

Table S1. Characteristic feature of each genomic subgroup with its detected numbers in 605 JPN samples.

Genome subgroup (GG)	N	MYCN - amp	17WG	17qG	1pL	11qL	% of total cohort	SCA	NCA only
GG-Pa	133								
GG-P1a	101	+	-	+	+	-	major (17%) 2.5%	101	-
GG-P2a	15	+	-	+	+	+		15	-
GG-P3a	4	+	-	+	-	+		4	-
GG-P4a	3	+	-	+	-	-		3	-
GG-P5a	10	+	-	-	any	any		10	-
GG-Ps	213								
GG-P1s	20	-	-	+	+	-	5.6% major (21%)	20	-
GG-P2s	34	-	-	+	+	+		34	-
GG-P3s	124	-	-	+	-	+		124	-
GG-P4s	27	-	-	+	-	-		27	-
GG-P5s	8	-	-	-	any	any		8	-
GG-Wa	5						rare		
GG-W1a	2	+	+	-	+	-		2	-
GG-W2a	0	+	+	-	+	+		0	-
GG-W3a	0	+	+	-	-	+		0	-
GG-W4a	3	+	+	-	-	-		3	-
GG-W5a	0	+	-	-	any	any		0	-
GG-Ws	173								
GG-W1s	5	-	+	-	+	-	major (25%)	5	-
GG-W2s	1	-	+	-	+	+		1	-
GG-W3s	11	-	+	-	-	+		11	-
GG-W4s	151	-	+	-	-	-		34	117
GG-W5s	5	-	-	-	any	any		2	3
GG-Sa	8	+	-	-	-	-	silent	-	-
GG-Ss	73	-	-	-	-	-	silent	-	-

GG: genome group; amp: amplification; 17WG: chromosome 17 whole gain (both short and long chromosomal arms); 17qG: chromosome 17q gain; 1pL: chromosome 1p loss; 11qL: chromosome 11q loss; SCA: segmental chromosome aberration; NCA: numerical chromosome aberration.

Table S2. Five-year overall and event-free survival rates of genomic subgroup.

Factor	N	5-year OS	± SE (%)	Log-rank- <i>p</i>	N	5-year EFS	± SE (%)	Log-rank- <i>p</i>
Genome Group								
GG-Pa	133	48	± 4.6		101	34	± 4.9	
GG-Ps	213	61	± 3.8		165	38	± 4.0	
GG-Wa	5	53	± 24.8		5	53	± 24.8	
GG-Ws	173	93	± 1.9		126	84	± 3.4	
GG-Pa subgroup								
GG-P1a	101	46	± 5.3		75	35	± 5.7	
GG-P2a	15	34	± 17.3		11	0	± 0.0	
GG-P3a	4	75	± 21.7		4	25	± 21.7	
GG-P4a	3	67	± 27.2		2	50	± 35.4	
GG-P5a	10	60	± 15.5		9	44	± 16.6	
GG-Ps subgroup								
GG-P1s	20	79	± 9.5		19	42	± 11.3	
GG-P2s	34	34	± 9.7		28	23	± 8.8	
GG-P3s	124	61	± 5.0		93	38	± 5.3	
GG-P4s	27	64	± 10.3		22	42	± 11.0	
GG-P5s	8	88	± 11.7		3	100	± 0.0	
GG-P2s subgroup				0.001				
GG-P2s	34	34	± 9.7		28	23	± 8.8	
Other GG*	179	65	± 4.0		137	41	± 4.4	
Genome Group				<0.0001				
GG-Ps	213	61	± 3.8		165	38	± 4.0	
GG-Ws	173	93	± 1.9		126	84	± 3.4	

OS: overall survival; EFS: event-free survival; SE: standard error; GG: genome group; *Other GG: GG-Wa, GG-Ws, GG-Pa (but no GG-P2a), or GG-Ps (but no GG-P2s).

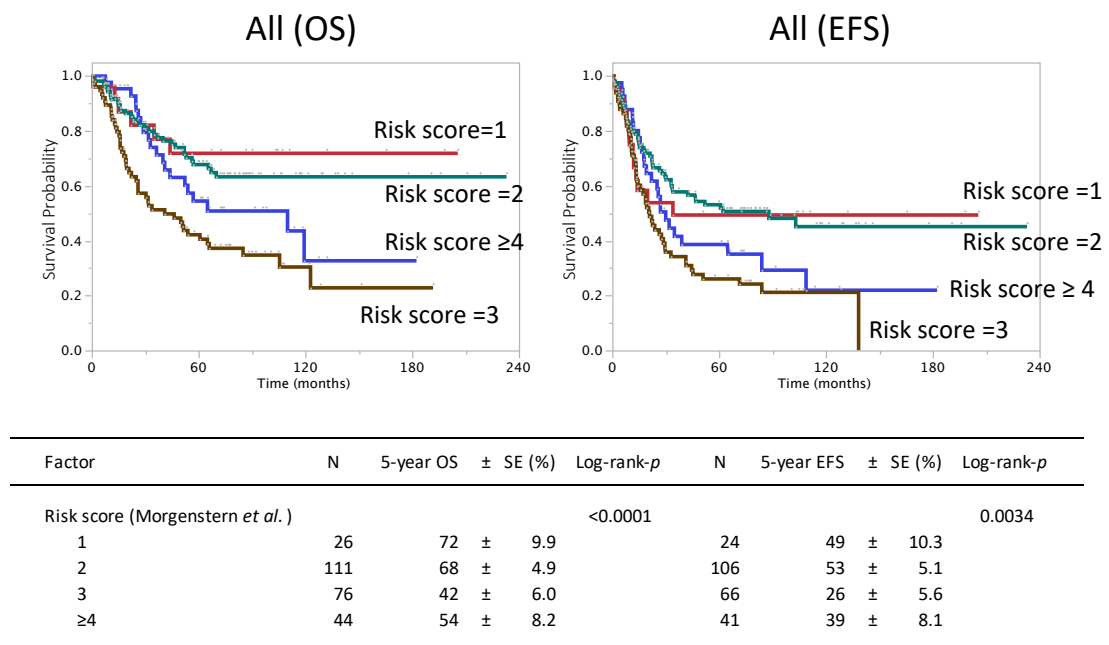
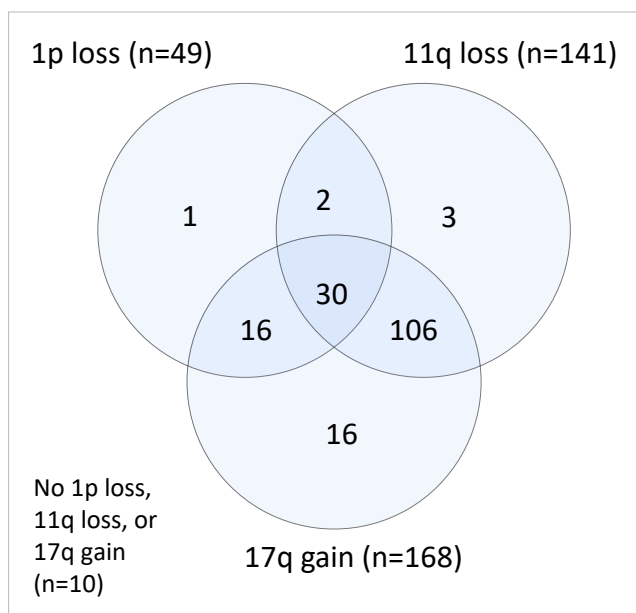


Figure S1. Prognostic significance of the risk score reported by Morgenstern *et al.*
 OS: overall survival; EFS: event-free survival; SE: standard error; MSI: metastatic site index

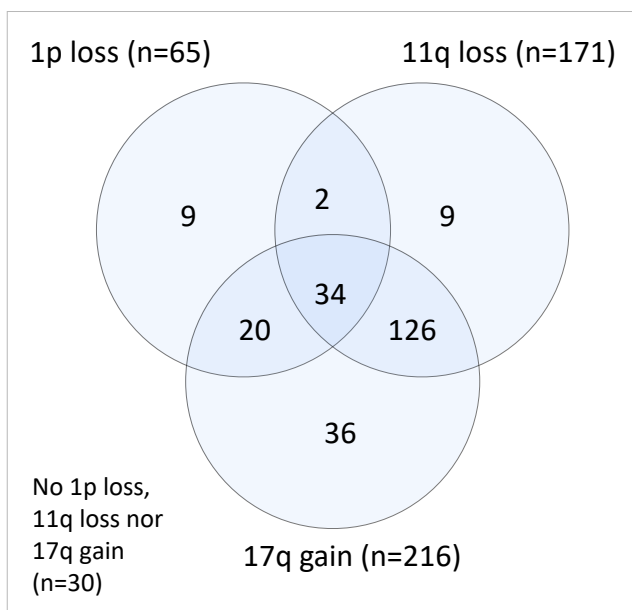
Genetic subtype “segmental (SCA)” detected in
Stage 4, *MYCN* non-amplified cases (n=184)



GG-P2 subtype (n=30) is
accompanying 1pL,11qL,
and 17qG.

Figure S2. Frequency of 1p loss, 11q loss, or 17q gain in 184 “segmental” subtypes detected in stage 4, *MYCN* non-amplified cases.

Genetic subtype “segmental (SCA)” detected in
MYCN non-amplified cases (n=266)



GG-P2 subtype (n=34) is
accompanying 1pL,11qL,
and 17qG.

Figure S3. Frequency of 1p loss, 11q loss, or 17q gain in 266 genetic “segmental” subtypes detected in *MYCN* non-amplified cases.