Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:30:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054577.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_SRR054577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:30:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,912,350
Mapped reads	5,045,957 / 63.77%
Unmapped reads	2,866,393 / 36.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	179 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,225,801 / 15.49%
Duplication rate	20.21%
Clipped reads	609,643 / 7.7%

2.2. ACGT Content

Number/percentage of A's	70,378,544 / 29.74%
Number/percentage of C's	46,786,526 / 19.77%
Number/percentage of T's	69,361,610 / 29.31%
Number/percentage of G's	50,078,033 / 21.16%
Number/percentage of N's	71,948 / 0.03%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0765

Standard Deviation	0.6505

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

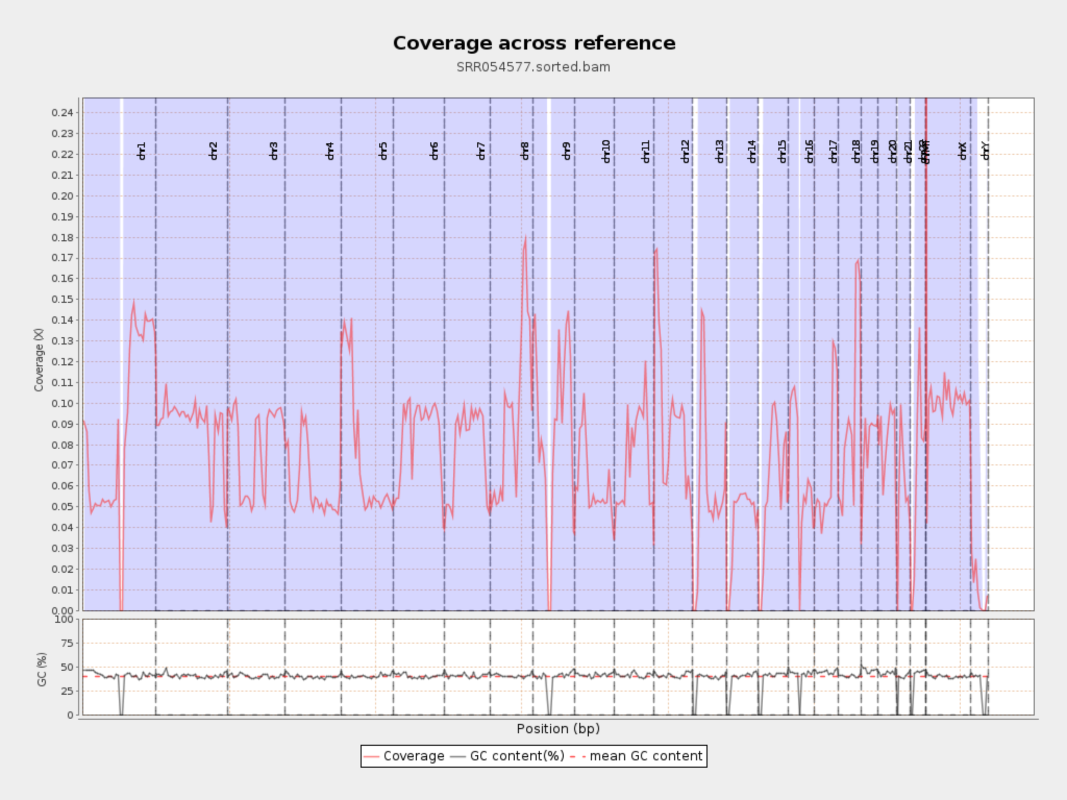
General error rate	0.7%
Mismatches	1,650,898
Insertions	10,416
Mapped reads with at least one insertion	0.21%
Deletions	31,113
Mapped reads with at least one deletion	0.62%
Homopolymer indels	46.32%

2.6. Chromosome stats

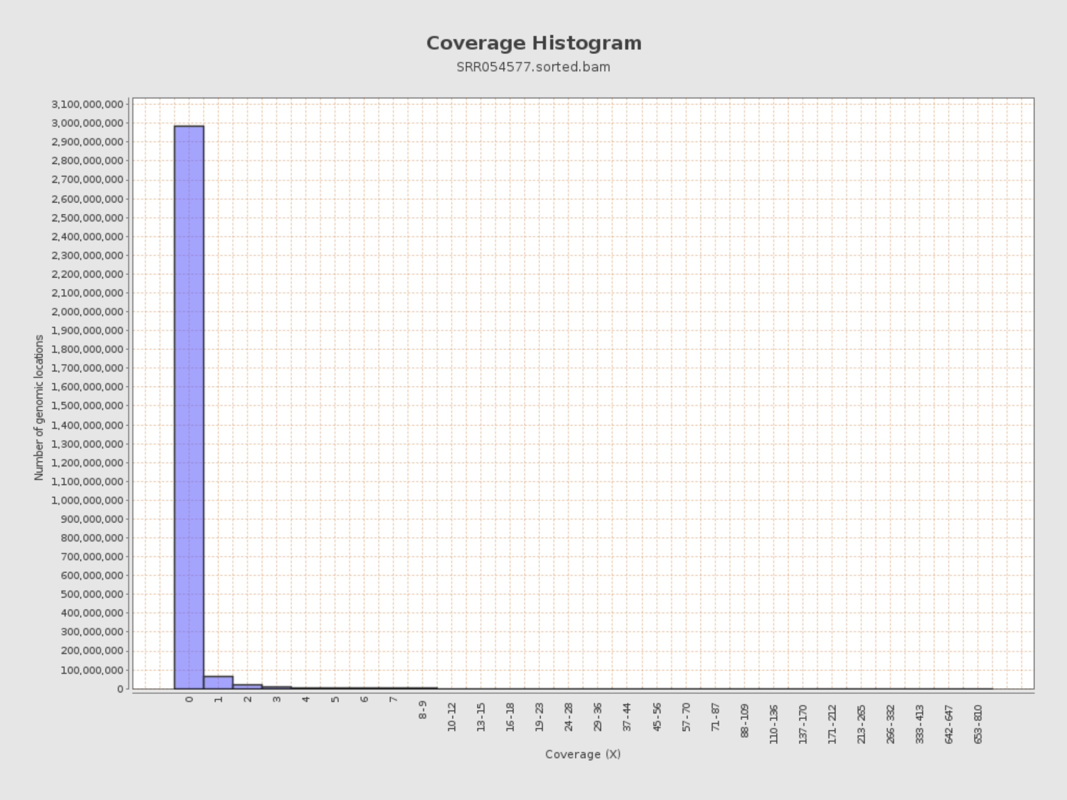
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21594805	0.0866	0.7209
chr2	243199373	21493224	0.0884	0.8994
chr3	198022430	15687996	0.0792	0.6031
chr4	191154276	11488929	0.0601	0.518
chr5	180915260	13571745	0.075	0.5838
chr6	171115067	14607245	0.0854	0.6693
chr7	159138663	12331313	0.0775	0.6924

chr8	146364022	13989884	0.0956	0.7185
chr9	141213431	12437556	0.0881	0.6625
chr10	135534747	8354262	0.0616	0.5711
chr11	135006516	10053221	0.0745	0.6348
chr12	133851895	12756637	0.0953	0.6763
chr13	115169878	6547545	0.0569	0.5263
chr14	107349540	4685932	0.0437	0.4896
chr15	102531392	6120938	0.0597	0.5109
chr16	90354753	5856667	0.0648	0.5693
chr17	81195210	5561850	0.0685	0.5582
chr18	78077248	7362549	0.0943	0.7369
chr19	59128983	4823254	0.0816	0.6707
chr20	63025520	5247127	0.0833	0.6355
chr21	48129895	2723598	0.0566	0.5333
chr22	51304566	3375925	0.0658	0.5512
chrMT	16571	21793	1.3151	2.5877
chrX	155270560	15448768	0.0995	0.7261
chrY	59373566	579312	0.0098	0.2169

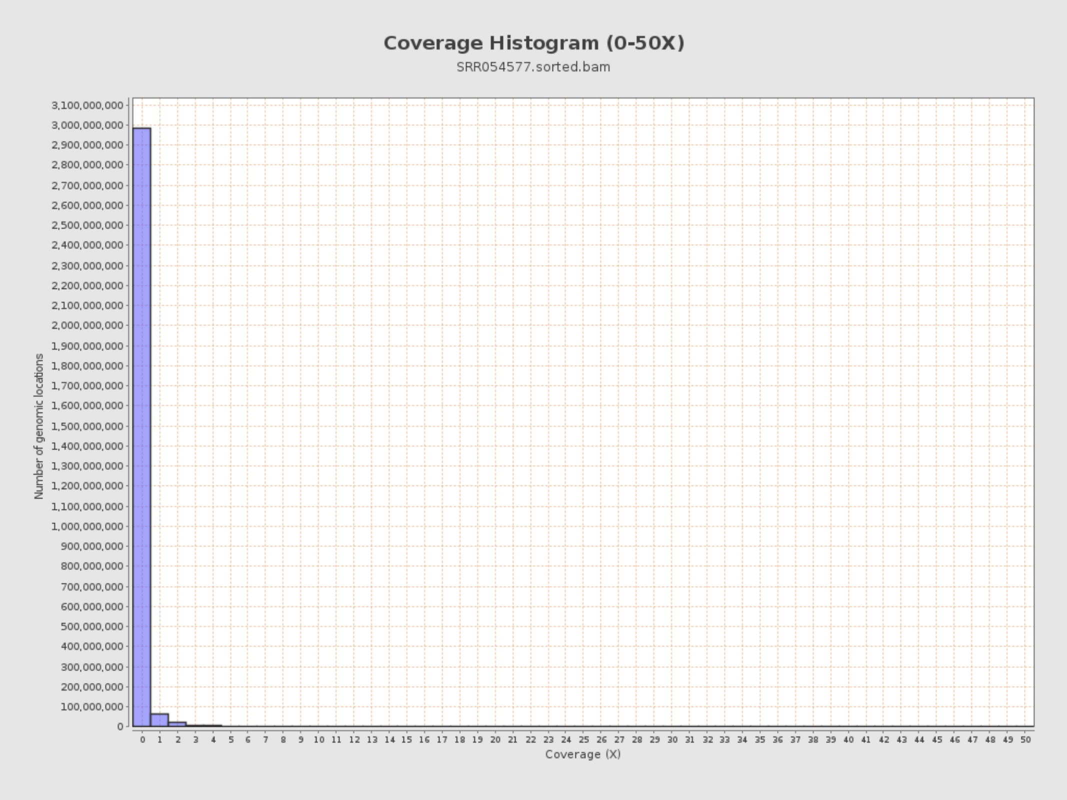
3. Results : Coverage across reference



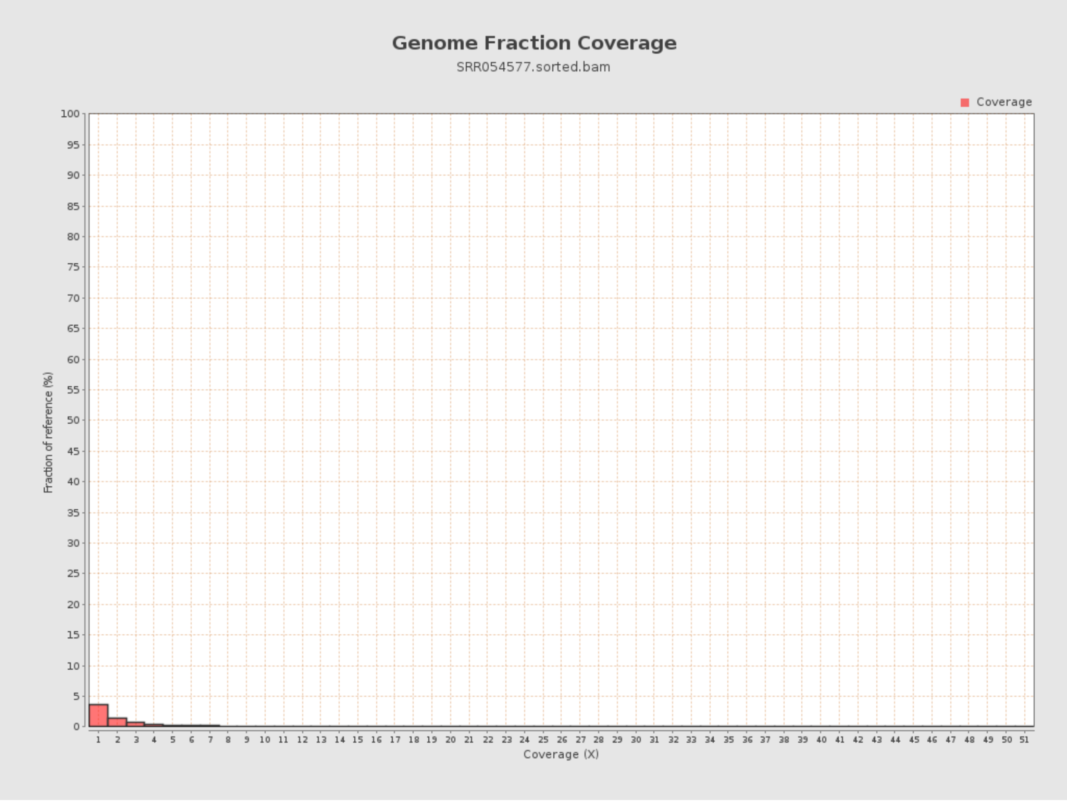
4. Results : Coverage Histogram



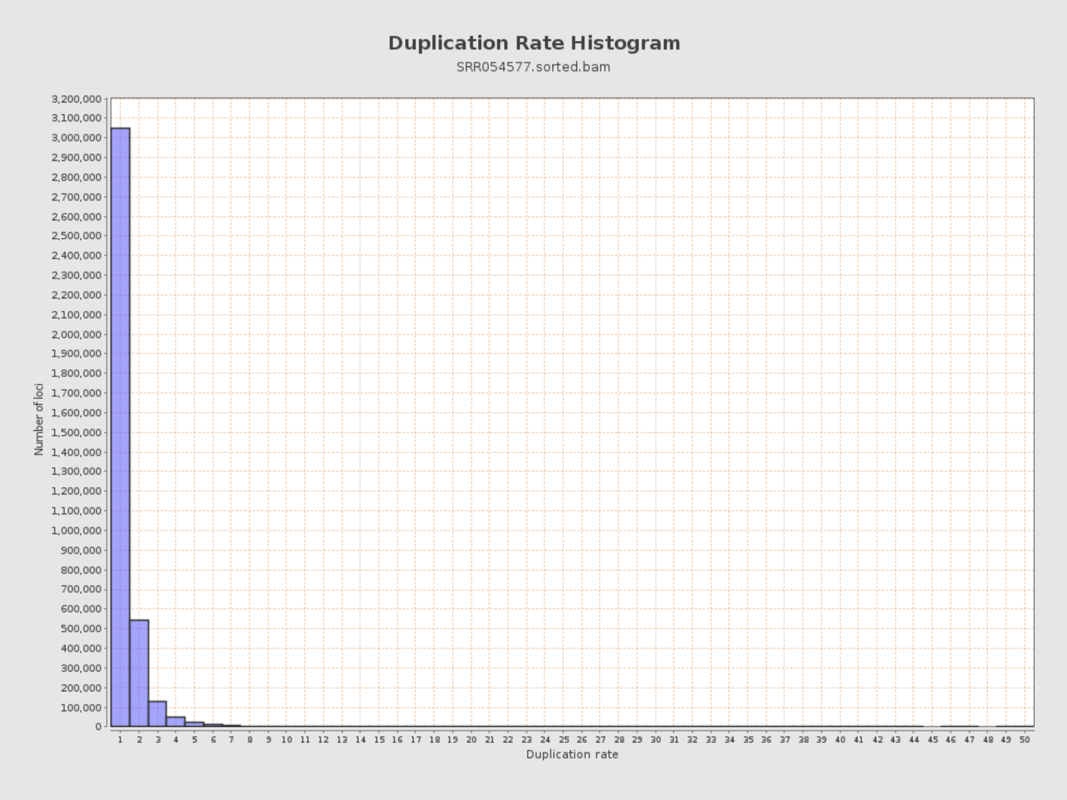
5. Results : Coverage Histogram (0-50X)



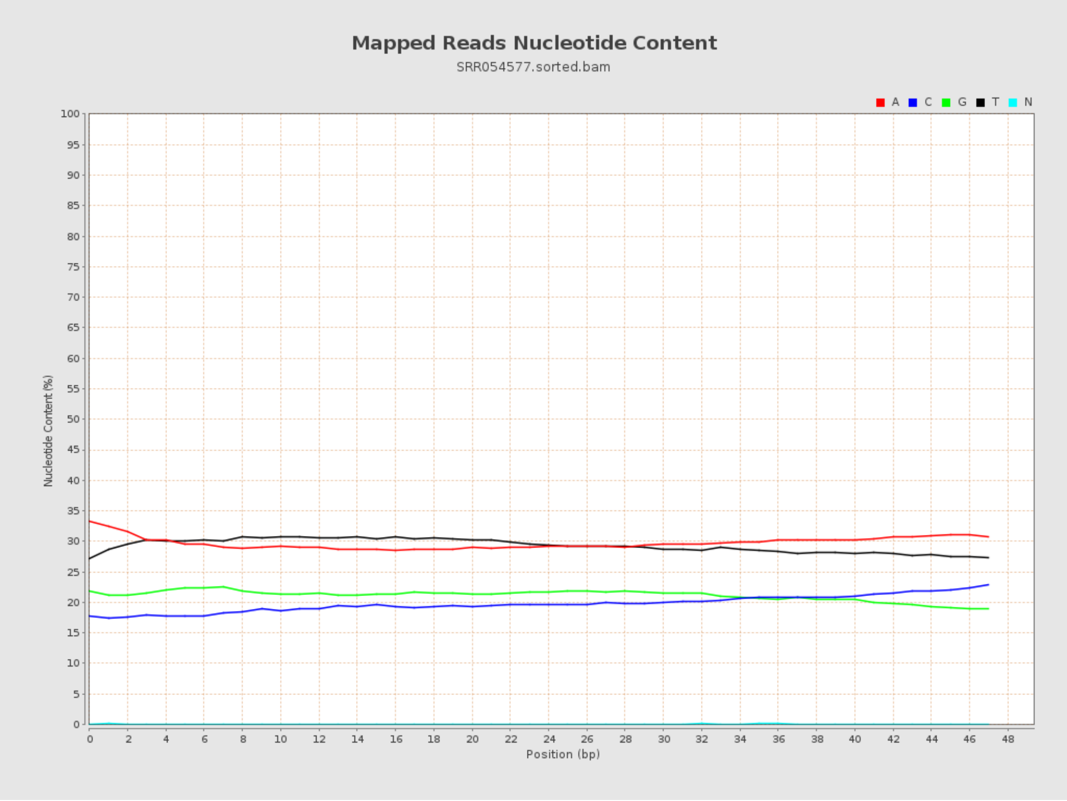
6. Results : Genome Fraction Coverage



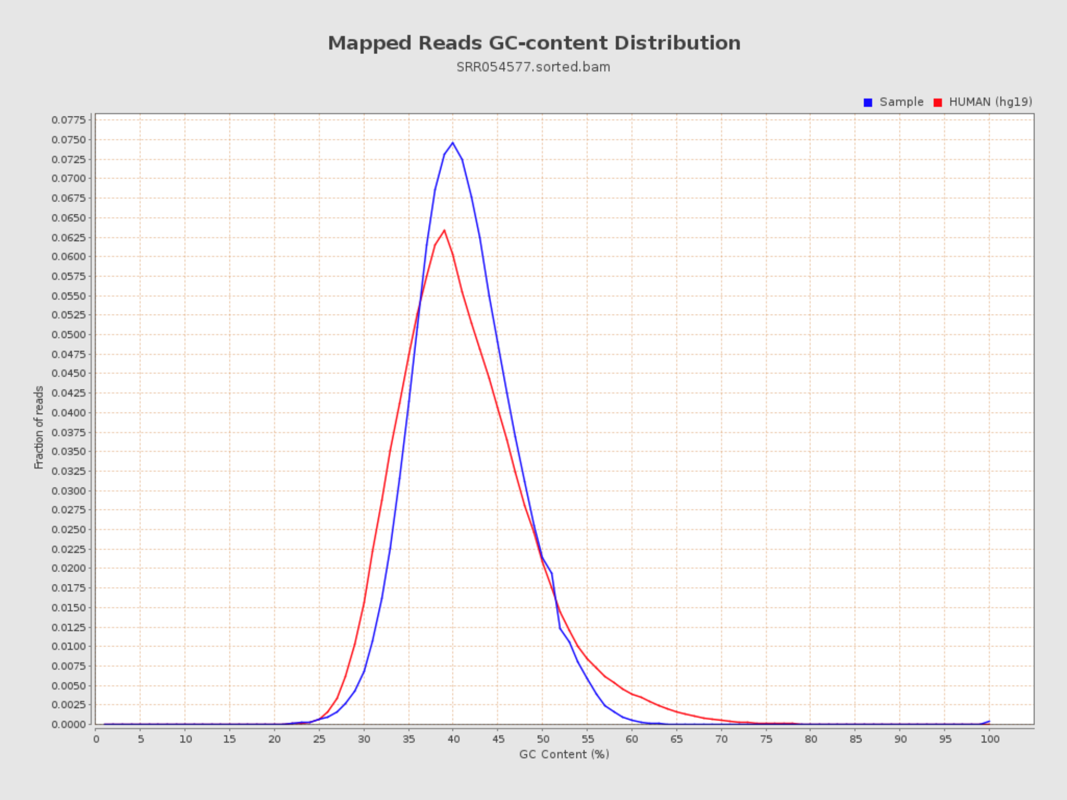
7. Results : Duplication Rate Histogram



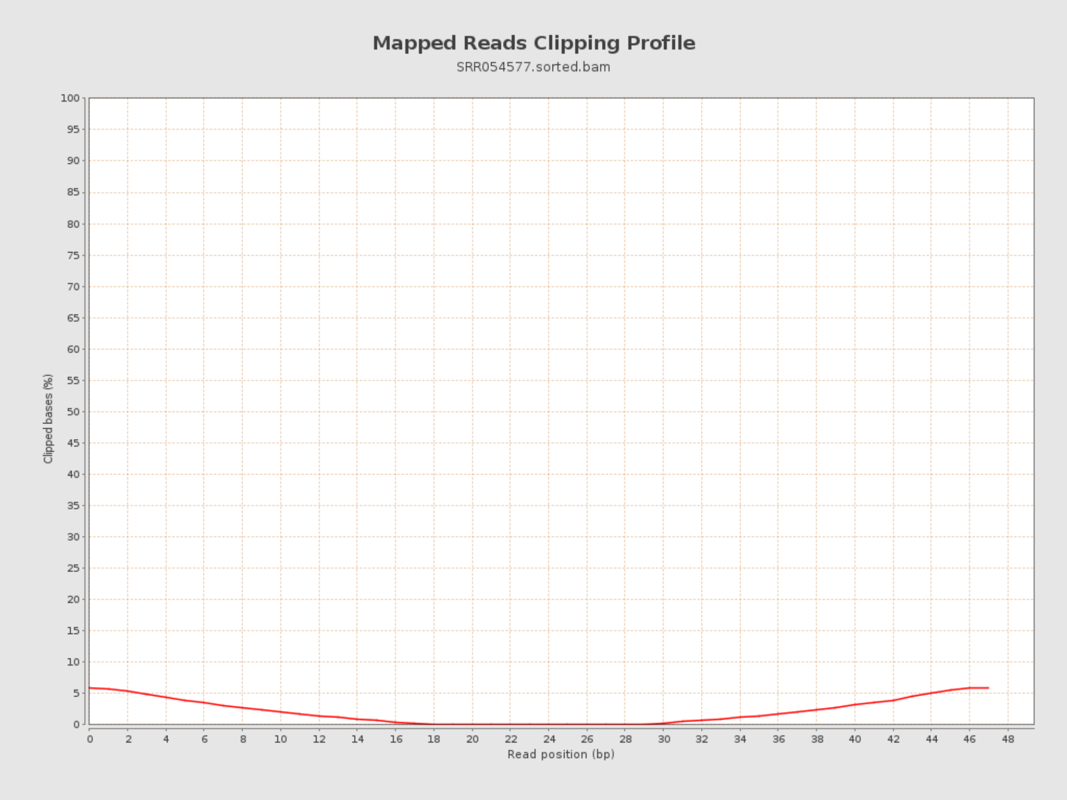
8. Results : Mapped Reads Nucleotide Content



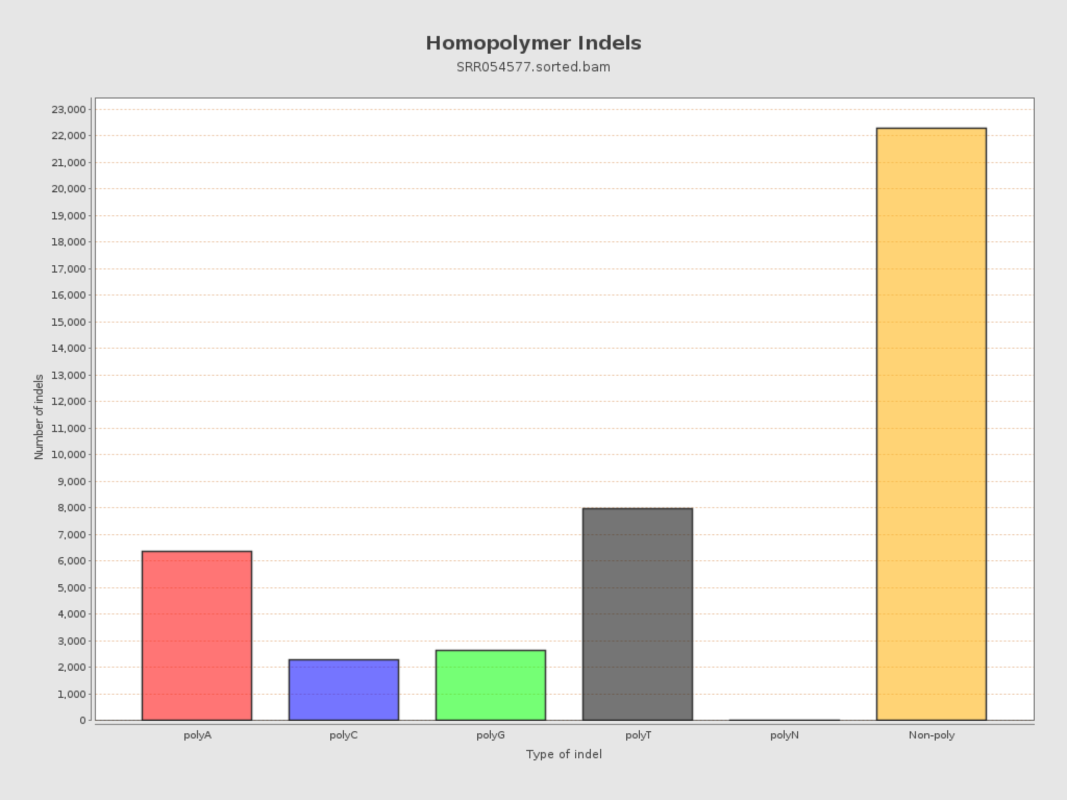
9. Results : Mapped Reads GC-content Distribution



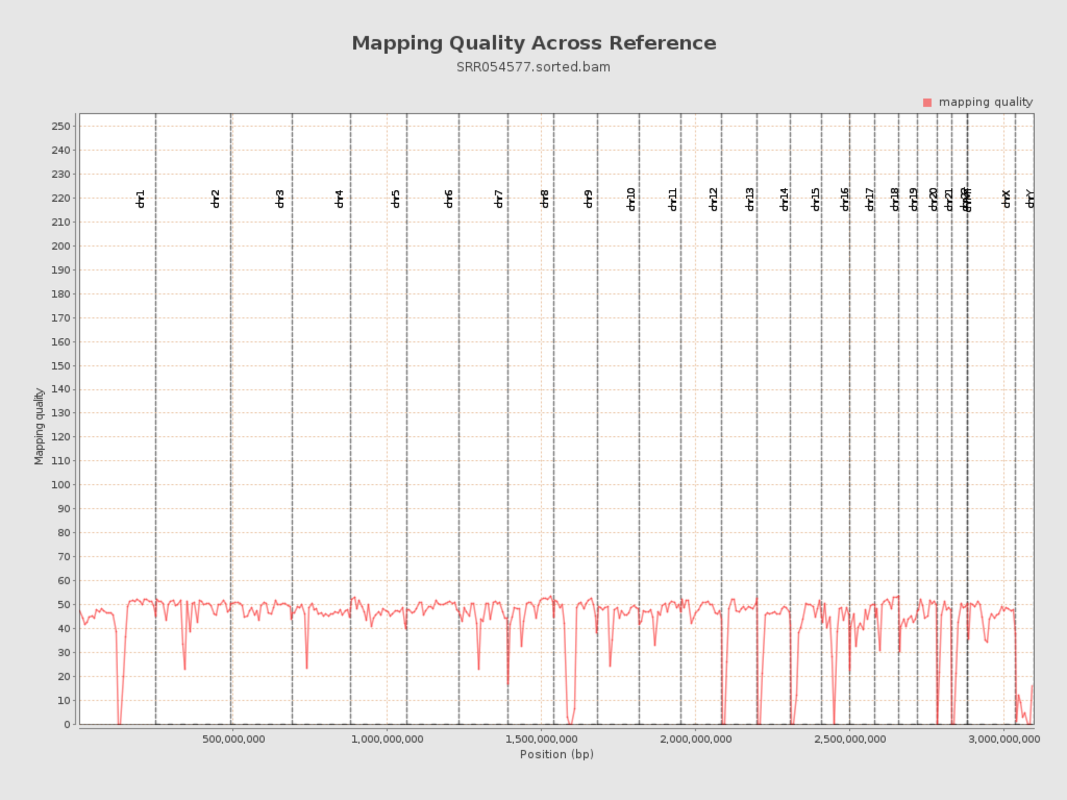
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram