

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:47:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013185.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_SRR6013185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:47:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,853,658
Mapped reads	2,569,665 / 90.05%
Unmapped reads	283,993 / 9.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,220 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	98,577 / 3.45%
Duplication rate	2.34%
Clipped reads	1,272,455 / 44.59%

2.2. ACGT Content

Number/percentage of A's	46,096,272 / 27.42%
Number/percentage of C's	32,063,250 / 19.07%
Number/percentage of T's	51,123,176 / 30.41%
Number/percentage of G's	38,823,018 / 23.09%
Number/percentage of N's	20,331 / 0.01%
GC Percentage	42.16%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.6018
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.02
----------------------	-------

2.5. Mismatches and indels

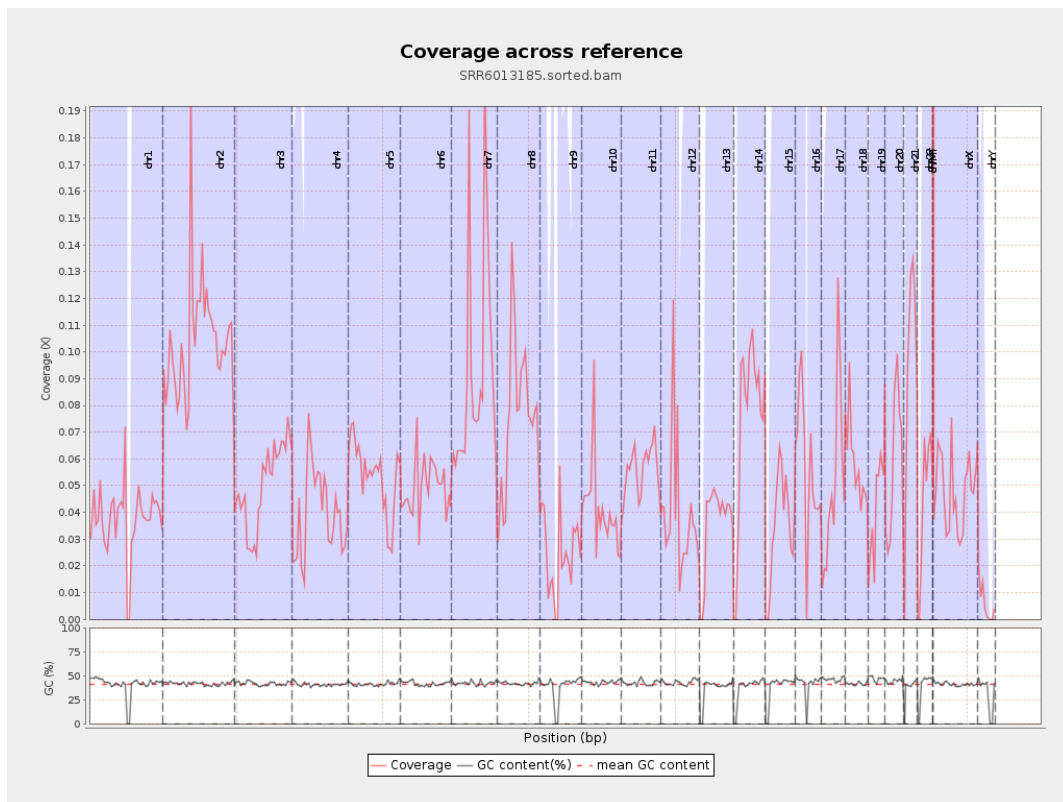
General error rate	0.79%
Mismatches	1,309,851
Insertions	11,957
Mapped reads with at least one insertion	0.46%
Deletions	46,069
Mapped reads with at least one deletion	1.77%
Homopolymer indels	44.7%

2.6. Chromosome stats

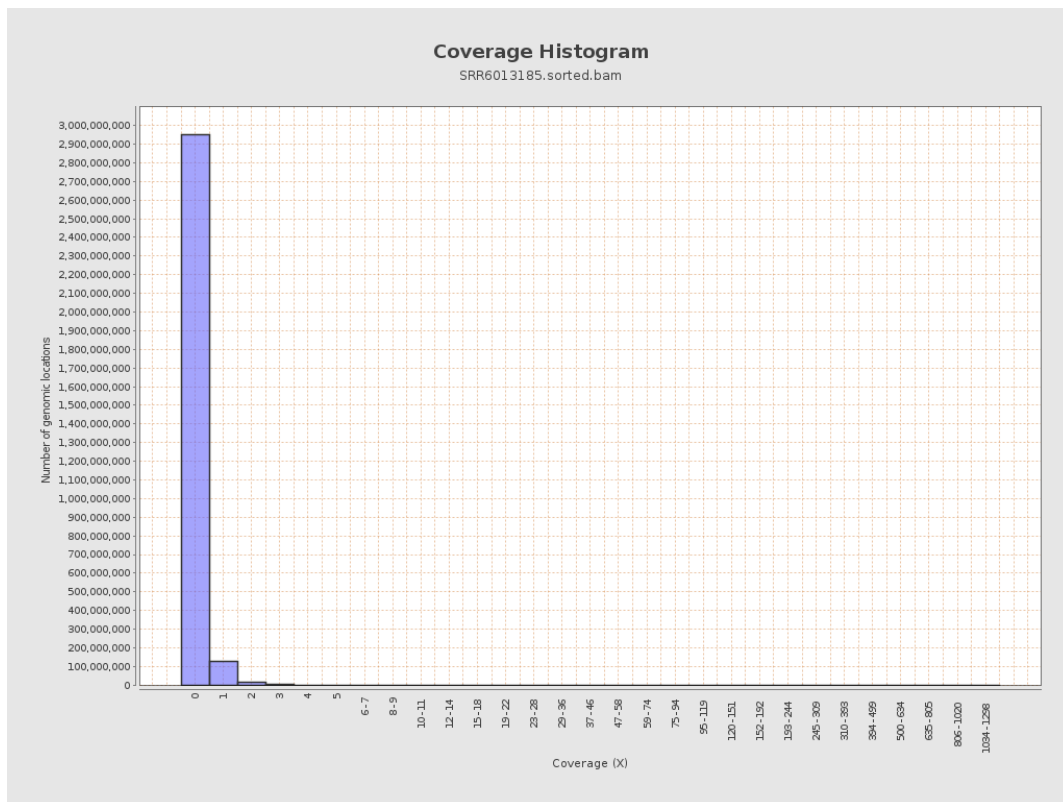
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9378824	0.0376	0.7317
chr2	243199373	25337245	0.1042	0.8362
chr3	198022430	9898161	0.05	0.2496
chr4	191154276	7747709	0.0405	0.2383
chr5	180915260	9666730	0.0534	0.2602
chr6	171115067	8486552	0.0496	0.3755
chr7	159138663	14522106	0.0913	1.6478

chr8	146364022	11100622	0.0758	0.5207
chr9	141213431	3412894	0.0242	0.4677
chr10	135534747	5559089	0.041	0.5329
chr11	135006516	7541385	0.0559	0.4222
chr12	133851895	5187252	0.0388	0.2387
chr13	115169878	4172054	0.0362	0.2096
chr14	107349540	8082388	0.0753	0.3292
chr15	102531392	3460635	0.0338	0.2168
chr16	90354753	5098563	0.0564	0.3231
chr17	81195210	4158044	0.0512	0.2631
chr18	78077248	4571238	0.0585	1.0561
chr19	59128983	2504632	0.0424	0.7054
chr20	63025520	3670692	0.0582	0.2947
chr21	48129895	4454684	0.0926	0.3596
chr22	51304566	2243129	0.0437	0.2353
chrMT	16571	57804	3.4883	2.6334
chrX	155270560	7541868	0.0486	0.3099
chrY	59373566	350691	0.0059	0.1096

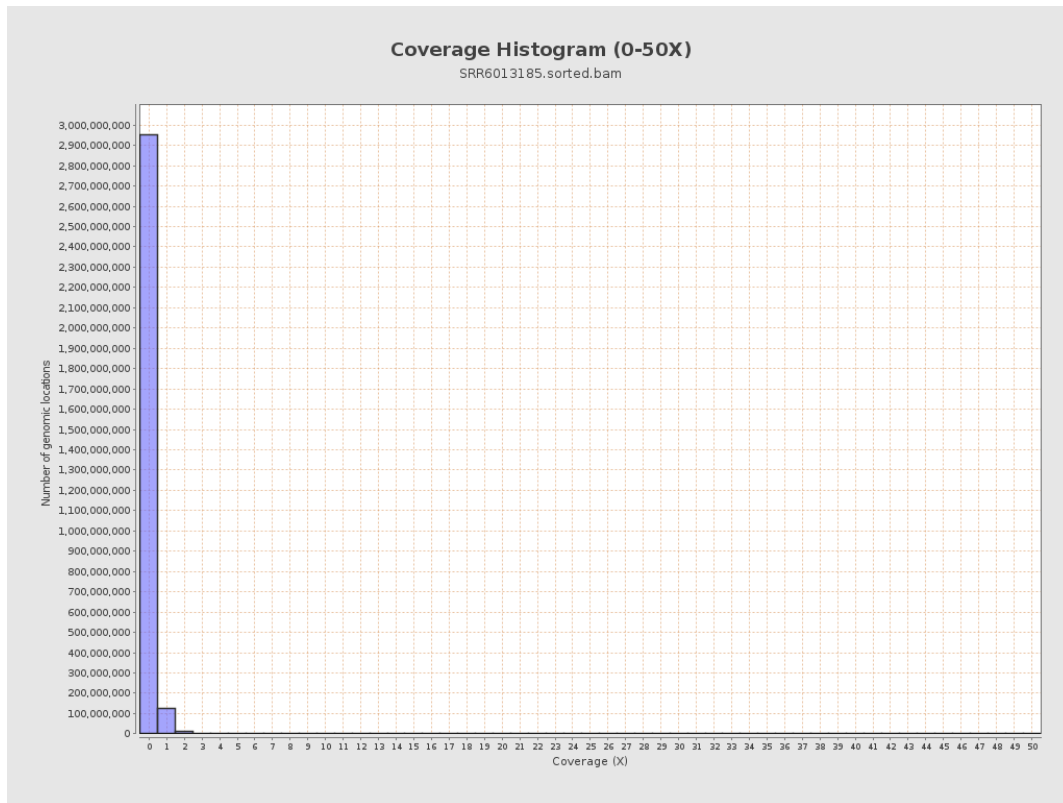
3. Results : Coverage across reference



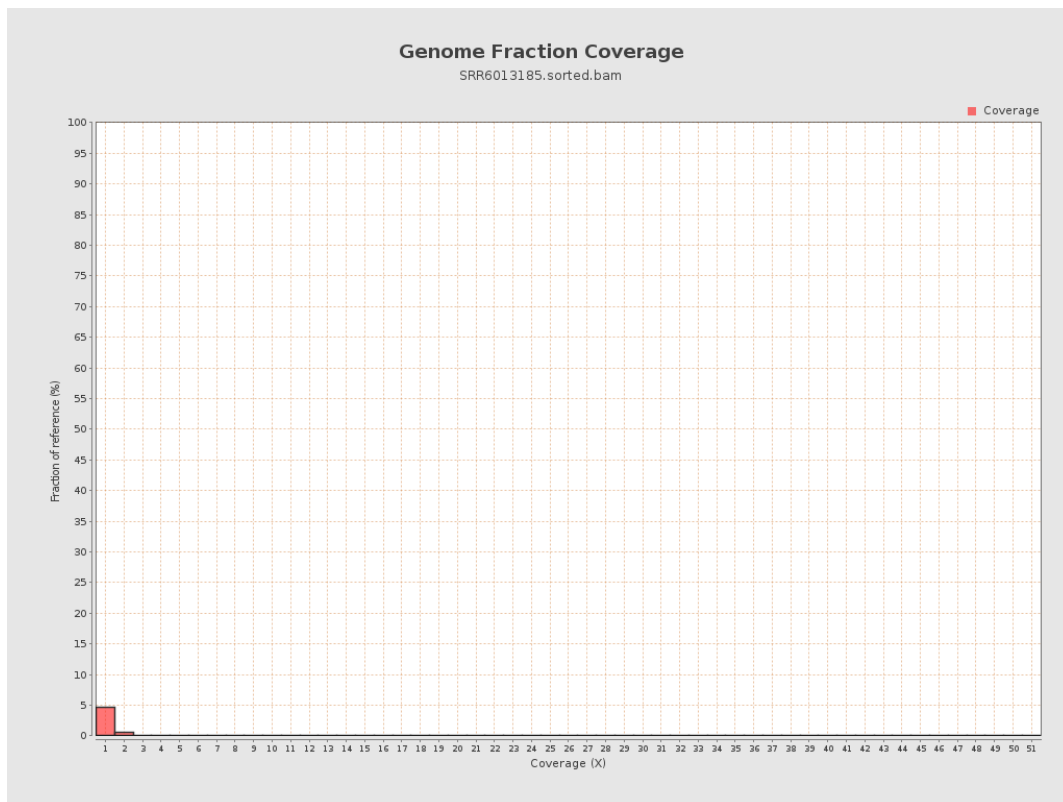
4. Results : Coverage Histogram



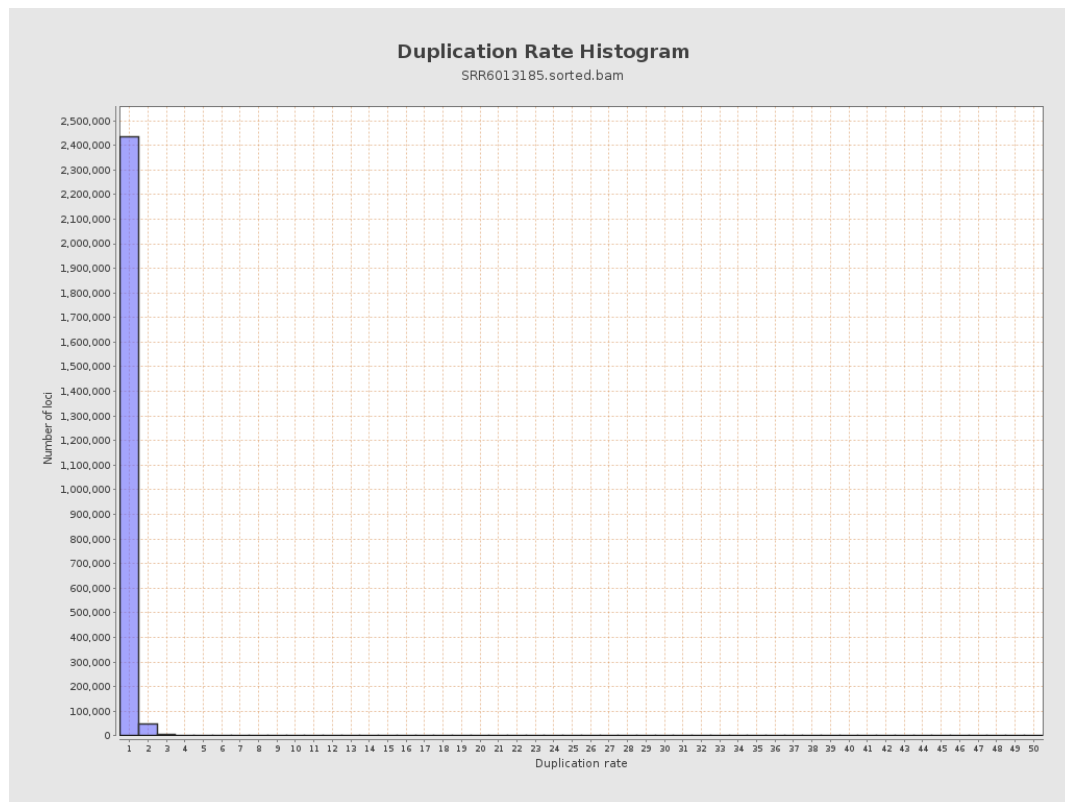
5. Results : Coverage Histogram (0-50X)



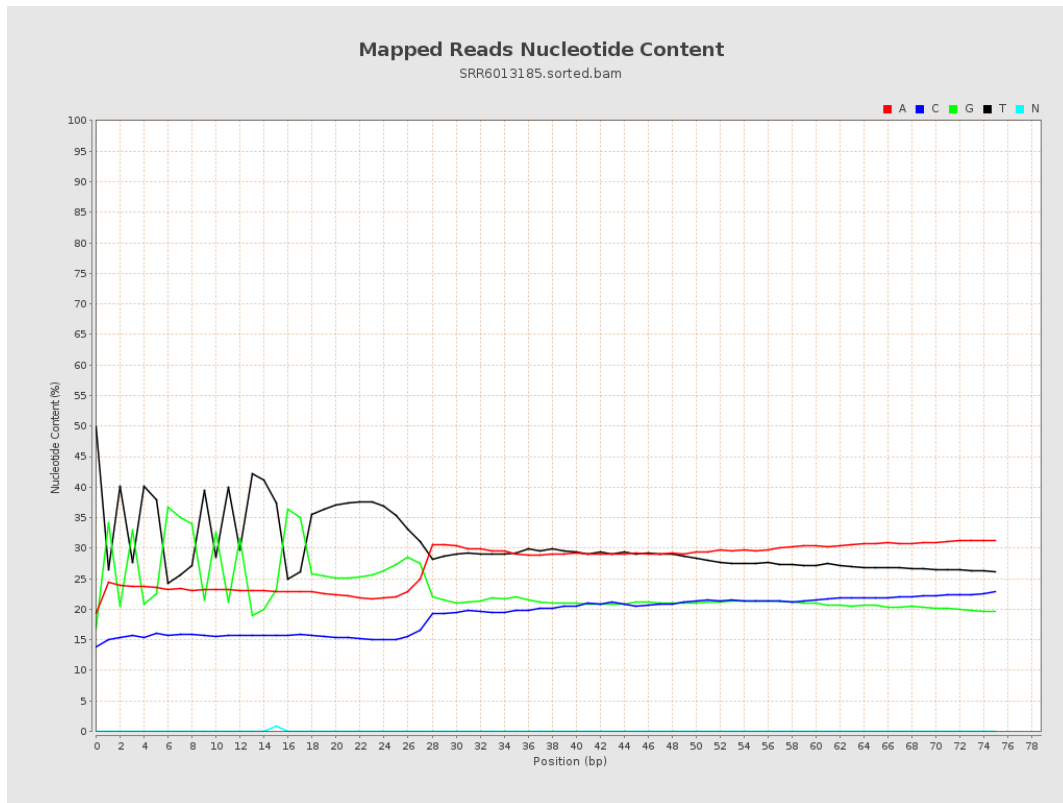
6. Results : Genome Fraction Coverage



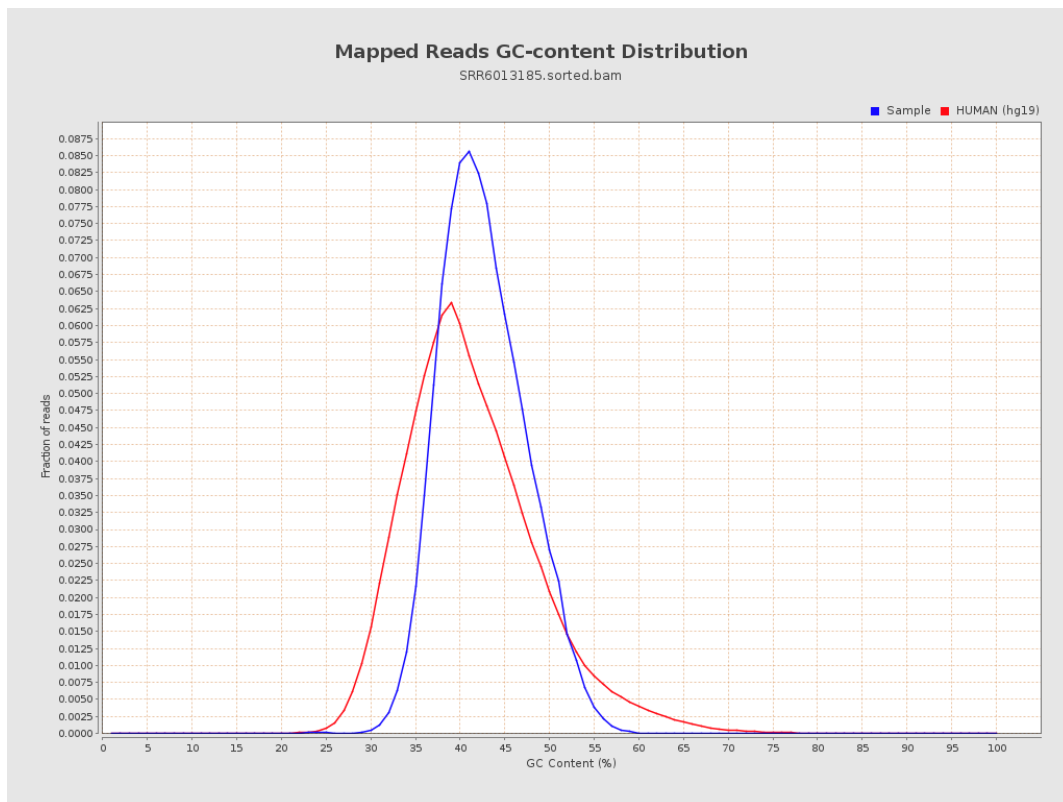
7. Results : Duplication Rate Histogram



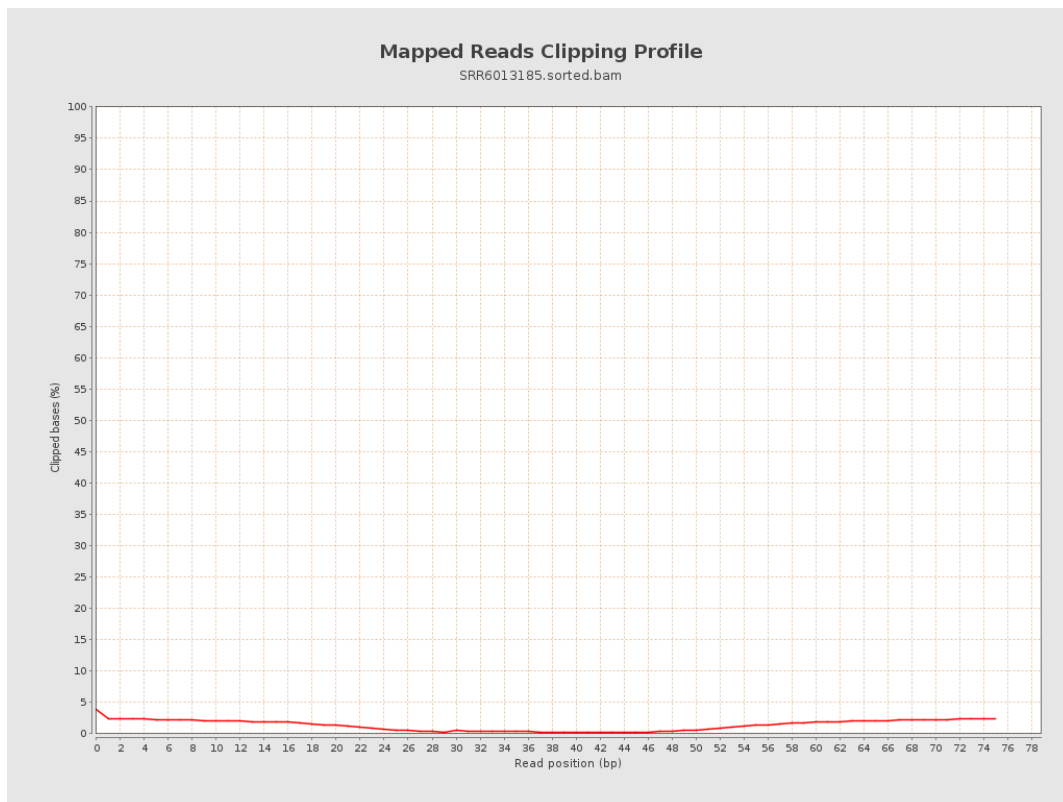
8. Results : Mapped Reads Nucleotide Content



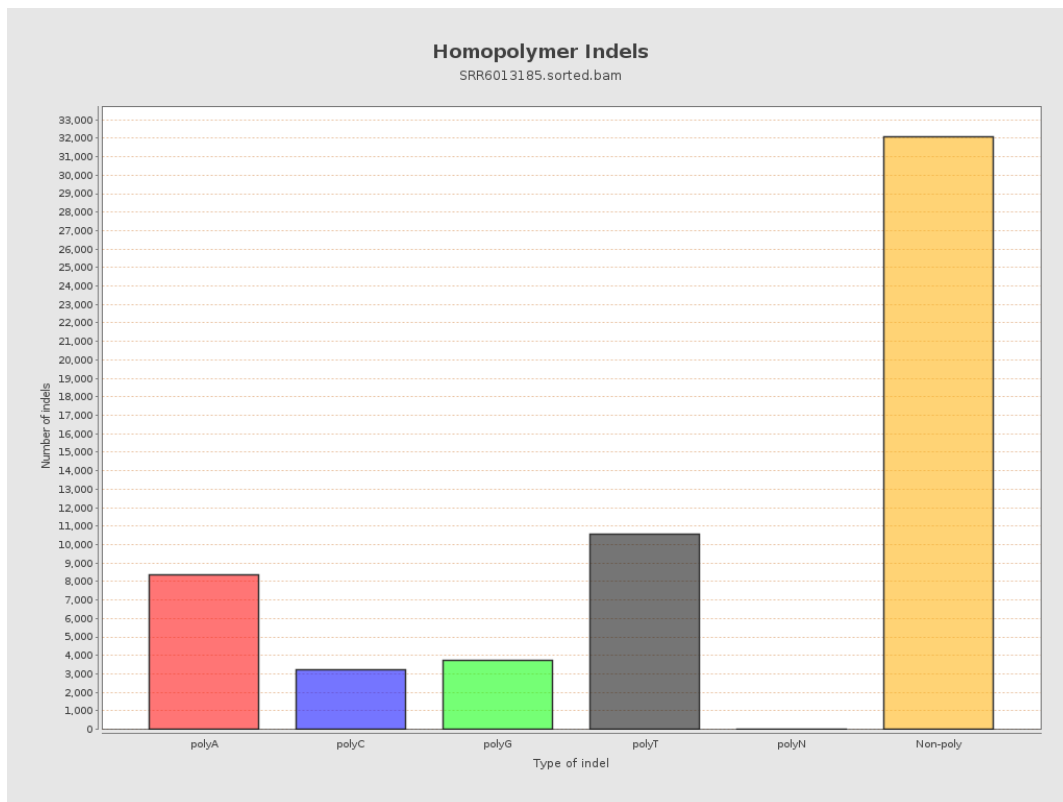
9. Results : Mapped Reads GC-content Distribution



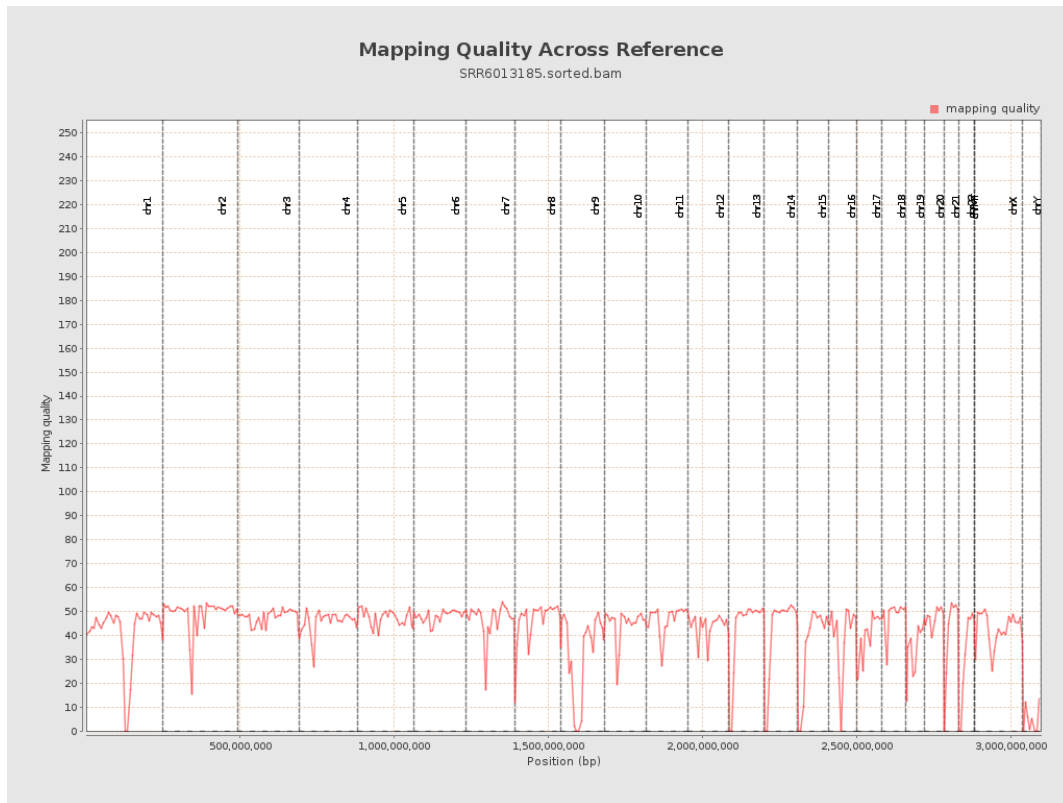
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

