

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:19:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068137.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_SRR6068137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:19:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,949,609
Mapped reads	1,629,258 / 83.57%
Unmapped reads	320,351 / 16.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,136 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	206,277 / 10.58%
Duplication rate	9.79%
Clipped reads	789,570 / 40.5%

2.2. ACGT Content

Number/percentage of A's	29,082,194 / 27.31%
Number/percentage of C's	18,819,992 / 17.67%
Number/percentage of T's	34,727,825 / 32.61%
Number/percentage of G's	23,755,802 / 22.31%
Number/percentage of N's	101,239 / 0.1%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0344

Standard Deviation	0.4166
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2.4. Mapping Quality

Mean Mapping Quality	43.23
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2.5. Mismatches and indels

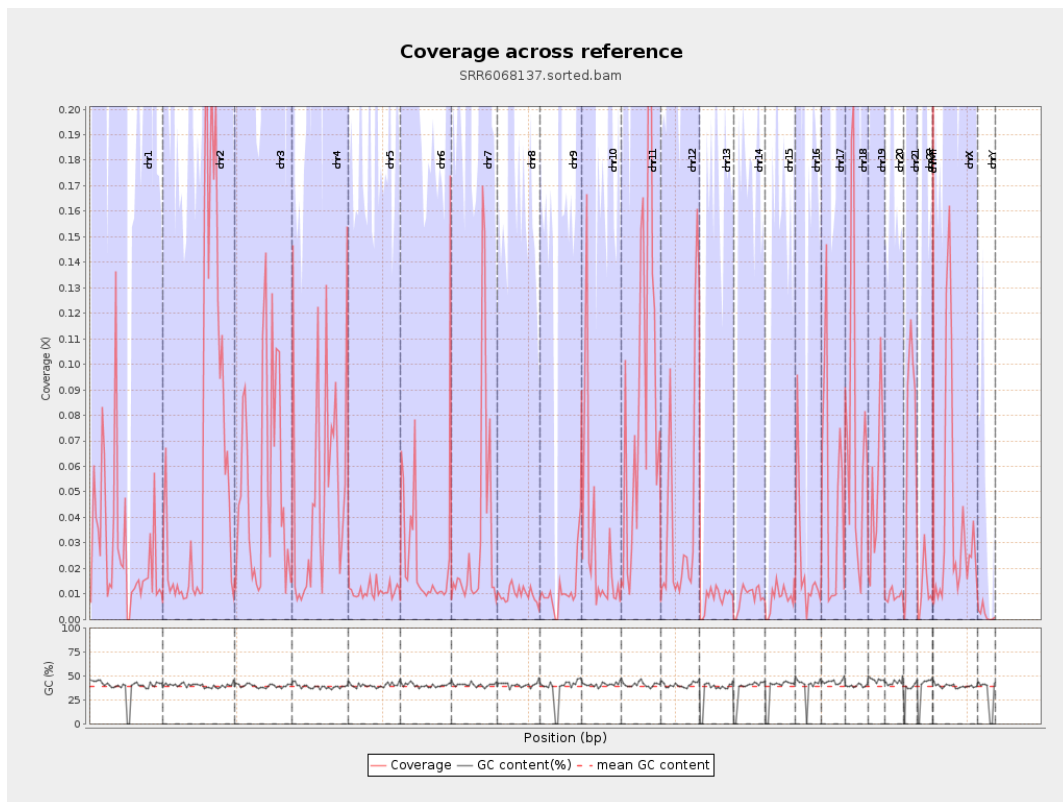
General error rate	0.89%
Mismatches	936,936
Insertions	7,620
Mapped reads with at least one insertion	0.46%
Deletions	33,948
Mapped reads with at least one deletion	2.06%
Homopolymer indels	45.74%

2.6. Chromosome stats

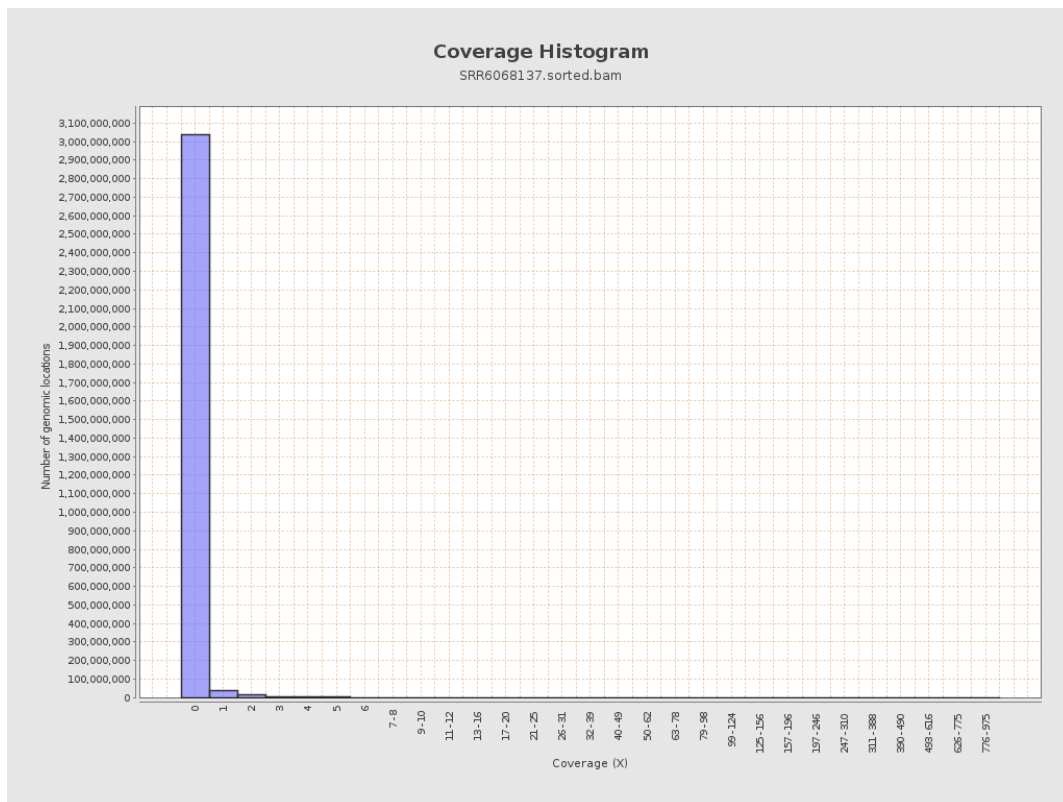
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6882068	0.0276	0.8444
chr2	243199373	15057560	0.0619	0.4816
chr3	198022430	10331597	0.0522	0.3685
chr4	191154276	9556301	0.05	0.3644
chr5	180915260	2015670	0.0111	0.1705
chr6	171115067	4173046	0.0244	0.2659
chr7	159138663	5204224	0.0327	0.3408

chr8	146364022	1425769	0.0097	0.2079
chr9	141213431	1705582	0.0121	0.2
chr10	135534747	3968310	0.0293	0.4489
chr11	135006516	12578608	0.0932	0.6089
chr12	133851895	5419105	0.0405	0.3297
chr13	115169878	977094	0.0085	0.1499
chr14	107349540	955469	0.0089	0.1553
chr15	102531392	851216	0.0083	0.1424
chr16	90354753	1866066	0.0207	0.2337
chr17	81195210	4183247	0.0515	0.4072
chr18	78077248	6082371	0.0779	0.5605
chr19	59128983	2927790	0.0495	0.5447
chr20	63025520	594484	0.0094	0.1651
chr21	48129895	3305433	0.0687	0.4255
chr22	51304566	618969	0.0121	0.1692
chrMT	16571	7340	0.4429	1.0088
chrX	155270560	5735030	0.0369	0.4375
chrY	59373566	120395	0.002	0.0659

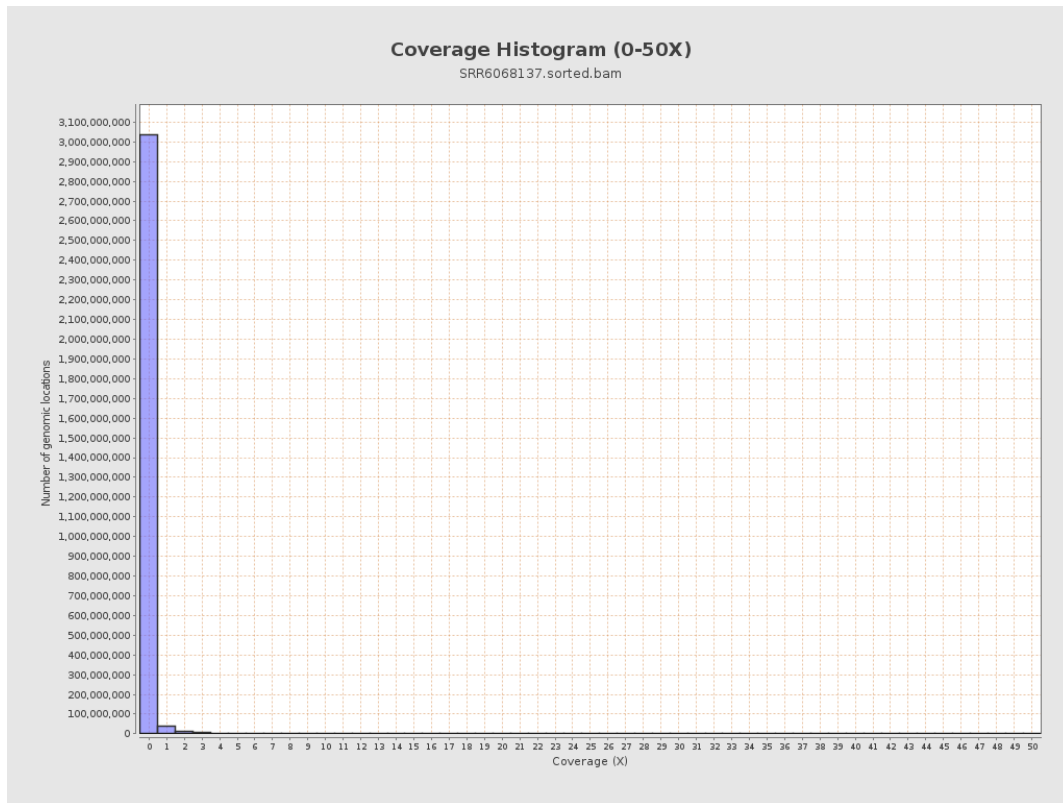
3. Results : Coverage across reference



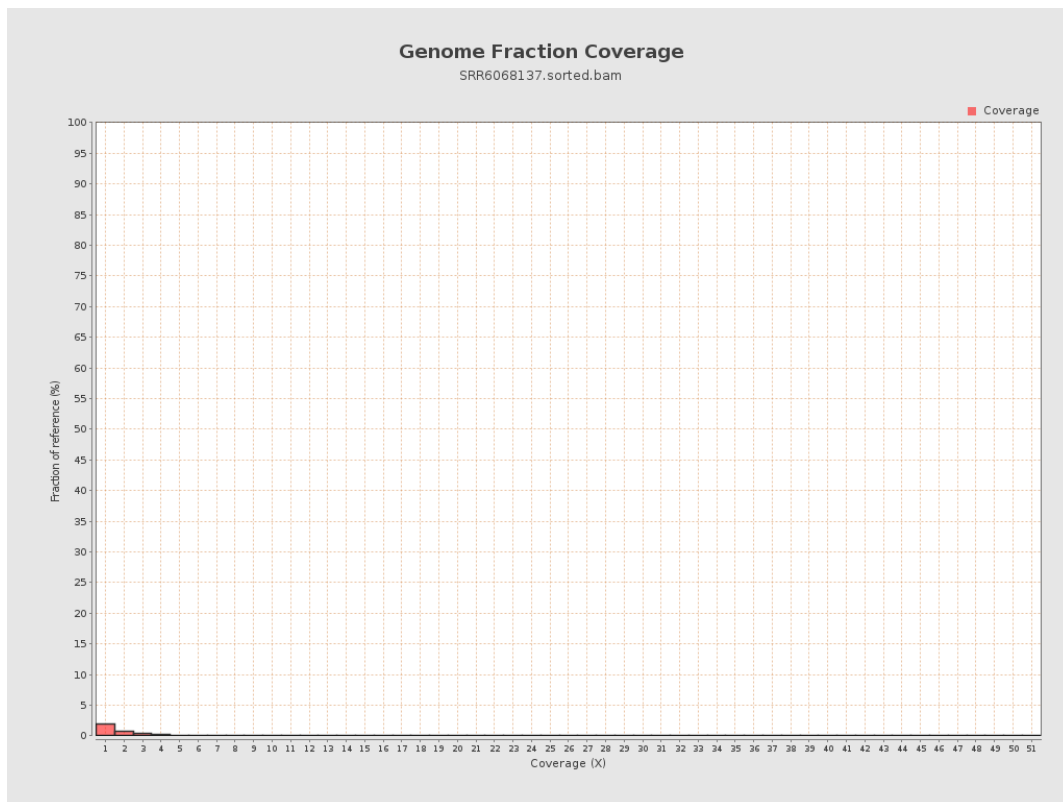
4. Results : Coverage Histogram



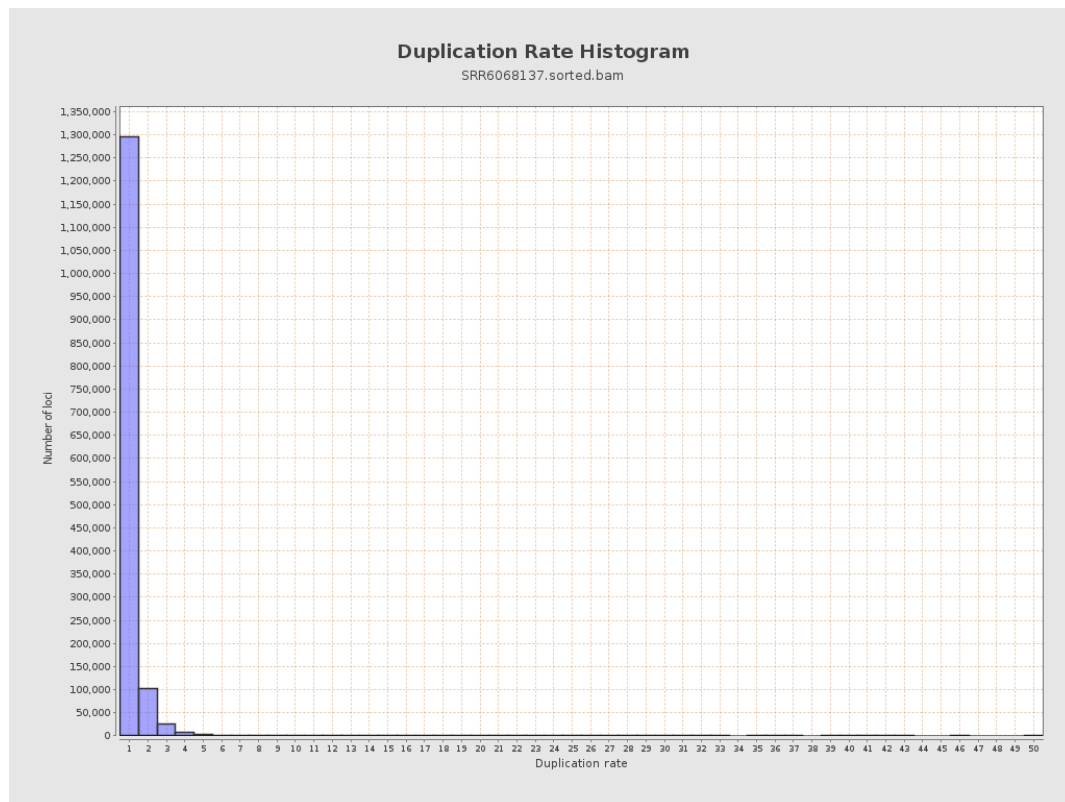
5. Results : Coverage Histogram (0-50X)



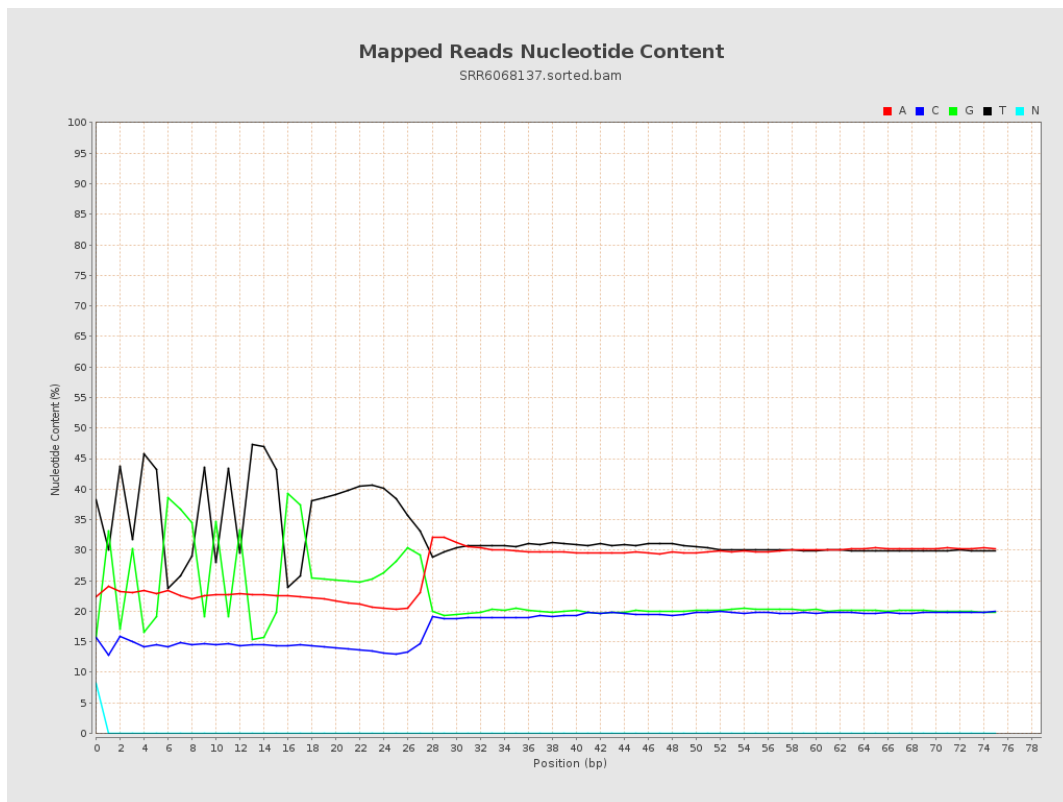
6. Results : Genome Fraction Coverage



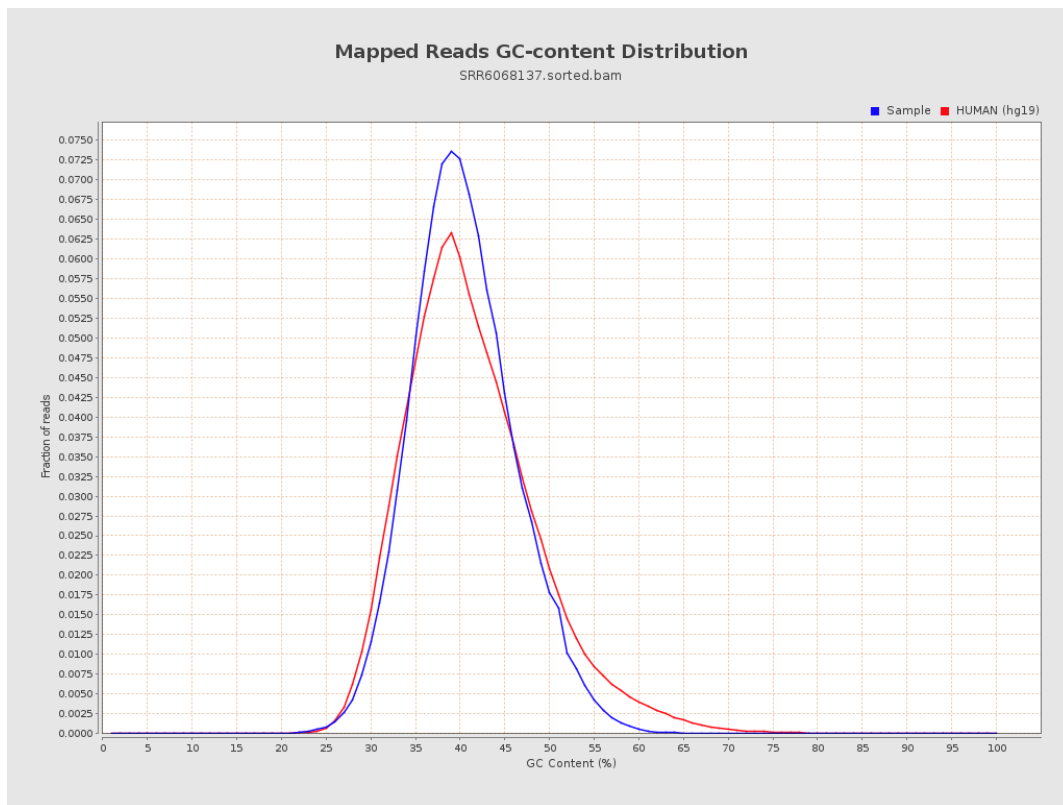
7. Results : Duplication Rate Histogram



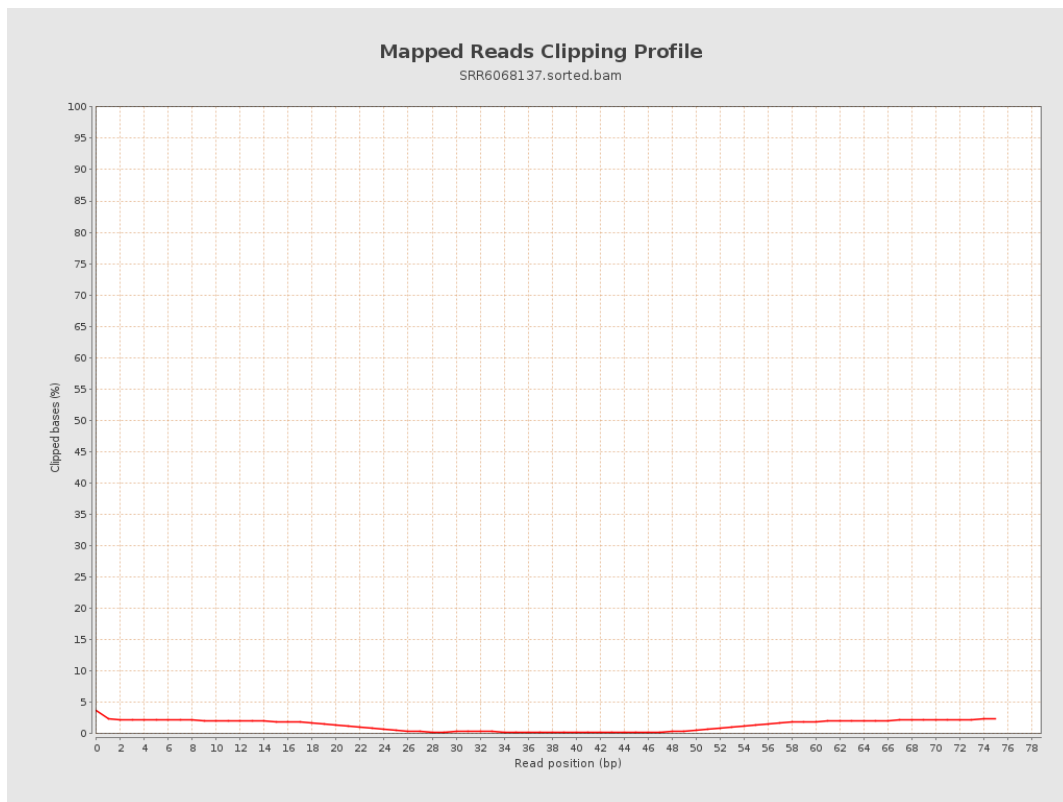
8. Results : Mapped Reads Nucleotide Content



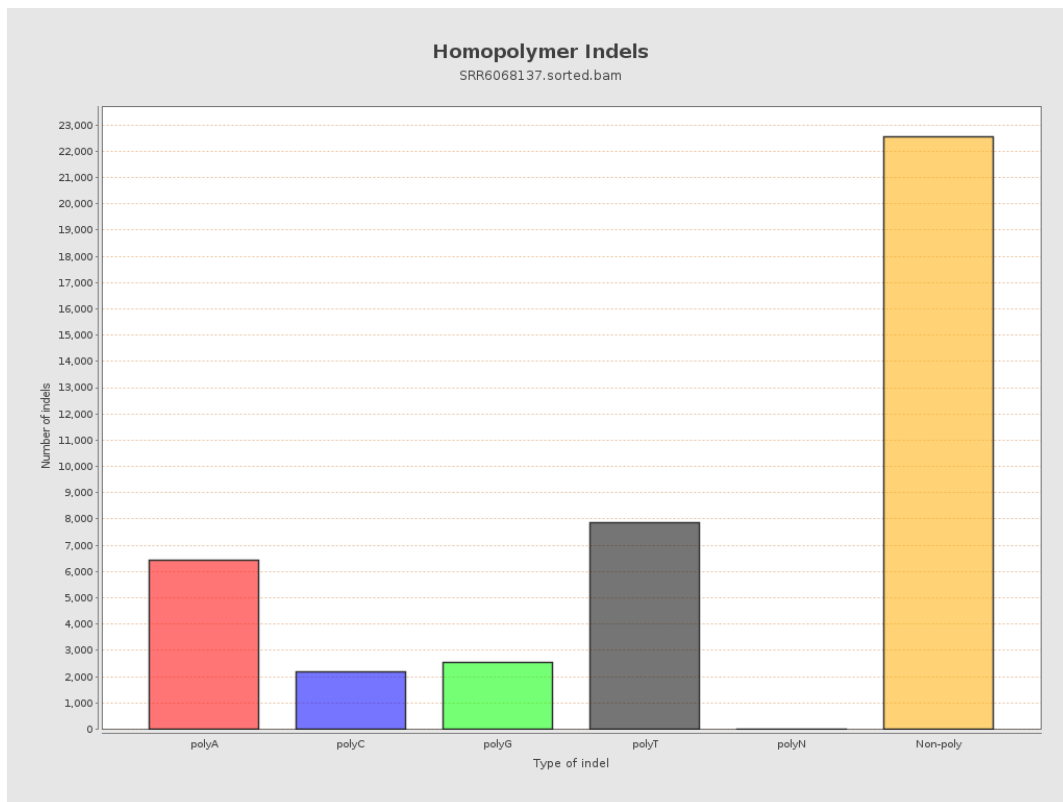
9. Results : Mapped Reads GC-content Distribution



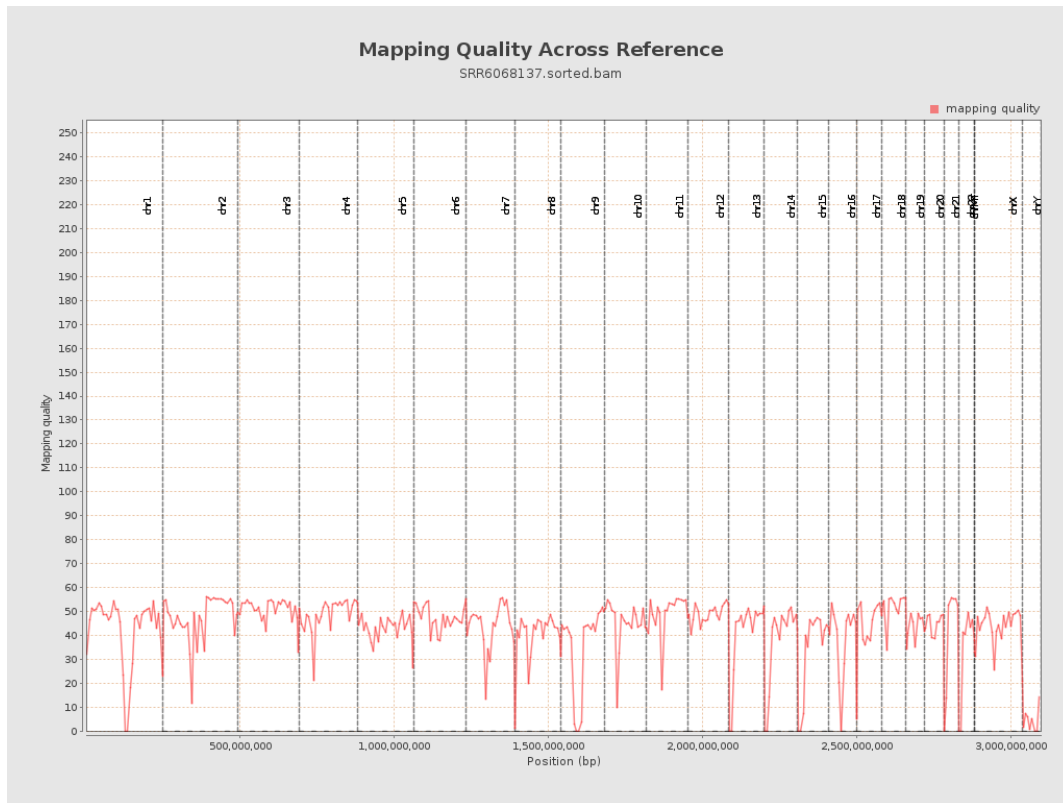
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

