Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:48:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004118.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_SRR6004118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:48:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,690,723
Mapped reads	2,746,320 / 74.41%
Unmapped reads	944,403 / 25.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,235 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	406,329 / 11.01%
Duplication rate	11.34%
Clipped reads	1,476,297 / 40%

2.2. ACGT Content

Number/percentage of A's	47,702,748 / 26.96%
Number/percentage of C's	30,796,131 / 17.4%
Number/percentage of T's	59,273,761 / 33.5%
Number/percentage of G's	39,150,012 / 22.13%
Number/percentage of N's	18,757 / 0.01%
GC Percentage	39.53%

2.3. Coverage

Mean	0.0572

Standard Deviation	0.5853

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

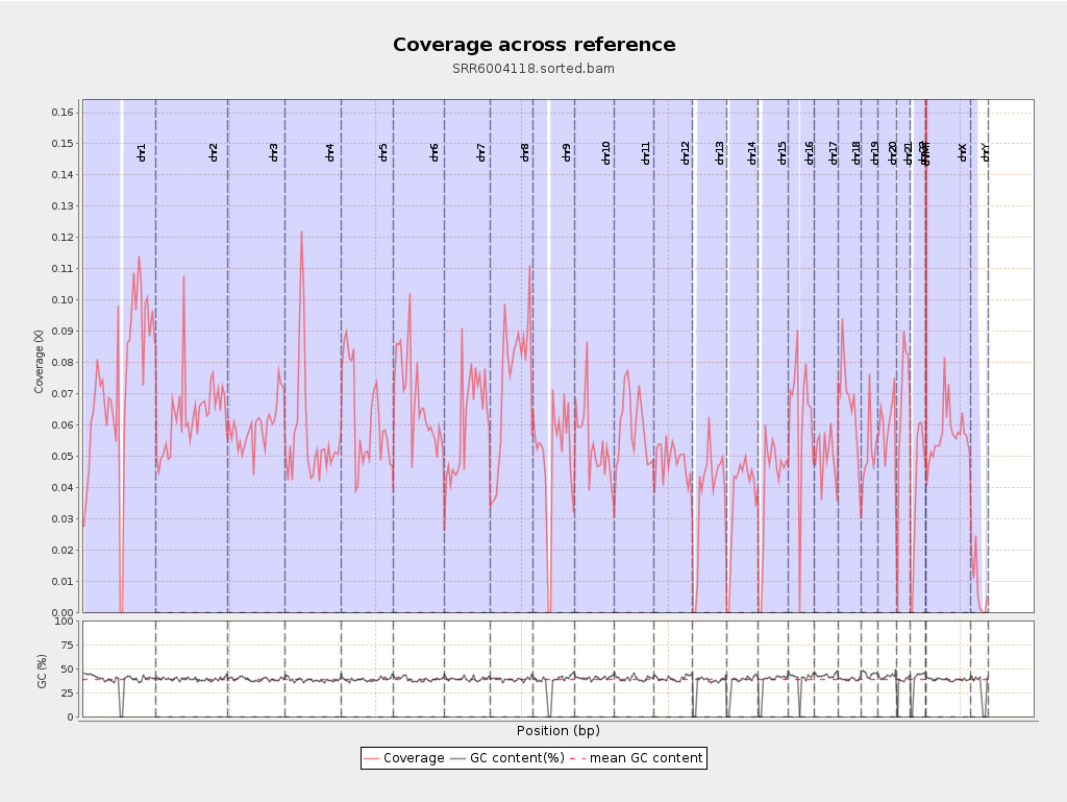
General error rate	1.03%
Mismatches	1,787,826
Insertions	16,031
Mapped reads with at least one insertion	0.58%
Deletions	52,587
Mapped reads with at least one deletion	1.89%
Homopolymer indels	49.37%

2.6. Chromosome stats

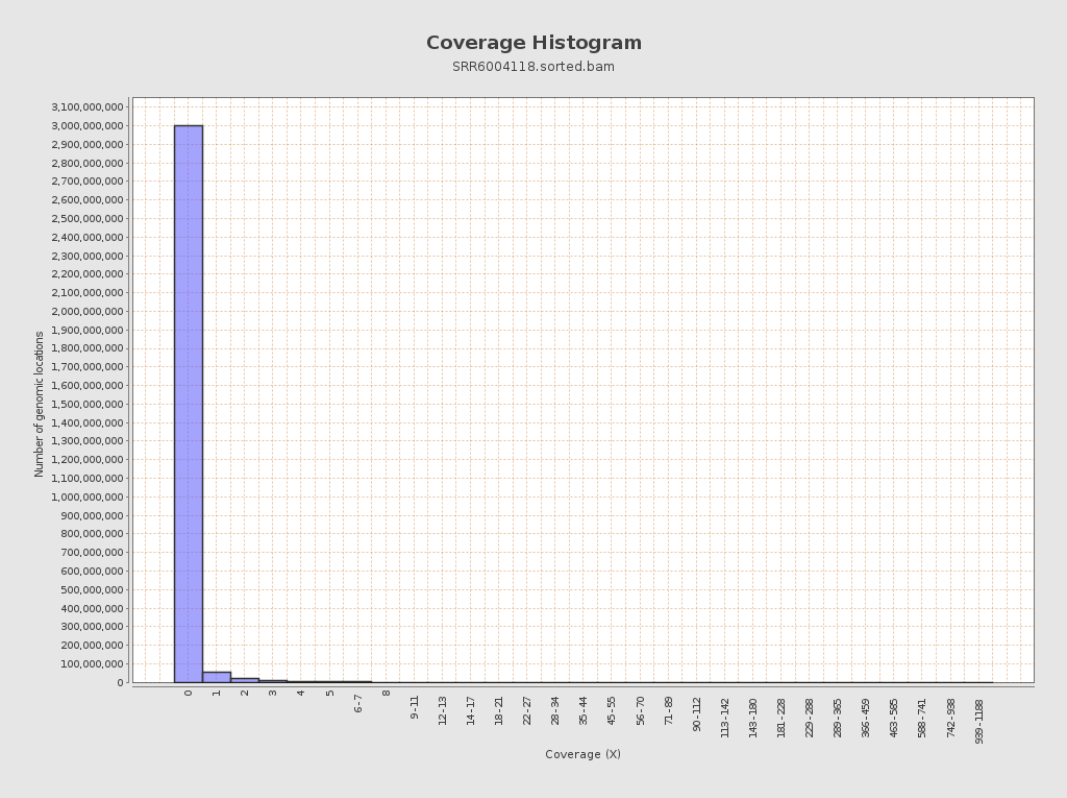
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18043527	0.0724	0.9484
chr2	243199373	15377439	0.0632	0.7167
chr3	198022430	11818690	0.0597	0.4082
chr4	191154276	10943098	0.0572	0.4172
chr5	180915260	11161338	0.0617	0.4154
chr6	171115067	11625145	0.0679	0.5073
chr7	159138663	9637332	0.0606	0.6707

chr8	146364022	10750331	0.0734	0.8588
chr9	141213431	6966435	0.0493	0.5622
chr10	135534747	7286346	0.0538	0.4819
chr11	135006516	7933590	0.0588	0.5278
chr12	133851895	6469976	0.0483	0.3695
chr13	115169878	4394287	0.0382	0.3275
chr14	107349540	3984795	0.0371	0.3519
chr15	102531392	4152860	0.0405	0.3334
chr16	90354753	5615575	0.0622	0.4327
chr17	81195210	4068934	0.0501	0.4059
chr18	78077248	5290277	0.0678	1.144
chr19	59128983	3052946	0.0516	0.6925
chr20	63025520	3809480	0.0604	0.4265
chr21	48129895	3164130	0.0657	0.4533
chr22	51304566	2054132	0.04	0.3189
chrMT	16571	123028	7.4243	6.8739
chrX	155270560	8836767	0.0569	0.4379
chrY	59373566	466802	0.0079	0.1827

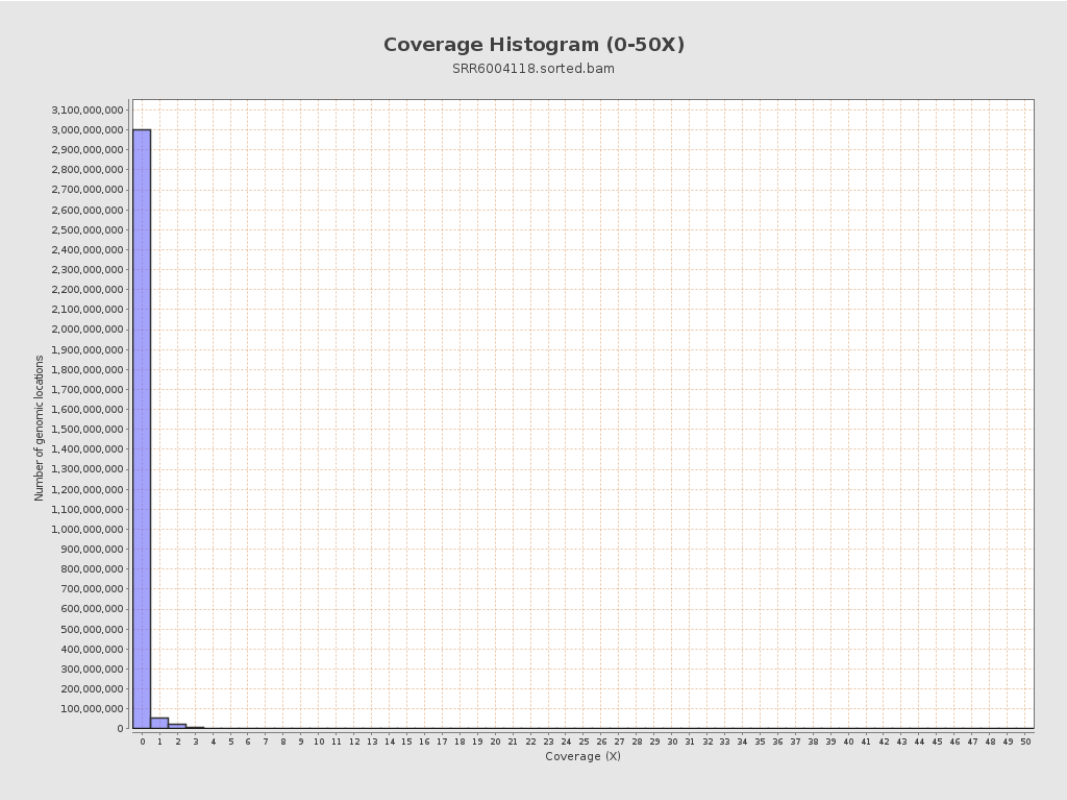
3. Results : Coverage across reference



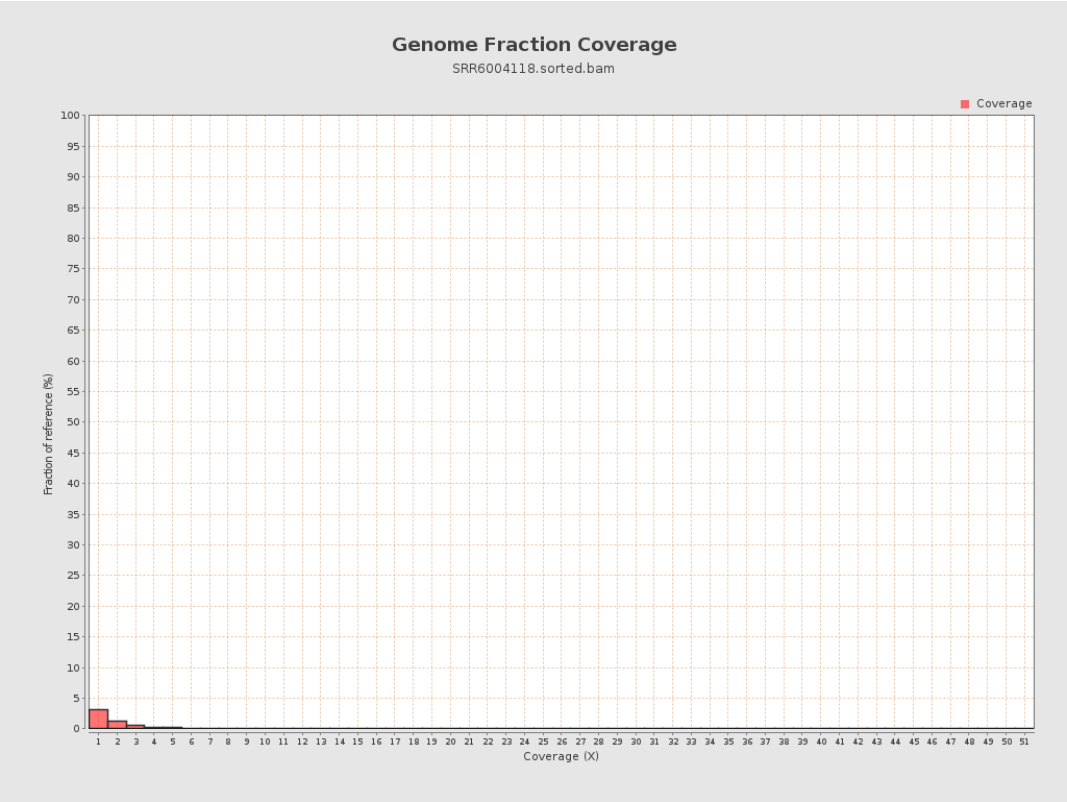
4. Results : Coverage Histogram



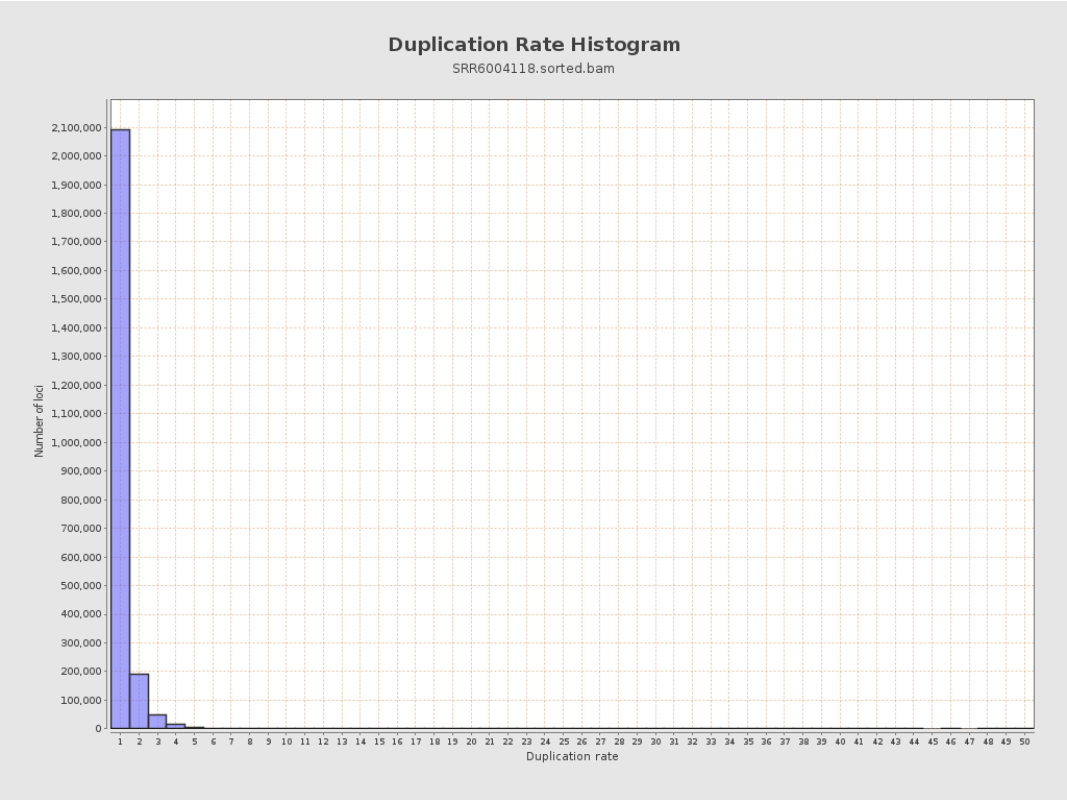
5. Results : Coverage Histogram (0-50X)



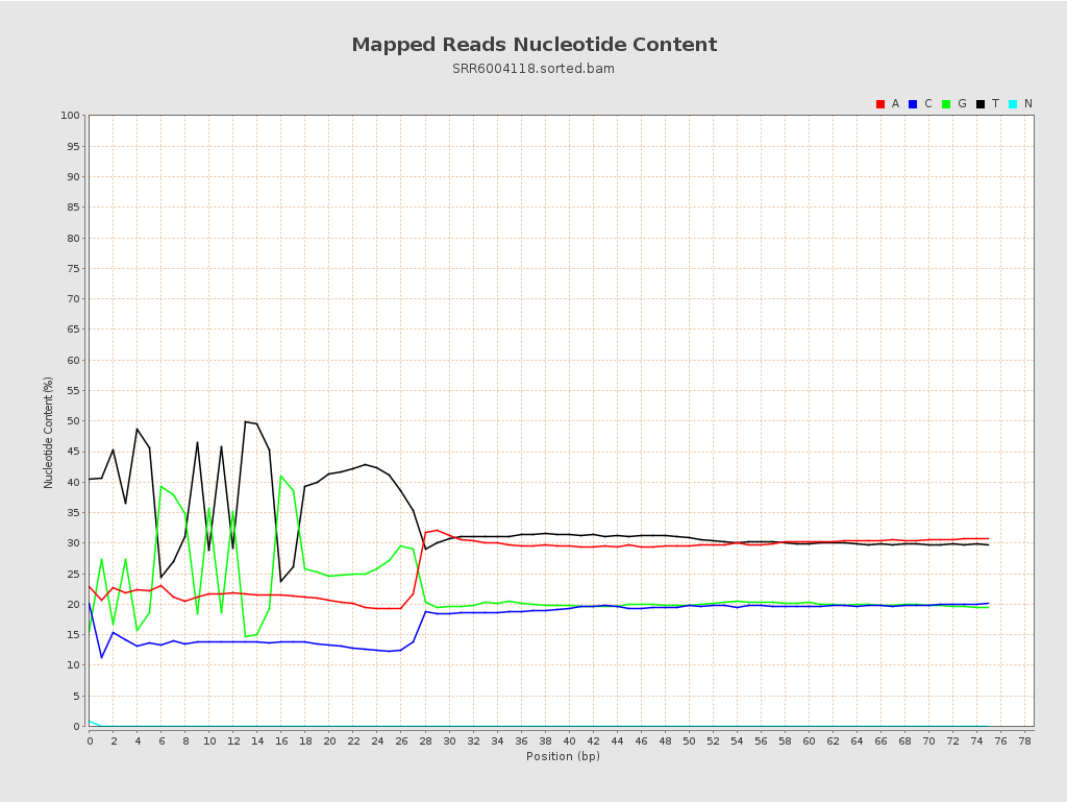
6. Results : Genome Fraction Coverage



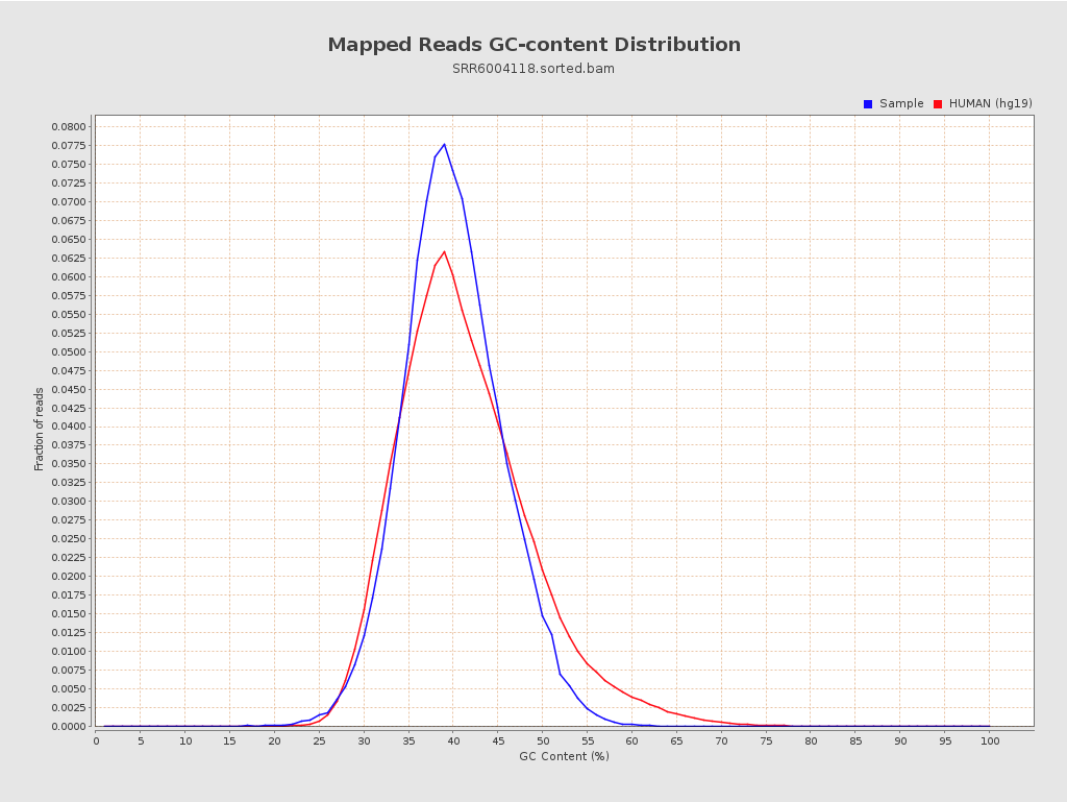
7. Results : Duplication Rate Histogram



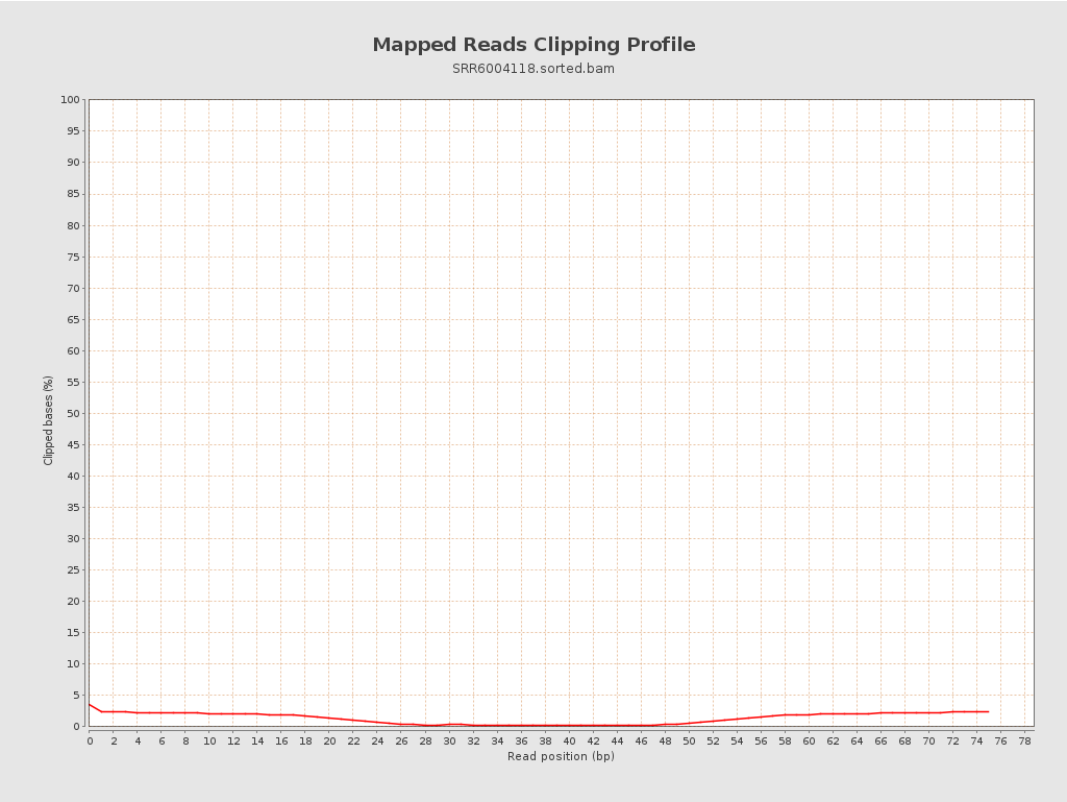
8. Results : Mapped Reads Nucleotide Content



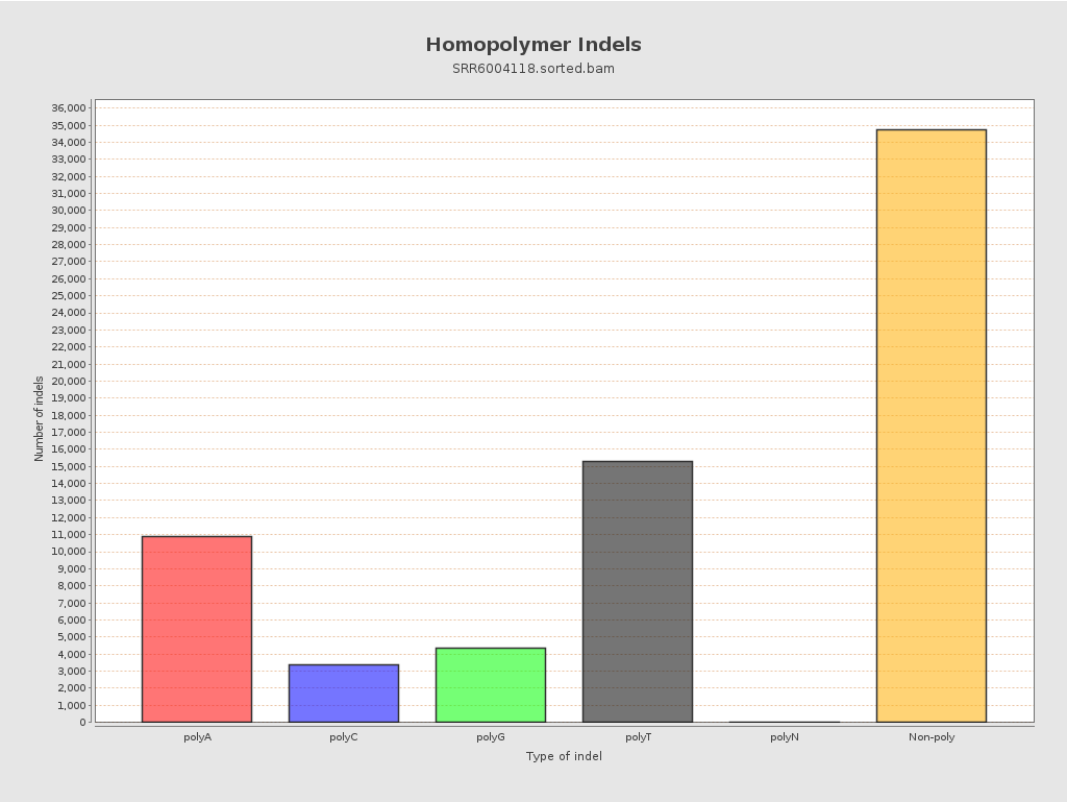
9. Results : Mapped Reads GC-content Distribution



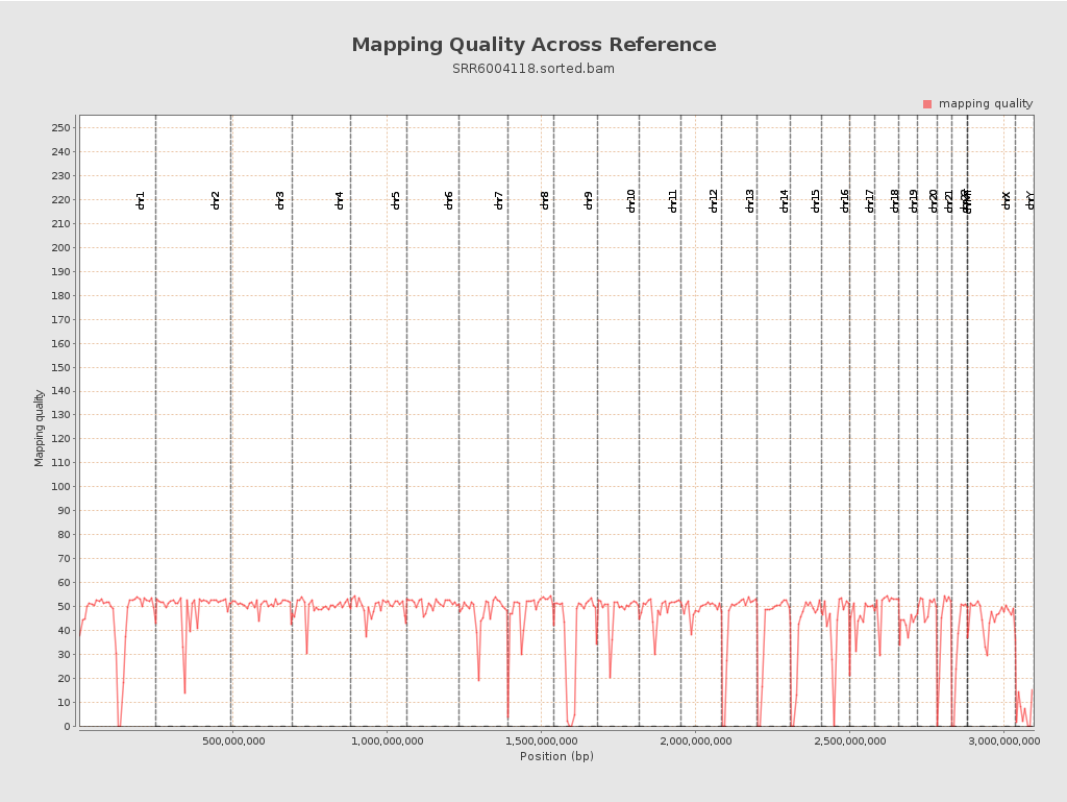
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram