

**Table W1.** Identification of N-CIN and S-CIN in Study Group of 10 OS.

Chromosome	Cytoband	Aberration Location ↔ CIN Type	Aberration Location ↔ CIN Type	
			N-CIN	S-CIN
chr1	p36.33	Telomere	■	
	p12 -p36.32	Arm	■	■
	p11.2	Centromere	■	
	q21.1	Centromere	□	
	q21.2-q43	Arm	■	■
chr2	q44	Telomere	■	
	p25.3	Telomere	■	
	p12-p25.2	Arm	■	■
	p11.2	Centromere	■	
	q11.2	Centromere	■	
chr3	q12.1-q37.2	Arm	□	
	q37.3	Telomere	■	
	p26.3	Telomere	■	
	p11.2-p26.2	Arm	■	■
	p11.1	Centromere	■	
chr4	q11.2	Centromere	■	
	q12.1-q28	Arm	□	
	q29	Telomere	■	
	p16.3	Telomere	■	
	p13-q16.2	Arm	■	■
chr5	p12	Centromere	■	
	q11	Centromere	■	
	q12-q35.1	Arm	□	
	q35.2	Telomere	■	
	p15.33	Telomere	■	
chr6	p12-p15.32	Arm	■	■
	p11	Centromere	■	
	q11.1	Centromere	■	
	q11.2-q35.3	Arm	□	
	q35.3	Telomere	■	
chr7	p25.3	Telomere	■	
	p12.1-p25.2	Arm	■	■
	p11.2	Centromere	■	
	q11.1	Centromere	■	
	q11.2-q26	Arm	□	
chr8	q27	Telomere	■	
	p22.3	Telomere	■	
	p11.2-p22.2	Arm	■	■
	p11.1	Centromere	■	
	q11.21	Centromere	■	
chr9	q11.22-q35.2	Arm	□	
	q36.3	Telomere	■	
	p23.3	Telomere	■	
	p11.22-p23.2	Arm	■	■
	p11.21	Centromere	■	
chr10	q11.1	Centromere	■	
	q11.21-q24.2	Arm	□	
	q24.3	Telomere	■	
	p24.3	Telomere	■	
	p13.2-p24.2	Arm	■	■
chr11	p13.1	Centromere	■	
	p12	Centromere	■	
	q12	Centromere	■	
	q13	Centromere	■	
	q21.11-q34.2	Arm	□	
chr12	q34.3	Telomere	■	
	p15.3	Telomere	■	
	p11.22-q15.2	Arm	■	■
	p11.21	Centromere	■	
	q11.21	Centromere	■	
chr13	q11.22-q26.2	Arm	□	
	q26.3	Telomere	■	
	p15.5	Telomere	■	
	p11.2-p15.4	Arm	■	■
	p11.12	Centromere	■	
chr14	q11	Centromere	■	
	q12.1-q24.3	Arm	□	
	q25	Telomere	■	

**Table W1.** (continued)

Chromosome	Cytoband	Aberration Location	CIN Type	
			N-CIN	S-CIN
chr12	p13.33	Telomere	Gray	
	p11.21-p13.32	Arm	Gray	Black
	p11.1	Centromere	Gray	
	q12	Centromere	White	
	q13.11-q24.32	Arm	Gray	Black
chr13	q24.33	Telomere	Gray	
	q12.11	Centromere	White	
	q12.12-q33.33	Arm	Gray	Black
chr14	q34	Telomere	Gray	
	q11.1	Centromere	White	
chr15	q11.2-q32.32	Arm	Gray	Black
	q32.33	Telomere	Gray	
chr16	q11.2	Centromere	White	
	q12-q26.2	Arm	Gray	Black
chr17	q26.3	Telomere	Gray	
	p13.3	Telomere	Gray	
	p12.1-p13.2	Arm	Gray	Black
	p11.2	Centromere	White	
	q12.1	Centromere	White	
chr18	q12.2-q24.2	Arm	Gray	Black
	q24.3	Telomere	Gray	
	p13.3	Telomere	Gray	
	p12-13.2	Arm	Gray	Black
	p11.2	Centromere	White	
chr19	q11.1	Centromere	White	
	q11.2-q25.2	Arm	Gray	Black
	q25.3	Telomere	Gray	
	p11.32	Telomere	Gray	
	p11.22-p11.31	Arm	Gray	Black
chr20	p11.21	Centromere	White	
	q11.2	Centromere	White	
	q12.1-q22.3	Arm	Gray	Black
	q23	Telomere	Gray	
	P13.3	Telomere	Gray	
chr21	p13.11-p13.2	Arm	Gray	Black
	p12	Centromere	White	
	q12	Centromere	White	
	q13.11-q13.42	Arm	Gray	Black
	q13.43	Telomere	Gray	
chr22	p13	Telomere	Gray	
	p11.22-p12.3	Arm	Gray	Black
	p11.21	Centromere	White	
	q11.21	Centromere	White	
	q11.22-q13.32	Arm	Gray	Black
chr23	q13.33	Telomere	Gray	
	p11.1	Centromere	White	
	q11.2	Centromere	White	
chr24	q21.1-q22.2	Arm	Gray	Black
	q22.3	Telomere	Gray	
	q11.1	Centromere	White	
chr25	q11.21-q13.32	Arm	Gray	Black
	q13.33	Telomere	Gray	

The position of genomic imbalance from all 10 OS is shown by cytoband location. Structural aberrations leading to S-CIN imbalance is mapped by black boxes and N-CIN imbalance is indicated by gray boxes.

**Table W2.** Estimation of the Overall Ploidy of 10 Samples.

OS	cen(3),* <i>n</i> (%)	cen(7),* <i>n</i> (%)	cen(17),* <i>n</i> (%)	Overall Ploidy Status <sup>†</sup>
OS1	2 (60%)	2 (70%)	2 (70%)	Diploid
	3 (15%)	3 (>10%)	3 (15%)	
	4 (<10%)			
OS4	1 (30%)	2 (60%)	2 (60%)	Diploid
	2 (60%)	3 (20%)	3 (20%)	
OS5	2 (70%)	2 (50%)	2 (40%)	Near-triploid
	3 (>10%)	3 (20%)	3 (40%)	
OS7	2	2 (50%)	2 (35%)	Near-triploid
		3 (20%)	3 (40%)	
		4 (>10%)	4 (>10%)	
OS9	2	2 (60%)	2 (>10%)	Polyploid (>5 <i>n</i> )
		3 (>10%)	3 (20%)	
		>5 (60%)		
OS11	2	2 (60%)	2 (70%)	Diploid
		3 (15%)	3 (>10%)	
OS12	2 (80%)	2 (30%)	3 (>10%)	Near-tetraploid
	3 (>10%)	3 (30%)	4 (20%)	
		4 (20%)	5 (20%)	
		5 (>10%)	>5 (30%)	
OS13	2	2 (50%)	ND	Diploid
		4 (15%)		
OS15	1 (30%)	2 (50%)	2 (40%)	Near-tetraploid
	2 (60%)	3 (20%)	3 (30%)	
		4 (20%)	4 (20%)	
OS18	2 (70%)	2 (53%)	2 (60%)	Near-triploid
	3 (>10%)	3 (27%)	3 (20%)	
		4 (>10%)		

\*For each sample, 200 nuclei were scored, and a population of cell was recorded if it was represented by more than 10% of the cells.

<sup>†</sup>Overall ploidy criteria are established according to Ventura et al. [39], with modification described in the Materials and Methods section.