Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:40:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068126.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_SRR6068126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:40:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,075,431
Mapped reads	3,816,444 / 93.65%
Unmapped reads	258,987 / 6.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,010 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	443,428 / 10.88%
Duplication rate	9.3%
Clipped reads	2,016,139 / 49.47%

2.2. ACGT Content

Number/percentage of A's	64,181,927 / 26.05%
Number/percentage of C's	44,480,803 / 18.05%
Number/percentage of T's	79,752,642 / 32.36%
Number/percentage of G's	57,981,782 / 23.53%
Number/percentage of N's	27,867 / 0.01%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0796

Standard Deviation	1.0632

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Mismatches and indels

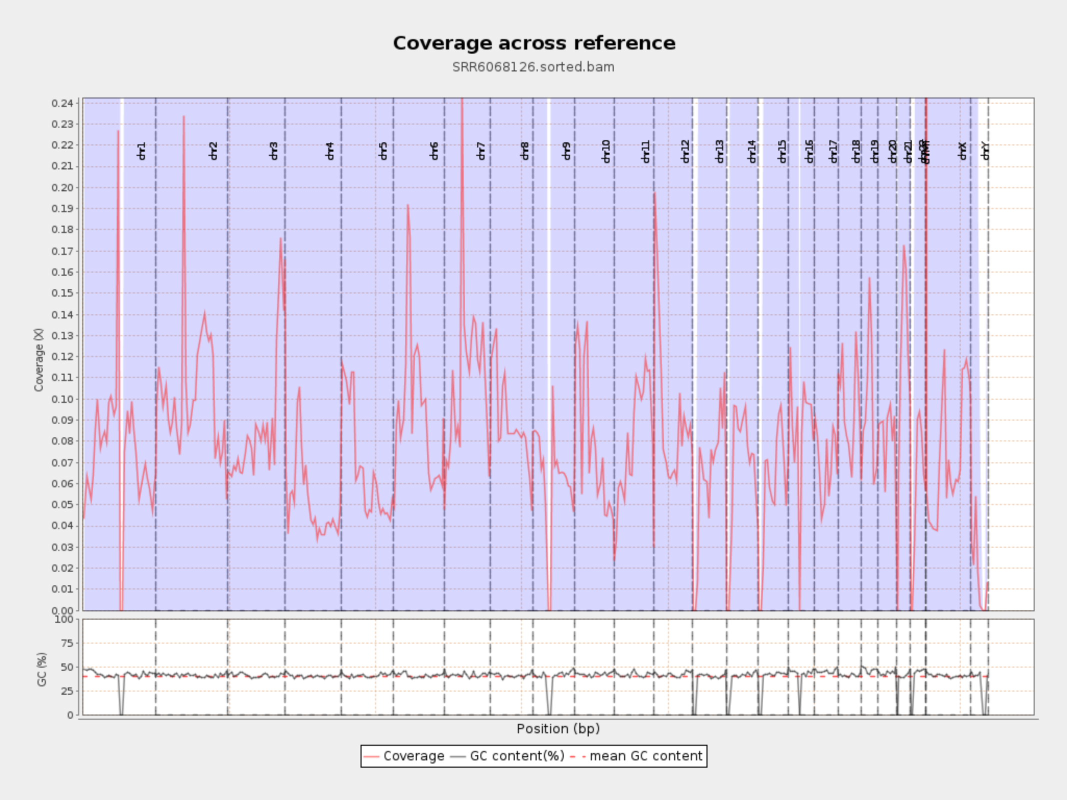
General error rate	0.61%
Mismatches	1,478,129
Insertions	17,395
Mapped reads with at least one insertion	0.45%
Deletions	66,010
Mapped reads with at least one deletion	1.71%
Homopolymer indels	45.03%

