

SURFSeq™ 5000

CMS™ Sequencing Kit V1.0

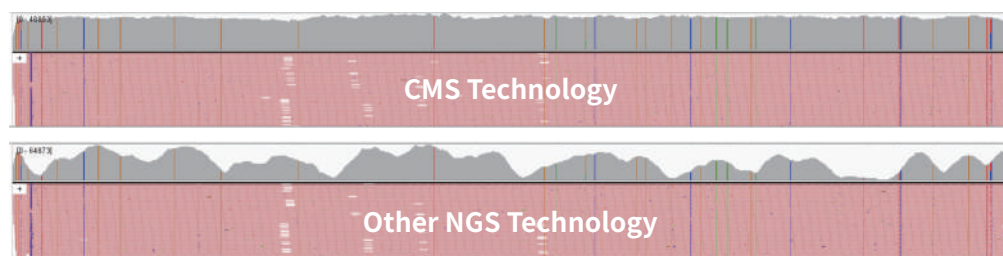


Pioneering the Unbiased Q50 Era
Redefining Speed with Tb-Level Desktop Sequencer

SURFSeq™ 5000 CMS™ Sequencing kit V1.0

Cross Mountains & Seas, Unlock Global Precision, Reach Unrivalled Speed

CMS™ (Cross Mountains and Seas) is an innovative sequencing chemistry developed by GeneMind. Through breakthroughs such as novel polymerase mutants, this technology significantly enhances sequencing capability in hard-to-sequence genomic regions, optimizes coverage uniformity across the whole genome, and delivers global unbiased Q50-level (99.999%) precision data output.



By integrating CMS™ and Lightning Chemistry Plus™, GeneMind introduces the SURFSeq™ 5000 CMS™ Sequencing Kit V1.0 series, fully empowering users to accelerate scientific discovery and enhance testing efficiency.



Navigate the "Difficult Terrain"

Overcome limits in hard-to-sequence regions
Achieve genome-wide coverage uniformity



Achieve Q50-Level Precision

Q40 > 95%
Q50 > 70%



Attain Unmatched Efficiency

1500 Gb + daily output
TAT for PE150 < 16 hrs

Lightning Chemistry Plus™ redefines sequencing efficiency with <1 minute per cycle—delivering rapid, high-quality results without compromise.

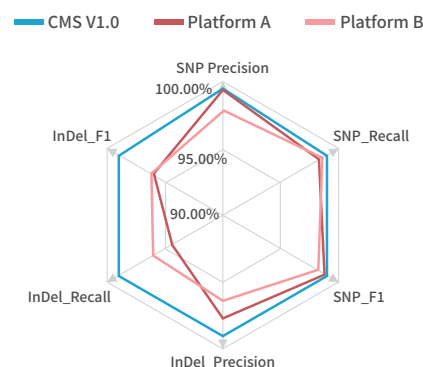
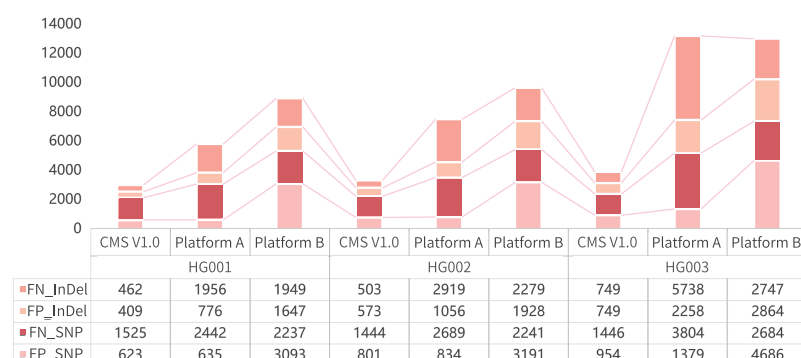
Detecting variants with high Accuracy in low-coverage regions^{1,2}

Test Sample: HG001–HG003 PCR-Free WGS Libraries.

Test Strategy: The same libraries were sequenced via CMS V1.0, Platform A, and Platform B with PE150.

Analysis Strategy: At 30× effective sequencing depth, SNP and InDel detection performance in low-coverage regions was evaluated across platforms.

Test Results: CMS V1.0 significantly outperformed Platform A and Platform B in both precision and sensitivity for SNP and InDel detection in low-coverage regions.



¹"Low-coverage regions" are defined as regions where the sequencing depth is less than 0.5× the median coverage.

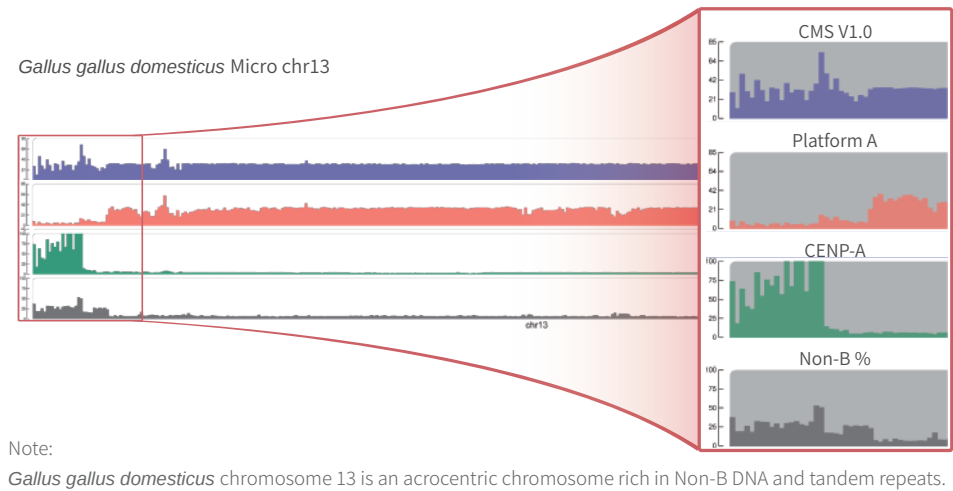
Unlocking hard-to-sequence Regions^{1,2}

Test Sample: *Gallus gallus domesticus* WGS library (Genome size: 2.18 Mb, GC content: 27.14%).

Test Strategy: The same libraries were sequenced via CMS V1.0, Platform A, and Platform B with PE150.

Analysis Strategy: Whole-genome coverage uniformity and sequencing performance in hard-to-sequence regions were evaluated.

Test Results: Using 25 Gb of data for comparative analysis, CMS V1.0 demonstrated significantly superior coverage uniformity and sequencing capability in hard-to-sequence regions compared to Platform A, as exemplified by chromosome 13.



Achieving More Data with Lower cost^{1,2}

Test Sample: *Fusobacterium nucleatum* WGS library (Genome size: 2.18 Mb, GC content: 27.14%).

Test Strategy: The same libraries were sequenced via CMS V1.0, Platform A, and Platform B with PE150.

Analysis Strategy: Reads from each platform were assessed at various depths for assembly quality using Unicycler.

Test Results: Assembly quality achieved with CMS V1.0 at 20× sequencing depth was equivalent to that achieved with Platform A at 100× or Platform B at 50× sequencing depth. This significantly reduces the data volume required for quality-assured detection, thereby lowering overall testing costs.

Assembly Core Metrics	Contigs	Largest contig	N50	L50	Genome fraction (%)
20×CMS V1.0	55	488,762	124,483	5	97.30
20×Platform A	96	95,303	40,492	21	94.49
20×Platform B	63	255,982	125,389	6	97.23
50×Platform A	71	255,982	94,810	7	97.40
50×Platform B	53	489,124	125,408	5	97.55
100×Platform A	58	488,871	125,408	5	97.53
100×Platform B	53	489,124	125,408	5	97.55

Product Parameter^{1,2}

Fowcell type	Lane	Throughput (Reads/FC)	Type	Read length	Data output (FC×2)	Q value (Q30)	Q value (Q40)	Q value (Q50)	TAT ³ (FC×1)	TAT ³ (FC×2)
FCP	4	3600 M	100cycles	SE100	360 Gb ×2	>97%	>95%	>70%	<14.0 hrs	<15.0 hrs
				PE50	360 Gb ×2	>97%	>95%	>70%	<14.0 hrs	<15.0 hrs
			200cycles	PE100	720 Gb ×2	>97%	>95%	>70%	<21.5 hrs	<24.5 hrs
			300cycles	PE150	1080 Gb ×2	>97%	>95%	>70%	<29.0 hrs	<34.0 hrs
FCH	4	2000 M	100cycles	SE100	200 Gb ×2	>97%	>95%	>70%	<12.5 hrs	<12.5 hrs
				PE50	200 Gb ×2	>97%	>95%	>70%	<12.5 hrs	<12.5 hrs
			200cycles	PE100	400 Gb ×2	>97%	>95%	>70%	<18.0 hrs	<18.0 hrs
			300cycles	PE150	600 Gb ×2	>97%	>95%	>70%	<24.0 hrs	<24.0 hrs
FCM	4	500 M	100cycles	SE100	50 Gb ×2	>97%	>95%	>70%	<9.0 hrs	<9.0 hrs
				PE50	50 Gb ×2	>97%	>95%	>70%	<9.0 hrs	<9.0 hrs
			200cycles	PE100	100 Gb ×2	>97%	>95%	>70%	<12.5 hrs	<12.5 hrs
			300cycles	PE150	150 Gb ×2	>97%	>95%	>70%	<16.0 hrs	<16.0 hrs

Ordering Information⁴

PN	Reagents
S000547	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCM 100cycles)
S000552	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCM 200cycles)
S000554	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCM 300cycles)
S000556	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCH 100cycles)
S000559	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCH 200cycles)
S000561	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCH 300cycles)
S000563	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCP 100cycles)
S000566	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCP 200cycles)
S000568	SURFSeq 5000 CMS Sequencing Kit V1.0 (FCP 300cycles)

Disclaimer:

1. Nature of the Data: This product evaluation is based on comparative testing conducted under specific controlled conditions. The conclusions presented are for research reference purposes only and do not constitute an express warranty or contractual commitment regarding product performance.

2. Result Variability: Actual performance may vary depending on factors such as sample type and quality. Results from a single test may deviate from the reference mean values.

3. turnaround time: Sequencing time refers to the runtime from sample loading to Basefile generation (based on the corresponding read length configuration plus dual-index setup).

4. This product is for research use only and shall not be used for clinical diagnostics. Not available in all regions, contact us for local availability.



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