Supporting Information

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SI Methods

DNA Purification and DNA Quantitation: UV Spectrometer, PicoGreen Assay, and Agarose Gel. The gDNA was made with DNeasy Blood and Tissue Kit (Qiagen). The purification of the amplicon was performed with QIAEXII (Qiagen), with its protocol option for purification of >4-kb products but with an additional wash and elution step. The two elutes were pooled. The original gDNA and purified amplicons were quantified by UV absorbance with a NanoDrop ND-1000 (NanoDrop Technologies) with the parameter set as ×50 for dsDNA, and/or measured by PicoGreen assay (Molecular Probes). The prepurified amplicons were usually preliminarily analyzed on ethidium bromide-stained agarose gels (1%). The band intensity was quantified with a Fluor-S MultiImager (Bio-Rad) when desired. When the prepurified products were measured with the PicoGreen assay, an N9 control with a complete reaction mixture except for phi29 DNA polymerase was applied in parallel, which value was subtracted from the read of the amplicons. The assay was performed on the MyiQ qPCR system (Bio-Rad) with the fluorophore set as SYBR Green, which shares the same range of excitation and emission wave as PicoGreen. The end-point reading was determined at 25°C. Alternatively, an end-point reading at 60°C was performed for the PicoGreen assay. With an end-reading at 60°C, the free excess oligonucleotides in the reaction system did not disturb the measurement of the true amplification product.

Preparation of Intact Cells for Amplification. White blood cells (WBC) were separated with Ficoll lymphocyte separation medium (Mediatech) and sorted by FACS (Cell Sorter Facility, Yale University School of Medicine) to remove red cells. The nucleated cells were collected and serially diluted with PBS, and 20 aliquots, each consisting of 1 μl of the cell suspension from the same tube, were counted separately on a hemacytometer under a microscope: The cell number per microliter ranged from 0 to 7.0 cells, with an average of 2.8 ± 1.9 cells (±SD). The cells were distributed into thin-walled PCR tubes, each at 1 μl, and stored at −80°C. When amplifying the gDNA from the cells, the tubes were taken from −80°C and placed on ice for 3 min before the amplification procedure started.

An Assay for Locus-Bias Assessment: The Locus-Bias Score (LBS). The ΔΔCt method is commonly used to quantify the copy number difference of the inputs for qPCR (1). Accordingly, it is reasonable to apply the ΔCt (the threshold cycle number difference of test vs. reference DNA) to represent the copy number (or fold) difference when an identical amount of tested samples and reference DNA control were used as input for parallel qPCR. However, the variation of repetitive tests of one single locus cannot reflect the variation in representation between loci. Therefore, we chose eight loci along the genome as a panel to validate the locus bias of amplified samples. The standard deviation of this panel of locus-based ΔCt was termed "locus-bias score" (LB score, or LBS).

Based on tests with a series of primer sets, ordered from Integrated DNA Technologies (IDT), for loci on different chromosomes (from ref. 2), eight loci from different chromosomes (2p, 3p, 4p, 5p, 7p, 10p, 13p, and 19p, from WIAF Whitehead Institute SNP database: 1004, 114, 1958, 1331, 349, 966, 474, and 893) (2) were chosen to construct a panel for locus-bias measurements. These loci were selected to represent regions with very different levels of amplification by standard MDA. The amplification products with these primers showed a single sharp on agarose gel, a single peak in the melting curve, and an amplification efficiency (the primer slope) ranging from 1.8 to 2.0.

ΔCt $(_n)$ for each locus (n = 1, 2, . . . , 8) was defined as

$$\Delta Ct_n = Ct\,(x_n) - Ct\,(r_n), \qquad \textbf{[S1]}$$

where Ct(x_n) denotes the Ct of the tested sample "x" in the locus n; Ct(r_n) denotes the Ct of the reference sample "r" in the locus n.

For a given sample, the average ΔCt and the standard deviation for the panel of loci (8-loci) were recorded as "AvΔCt" and "SdΔCt"

$$\begin{aligned} Av\Delta Ct &= [\Delta Ct\,(_1) + \Delta Ct\,(_2) + \ldots + \Delta Ct\,(_8)]/8 \\ &= [\Sigma \Delta Ct\,(_n)]/8, n = 1{-}8 \\ LBS &= Sd[\Delta Ct\,(_n)], n = 1{-}8. \end{aligned} \qquad \textbf{[S2]}$$

The standard deviation of LBS (Sd_LBS) was calculated from amplification and qPCR repeated experiment (Table S3). In addition, we observed that different loci varied slightly in Ct value in different repetitions, even for the original reference gDNA. Therefore, some variations were solely due to the nature of qPCR. Assuming that the qPCR variability is independent of the locus variability, the qPCR variation was subtracted from the total variability measured with the samples when we estimated the net amplification variation between loci:

$$Net\_LBS = (LBS_x^2 - LBS_r^2)^{1/2} \qquad \textbf{[S3]}$$

Here, LBS_x denotes LBS for test sample x, and LBS_r denotes LBS for reference control "r." LBS_r was the average of 9 samples of genomic DNA that were measured as tests, against another randomly chosen sample of genomic DNA that was taken as their reference.

When the total input of gDNA for qPCR was varied from 50 to 2.5 ng, the LBS in our tests essentially did not exhibit significant variation, although the AvΔCt did increase proportionally (data not shown). Thus, LBS could be regarded as a reliable indicator for locus bias, which remains consistent even if the amount of input DNA for qPCR changes within a wide range.

LBS qPCR was performed on a MyiQ cycler, using iQ SYBR Green SuperMix (Bio-Rad). For each locus, a qPCR master mix including specific primers was prepared, and aliquots of 20 μl were distributed to each well. A 5-μl aliquot of purified amplicon or native gDNA was added as template, respectively, with their concentration pre-adjusted in water to 2 ng/μl. Therefore, for all samples, an identical 10 ng DNA was input for one qPCR reaction. The final reaction volume was 25 μl. The PCR program was as follows: 3 min at 94°C for 1 cycle; 10 s at 94°C, 30 s at 60°C, and 30 s at 72°C for 45 cycles; followed by the standard melt curve analysis program.

1. Pfaffl MW (2001) A new mathematical model for relative quantification in real-time RT-PCR. *Nucleic Acids Res* 29:e45.

2. Hosono S, *et al.* (2003) Unbiased whole-genome amplification directly from clinical samples. *Genome Res* 13:954–964.

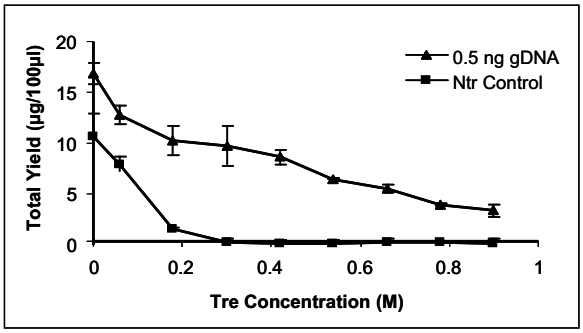

Fig. S1. Products of amplification with 0.5 ng of gDNA vs. Ntr control in the presence of Tre at various concentrations, measured by the intensity on an ethidium bromide-stained agarose gel (duplicate agarose gels and measurements). Each 5 (or 10) μl of amplicon from a 100-μl total reaction was loaded on the ethidium bromide-containing agarose gel side-by-side, with a serially diluted 1-kb DNA ladder marker loaded as control. The photos were taken at different times of electrophoresis. The band intensity was quantified with the Fluor-S MultiImager and Quantity One 4.5.2 software (Bio-Rad). The result demonstrated that the Ntr at 0.2 M Tre produced some positive TIP, showing a slight difference from Fig. 1*C* (PicoGreen assay), and that at 0.7–0.9 M Tre, the specific product was higher than that detected by PicoGreen. Because PicoGreen assay detects only dsDNA, and the early report that the ssDNA products increased with the reduction of starting DNA input [Bergen AW, Qi Y, Haque KA, Welch RA, Chanock SJ (2005) *BMC Biotechnol* 5:24], we proposed that this difference was due to the fact that, under these circumstances (Ntr at low Tre, specific DNA input at high Tre, or low input of DNA), ssDNA product may represent a significant portion of the product. However, we confirmed that NTR was indeed completely avoided in our optimized amplification system by using the initial amplicons from the control tubes with Tre at $>$0.54 M as input for a second round of amplification. Even after two rounds of amplification, no product was detected. However, the demonstrated yields with low Tre (e.g., 0, 0.06, 0.18 M Tre) were a little less than the result measured with PicoGreen assay. This may be an underestimation because the DNA signal in agarose gel was saturated when the amount of DNA exceeded certain limitation, captured by the Fluor-S MultiImager.

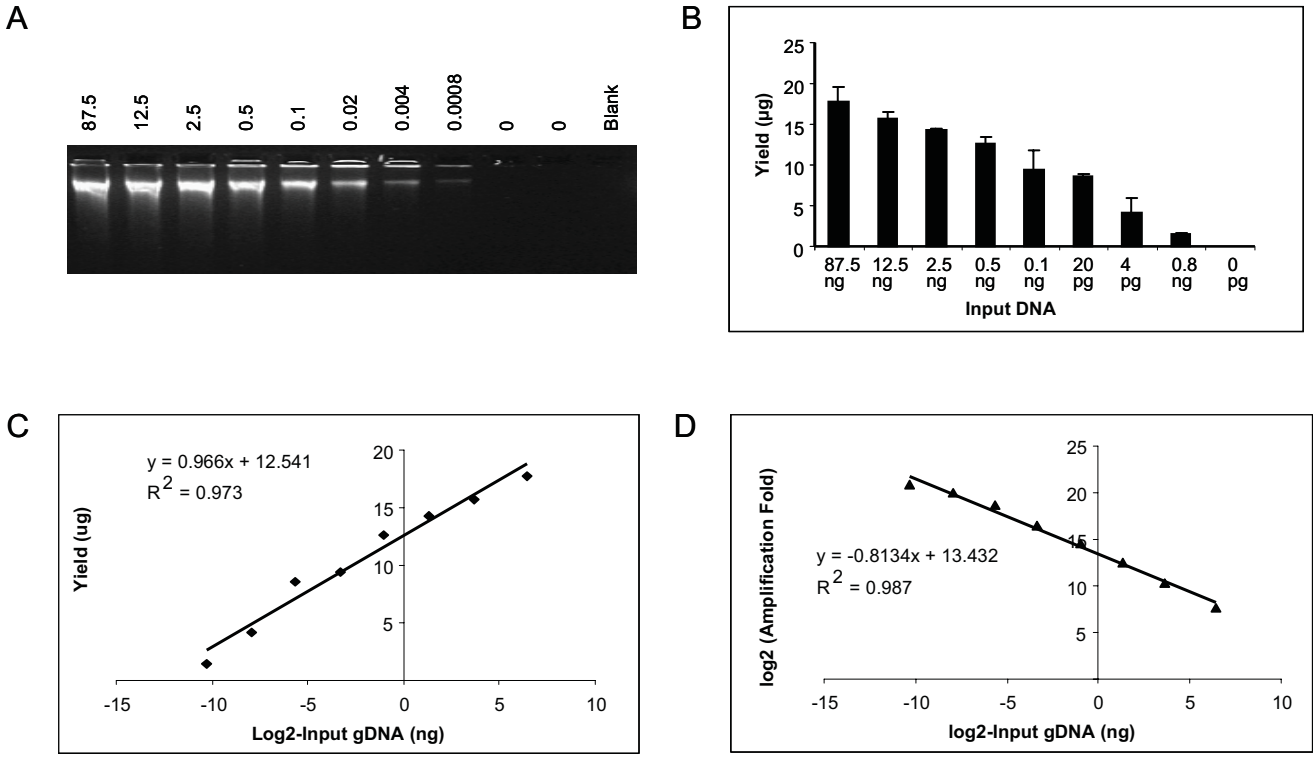

Fig. S2. The yield of products of reactions stopped at 16 h was input DNA-dependent. The amplification reaction was at 0.75 M Tre (Tre preparation lot T913) and followed the general amplification procedure. (*A*) Agarose gel showing the amplicon products for various inputs of gDNA (ng), all loaded with the same volume of nonpurified products (10 μl). Blank, well control without loading. (*B*) The yield was increased by increasing gDNA input, measured by PicoGreen assay (two times). (*C*) The yield was increased with the gDNA input increasing. (*D*) The amplification fold was increased with the reduction of the gDNA input.

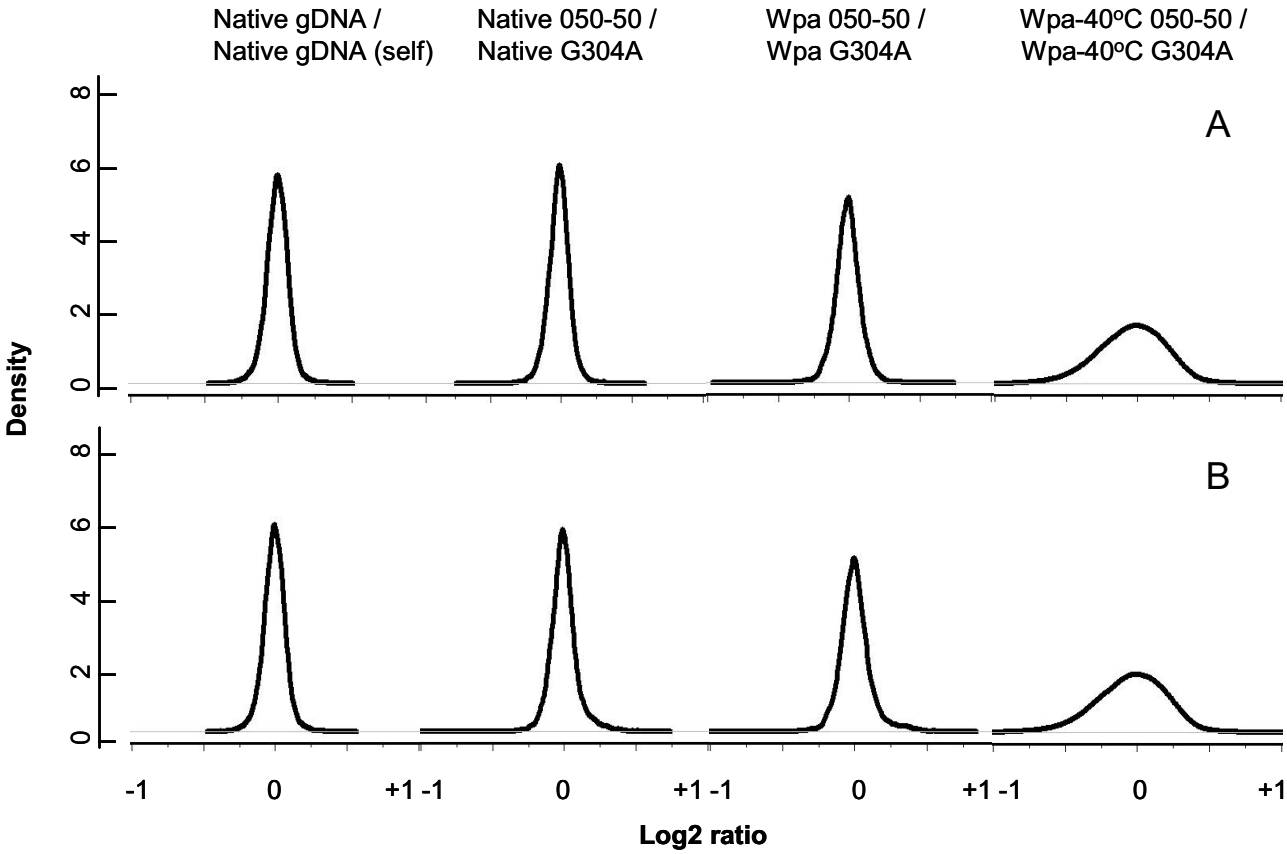

Fig. S3. Density distribution of log2 ratio for variant sample pairs on tiling array for chromosome 22 long arm with a 2,000-bp sliding window. With normalization applied by NimbleScan 2.3, the average log2 ratio is close to 0. The density graphs show the variability of log2 ratio of each data set of fluorescent intensities as marked on the top. (*A*) The previously known or predicted CNV regions were excluded from all data to eliminate the possible effect of CNVs on the deviation. (*B*) All probes were included.

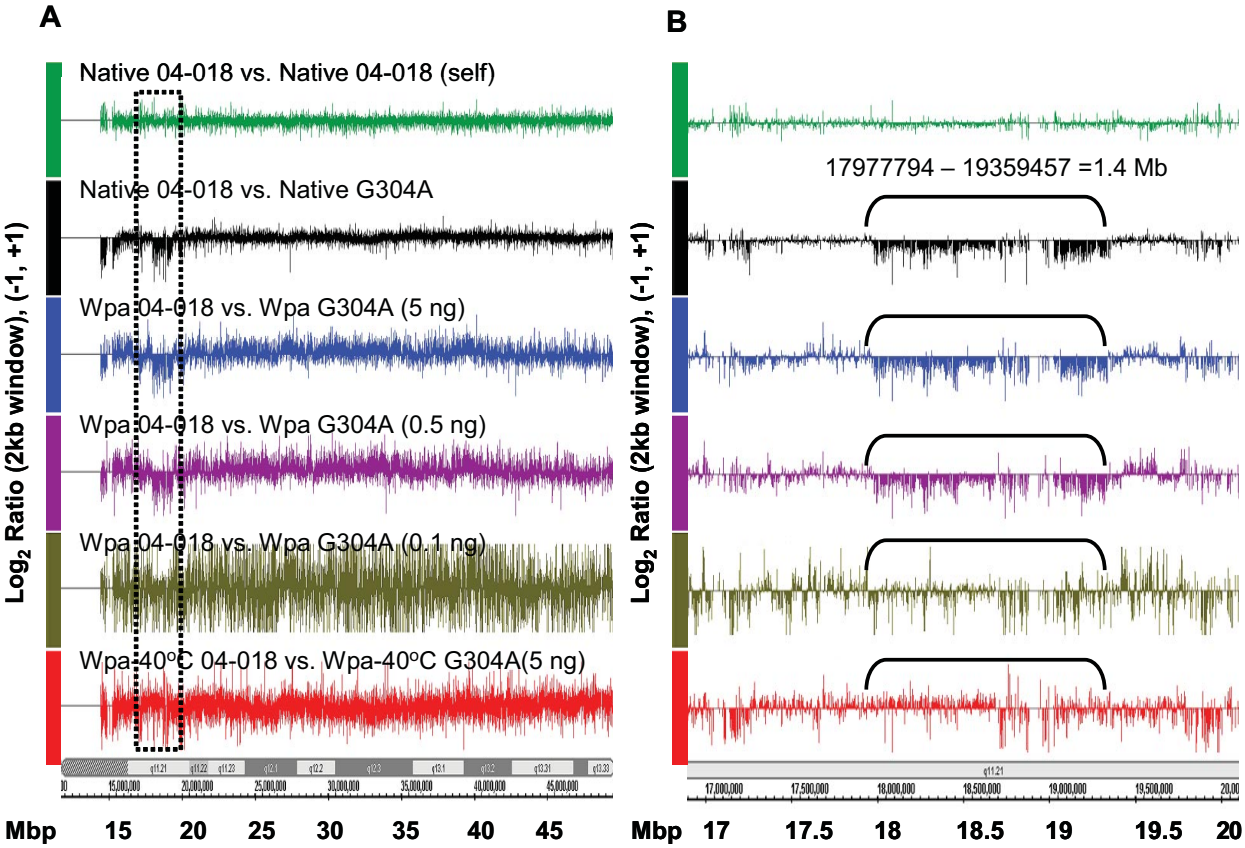

Fig. S4. Amplicon hybridization on a chromosome 22 tiling array reproduced the known segment copy number variation seen with native DNA (sample 04-018), showing known/confirmed heterozygous deletions with different amplification methods and different starting inputs (5, 0.5, and 0.1 ng) for the amplifications. The data processing and the method of labeling in this figure are the same as in Fig. 4. The sample 04-018 was slightly degraded. The ''Native gDNA vs. Native gDNA self'' (green) is an unamplified gDNA (04-018) against itself. All other Cy5/Cy3 sets are the amplified tested sample (04-018) vs. the amplified normal DNA control (G304A). The labels at the bottom are the chromosome 22 coordinates. (*A*) Through the whole chromosome 22 long arm at a 2-kb sliding window. The dot rectangle is the segment enlarged in *B*. (*B*) Expansion of a segment with a known heterozygous duplication (1.4 Mb) and analyzed with a 2-kb sliding window. (*C*) Expansion of a confirmed 18.2-kb heterozygous deletion (half brackets) with a 400-bp sliding window. This deletion was confirmed independently ahead of this research. (*D*) Expansion of a confirmed 975-bp homologous deletion (filled arrows) with a 400-bp sliding window.

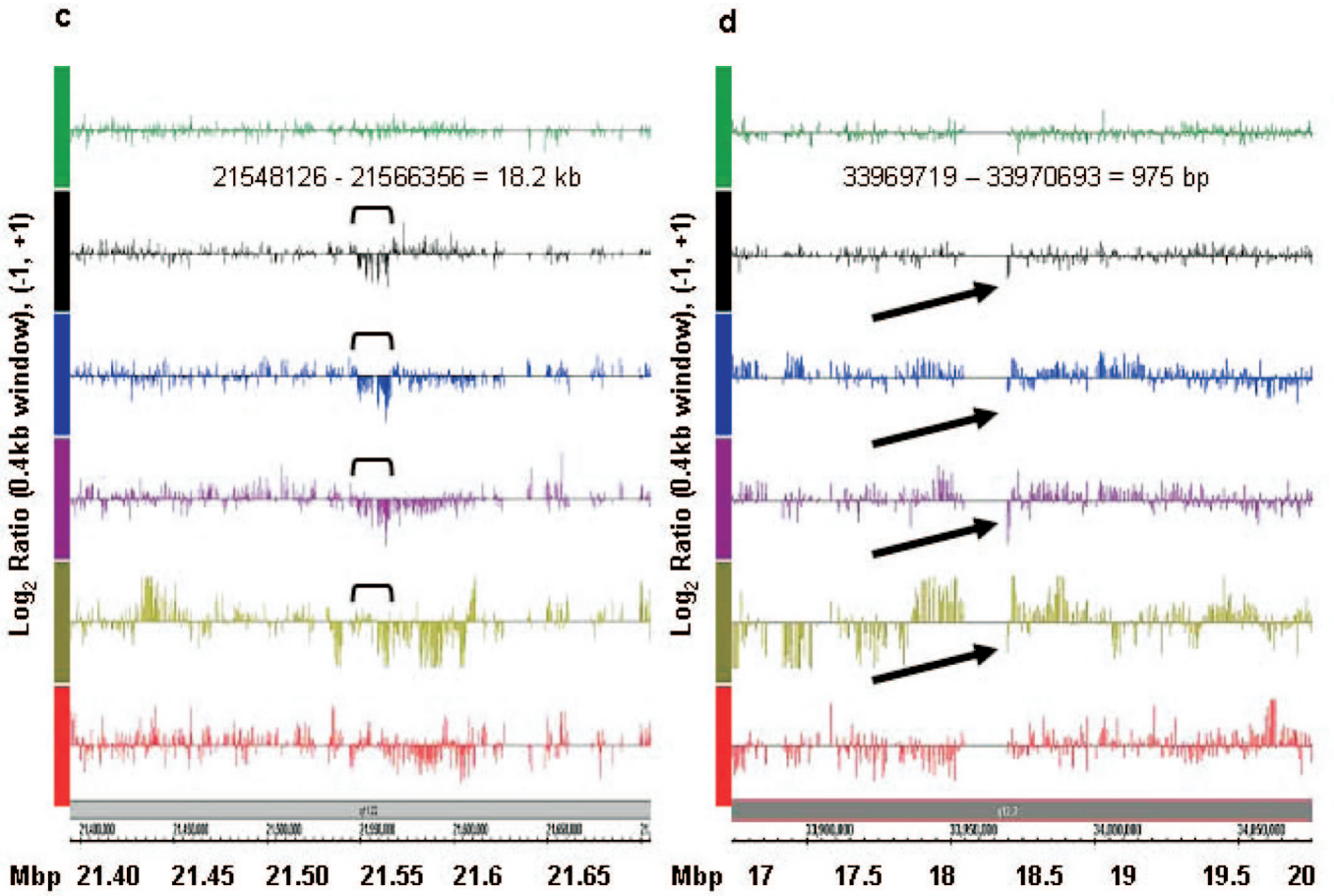

Fig. S4. *Continued*

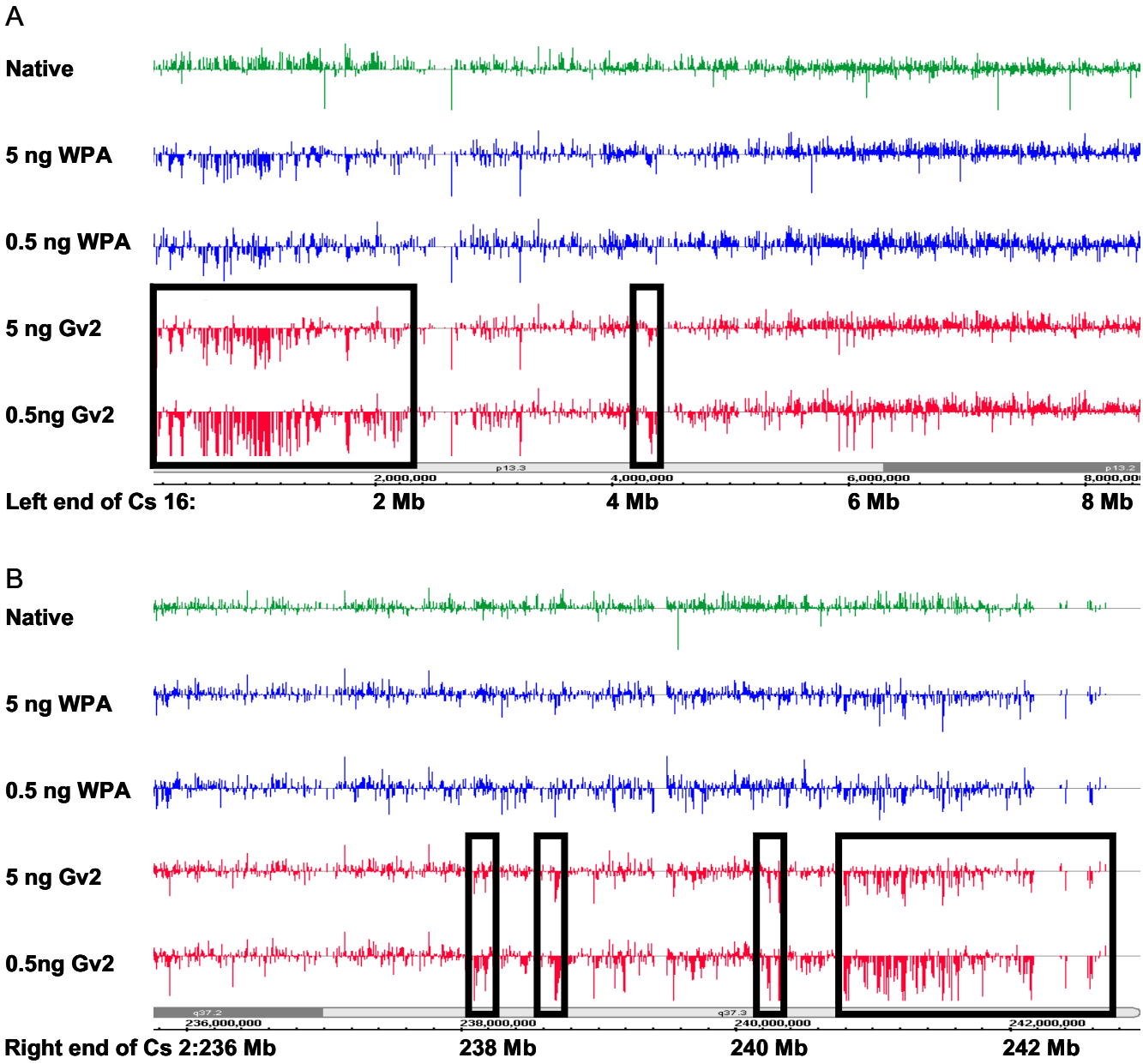

Fig. S5. Examples of a left and a right chromosome terminal region in LRR for amplicons with variants of input, showing that Wpa rescued the sequences that were underrepresented with Gv2 amplification. Generated by using BeadStudio 3.1.3.0 (Illumina), LRR is the log2 relative ratio of the observed normalized signal intensity of both alleles and the expected intensity based on ≈120 normal samples. The LRR data for each sample were exported and processed to generate an .sgr file for visualization in the IGB browser software, and all samples are shown with the same scale (+3, −3). Rectangular frames refer to some example segments underrepresented. (*A*) Left terminus of chromosome 16 for sample 05-050. (*B*) Right terminus of chromosome 2 for sample 05-050. The whole panel of the termini for two samples is shown in Tables S6 and S7.

Table S1. PicoGreen assayed yield and amplification fold with various amounts of input gDNA in the presence of 0.75 M Tre, as shown in Fig. S2 (duplicate estimates on PicoGreen assay)

	Concentration, ng/μl		Total yield, μg/100 μl		
Input gDNA	Average	SD	Average	SD	Amplification fold
		First round of amplification			
87.5 ng	177.9	17.9	17.8	1.8	203
12.5 ng	157.6	7.7	15.8	0.8	1,261
2.5 ng	142.4	2.7	14.2	0.3	5,697
0.5 ng	126.0	8.3	12.6	0.8	25,202
0.1 ng	94.5	23.1	9.4	2.3	94,494
20 pg	85.7	3.2	8.6	0.3	428,488
4 pg	42.1	17.7	4.2	1.8	1,053,396
0.8 pg	14.8	2.1	1.5	0.2	1,850,722
0 pg	ND		ND		ND
		Second round of amplification*			
12.5 ng	944.5	72.0	94.5	7.2	9,445
2.5 ng	734.8	25.9	73.5	2.6	7,348
0.5 ng	375.7	71.0	37.6	7.1	3,757
0.1 ng	406.5	38.7	40.6	3.9	4,065
0 ng	ND		ND		ND

ND, not detectable.

*With 10 ng of purified amplicons from first round and various inputs of gDNA. However, the second round of amplification for the original 0-ng input was initiated with 1 μl (concentration undetectable) of elute from the totally 30 μl of elute purified from the 1st round of amplification.

Table S2. LBS of amplicons with various inputs

Wpa amplification procedures	General procedure					Trace DNA procedure		Intact cell (three cells)*	Reference
	12.5 ng	2.5 ng	0.5 ng	0.1 ng	20 pg	0.1 ng	20 pg		
Test repeats: Amp × LBS	2 × 3	2 × 3	2 × 3	2 × 3	2 × 3	9 × 1	4 × 1	19 × 1	9 × 1
Av_LBS (of tests)	0.71	0.73	0.86	1.73	4.09	1.21	2.57	0.77	0.52
Sd_LBS (among tests)	0.17	0.01	0.07	0.45	0.92	0.23	1.00	0.17	0.10
Net_LBS (reference subtracted)	0.49	0.52	0.69	1.66	4.06	1.09	2.51	0.57	0.00

The general procedure was employed for 12.5-ng to 20-pg inputs. In addition, the trace-input-specific procedure was employed for 0.1-ng and 20-pg inputs, and the intact-cell procedure was used for intact cells, of which all were at 100-μ l volume reaction without real-time monitor applied.

*Of the 23 samples of intact cells, the results for 4 samples were discrepant relative to others and, therefore, excluded. In one sample from the cell dilution, there was no amplicon and this presumably represented a well in which there were no cells. The average and standard deviation of LBS (Av_LBS, Sd_LBS) were calculated among the repeats of test of amplification and qPCR. See *SI Text* for detail of LBS estimation.

Table S3. qPCR measured locus bias of amplicons from various levels of starting material with native gDNA as reference

	Wpa Repeat 1					Wpa Repeat 2				
Locus	12.5 ng	2.5 ng	0.5 ng	0.1 ng	20 pg	12.5 ng	2.5 ng	0.5 ng	0.1 ng	20 pg
2p	0.58	−0.11	0.25	*1.45*	**7.21**	−0.11	−0.40	0.35	*−1.03*	**6.19**
3p	−0.69	−0.66	−0.39	0.34	**0.06**	−0.28	−0.68	−1.07	−1.46	**0.04**
4p	−0.36	−0.32	−0.30	0.93	6.56	−0.78	−0.77	0.83	−0.16	2.81
5p	1.75	1.33	1.86	**3.40**	*−0.21*	0.63	1.14	1.56	**2.51**	*2.00*
7p	−0.56	−0.42	−0.70	**1.21**	4.71	0.41	−0.15	−0.17	**1.04**	7.00
10p	0.42	0.09	0.94	2.67	**8.99**	−0.17	−0.08	0.51	0.98	**2.05**
13p	0.76	0.96	1.09	*0.53*	*9.68*	0.84	0.93	1.16	*5.07*	*0.09*
19p	0.42	0.24	0.14	0.46	2.32	0.14	0.13	0.75	2.23	0.79
AvΔCt	0.29	0.14	0.36	1.37	4.91	0.08	0.01	0.49	1.15	2.62
SdΔCt	0.81	0.69	0.87	1.11	3.85	0.53	0.70	0.82	2.13	2.65

Each amplification was performed twice, and qPCR-LBS assessments of each sample were repeated three times, of which one qPCR result is displayed here. Boldface numbers show apparently consistent bias between two amplification repeats, and boldface, italic numbers show apparently inconsistent bias between two amplification repeats. SdΔCt was denoted as LBS (*SI Text*).

Table S4. Standard deviation of log2 ratio of signals for sample 05-050 vs. a genomic DNA pool from seven individuals (Cy3 and Cy5 labeled separately) on the tiling array for chromosome 22 long arm

Cy3/Cy5	Native g/native g (self)	Native 05-050/native G304A	Wpa 05-050/Wpa G304A	Wpa-40° C 05-050/Wpa-40° C G304A
log2 ratio for probes excluding the previously known and confirmed, and previous predicted segmental CNVs sequences (23 segments) in earlier investigations				
Array ID	47750	42762	141539	94902
2,000-bp window	0.079	0.079	0.095	0.251
800-bp window	0.104	0.104	0.119	0.293
400 bp window	0.121	0.123	0.135	0.325
Unaveraged	0.161	0.168	0.175	0.407
log2 ratio with all probes included				
Array ID	47750	42762	141539	94902
2,000-bp window	0.081	0.099	0.117	0.256
800-bp window	0.122	0.135	0.149	0.327
400-bp window	0.105	0.119	0.135	0.296
Unaveraged	0.161	0.178	0.185	0.408

Table S5. Analysis of SNP genotyping with the HumanHap550-Duo genotyping BeadChip for amplicons with Wpa vs. Gv2 and native gDNA

Sample	No. calls	% calls	No. calls both	% discordance	% concordance
			Whole-genome SNP analysis		
05-050					
Native gDNA	551,904	98.30%	551,904	N/A	N/A
5-ng input Wpa	551,542	98.23%	543,751	0.15%	99.85%
5-ng input Gv2	556,253	99.07%	547,943	0.10%	99.90%
0.5-ng input Wpa	542,484	96.62%	534,837	0.12%	99.88%
0.5-ng input Gv2	543,454	96.79%	535,086	0.16%	99.84%
04-018*					
Native gDNA	560,048	99.75%	560,048	N/A	N/A
5-ng input Wpa	546,303	97.30%	545,622	0.07%	99.93%
5-ng input Gv2	553,899	98.65%	553,068	0.03%	99.97%
0.5-ng input Wpa	516,870	92.06%	516,176	0.31%	99.69%
0.5-ng input Gv2	508,308	90.53%	507,589	0.54%	99.46%
			Analysis of the SNPs in 5 Mb of the terminal regions for all chromosomes applicable		
05-050					
Native gDNA	48,524	98.53%	48,524	N/A	N/A
5-ng input Wpa	48,363	98.20%	47,755	0.14%	99.86%
5-ng input Gv2	48,212	97.90%	47,591	0.13%	99.87%
0.5-ng input Wpa	47,545	96.54%	46,961	0.11%	99.89%
0.5-ng input Gv2	45,827	93.06%	45,234	0.38%	99.62%
04-018*					
Native gDNA	49,078	99.66%	49,078	N/A	N/A
5-ng input Wpa	47,700	96.86%	47,613	0.11%	99.89%
5-ng input Gv2	46,766	94.96%	46,653	0.15%	99.85%
0.5-ng input Wpa	44,858	91.09%	44,770	0.43%	99.57%
0.5-ng input Gv2	41,591	84.45%	41,508	1.38%	98.62%

Calls both, discordance, and concordance are based on a tested sample vs. its native reference. N/A, not applicable.
*Native or amplified with partially degraded gDNA.

Table S6. Analysis of LRR of SNP genotyping on 5-Mb left-terminal regions of each of chromosomes with the HumanHap550-Duo genotyping BeadChip for amplicons with Wpa vs. Gv2 and native gDNA

Chr.	SNP no. covered	Native gDNA	5-ng input		0.5-ng input	
			Wpa	Gv2	Wpa	Gv2
			Sample 05-050			
1	844	0.251	−0.006	−0.141	0.184	−0.485
2	1,192	0.115	0.009	−0.034	−0.107	−0.164
3	1,800	−0.020	−0.005	0.061	−0.262	0.071
4	729	0.189	−0.025	−0.133	0.024	−0.405
5	1,240	0.144	−0.012	−0.065	−0.067	−0.217
6	1,518	0.063	0.029	0.029	−0.024	−0.037
7	902	0.146	0.017	−0.056	0.116	−0.216
8	2,683	0.041	−0.030	−0.005	−0.294	−0.074
9	2,058	0.002	0.018	0.046	−0.098	0.044
10	1,480	0.064	0.003	0.003	−0.134	−0.061
11	1,093	0.182	−0.084	−0.208	0.012	−0.513
12	1,351	0.095	0.073	0.050	0.170	0.000
13	0	N/A	N/A	N/A	N/A	N/A
14	0	N/A	N/A	N/A	N/A	N/A
15	0	N/A	N/A	N/A	N/A	N/A
16	861	0.276	−0.125	−0.222	0.084	−0.618
17	1,123	0.168	0.038	−0.032	0.304	−0.186
18	1,252	−0.020	−0.054	−0.006	−0.197	−0.045
19	872	0.322	−0.080	−0.292	0.342	−0.836
20	1,516	0.113	0.093	0.056	0.182	−0.011
21	0	N/A	N/A	N/A	N/A	N/A
22	0	N/A	N/A	N/A	N/A	N/A
Average	1,324*	0.125	−0.009	−0.056	0.014	−0.221
SD	501*	0.100	0.058	0.107	0.187	0.261
Filter cut-off		Less than −0.15	Less than −0.15	Less than −0.15	Less than −0.3	Less than −0.3
Filter call no.		0	0	3	0	5
			Sample 04-018			
1	844	0.155	−0.051	−0.656	−0.095	−0.838
2	1,192	0.067	−0.144	−0.206	−0.224	−0.291
3	1,800	−0.015	−0.186	0.092	−0.312	0.078
4	729	0.113	−0.084	−0.471	−0.129	−0.634
5	1,240	0.101	−0.162	−0.311	−0.247	−0.422
6	1,518	0.068	−0.018	−0.033	−0.054	−0.023
7	902	0.093	0.000	−0.311	−0.001	−0.373
8	2,683	0.024	−0.274	−0.082	−0.432	−0.142
9	2,058	0.023	−0.020	0.088	−0.088	0.099
10	1,480	0.050	−0.124	−0.104	−0.233	−0.157
11	1,093	0.115	−0.086	−0.545	−0.144	−0.733
12	1,351	0.074	0.119	−0.078	0.135	−0.052
13	0	N/A	N/A	N/A	N/A	N/A
14	0	N/A	N/A	N/A	N/A	N/A
15	0	N/A	N/A	N/A	N/A	N/A
16	861	0.194	−0.119	−0.760	−0.154	−0.896
17	1,123	0.104	0.208	−0.277	0.277	−0.297
18	1,252	0.001	−0.119	0.040	−0.208	0.015
19	872	0.203	0.142	−0.827	0.180	−1.018
20	1,516	0.080	0.145	−0.063	0.172	−0.059
21	0	N/A	N/A	N/A	N/A	N/A
22	0	N/A	N/A	N/A	N/A	N/A
Average	1,324*	0.085	−0.045	−0.265	−0.078	−0.338
SD	501*	0.061	0.133	0.293	0.189	0.362
Filter cut-off		Less than −0.15	Less than −0.15	Less than −0.15	Less than −0.3	Less than −0.3
Filter call no.		0	3	9	2	7

Chromosome terminal regions without SNP are not applied, nor was chromosome X/Y. Mean LRR for each chromosome end are shown. SD, standard deviation. N/A, not applicable. The cut-off was set manually.

Table S7. Analysis of LRR of SNP genotyping on 5-Mb right-terminal regions of each of chromosomes generated in the same way as in Table S6

Chr.	SNP no. covered	Native gDNA	5-ng input		0.5-ng input	
			Wpa	Gv2	Wpa	Gv2
			Sample 05-050			
1	1,106	0.063	0.021	0.016	−0.033	−0.041
2	1,105	0.183	−0.059	−0.162	−0.033	−0.427
3	755	0.080	−0.004	−0.017	0.098	−0.137
4	1,124	0.024	−0.025	0.003	−0.225	−0.067
5	909	0.178	0.033	−0.022	0.151	−0.204
6	1,462	0.110	−0.045	−0.076	−0.157	−0.234
7	1,223	0.129	0.020	−0.055	0.021	−0.228
8	932	0.247	−0.038	−0.205	0.086	−0.532
9	1,061	0.297	−0.080	−0.292	0.125	−0.735
10	1,314	0.180	−0.010	−0.066	−0.039	−0.242
11	1,583	0.110	0.153	0.130	0.182	0.125
12	1,531	0.158	0.109	0.020	0.179	−0.107
13	1,128	0.137	−0.016	−0.073	−0.049	−0.247
14	531	0.202	−0.077	−0.205	0.069	−0.494
15	1,400	0.069	0.005	0.027	−0.066	−0.022
16	1,372	0.206	0.033	−0.065	0.220	−0.286
17	1,011	0.250	0.004	−0.118	0.210	−0.393
18	1,420	0.082	−0.037	−0.084	−0.149	−0.230
19	1,160	0.144	0.100	0.021	0.300	−0.110
20	1,326	0.197	0.014	−0.109	0.114	−0.370
21	1,510	0.197	−0.013	−0.143	0.081	−0.409
22	1,501	0.201	0.001	−0.092	0.099	−0.303
Average	1,203	0.157	0.004	−0.071	0.054	−0.259
SD	271	0.069	0.058	0.095	0.135	0.195
Filter cut-off		Less than −0.15	Less than −0.15	Less than −0.15	Less than −0.3	Less than −0.3
Filter call no.		0	0	4	0	8
			Sample 04-018			
1	1,106	0.044	−0.024	−0.004	−0.058	−0.008
2	1,105	0.107	−0.130	−0.501	−0.198	−0.637
3	755	0.066	0.085	−0.115	0.065	−0.155
4	1,124	0.021	−0.202	−0.027	−0.324	−0.063
5	909	0.115	0.043	−0.280	0.043	−0.350
6	1,462	0.062	−0.195	−0.250	−0.284	−0.371
7	1,223	0.094	−0.041	−0.246	−0.090	−0.323
8	932	0.167	−0.090	−0.661	−0.141	−0.852
9	1,061	0.183	−0.073	−0.828	−0.130	−1.056
10	1,314	0.084	−0.173	−0.410	−0.251	−0.503
11	1,583	0.057	0.114	0.014	0.120	0.023
12	1,531	0.093	0.100	−0.170	0.065	−0.234
13	1,128	0.086	−0.116	−0.298	−0.214	−0.412
14	531	0.134	−0.086	−0.576	−0.133	−0.692
15	1,400	0.062	−0.067	−0.063	−0.119	−0.098
16	1,372	0.133	0.058	−0.447	0.057	−0.528
17	1,011	0.158	0.037	−0.568	0.041	−0.658
18	1,420	0.054	−0.180	−0.228	−0.260	−0.335
19	1,160	0.080	0.229	−0.148	0.264	−0.169
20	1,326	0.114	−0.037	−0.480	−0.075	−0.626
21	1,510	0.128	−0.041	−0.491	−0.086	−0.620
22	1,501	0.128	−0.057	−0.447	−0.069	−0.570
Average	1,203	0.099	−0.038	−0.328	−0.081	−0.420
SD	271	0.042	0.112	0.230	0.147	0.283
Filter cut-off		Less than −0.15	Less than −0.15	Less than −0.15	Less than −0.3	Less than −0.3
Filter call no.		0	4	17	1	15