Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 04:39:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054570.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_SRR054570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054570.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 04:39:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,971,268
Mapped reads	9,378,870 / 72.3%
Unmapped reads	3,592,398 / 27.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	288 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,123,811 / 24.08%
Duplication rate	21.89%
Clipped reads	1,068,911 / 8.24%

2.2. ACGT Content

Number/percentage of A's	134,695,213 / 30.57%
Number/percentage of C's	86,104,071 / 19.54%
Number/percentage of T's	130,958,973 / 29.72%
Number/percentage of G's	88,830,493 / 20.16%
Number/percentage of N's	57,640 / 0.01%
GC Percentage	39.7%

2.3. Coverage

Mean	0.1424

Standard Deviation	1.352

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

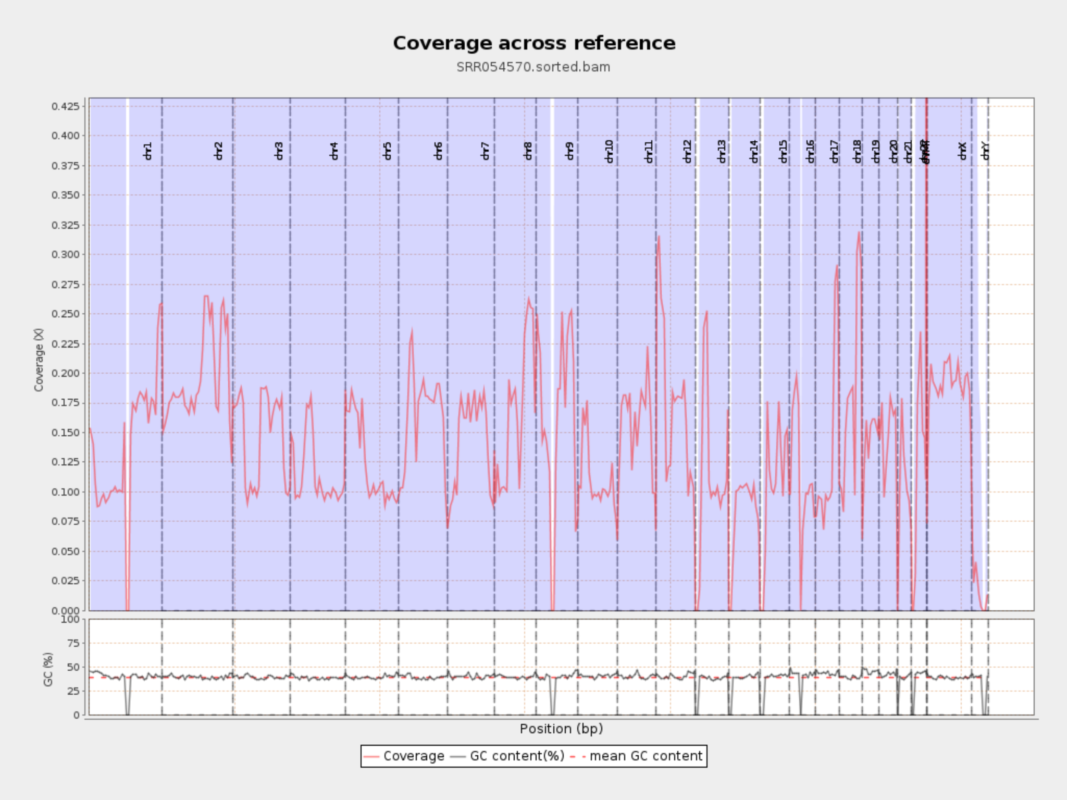
General error rate	0.55%
Mismatches	2,400,734
Insertions	20,386
Mapped reads with at least one insertion	0.22%
Deletions	64,122
Mapped reads with at least one deletion	0.68%
Homopolymer indels	46.94%

2.6. Chromosome stats

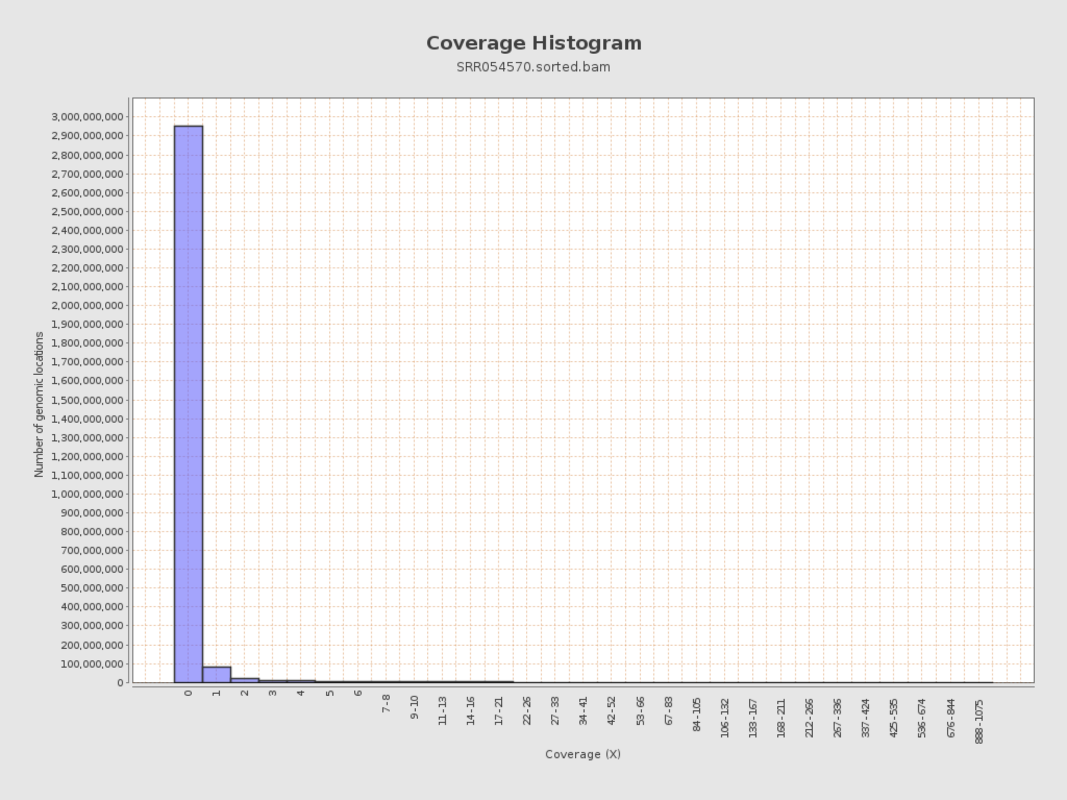
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33648243	0.135	1.3353
chr2	243199373	47775970	0.1964	1.684
chr3	198022430	29070185	0.1468	1.3203
chr4	191154276	21980481	0.115	1.1488
chr5	180915260	22537237	0.1246	1.175
chr6	171115067	28201959	0.1648	1.531
chr7	159138663	23044736	0.1448	1.4152

chr8	146364022	24810735	0.1695	1.5062
chr9	141213431	23063365	0.1633	1.4436
chr10	135534747	15172848	0.1119	1.1357
chr11	135006516	21076136	0.1561	1.3987
chr12	133851895	23620490	0.1765	1.4834
chr13	115169878	12201432	0.1059	1.1103
chr14	107349540	8792921	0.0819	1.121
chr15	102531392	10815598	0.1055	1.0732
chr16	90354753	10429246	0.1154	1.1553
chr17	81195210	11053224	0.1361	1.2864
chr18	78077248	14255407	0.1826	1.6004
chr19	59128983	8560090	0.1448	1.3402
chr20	63025520	9273209	0.1471	1.3571
chr21	48129895	5014375	0.1042	1.1452
chr22	51304566	5918042	0.1154	1.1238
chrMT	16571	31918	1.9261	4.7511
chrX	155270560	29381283	0.1892	1.5753
chrY	59373566	1011920	0.017	0.3759

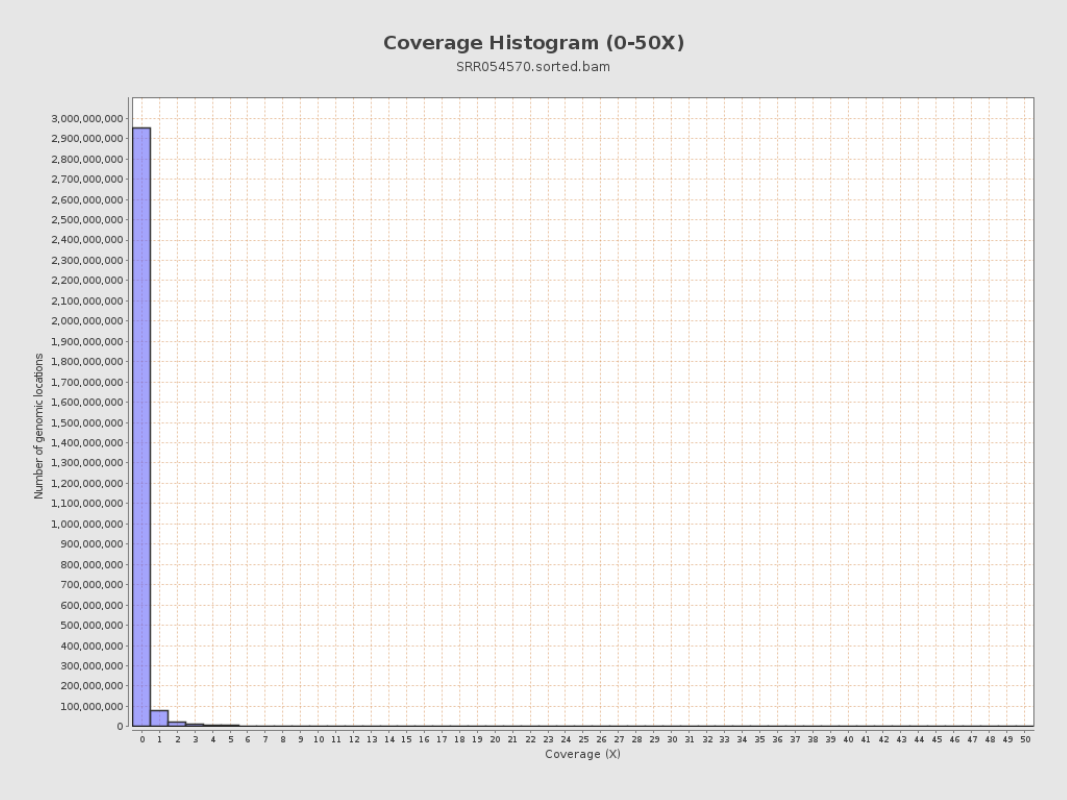
3. Results : Coverage across reference



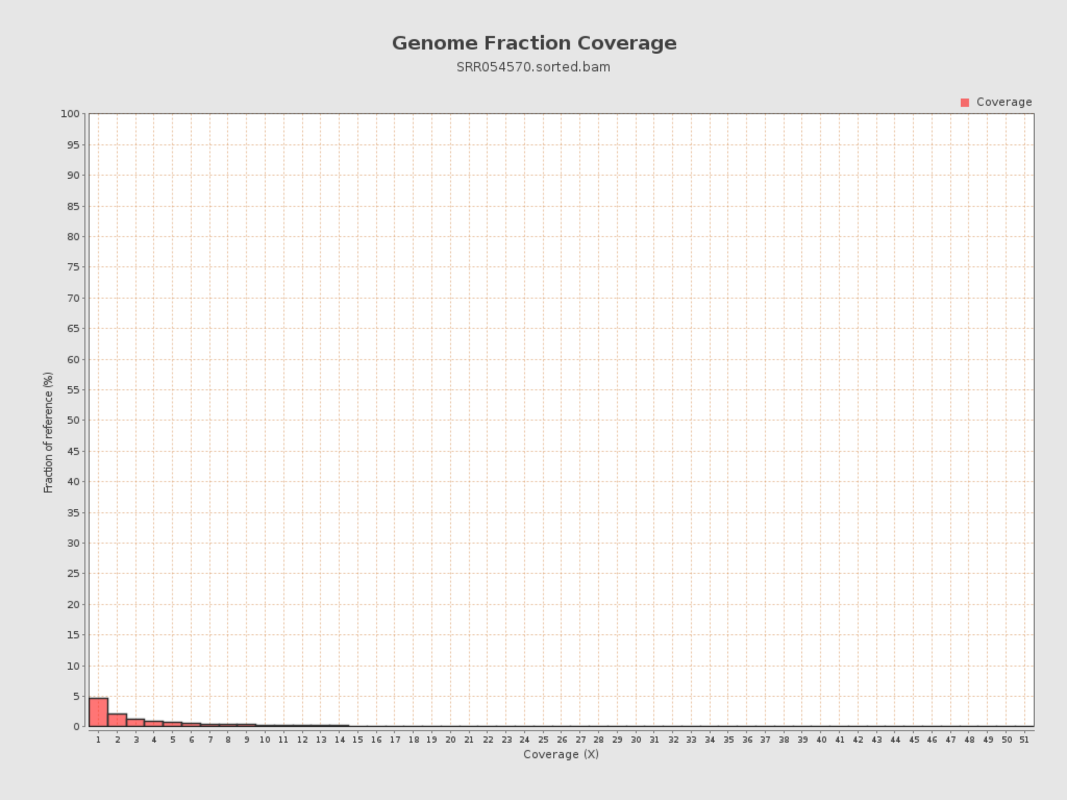
4. Results : Coverage Histogram



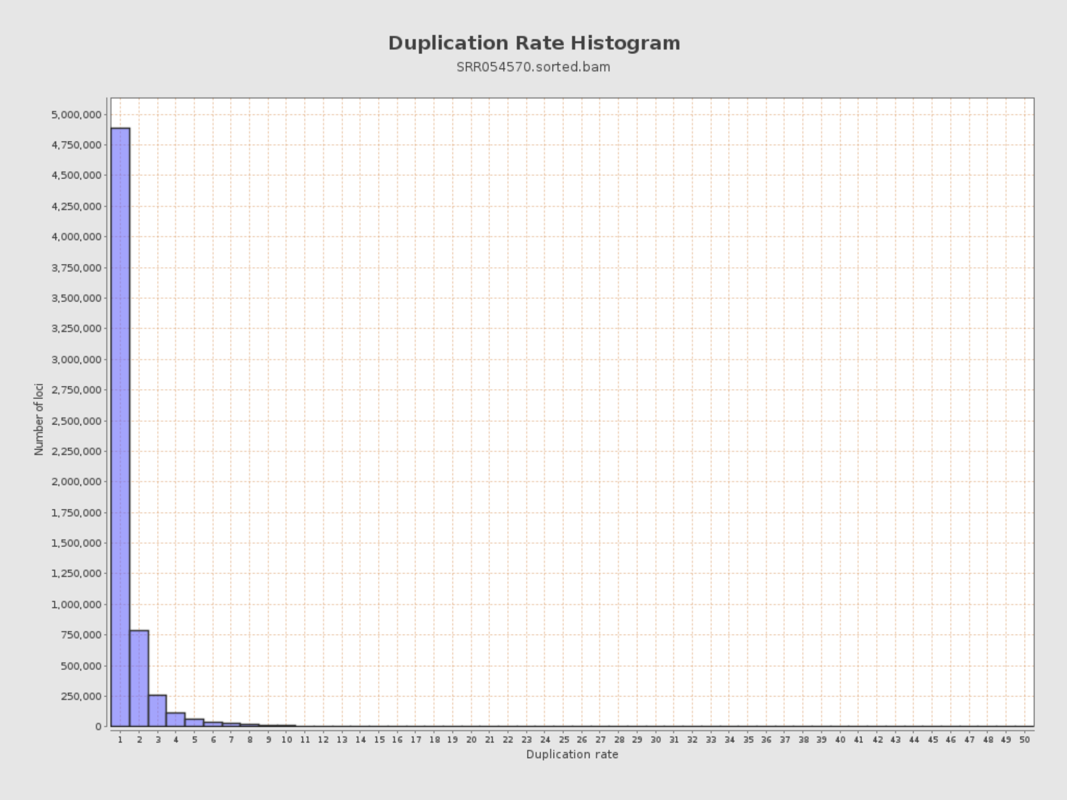
5. Results : Coverage Histogram (0-50X)



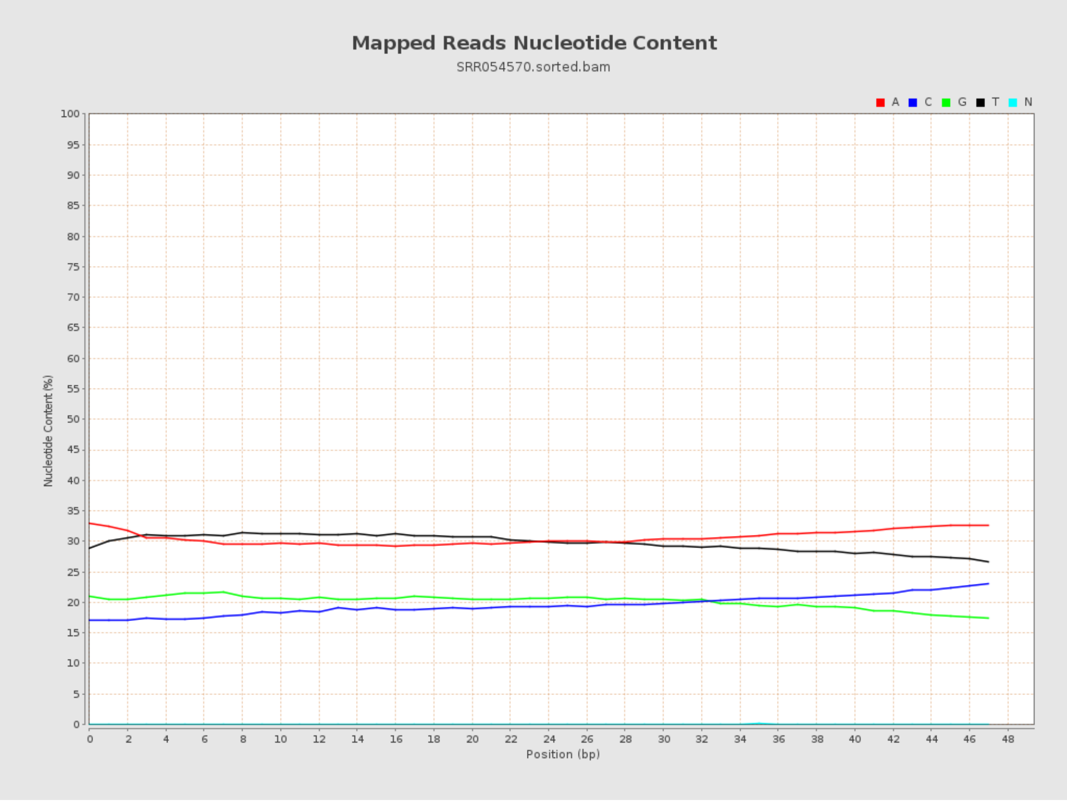
6. Results : Genome Fraction Coverage



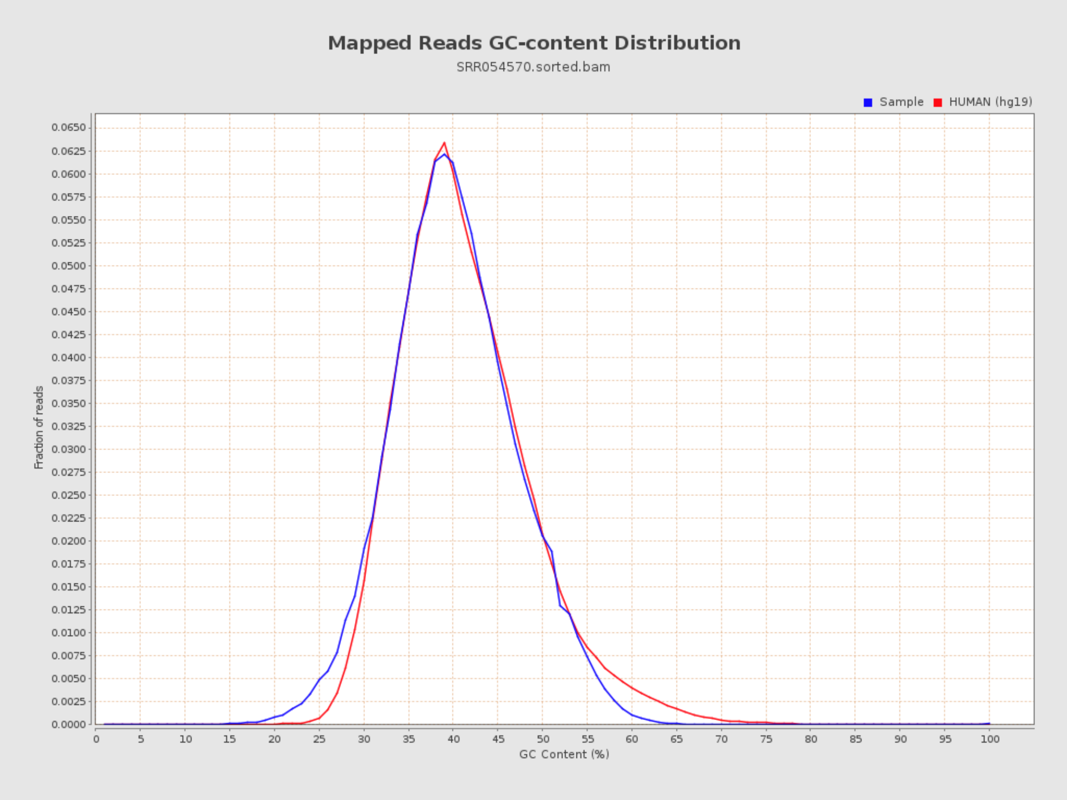
7. Results : Duplication Rate Histogram



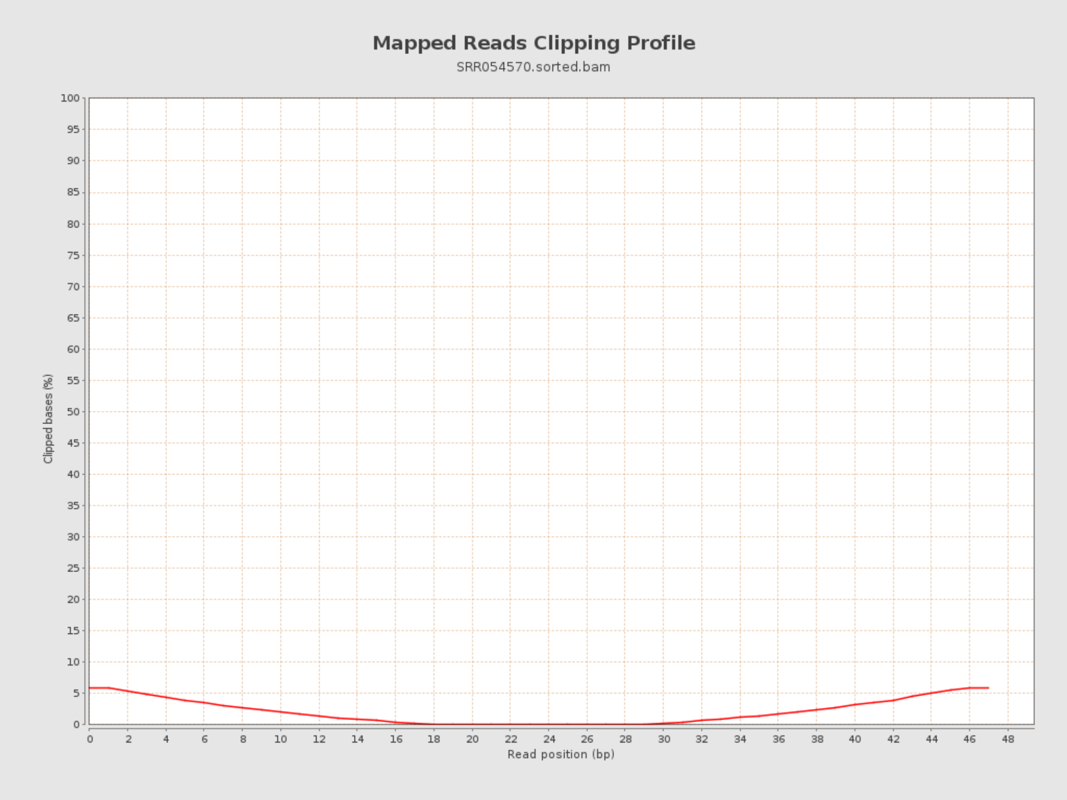
8. Results : Mapped Reads Nucleotide Content



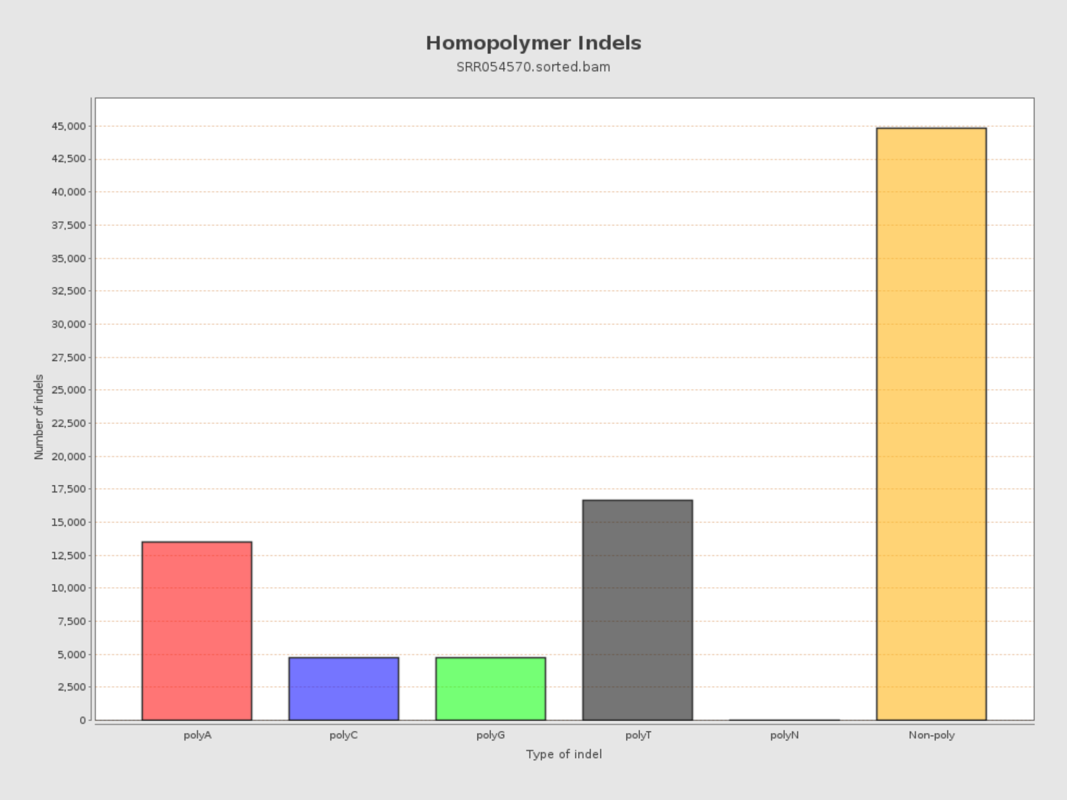
9. Results : Mapped Reads GC-content Distribution



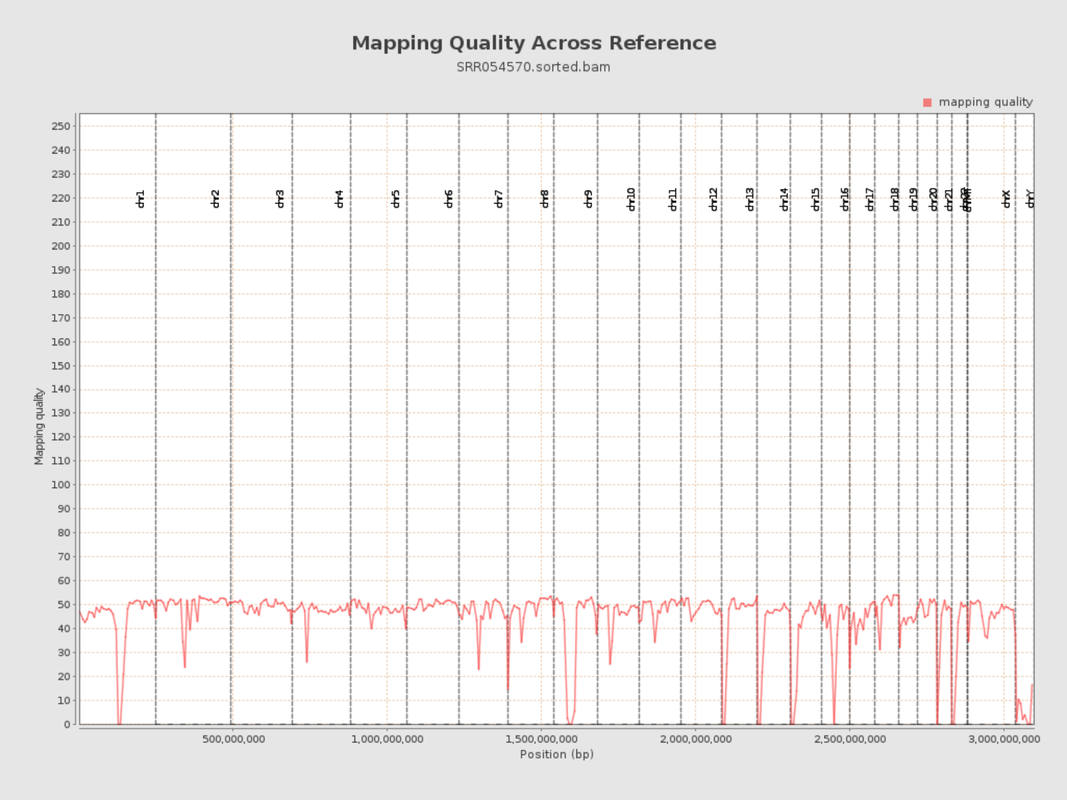
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram