Supplementary Table 1. Oligonucleotide primers in this study

Name	Ori	Primer sequence (5’- 3’)	Method
MYB1	For	GGCAGAAATCGCAAAGCTAC	RT-PCR (Exon5)
MYB2	For	GCAGGATGTGATCAAACAGG	RT-PCR (Exon13)
NFIB1	Rev	CTATTTCCCAGCGGACTTCA	RT-PCR (Exon12)
MYB3	For	CTCCGCCTACAGCTCAACTC	RT-PCR (Exon6)
MYB4	For	GCACCAGCATCAGAAGATGA	RT-PCR (Exon15)
NFIB3	Rev	TCAGTTGCTTGTTTCTGCTTGAAGG	RT-PCR (Exon12)
ACTB-F	For	CTGTCTGGCGGCACCACCAT	RT-PCR
ACTB-R	Rev	GCAACTAAGTCATAGTCCGC	RT-PCR
MYB-QE2	For	GACTATGGATGGGCTGCTTCC	QRT-PCR (Exon2)
MYB-QE3	Rev	TGTTCCATTCTGTTCCACCA	QRT-PCR (Exon3)
MYB-QE15	For	GCATTTACAGTACCTAAAAACAGGTC	QRT-PCR (Exon15)
MYB-QE16	Rev	CCCAAGTCAACTTGAAGTGTTC	QRT-PCR (Exon16)
ACTB-QF	For	TCACCGAGCGCGGCT	QRT-PCR
ACTB-QR	Rev	TAATGTCACGCACGATTTCCC	QRT-PCR
MYB-GSP1	For	CTCCGCCTACAGCTCAACTC	3’RACE (Exon6)
MYB-GSP2	For	GCCGCAGCCATTCAGAGACACTATAA	3’RACE (Exon7-8)
MYB-GSP3	For	CTCAGACTTGGAAATGCCTTC	3’RACE (Exon11)
MYB-GSP4	For	GCAGGATGTGATCAAACAGG	3’RACE (Exon13)
AP	Rev	GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTTTT	3’RACE
AUAP	Rev	GGCCACGCGTCGACTAGTAC	3’RACE
NFIB-AIG1-F	For	GCATGAGAAGCGAATGTCAA	RT-PCR
NFIB-AIG1-R	Rev	TCCAAGGTCCAATTCTGGTT	RT-PCR

Note: Ori, Orientation; For, Forward; Rev, Reverse; AP, Adapter Primer; AUAP, Abridged Universal Amplification Primer.

Supplementary Table 2. Alternative breakpoint detected by FISH

	Fusion Status	
Case#	**RP11-378M4/NFIB (5')**	**RP11-55H4/NFIB (3')**
78-C8	Positive	Positive
124-C1	Negative	Positive
288-F7	Negative	Positive
405-B2	Negative	Positive
436-H3	Negative	Positive
471-F2	Positive	Positive
484-H3	Negative	Positive
485-F7	Negative	Positive
502-A5	Positive	Negative
526-B5	Negative	Positive
594-D3	Negative	Positive

FISH analysis used BAC clones of *MYB* (RP11-378M4 or RP11-55H4) and *NFIB* (RP11-79B9 and RP11-54D21) genes. All of these cases are *MYB-NFIB* transcript negative by RT-PCR and 3'RACE, but FISH positive (*MYB*; RP11-104D9) samples.

Supplementary Table 3. Summary of rearrangement patterns in 485F7 case

Rearrangement pattern	**[a]Chr**	**[b]Pos**	**[a]Chr**	**[b]Pos**	**Size**	**Rearrangement consequence**
Translocation	6	135403192	9	14213172	N/A	Breaks *NFIB* intron 7, Breaks upstream of *MYB*
Translocation	6	143599570	9	14212301	N/A	Breaks *NFIB* intron 7, Breaks *AIG1* intron 2
Inverted orientation	6	143599106	6	145105794	1506688	Breaks *AIG1* intron2, Breaks *UTRN* intron 11
Intrachromosomal	6	135316882	6	145106331	9789449	Breaks *HBS1L* intron 7, Breaks *UTRN* intron 60
Inversion	6	55851114	6	146674745	90823631	Breaks *GRM1* intron 4
Inversion	6	55851947	6	146675822	90823875	Breaks *GRM1* intron 4
Intrachromosomal	3	75755145	3	197845654	122090509	Breaks no annatated genes
Deletion	4	35374876	4	35412355	37479	Breaks no annatated genes
Intrachromosomal	4	83621546	4	176884816	93263270	Breaks *SCD5* intron 2, Breaks *GPM6A* 5' UTR
Intrachromosomal	11	47349411	11	48359707	1010296	Breaks *MADD* intron 33
Intrachromosomal	13	23487983	13	24901910	1413927	Breaks no annatated genes
Intrachromosomal	14	48690021	14	49436046	746025	No annotated genes in deletion
Deletion	16	79260215	16	79280247	20032	No annotated genes in deletion
Inverted orientation	19	15819768	19	16018350	198582	Breaks no annatated genes

[a]Chr, Chromosome location. [b]Pos, break position

Supplementary Table 4. Correlation between Clinicopathologic and fusion gene status and *MYB* expression in ACC

Factor	number	***MYB* exon 2-3**		***MYB* exon 15-16**	
		Mean ± SE	[a]p-value	Mean ± SE	[a]p-value
Fusion transcript					
positive	39	605.2 ± 105.2		12.7 ± 2.8	
negative	63	239.7 ± 41.2	< 0.001	132.4 ± 22.3	0.003
FISH					
positive	54	519.7 ± 93.1		63.1 ± 18.3	
negative	48	221.7 ± 51.9	< 0.001	113.1 ± 26.3	0.50
Age					
<60	67	447.3 ± 70.0		90.6 ± 19.1	
≥60	35	249.6 ± 55.8	0.044	79.2 ± 24.5	0.95
Gender					
Male	61	435.0 ± 74.8		89.9 ± 18.8	
Female	41	296.9 ± 56.8	0.18	81.9 ± 24.9	0.22
Size					
<4cm	63	373.0 ± 64.2		99.1 ± 20.8	
≥4cm	35	426.8 ± 89.9	0.46	73.7 ± 22.4	0.98
Pattern[b]					
T/C	60	377.9 ± 75.8		91.5 ± 20.4	
S	41	357.6 ± 54.9	0.26	81.6 ± 22.6	0.79
Stage[c]					
I-II	20	399.1 ± 147.1		63.7 ± 24.9	
III-IV	35	343.1 ± 80.7	0.55	109.9 ± 28.7	0.12
PNI[d]					
Yes	78	369.3 ± 51.4		83.9 ± 15.8	
No	7	554.6 ± 348.8	0.80	47.0 ± 26.1	0.94
Metastasis					
Yes	52	477.5 ± 86.9		76.5 ± 20.0	
No	50	277.5 ± 46.1	0.12	97.2 ± 22.6	0.98

[a]Mann-Whitney U test. [b]T/C, tubular/cribriform; S, solid pattern; [c]55 patients are available for the staging analysis. [d]PNI, Perineural invasion.