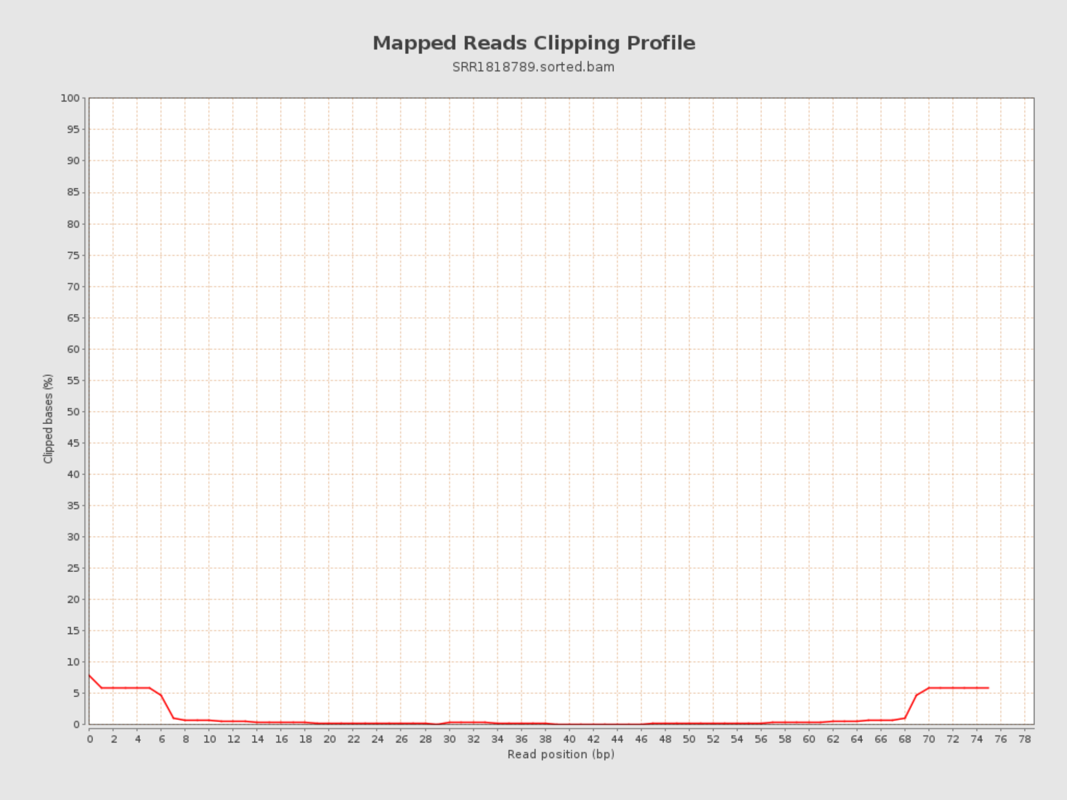
8. Results : Mapped Reads Nucleotide Content



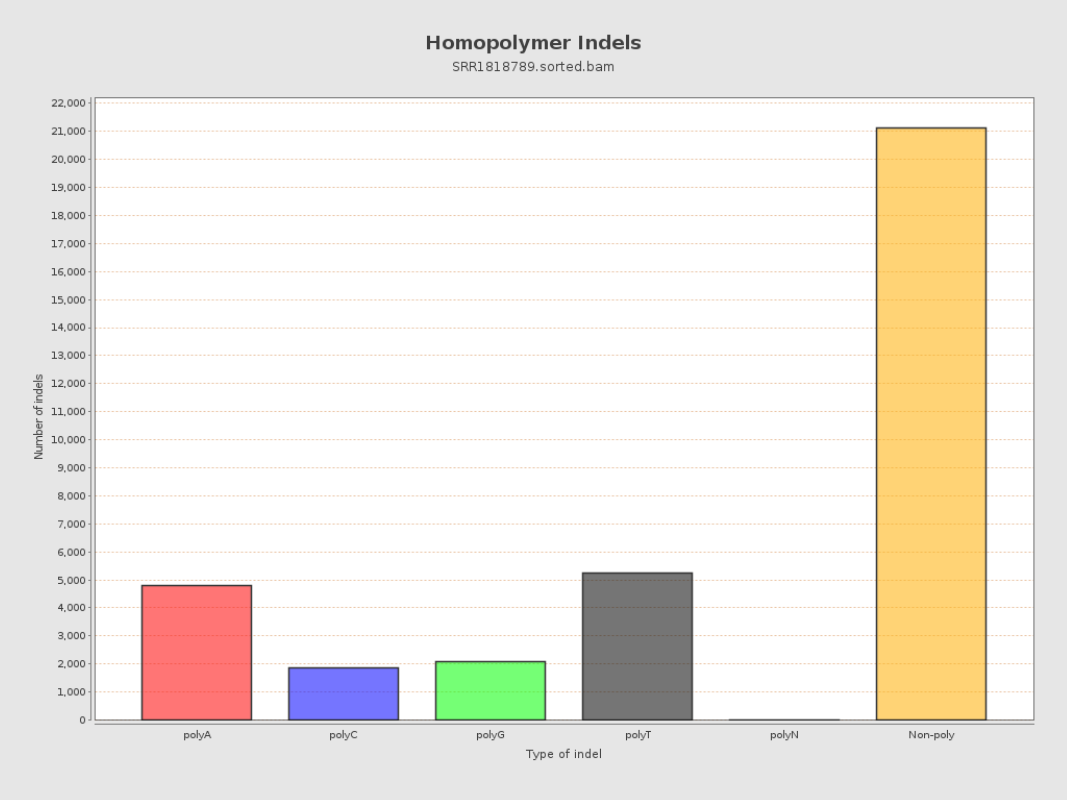
9. Results : Mapped Reads GC-content Distribution



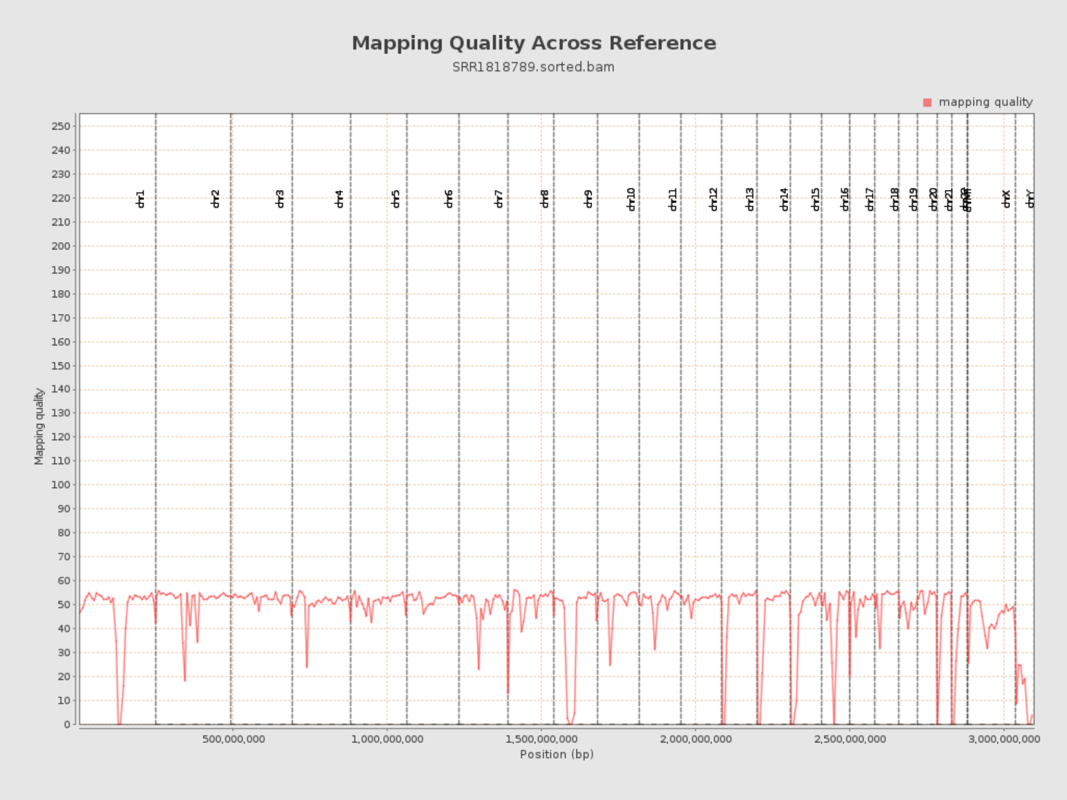
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram