Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:02:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008687.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_SRR6008687 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008687.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:02:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008687.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,027,042
Mapped reads	1,776,620 / 87.65%
Unmapped reads	250,422 / 12.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,748 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	65,813 / 3.25%
Duplication rate	2.46%
Clipped reads	998,204 / 49.24%

2.2. ACGT Content

Number/percentage of A's	29,175,229 / 25.81%
Number/percentage of C's	21,284,024 / 18.83%
Number/percentage of T's	34,789,079 / 30.78%
Number/percentage of G's	27,737,350 / 24.54%
Number/percentage of N's	47,258 / 0.04%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.4118

2.4. Mapping Quality

Mean Mapping Quality	42.16

2.5. Mismatches and indels

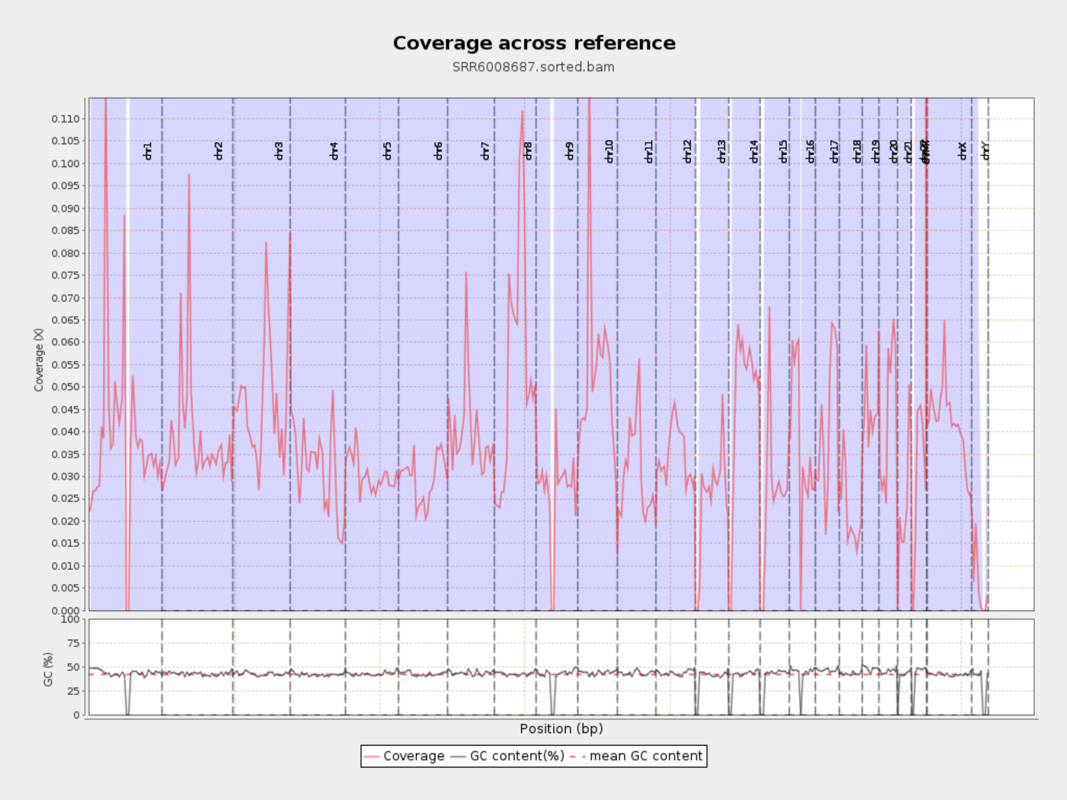
General error rate	0.87%
Mismatches	972,192
Insertions	7,735
Mapped reads with at least one insertion	0.43%
Deletions	40,326
Mapped reads with at least one deletion	2.24%
Homopolymer indels	42.64%

2.6. Chromosome stats

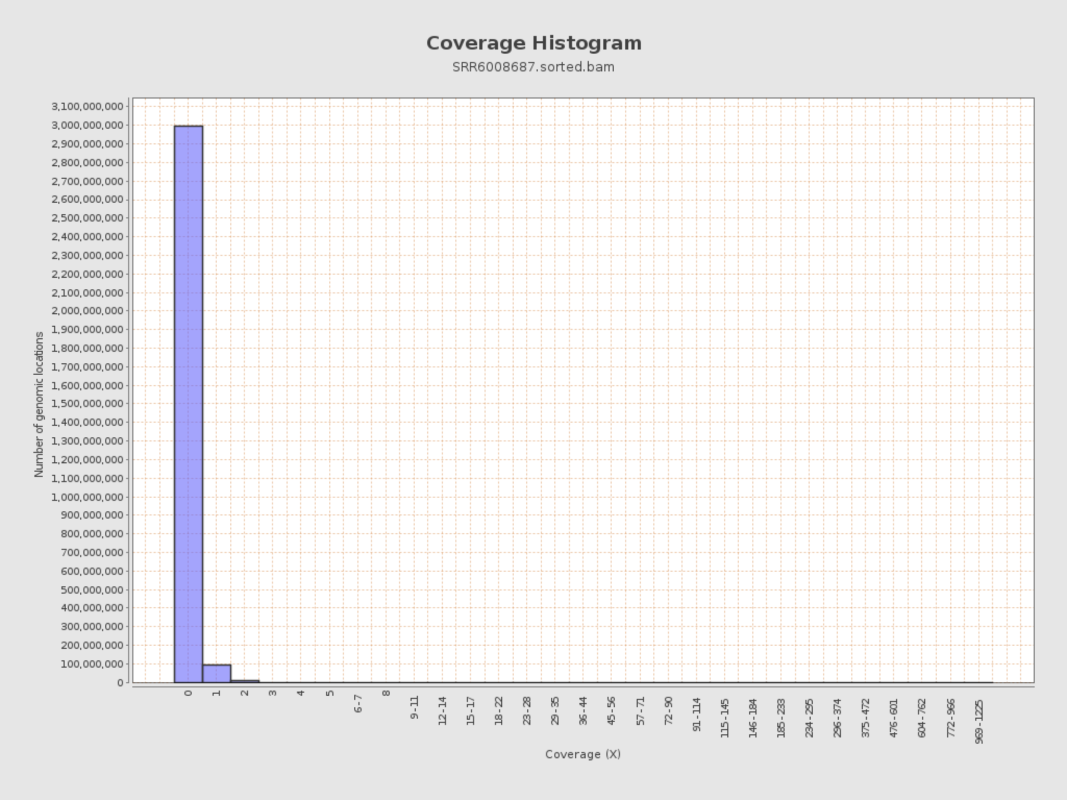
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9573564	0.0384	0.8955
chr2	243199373	9419253	0.0387	0.4646
chr3	198022430	9231574	0.0466	0.2634
chr4	191154276	5966348	0.0312	0.2086
chr5	180915260	5520869	0.0305	0.1922
chr6	171115067	5041675	0.0295	0.2214
chr7	159138663	6401697	0.0402	0.4749

chr8	146364022	8035528	0.0549	0.3528
chr9	141213431	3717800	0.0263	0.3202
chr10	135534747	7216367	0.0532	0.6537
chr11	135006516	4162988	0.0308	0.298
chr12	133851895	4691928	0.0351	0.2077
chr13	115169878	2881299	0.025	0.1694
chr14	107349540	5032574	0.0469	0.2444
chr15	102531392	2718411	0.0265	0.182
chr16	90354753	3369381	0.0373	0.2635
chr17	81195210	3369312	0.0415	0.2746
chr18	78077248	1720919	0.022	0.5586
chr19	59128983	2644551	0.0447	0.5803
chr20	63025520	2751580	0.0437	0.2352
chr21	48129895	1163800	0.0242	0.1855
chr22	51304566	1444803	0.0282	0.1824
chrMT	16571	130691	7.8867	5.1079
chrX	155270560	6541463	0.0421	0.2685
chrY	59373566	354961	0.006	0.1615

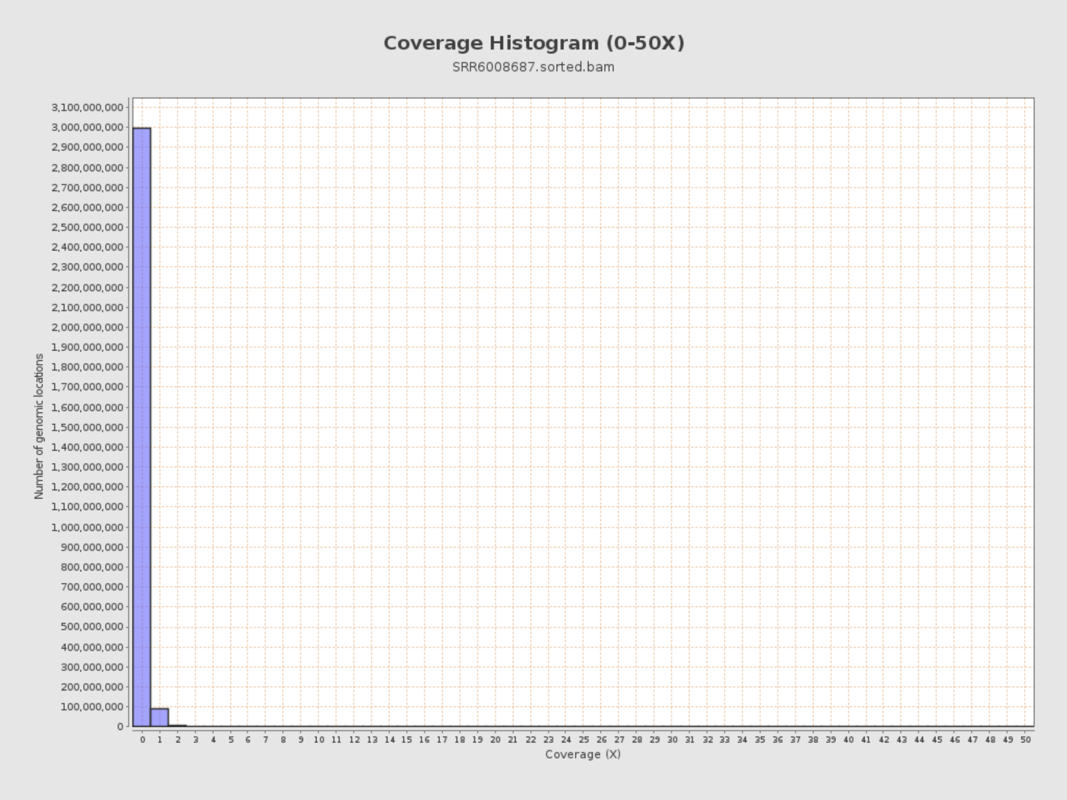
3. Results : Coverage across reference



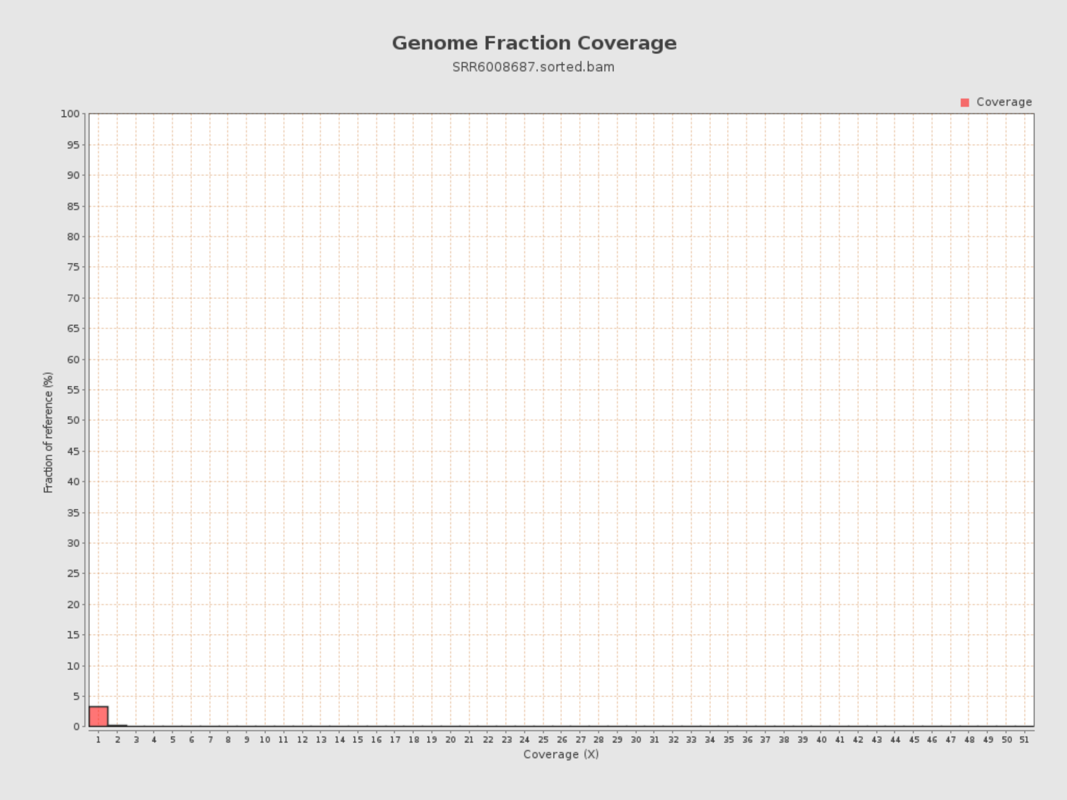
4. Results : Coverage Histogram



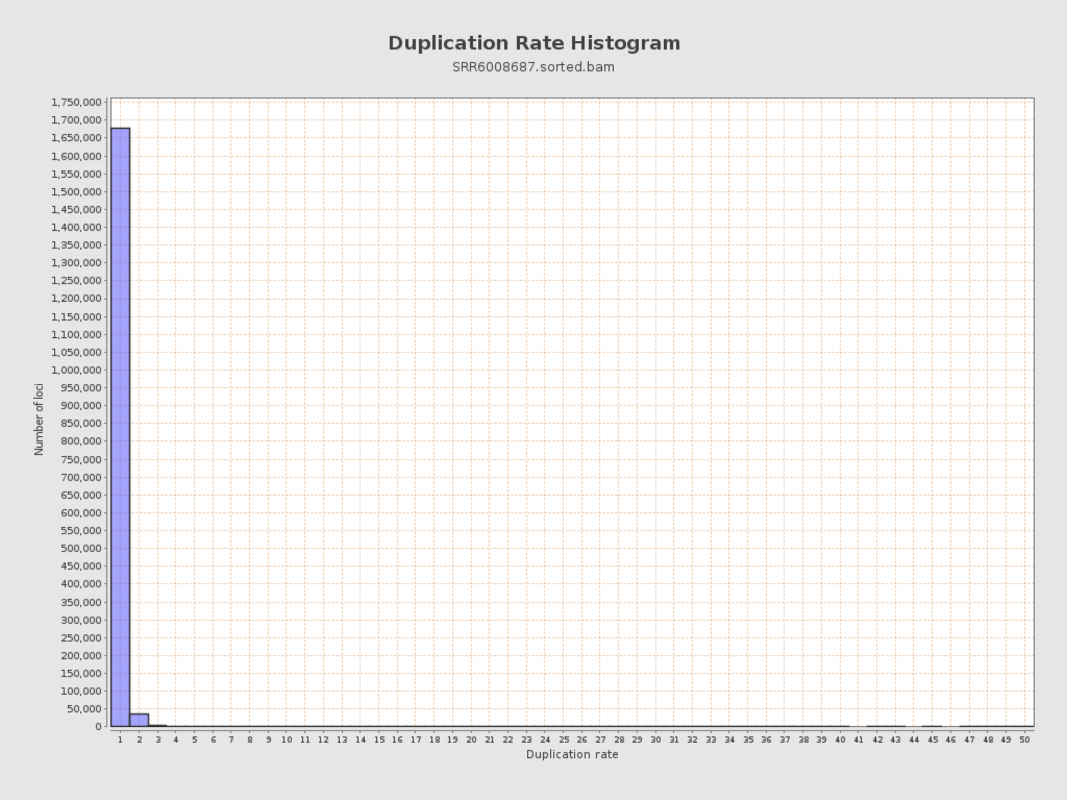
5. Results : Coverage Histogram (0-50X)



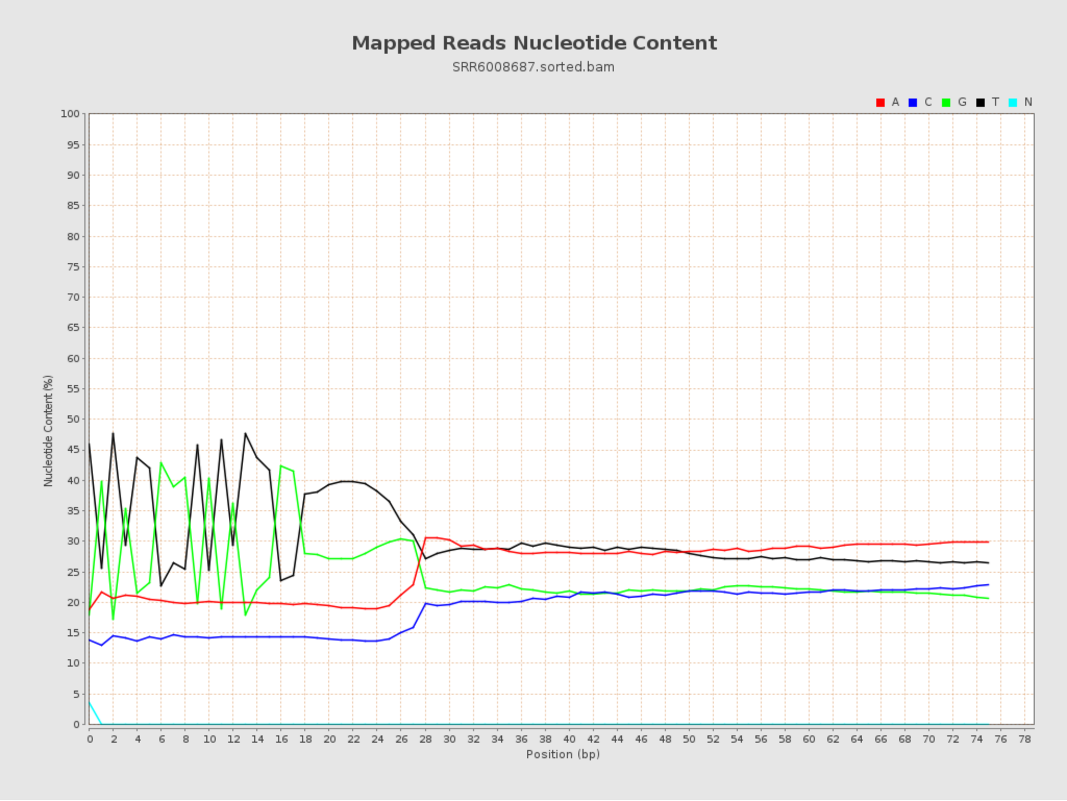
6. Results : Genome Fraction Coverage



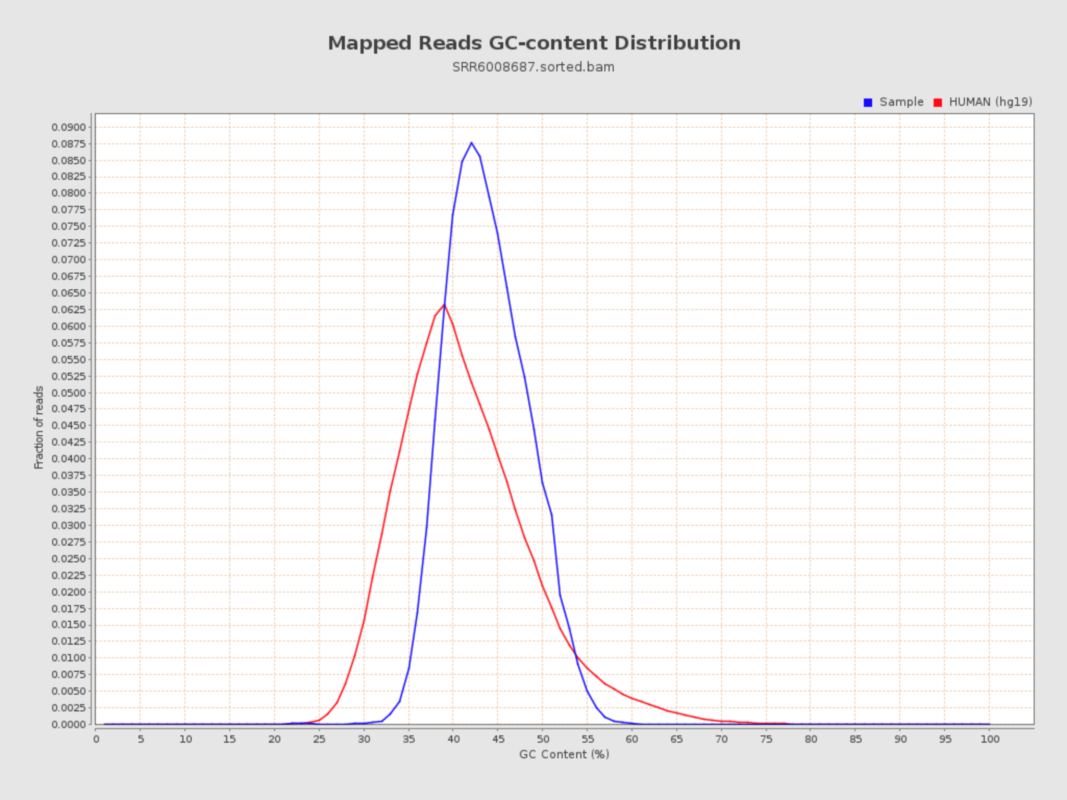
7. Results : Duplication Rate Histogram



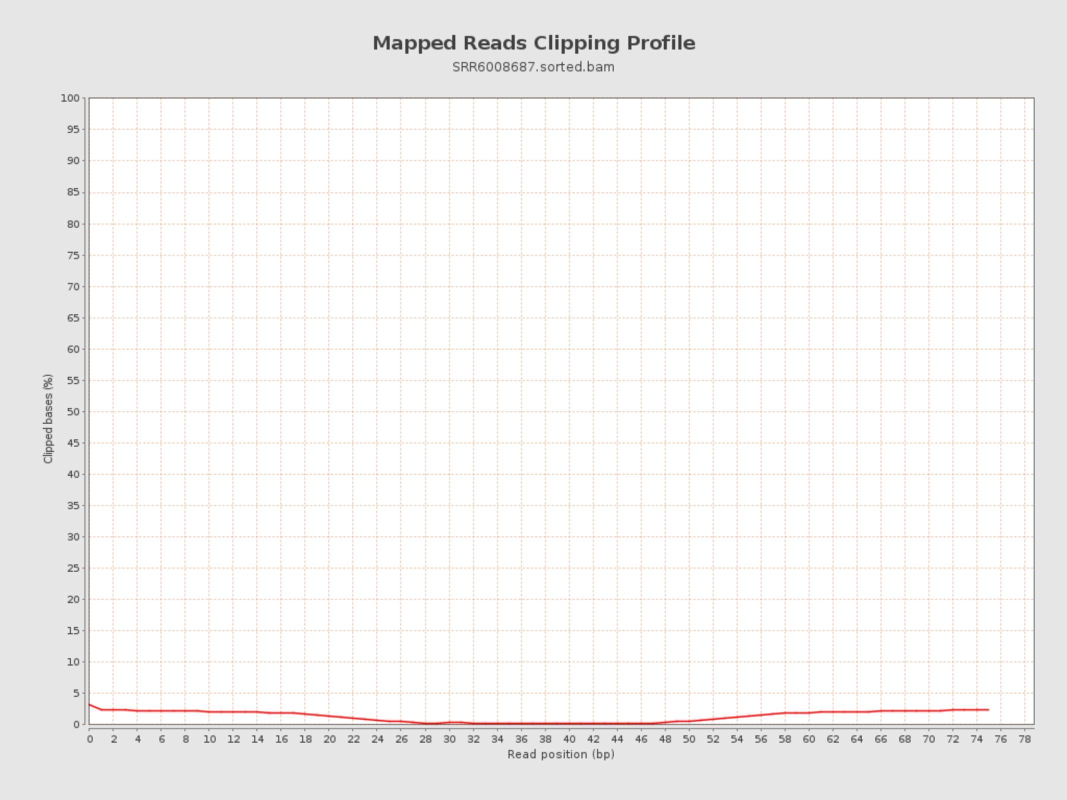
8. Results : Mapped Reads Nucleotide Content



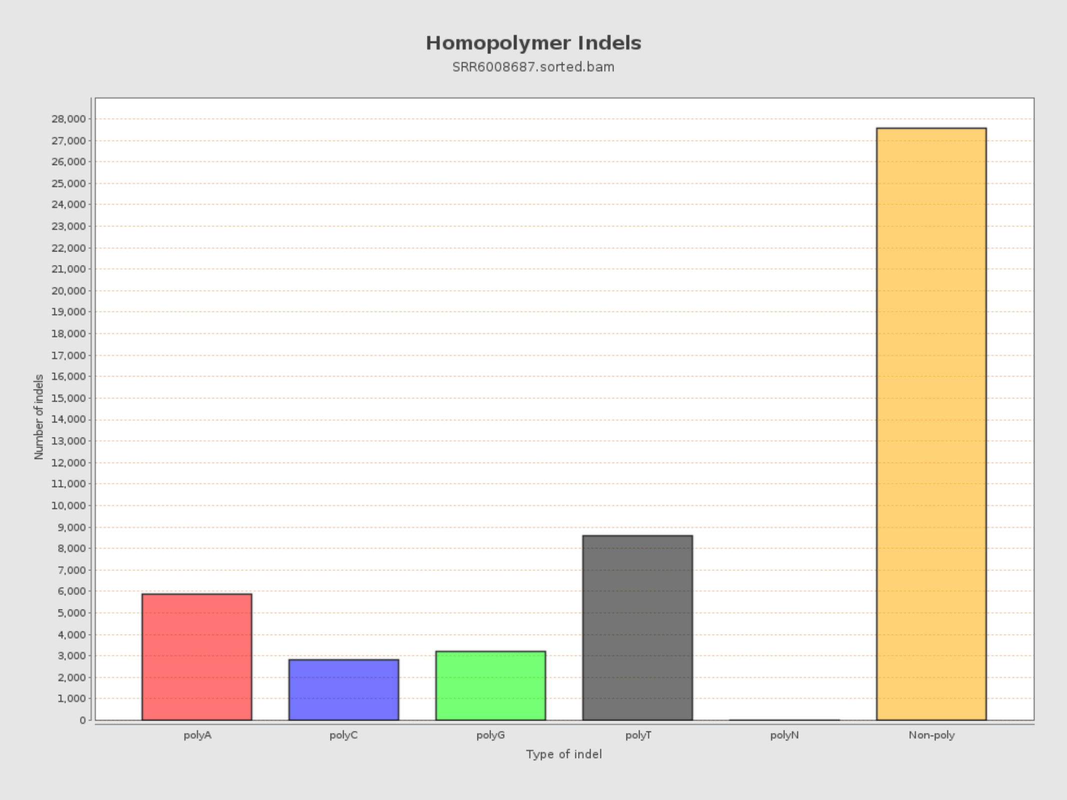
9. Results : Mapped Reads GC-content Distribution



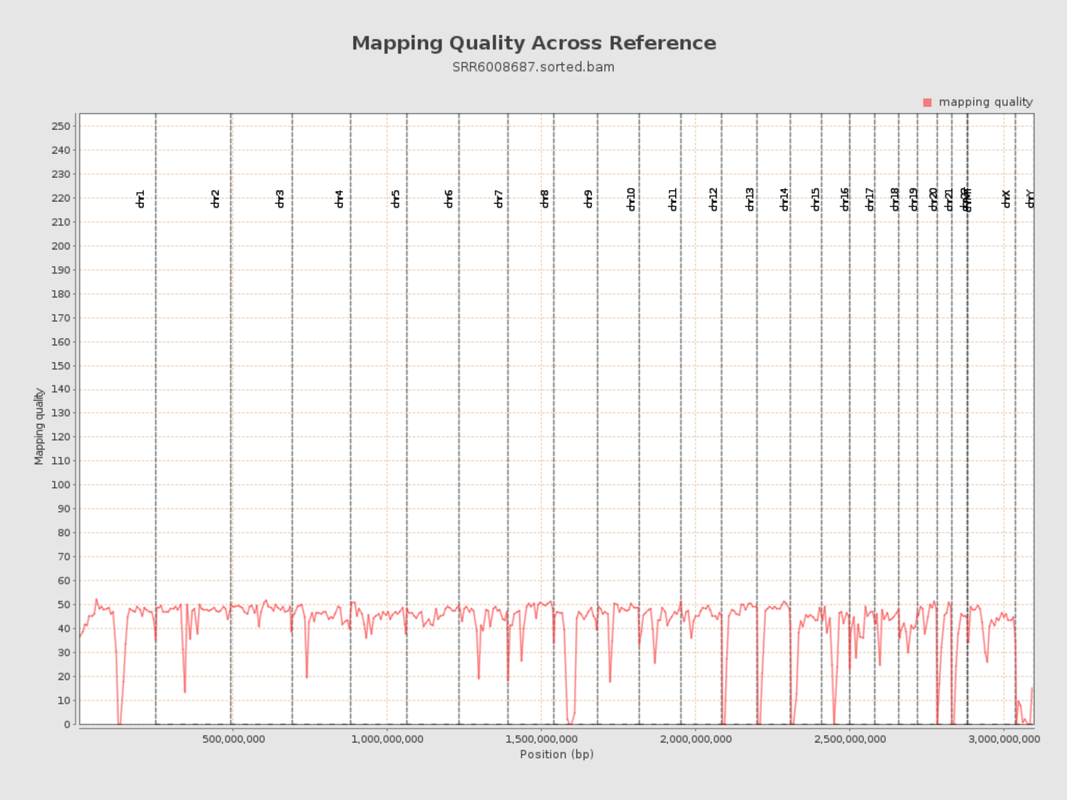
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram