

Supplementary Table S1.

Distribution of the rearrangement-positive myeloma cases according to immunohistochemical positivity

	Cohort 1			Cohort 2			Total		
	Rearranged gene			Rearranged gene			Rearranged gene		
IHC	CCND1	NSD2	MAF	CCND1	NSD2	MAF	CCND1	NSD2	MAF
Class*	(n=20)	(n=20)	(n=10)	(n=26)	(n=13)	(n=4)	(n=46)	(n=33)	(n=14)
0% - 5%	0	1	1	0	0	0	0	1	1
5 - 10	1	0	0	1	1	0	2	1	0
10 - 15	2	1	1	0	0	0	2	1	1
15 - 20	0	0	0	0	0	0	0	0	0
20 - 25	1	0	0	4	0	0	5	0	0
25 - 30	0	0	0	0	0	0	0	0	0
30 - 35	2	1	0	1	0	1	3	1	1
35 - 40	0	0	0	0	0	0	0	0	0
40 - 45	2	0	0	2	0	0	4	0	0
45 - 50	0	0	0	0	0	0	0	0	0
50 - 55	0	0	0	1	1	0	1	1	0
55 - 60	0	0	0	0	0	0	0	0	0
60 - 65	3	1	1	1	0	0	4	1	1
65 - 70	0	0	0	0	0	0	0	0	0
70 - 75	0	1	1	3	0	0	3	1	1
75 - 80	0	0	0	0	0	0	0	0	0
80 - 85	2	5	1	4	1	0	6	6	1
85 - 90	0	0	0	0	0	0	0	0	0
90 - 95	5	1	0	4	2	2	9	3	2
95 - 100	2	9	5	5	8	1	7	17	6

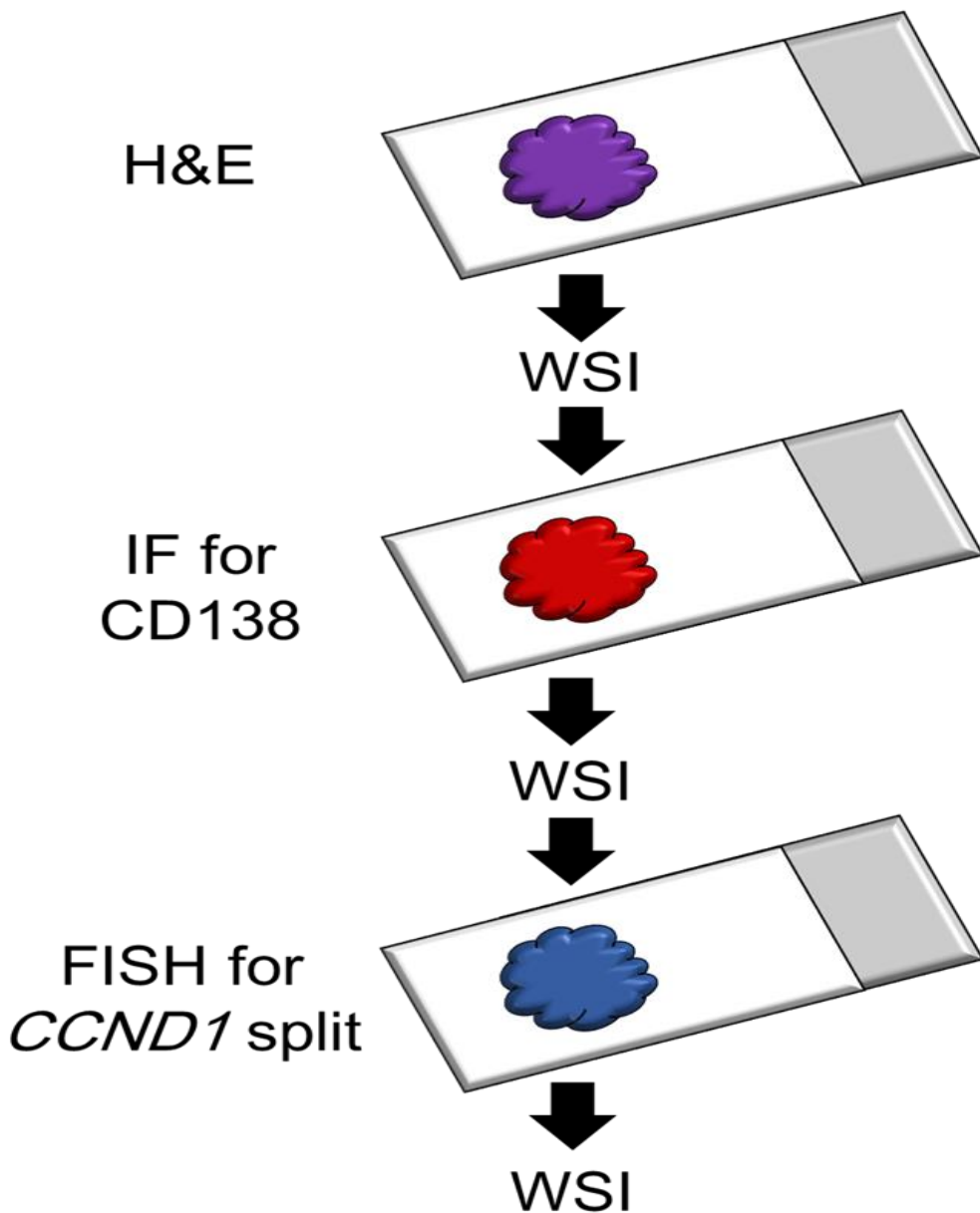
IHC, immunohistochemistry; *, immunohistochemically positive tumor cells

Supplementary Table S2. Cohort 1 and Cohort 2 myeloma cases (n=190)

Molecule	Sensitivity (95% CI)	Specificity (95% CI)	Accuracy (95% CI)
CCND1	1.00 (0.92-1.00)	0.99 (0.95-1.00)	0.99 (0.96-1.00)
NSD2	0.94 (0.80-0.99)	0.98 (0.95-1.00)	0.97 (0.94-0.99)
MAF	0.93 (0.66-1.00)	0.99 (0.97-1.00)	0.99 (0.96-1.00)

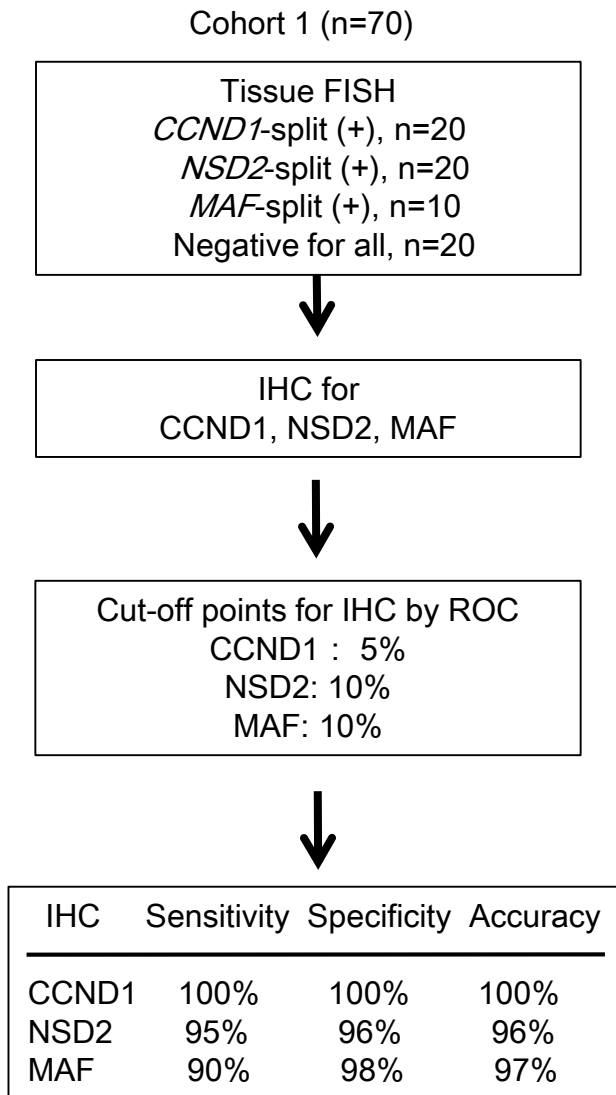
Supplementary Fig. S1.

Sequential retrieval of whole-slide imaging (WSI) data of H&E staining, immunofluorescence (IF) for CD138, and fluorescence in situ hybridization (FISH) for the *CCND1* gene split



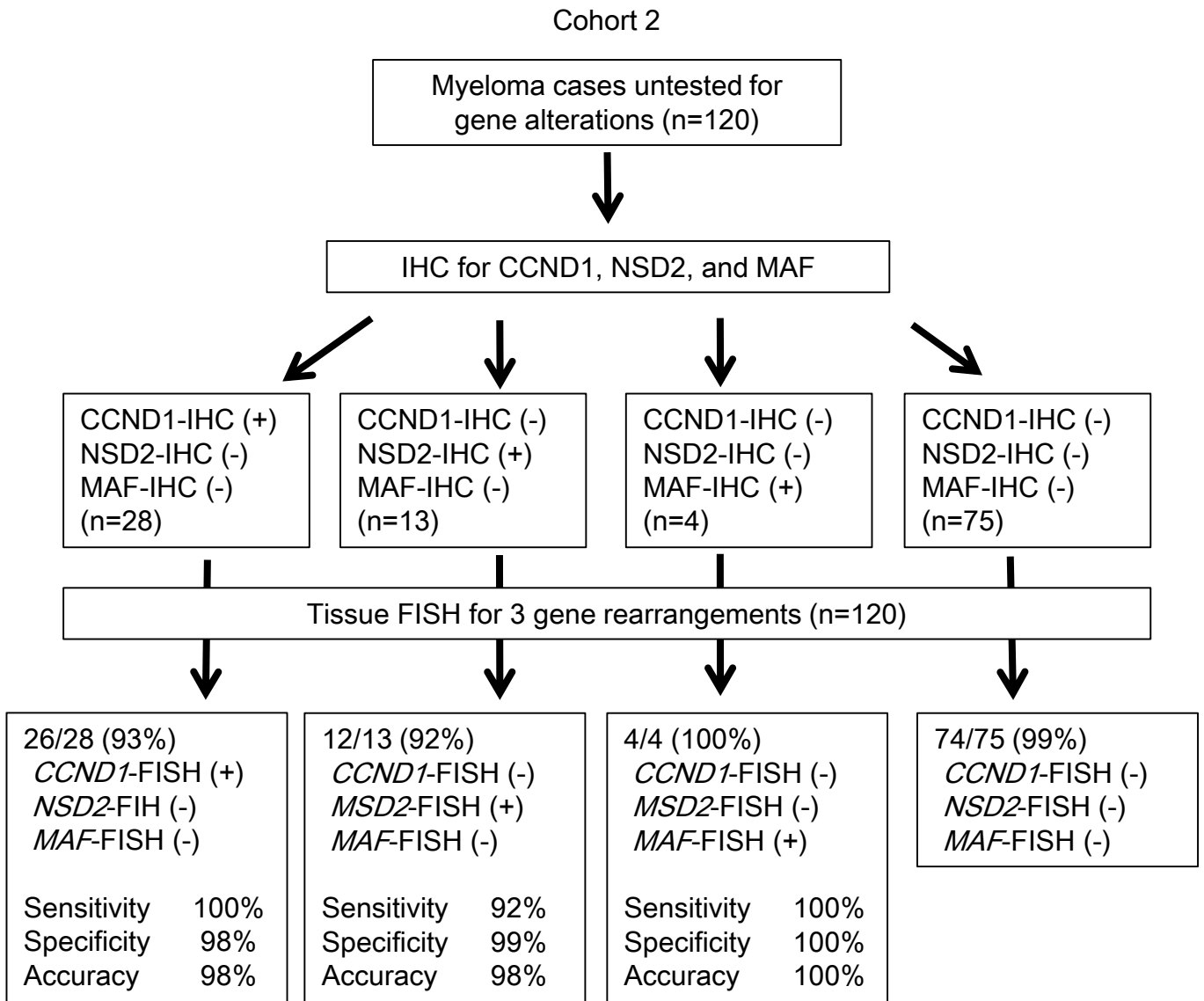
Supplementary Fig. S2.

Cohort 1 flowchart illustrating the number of myeloma cases and study data. FISH, fluorescence *in situ* hybridization; IHC, immunohistochemistry; and ROC, receiver operating characteristics



Supplementary Fig. S3.

Cohort 2 flowchart illustrating the number of myeloma cases and study data. IHC, immunohistochemistry and FISH, fluorescence *in situ* hybridization



Supplementary Fig. S4.

Evaluation of FISH signals in formalin-fixed paraffin-embedded tissue sections. When using a dual-color FISH probe, the number of FISH signals to be evaluated is greater than when using a break-apart FISH probe. FISH, fluorescence *in situ* hybridization

