

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:45:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008660.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_SRR6008660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:45:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,107,875
Mapped reads	1,747,941 / 82.92%
Unmapped reads	359,934 / 17.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,657 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	318,869 / 15.13%
Duplication rate	12.54%
Clipped reads	925,295 / 43.9%

2.2. ACGT Content

Number/percentage of A's	29,869,328 / 26.53%
Number/percentage of C's	21,460,806 / 19.06%
Number/percentage of T's	34,882,623 / 30.98%
Number/percentage of G's	26,293,036 / 23.35%
Number/percentage of N's	91,953 / 0.08%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.4034
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2.4. Mapping Quality

Mean Mapping Quality	45.2
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2.5. Mismatches and indels

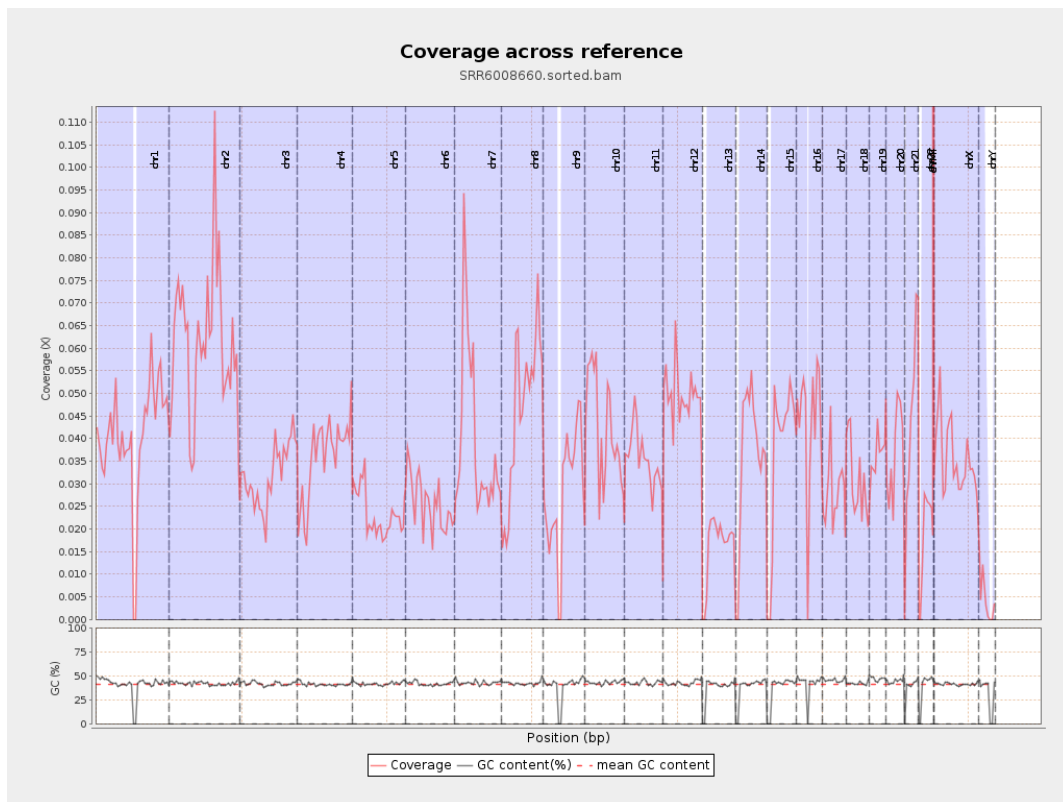
General error rate	0.9%
Mismatches	995,087
Insertions	8,033
Mapped reads with at least one insertion	0.46%
Deletions	33,516
Mapped reads with at least one deletion	1.9%
Homopolymer indels	49.56%

2.6. Chromosome stats

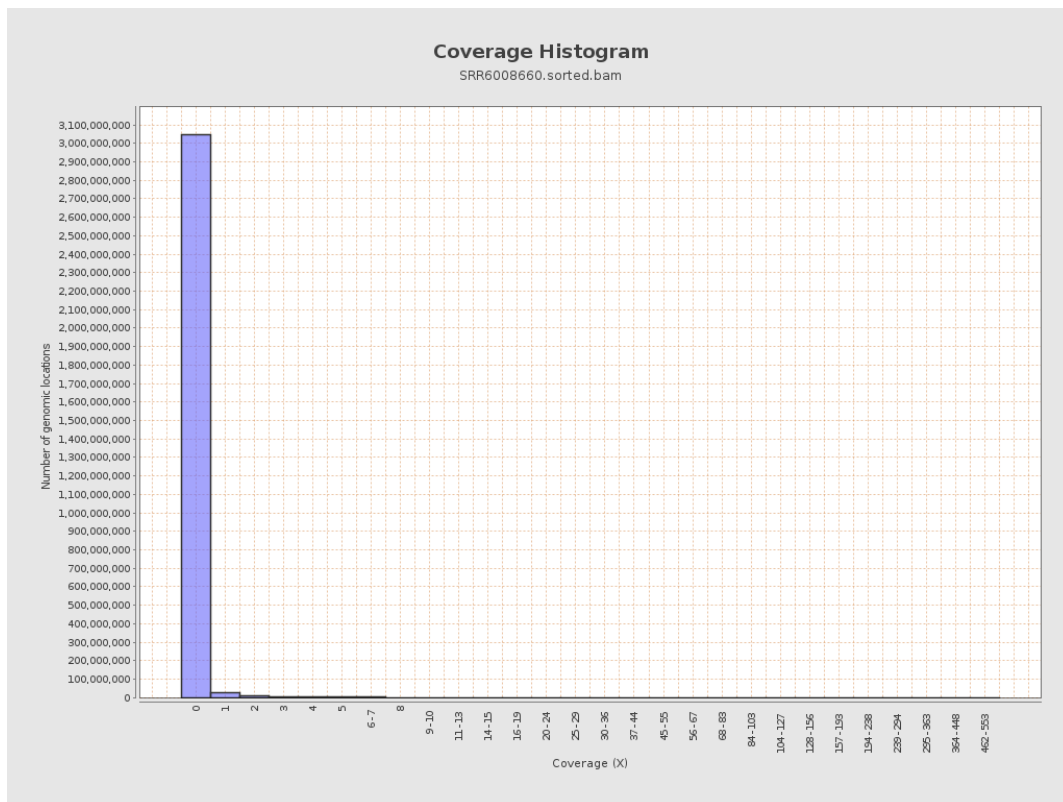
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10097948	0.0405	0.5055
chr2	243199373	14864079	0.0611	0.555
chr3	198022430	6307894	0.0319	0.3246
chr4	191154276	6865552	0.0359	0.3596
chr5	180915260	4215736	0.0233	0.2795
chr6	171115067	4400104	0.0257	0.3178
chr7	159138663	6362313	0.04	0.5306

chr8	146364022	6780578	0.0463	0.4352
chr9	141213431	3989987	0.0283	0.3501
chr10	135534747	5784690	0.0427	0.4241
chr11	135006516	4772615	0.0354	0.3972
chr12	133851895	6677534	0.0499	0.416
chr13	115169878	1861481	0.0162	0.233
chr14	107349540	3910369	0.0364	0.4043
chr15	102531392	3818804	0.0372	0.3906
chr16	90354753	3896404	0.0431	0.3928
chr17	81195210	2280701	0.0281	0.3254
chr18	78077248	2418150	0.031	0.4706
chr19	59128983	2162020	0.0366	0.4042
chr20	63025520	2295775	0.0364	0.3565
chr21	48129895	2111036	0.0439	0.4006
chr22	51304566	933065	0.0182	0.2414
chrMT	16571	73656	4.4449	4.8848
chrX	155270560	5520544	0.0356	0.3583
chrY	59373566	255410	0.0043	0.1104

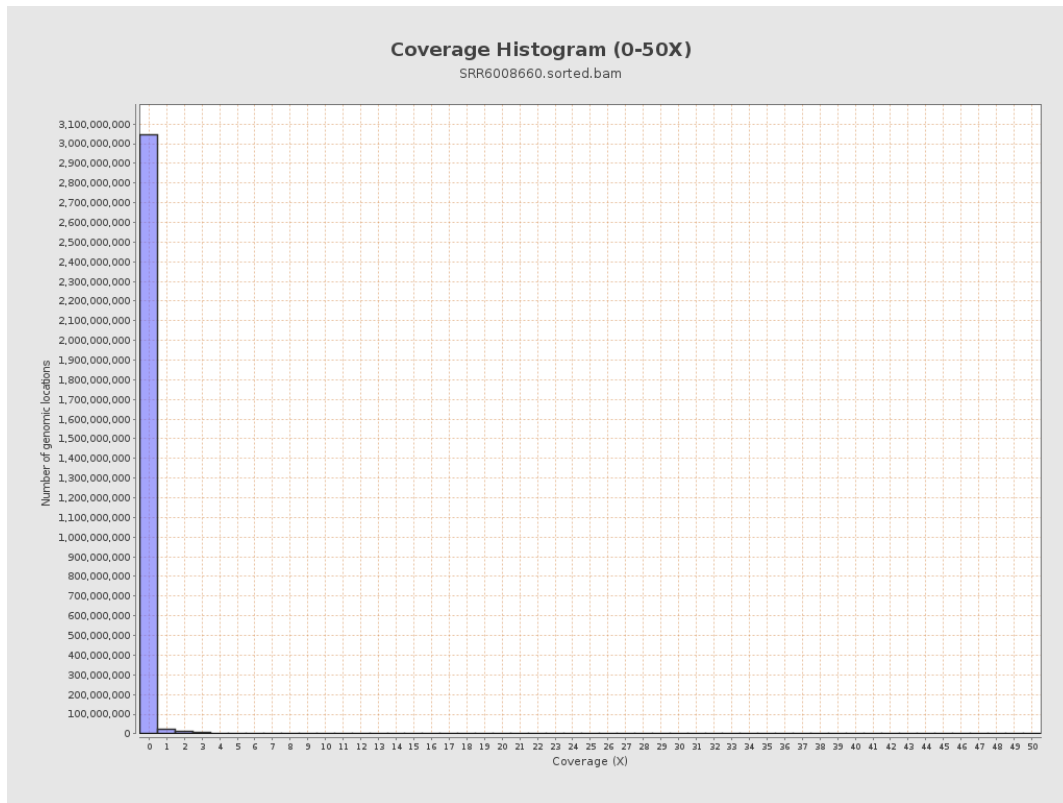
3. Results : Coverage across reference



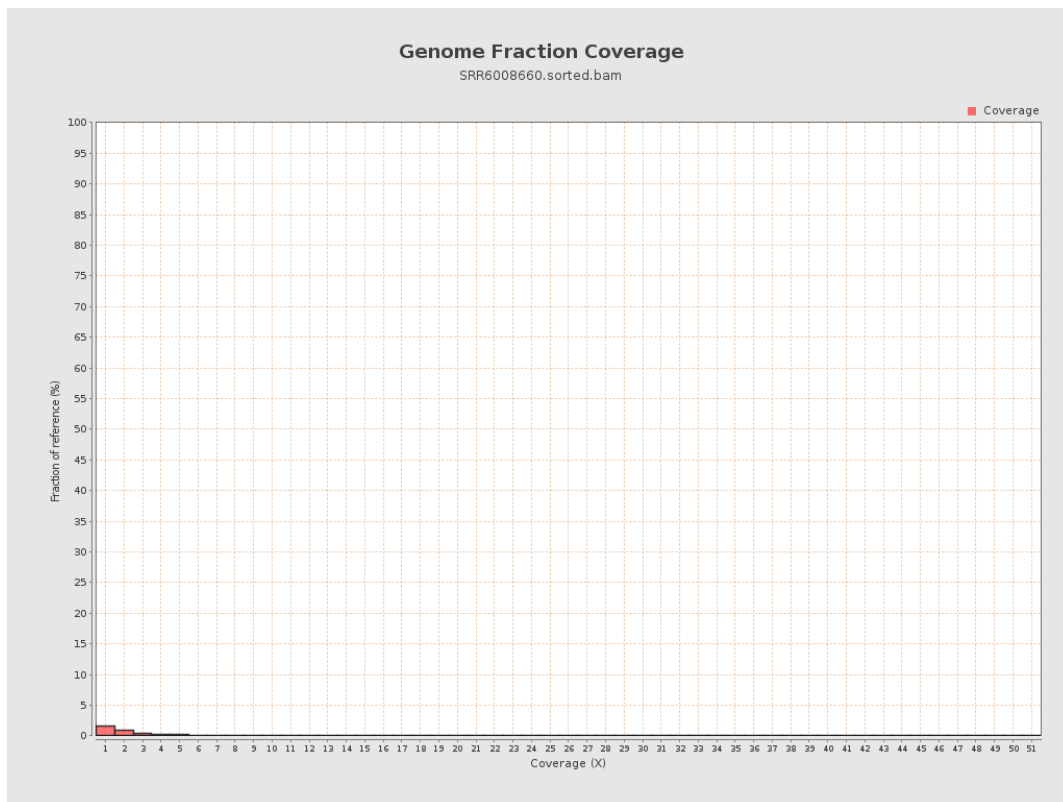
4. Results : Coverage Histogram



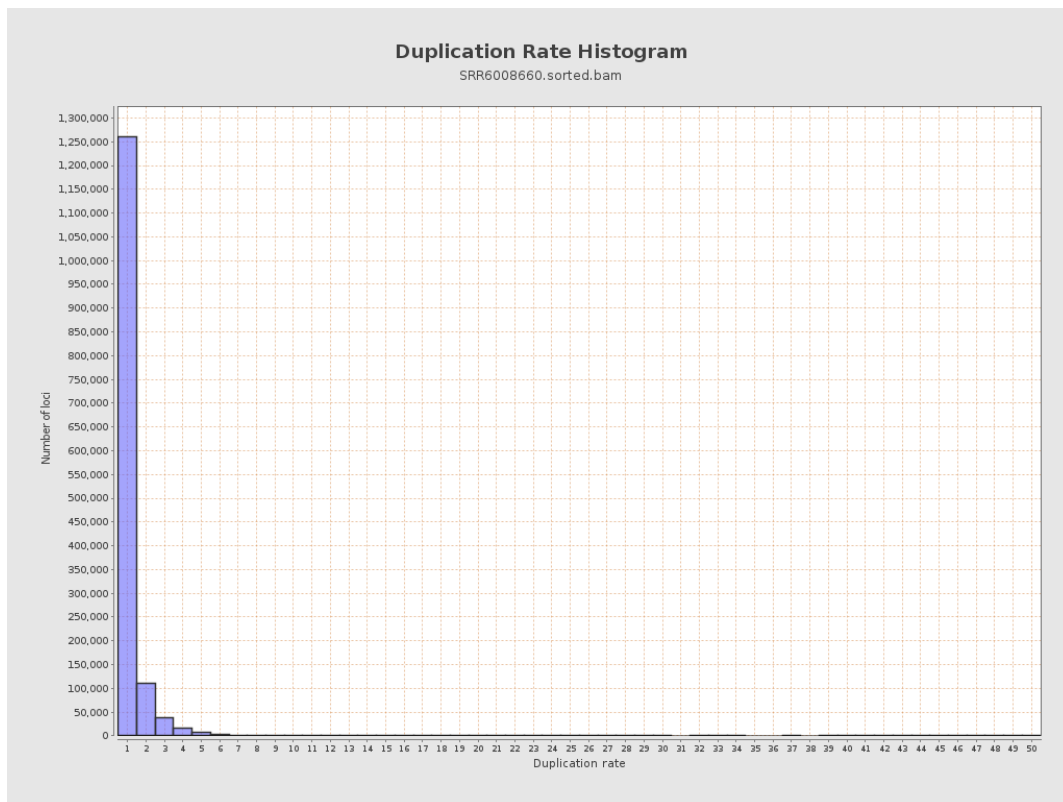
5. Results : Coverage Histogram (0-50X)



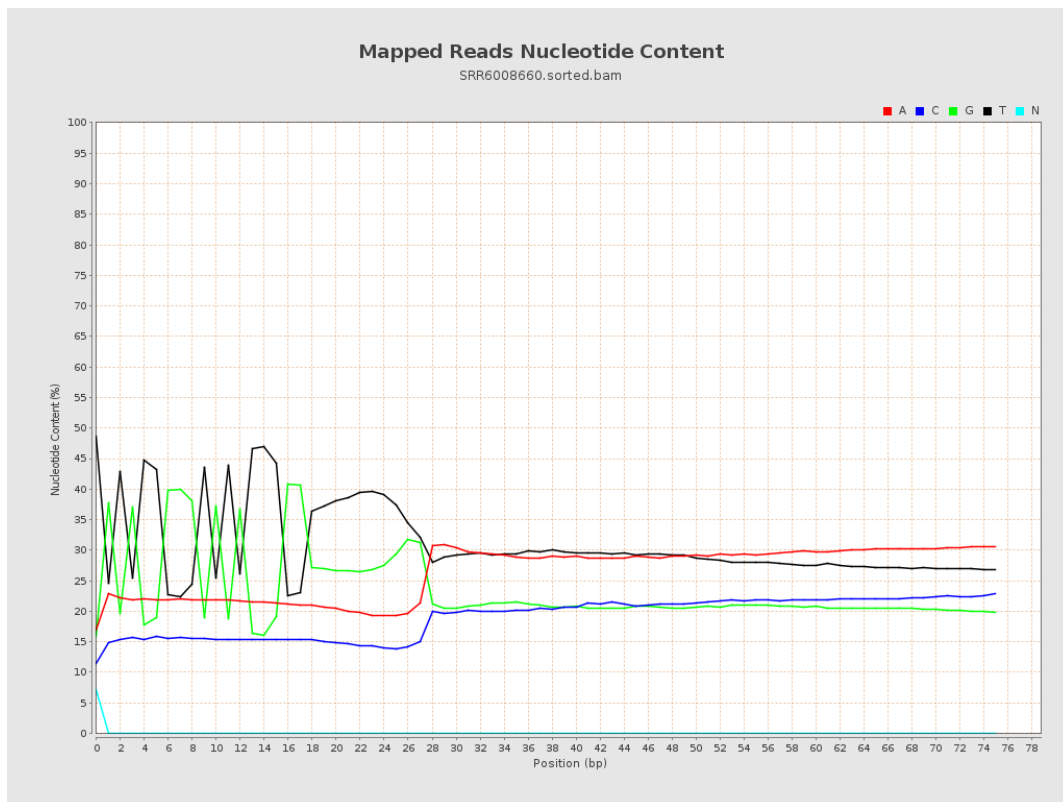
6. Results : Genome Fraction Coverage



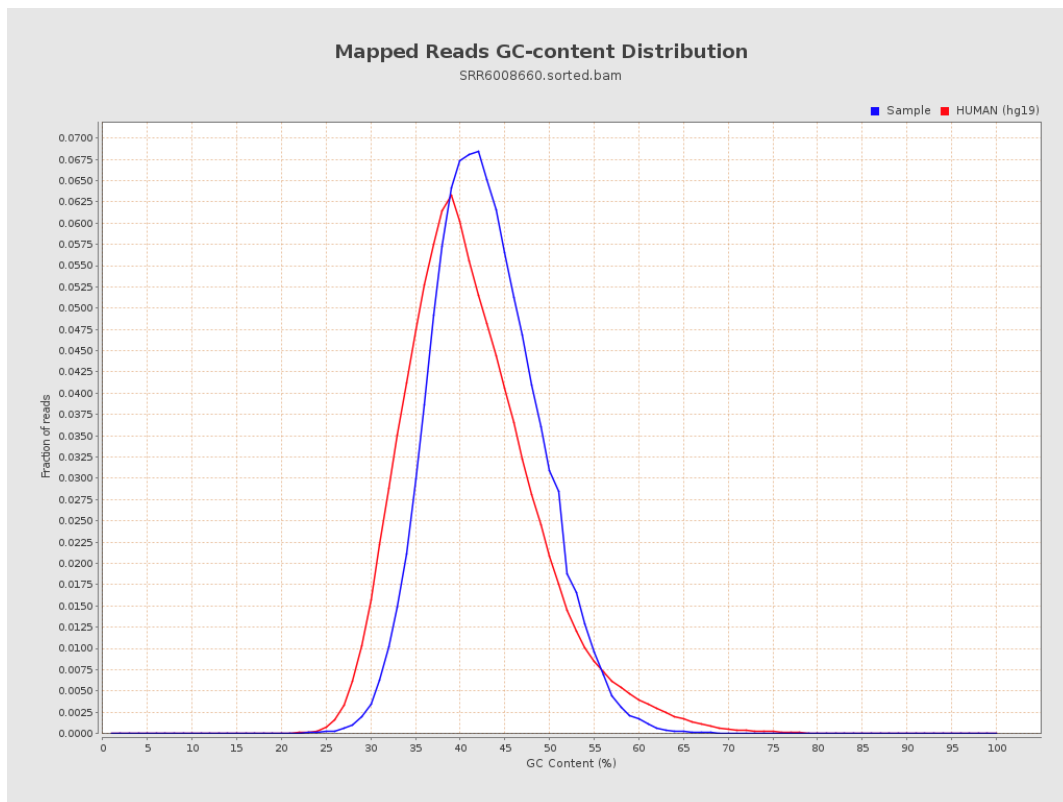
7. Results : Duplication Rate Histogram



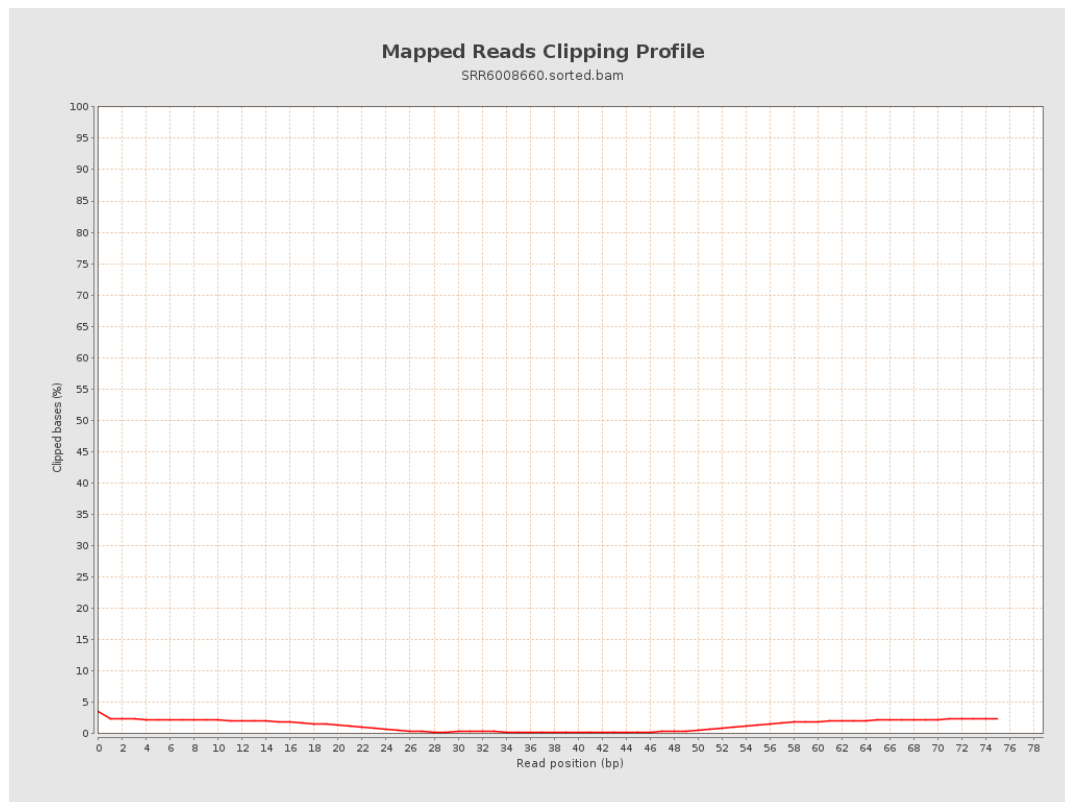
8. Results : Mapped Reads Nucleotide Content



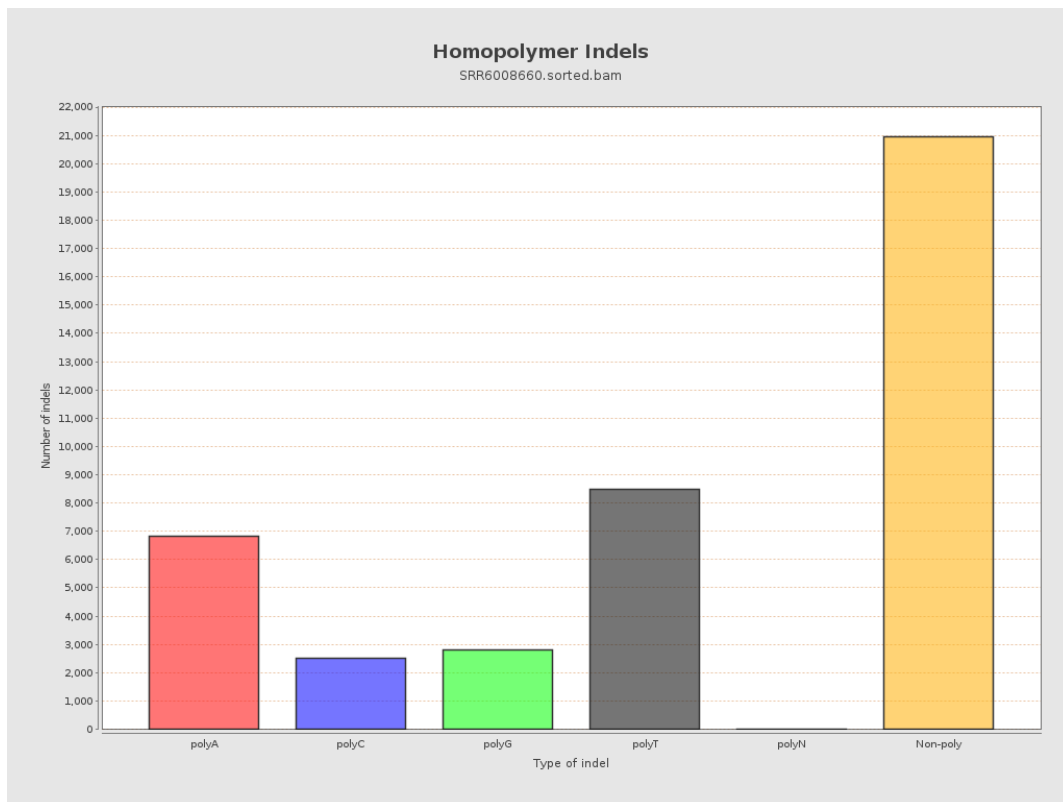
9. Results : Mapped Reads GC-content Distribution



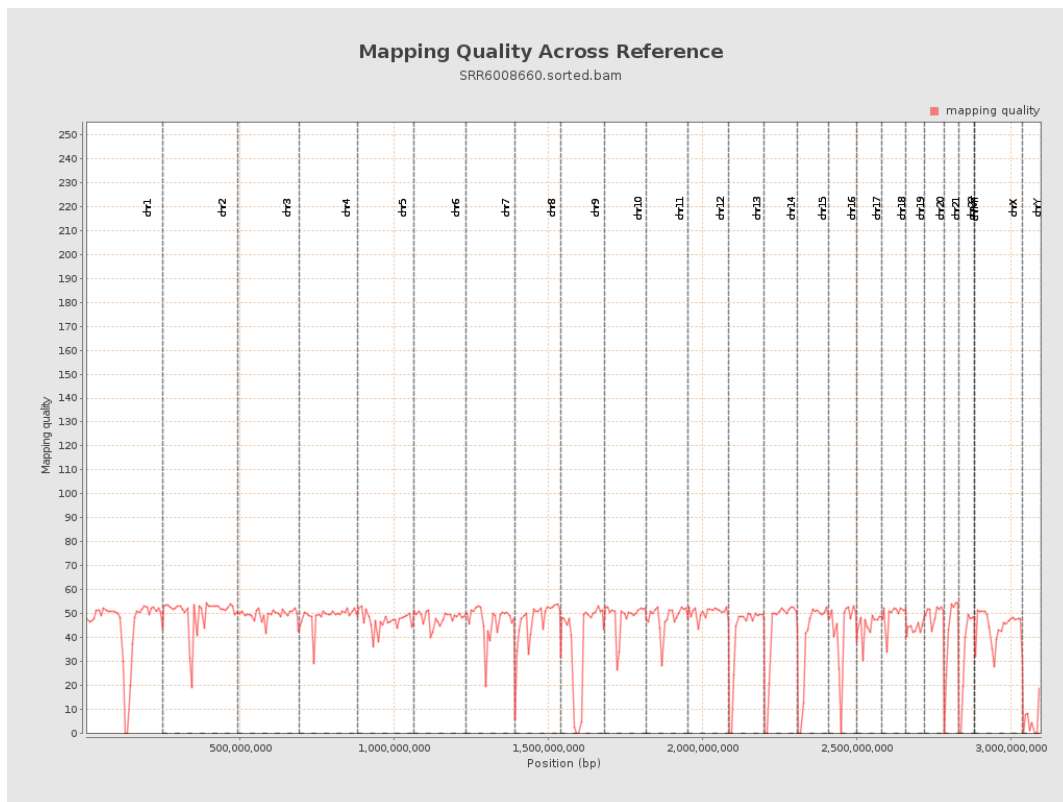
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

