Supplementary Table S1: Primers

Name and Description			Sequence	Product Size
Primers designed to test whether there was a chromosomal rearrangement between NR5A2 and KLHL29	Primer 1	F	5'-GGCATAGTGAAAGAGCACTGG-3'	108 bps
		R	5'-GCCACTCGGAGTACTCTGCTA-3'	
	Primer 2	F	5'-TGCAGGAAAGAAACTGGGCA-3'	208 bps
		R	5'-GCCTCATATCTGCCACTCGG-3'	
	Primer 3	F	5'-CCCCAAATCGGAAGGAGTGT-3'	408 bps
		R	5'-TGTGTATTCGGAGGATGGGC-3'	
	Primer 4	F	5'-CTGGCCAGGACAAGGAAACT-3'	643 bps
		R	5'-GGGGATGCCTCATATCTGCC-3'	
NR5A2 gene primers (spanning fusion site)		F	5'-TGCAGGAAAGAAACTGGGCA-3'	856 bps
		R	5'-GGCAGTTGGCCAAAGAAAGG-3'	
KLHL29 gene primers (spanning fusion site)		F	5'-GCTCTGCCTCCCCGTAATAG-3'	853 bps
		R	5'-AAATCGCACTGAGGAAGAGGG-3'	
GAPDH mRNA		F	5'-AGAAGGCTGGGGCTCATTTG-3'	258 bps
		R	5'-AGGGGCCATCCACAGTCTTC-3'	

Supplementary Table S2: Fusion transcript candidates grouped by genomic location (sample A1).

Fusion transcript [a]	**Left gene**	**Left chr ID**	**Coordinates on the left**	**Right gene**	**Right chr ID**	**Coordinates on the right**	**N[b]**	**N[c]**	**N[d]**
Chr10-chr10 ff	C10orf68	Chro10	32873231	CCDC7	Chr10	32832227	56	1	10
Chr13-chr13 rr	ENSG00000139597	Chr13	33006925	N4BP2L2	Chr13	33095585	2	2	0
Chr9-chr9 rr	MPDZ	Chr9	13205034	ENSG00000234740	Chr9	13276769	3	2	0
Chr1-chr2 fr	NR5A2	Chr1	200067672	KLHL29	Chr2	23698253	6	1	9
Chr6-chr6 rr	MYLIP	Chr6	16148001	ENSG00000251793	Chr6	16148559	3	56	0
Chr3-chr3 ff	ENSG00000242086	Chr3	195416308	SDHAP2	Chr3	195415403	15	99	2
Chr20-chr20 rr	ENSG00000225065	Chr20	33302393	NCOA6	Chr20	33303168	7	129	0
ChrX-chrX rr	CLIC2	ChrX	154563679	ENSG00000224216	ChrX	154564557	3	14	0
Chr12-chr12 rr	ENSG00000212127	Chr12	11148552	TAS2R20	Chr12	11150115	2	53	0
Chr3-chr3 rr	ENSG00000249598	Chr3	195686053	SDHAP1	Chr3	195686956	10	13	0
Chr12-chr5 ff	SUDS3	Chr12	118825300	ENSG00000249129	Chr5	177398635	8	33	0

ff, sense strand of left gene fused to sense strand of right gene; *fr,* sense strand of left gene fused to antisense strand of right gene; *rr*, antisense strand of left gene fused to antisense strand of right gene; N^b, number of reads showing fusion breakpoint; N^c, number of paired reads where one read maps entirely on the left and the other read maps entirely on the right of the fusion breakpoint; N^d, number of spanning mate-pairs where one end spans fusion (reads spanning fusion with only a few bases are included).

Supplementary Table S3a. Expression levels of NR5A2-KLHL29FT in 15 matched colon cancer

Sample ID	Database ID	Log2 relative RNA expression by qRT-PCR	Log2 RNA relative expression in tumor normalized to matched normal tissue
Sample 1-N	3848 N	-4.7108	
Sample 1-T	3848 T	-12.1294	-7.4186
Sample 5-N	3791 N	-7.6937	
Sample 5-T	3791 T	-3.6668	4.0269
Sample 7-N	3457 N	-5.1908	
Sample 7-T	3457 T	-7.6636	-2.4728
Sample 8-N	3615 N	-4.7504	
Sample 8-T	3615 T	-13.9279	-9.1775
Sample 11-N	3841 N	-7.9602	
Sample 11-T	3841 T	-10.0088	-2.0486
Sample 12-N	3785 N	-10.8391	
Sample 12-T	3785 T	No products	-5
Sample 16-N	3876 N	-8.5618	
Sample 16-T	3876 T	-11.4129	-2.8511
Sample 17-N	3891 N	-11.3752	
Sample 17-T	3891 T	-9.2948	2.0826
Sample 18-N	3900 N	-5.4584	
Sample 18-T	3900 T	-8.571	-3.0987
Sample 20-N	3849 N	-10.7722	
Sample 20-T	3849 T	-10.7164	0.0558
Sample 21-N	3896 N	-8.7955	
Sample 21-T	3896 T	-11.1227	-2.3271
Sample 22-N	3901 N	-10.2564	
Sample 22-T	3901 T	-11.06	-0.8036
Sample 23-N	3915N	-10.9447	
Sample 23-T	3915 T	-13.5562	-2.6115
Sample 24-N	3929 N	-11.0378	
Sample 24-T	3929 T	-9.8847	1.1531
Sample 25-N	3940 N	-8.8420	
Sample 25-T	3940 T	-10.3876	-1.5456

Supplementary Table S3b. Sample IDs and matched primary sample IDs in our sample database

Sample ID	Primary sample ID in our sample databases	Sample ID	Primary sample ID in our sample database
1	3848 (++)	14	3836 (-)
2	H69 (-)	15	3860 (-)
3	H95 (+)	16	3876 (+)
4	H96 (+)	17	3891 (+)
5	3791 (+)	18	3900 (+)
6	2874 (-)	19	3925 (-)
7	3457 (+)	20	3849 (+)
8	3615 (+)	21	3896 (++)
9	3923 (-)	22	3901 (+)
10	3908 (-)	23	3915 (+)
11	3841 (+)	24	3929 (+)
12	3785 (+)	25	3940 (+)
13	2945 (-)		

++, homozygous for KLHL29 insertion; + heterozygous for KLHL29 insertion; -, homozygous wild-type