

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:24:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013215.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_SRR6013215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013215.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:24:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,602,850
Mapped reads	2,717,310 / 75.42%
Unmapped reads	885,540 / 24.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,766 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	218,205 / 6.06%
Duplication rate	6.56%
Clipped reads	1,679,208 / 46.61%

2.2. ACGT Content

Number/percentage of A's	47,372,087 / 27.95%
Number/percentage of C's	31,877,714 / 18.81%
Number/percentage of T's	52,434,782 / 30.94%
Number/percentage of G's	37,724,054 / 22.26%
Number/percentage of N's	59,580 / 0.04%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.451
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2.4. Mapping Quality

Mean Mapping Quality	44.8
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2.5. Mismatches and indels

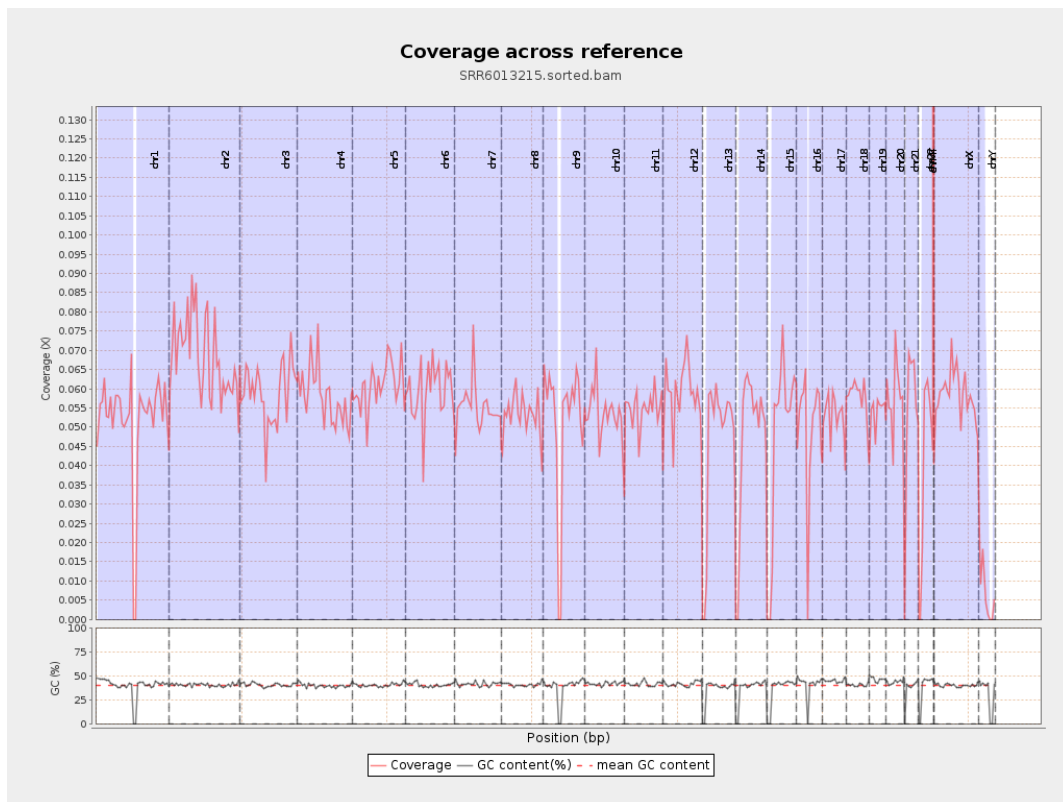
General error rate	0.85%
Mismatches	1,409,771
Insertions	12,477
Mapped reads with at least one insertion	0.45%
Deletions	40,799
Mapped reads with at least one deletion	1.49%
Homopolymer indels	44.74%

2.6. Chromosome stats

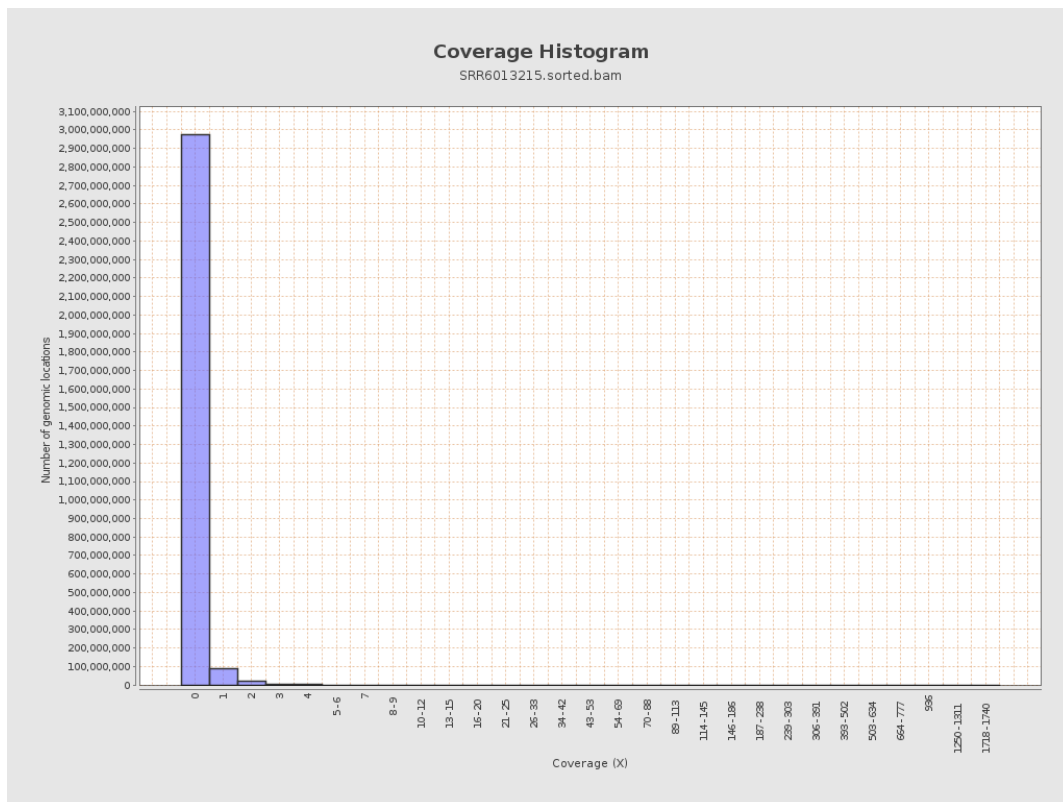
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12904552	0.0518	0.5772
chr2	243199373	16681967	0.0686	0.8112
chr3	198022430	11665214	0.0589	0.3263
chr4	191154276	11043480	0.0578	0.3322
chr5	180915260	11027534	0.061	0.3314
chr6	171115067	10221507	0.0597	0.4266
chr7	159138663	8833827	0.0555	0.5262

chr8	146364022	7775403	0.0531	0.5515
chr9	141213431	7210207	0.0511	0.3764
chr10	135534747	7263016	0.0536	0.4026
chr11	135006516	7356449	0.0545	0.3568
chr12	133851895	7904247	0.0591	0.3309
chr13	115169878	5271545	0.0458	0.3082
chr14	107349540	5096988	0.0475	0.3083
chr15	102531392	4874535	0.0475	0.2929
chr16	90354753	4461516	0.0494	0.3236
chr17	81195210	4258182	0.0524	0.3157
chr18	78077248	4554231	0.0583	0.5879
chr19	59128983	3175020	0.0537	0.4557
chr20	63025520	3608009	0.0572	0.3264
chr21	48129895	2599976	0.054	0.3285
chr22	51304566	2003628	0.0391	0.2597
chrMT	16571	320789	19.3585	13.5732
chrX	155270560	9025468	0.0581	0.3438
chrY	59373566	399819	0.0067	0.1385

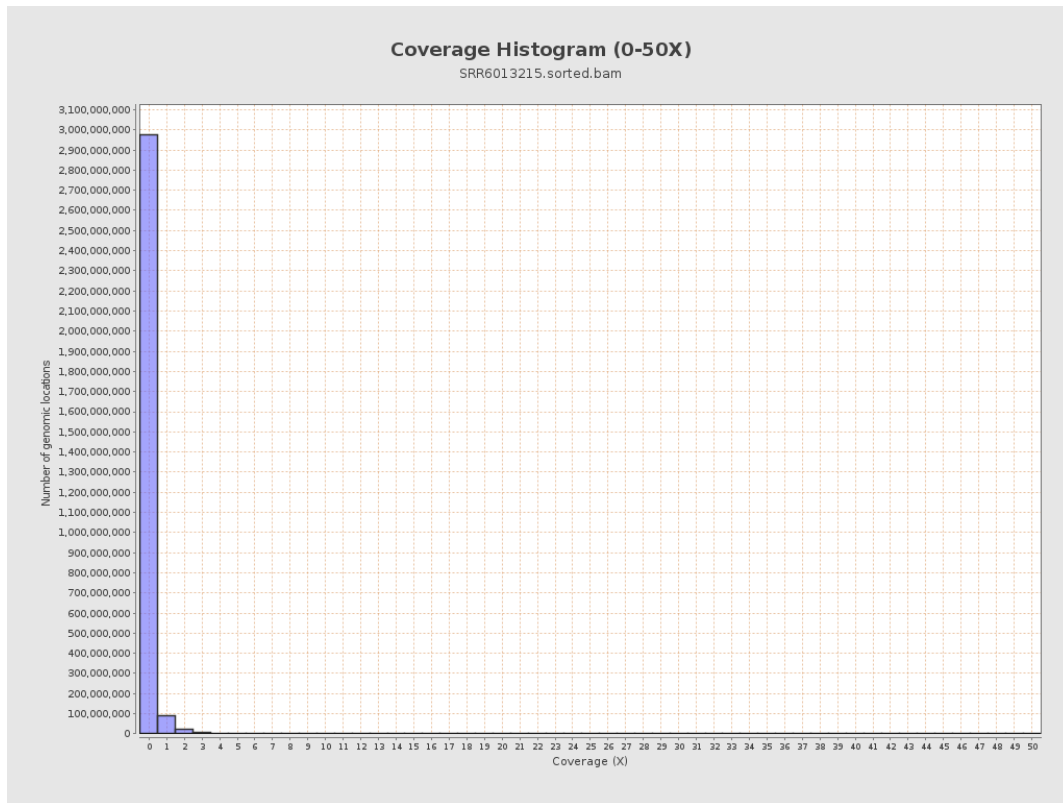
3. Results : Coverage across reference



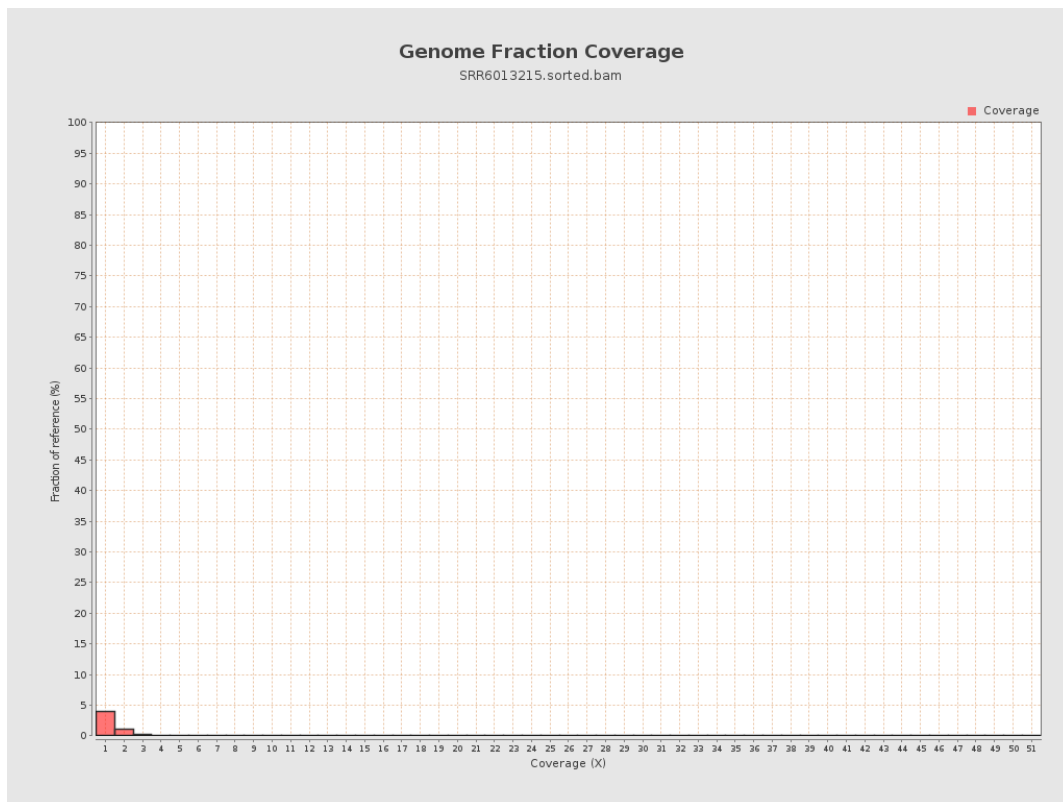
4. Results : Coverage Histogram



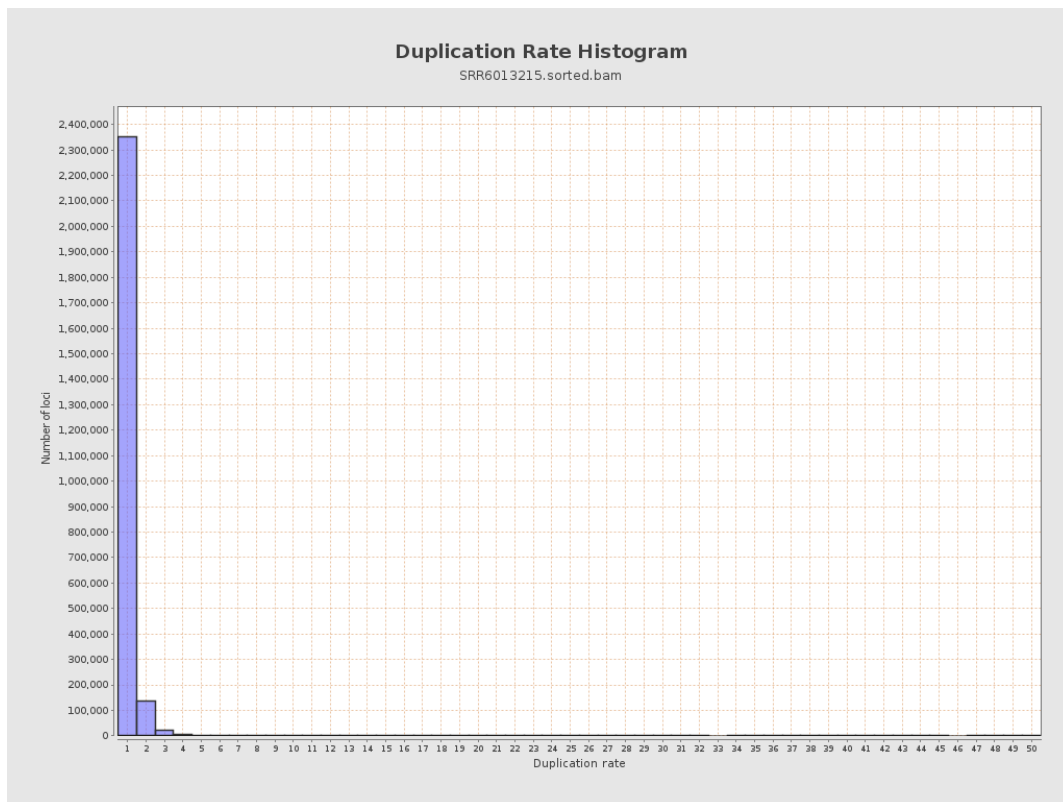
5. Results : Coverage Histogram (0-50X)



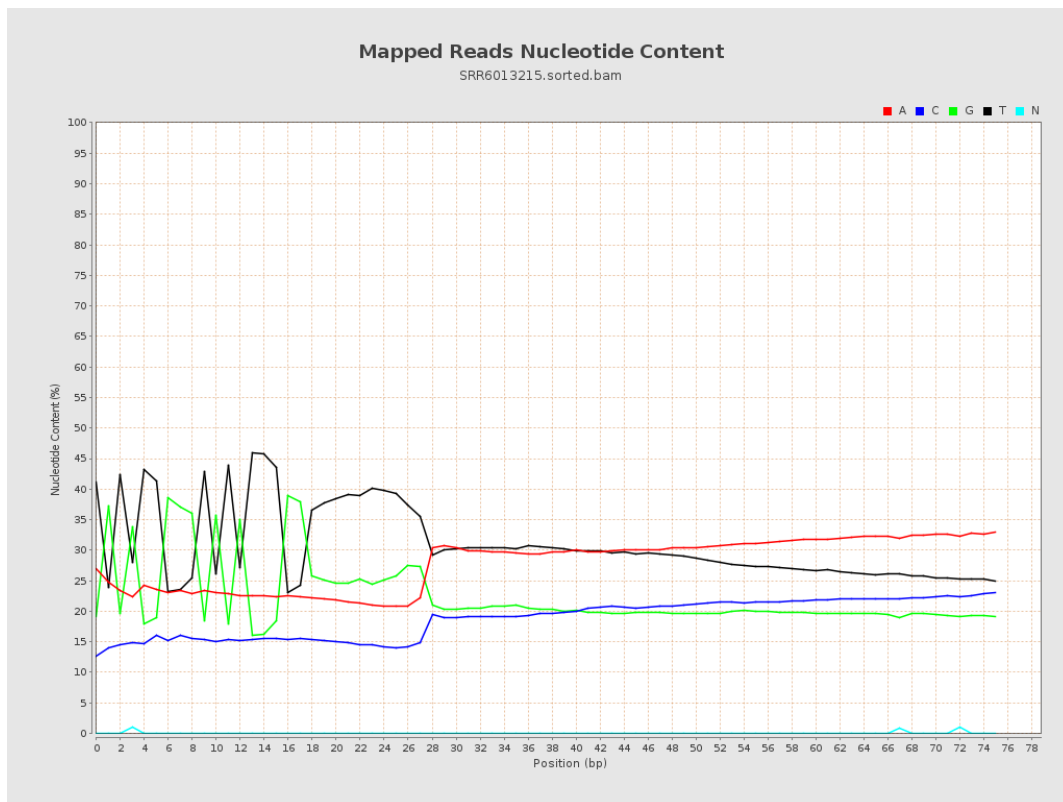
6. Results : Genome Fraction Coverage



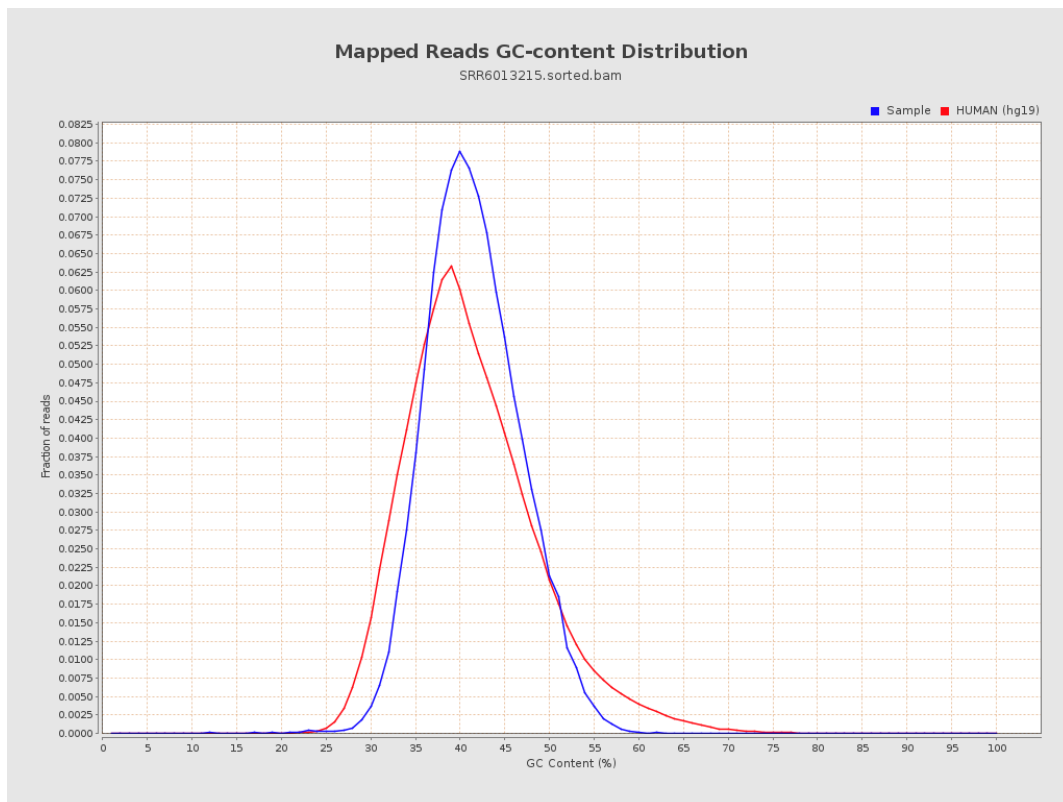
7. Results : Duplication Rate Histogram



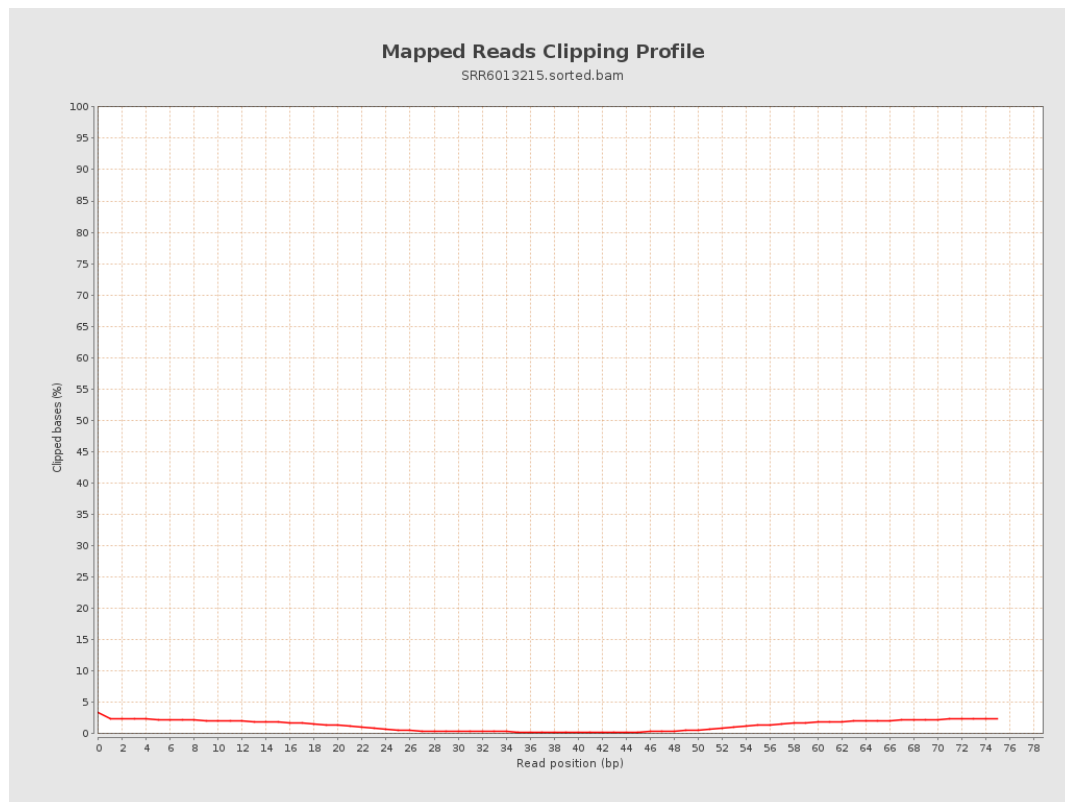
8. Results : Mapped Reads Nucleotide Content



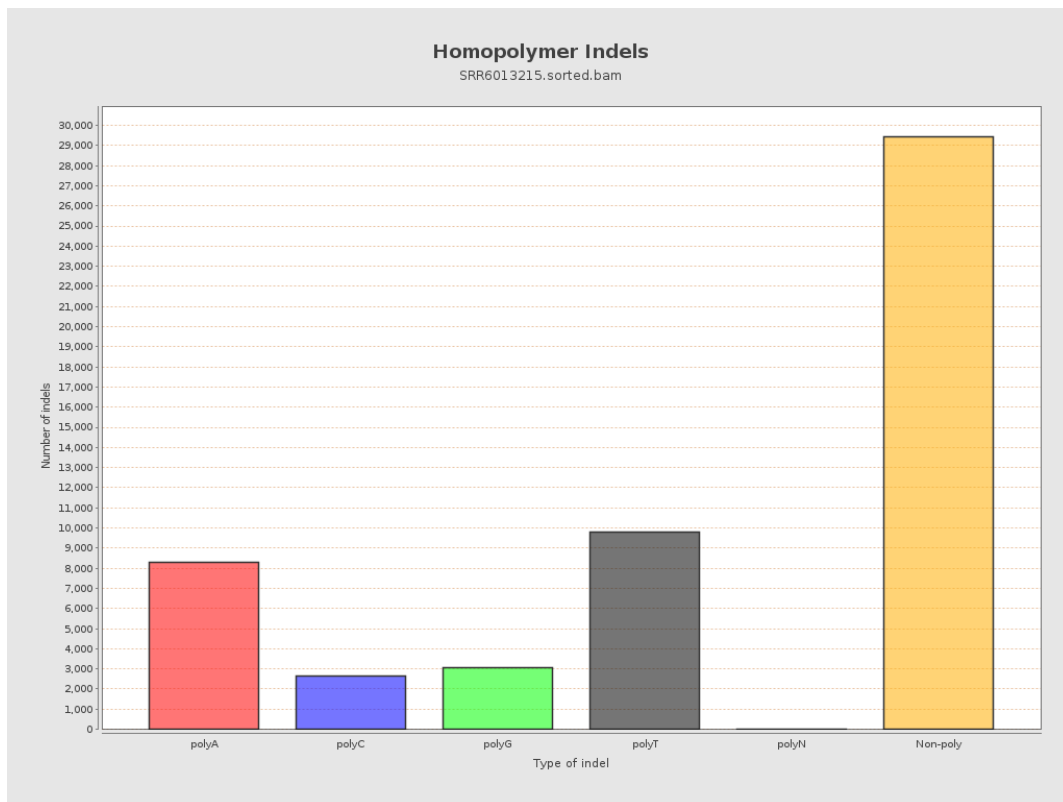
9. Results : Mapped Reads GC-content Distribution



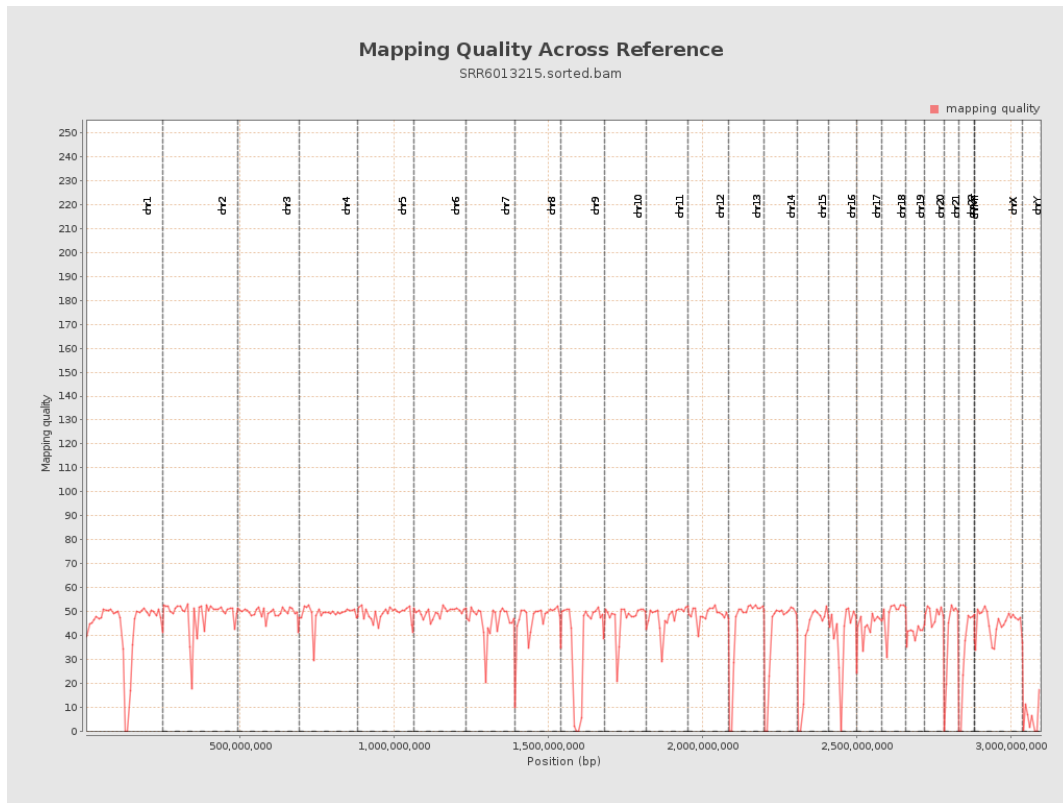
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