2.6. Chromosome stats

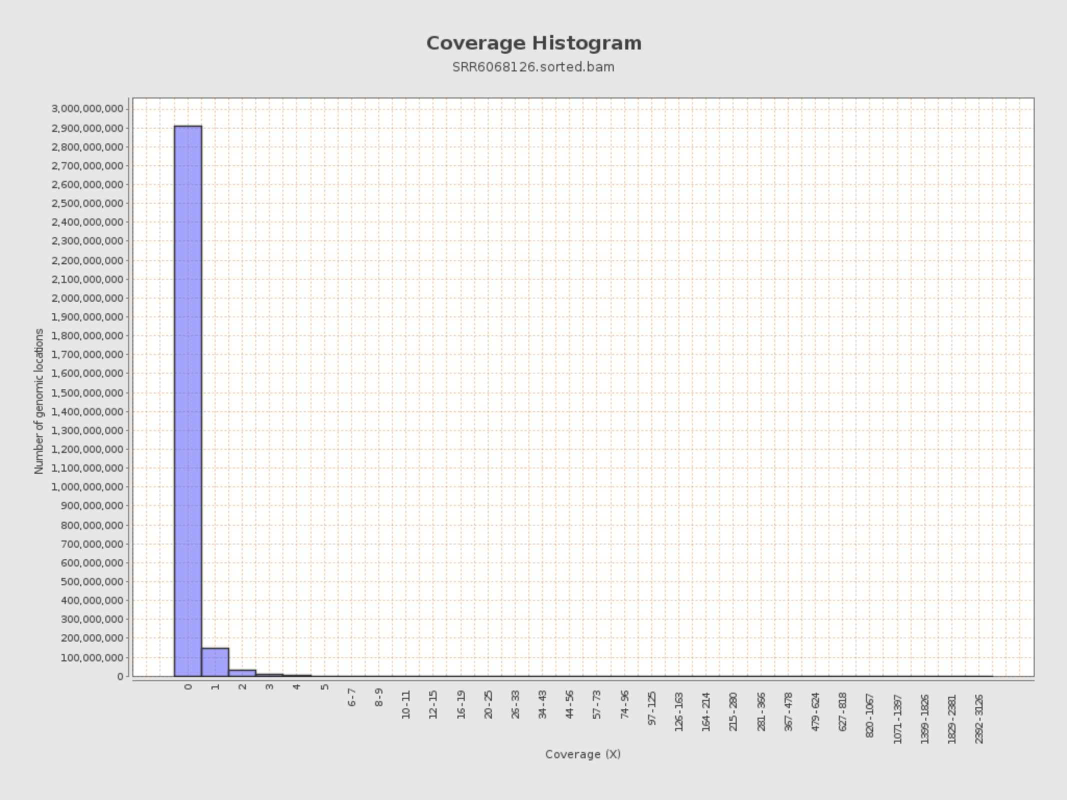
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18601700	0.0746	2.4954
chr2	243199373	25399395	0.1044	1.2535
chr3	198022430	17313346	0.0874	0.3854
chr4	191154276	9853605	0.0515	0.3418
chr5	180915260	12270993	0.0678	0.3493
chr6	171115067	16180369	0.0946	0.5299
chr7	159138663	17518819	0.1101	1.7932

chr8	146364022	13078367	0.0894	1.1848
chr9	141213431	8718926	0.0617	0.8135
chr10	135534747	10789305	0.0796	0.6654
chr11	135006516	11002421	0.0815	0.5857
chr12	133851895	12652534	0.0945	0.4227
chr13	115169878	7368712	0.064	0.3397
chr14	107349540	7334299	0.0683	0.4141
chr15	102531392	5719495	0.0558	0.3805
chr16	90354753	7676069	0.085	0.4467
chr17	81195210	5667925	0.0698	0.3778
chr18	78077248	7603141	0.0974	1.6141
chr19	59128983	5744700	0.0972	1.5908
chr20	63025520	5292881	0.084	0.4143
chr21	48129895	5445596	0.1131	0.4621
chr22	51304566	2913426	0.0568	0.2996
chrMT	16571	155090	9.3591	6.0366
chrX	155270560	11229660	0.0723	0.4626
chrY	59373566	1011693	0.017	0.432

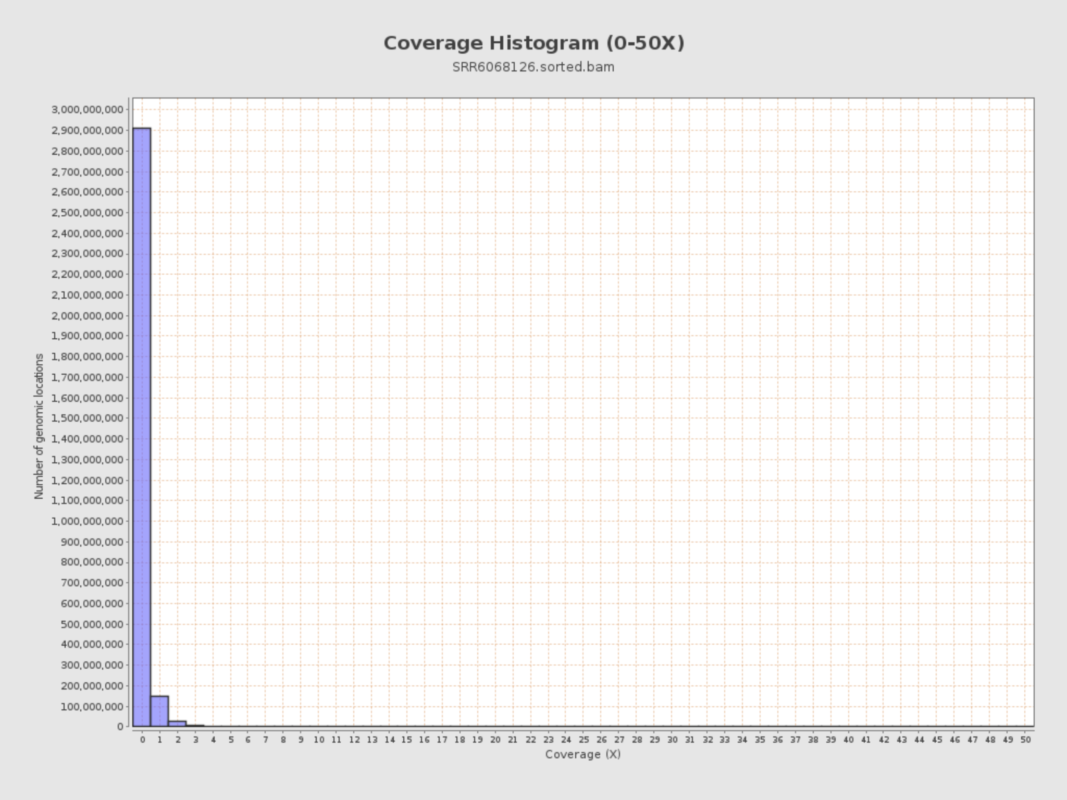
3. Results : Coverage across reference



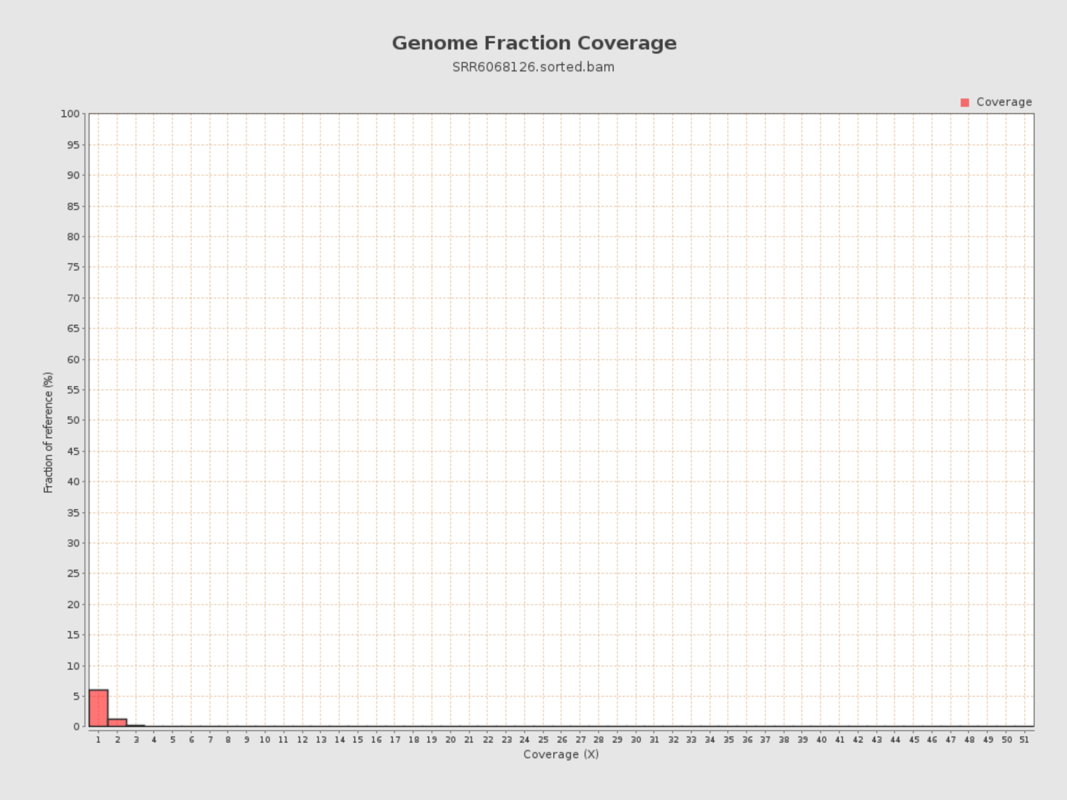
4. Results : Coverage Histogram



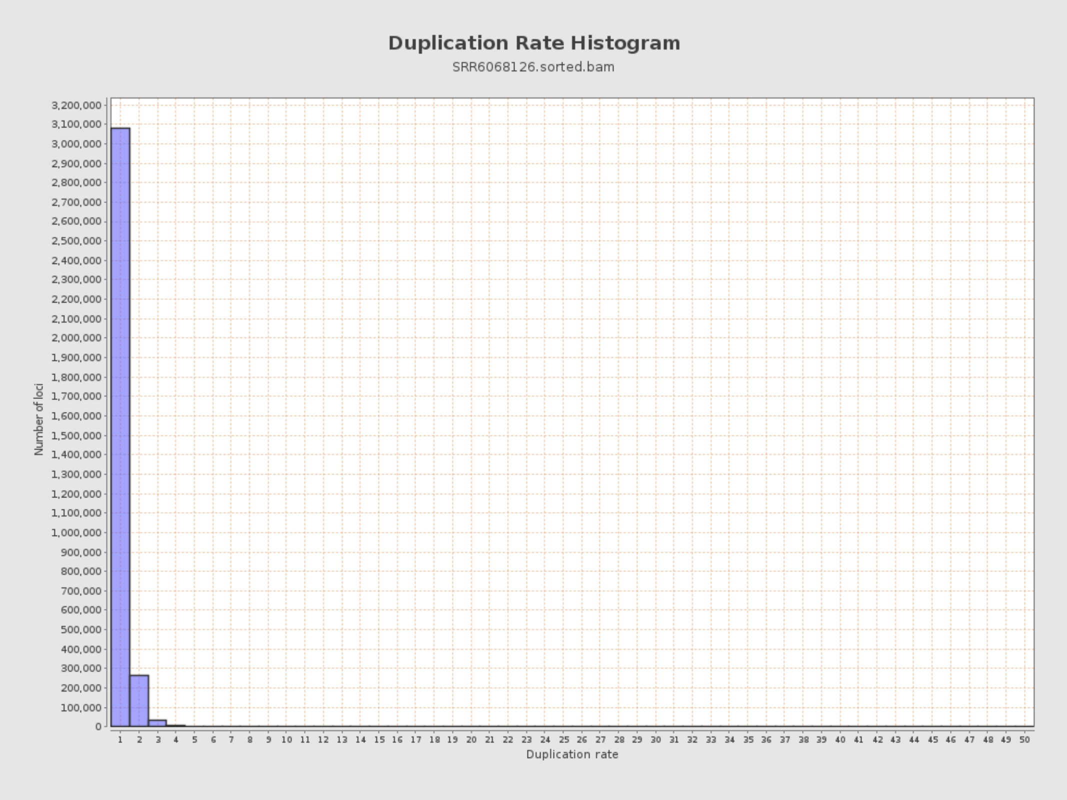
5. Results : Coverage Histogram (0-50X)



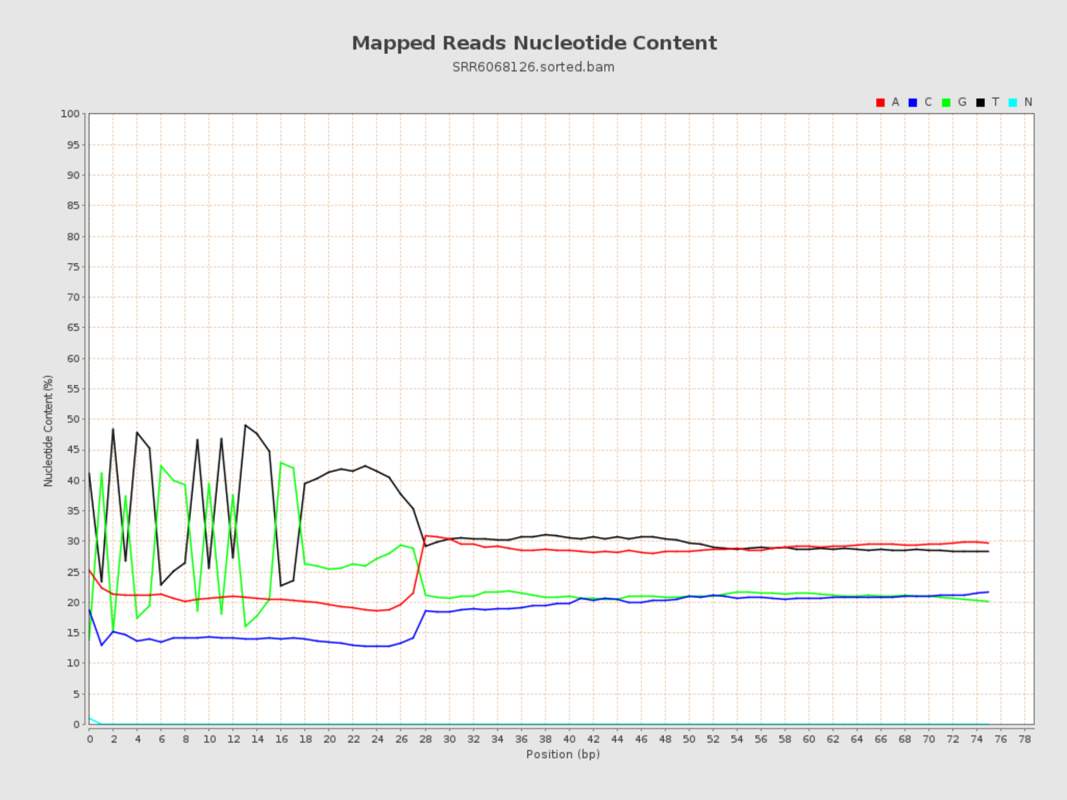
6. Results : Genome Fraction Coverage



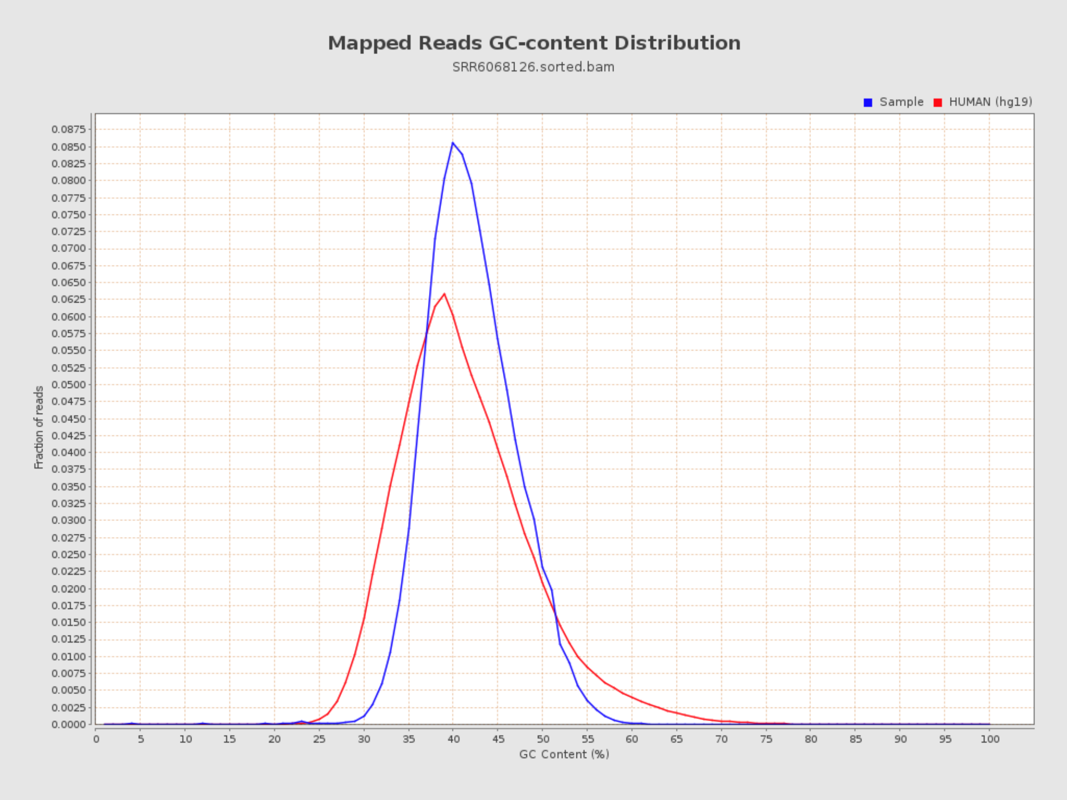
7. Results : Duplication Rate Histogram



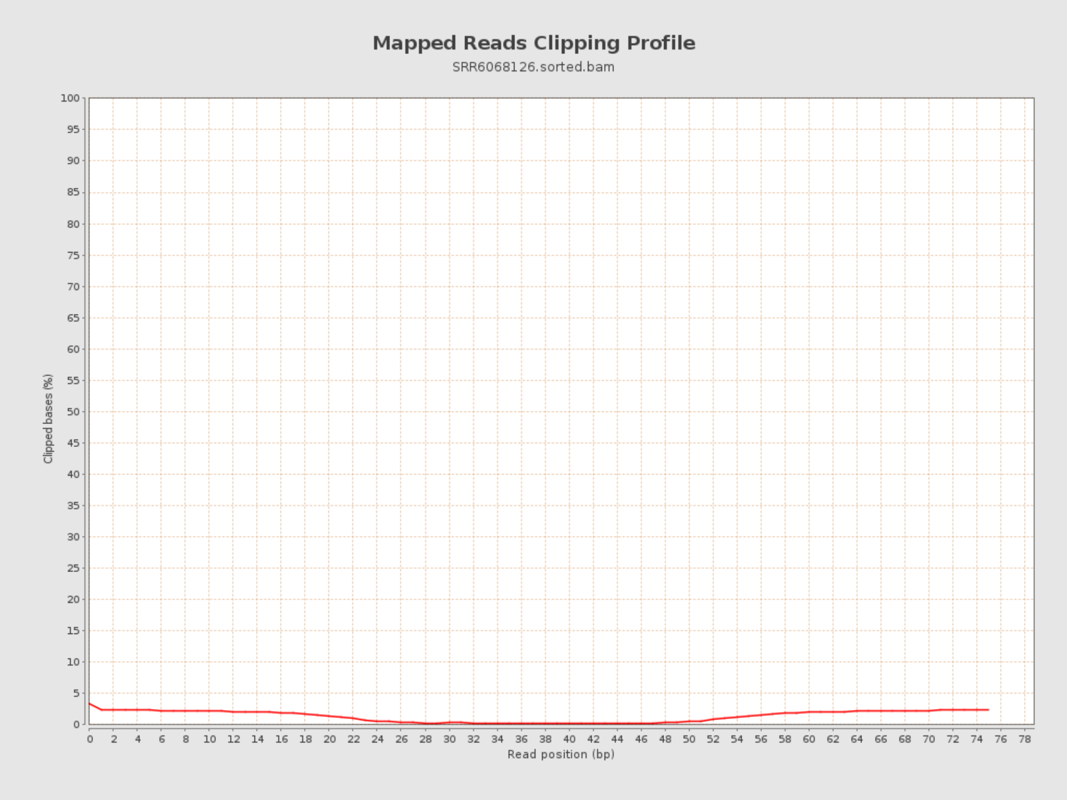
8. Results : Mapped Reads Nucleotide Content



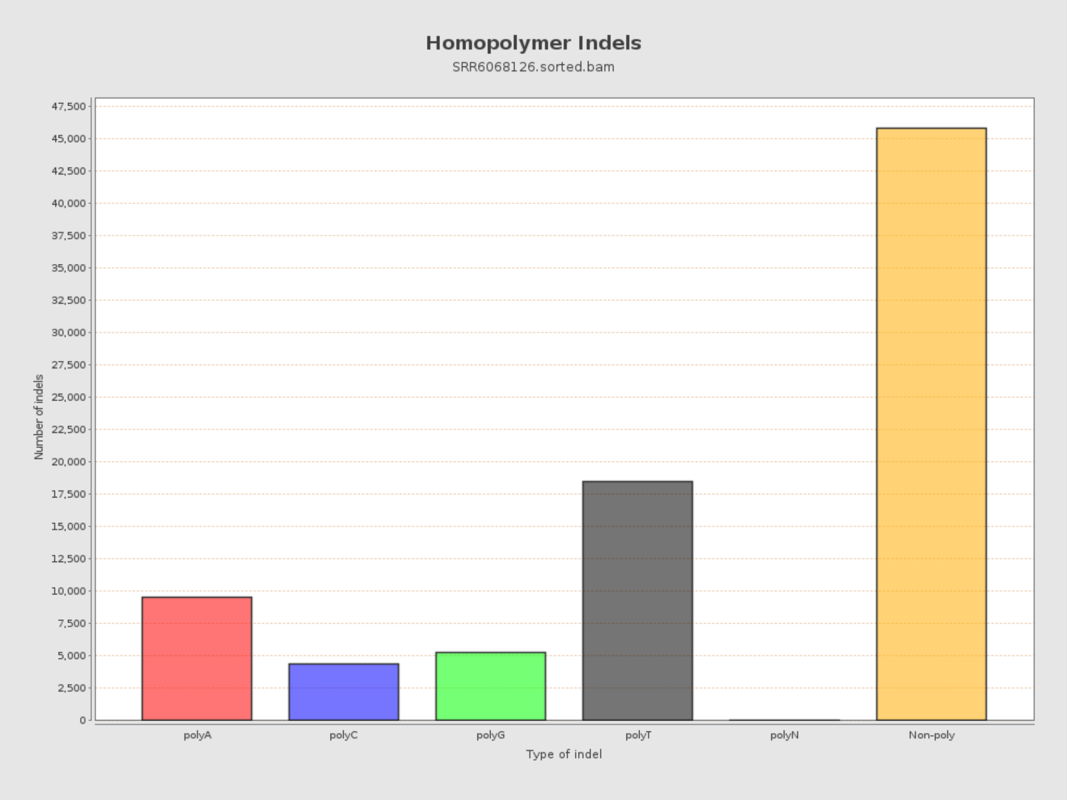
9. Results : Mapped Reads GC-content Distribution



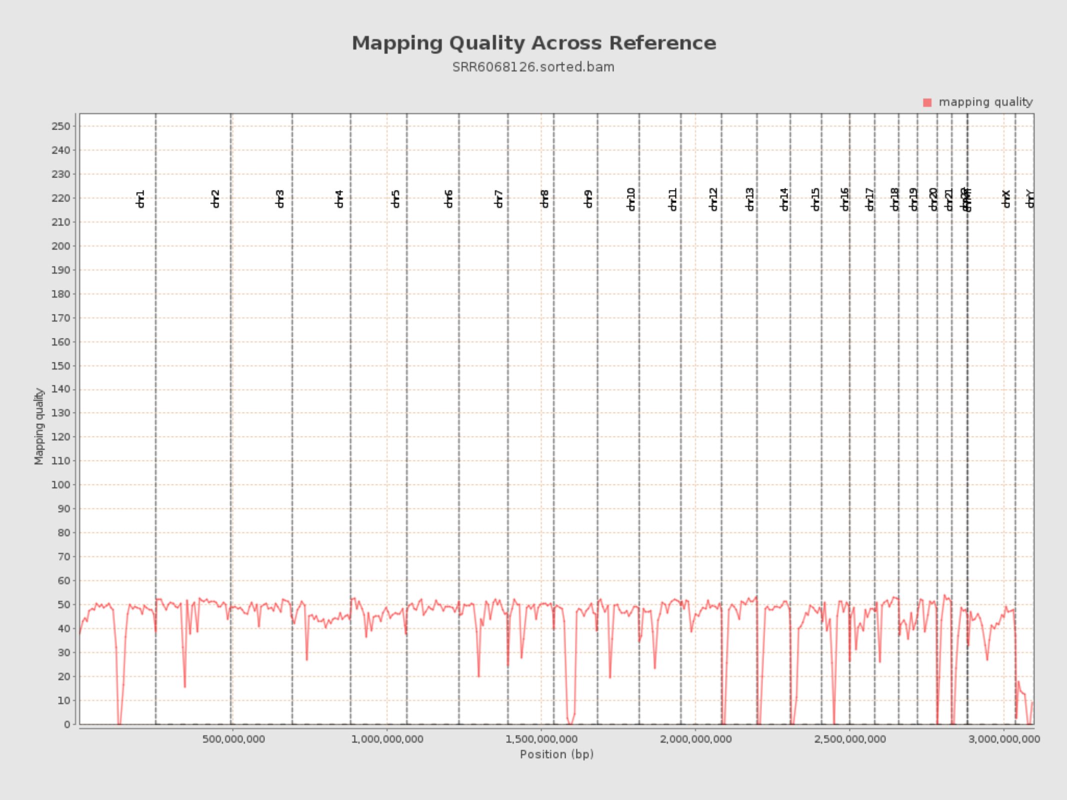
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram