Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:39:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068077.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_SRR6068077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:39:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,446,800
Mapped reads	1,779,897 / 72.74%
Unmapped reads	666,903 / 27.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,770 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	311,866 / 12.75%
Duplication rate	13.16%
Clipped reads	1,149,211 / 46.97%

2.2. ACGT Content

Number/percentage of A's	28,100,595 / 25.58%
Number/percentage of C's	20,145,192 / 18.34%
Number/percentage of T's	34,940,639 / 31.81%
Number/percentage of G's	26,647,938 / 24.26%
Number/percentage of N's	2,000 / 0%
GC Percentage	42.6%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.4062

2.4. Mapping Quality

Mean Mapping Quality	42.9

2.5. Mismatches and indels

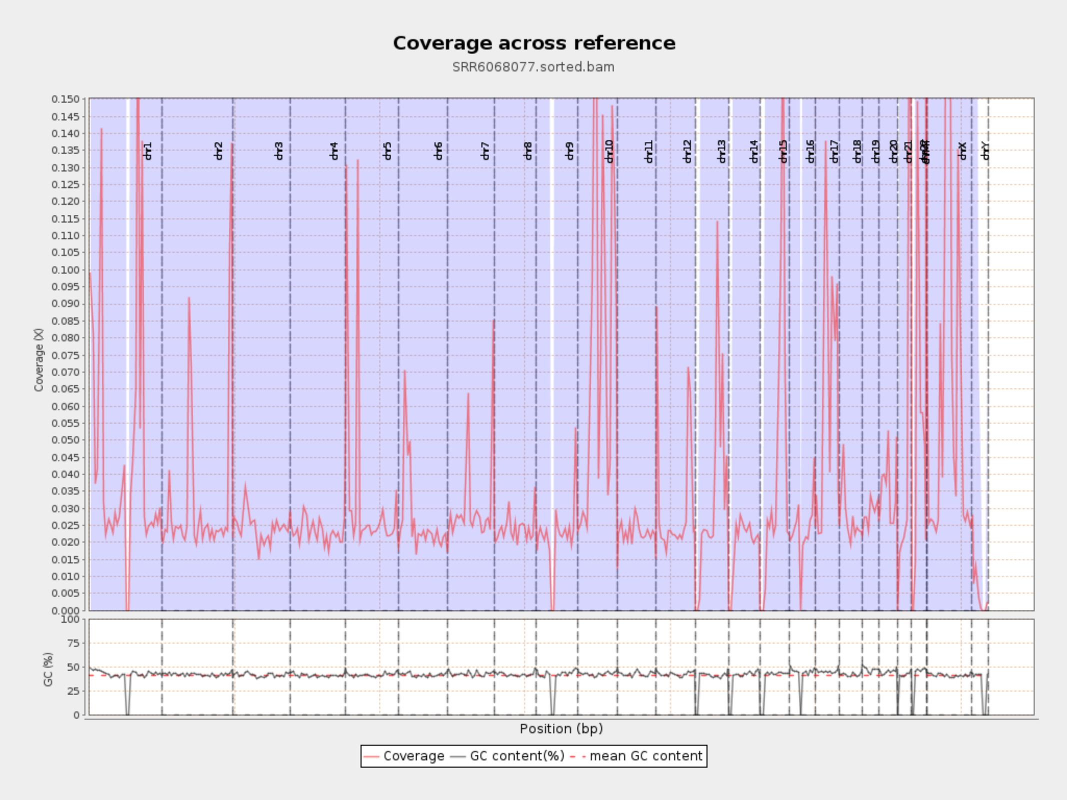
General error rate	0.83%
Mismatches	901,800
Insertions	7,719
Mapped reads with at least one insertion	0.43%
Deletions	27,812
Mapped reads with at least one deletion	1.55%
Homopolymer indels	45.16%

2.6. Chromosome stats

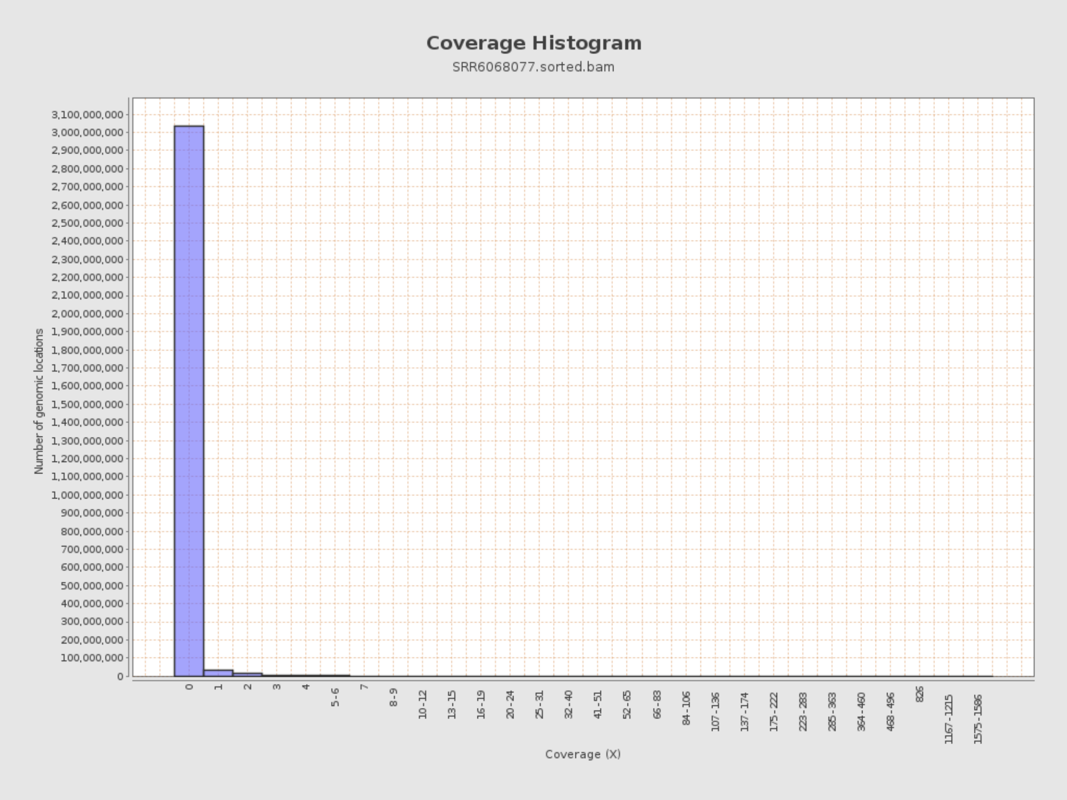
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11807716	0.0474	0.5251
chr2	243199373	7894321	0.0325	0.7516
chr3	198022430	4819588	0.0243	0.262
chr4	191154276	4396438	0.023	0.2844
chr5	180915260	6179722	0.0342	0.3145
chr6	171115067	4539069	0.0265	0.3174
chr7	159138663	5023579	0.0316	0.3693

chr8	146364022	3519202	0.024	0.3234
chr9	141213431	3093611	0.0219	0.3012
chr10	135534747	10795803	0.0797	0.4948
chr11	135006516	3106640	0.023	0.2663
chr12	133851895	4180133	0.0312	0.3014
chr13	115169878	3907943	0.0339	0.3233
chr14	107349540	2095813	0.0195	0.2749
chr15	102531392	4576911	0.0446	0.3997
chr16	90354753	2160223	0.0239	0.2659
chr17	81195210	5583185	0.0688	0.4473
chr18	78077248	2182454	0.028	0.3589
chr19	59128983	1701018	0.0288	0.3991
chr20	63025520	2280374	0.0362	0.3274
chr21	48129895	2703363	0.0562	0.4172
chr22	51304566	2580715	0.0503	0.3828
chrMT	16571	51166	3.0877	3.0557
chrX	155270560	10341042	0.0666	0.4555
chrY	59373566	359956	0.0061	0.1332

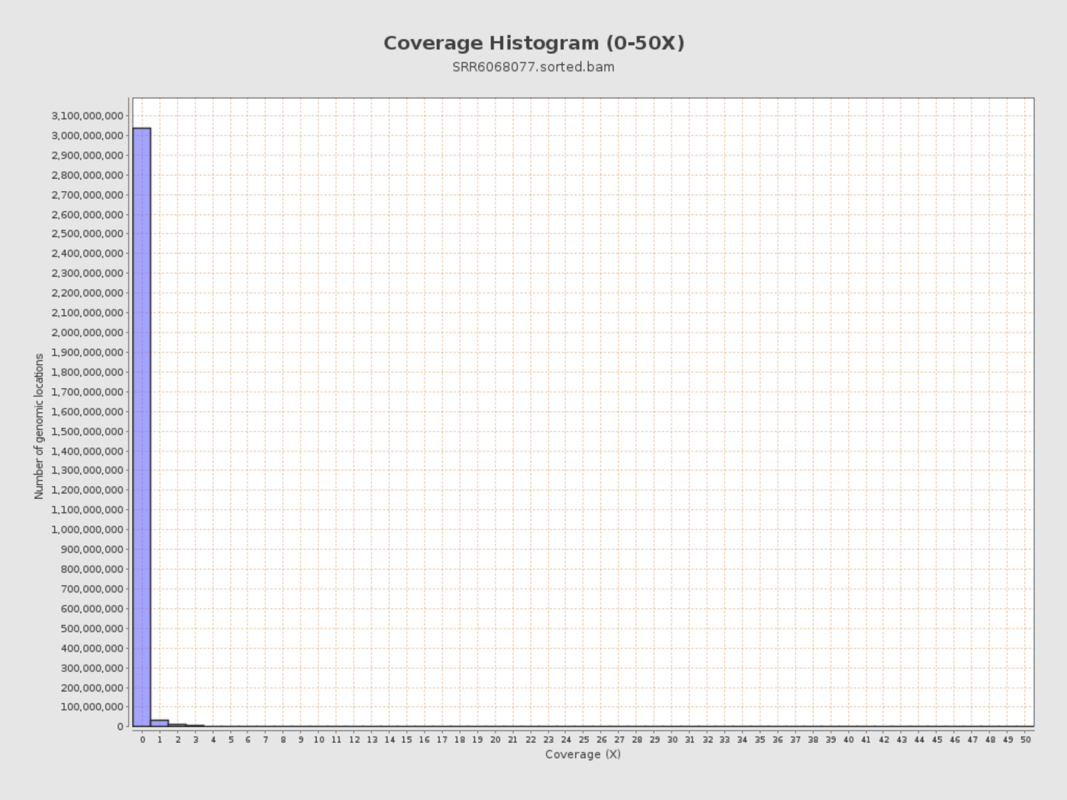
3. Results : Coverage across reference



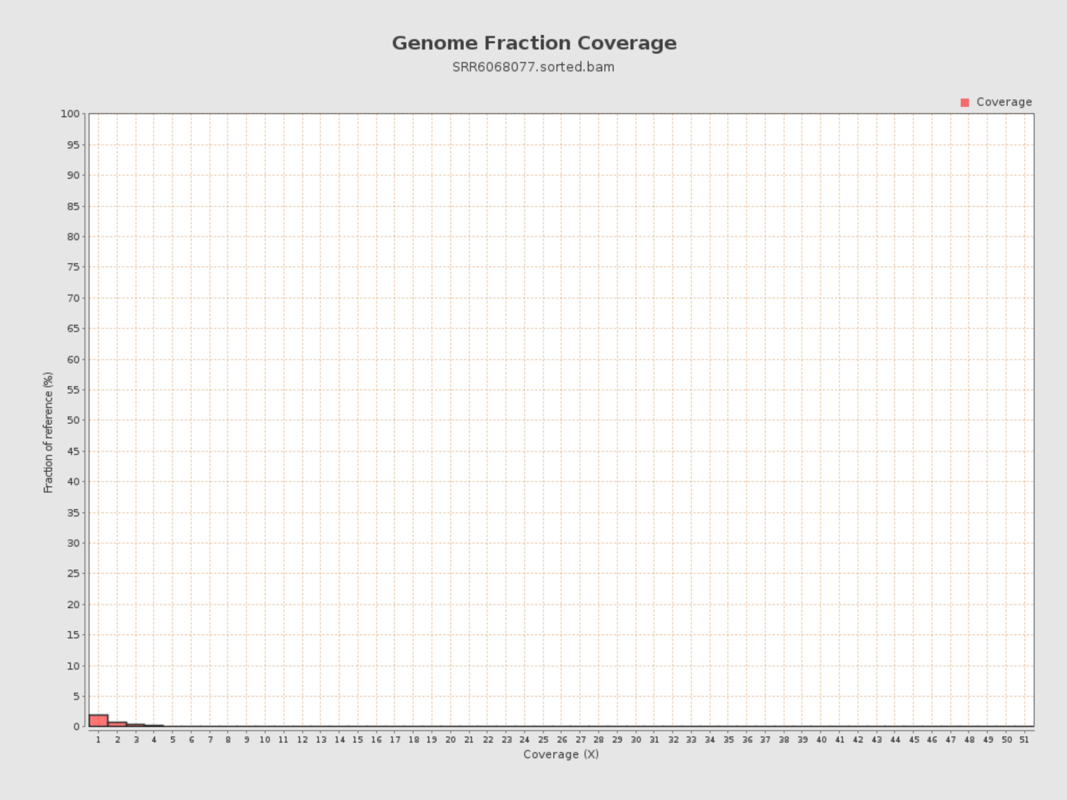
4. Results : Coverage Histogram



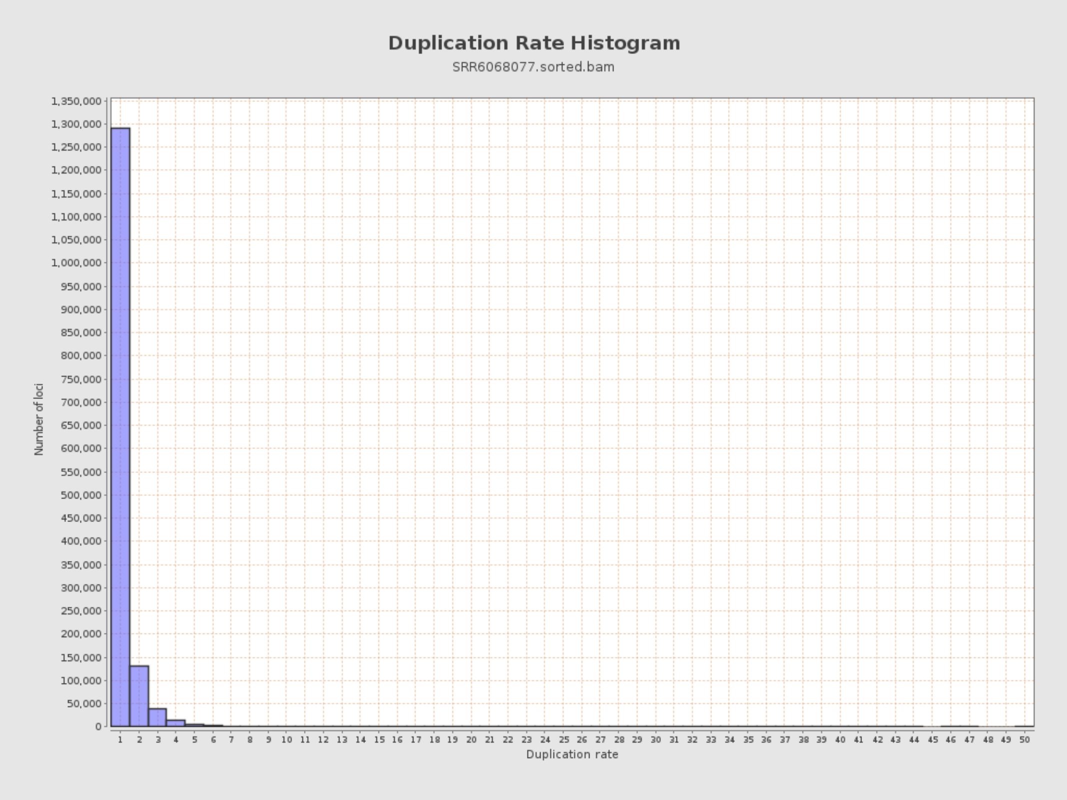
5. Results : Coverage Histogram (0-50X)



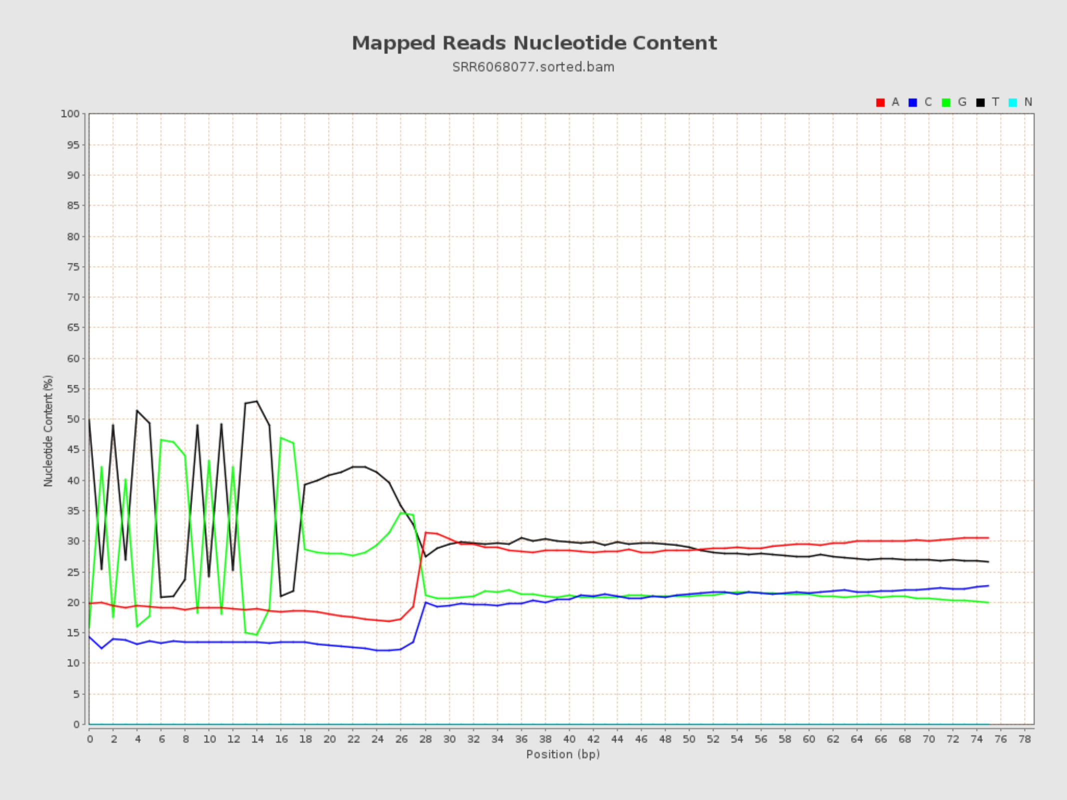
6. Results : Genome Fraction Coverage



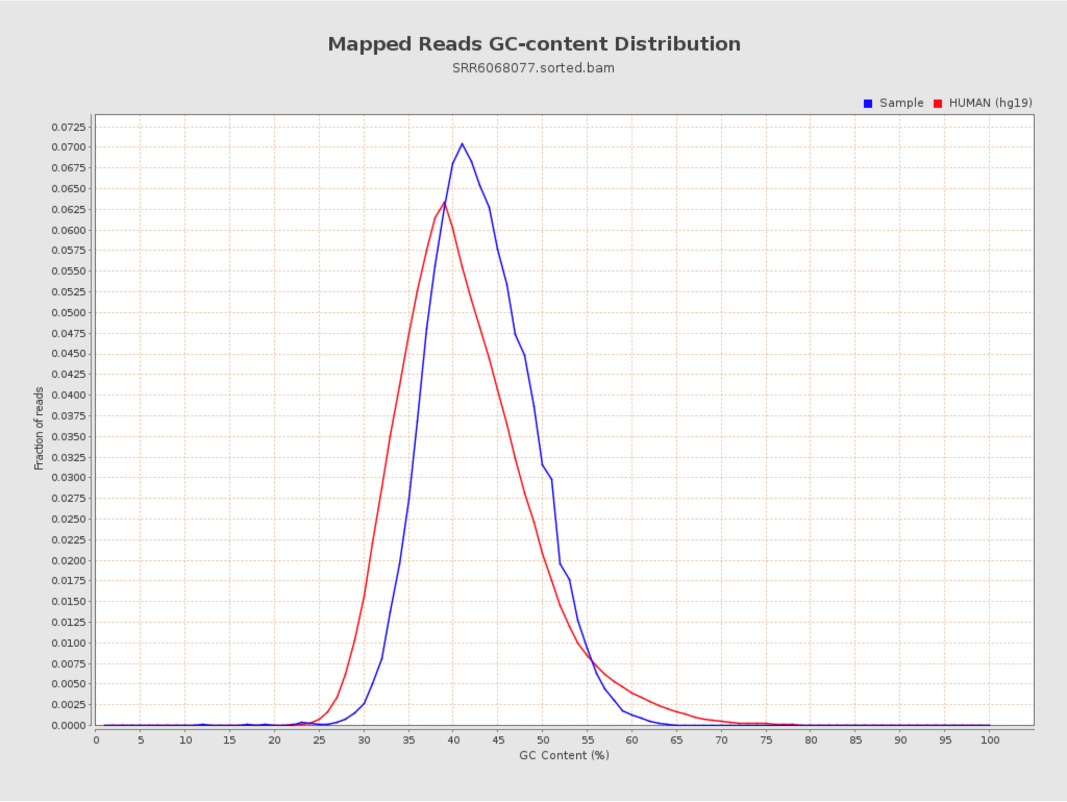
7. Results : Duplication Rate Histogram



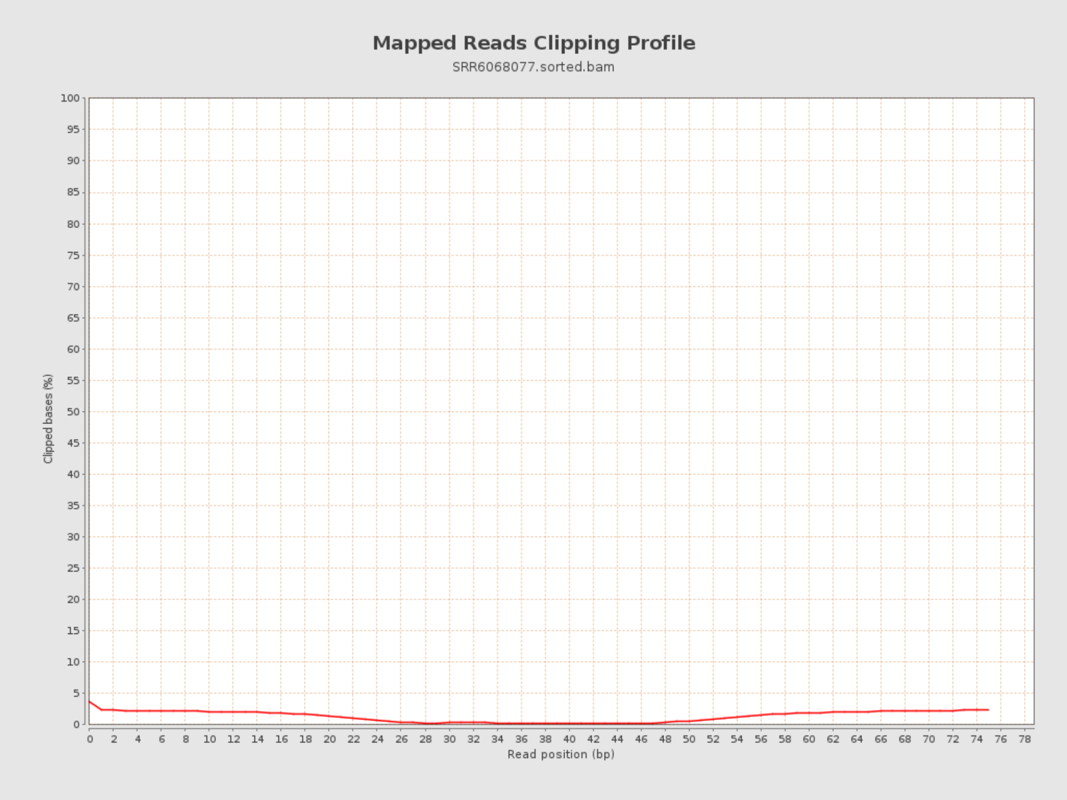
8. Results : Mapped Reads Nucleotide Content



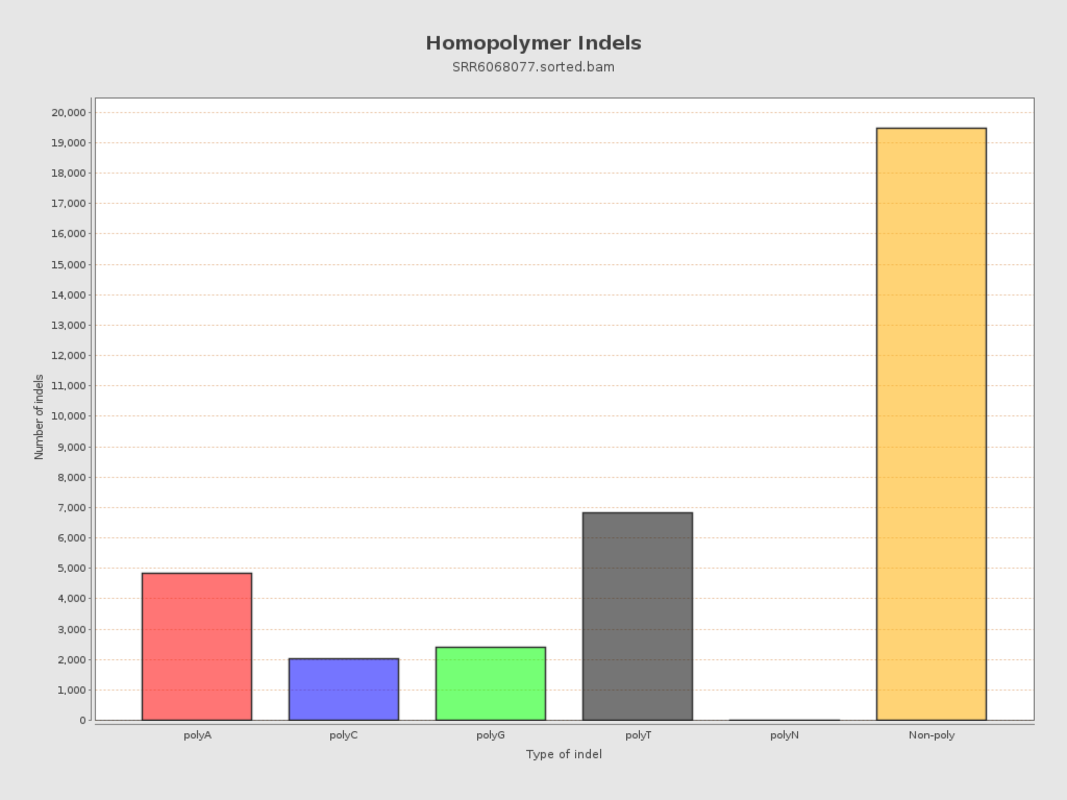
9. Results : Mapped Reads GC-content Distribution



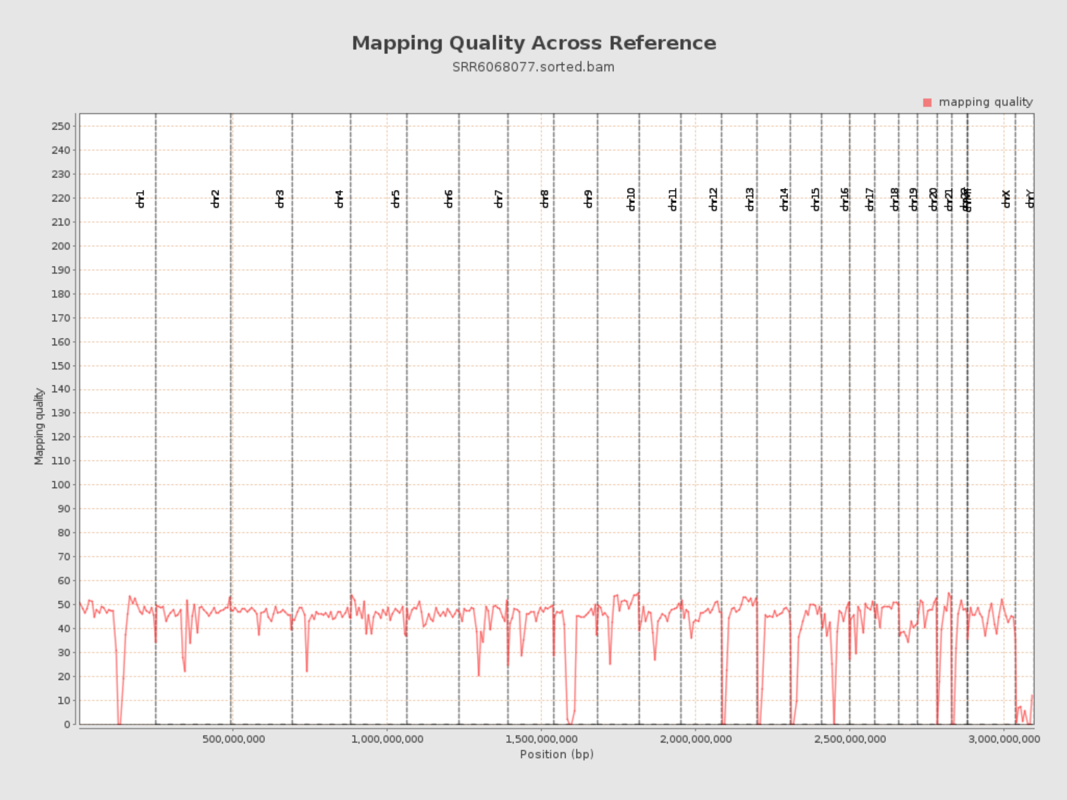
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram