Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:08:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054601.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_SRR054601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:08:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,500,766
Mapped reads	6,459,692 / 75.99%
Unmapped reads	2,041,074 / 24.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	222 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,305,946 / 15.36%
Duplication rate	15.08%
Clipped reads	652,450 / 7.68%

2.2. ACGT Content

Number/percentage of A's	93,486,546 / 30.74%
Number/percentage of C's	56,506,696 / 18.58%
Number/percentage of T's	93,670,236 / 30.8%
Number/percentage of G's	60,418,023 / 19.86%
Number/percentage of N's	82,600 / 0.03%
GC Percentage	38.44%

2.3. Coverage

Mean	0.0983

Standard Deviation	0.7316

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

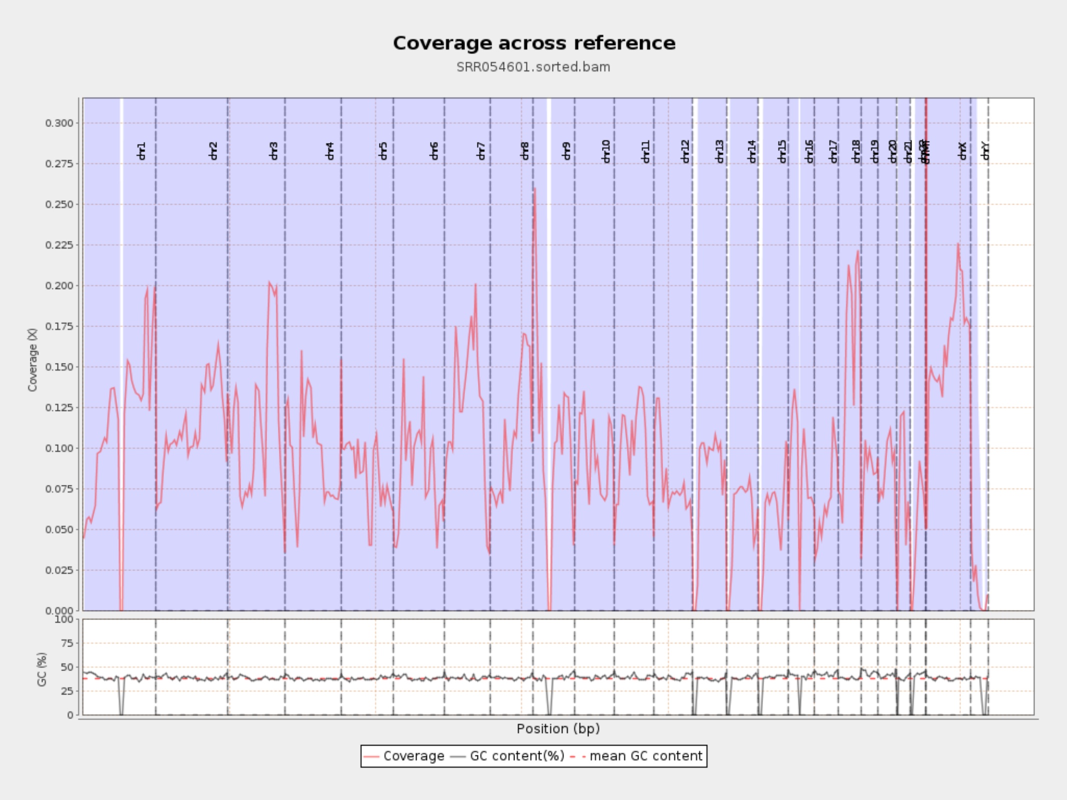
General error rate	0.58%
Mismatches	1,757,767
Insertions	13,894
Mapped reads with at least one insertion	0.21%
Deletions	45,799
Mapped reads with at least one deletion	0.71%
Homopolymer indels	48.82%

2.6. Chromosome stats

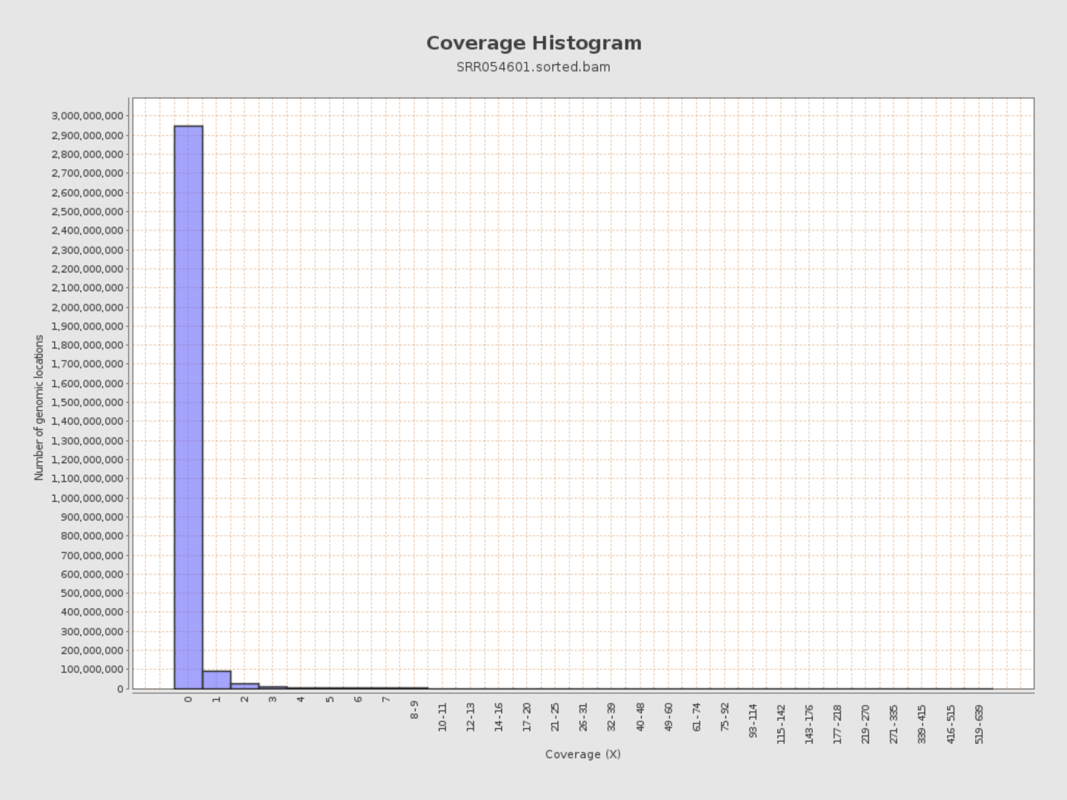
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28186173	0.1131	0.8269
chr2	243199373	27615949	0.1136	0.855
chr3	198022430	22818496	0.1152	0.7515
chr4	191154276	18439640	0.0965	0.685
chr5	180915260	15116502	0.0836	0.5922
chr6	171115067	14927362	0.0872	0.678
chr7	159138663	19907550	0.1251	0.9497

chr8	146364022	15952868	0.109	0.7799
chr9	141213431	14995743	0.1062	0.7522
chr10	135534747	12829294	0.0947	0.7091
chr11	135006516	13349163	0.0989	0.7065
chr12	133851895	10893539	0.0814	0.5943
chr13	115169878	9323217	0.081	0.5926
chr14	107349540	6124831	0.0571	0.5416
chr15	102531392	5769952	0.0563	0.4756
chr16	90354753	7784528	0.0862	0.6371
chr17	81195210	5449242	0.0671	0.5338
chr18	78077248	11920693	0.1527	0.9334
chr19	59128983	5127771	0.0867	0.6916
chr20	63025520	5456798	0.0866	0.6259
chr21	48129895	3393483	0.0705	0.6193
chr22	51304566	2654445	0.0517	0.4512
chrMT	16571	50733	3.0616	6.9441
chrX	155270560	25426791	0.1638	1.0094
chrY	59373566	715504	0.0121	0.2351

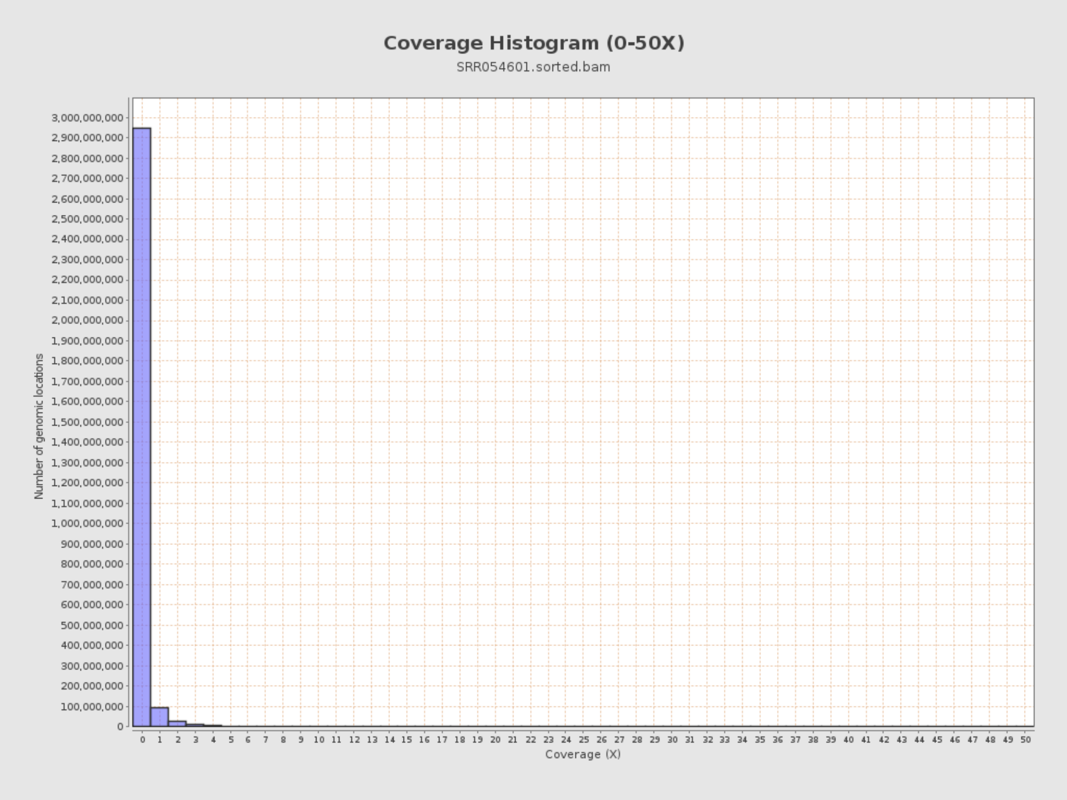
3. Results : Coverage across reference



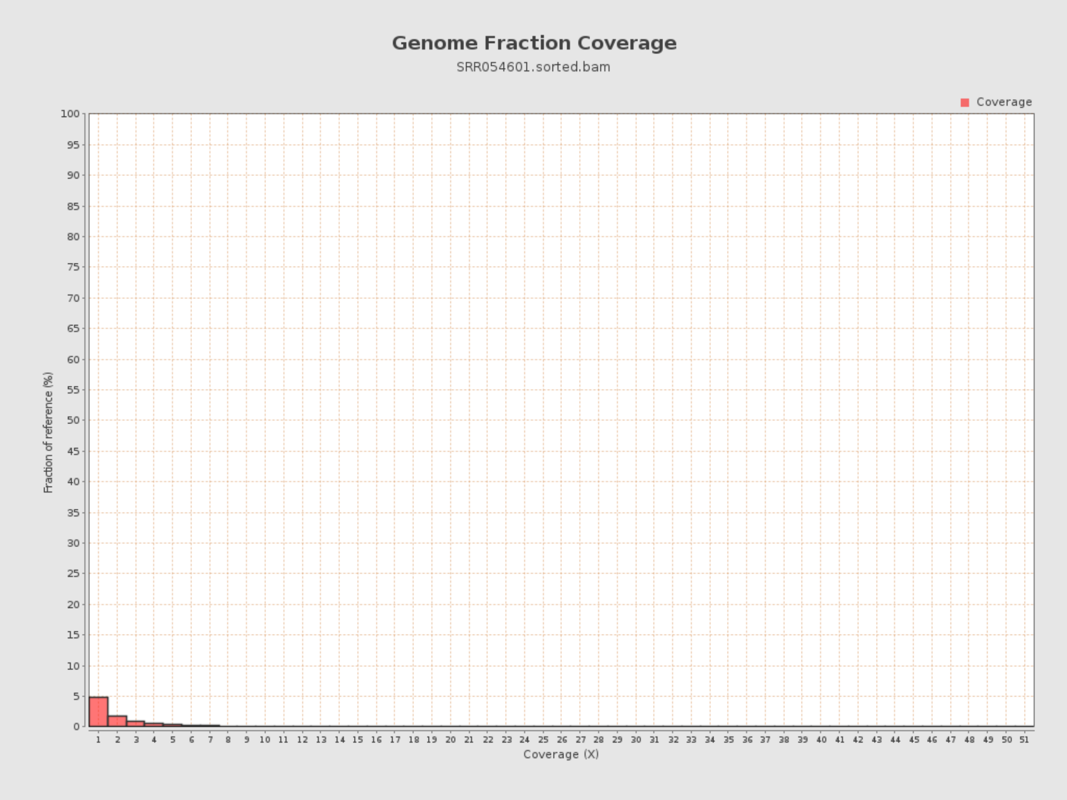
4. Results : Coverage Histogram



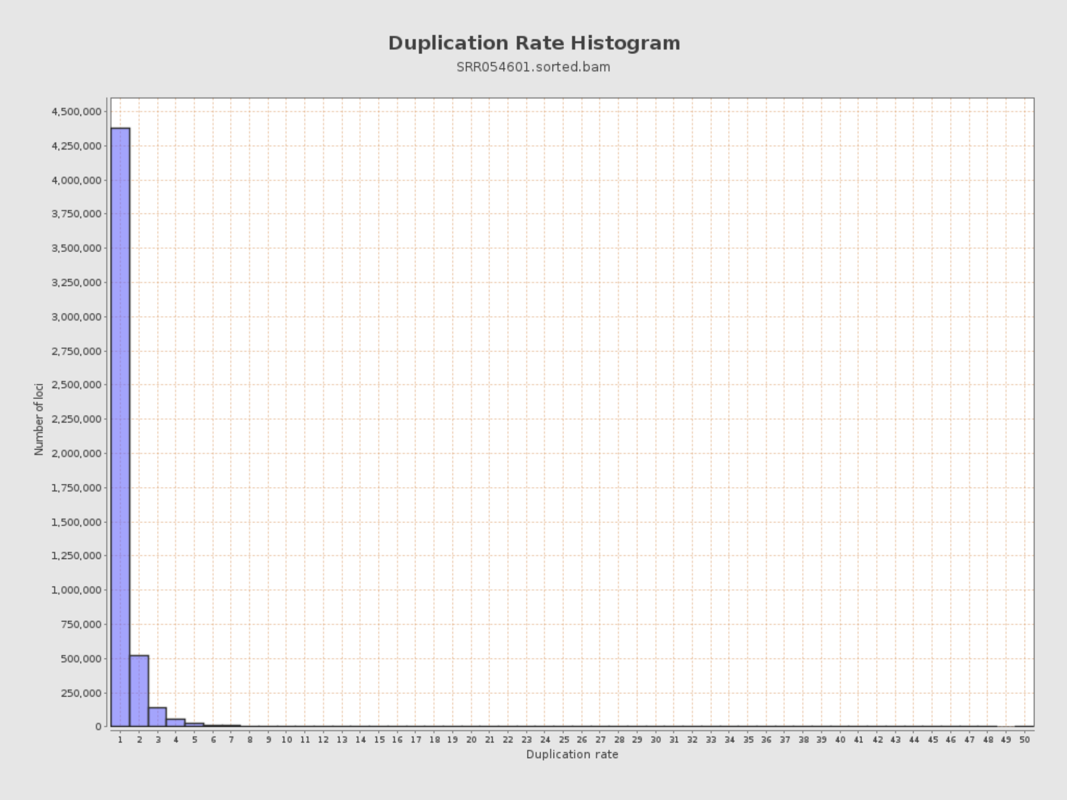
5. Results : Coverage Histogram (0-50X)



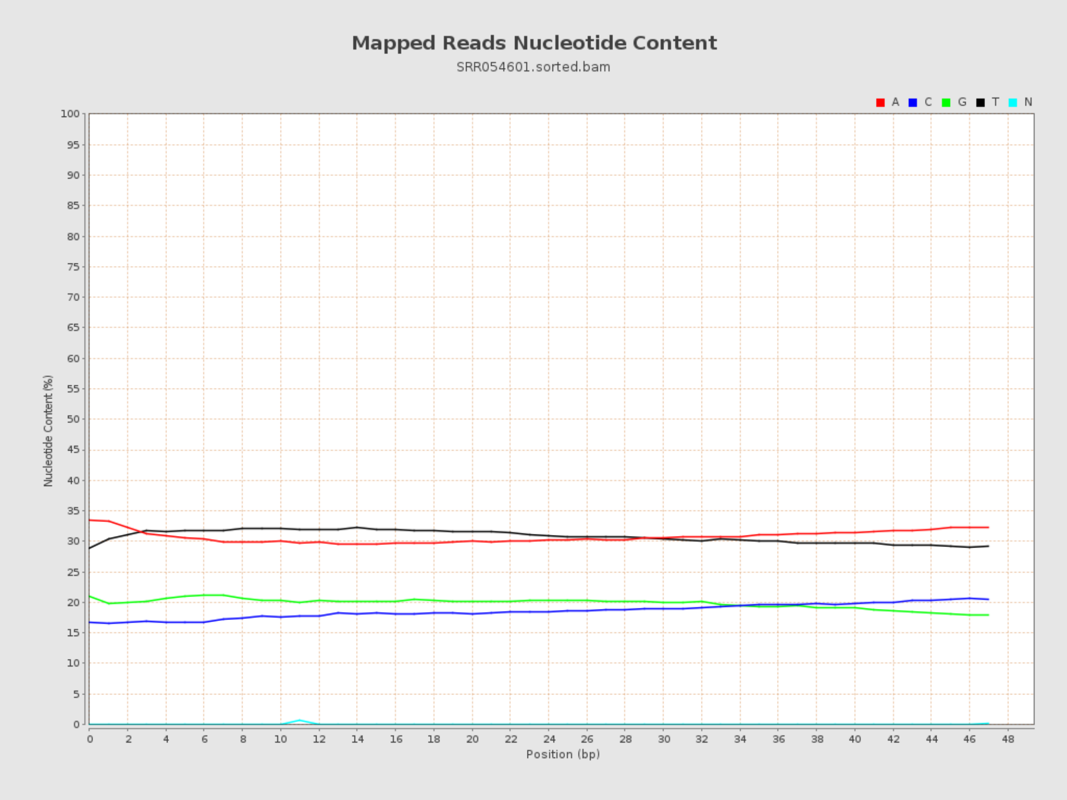
6. Results : Genome Fraction Coverage



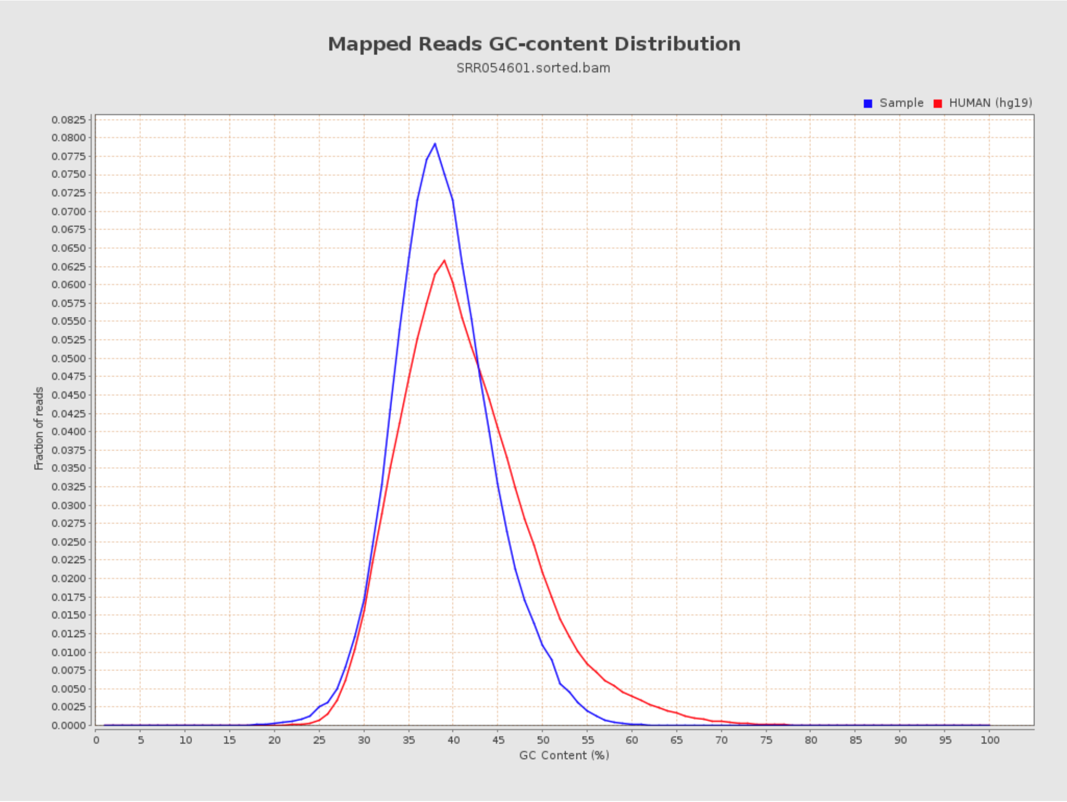
7. Results : Duplication Rate Histogram



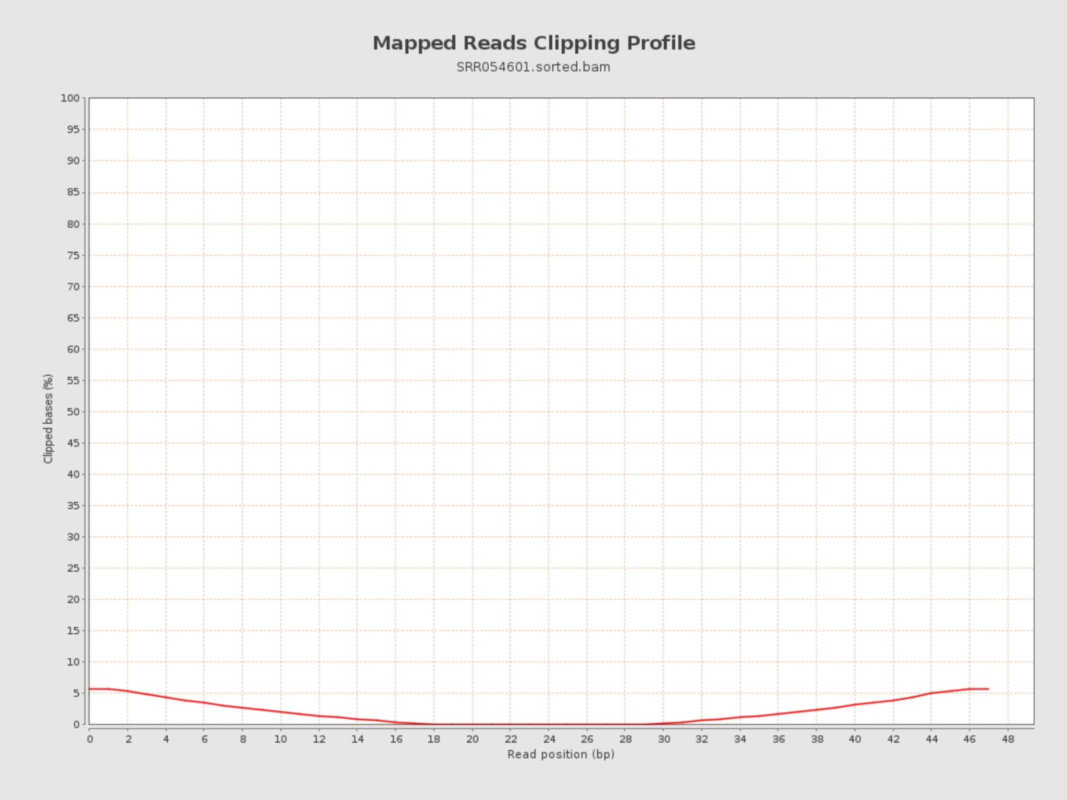
8. Results : Mapped Reads Nucleotide Content



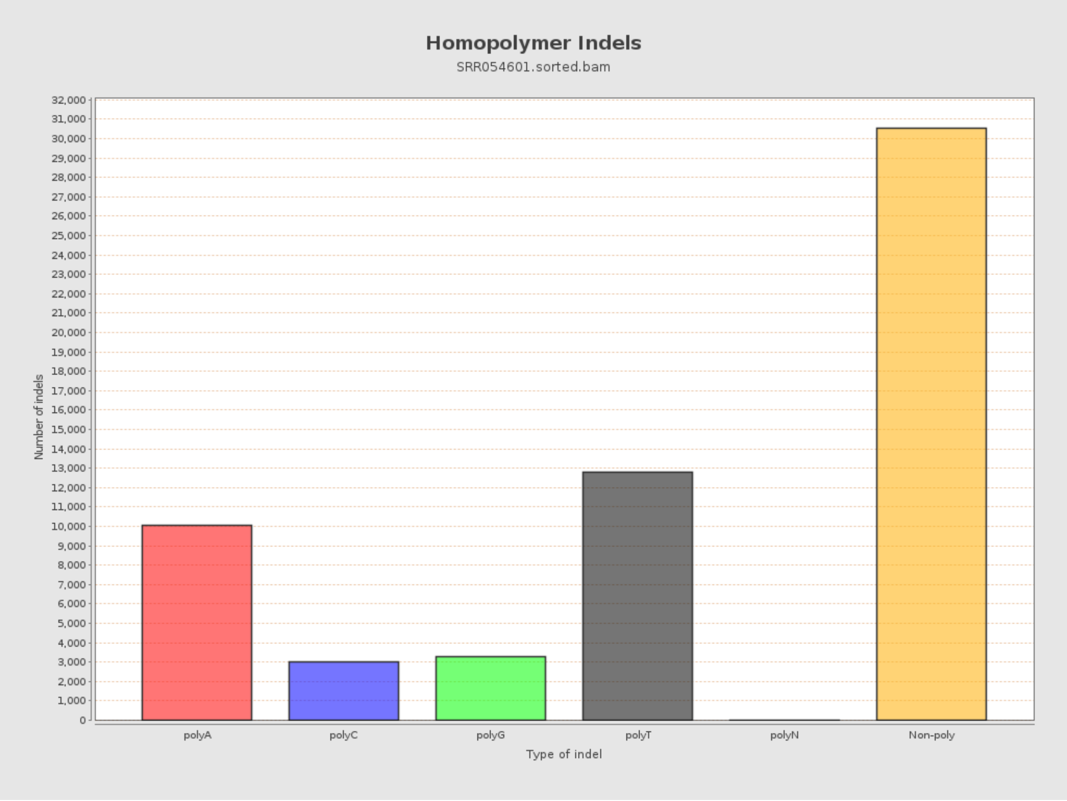
9. Results : Mapped Reads GC-content Distribution



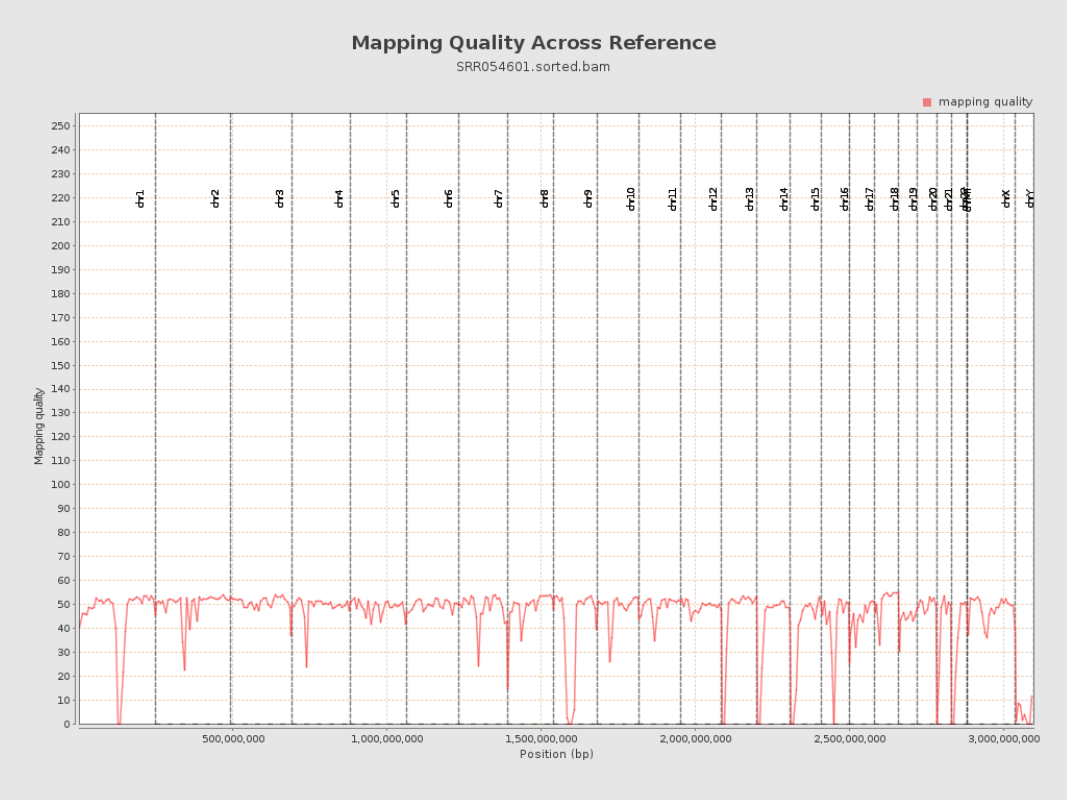
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram