Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:38:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054620.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_SRR054620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:38:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,232,344
Mapped reads	10,661,002 / 80.57%
Unmapped reads	2,571,342 / 19.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	333 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,565,423 / 19.39%
Duplication rate	17.16%
Clipped reads	823,223 / 6.22%

2.2. ACGT Content

Number/percentage of A's	145,419,876 / 28.84%
Number/percentage of C's	98,959,756 / 19.63%
Number/percentage of T's	148,373,590 / 29.43%
Number/percentage of G's	111,256,616 / 22.07%
Number/percentage of N's	198,206 / 0.04%
GC Percentage	41.69%

2.3. Coverage

Mean	0.1629

Standard Deviation	1.1381

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

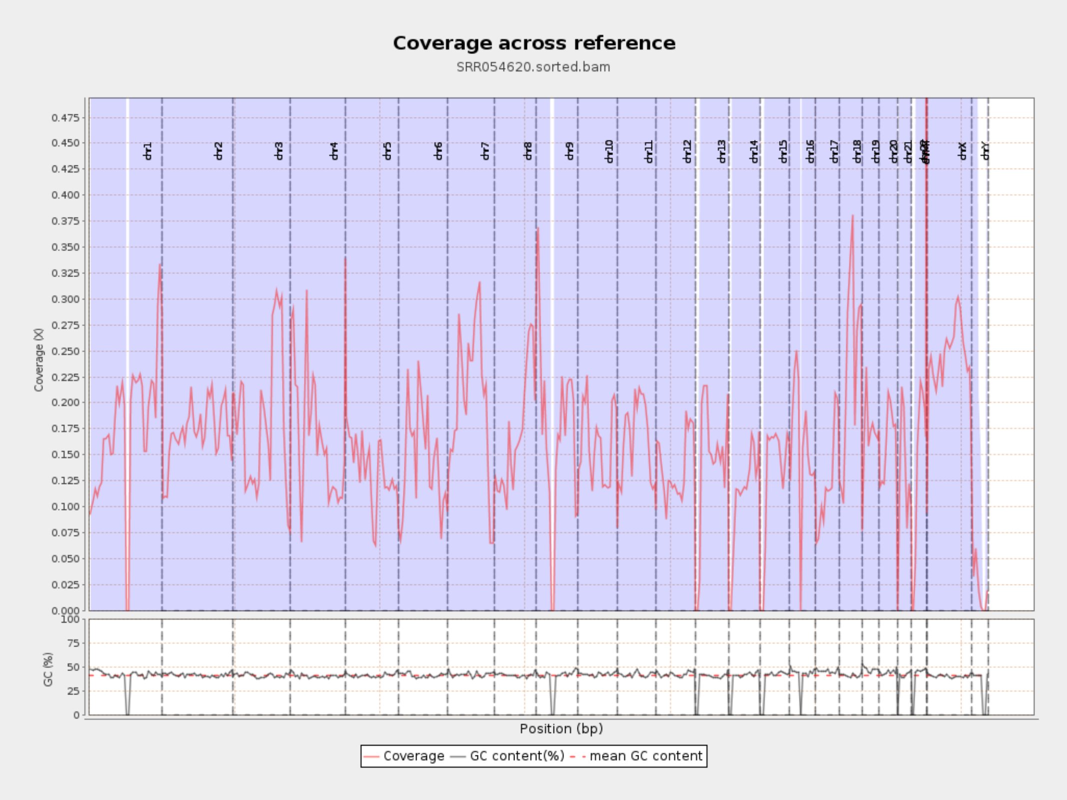
General error rate	0.48%
Mismatches	2,400,402
Insertions	19,584
Mapped reads with at least one insertion	0.18%
Deletions	67,118
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.18%

2.6. Chromosome stats

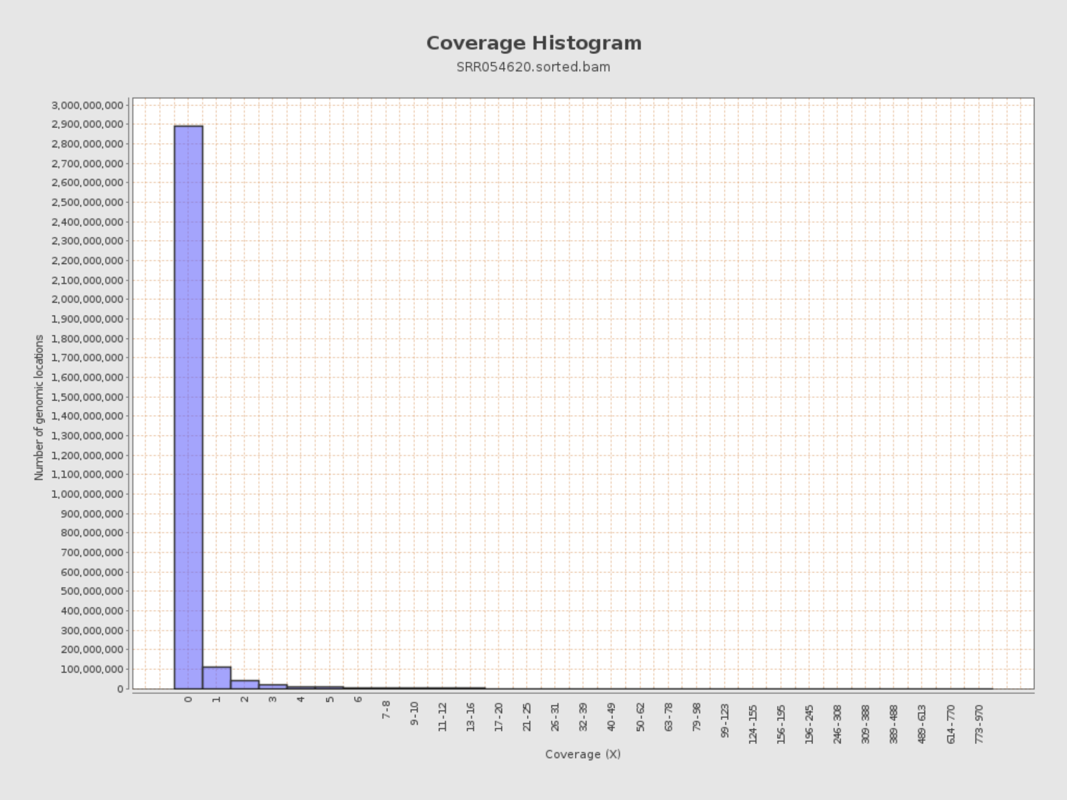
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43509202	0.1746	1.2875
chr2	243199373	41918576	0.1724	1.2382
chr3	198022430	36213368	0.1829	1.119
chr4	191154276	31767023	0.1662	1.1229
chr5	180915260	24711607	0.1366	0.9035
chr6	171115067	24553517	0.1435	1.0118
chr7	159138663	32613272	0.2049	1.3118

chr8	146364022	25108816	0.1716	1.119
chr9	141213431	24537469	0.1738	1.1547
chr10	135534747	21980444	0.1622	1.1569
chr11	135006516	22403275	0.1659	1.1081
chr12	133851895	18442401	0.1378	0.9254
chr13	115169878	15942762	0.1384	0.9361
chr14	107349540	11620430	0.1082	0.9289
chr15	102531392	13102928	0.1278	0.8634
chr16	90354753	14487493	0.1603	1.128
chr17	81195210	10092166	0.1243	0.8619
chr18	78077248	18647630	0.2388	1.5035
chr19	59128983	10276815	0.1738	1.514
chr20	63025520	10172433	0.1614	1.1628
chr21	48129895	6189970	0.1286	1.1653
chr22	51304566	6766571	0.1319	0.9776
chrMT	16571	27899	1.6836	3.5383
chrX	155270560	37835872	0.2437	1.4517
chrY	59373566	1387678	0.0234	0.5216

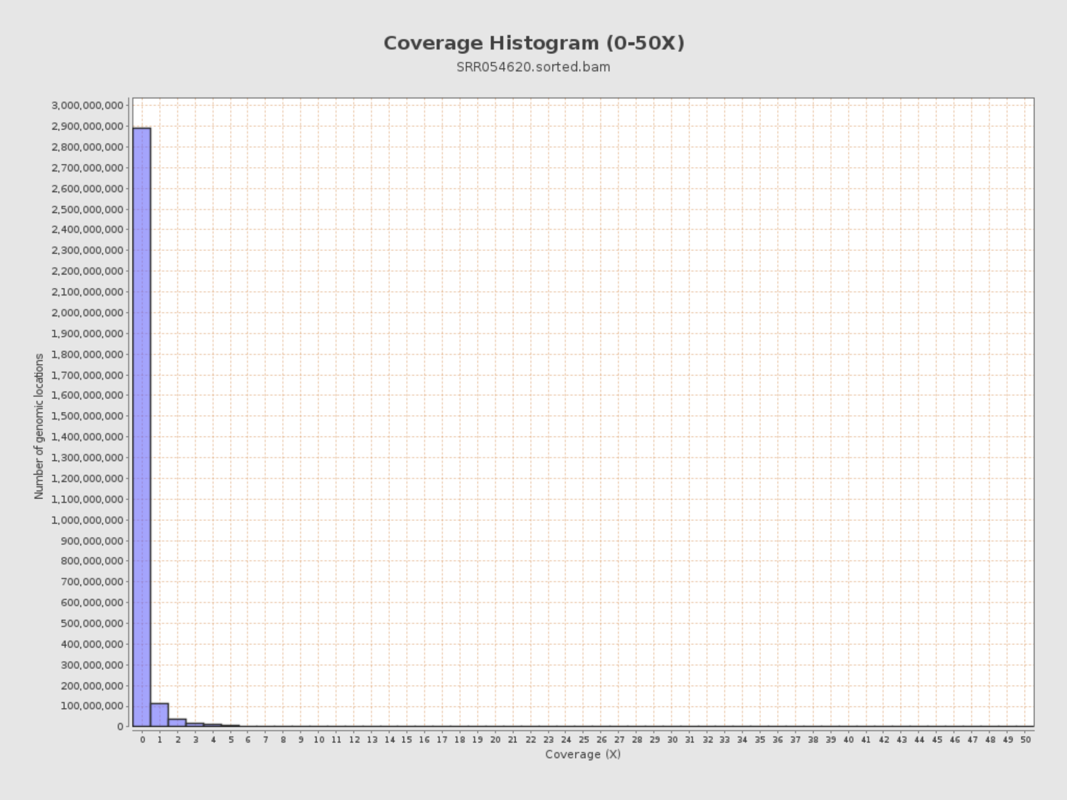
3. Results : Coverage across reference



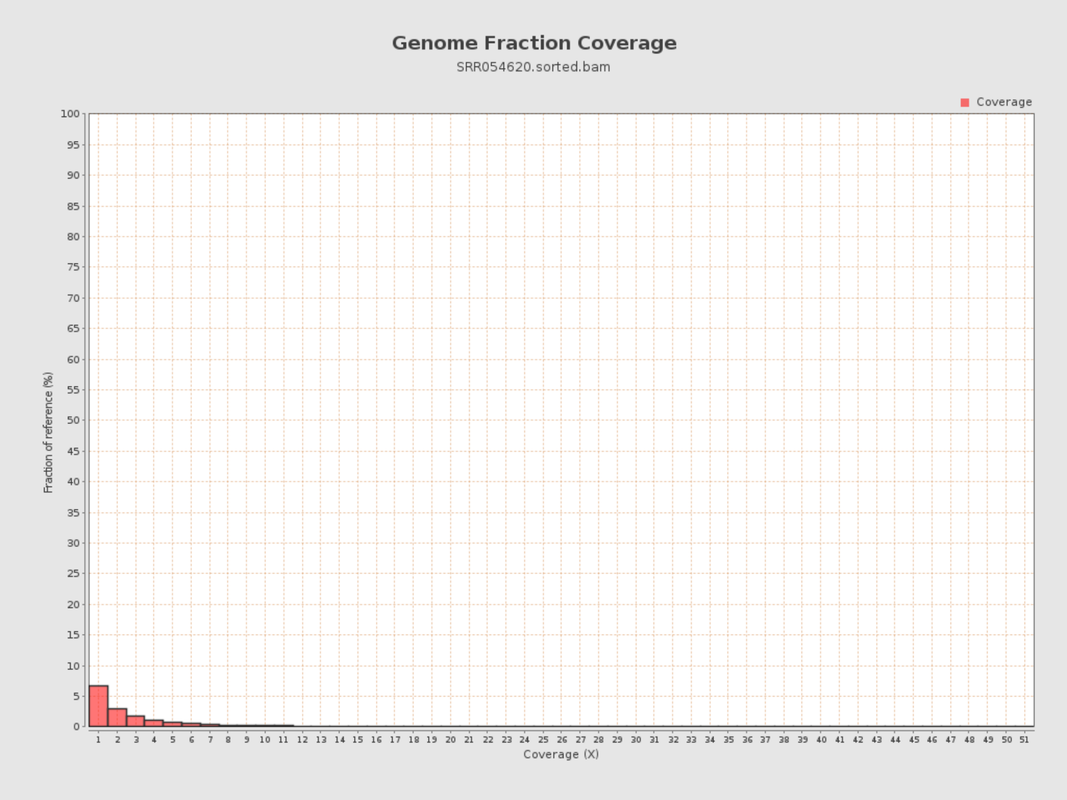
4. Results : Coverage Histogram



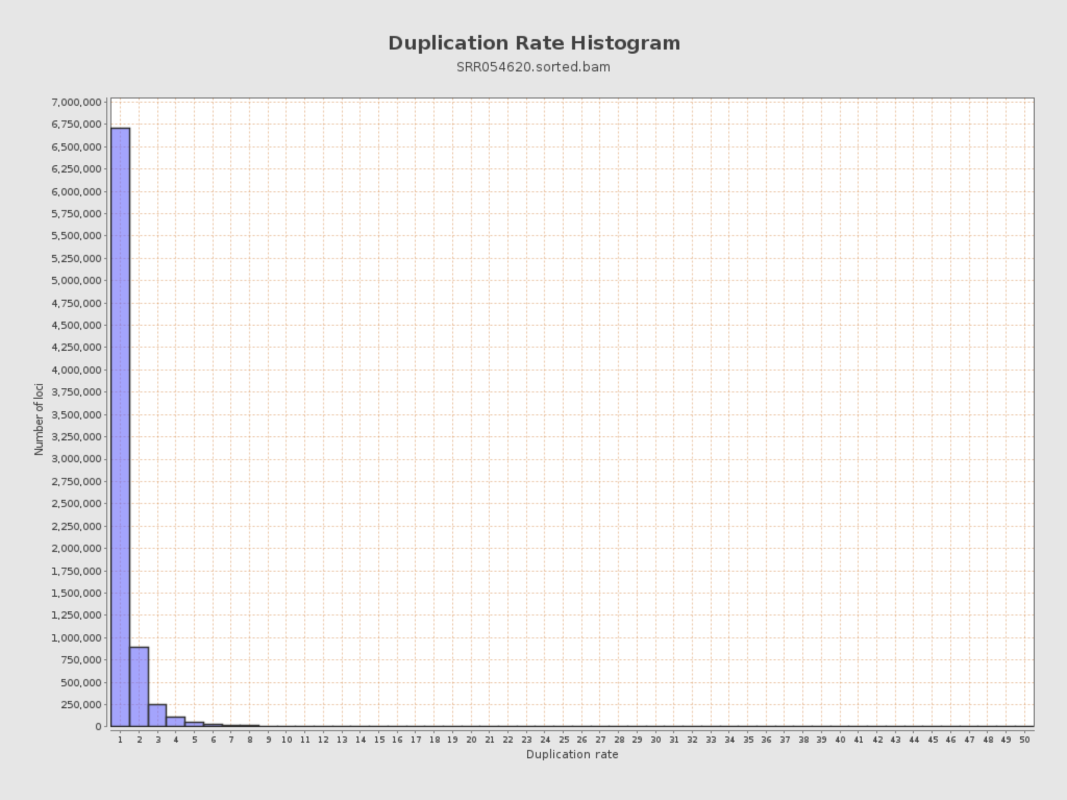
5. Results : Coverage Histogram (0-50X)



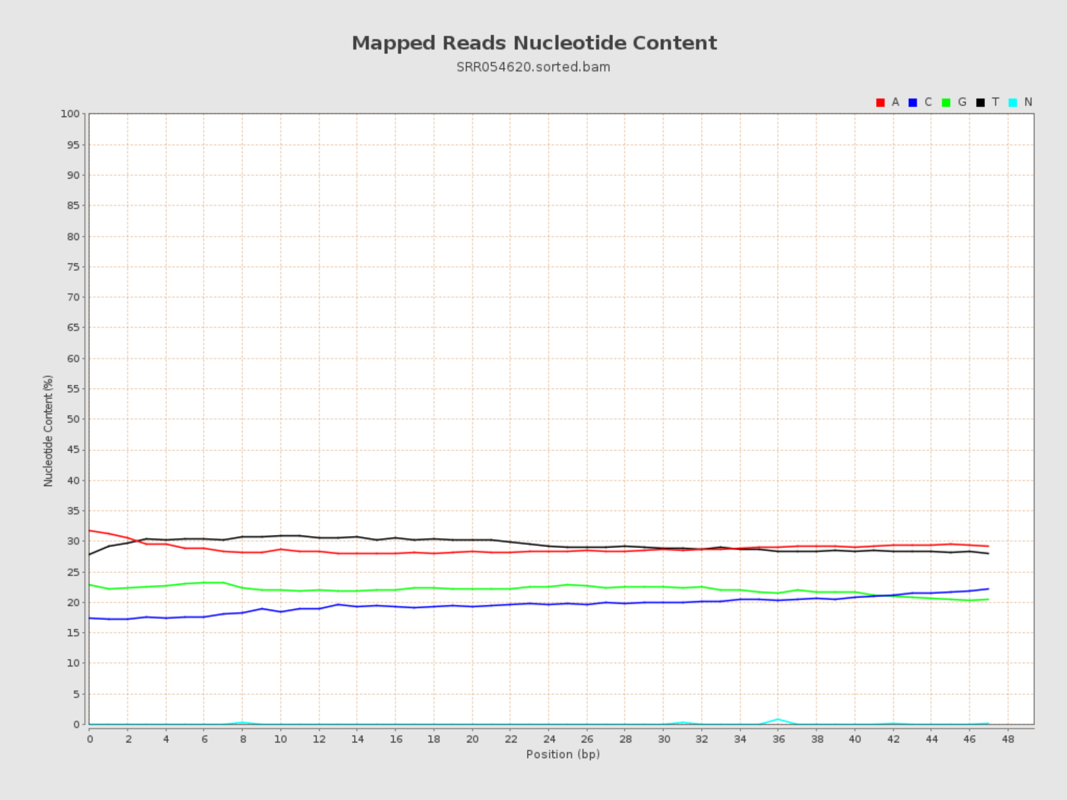
6. Results : Genome Fraction Coverage



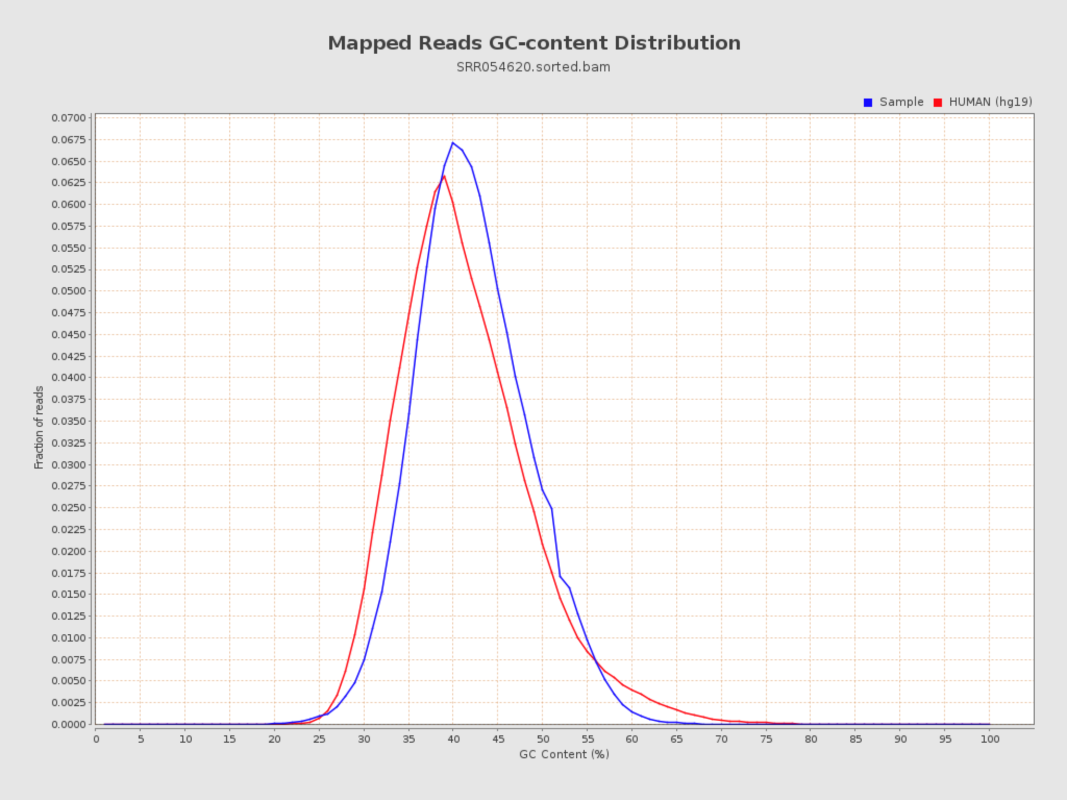
7. Results : Duplication Rate Histogram



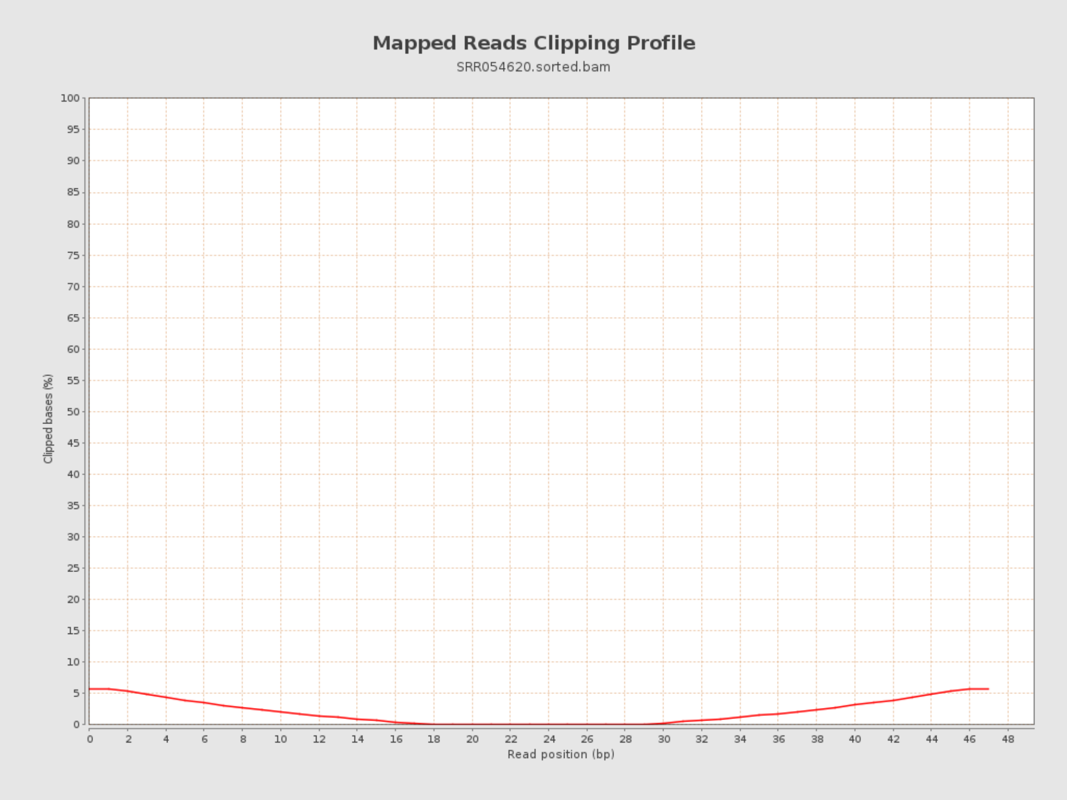
8. Results : Mapped Reads Nucleotide Content



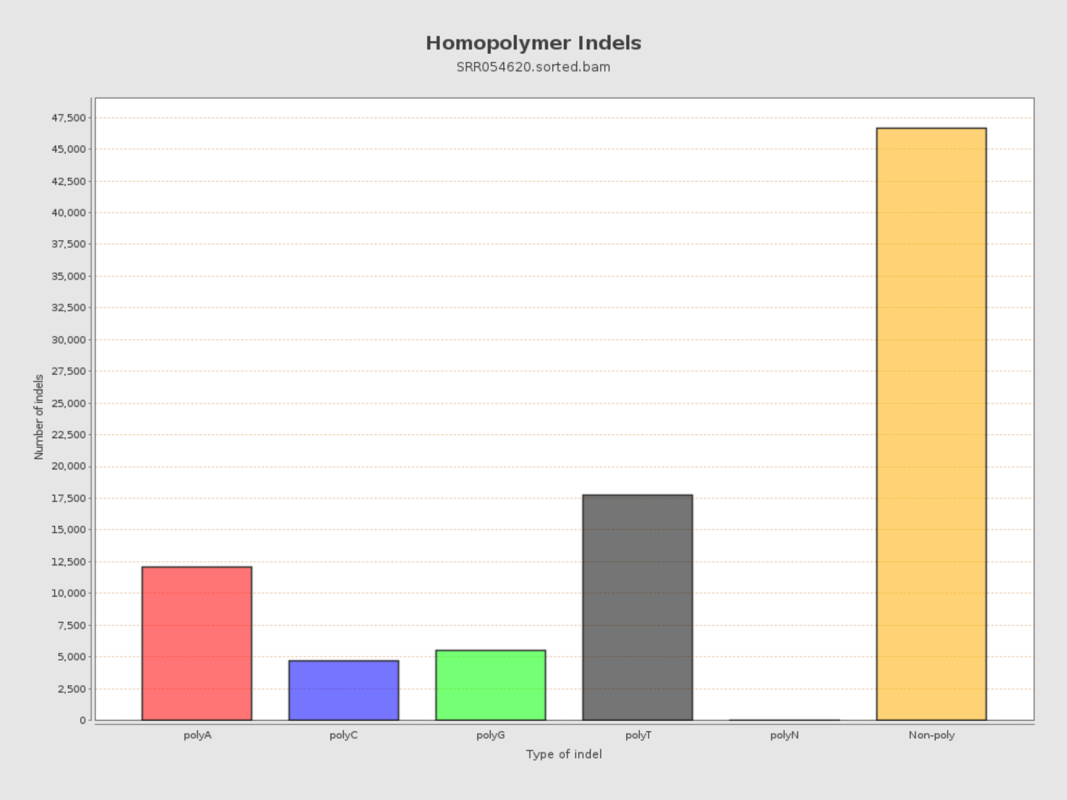
9. Results : Mapped Reads GC-content Distribution



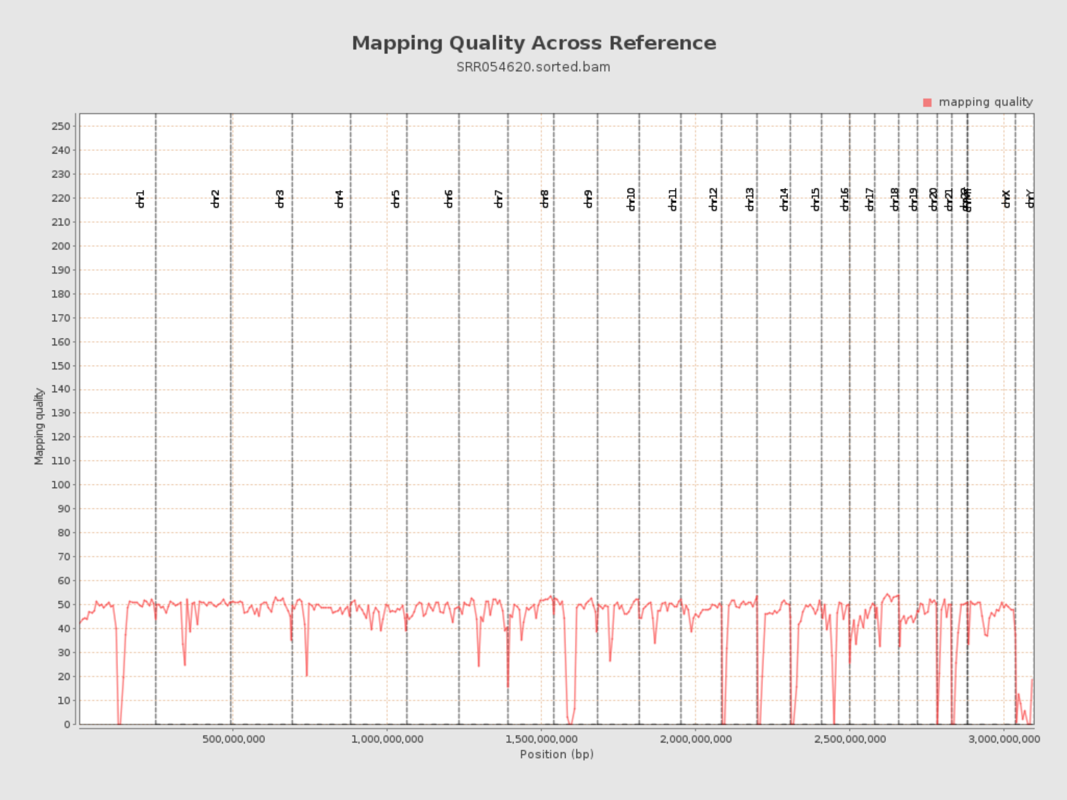
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram