Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:37:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008657.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_SRR6008657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008657.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:36:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,567,399
Mapped reads	1,374,487 / 87.69%
Unmapped reads	192,912 / 12.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,674 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	90,479 / 5.77%
Duplication rate	4.88%
Clipped reads	680,084 / 43.39%

2.2. ACGT Content

Number/percentage of A's	24,300,550 / 27.08%
Number/percentage of C's	17,350,261 / 19.34%
Number/percentage of T's	27,564,485 / 30.72%
Number/percentage of G's	20,399,643 / 22.73%
Number/percentage of N's	117,579 / 0.13%
GC Percentage	42.07%

2.3. Coverage

Mean	0.029

Standard Deviation	0.3835

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Mismatches and indels

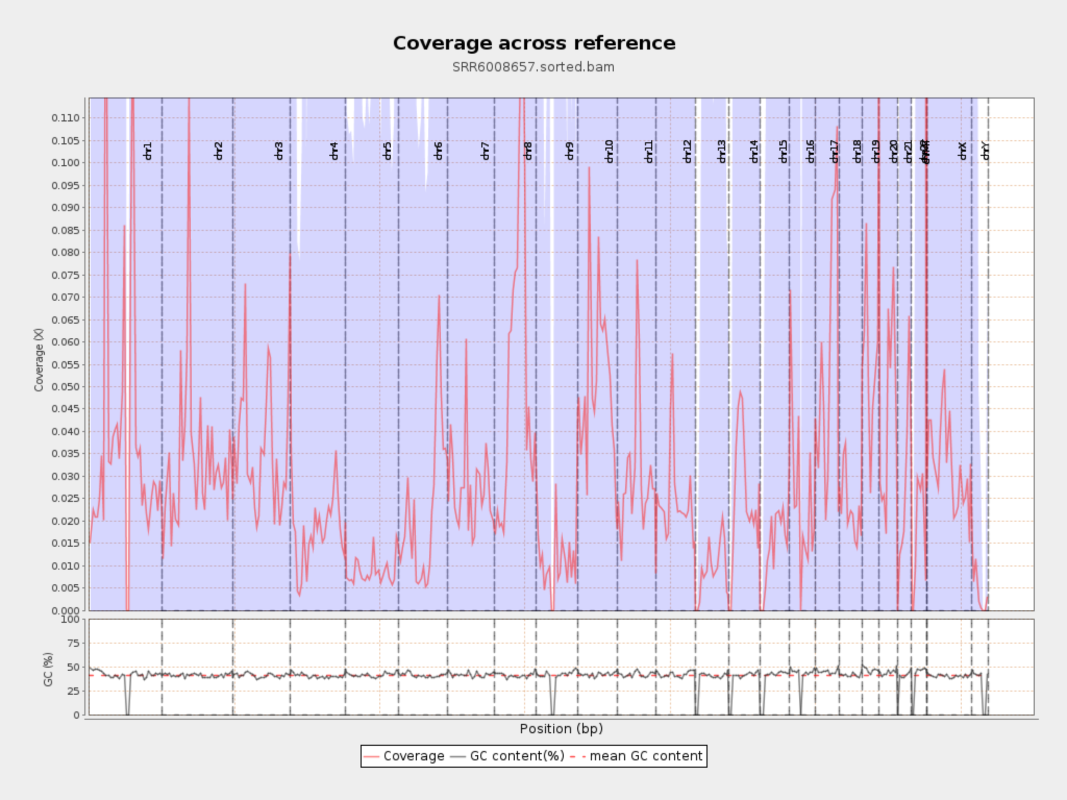
General error rate	0.92%
Mismatches	815,417
Insertions	6,734
Mapped reads with at least one insertion	0.49%
Deletions	31,478
Mapped reads with at least one deletion	2.26%
Homopolymer indels	44.67%

2.6. Chromosome stats

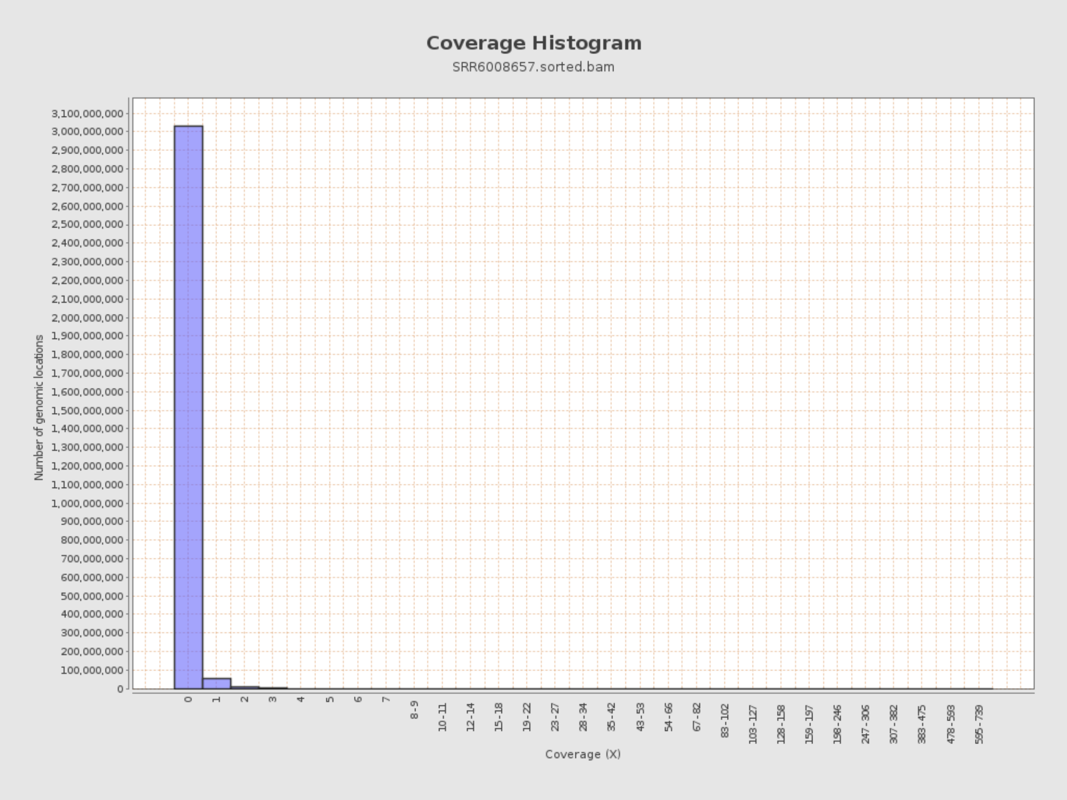
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9553715	0.0383	0.6837
chr2	243199373	8357990	0.0344	0.5077
chr3	198022430	7121656	0.036	0.2681
chr4	191154276	3394252	0.0178	0.1734
chr5	180915260	1593552	0.0088	0.1198
chr6	171115067	3868568	0.0226	0.2033
chr7	159138663	4394554	0.0276	0.5659

chr8	146364022	7844277	0.0536	0.469
chr9	141213431	1468680	0.0104	0.2509
chr10	135534747	7032291	0.0519	0.6764
chr11	135006516	4170274	0.0309	0.2741
chr12	133851895	3382617	0.0253	0.203
chr13	115169878	1078479	0.0094	0.1224
chr14	107349540	2715087	0.0253	0.2022
chr15	102531392	1465287	0.0143	0.1518
chr16	90354753	2247181	0.0249	0.2933
chr17	81195210	4561097	0.0562	0.4101
chr18	78077248	1804777	0.0231	0.3852
chr19	59128983	3384684	0.0572	0.4739
chr20	63025520	2740493	0.0435	0.2688
chr21	48129895	1345741	0.028	0.2165
chr22	51304566	881075	0.0172	0.1611
chrMT	16571	80519	4.859	4.081
chrX	155270560	5050228	0.0325	0.2712
chrY	59373566	250541	0.0042	0.1369

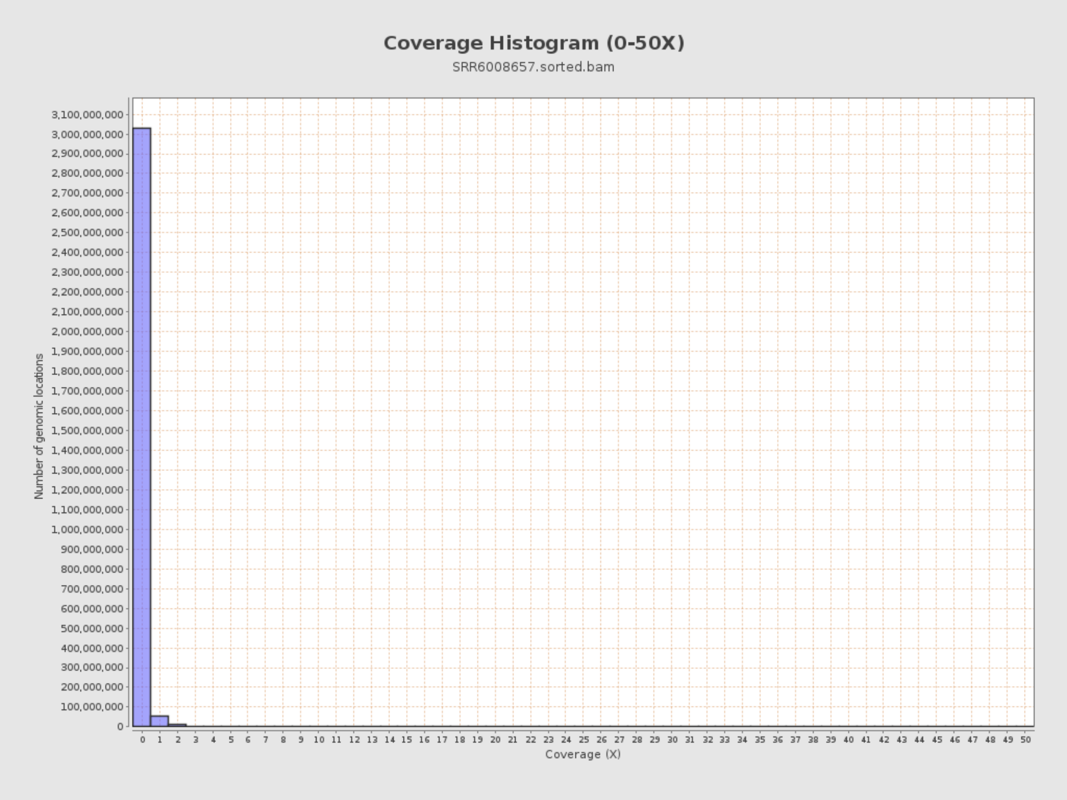
3. Results : Coverage across reference



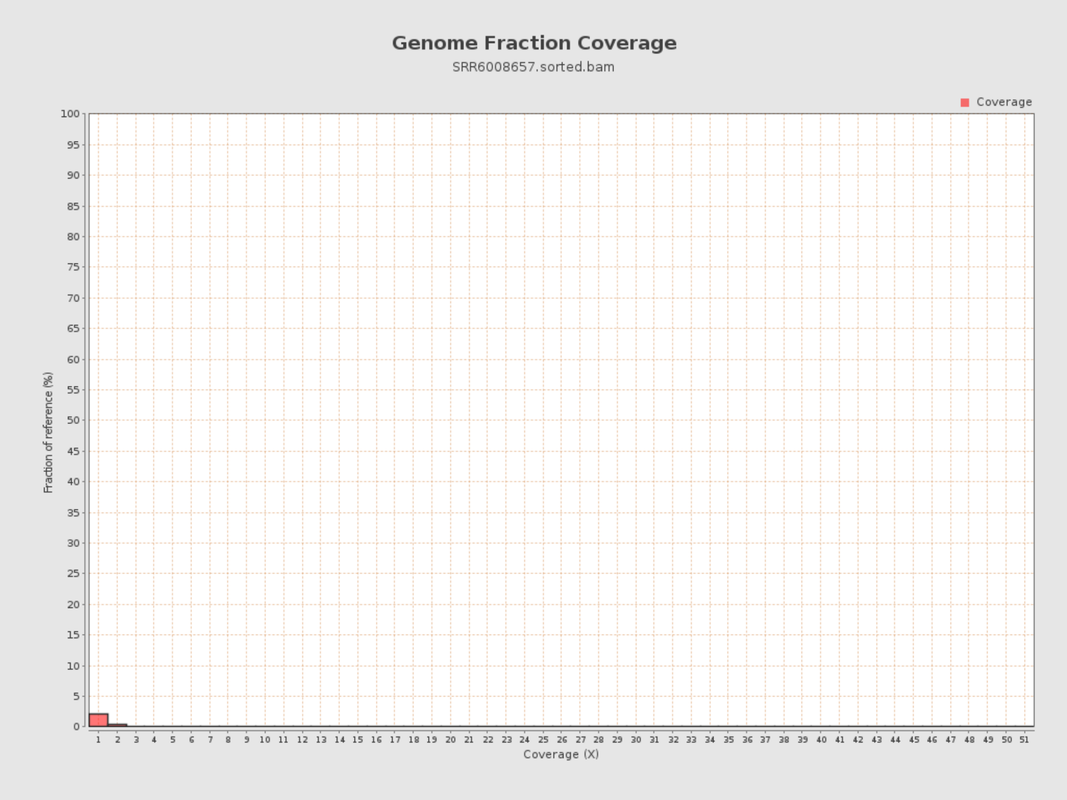
4. Results : Coverage Histogram



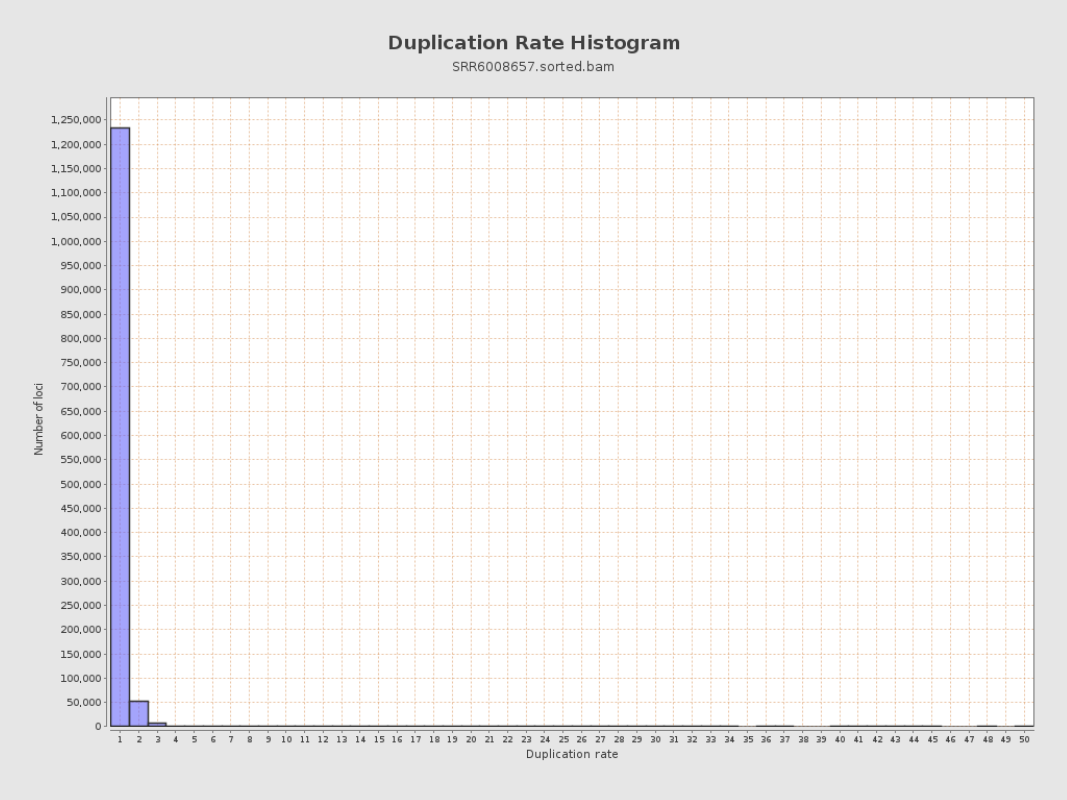
5. Results : Coverage Histogram (0-50X)



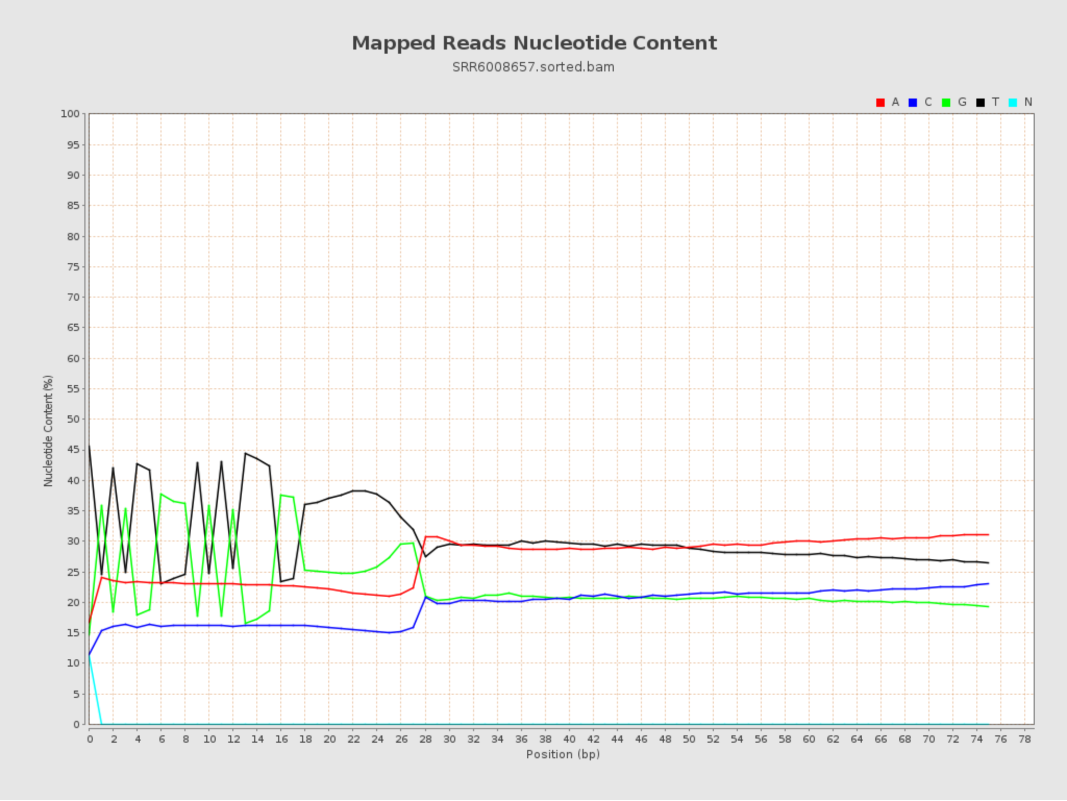
6. Results : Genome Fraction Coverage



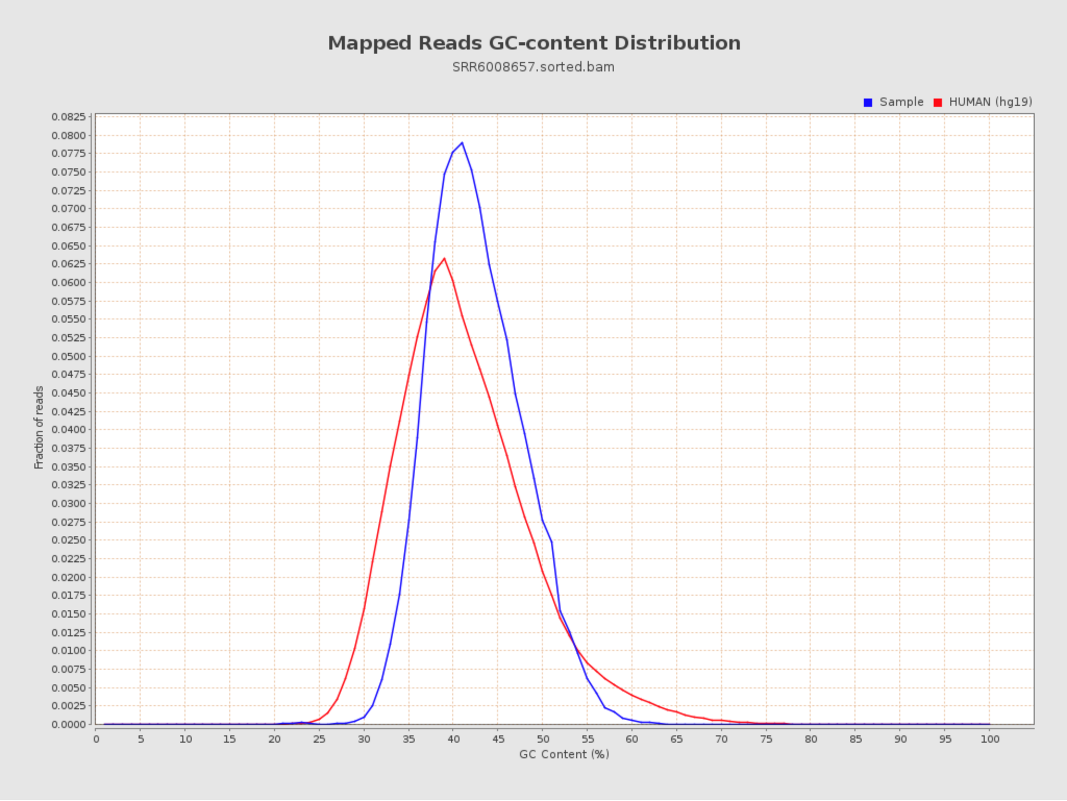
7. Results : Duplication Rate Histogram



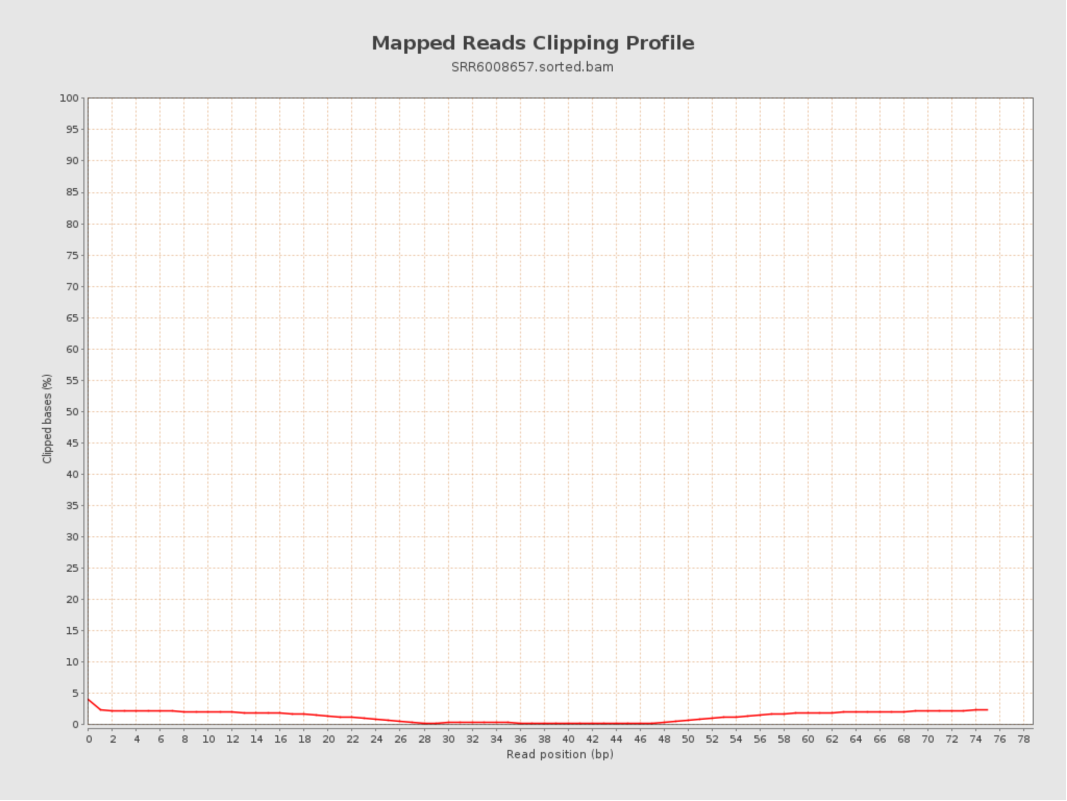
8. Results : Mapped Reads Nucleotide Content



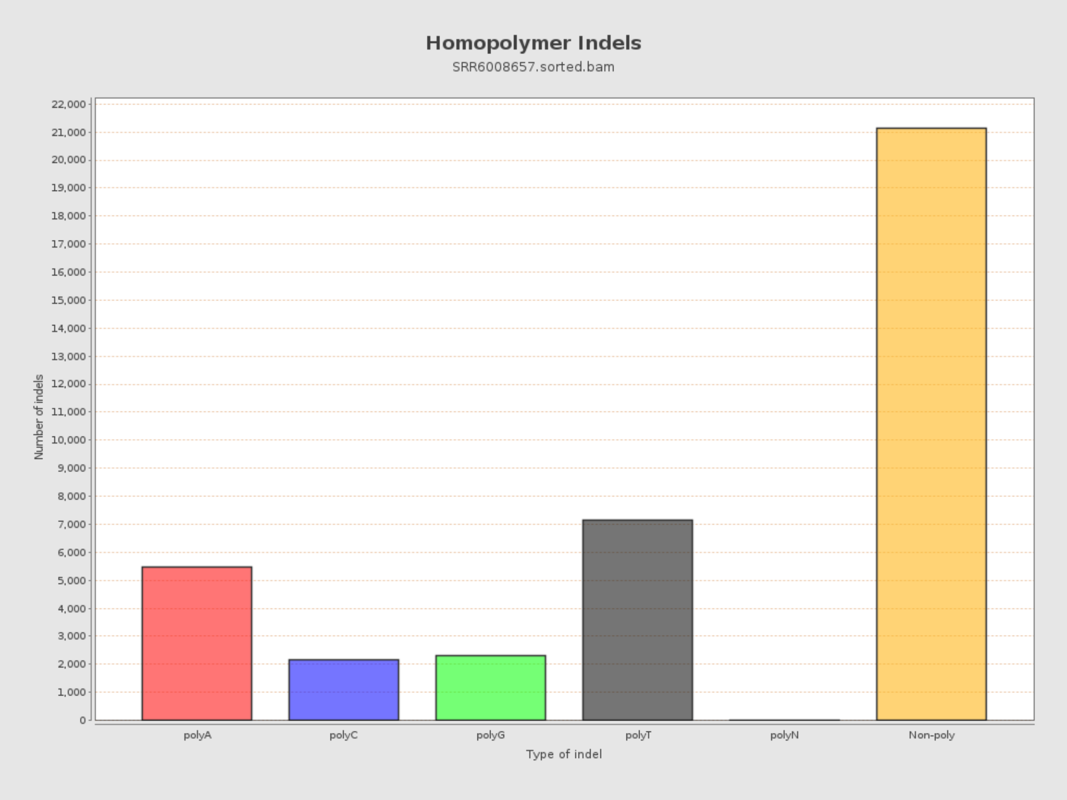
9. Results : Mapped Reads GC-content Distribution



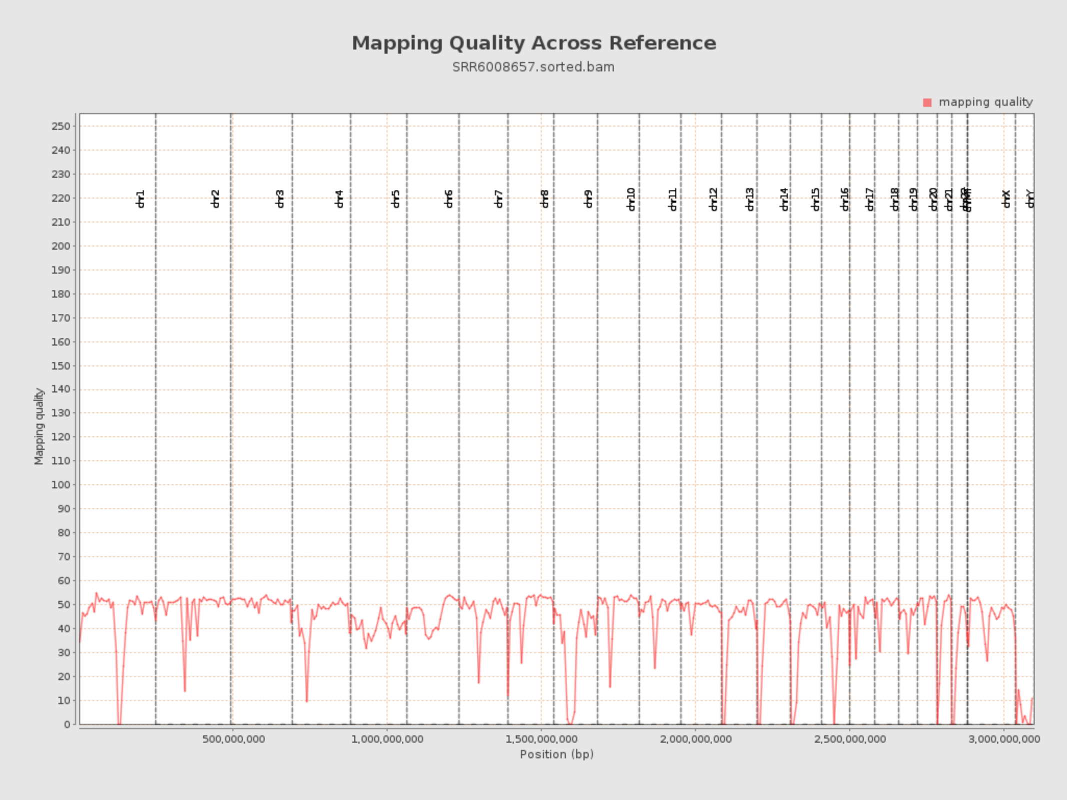
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram