Supplementary Material

Highly-accurate long-read sequencing improves variant detection and assembly of a human genome

Authors

Aaron M. Wenger[1*], Paul Peluso[1*], William J. Rowell[1], Pi-Chuan Chang[2], Richard J. Hall[1], Gregory T. Concepcion[1], Jana Ebler[3,4,5], Arkarachai Fungtammasan[6], Alexey Kolesnikov[2], Nathan D. Olson[7], Armin Töpfer[1], Chen-Shan Chin[6], Michael Alonge[8], Medhat Mahmoud[9], Yufeng Qian[1], Adam M. Phillippy[10], Michael C. Schatz[8], Gene Myers[11], Mark A. DePristo[2], Jue Ruan[12], Tobias Marschall[3,4], Fritz J. Sedlazeck[9], Justin M. Zook[7], Heng Li[13], Sergey Koren[10], Andrew Carroll[2], David R. Rank[1]†, Michael W. Hunkapiller[1]†

* These authors contributed equally to this work.
† Address correspondence to M.W.H. (mhunkapiller@pacb.com) or D.R.R. (drank@pacb.com).

1. Pacific Biosciences, Menlo Park, CA, USA
2. Google Inc., Mountain View, CA, USA
3. Center for Bioinformatics, Saarland University, Saarbrücken, Germany
4. Max Planck Institute for Informatics, Saarland Informatics Campus E1.4, Saarbrücken, Germany
5. Graduate School of Computer Science, Saarland University, Saarland Informatics Campus E1.3, Saarbrücken, Germany
6. DNAnexus, Mountain View, CA, USA
7. National Institute of Standards and Technology, Gaithersburg, MD, USA
8. Department of Computer Science, Johns Hopkins University, Baltimore, MD, USA
9. Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA
10. Genome Informatics Section, Computational and Statistical Genomics Branch, National Human Genome Research Institute, Bethesda, MD, USA
11. Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany
12. Agricultural Genomics Institute, Chinese Academy of Agriculture Sciences, Shenzen, China
13. Dana-Farber Cancer Institute, Boston, MA, USA

Detailed Author Contributions

CCS Library Preparation and Sequencing: DRR, PP, YQ

Quality Evaluation of CCS Reads: AMW, GM, RJH

Increased Mappability of CCS Reads: RJH

Small Variant Detection in CCS Reads: AC, AK, CSC, FJS, JMZ, MAD, NDO, PC, WJR

Phasing Small Variants: JE, TM, WJR

Improving Small Variant Detection with Haplotype Phasing: AC, AK, MAD, PC, WJR

Structural Variant Detection in CCS Reads: AMW, AT, FJS, HL, MCS, MA, MM

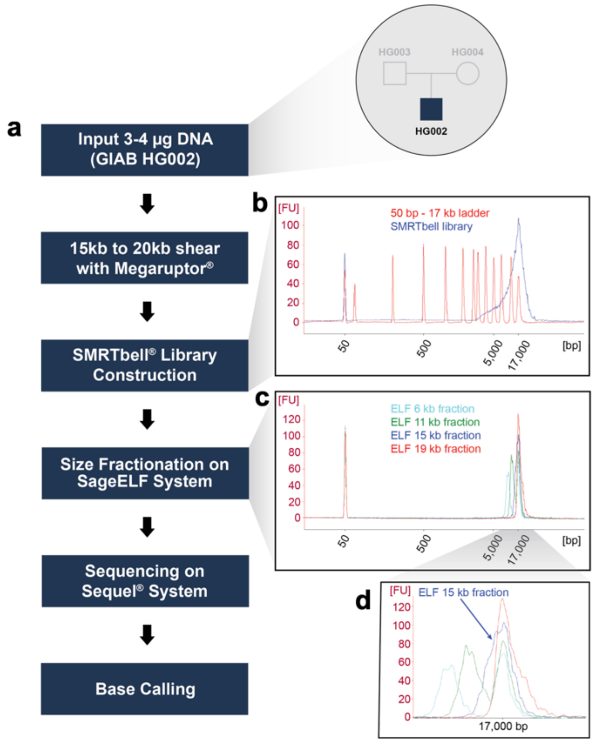
De Novo Assembly of CCS Reads: AF, AMP, AMW, DRR, JR, GTC, SK

Coverage Requirements for Variant Calling and De Novo Assembly: AC, AK, AMW, GTC, JE, TM, WJR

Revising and Expanding Genome in a Bottle Benchmarks: AMW, JMZ, NDO

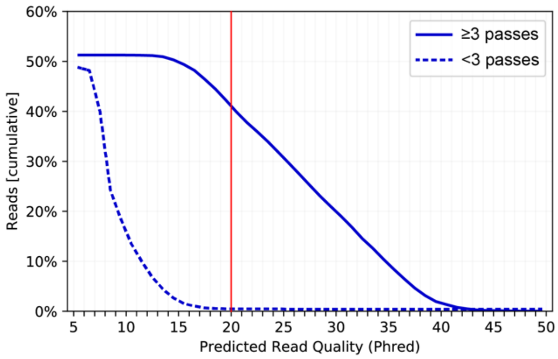
Supplementary Figures

Supplementary Figure 1



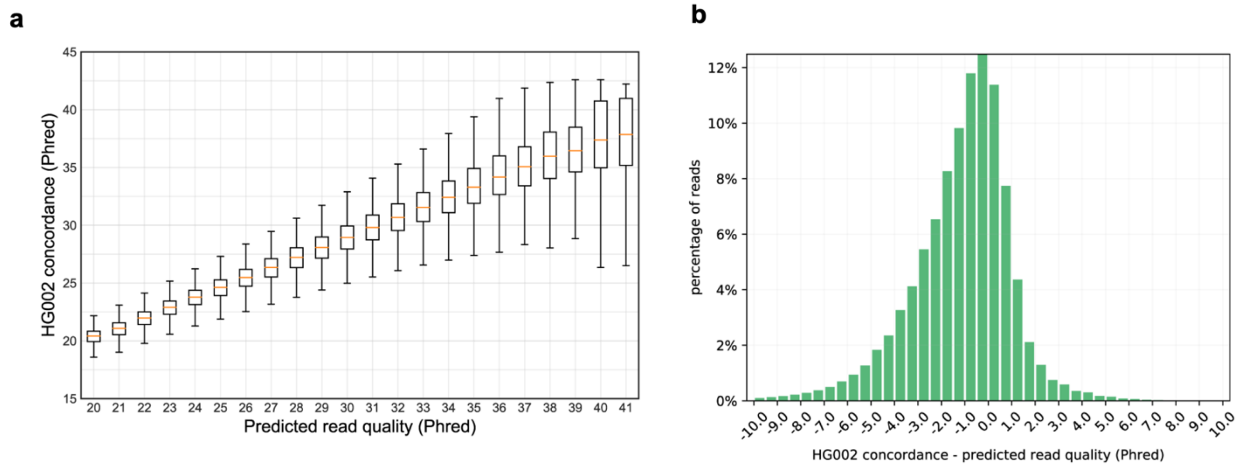
Supplementary Figure 1. CCS protocol. (a) Sample preparation and sequencing workflow. (b) BioAnalyzer trace for the SMRTbell library, sheared to target 15-20 kb fragments. "FU" is fluorescence units. (c) BioAnalyzer trace for ELF fractions of the SMRTbell library. (d) The fraction centered around 15 kb was used for sequencing.

Supplementary Figure 2



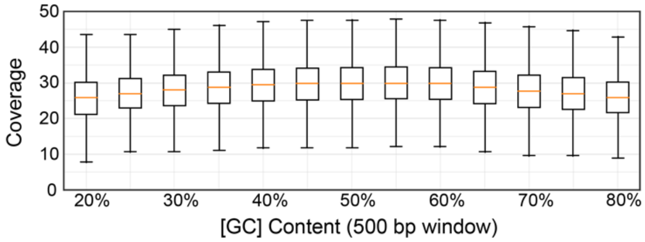
Supplementary Figure 2. Relationship between predicted CCS read quality and number of passes. Distribution of predicted quality for reads with fewer than 3 passes and at least 3 passes, which we consider a minimum pass count for CCS. Approximately half of reads have 3 or more passes; among those nearly all achieve Q20 predicted accuracy.

Supplementary Figure 3



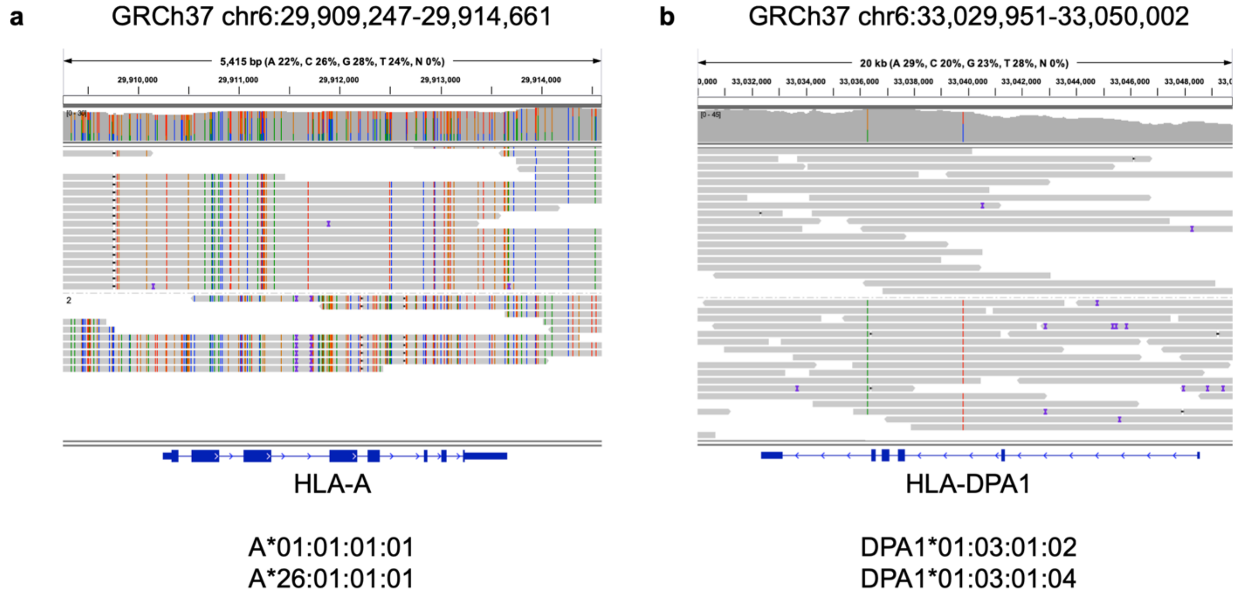
Supplementary Figure 3. Agreement between empirical concordance and predicted read quality for CCS reads. Empirical concordance is measured from alignments to GRCh37 at HG002 Genome in a Bottle high-confidence, non-variant positions. Predicted read quality is output by the CCS algorithm. (a) Distribution of HG002 concordance at levels of predicted read quality (R^2 of median = 0.9994), and (b) difference between concordance and predicted read quality show that the predicted read quality is well-calibrated to the empirical read quality.

Supplementary Figure 4



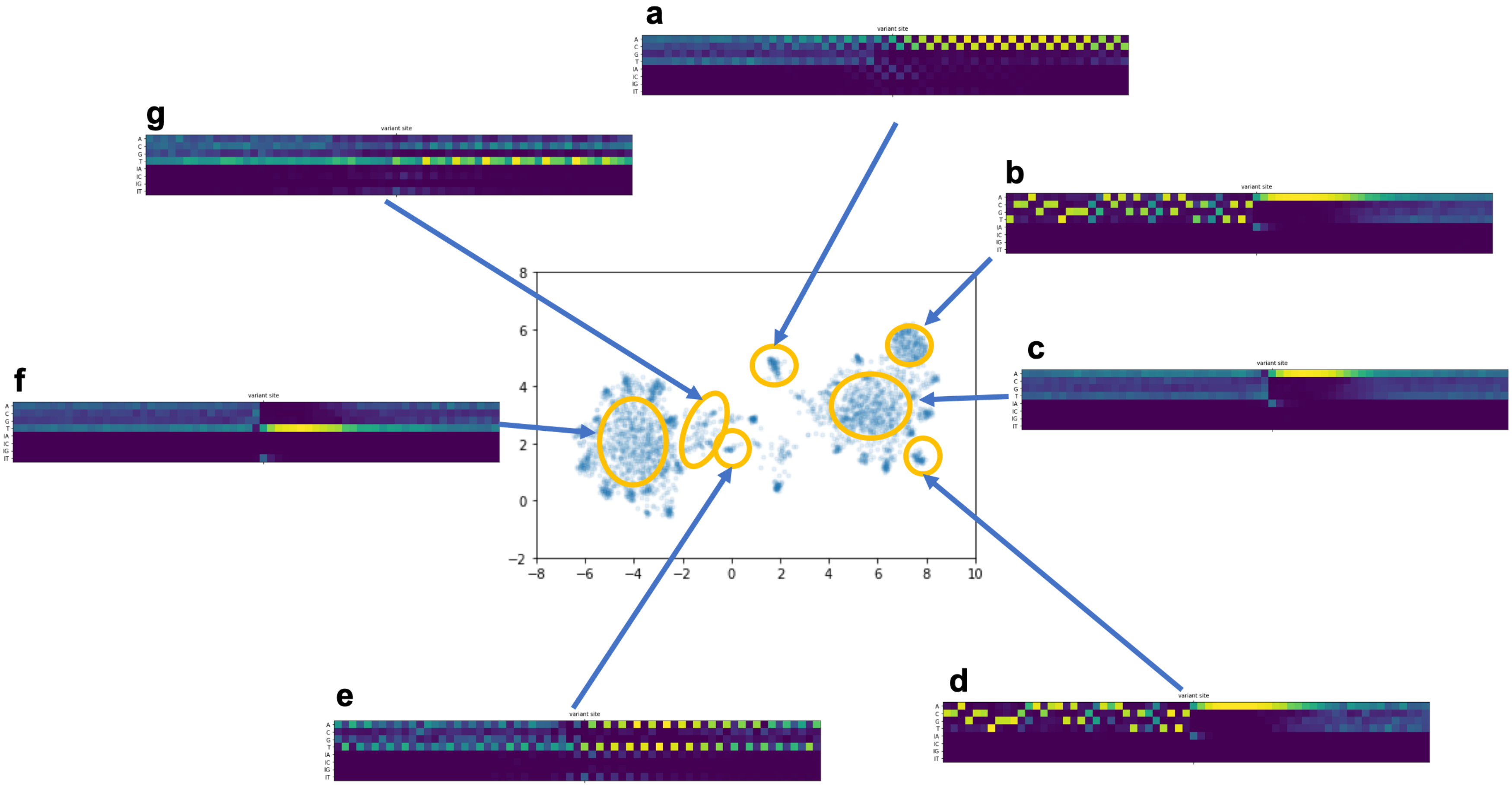
Supplementary Figure 4. Coverage as a function of genome [GC] content. Average coverage from 89 Gb of total yield, measured in 500 bp windows.

Supplementary Figure 5



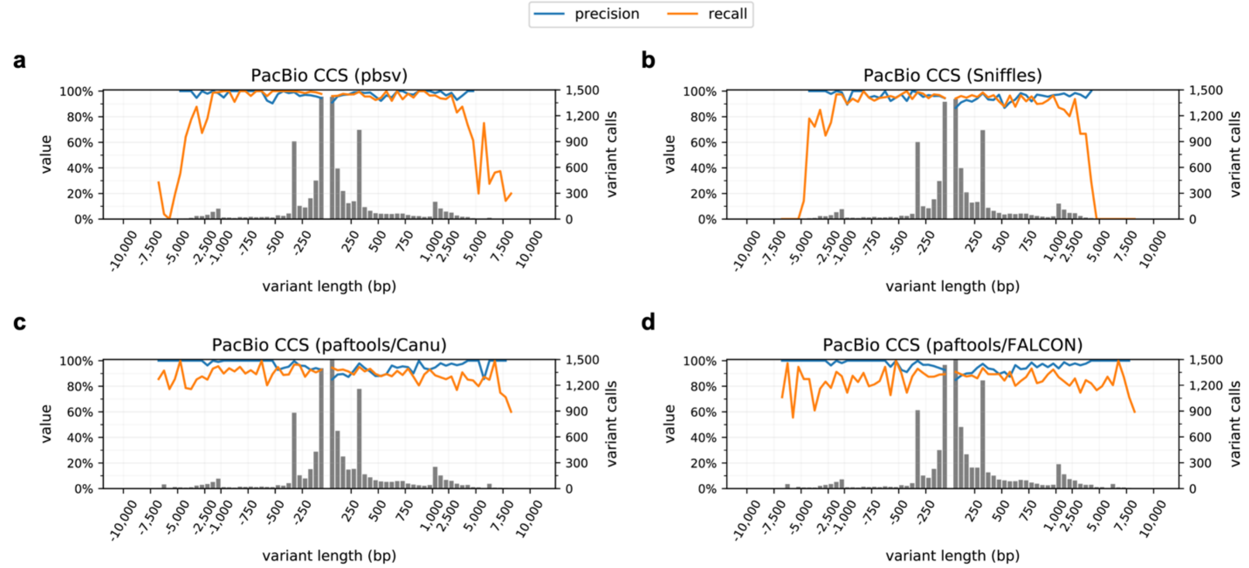
Supplementary Figure 5. CCS read pileups at HLA genes. The 13.5 kb CCS reads provide phasing and full four-field resolution of HLA class I and II genes[1], including (a) *HLA-A* for which HG002 has alleles that differ in the first field, and (b) *HLA-DPA1* for which HG002 has alleles that differ only in the fourth field from two intronic single nucleotide polymorphisms across 20 kb.

Supplementary Figure 6



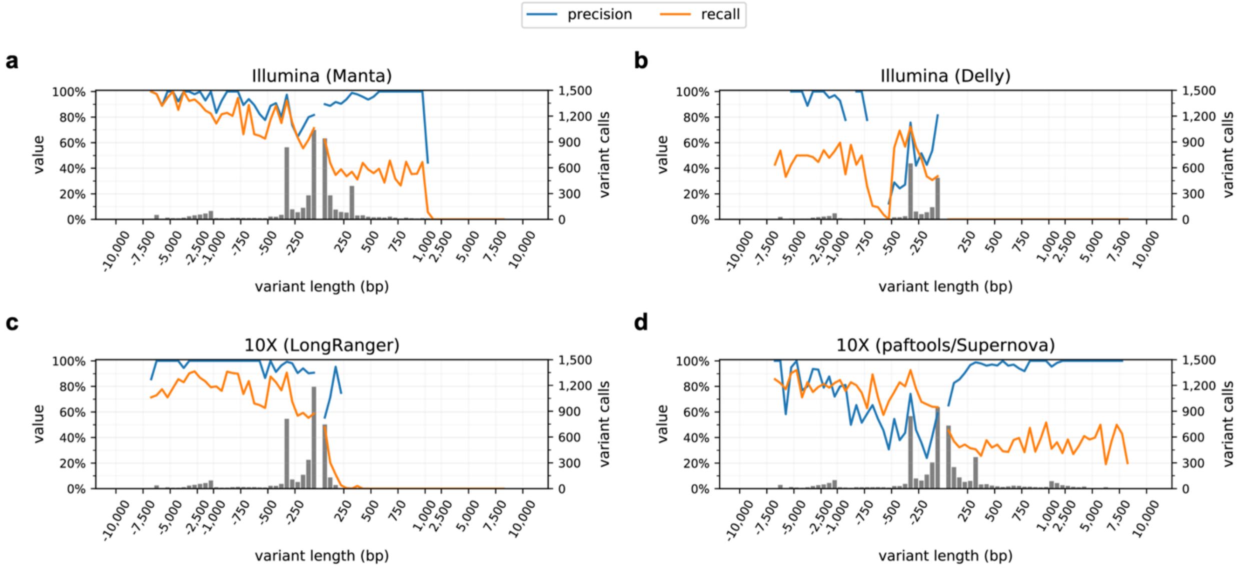
Supplementary Figure 6. Alignment contexts around DeepVariant (CCS) discordances. For all positions where the DeepVariant (CCS) callset is discordant with the Genome in a Bottle benchmark, CCS read alignments to the position +/- 32 bp were encoded as a matrix (4 rows for A/C/G/T match, 4 rows for A/C/G/T insertion). The matrices were deflated into vectors with length 65×8=520 and embedded into two dimensions using UMAP[2]. Some distinct clusters represent simple, identifiable patterns: (a)(e) di-nucleotide repeats; (b)(d) poly-A tails of ALU elements[3]; (c)(f) homopolymer A/T runs without a specific prefix; and (g) [CT]-rich simple repeats.

Supplementary Figure 7



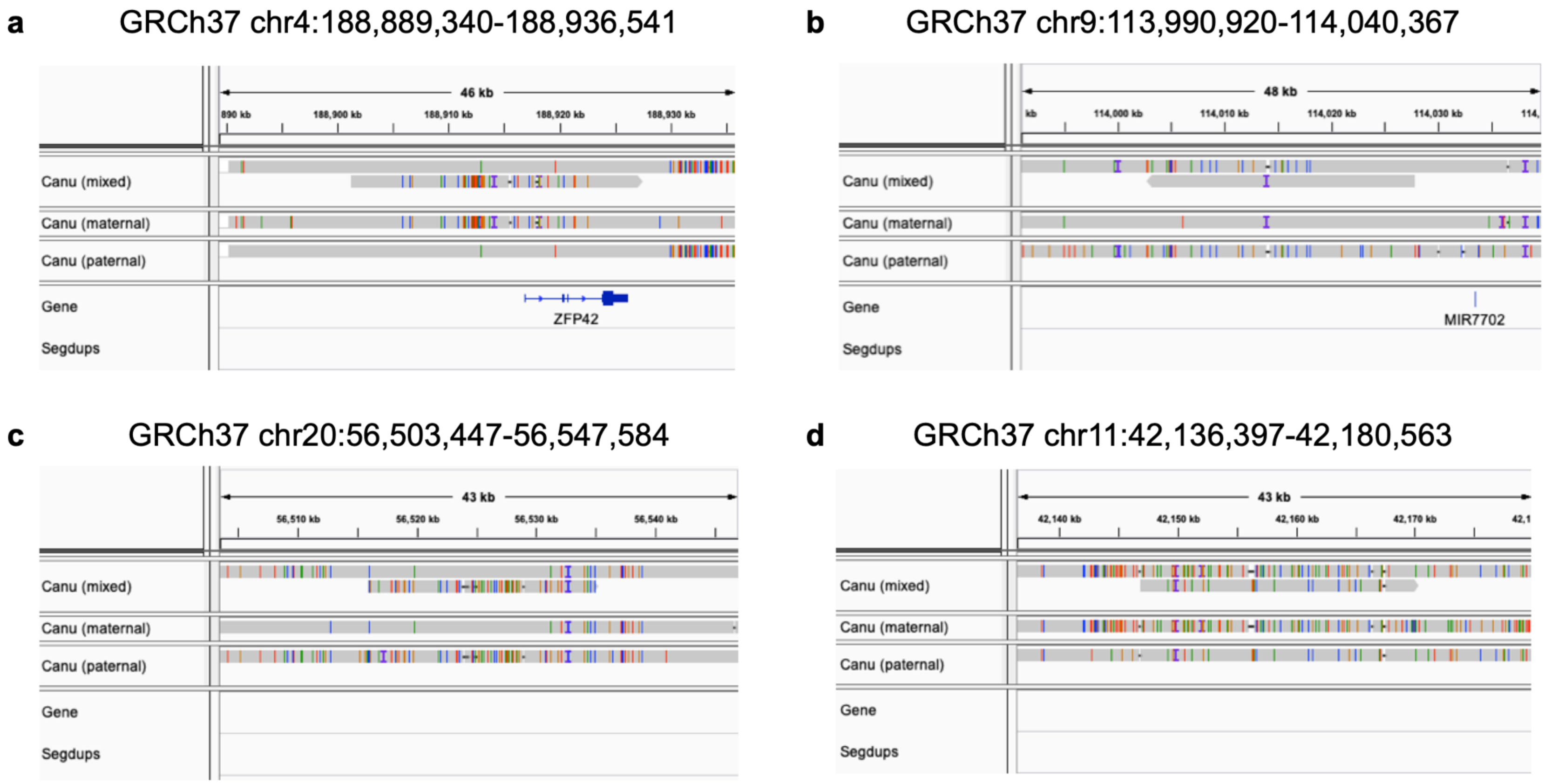
Supplementary Figure 7. Structural variant calling performance for mapping and assembly-based callers with PacBio CCS reads. Precision, recall, and number of variant calls in the GIAB HG002 SV high-confidence regions for PacBio CCS reads analyzed with the mapping-based variant callers (a) pbsv and (b) Sniffles and the assembly-based callers (c) paftools/Canu (polished) and (d) paftools/FALCON (unpolished). Negative length indicates a deletion; positive length indicates an insertion. The histogram bin size is 50 bp for variants shorter than 1 kb, and 500 bp for variants >1 kb. Precision and recall are measured with Truvari against the GIAB HG002 SV benchmark in high-confidence regions.

Supplementary Figure 8



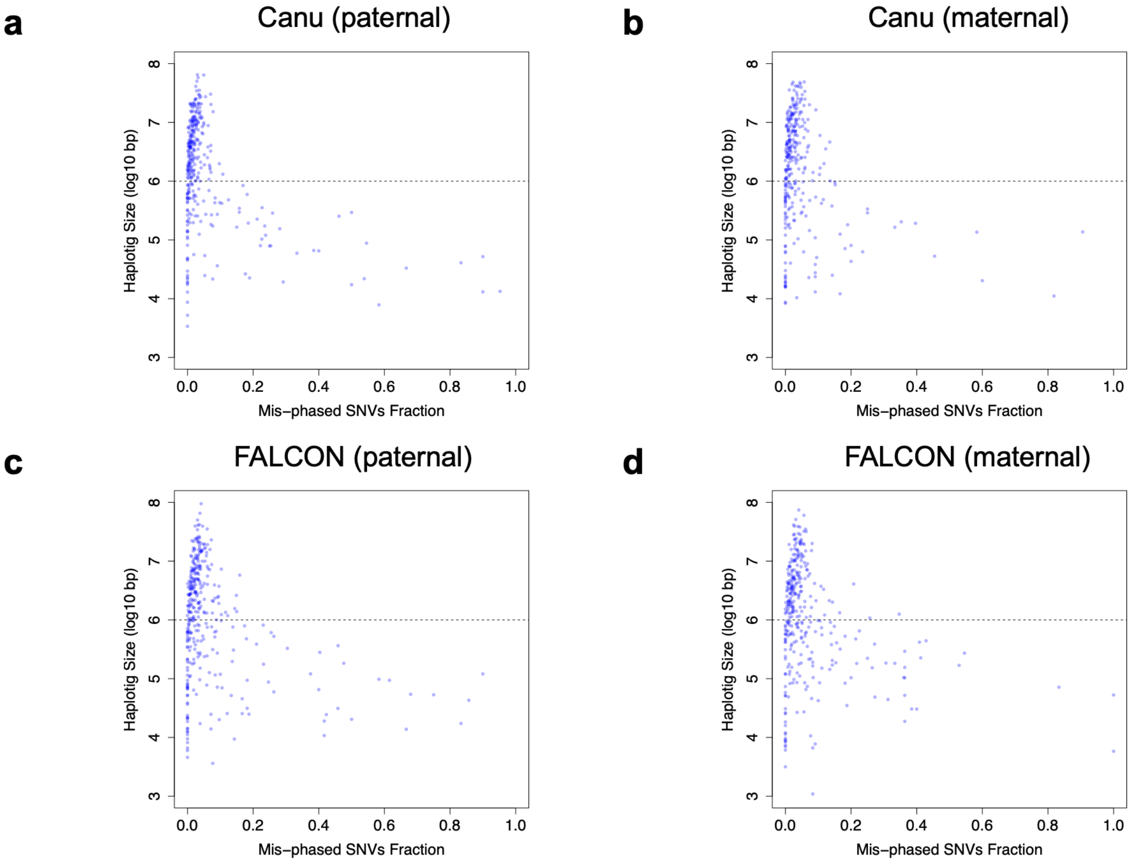
Supplementary Figure 8. Structural variant calling performance for Illumina and 10X Genomics variant callers. Precision, recall, and number of variant calls in the GIAB HG002 SV high-confidence regions for the Illumina short-read callers (a) Manta and (b) Delly and the 10X Genomics callers (c) LongRanger and (d) paftools/Supernova. Negative length indicates a deletion; positive length indicates an insertion. The histogram bin size is 50 bp for variants shorter than 1 kb, and 500 bp for variants >1 kb. Precision and recall are measured with Truvari against the GIAB HG002 SV benchmark in high-confidence regions.

Supplementary Figure 9



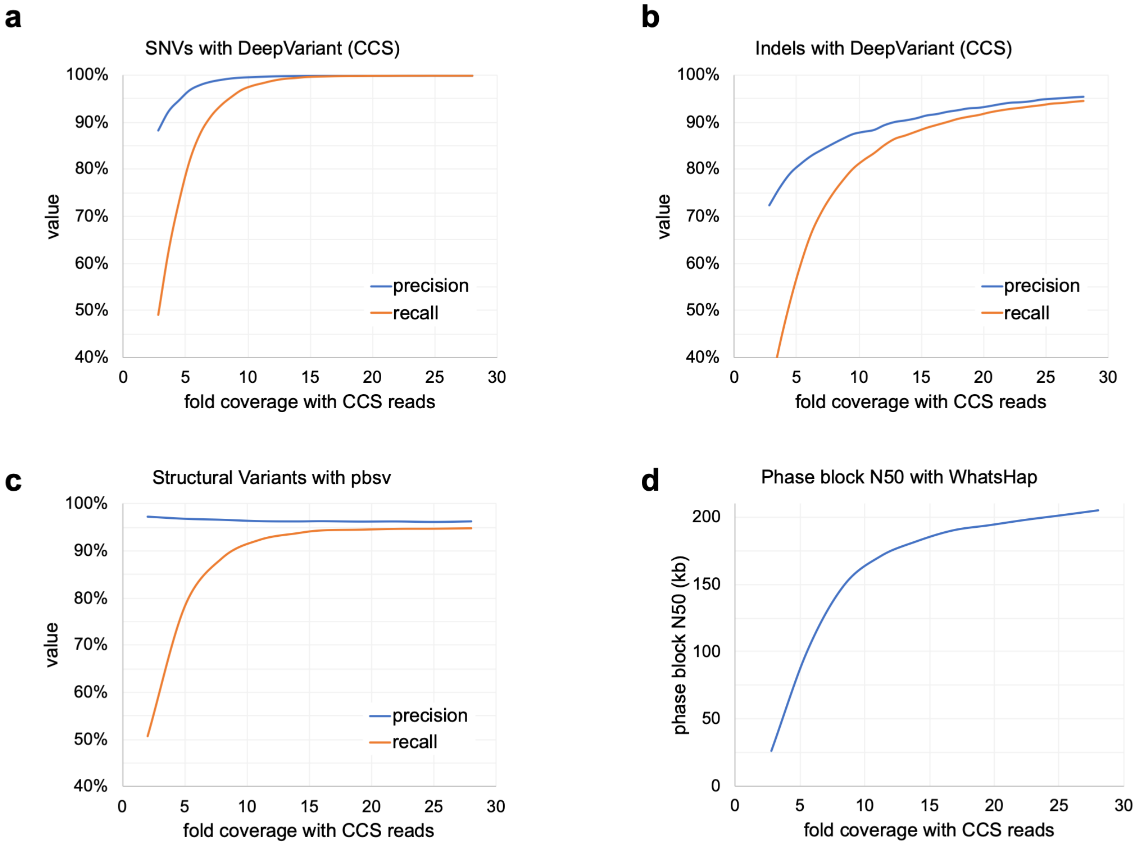
Supplementary Figure 9. Haplotype resolution in the Canu mixed assembly. The Canu mixed assembly is larger than the haploid human genome size because it resolves some heterozygous loci into separate maternal and paternal haplotypes. (a) (b) Loci where the long primary contig matches the paternal haplotype and a smaller contig matches the maternal haplotype. (c) (d) Similar loci where the long primary contig matches the maternal haplotype and a smaller contig matches the paternal haplotype.

Supplementary Figure 10



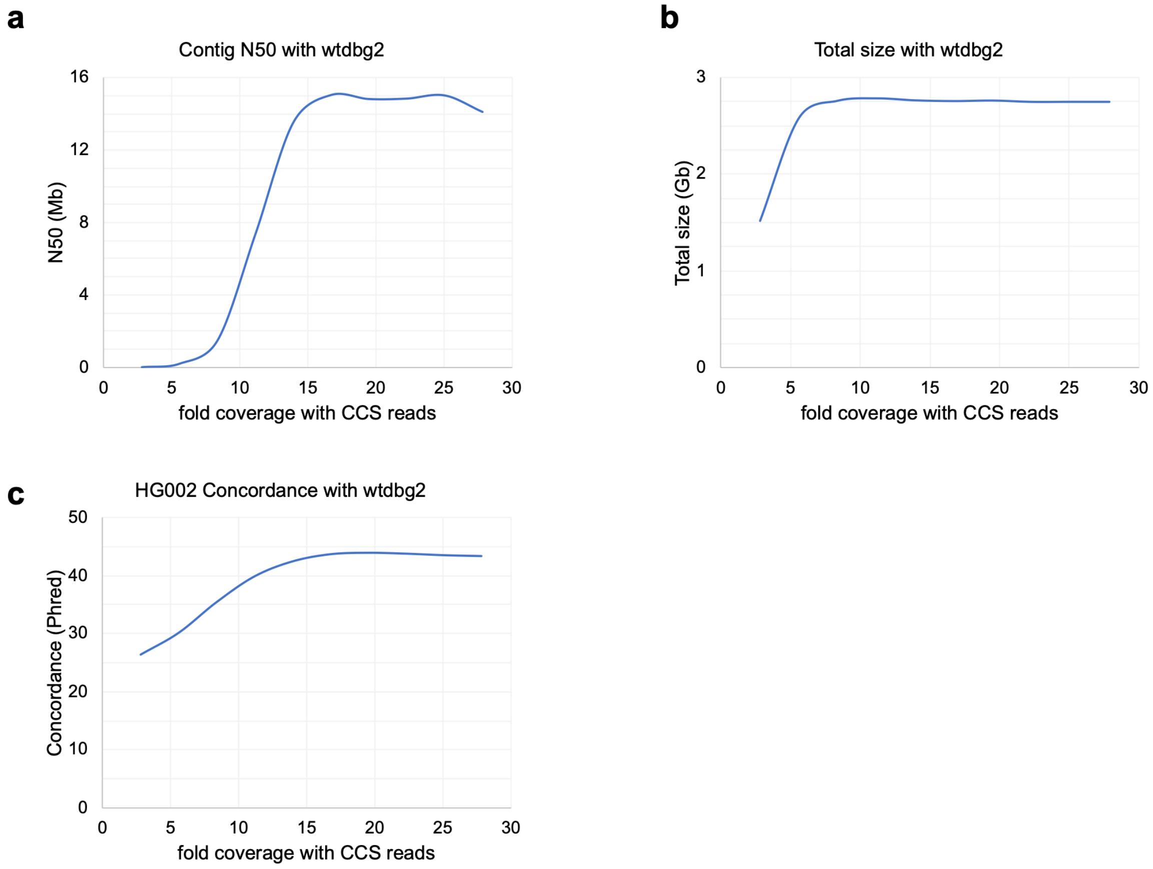
Supplementary Figure 10. Mis-phasing analysis of parental assemblies. Parent-specific heterozygous SNVs were identified in the Genome in a Bottle phased high-confidence callset. The "mis-phased SNVs fraction" is the fraction of parent-specific SNVs from the wrong parent (e.g. [SNV_{pat}]/[SNV_{pat}+SNV_{mat}] in a maternal contig). No large contigs have a high mis-phased SNVs ratio, which suggests proper phasing of the (a) Canu paternal, (b) Canu maternal, (c) FALCON paternal, and (d) FALCON maternal assemblies.

Supplementary Figure 11



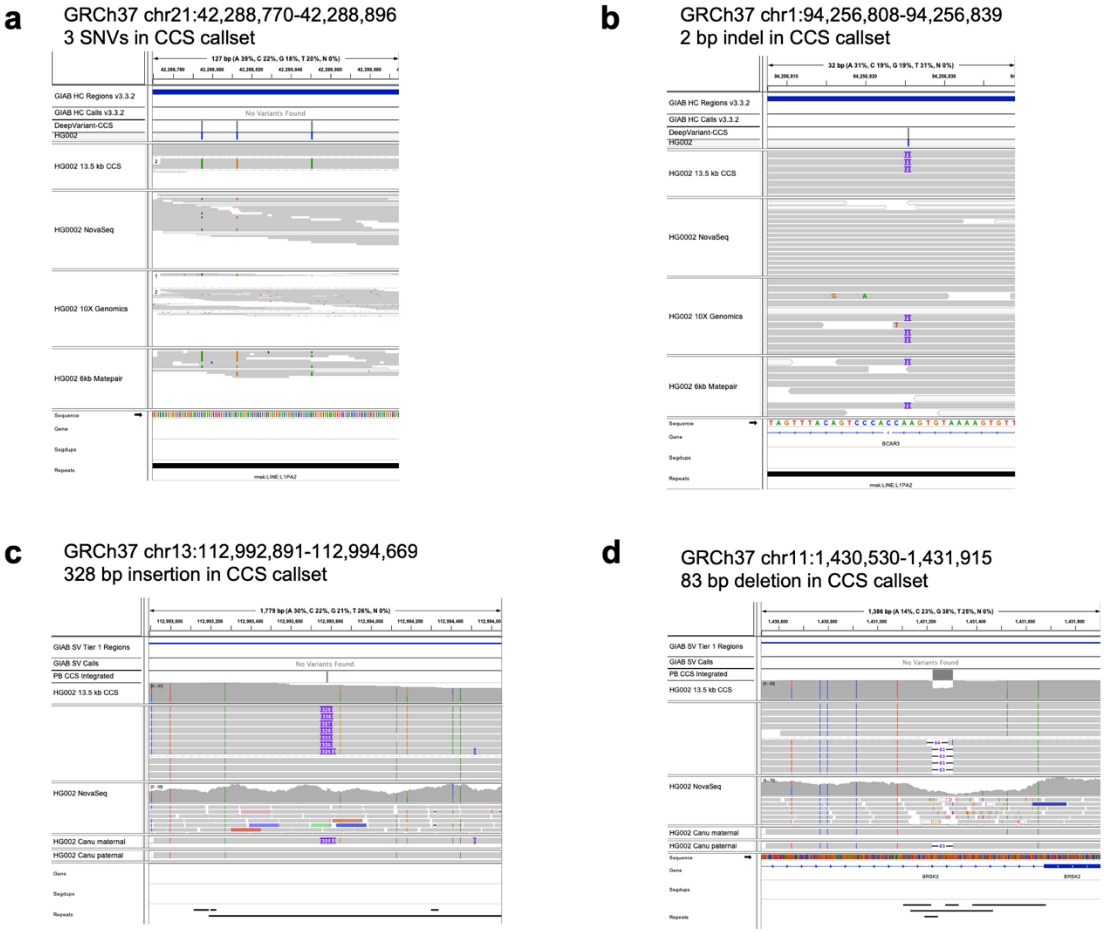
Supplementary Figure 11. Coverage titration for variant calling and phasing. Alignments of the 13.5 kb CCS reads were subsampled from 28-fold total coverage to evaluate variant calling and phasing performance at different coverage levels. Precision and recall for (a) SNVs and (b) indels called with DeepVariant (CCS), subsampling in steps of 3%. (c) Precision and recall for structural variants called with pbsv, subsampling in steps of 10%. (d) Phase block N50 for phasing of the 28-fold DeepVariant (CCS) callset with WhatsHap, subsampling in steps of 10%. Phasing performance is similar with a callset produced at matched coverage (not shown).

Supplementary Figure 12



Supplementary Figure 12. Coverage titration for *de novo* assembly. The 13.5 kb CCS reads were subsampled from 28-fold total coverage in steps of 10% to evaluate *de novo* assembly at different coverage levels. Reads were assembled with wtdbg2. (a) Contiguity measured as contig N50. (b) Completeness measured as total assembly size. (c) Correctness measured as concordance to HG002 at high-confidence, non-variant positions.

Supplementary Figure 13



Supplementary Figure 13. Likely errors in the Genome in a Bottle benchmark identified by CCS callsets. The high-quality Genome in a Bottle benchmark and CCS variant callsets have strong, but not perfect, concordance. Manual curation of discrepancies identifies benchmark errors for all variant types that are correctable using the CCS variant callsets. Shown are four loci that the Genome in a Bottle benchmark records as homozygous reference where CCS reads identify likely heterozygous variation: (a) Three SNVs supported by CCS reads and 6 kb matepair reads. (b) A 2 bp insertion supported by CCS reads, 10X Genomics reads, and 6 kb matepair reads. (c) A 328 bp insertion supported by CCS reads and assemblies. (d) An 83 bp insertion supported by CCS reads.

Supplementary Tables

Supplementary Table 1

	Total across CCS reads				
Discordance	**Count**	**Percentage**	**Frequency (1 / bp)**	**Concordance**	**(Phred)**
Mismatch	5,399,441	3.4%	13,048	99.992%	(Q41)
Non-homopolymer indel	7,286,391	4.6%	9,669	99.990%	(Q39)
Non-homopolymer insertion	5,700,531	3.6%	12,359	99.991%	(Q41)
Non-homopolymer deletion	1,585,860	1.0%	44,425	99.998%	(Q46)
Homopolymer indel	147,629,196	92.0%	477	99.790%	(Q27)
Homopolymer insertion	67,916,571	42.3%	1,037	99.903%	(Q30)
Homopolymer deletion	79,712,625	49.7%	884	99.887%	(Q29)
Total	**160,315,028**	**100%**	**439**	**99.772%**	**(Q26)**

Supplementary Table 1. Discordances between CCS read alignments and HG002 at high-confidence, non-variant positions. An indel is considered a homopolymer event if the inserted/deleted basepairs match either the preceding or following reference basepair. “Count” is the total number of discordances across CCS reads. “Percentage” is over all discordances, by type. “Concordance (Phred)” considers only discordances of the given type. A large majority of discordances between the CCS reads and HG002 are homopolymer indels, which likely represent indel errors in the CCS reads.

Supplementary Table 2

			SNVs			Indels		
Platform	**Coverage**	**Variant caller (training model)**	**Precision**	**Recall**	**F1 ^**	**Precision**	**Recall**	**F1**
Illumina (Novaseq)	30-fold	DeepVariant (Illumina model)	**99.925%**	**99.940%**	**99.933%**	**99.450%**	**99.233%**	**99.341%**
Illumina (Novaseq)	30-fold	GATK HaplotypeCaller (no filter)	99.824%	99.920%	99.872%	99.230%	98.898%	99.064%
PacBio (CCS)	28-fold	DeepVariant (haplotype-sorted CCS model)	99.778%	99.937%	99.858%	96.860%	96.035%	96.446%
PacBio (CCS)	28-fold	DeepVariant (CCS model)	99.807%	99.904%	99.855%	95.387%	94.501%	94.942%
PacBio (CCS)	28-fold	DeepVariant (Illumina model)	99.533%	99.793%	99.663%	23.991%	81.692%	37.090%
PacBio (CCS)	28-fold	GATK HaplotypeCaller (hard filter)	99.408%	99.531%	99.469%	77.137%	79.941%	78.514%

Supplementary Table 2. Performance of small variant calling with CCS reads on chromosome 20. DeepVariant models were not presented with chromosome 20 data before variant calling, so accuracy evaluations between GATK and DeepVariant are most comparable for chromosome 20. **Bold** indicates the highest value in each column. Underline indicates a value higher than the GATK HaplotypeCaller run on 30-fold Illumina NovaSeq reads. Callers are sorted (“^”) based on F1 for SNVs.

Supplementary Table 3

GRCh37 chrom	Heterozygous variants	% phased	Phase blocks	Phase block N50 (bp)	Hamming error rate	Switch errors	Switch error rate
1	220,180	99.61%	1,585	225,534	1.53%	1,168	0.65%
2	212,809	99.62%	1,879	179,190	1.53%	373	0.21%
3	193,762	99.73%	1,312	259,761	1.63%	408	0.25%
4	199,451	99.70%	1,338	238,088	1.65%	547	0.33%
5	186,023	99.75%	1,115	277,697	1.06%	237	0.15%
6	177,458	99.71%	1,160	265,656	0.96%	303	0.20%
7	166,051	99.70%	1,048	246,748	2.23%	1,105	0.80%
8	153,941	99.71%	1,002	250,705	1.22%	322	0.25%
9	119,897	99.72%	778	207,951	1.30%	362	0.36%
10	141,433	99.72%	840	255,026	2.13%	344	0.29%
11	128,503	99.67%	948	203,073	1.24%	169	0.16%
12	135,470	99.72%	832	292,306	3.51%	229	0.20%
13	100,628	99.69%	638	244,289	2.19%	123	0.14%
14	93,645	99.68%	548	292,617	2.70%	520	0.66%
15	81,981	99.61%	609	188,168	0.71%	411	0.61%
16	87,697	99.71%	596	198,059	4.69%	455	0.63%
17	78,865	99.65%	569	209,363	3.06%	380	0.61%
18	74,575	99.68%	568	215,577	2.44%	95	0.15%
19	70,975	99.78%	345	283,264	2.17%	149	0.26%
20	61,413	99.65%	425	207,556	3.53%	165	0.33%
21	44,142	99.49%	257	178,353	4.29%	545	1.60%
22	38,604	99.71%	249	221,143	1.29%	87	0.28%
Autosomes	**2,779,801**	**99.64%**	**19,215**	**206,063**	**1.91%**	**8,497**	**0.37%**

Supplementary Table 3. WhatsHap phasing performance on DeepVariant (CCS) callset. WhatsHap provides highly complete phasing (99.64%) of heterozygous variants in the DeepVariant (CCS) callset that is concordant with the Genome in a Bottle Trio/10X Genomics phasing truth set. Statistics are reported by WhatsHap with Hamming and switch error rates evaluated against the truth set.

Supplementary Table 4

		All variants			Deletions			Insertions		
Platform	**Caller**	*Precision*	*Recall*	*F1 ^*	*Precision*	*Recall*	*F1*	*Precision*	*Recall*	*F1*
PacBio (CCS)	integrated	96.13%	**95.99%**	**96.06%**	**97.66%**	**96.88%**	**97.27%**	94.97%	**95.30%**	95.13%
PacBio (CCS)	pbsv	**96.26%**	94.93%	95.59%	96.71%	94.98%	95.84%	**95.95%**	94.89%	**95.42%**
PacBio (CCS)	Sniffles	94.28%	91.76%	93.01%	96.56%	92.19%	94.32%	92.59%	91.44%	92.01%
PacBio (CCS)	paftools (Canu †‡)	93.16%	92.32%	92.74%	95.84%	92.76%	94.28%	91.48%	91.99%	91.73%
PacBio (CCS)	paftools (FALCON †)	93.25%	89.14%	91.15%	95.99%	89.00%	92.36%	91.64%	89.25%	90.43%
Illumina	Manta	85.34%	55.88%	67.53%	85.95%	76.90%	81.17%	92.12%	39.65%	55.44%
10X	paftools (Supernova)	64.52%	52.74%	58.04%	55.37%	73.71%	63.24%	82.74%	36.57%	50.72%
10X	LongRanger	83.79%	39.83%	53.99%	94.66%	70.18%	80.60%	59.39%	16.41%	25.71%
Illumina	Delly	65.92%	19.90%	30.58%	65.92%	45.70%	53.98%	0.00%	0.00%	0.00%

Supplementary Table 4. Structural variant calling performance as measured with Truvari against the GIAB HG002 SV benchmark. **Bold** indicates the highest value in each column; callers are sorted (“^”) based on F1 for all variants. † union of maternal and paternal assemblies; ‡ polished with arrow.

Supplementary Table 5

		CPU core hours		
Haplotype	**Assembler**	**Trio binning**	**Assembly**	**Arrow polishing**
Mixed	Canu	n/a	2,136	-
Mixed	FALCON	n/a	2,650	-
Mixed	wtdbg2	n/a	380	-
Maternal	Canu	350	751	71,226*
Maternal	FALCON	350	1,683	26,137
Maternal	wtdbg2	350	182	-
Paternal	Canu	350	841	70,069*
Paternal	FALCON	350	1,568	26,183
Paternal	wtdbg2	350	187	-

Supplementary Table 5. CPU core hours for *de novo* assembly and polishing. The CPU core hours required for trio binning, assembly, and polishing were recorded using the Unix `time` command. Assembly time includes read correction built into the assembler but excludes the total upfront CCS read generation (118,365 CPU core hours). The assemblers were run by different groups on different hardware, and thus times are not directly comparable. "*" Arrow polishing was run for one round on FALCON and two rounds on Canu; "n/a" = not applicable; "-" = not done

Supplementary Table 6

	% reads assigned to haplotype		
k-mer (bp)	**Maternal**	**Paternal**	**Unassigned**
21	35.3%	33.6%	31.1%
51	40.4%	38.1%	21.5%
91	40.5%	38.7%	20.8%

Supplementary Table 6. CCS read classification by trio binning. The percentage of CCS reads assigned to the maternal and paternal haplotype by k-mer size used in trio binning. CCS reads with an insufficient number of distinguishing k-mers are assigned to the "unassigned" haplotype, which includes reads from homozygous regions of genome.

Supplementary Table 7

NCBI/ENA Accession	Platform	Sample	Assembler	Polish	Concordance ^	(Phred)
-	PacBio (CCS)	HG002 (paternal)	Canu	Arrow	99.9983%	(Q47.7)
-	PacBio (CCS)	HG002 (maternal)	Canu	Arrow	99.9981%	(Q47.2)
-	PacBio (CCS)	HG002	wtdbg2	-	99.9965%	(Q44.6)
GCA_001542345	PacBio (CLR)	HG002	PBcR	Quiver	99.9899%	(Q40.0)
GCA_002077035	PacBio (CLR)	HG001	FALCON	Quiver	99.9893%	(Q39.7)
ERZ781176	ONT + Illumina	HG001	Canu	Nanopolish×2, Pilon×2, Racon×2	99.8693%	(Q28.8)
-	ONT	HG001	Canu	Nanopolish×2	99.6565%	(Q24.6)

Supplementary Table 7. Reference concordance of assemblies from different platforms. Concordance is measured at non-variant positions in Genome in a Bottle high-confidence regions. The three CCS read assemblies have higher concordance than accessioned assemblies provided with PacBio continuous long reads (CLR) or Oxford Nanopore read (ONT). ONT HG001 assembly is from https://obj.umiacs.umd.edu/marbl_publications/triobinning/albacore_canu_nanopolish2.fasta.

Supplementary Table 8

		Segdups	
Haplotype	**Assembler**	**Resolved (Mb)**	**Unresolved (Mb)**
Mixed	Canu	63.6	111.8
Mixed	FALCON	46.1	129.3
Mixed	wtdbg2	26.4	149.0
Maternal	Canu	60.2	115.2
Maternal	FALCON	43.2	132.2
Maternal	wtdbg2	28.9	146.5
Paternal	Canu	60.0	115.4
Paternal	FALCON	41.7	133.7
Paternal	wtdbg2	27.2	148.2

Supplementary Table 8. Resolution of segmental duplications. A segmental duplication in GRCh38 is considered resolved by an assembly if it is spanned by a contig with at least 50 kb on each flank, as measured by segDupPlots (https://github.com/mvollger/segDupPlots).

Supplementary Table 9

Discrepancy	Variant Type	Repeat family (if ≥1 kb)	Homopolymer Length (bp) (if ≥6 bp)	Correct Call	Chr	Position	Variant
AM	INDEL		19	GIAB	2	9,591,845	CT/C
AM	INDEL			GIAB	2	232,051,483	GCA/GCATCATGGAGAATGGGACATCTC
AM	INDEL			GIAB	3	37,083,407	G/GA
AM	INDEL			CCS	4	11,468,804	CACACATATAT/C
AM	INDEL	L1PA2		CCS	5	42,740,225	CT/C
AM	INDEL		Nearby 17	GIAB	6	41,984,320	ACTAT/A
AM	INDEL		16	GIAB	8	73,675,279	TAAAA/T
AM	INDEL		13	GIAB	13	76,646,445	G/GA
AM	INDEL		16	GIAB	15	44,350,983	C/CA
AM	INDEL		13	GIAB	19	1,586,670	A/ATTT
AM	SNP	HERVH-int		CCS	2	5,143,996	G/A
AM	SNP			GIAB	2	230,174,543	A/G
AM	SNP	L1PA2		CCS	4	165,276,021	T/C
AM	SNP		8	GIAB	5	16,287,108	A/C
AM	SNP		8	GIAB	11	41,384,344	C/T
AM	SNP		20	GIAB	12	51,793,781	A/C
AM	SNP		9	GIAB	13	34,840,815	G/T
AM	SNP	L1PA3		CCS	13	48,291,499	A/C
AM	SNP		12	GIAB	13	71,512,745	A/T
AM	SNP			GIAB	21	25,668,597	G/A
FN	INDEL			GIAB	1	162,491,859	A/ATGTCTAG
FN	INDEL		12	GIAB	2	152,262,374	G/GTT
FN	INDEL		14	GIAB	2	236,062,930	G/GTT
FN	INDEL	L1PA2	9	GIAB	3	107,982,543	AT/A
FN	INDEL		18	GIAB	4	149,672,221	A/ATT
FN	INDEL			CCS	8	5,930,728	TACAC/T
FN	INDEL		6	GIAB	10	29,087,199	T/TCC
FN	INDEL			GIAB	15	26,120,981	C/CTTACACTGGGCTTTTTGTAAGGA
FN	INDEL			CCS	15	41,943,823	T/TCCTCTTCTCTCCTCTCC
FN	INDEL		15	GIAB	17	5,198,683	C/CA
FN	SNP		16	GIAB	5	55,201,041	A/G
FN	SNP			GIAB	6	8,353,625	C/T
FN	SNP			CCS	6	9,737,425	T/C
FN	SNP			GIAB	6	57,283,620	T/C
FN	SNP		13	GIAB	7	135,981,582	T/A
FN	SNP			CCS	7	157,385,671	A/G
FN	SNP			GIAB	9	117,917,190	A/C
FN	SNP		13	GIAB	9	129,471,234	T/A
FN	SNP		5	CCS	17	32,064,214	A/G
FN	SNP		25	GIAB	17	68,021,050	T/A
FP	INDEL	L1PA2		CCS	1	94,256,825	A/AAC
FP	INDEL	L1HS		CCS	2	153,864,971	AT/A
FP	INDEL	L1M2	13	GIAB	3	97,014,398	AT/A
FP	INDEL	L1HS	7	CCS	4	112,819,087	GA/G
FP	INDEL	L1PA2		CCS	4	165,026,074	A/AG
FP	INDEL		10	GIAB	6	64,897,720	A/AT
FP	INDEL		15	GIAB	7	38,338,238	C/CA
FP	INDEL			GIAB	8	132,575,025	C/CAAAAAAAAA
FP	INDEL	L1P1		CCS	11	23,338,682	C/CT
FP	INDEL		20	GIAB	11	61,993,476	CA/C
FP	SNP	L1HS		CCS	1	35,034,071	T/C
FP	SNP	L1HS		CCS	3	79,181,734	C/T
FP	SNP		Nearby 8	GIAB	4	55,520,593	G/A
FP	SNP	L1HS	7	CCS	4	94,532,444	T/G
FP	SNP	ALR/Alpha		CCS	8	46,873,565	C/T
FP	SNP		11	GIAB	9	6,900,971	C/T
FP	SNP	L1PA2		CCS	9	22,350,168	A/C
FP	SNP		13	GIAB	20	1,347,896	A/G
FP	SNP		12	GIAB	20	4,159,335	C/T
FP	SNP	L1PA2		CCS	21	42,288,851	C/A

Supplementary Table 9. Manual curation of small variant discrepancies between CCS callset and Genome in a Bottle benchmark. For the "Discrepancy" column, "AM" means genotype difference, "FN" means false negative (in benchmark but not callset), and "FP" means false positive (in callset but not benchmark). "Repeat family" column is from the RepeatMasker track from the UCSC Genome Browser. "Correct Call" column is "GIAB" when the benchmark was deemed correct by expert curators, and "CCS" when the CCS callset was deemed correct. Rows where the correct call is from the CCS callset are colored blue.

Supplementary Table 10

Discrepancy	SV Type	SV Length (bp)	Simple Repeat Length (bp) (if ≥100 bp)	Simple Repeat Period (bp)	Correct Call	Chr	Position
FN	DEL	-32,196			GIAB	1	152,555,543
FN	DEL	-2,269			GIAB	2	159,958,799
FN	DEL	-49,058	172	71	-	4	34,779,881
FN	DEL	-127	466	127	GIAB	4	123,733,539
FN	DEL	-357	1,921	20	GIAB	13	30,131,788
FN	DEL	-108	589	54	GIAB	13	114,841,327
FN	DEL	-52			GIAB	16	85,800,468
FN	DEL	-565	1,403	561	-	19	4,884,873
FN	DEL	-55			GIAB	19	57,683,315
FN	DEL	-120	917	40	GIAB	20	62,510,913
FN	INS	62			GIAB	2	228,113,946
FN	INS	104	163	27	GIAB	3	66,992,107
FN	INS	52			GIAB	3	172,678,665
FN	INS	125	230	23	GIAB	5	105,107,607
FN	INS	727	651	65	-	6	40,459,830
FN	INS	172	815	4	-	9	135,394,538
FN	INS	6,179			GIAB	12	71,053,961
FN	INS	51	125	3	GIAB	13	29,161,602
FN	INS	3,268			GIAB	14	67,862,850
FN	INS	58	472	33	CCS	19	14,488,489
FP	DEL	-1,432			-	1	108,735,819
FP	DEL	-50			CCS	2	65939,406
FP	DEL	-80	1,274	16	CCS	6	167,162,349
FP	DEL	-80	332	40	CCS	7	129,149
FP	DEL	-65	632	168	-	10	134,253,963
FP	DEL	-83	333	83	CCS	11	1,431,223
FP	DEL	-74	1,674	74	CCS	12	6,038,958
FP	DEL	-128			-	13	107,435,844
FP	DEL	-63	1,227	22	GIAB	17	230,498
FP	DEL	-300	1,923	60	GIAB	18	77,569,248
FP	INS	103			CCS	4	141,283,453
FP	INS	52	588	26	CCS	4	190,329,327
FP	INS	202	893	18	-	8	146,172,196
FP	INS	176	1,184	24	-	10	132,840,681
FP	INS	783	1,184	24	-	10	132,841,387
FP	INS	328			CCS	13	112,993,782
FP	INS	60	312	4	CCS	16	85,867,748
FP	INS	54	527	18	-	17	10,662,861
FP	INS	84			CCS	18	53,029,667
FP	INS	267	641	37	CCS	X	67,035,046

Supplementary Table 10. Manual curation of structural variant discrepancies between CCS callset and Genome in a Bottle benchmark. For the “Discrepancy” column, “FN” means false negative (in benchmark but not callset), and “FP” means false positive (in callset but not benchmark). “Simple Repeat Length” and “Simple Repeat Period” are from the simpleRepeat track from the UCSC Genome Browser. “Correct Call” column is “GIAB” when the benchmark was deemed correct by expert curators, “CCS” when the CCS callset was deemed correct, and “-“ when it is unclear which callset is correct (typically due to complex tandem repeats that permit multiple representations of the same variant). Rows where the correct call is from the CCS callset are colored blue.

Supplementary References

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3. Myers, S., Freeman, C., Auton, A., Donnelly, P. & McVean, G. A common sequence motif associated with recombination hot spots and genome instability in humans. *Nat. Genet.* **40**, 1124–1129 (2008).