

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:24:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819016.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_SRR1819016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:24:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,936,914
Mapped reads	2,707,615 / 92.19%
Unmapped reads	229,299 / 7.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,016 / 1.26%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	1,307,637 / 44.52%
Duplication rate	37.18%
Clipped reads	2,730,394 / 92.97%

2.2. ACGT Content

Number/percentage of A's	71,937,314 / 28.69%
Number/percentage of C's	53,174,387 / 21.21%
Number/percentage of T's	71,771,481 / 28.63%
Number/percentage of G's	53,833,054 / 21.47%
Number/percentage of N's	12,009 / 0%
GC Percentage	42.68%

2.3. Coverage

Mean	0.081

Standard Deviation	0.9565
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2.4. Mapping Quality

Mean Mapping Quality	49.3
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2.5. Mismatches and indels

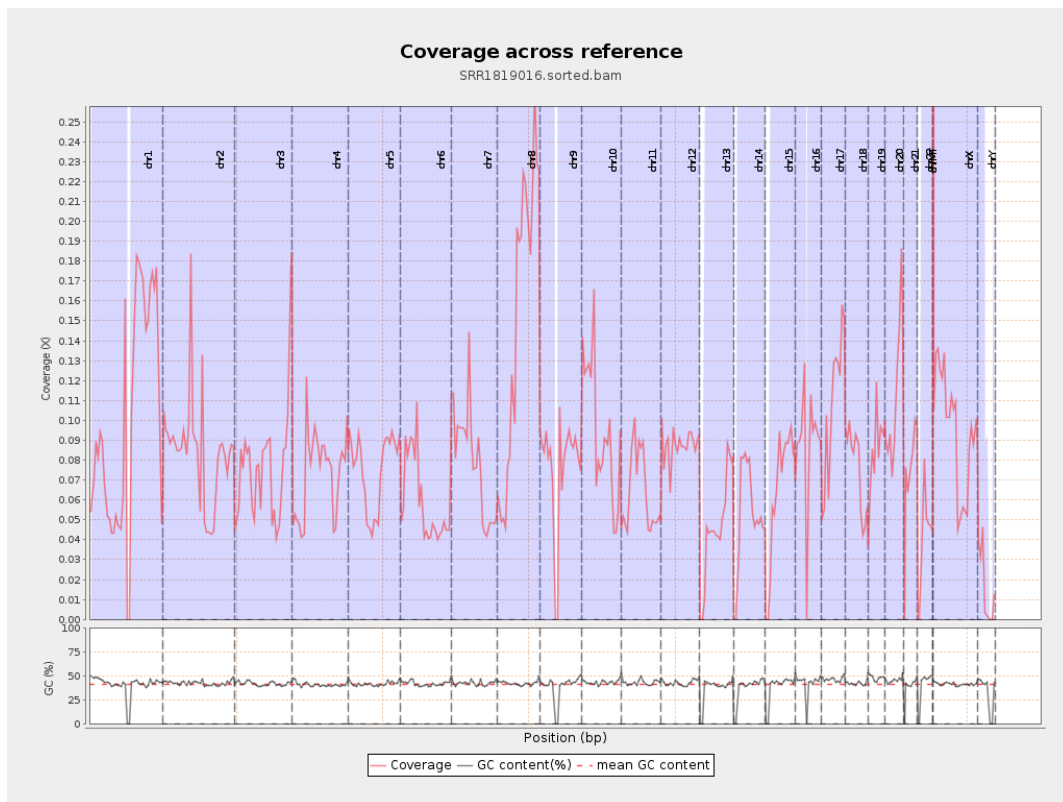
General error rate	0.65%
Mismatches	1,538,326
Insertions	41,384
Mapped reads with at least one insertion	1.48%
Deletions	79,777
Mapped reads with at least one deletion	2.88%
Homopolymer indels	41.58%

2.6. Chromosome stats

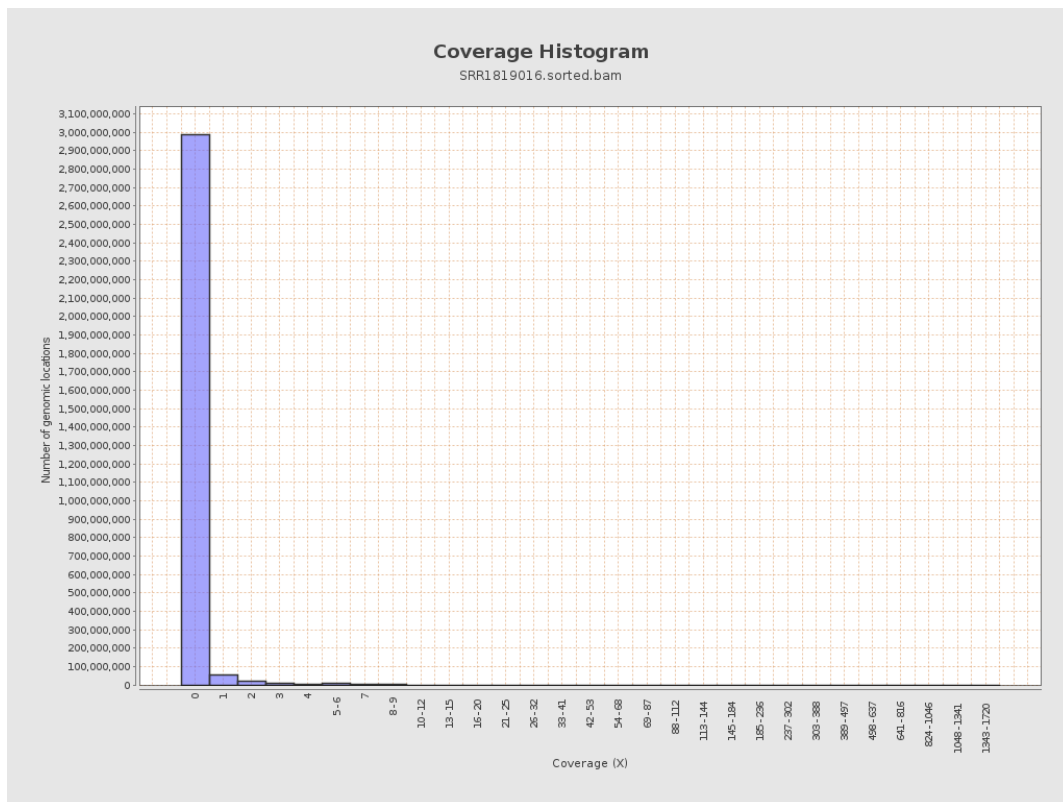
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24882062	0.0998	1.6177
chr2	243199373	20417625	0.084	1.431
chr3	198022430	15117512	0.0763	0.5589
chr4	191154276	14029626	0.0734	0.6509
chr5	180915260	13649165	0.0754	0.5895
chr6	171115067	10164879	0.0594	0.5981
chr7	159138663	12552232	0.0789	1.1967

chr8	146364022	22494551	0.1537	0.9067
chr9	141213431	10742141	0.0761	0.89
chr10	135534747	12680226	0.0936	1.1327
chr11	135006516	8550814	0.0633	0.613
chr12	133851895	11745087	0.0877	0.6171
chr13	115169878	5374161	0.0467	0.4386
chr14	107349540	5727251	0.0534	0.5131
chr15	102531392	6469497	0.0631	0.5159
chr16	90354753	7814701	0.0865	1.096
chr17	81195210	8718710	0.1074	0.7832
chr18	78077248	5908332	0.0757	1.0588
chr19	59128983	5071034	0.0858	1.5029
chr20	63025520	7171540	0.1138	0.7408
chr21	48129895	3601375	0.0748	0.6274
chr22	51304566	2053035	0.04	0.4476
chrMT	16571	167337	10.0982	9.6718
chrX	155270560	14838389	0.0956	0.7595
chrY	59373566	936732	0.0158	1.0362

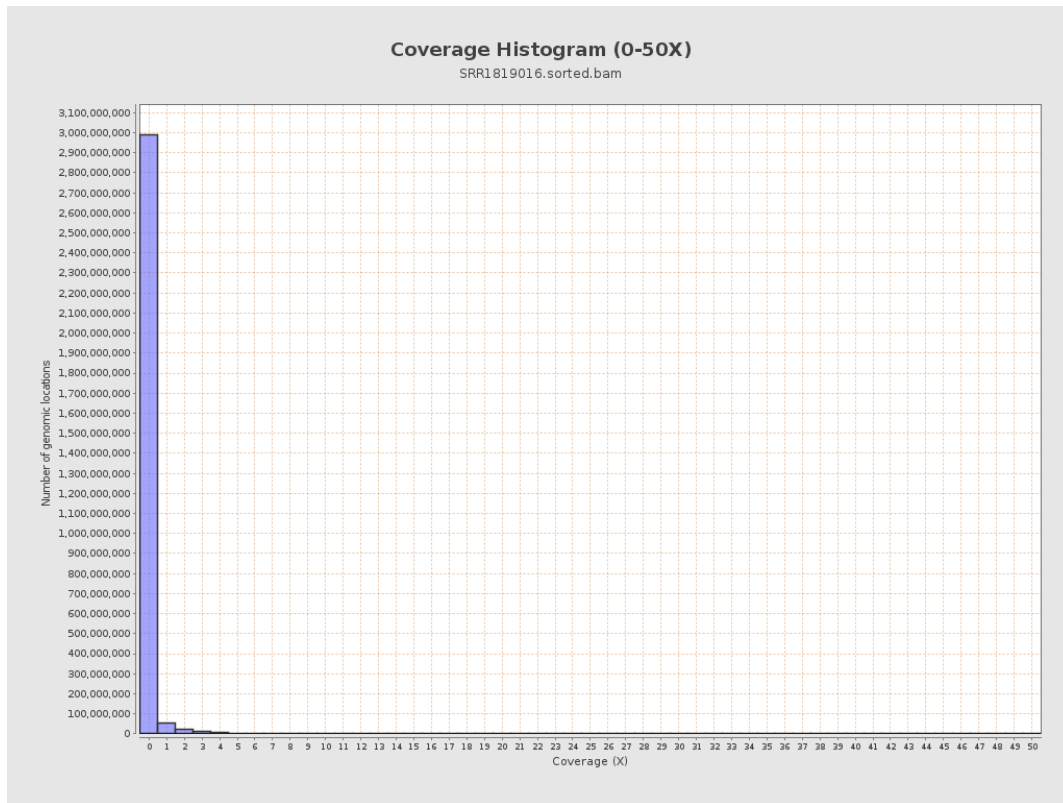
3. Results : Coverage across reference



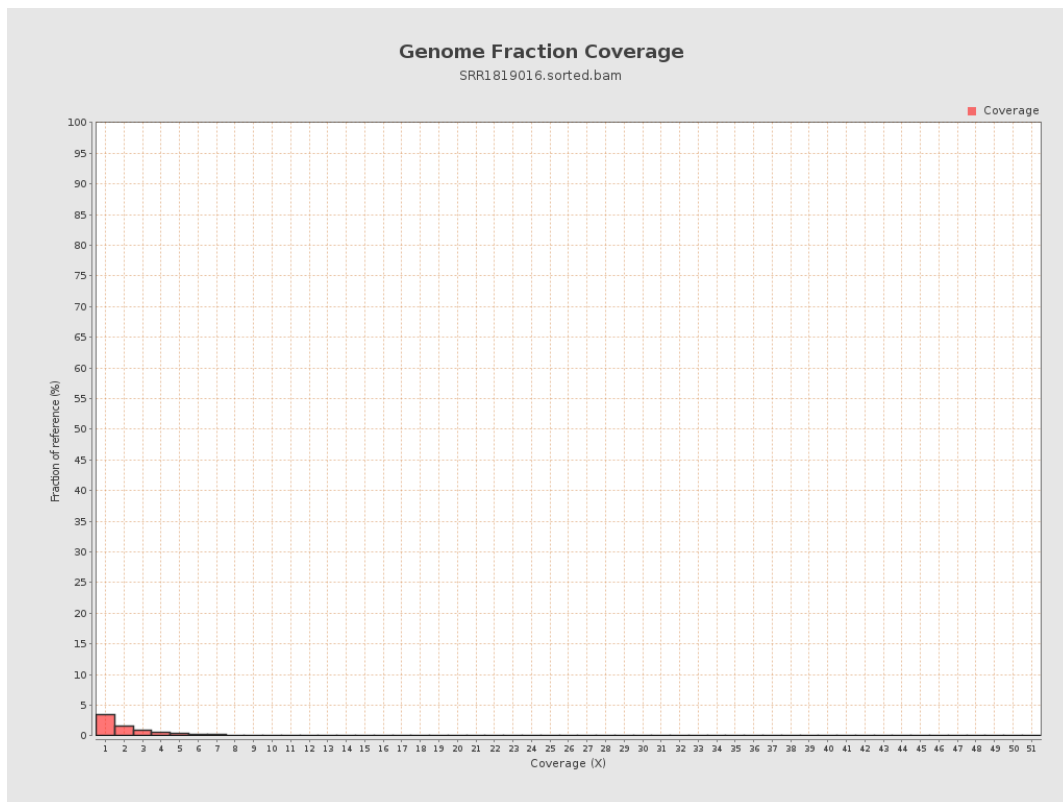
4. Results : Coverage Histogram



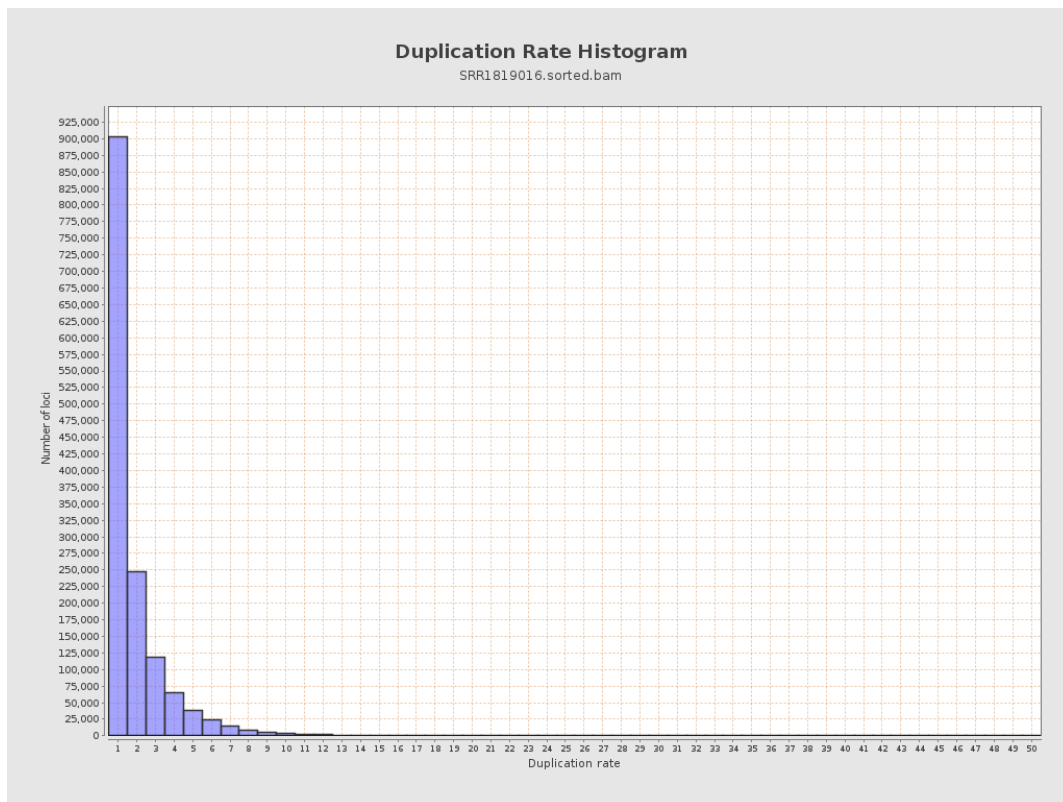
5. Results : Coverage Histogram (0-50X)



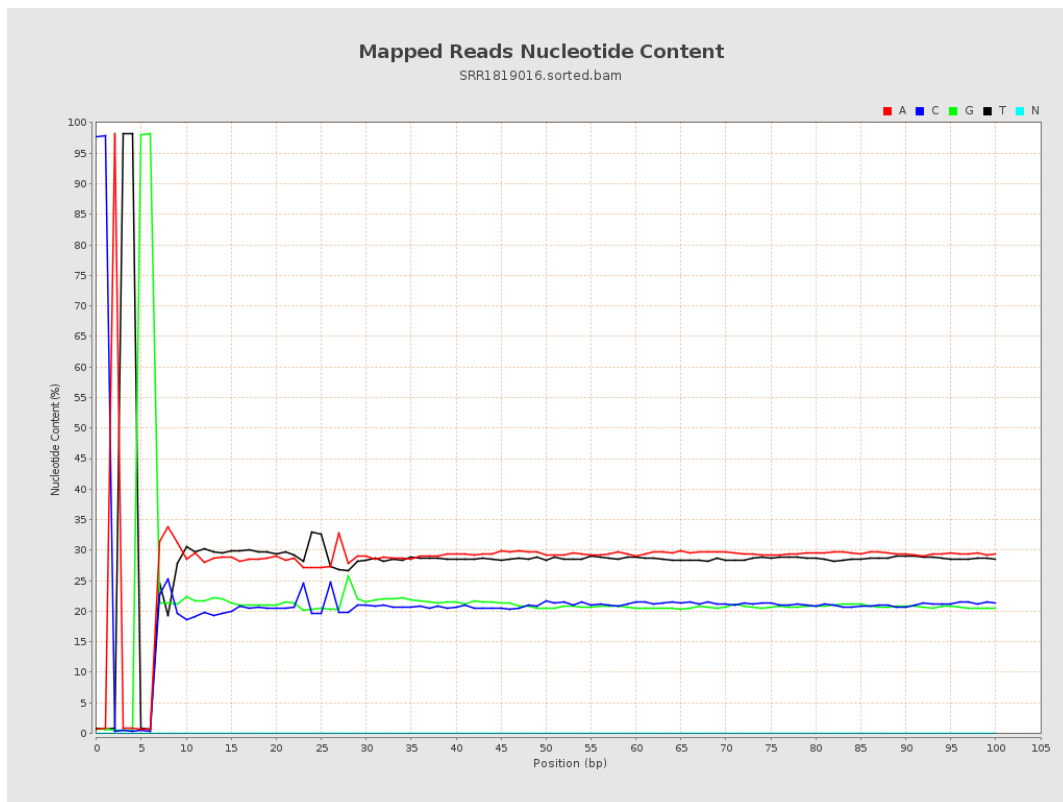
6. Results : Genome Fraction Coverage



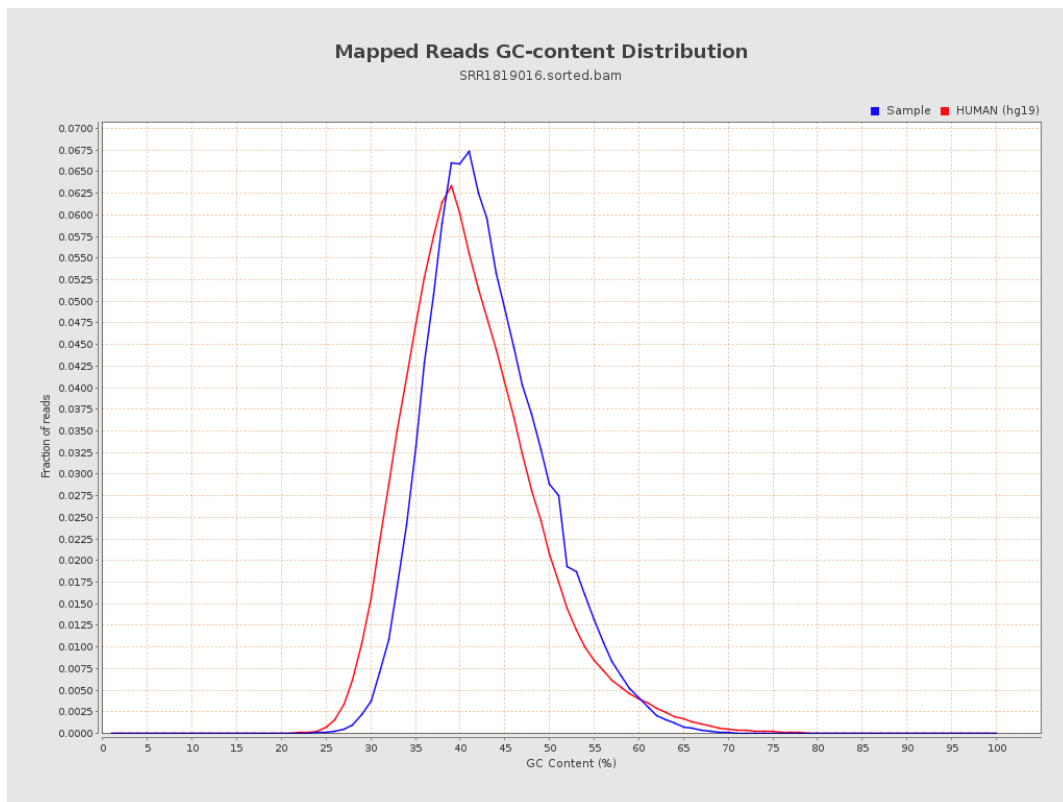
7. Results : Duplication Rate Histogram



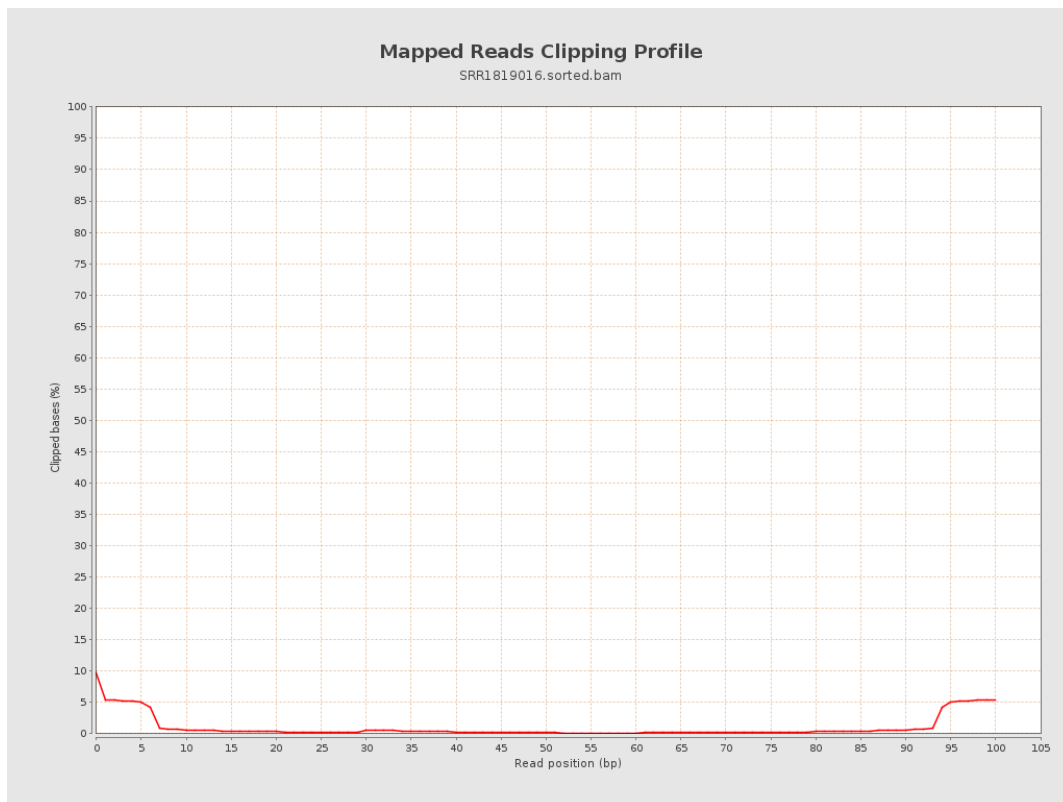
8. Results : Mapped Reads Nucleotide Content



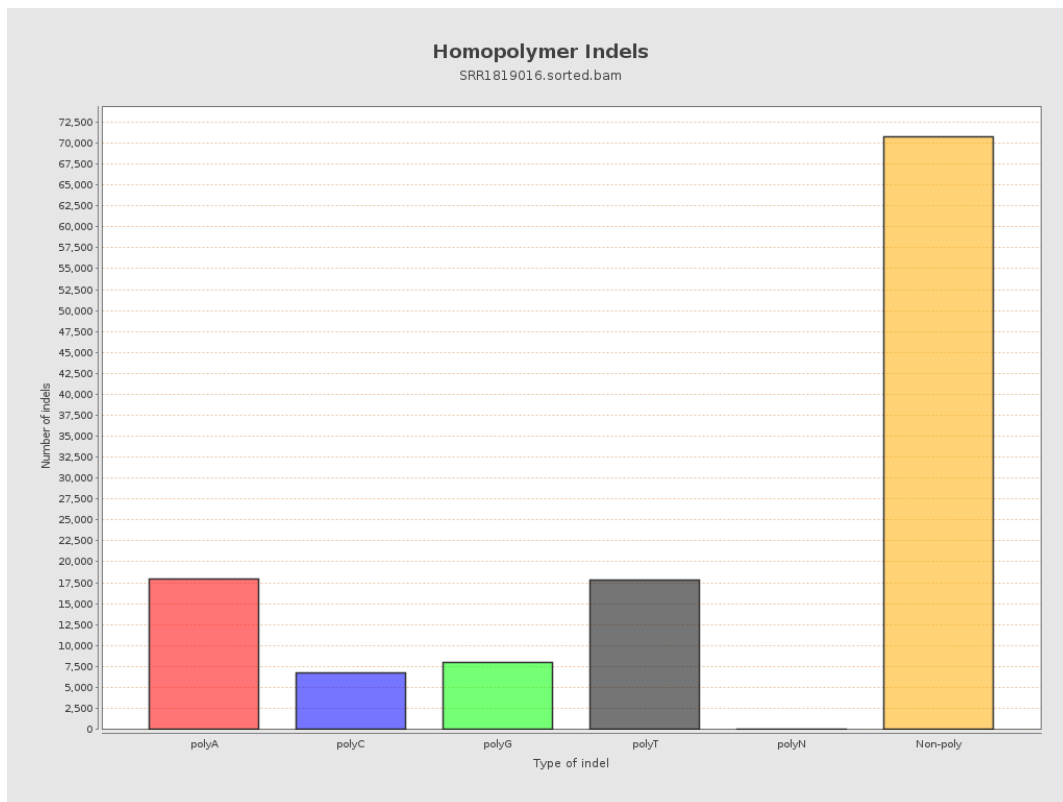
9. Results : Mapped Reads GC-content Distribution



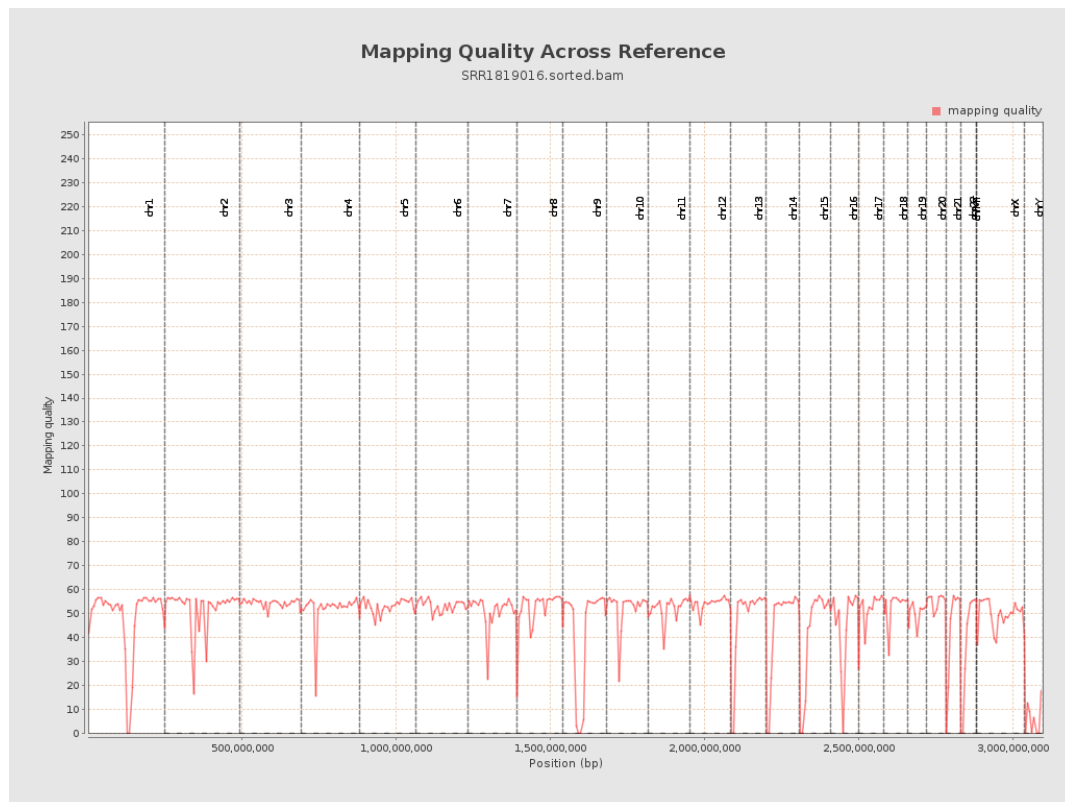
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

