Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:22:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068167.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_SRR6068167 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068167.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:22:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,434,934
Mapped reads	1,206,279 / 84.07%
Unmapped reads	228,655 / 15.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,220 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	156,728 / 10.92%
Duplication rate	9.95%
Clipped reads	597,456 / 41.64%

2.2. ACGT Content

Number/percentage of A's	22,481,886 / 28.36%
Number/percentage of C's	14,846,309 / 18.73%
Number/percentage of T's	24,896,215 / 31.41%
Number/percentage of G's	16,956,807 / 21.39%
Number/percentage of N's	87,310 / 0.11%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0256

Standard Deviation	0.3647

2.4. Mapping Quality

Mean Mapping Quality	46.64

2.5. Mismatches and indels

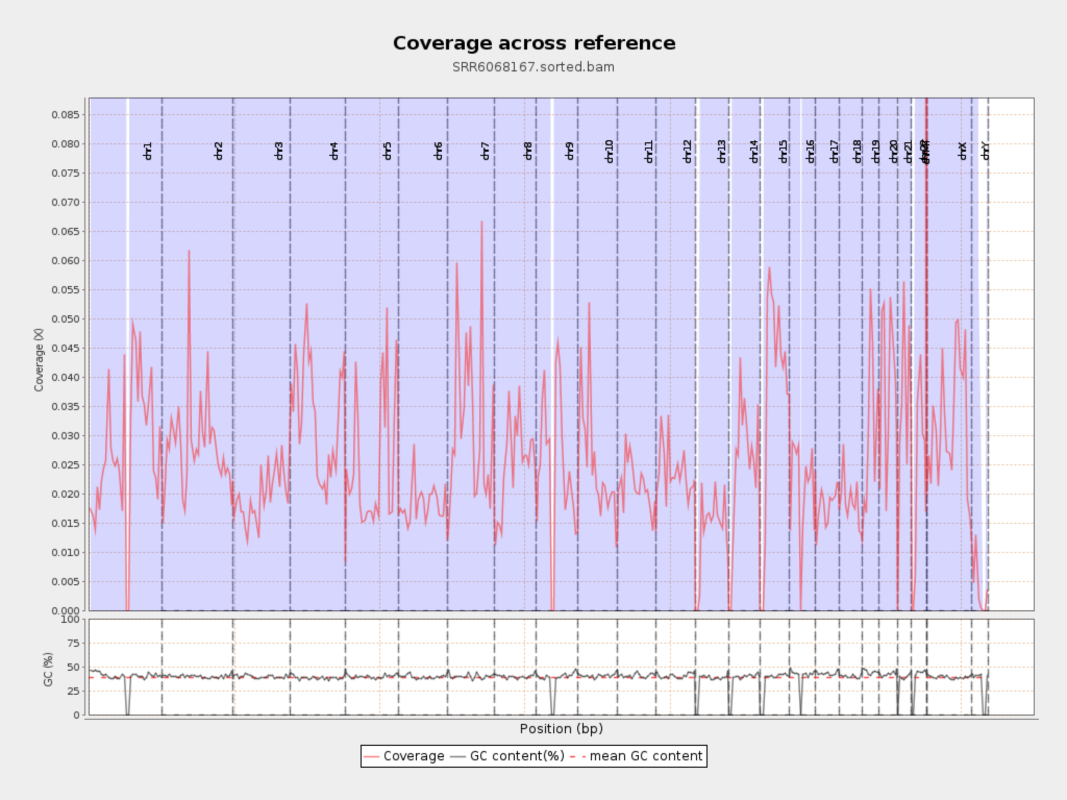
General error rate	0.92%
Mismatches	718,056
Insertions	5,580
Mapped reads with at least one insertion	0.46%
Deletions	23,689
Mapped reads with at least one deletion	1.94%
Homopolymer indels	47.1%

2.6. Chromosome stats

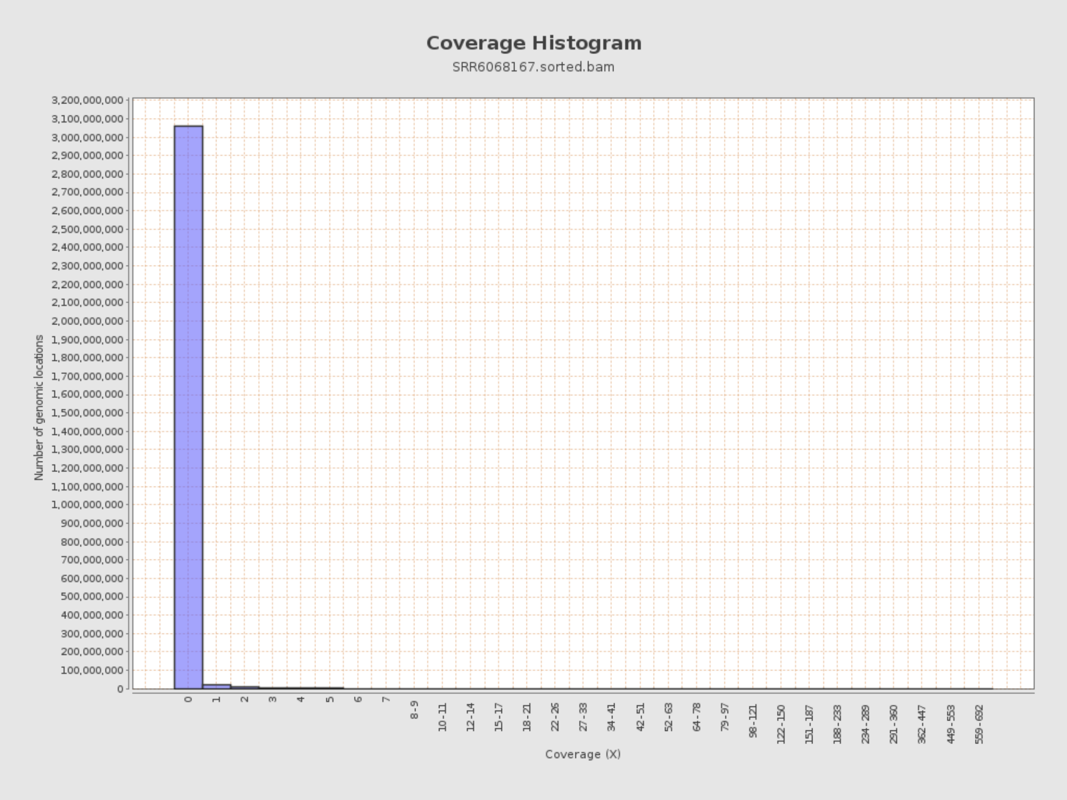
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6843330	0.0275	0.6381
chr2	243199373	6906081	0.0284	0.4044
chr3	198022430	3892490	0.0197	0.2646
chr4	191154276	6386542	0.0334	0.3324
chr5	180915260	4700385	0.026	0.2951
chr6	171115067	3137113	0.0183	0.2625
chr7	159138663	5234585	0.0329	0.4057

chr8	146364022	3717979	0.0254	0.3914
chr9	141213431	3551967	0.0252	0.342
chr10	135534747	3452054	0.0255	0.3917
chr11	135006516	2882333	0.0213	0.2984
chr12	133851895	3186110	0.0238	0.2875
chr13	115169878	1594367	0.0138	0.2243
chr14	107349540	2681855	0.025	0.2912
chr15	102531392	3920610	0.0382	0.3454
chr16	90354753	1917742	0.0212	0.2692
chr17	81195210	1452434	0.0179	0.2498
chr18	78077248	1480898	0.019	0.4403
chr19	59128983	1879025	0.0318	0.3939
chr20	63025520	2452733	0.0389	0.3612
chr21	48129895	1670548	0.0347	0.3351
chr22	51304566	1156812	0.0225	0.2569
chrMT	16571	16030	0.9674	1.6298
chrX	155270560	4965660	0.032	0.3357
chrY	59373566	230897	0.0039	0.1361

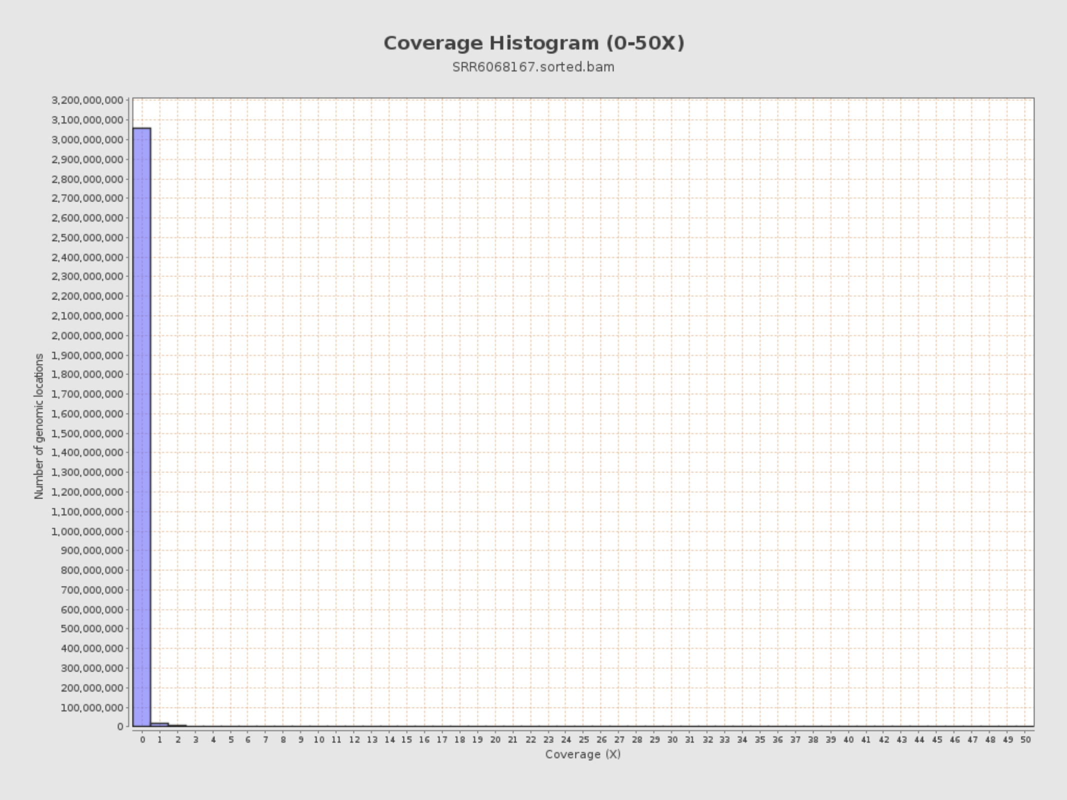
3. Results : Coverage across reference



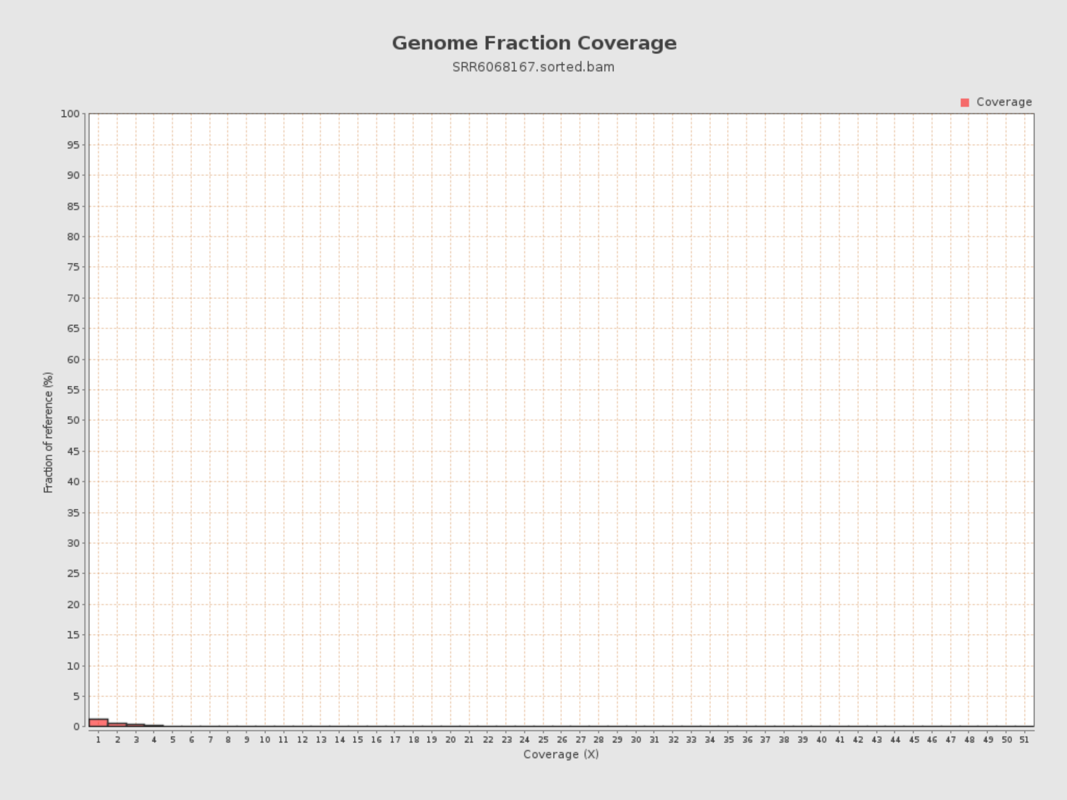
4. Results : Coverage Histogram



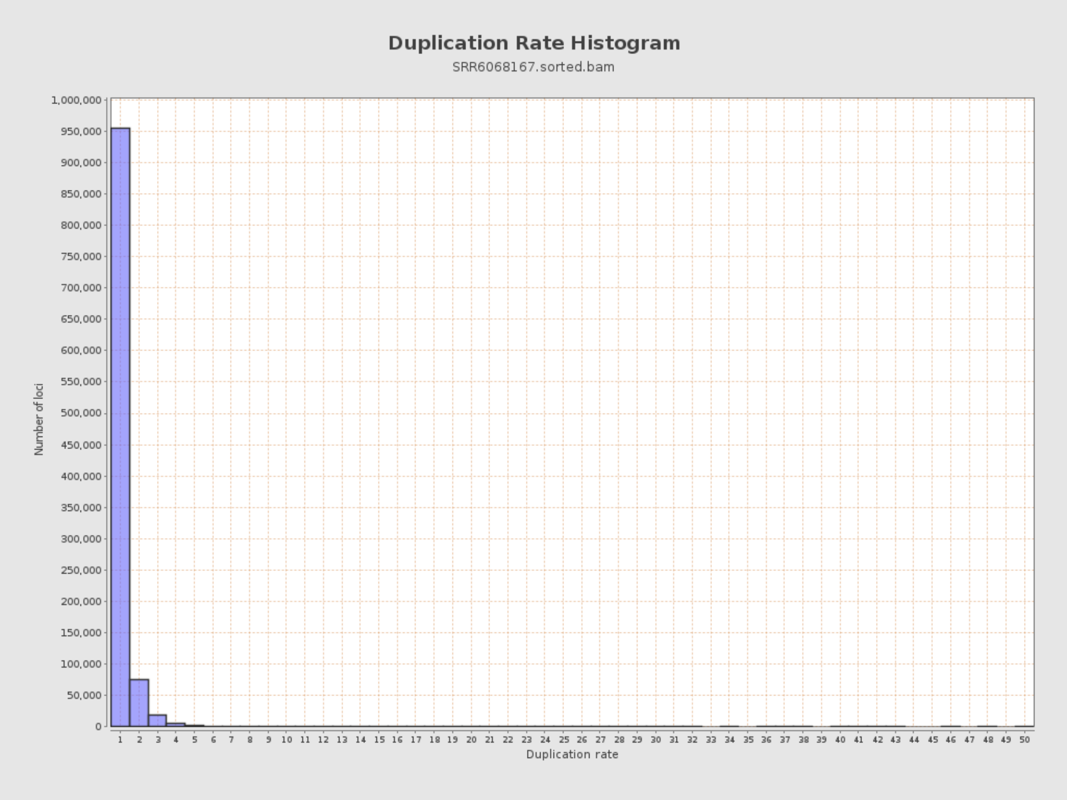
5. Results : Coverage Histogram (0-50X)



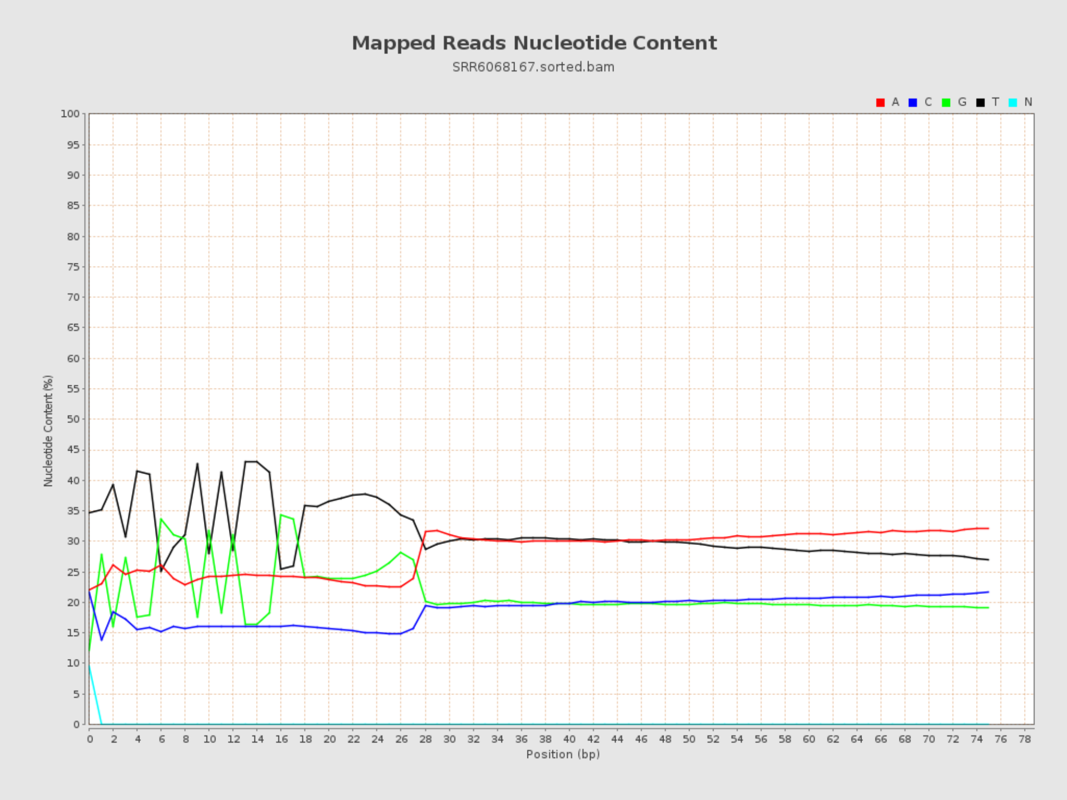
6. Results : Genome Fraction Coverage



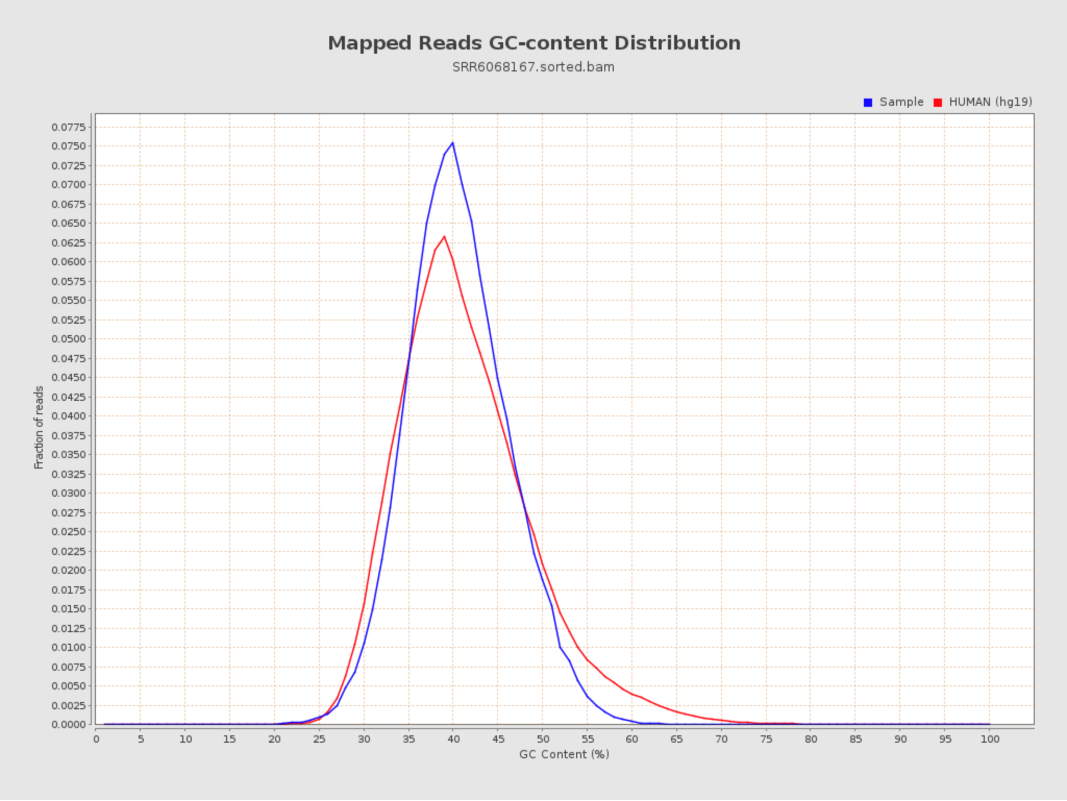
7. Results : Duplication Rate Histogram



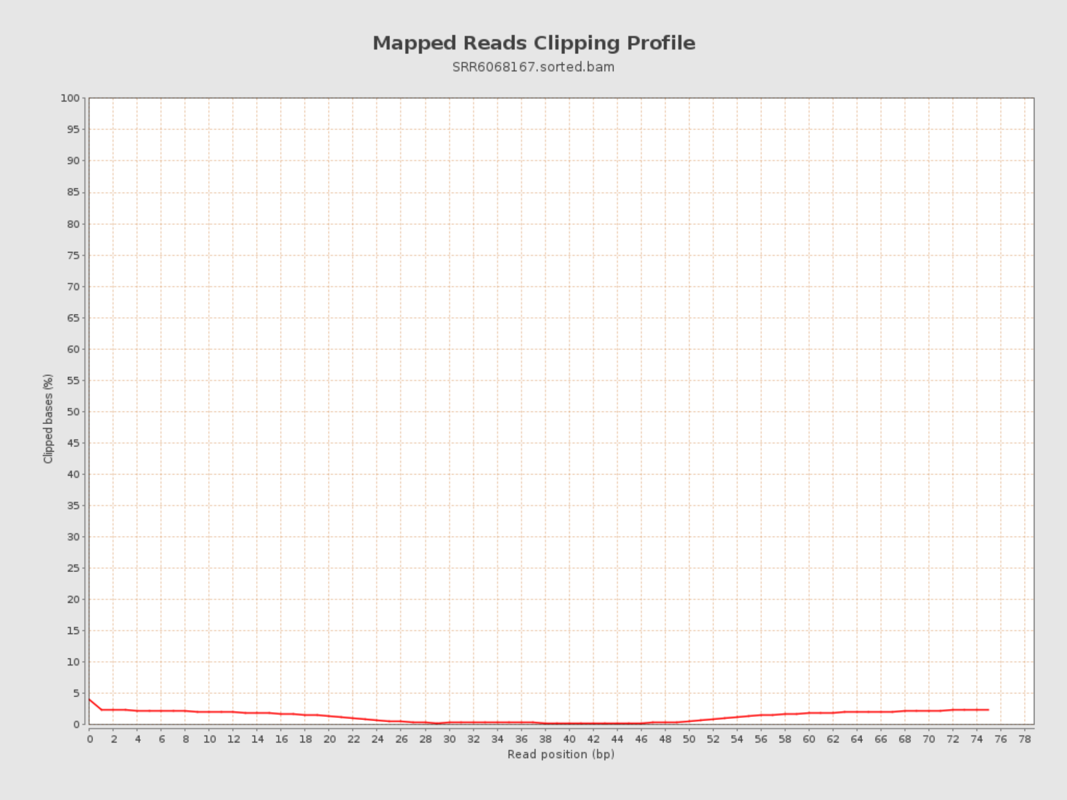
8. Results : Mapped Reads Nucleotide Content



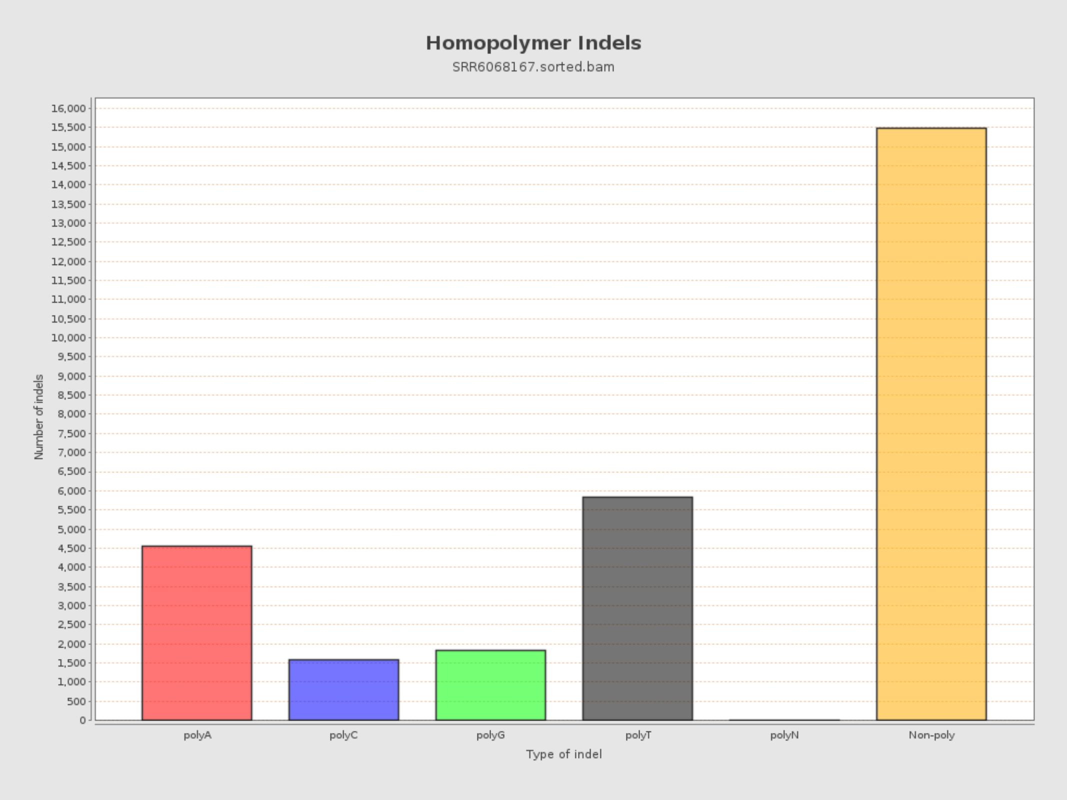
9. Results : Mapped Reads GC-content Distribution



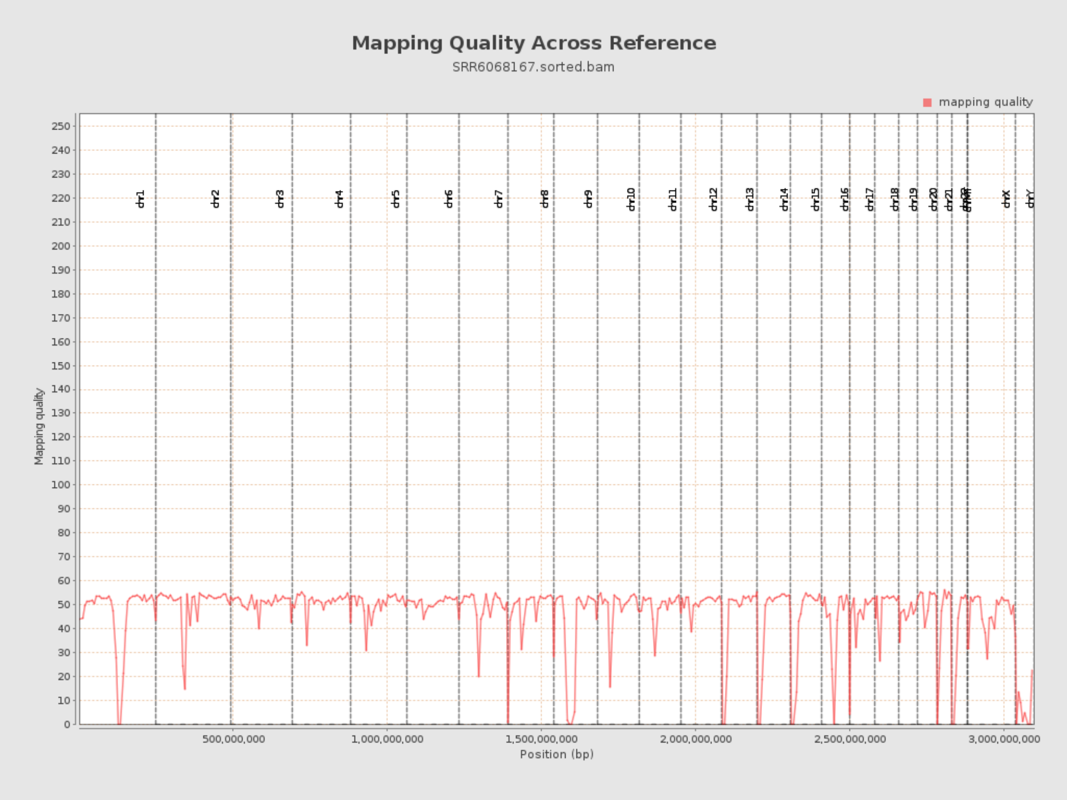
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram