Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:18:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054575.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_SRR054575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054575.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:18:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054575.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,798,840
Mapped reads	6,896,583 / 70.38%
Unmapped reads	2,902,257 / 29.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	197 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,877,550 / 19.16%
Duplication rate	21.21%
Clipped reads	535,660 / 5.47%

2.2. ACGT Content

Number/percentage of A's	94,752,249 / 29.05%
Number/percentage of C's	64,048,925 / 19.63%
Number/percentage of T's	96,489,310 / 29.58%
Number/percentage of G's	70,703,858 / 21.67%
Number/percentage of N's	214,324 / 0.07%
GC Percentage	41.31%

2.3. Coverage

Mean	0.1054

Standard Deviation	0.8483

2.4. Mapping Quality

Mean Mapping Quality	44.32

2.5. Mismatches and indels

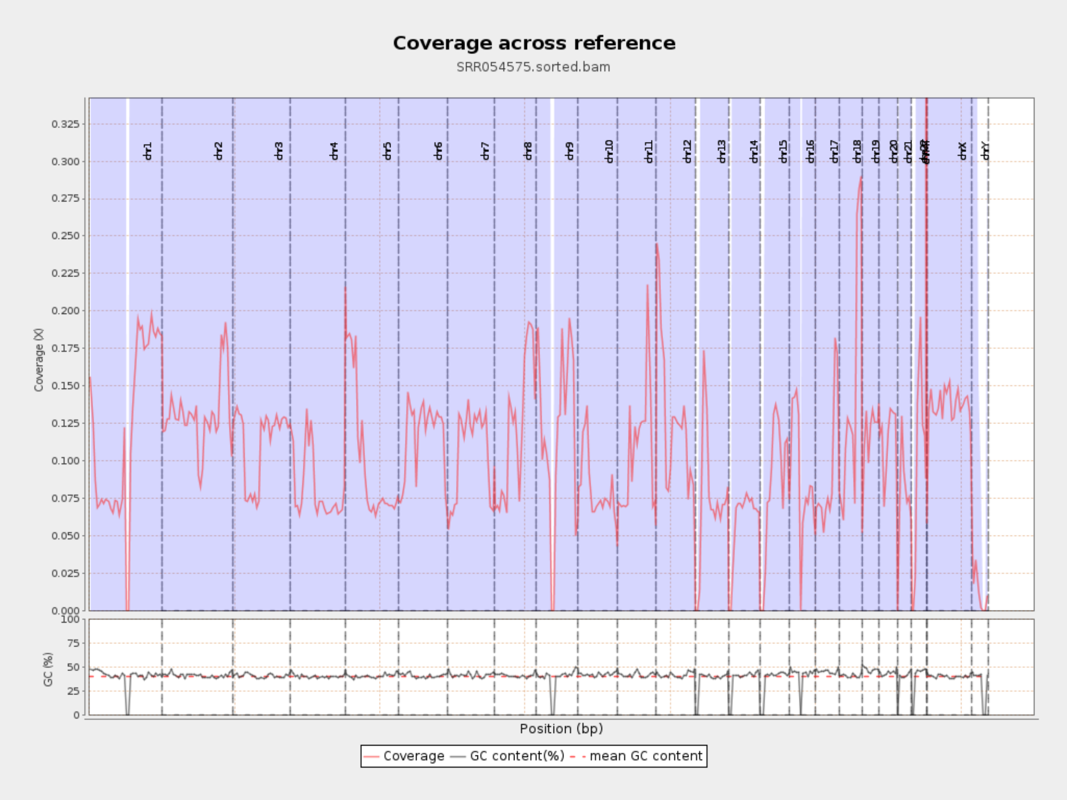
General error rate	0.61%
Mismatches	1,985,723
Insertions	13,741
Mapped reads with at least one insertion	0.2%
Deletions	44,738
Mapped reads with at least one deletion	0.65%
Homopolymer indels	47.41%

2.6. Chromosome stats

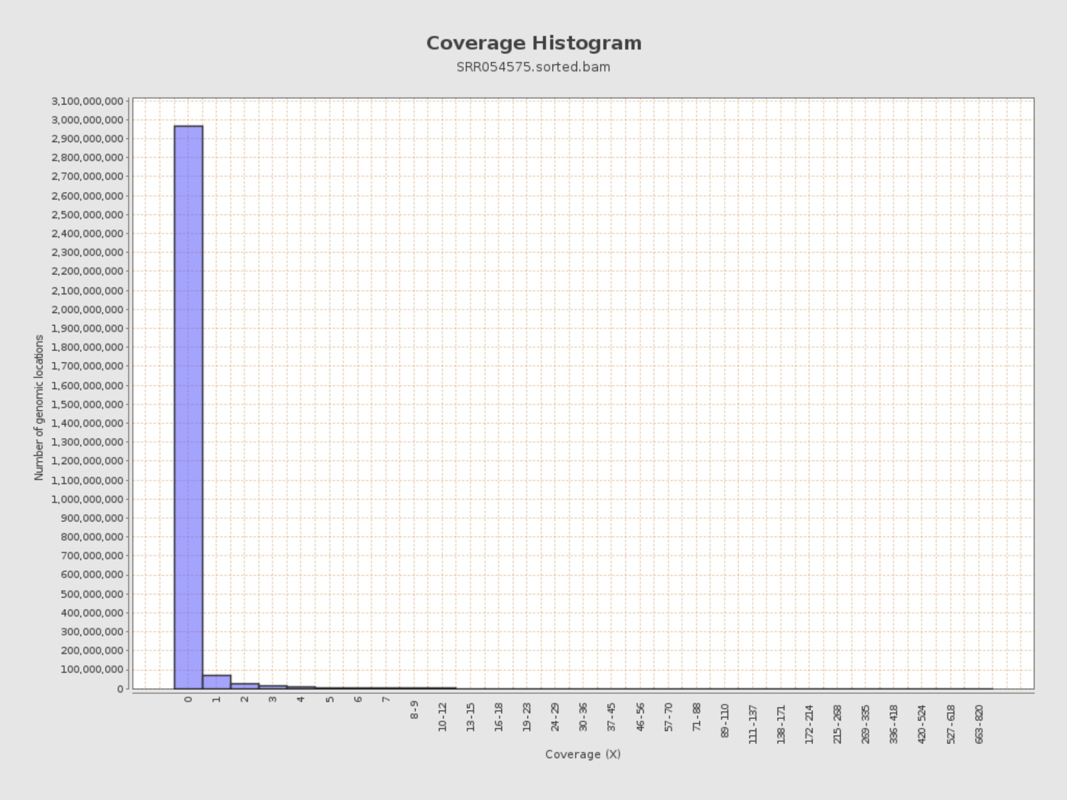
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29628854	0.1189	0.9441
chr2	243199373	31891222	0.1311	1.1365
chr3	198022430	22146867	0.1118	0.8014
chr4	191154276	15591060	0.0816	0.6776
chr5	180915260	18153851	0.1003	0.7472
chr6	171115067	19879925	0.1162	0.8837
chr7	159138663	16942549	0.1065	0.9285

chr8	146364022	17991450	0.1229	0.889
chr9	141213431	17035221	0.1206	0.882
chr10	135534747	11241794	0.0829	0.7395
chr11	135006516	14209482	0.1053	0.8376
chr12	133851895	17267477	0.129	0.8876
chr13	115169878	8154207	0.0708	0.6245
chr14	107349540	6339276	0.0591	0.6735
chr15	102531392	8417050	0.0821	0.6757
chr16	90354753	8143857	0.0901	0.7458
chr17	81195210	7527041	0.0927	0.7227
chr18	78077248	11186638	0.1433	1.0289
chr19	59128983	7015942	0.1187	0.927
chr20	63025520	7160529	0.1136	0.8145
chr21	48129895	3709309	0.0771	0.6996
chr22	51304566	4806582	0.0937	0.7571
chrMT	16571	32875	1.9839	5.0339
chrX	155270560	21030901	0.1354	0.9389
chrY	59373566	771527	0.013	0.263

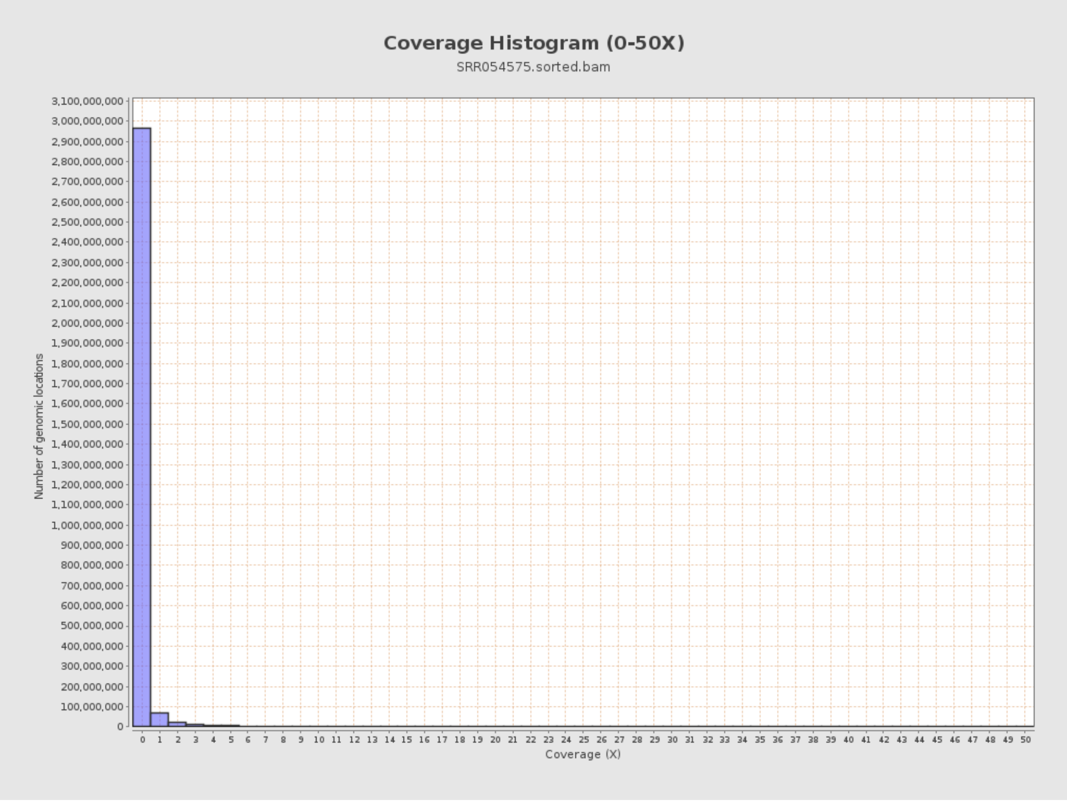
3. Results : Coverage across reference



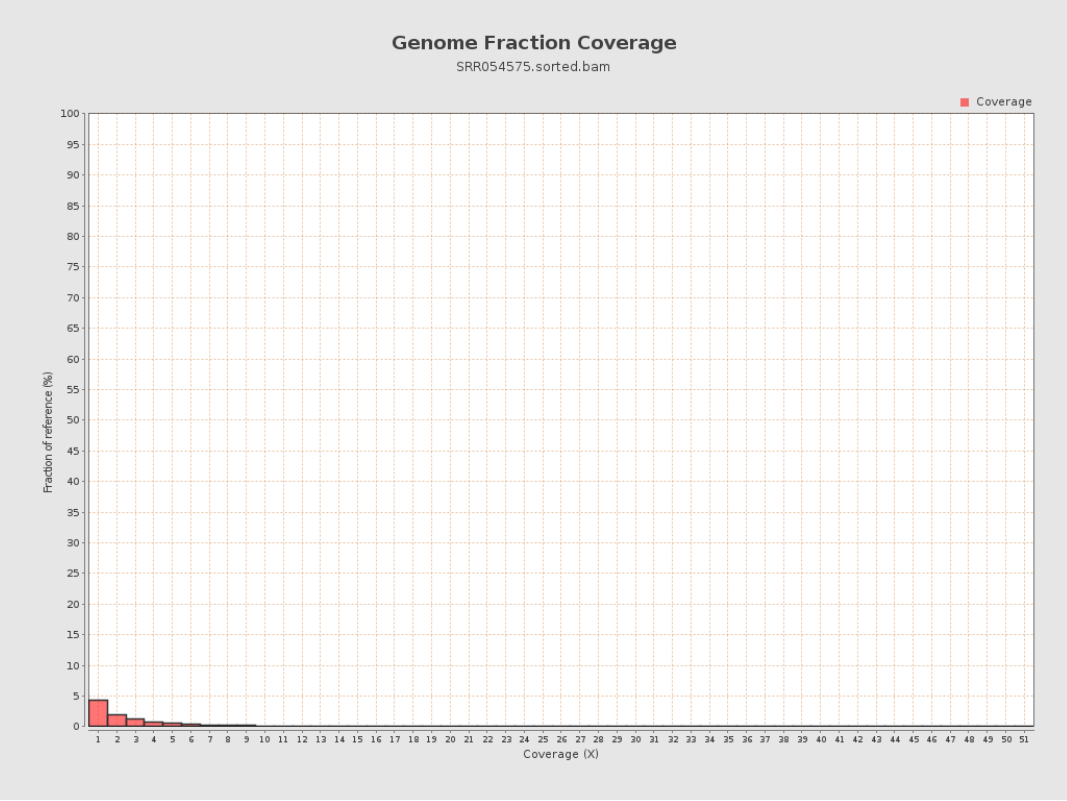
4. Results : Coverage Histogram



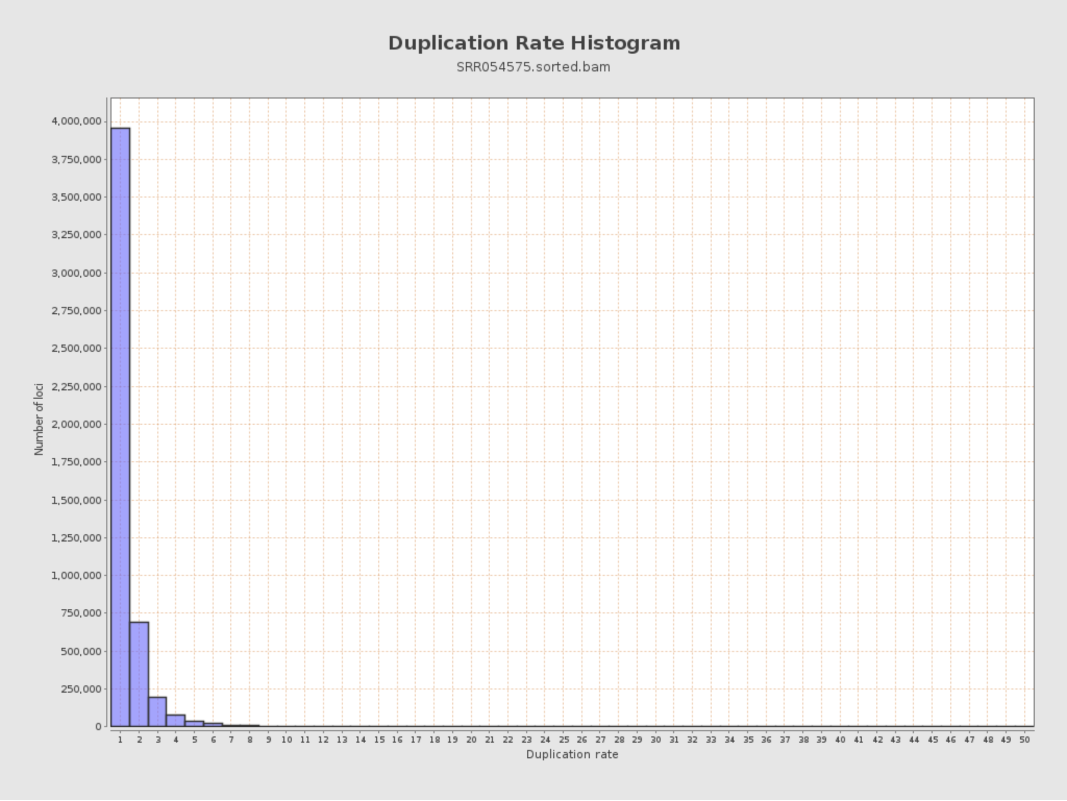
5. Results : Coverage Histogram (0-50X)



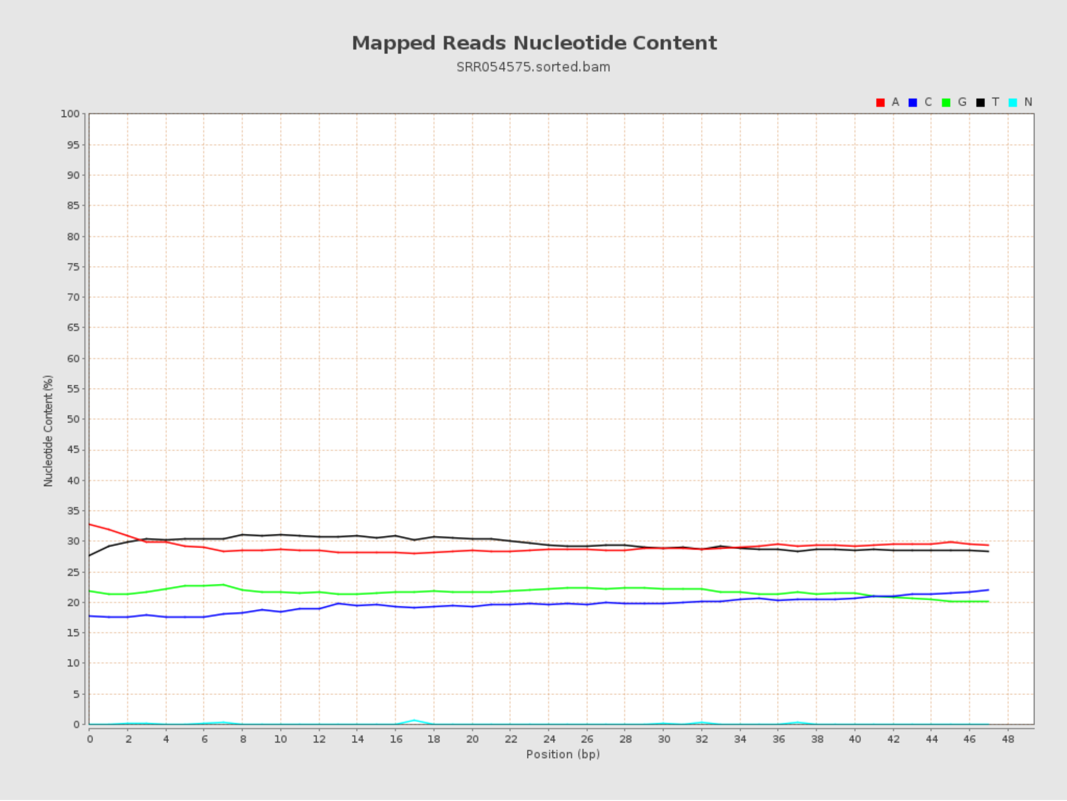
6. Results : Genome Fraction Coverage



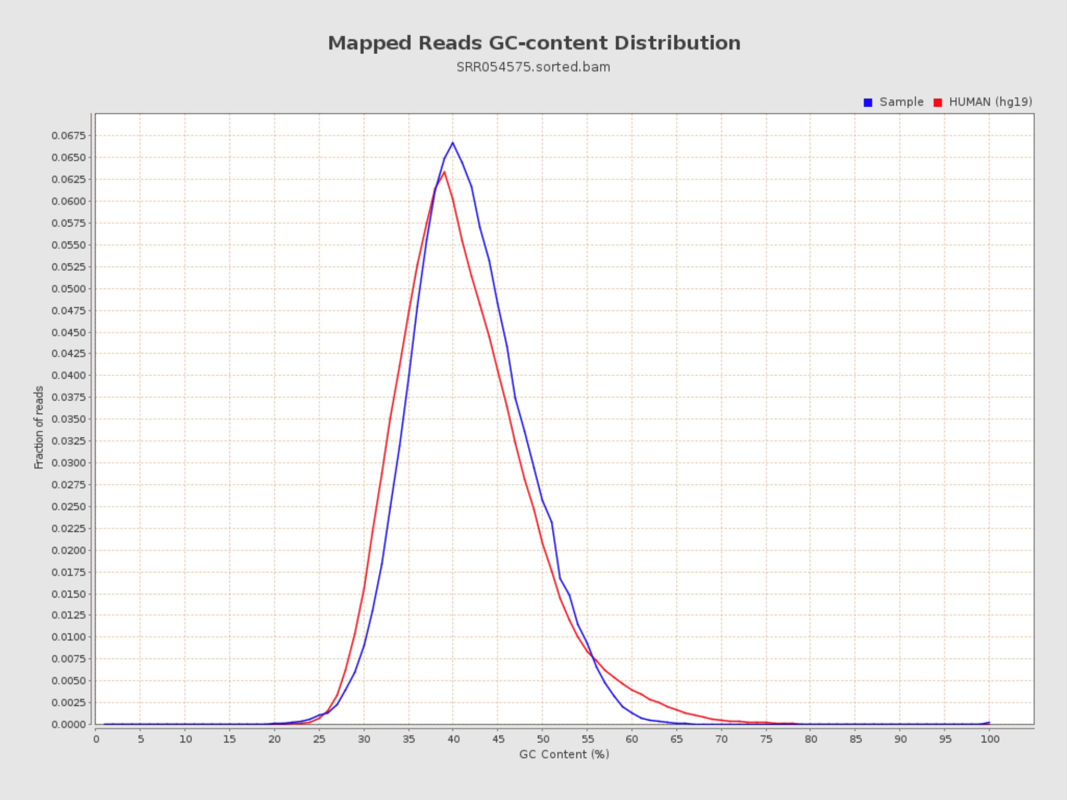
7. Results : Duplication Rate Histogram



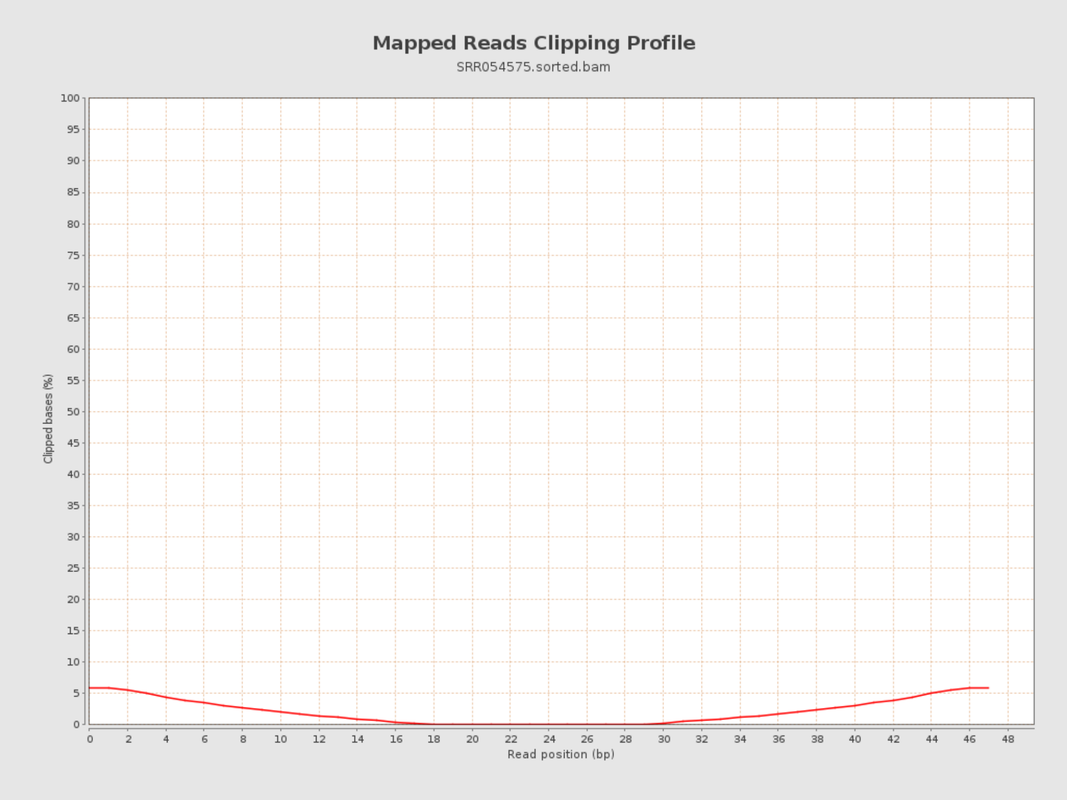
8. Results : Mapped Reads Nucleotide Content



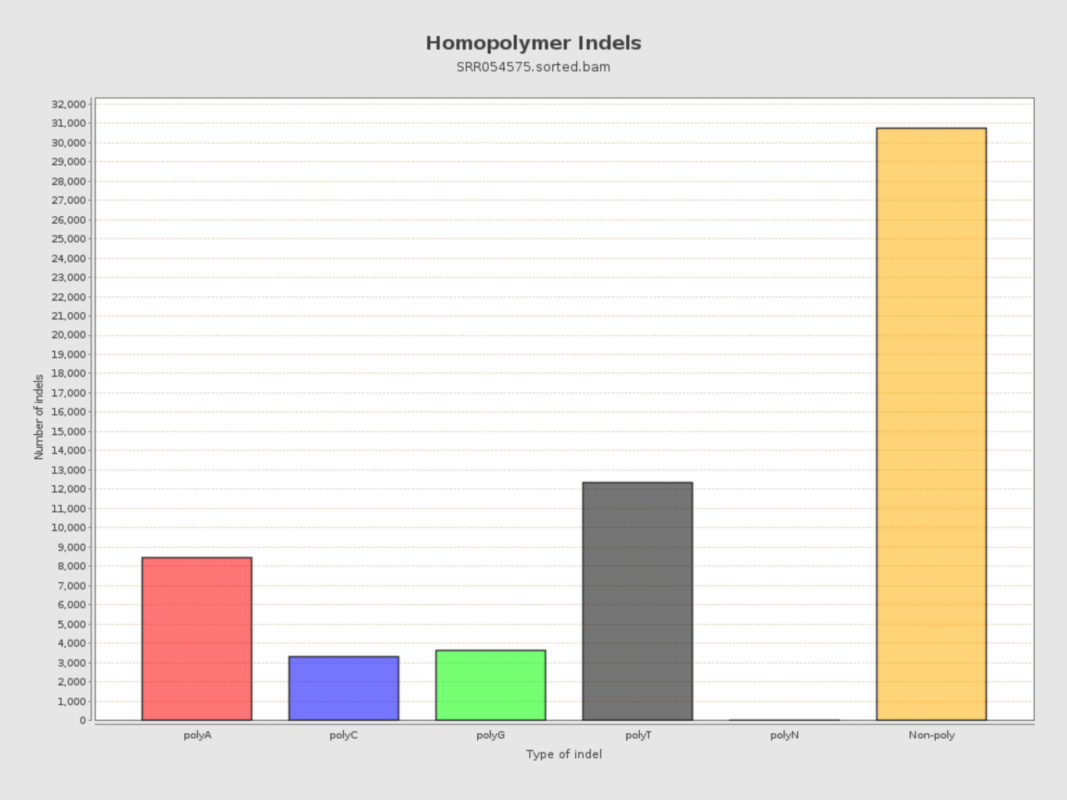
9. Results : Mapped Reads GC-content Distribution



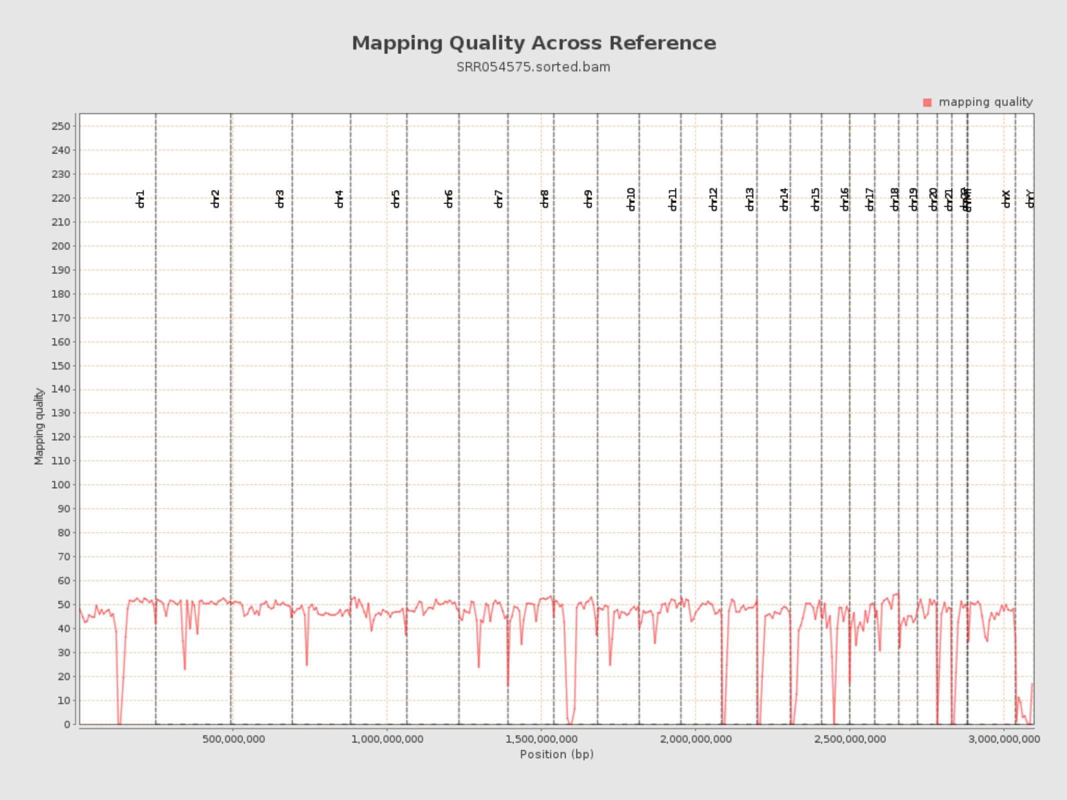
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram