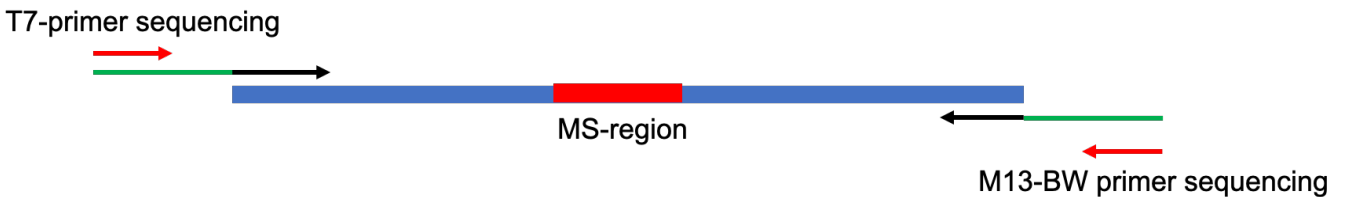


**Data S1.** Sanger sequencing results for MS-indel recalling using selected CCLE cell lines: HCT116, Hec59, Hec1B, LOVO. Related to the **Figure 4**.

Protocol steps:

0) **Cell growth.** Cell lines were purchased from ATCC: HCT116 (ID: CCL-247), Hec1B (ID: HTB-113), LOVO (ID: CCL-229) or Addexbio Technologies: Hec59 (ID: C0026001). Obtained cell lines were grown for 2 passages in cell culture conditions recommended by manufacturer: DMEM media (Corning-Cellgro, cat: 10-013-CM) supplemented with 10% FBS (Sigma-Aldrich, cat: F4135). Genomic DNA extraction was done from 107 cells using DNeasy Blood&Tissue Kit from Qiagen following manufacturer recommendations (Qiagen, ID: 69504).

1) **Primer Design.** Primers are designed to anneal around the microsatellite region of interest. Each primer has 5'-end overhangs encoding T7 or M13-BW complementary sequences suitable for sanger sequencing using T7 or M13-BW primers.



2) **High-fidelity PCR.** PCR was performed using ready-to-use 2x CloneAmp HiFi PCR premix (Takara, cat: 639298). PCR amplifications were done using standard BioRad thermocycle with PCR cycle setup as following: first melting step 95C – 2m; cycle repeated 35x: 95C – 15s, 55C – 30s, 72C – 30s; final extension step 72C – 2m; hold at 16C. Primers used for amplification are listed in the table below:

oVR1011	COBL1_fw	TAATACGACTCACTATAGGGTGTAAACGACGGCCAGT GTACCAGTTTGAAAGTCAGGAGG
oVR1012	COBL1_bw	CAGGAAACAGCTATGAC ATTTAGGTGACACAG CCTCTAGAACTCTAGAATATCCTGTGTG
oVR1013	DOCK3_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCA GTTTATCCATAGCCCTCAATGCTG
oVR1014	DOCK3_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CTGCAGCTCAAGTGTGGCTCTG
oVR1015	GRIK2_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCA CAATTCTTCAGCTGCAAGAGGAAG
oVR1016	GRIK2_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG GAATGACATAAGACAATTTAGAGCAATAGTTC
oVR1017	KMT2C_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCAG CTGAGTGAGCAGAAGCCTGTGAG
oVR1018	KMT2C_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CTGGATGACCTCTTAAGGTGAGGAG
oVR1019	RNF43_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCA CACACTGGCTGTGAATTTGAGTAA
oVR1020	RNF43_bw	CAGGAAACAGCTATGACATTTAGGTGACACTA CTGATCAGCAAGTCACCAGATCCAACCTC
oVR1021	SEC31A_fw	TAATACGACTCACTATAGGGTGTAAAACG GCTCTTTATAAGGCTCTTAATTTTCATGATG
oVR1022	SEC31A_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CTTCATCAGGGAGCTGAGCAG
oVR1023	XYLT2_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCAGT GAAAAGCCGACGAGGGCTGAG
oVR1024	XYLT2_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG GGCCTGCTGTATGTCAGAAGGG
oVR1025	ZBTB20_fw	TAATACGACTCACTATAGGGTGTAAAACGAC GAGAGAAAGATACTACTTATCCGTCAGAC
oVR1026	ZBTB20_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CACACACAGGAGTGAGGGCATAAC
oVR1027	BMPR2_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCC CAACCTGTACATAATAGGCGTGTG
oVR1028	BMPR2_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CTGTGCAACATTTGTGGTATGCAG
oVR1029	CCDC168_fw	TAATACGACTCACTATAGGGTGTAAAACGA GTAATGTCAGCTATGAAAAACGGTAGTAAG
oVR1030	CCDC168_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CAGCAGTCATTGGACCCAGATTAC
oVR1031	EIF2B3_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCC CATCAACTCTAGCACAGAATCTGT
oVR1032	EIF2B3_bw	CAGGAAACAGCTATGACATTTAGGTGACA ATTGTCCTTTATGATATTGACTTTTCCATC
oVR1033	PLEKHA6_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCA GATTGGGCAAGCCAGGAAGCATG
oVR1034	PLEKHA6_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG AACAGCCTGCCAGCCCAATG
oVR1035	SETD1B_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCCAG GAGCCAGCGAGACAGCTCCTTC
oVR1036	SETD1B_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CTACTACC GCCAGGCTGAAATG

oVR1037	SLAMF1_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCC CACTGACGTTTAGTGACTTTAGGAG
oVR1038	SLAMF1_bw	CAGGAAACAGCTATGACATTTAGGTGACACTATAG CAGGGCTTTGTTCCATTGTGCC
oVR1039	SLC35G2_fw	TAATACGACTCACTATAGGGTGTAAAACGA GATTATCTGAAGAAATGGATACTTCTCCCT
oVR1040	SLC35G2_bw	CAGGAAACAGCTATGACATTTAGGTGACACTA CAGAAACAAGCCTAGTGATAAGAGCTAC
oVR1041	TTK_fw	TAATACGACTCACTATAGGGTGTAAAACGAC CAACTGTAAGAACAAGAGAGAAATAATG
oVR1042	TTK_bw	CAGGAAACAGCTATGACATTTAGGTGACAC CAGTGCCATAAGTGTTGCTATTTTTACAG
oVR1043	VCP_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGCC GAGGACTCATGCAAGTCTCCACAG
oVR1044	VCP_bw	CAGGAAACAGCTATGACATTTAGGTGACAC GAGACATCTAGTTTTGTTAGTGCTTGAATC
oVR1045	DCAF13_fw	TAATACGACTCACTATAGGGTGTAAAACGACGGC CAGTGTATACTGGGATTGATCATCAC
oVR1046	DCAF13_bw	CAGGAAACAGCTATGACATTTAGGTGACACTA CTCTAGTATCTGGGACTAAACTGCTGGG

3) **Sanger Sequencing.** After amplification, PCR reactions were purified on the PCR cleanup column (Qiaquick PCR purification kit, Qiagen cat: 28104). Obtained DNA was sent for sanger sequencing with standard T7-and M13-BW primers at Genscript (<https://www.genscript.com>).

4) **Analysis of sequencing results.** Obtained sequencing results and reference sequences of target genomic loci (shown in FASTA format below) were aligned using Clustal Omega multiple sequence alignment tool. Alignments were visualized using EBI available visualization tools (<https://www.ebi.ac.uk/Tools/msa/>).

#### **AASDH MS locus analysis:**

>AASDH\_reference

```
ATAATAGAGACCCAGCACAGAAAATTGGTGGTGGCTGCTTCTACTACTTACATATATTAATAGATATTC
AATATTTAAATAGTTCTACCTGTTGCACAAGTTCAATGTTAAGACGTTTGCCATGACGTTTGATCTGACTG
TCTTTTCGTCCCAAAAAAAAAAATCTCTCCATCTTTCACAGTCACAAAGTCTCCTGTAGCTCGCATTGTGCC
AAGTGGTACTGTCACCTTCATCATCAAGAAAACACACTCTGTTTCTGCCACCTTCCCAAGATATAAACACCA
ATGTCATAAAAATCCAAGGG
```

>HCT116\_AASDH\_T7

```
ACGACTGCAGTGAGACCAGCACAGAGATTCCGTGCTAGTGACGTGCTCACTCACAACCTTACATATACTG
ATATACGCATATTCAATATTTAAATAGTTCTACCTGTTGCACAAGTTCAATGTTAAGACGTTTGCCATGAC
GTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAAATCTCTCCATCTTTCACAGTCACAAAGTCTCCTGTA
GCTCGCATTGTGCCAAGTGGTACTGTCACTTCATCATCAAGAAAACACACTCTGTTTCTGCCACCTTCCCA
AGATATAAACACCAATGTCATAAAAATCCAAGCTATAGTGTACCTAAATGTCAAGCAGTTTTCTGAGA
AATCGGCTACTGAAGAGCTGTGGCCTTCGTTTTACACCCTATATGGAAAAAAGAAAAAATTAGTCAGATT
GGGAAG
```

>HCT116\_AASDH\_M13

```
AAACACCTCGAAATATAGGGGGCCCATATGGTTTATACGACTCCCCTATAGGGTGTAAAACGAAGGCC
ACCCAACCAGGGCAACCGTTTTTAAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGAGACCCC
AGCACAGAAAATTGGTGGTGGCTGCTTCTACTACTTACATATATTAATAGATATTCAATATTTAAATAGTT
CTACCTGTTGCACAAGTTCAATGTTAAGACGTTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAA
AAAAAATCTCTCCATCTTTCACAGTCACAAAGTCTCCTGTAGCTCGCATTGTGCCAAGTGGTACTGTCAC
TTCATCATCATTAAACGACATCTACGATTGGGCGTACAATTGACCGGCGCATGTGAGACACCCAGCGTC
AGAAATCCAGCTGTAGCCC
```

>Hec59\_AASDH\_T7

```
ACAACGACTGCAGTGAGACCAGCACAGAAAATTCCGTGCGTAGTGACGTGGTCACTCACTACTGACATATGAC
TGATATTCGCATATTCAATATTTAAATAGTTCTACCTGTTGCACAAGTTCAATGTTAAGACGTTTGCCATG
ACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAAATCTCTCCATCTTTCACAGTCACAAAGTCTCCTGTA
```

GCTCGCATTGTGCCAAGTGGTACTGTCACTTCATCATCAAGAAAACACACTCTGTTTCTGCCACCTTCCCA  
AGAAATAAACACCAATGTCATAAAAATCCAAGCTATAGTGTACCTAAATGTCAAACTTTTTCTGGAA  
AA

>Hec59\_ AASDH \_M13

GCATTTTTTAAACCGACTCCCTTTAGGGTGAAAACGCCGCCAGTGGGCCCCAGCACAGAAATTTGGT  
GGTGGCTGCTTCACTACTTACAAATATTAATAGATATTCAAATTTAAATAGTTCTACCTGTTCCACAAG  
TTCAAGGTTAAGACGTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCATC  
TTTACAGTCACAAAGTCTCCTGTAGCTCGCATTGTGCCAAGTGGTACTGTCACTTCATCATCTTTAATAC  
GACTCACTATAGGGCGTAAACGACGGCCAGTGAGACCCCAATTCCATAAAAATGGCAAGTCTTTCCATT

>Hec1B\_ AASDH \_T7

ACGCTGCGTGAACCAGCAAGAGATCCGTGCTGGCTGGTTCTACAACGACATATCTGTTTCCTATAACAAT  
ATTTAAATAGTTCTACCTGTTGCACAAGTTCAATGTTAAGACGTTTGCCATGACGTTTGATCTGACTGTCT  
TTTCGTCCCAAAAAAAAAATCTCTCCATCTTTACAGTCACAAAGTCTCCTGTAGCTCGCATTGTGCCAAG  
TGGTACTGTCACTTCATCATCAAGAAAACACACTCTGTTTCTGCCACCTTCCAAGATATAAACACCAATG  
TCATAAAAATCCAAGCTATAGTGTACCTAAATGTCATAACTGTTTCTGGGAAAAA

>Hec1B\_ AASDH \_M13

CTTTTCCTTTAACATATCAGTTTCTTACTCCCGTCCACTTTTCGGCGTAAAAGGGCCGCCAGCGGCGG  
CCGCTCTTTAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGAGACCCAGCACAGAAAATTGG  
TGGTGGCTGCTTCTACTACTTACATATTAATAGATATTCAATATTTAAATAGTTCTACCTGTTGCACAA  
GTTCAATGTTAAGACGTTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCA  
TCTTTACAGTCACAAAGTCTCCTGTAGCTCGCATTGTGCCAAGTGGTACTGTCACTTCATCATCATTAAAT  
ACGACCTCTACGATTGGGCGTACAACGACGGCGCATGTGAGACACCCAGCACAGAAAATCCAAGGCTCT  
ACCC

**Alignment\_result\_AASDH\_MS\_region:**

Hec59_1_M13	TTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAA-AAAAATCTCTCCATCTTT	214
HCT116_1_M13	TTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCATCTTT	300
Hec1B_1_M13	TTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCATCTTT	287
Hec1B_1_T7	TTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCATCTTT	173
AASDH_reference	TTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCATCTTT	176
HCT116_T7_1	TTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAAAAAAAAAATCTCTCCATCTTT	189
Hec59_1_T7	TTTGCCATGACGTTTGATCTGACTGTCTTTTCGTCCCAA-AAAAATCTCTCCATCTTT	190
	** *****	

**Conclusion: Hec59 has deletion**

**ACVR2A MS locus analysis:**

>ACVR2A\_reference

ATATTTTAGAAAGTTTGTACCAGTTTGAAAGTCAGGAGGATTTAATGAAAATGATTTATTTACTTTTCT  
TACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTCTTG  
AAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATG  
CTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATCCAATAAACACTTTTCAGAGGAATTATTTATCTCTG  
CACATTTCTCTTCTCTGCAAGTATTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTCTAGAG  
GCAGAATTAGGGCT

>LoVo\_ ACVR2A\_T7

CCGAAGGCAGTGTACAGTTTGAGTCAGGAGGATCTAAAGGTCTATGATGCTAGTGTTACTTTTCTGACTT  
ATCTGGATCCGTAAATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTCTTGAAGAC  
ATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTGTAA

GTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACACTTTTCAGAGGAATTATTTATCTCTGCACATT  
TCTCTTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTCTAGAGGCTGTG  
TCACCTAAATGTCATAGCAAATTTCTGGGGAGAGGG

>LoVo\_ ACVR2A\_M13

TTAATTTTTGTTTCACTTTTGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATTTTAA  
TGAAAATGATTTATTTTACTTTTTCTTACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGGAGG  
AAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTT  
AAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACAC  
TTTTCAGAGGAATTATTTTATTACCACTCTTCTTATGGTGTAAACAGACGGCCAGGTACCAGTCGAAACTCA  
GGATTTCTAGAGTCTAGAGGTTATTCCT

>Hec1B\_ ACVR2A\_T7

ACGACTGCAGTGTACAGTTTGAGTCAGGAGATATCTATAATGTTCTATGAAGTGTCTAGTGTTCACTCTT  
TCTGACTTTTTCTGGACCCGGAATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTC  
TTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAAC  
ATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACACTTTTCAGAGGAATTATTTATCT  
CTGCACATTTCTCTTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTCTA  
GAGGCTGTGTCACCTAAATGTCATAGCTGTTTCCTAAAGA

>Hec1B\_ ACVR2A\_M13

TTTTTTAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATTT  
TAATGAAAATGATTTATTTTACTTTTTCTTACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGG  
AGGAAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTG  
TTTTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAA  
CACTTTTCAGAGGAATTATTTTATTTGCACTCTTCTTTGGTGTAAAAGACGGCCAGGAACCAGTCGAAA  
CTCAGGATATCTAGAGTCAGAGGGAACCCTC

>Hec59\_ ACVR2A\_T7

TCGAGGGGGGCGGTGTTTCAGTTTGAAGTCAGGAGGATTTAATGAAAATGATTTATTTTACTTTTTCTTAC  
TTTTCAGGACCTGGAGATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTCTTGAA  
GACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG  
TAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACACTTTTCAGAGGAATTATTTATCTCTGCAC  
ATTTCTCTTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTCTAGAGGCT  
GTGTCACCTAAATGTCATAGCTGTTTCCTGAAGA

>Hec59\_ ACVR2A\_M13

TATTTTTAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATTT  
TAATGAAAATGATTTATTTTACTTTTTCTTACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGG  
AGGAAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGT  
TTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAAC  
ACTTTTCAGAGGAATTATTTATCTTTGCACATTTCTCTTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTCA  
CACAGGATATCTAGAGTCAGAGGACCCC

>HCT116\_ ACVR2A\_T7

ACAACGCAGTGTACAGTTTGAGTCAGGATATTCTAGAGTTCTATGAGGCTGTGTCACCTATCTGTCTTAT  
CTGTTTCCGTAGATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTCTTGAAGACAT  
GCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTGTAAGT  
TATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACACTTTTCAGAGGAATTATTTATCTCTGCACATTTT

TCTTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTCTAGAGGCTGTGTC  
 ACCTAAATGTCATAGCTGTTTCCTAAAAA  
 >HCT116\_ACVR2A\_M13  
 TCTTTTTAATACGACTCACTATAGGGTGTAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATT  
 TAATGAAAATGATTTATTTTACTTTTCTTACTTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGG  
 AGGAAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGT  
 TTTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAAC  
 ACTTTTCAGAGGAATTATTTTATTACGACTCACTATAGGGTGTAAGACGGCCAGTGTACGCAGATCTG  
 AAAGTCAGGATATCTAGAGTCAGAGGTACCCC

**Alignment\_result\_ACVR2A\_MS\_region:**

Hec1B_2_T7	AAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	215
LoVo_T7_2	AAGTTGTTGTGCATAAAAA-AAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	206
HCT116_2_T7	AAGTTGTTGTGCATAAAAA-AAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	204
HCT116_2_M13	AAGTTGTTGTGCATAAAAA-AAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	239
LoVo_2_M13	AAGTTGTTGTGCATAAAAA-AAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	236
Hec1B_2_M13	AAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	240
Hec59_2_M13	AAGTTGTTGTGCATAAAAA-AAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	239
ACVR2A_reference	AAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	213
Hec59_2_T7	AAGTTGTTGTGCATAAAAA-AAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG	208
	*****	

**Conclusion: LoVo, HCT116, Hec59 has MS-related deletion**

**DOCK3 MS locus analysis:**

>DOCK3\_reference  
 GCCAGTGTAAGAGAGGTTTATCCATAGCCCTCAATGCTGAGGGGTCCCCAGGGGACTCTTCTCATGCC  
 TGCCCAGTTGGCCAGCAAGATGGTGTGCTGGCATGAAGTCTGTGCAGGGCCCCCAGCTGAGGCTCTGGTT  
 CTGTTCCCTTTGCAGGTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCCCCA  
 GCCCTCCCTGCCCGACCCTGCGCAAGGTAATGTACTGAAGCGGCAGCCCCACCAGGCTGTGAGATGA  
 GTCATCTCGTCTGCTCTAGAACCACCCTTGGGGTCTACAGGAGGAACTGGAGCCCTCCCCTTACCTCTC  
 TCCCCAGCCTGGCAGAAGCTGGGGGTGGCCAGAGCCACACTTGAGCTGCAGGTG  
 >Hec1B\_DOCK3\_T7  
 ACGCGGCAGTATCCATAGCCCTCTTGGACTGGCCTTATATGGCACCAAATTGTCAAACTTTTTTCGGGAA  
 TCAAGATGGTGCTGGCATGAAGTCTGTGCAGGGCCCCCAGCTGAGGCTCTGGTTCTGTTCCCTTTGCAG  
 GTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCCCCAGCCCTCCCTGCCCGG  
 ACCCTGCGCAAGGTAATGTACTGAAGCGGCAGCCCCACCAGGCTGTGAGATGAGTCATCTCGTCTGCTC  
 TAGAACCACCCTTGGGGTCTACAGGAGGAACTGGAGCCCTCCCCTTACCTCTCTCCCCAGCCTGGCAGA  
 AGCTGGGGGTGGCCAGAGCCACACTTGAGCTGCAGCAATAGTGCA  
 >Hec1B\_DOCK3\_M13  
 GGGACTTTTGTGCATGCATGTCAAGGTCAGCCAGCAAGATGGTGTGTCGTAAGTTTGGGCAGGCCCCC  
 AGCCGAGGCTCTCAATTTTTTCCGTCACCATGTAATTAGCCCGGAGCCTAAAGCCCTTCCACCACCCTCTG  
 GGTGATACCCCCCAGCCCTCCCTGCCCGACCCTGCGCAAGGTAATGTACTGAAGCGGCAGCCCCACC  
 AGGCTGTGAGATGAGTCATCTCGTCTGCTCTAGAACCACCCTTGGGGTCTACAGGAGGAACTGGAGTTT  
 TTATATGAATCACTATAGGGTGTAAGACGACGGCCCGTTTATCCATAGCCACACTGAGCGCAGCTTTAG  
 CCTTTT  
 >Hec59\_DOCK3\_T7  
 ACAGCTGCAGTATCCATAGCCCTCCTGGAGCTGCAGCTATAGTGTACCTAAATGTCAAAGCTTTTTTCGG  
 GAAGCAAGATGGTGCTGGCATGAATTCTGTGCAGGGCCCCCAGCTGAGGCTCTGGTTCTGTTCCCTTTG

CAGGTCATTACTCCCTACACTTTGACGCCGTCCACCACCCTCTGGGTGATACCCCCCAGCCCTCCCTGCC  
 CGGACCCTGCGCAAGGTAATGTAAGCGGCACCCCCACCAGGCTGTGAGATGAGTCATCTCGTCTG  
 CTCTAGAACCACCTTGGGGTCTACAGGAGGAACTGGAGCCCTCCCCTTACCTCTCTCCCCAGCCTGGC  
 AGAAGCTGGGGGTGGCCAGAGCCACACTTGAGCTGCAGCTATAGTGTC

>Hec59\_DOCK3\_M13

CACACCCTTAATAAGACTCACAATAGGGTGTAAAACGACGGTCAGTTAATCCATAGCCCTCAAAGCTGA  
 GGGGTCCCCAGGGGACTCTTCTCATGCCTGCCAGTTGGCCCAGCAAGATGGTGATGGCATGAAGTCTG  
 TCGGGGCCCCCATCCAAGGCTCTGAATGTGTTCCCTCACCATGTCATTACTCCCTACACTTTGACGCCTT  
 CCACCACCCTCTGGGTGATACCCCCCAGCCCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGC  
 GGCAGCCCCACCAGGCTGTGAGATGAGTCATCTCGTCTGCTCTAGAACCACCTTGGGGTCTACAGGAG  
 GAACTGGAGTTTTATACGACTCACTATAGGGTGTAAAACGACGGCCAGTTTATCCATAGCCCACACTGA  
 GCGCAGGCTAAAG

>HCT116\_DOCK3\_T7

CCAGCTGGCAGTATCCATAGCCCTCCTTGAGCTGCAGCTATAGTGTACCTAATTGTCAAACCTTTTTCGG  
 GAAGCAAGATGGTGCTGGCATGAATCTGTGCAGGGCCCCAGCTGAGGCTCTGGTTCTGTTCCCTTTCG  
 AGGTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCCCCAGCCCTCCCTGCCCG  
 GACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTGAGATGAGTCATCTCGTCTGCT  
 CTAGAACCACCTTGGGGTCTACAGGAGGAACTGGAGCCCTCCCCTTACCTCTCTCCCCAGCCTGGCAG  
 AAGCTGGGGGTGGCCAGAGCCACACTTGAGCTGCAGCTATAATGTAGCAAAAAT

>HCT116\_DOCK3\_M13

GGGGGTTTATCCGTGACACCCTTTTATCCTTCAAAAAAATCGTTGAAGGTCAGGGAACAGATCAGCAA  
 GATTGACCTGAGGGAGAAGAAGTAAGTGGTGCCGTCCGTGCGGTCCATCACGCCTGGGGGGTCTCCAA  
 GGGCACATGCGGGTGGGCATACTGGACGTGCCGACACAAGCACTGGCAGAGTCATATATGGCTCCCA  
 GAGGGTAATATAGTGCCTTGGTGCTTCTTTAAAATGAAGCACCTCCTCGTCAGGGCCCTTTTTTTAATAC  
 GACTCACTATAGGGTGTAAAACGACGGCCAGTTATCCATAGCCCACACTGAGCTGCAGCGTTAGCCCC

**Alignment\_result\_DOCK3\_MS\_region:**

HCT116_4_M13	-----CCTGGGGGTCTCCAAGGGCACATGCGGGTGGGCATACTGGA	163
DOCK3_reference	AGGTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCCCCAGC	211
Hec1B_4_T7	AGGTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCCCCAGC	197
Hec59_4_T7	AGGTCATTACTCCCTACACTTTGACGCCGTCCACCACCCTCTGGGTGATACCCCCCAGC	200
HCT116_4_T7	AGGTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCC--CCAGC	199
Hec1B_4_M13	ATGTAATTAGCCCGG-AGCCTAAAGCCCTTCCACCACCCTCTGGGTGATACCCCCCAGC	157
Hec59_4_M13	ATGTCATTACTCCCTACACTTTGACGCCTTCCACCACCCTCTGGGTGATACCCCCCAGC	239
	* *           ****   *   * * * *   *   * * *	
HCT116_4_M13	CGTGTCCGACACAAGCACTGGCAGAGTCATATATGGCTC-----CCAGAGGGTA	212
DOCK3_reference	CCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTG	271
Hec1B_4_T7	CCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTG	257
Hec59_4_T7	CCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTG	260
HCT116_4_T7	CCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTG	259
Hec1B_4_M13	CCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTG	217
Hec59_4_M13	CCTCCCTGCCCGGACCCTGCGCAAGGTAATGTAAGCGGCAGCCCCACCAGGCTGTG	299
	* * * * *   * *   ****   * * * * *   *                   ****   **	

**Conclusion: HCT116 has MS-related deletion**

**GRIK2 MS locus analysis:**

>GRIK2\_reference

ATAGCAATTCTTCAGCTGCAAGAGGAAGGCAAACCTGCATATGATGAAGGAGAAATGGTGGAGGGGCAA  
 TGTTGCCAGAAAGAGGAGAGCAAAGAGGCCAGTGCCCTGGGGGTTTCAAGATATTGGTGGCATCTTCA

TTGTTCTGGCAGCCGGCTTGGTGCTTTCAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAAAA  
AAACGCTCAATTGAAAAGGTAATGTTACTTGTTCAGTTTAAATTTAAAACAATTTTTGTTGTTACAAT  
AAAACACAAACCAAAGAGTTTTTATGTTACCACTAATGATAATGCATAGAACTATTGCTCTAAATTGT  
CTTATGTCATTCATTACATAACAAAATATTATATTTTGTGAAATTTACAGAAA

>LoVo\_ GRIK2\_T7

GCGGGCTGACAAGTCTTCAGCTGCAGAGGAGGCAAACCTGCATATGATGAAGGAGAAATGGTGGAGG  
GGCAATGGTTGCCAGAAGAGGAGAGCAAAGAGGCCAGTGCCTGGGGTTT CAGAATATTGGTGGCA  
TCTTCATTGTTCTGGCAGCCGGCTTGGTGCTTTCAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCC  
AAAAAAAACGCTCAATTGAAAAGGTAATGTTACTTGTTCAGTTTAAATTTAAAACAATTTTTGTTGTT  
ACAATAAACACAAACCAAAGAGTTTTTATGTTACCACTAATGATAATGCATAGAACTATTGCTCTAA  
ATTGCTTATGTCATTCCTATAGTGTACCTAAATGTCATAGCTGTTCCGAAAGGAG

>LoVo\_ GRIK2\_M13

AGAAGACTCATCATTGGGTGTAAAACGACGGCCACAATTCTTCAGCTGCAAGAGGAAGGCCAACTGCAT  
ATGATAAGGAGAAATGGTGGAGGGGCAATGGTTGCCAGAAGAGGAGAGCAAAGAGGCCAGTGCCT  
GGGGTTT CAGAATATTGGTGGCATCTTCATTGTTCTGGCAGCCGGCTTGGTGCTTTCAGTTTTTGTGGCA  
GTGGGAGAATTTTTATACAAATCCAAAAAAAACGCTCAATTGAAAAGGTAATGTTACTTGTTCCTTGC  
CTCATTATATAAAACAATTTTTGTTGTTACAATAAACACAAAGGAGAATTTTTATGTTACCACTAATTG  
ATAATGCATAGAACTATTTGCTCTTAAATTGTCCTTGTCTTGCCATACCGGTTTCG

>Hec1B\_ GRIK2\_T7

ACCCACTGGCCAATTCTTCAGCTGCAGAGGAGGCCAACTGCATATGATGAAGGAGAAATGGTGGAGGGG  
CAATGGTTGCCAGAAGAGGAAAGCAAAGAGGCCAGTGCCTGGGGTTT CAGAATATTGGTGGCATCT  
TCATTGTTCTGGCAGCCGGCTTGGTGCTTTCAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA  
AAAAACGCTCAATTGAAAAGGTAATGTTACTTGTTCAGTTTAAATTTAAAACAATTTTTGTTGTTACA  
ATAAAACACAAACCAAAGAATTTTTATGTTACCACTAATGATAATGCATAAACTATTGCTCTAAATTG  
TCTTATGTCATTCCTATAGTGTACCTAAATGTCATAACTGTTTCCTGGAGGA

>Hec1B\_ GRIK2\_M13

TTTTTATTTTTGACCACTATAGGGTGTAAAACGACGGCCACAATTCTTCAGCTGCAAGAGGAAGGCCAAA  
CTGCATTTGATGAAGGAGAAATGGTGGAGGGGCAATGGTTGCCAGAAGAGGAAAGCAAAGAGGCCA  
GTGCCCGGGGGTTT CAGAATATTGGTGGCATTTTTATTGTTCTGGCAGCCGGCTTGGTGCTTTCAGTTTT  
TGTGGCAGTGGGAGAATTTTTATACAAATCCAAAAAAAACGCTCAATTGAAAAGGTAATGTTACTTGT  
TTCAGTTTAAATTTAAAACAATTTTTGTTGTTACAATAAACACAAACCAAAGAGTTTTTATGTTACCAA  
CTAATGATAATGCATAGAACTATTGCTCTAAATTGCTTAGGGCATCCCTTTAGTGCC

>Hec59\_ GRIK2\_T7

AAAATCGTACAAAATTTCTTTCGGCTGCAAGAGGAGGCCAACTGCATATGATGAAGGAGAAATGGTGG  
AGGGGCAATGGTTGCCAGAAGAGGAAAGCAAAGAGGCCAGTGCCTGGGGTTT CAGAATATTGGTG  
GCATCTTCATTGTTCTGGCAGCCGGCTTGGTGCTTTCAGTTTTTGTGGCAGTGGGAGAATTTTTATACAA  
ATCCAAAAAAAACGCTCAATTGAAAAGGTAATGTTACTTGTTCATTTTAAATTTAAAACAATTTTTGT  
TGTTACAATAAACACAAACCAAAGAGTTTTTATGTTACCACTAATGATAATGCATAAACTATTGCTC  
TAAATTGCTTATGTCATTCCTATAGTGCCACCTAATTGCTTACCTGTTCCGGAAGAA

>Hec59\_ GRIK2\_M13

TTTTTATACGACTCACTATAGGGTGTAAAAGAAGGCCACAATTTTTTAGGTGCAAGAGGAAGGCCAAA  
TGCATTTGATGAAGGAGAAATGGTGGAGGGGCAATGGTTGCCAGAAGAGGAAAGCAAAGAGGCCAG  
TGCCCTGGGGTTT CAGAATATTGGTGGCATTTTTATTGTTTGGCCGCGGCTTGGTGCTTTCAGTTTTTGT  
TGGCAGTGGGAGAATTTTTATACAAATCCAAAAAAAACGCTCAATTGAAAAGGTAATGTTACTTGT

CAGTTTAAATTTAAAACAATTTTTGTTGTTACAATAAAACACAAACCAAAGAGTTTTTATGTTACCAACT  
AATGATAATGCATAGAACTATTGCTCTAAATTGCTTAGTCATCGCCTTAACCCC

>HCT116\_GRIK2\_T7

GCCACTGGCCATTCTTCAGCTGCAGAGGAGGCAAACCTGCATATGATGAAGGAGAAATGGTGGAGGGGC  
AATGGTTGCCAGAAGAGGAAAGCAAAGAGGCCAGTGCCCTGGGGGTTTCCAGAATATTGGTGGCATCTT  
CATTGTTCTGGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAAA  
AAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAATTTTTGTTGTTACA  
ATAAAACACAAACCAAAGAGTTTTTATGTTACCAACTAATGATAATGCATAGAACTATTGCTCTAAATT  
GTCTTATGTCATTCTATAGTGTACCTAAATGTCATACTGTTTTCTGAAAAA

>HCT116\_GRIK2\_M13

TTTTTATAACGAACACTATAGGGTGTAAAACGACGGCCACAATTCTTCAGCTGCAAGAGGAAGGCAA  
ACTGCATATGATGAAGGAGAAATGGTGGAGGGGCAATGGTTGCCAGAAGAGGAAAGCAAAGAGGCC  
AGTGCCCTGGGGGTTTCCAGAATATTGGTGGCATCTTCATTGTTCTGGCAGCCGGCTTGGTGCTTTAGTTT  
TTGTGGCAGTGGGAGAATTTTTATACAAATCCAAAAAAACGCTCAATTGAAAAAGGTAAATGTTACTT  
GTTTCAGTTTAAATTTAAAACAATTTTTGTTGTTACAATAAAACACAAACCAAAGAGTTTTTATGTTACC  
AACTAATGATAATGCATAGAACTATGCTCTAAATGTCTTAGGCATGCGTGTTGGCG

### Alignment\_result\_GRIK2\_MS\_region:

LoVo_5_M13	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	232
Hec59_5_M13	GGCCGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	238
Hec1B_5_M13	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	240
HCT116_5_M13	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	240
GRIK2_reference	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	203
Hec59_5_T7	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	211
Hec1B_5_T7	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	206
LoVo_5_t7	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	207
HCT116_5_T7	GGCAGCCGGCTTGGTGCTTTAGTTTTTGTGGCAGTGGGAGAATTTTTATACAAATCCAA	205
	*** ****	

LoVo_5_M13	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCCTCATTATATAAAAA	292
Hec59_5_M13	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	297
Hec1B_5_M13	A-AAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	298
HCT116_5_M13	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	299
GRIK2_reference	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	262
Hec59_5_T7	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCATTTTAAATTTAAAACAAT-	270
Hec1B_5_T7	A-AAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	264
LoVo_5_t7	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	266
HCT116_5_T7	AAAAAACGCTCAATTGAAAAAGGTAAATGTTACTTGTTCAGTTTAAATTTAAAACAAT-	264
	* **** ** * * *	

### Conclusion: Hec1B has MS-related deletion

### KMT2C MS locus analysis:

>KMT2C\_reference

TCATTTAGGTCTGAGTGAGCAGAAGCCTGTGAGCAAGGAGTGTCAACATTATCTTTATTCTCATCTTTT  
TTCAGTTTCACATTTGGATTCCACCTTAGAATTTGGAGACAGTACTTCCGTTTTTACCTCATTGGTAACAG  
TGGATTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTCTTTTTTTTTGGTT  
CAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGTTCCTCATTAAACATGCTTTTC  
TTATCTCCCATGTCAAGTCTGGATCTGTATATGCAATGATATCAAACCTCCTGACCTTAAGAGGTCATC  
CAGGTTGGGATCATTAGTTTCAAATTATCTAAAGTATCCAATTC

>HCT116\_KMT2C\_T7

CCAACCTGGCAGCTGAGTGAGCAGAGCCTGTGAGCAGGAGTGTCAACATTATCTTTATTCTCATCTTTT  
TTCAGTTTCACATTTGGATTCCACCTTAGAATTTGGAGACAGTACTTCCGTTTTTACCTCATTGGTAACAG



TGGATTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCTTTTTTTTTGGTTC  
AACAAATACCCACGGATAATCTAATTTATCACCATTTGAAAGGTCTATTTCCCATTA AACAGGCTTTTTCT  
TATCTCCAGGTCAAGTTCGGAATCTGTATATGCAAGGATTTCAAACCTCTCCGGACCTTAAAAGGTCATC  
CACCTATATGGCCACCAAATTGTCAACCTTTTTCCCGGAGGCCCGTTAAACGGGGTGATTCCCTCGGGCA  
GCCAAGGGTCCGGGGTGAATCCATGGGCTAGGAATGAGAAGAG

>HCT116\_KMT2C\_M13

TCCTTTTTATAAGAATCATATTGGGGGTAAAAGAAGGCCAGGTGAGTGAGCCGAAGCCTGTGAGCAA  
GGAGGGTCAACCTTATTTTTATTTTTATCATTTTTTTCAGTTTCACATTTGGATTCCCTTAGAATTTGGA  
GACCGTAATTCCGTTTTACCTCATTGGTAACCGGGGATTTTTTTTTGTGGGAAAGTTTATTAGAGAGAA  
CCAGAGTTTTGTTTTTTGTTCTTTTTTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATT  
GGAAGGTCTAGTTCCTCATTAAACATGCTTTTTTTATCTCCCATGTCAAGTTCTGGATCGGTATATGCAAT  
GATATCAAACCTCCTGACCTAAGAGTCTCCAGCTTAGCCC

>LoVo\_KMT2C\_T7

CAGAGGAGGGCAGCTGAGTGAGCAGAGCCTGTGAGCAAGGAGTGTCAACATTATCTTTATTCTCATCAT  
TTTTTTCAGTTTCACATTTGGATTCCACCTTAGAATTTGGAGACAGTACTTCCGTTTTTACCTCATTGGTAA  
CAGTGGATTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCTTTTTTTTTGG  
TTCAACAGATACACACTGGTTATCTAACTTATCATCAATTGGAAGGGCTAGTTCCTCATTAAACATGCTTT  
TCTTATCTCCCATGTCAAGTTCTGGATCTGTATATGCAATGATATCAAACCTCCTGACCTTAAAAGTCA  
TCCAGCTATAGTGGCACCTAAATGTCATAACTGTTTCCAAGGGA

>LoVo\_KMT2C\_M13

TCCTTTTTAATAGGACTCACTATGGGGTGTAAAAGGACGGCCAGCTGAGTGAGCAGAAGCCTGTGAGC  
AAGGAGTGTCAACATTATCTTTATTTTCATCATTTTTTTCAGTTTCACATTTGGATTCCCTTAGAATTGG  
GAGCCAGTACTTCCGTTTTTACCTCATTGGTACCAGTGGATTTTTTTTTGTGGGGAATGTTTTTCAGAGAGA  
ACCAGAGTTTTGTTTTCTTGTTCTTTTTTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAA  
TTGGAAGGTCTAGTTCCTCATTAAACATGCTTTTTTTATCTCCCATGTCAAGTTCTGGATCTGTATATGCA  
ATGATATCAAACCTCCTGACCTAAGAGGTCATCCAGGCTATTCGCCCT

>Hec1B\_KMT2C\_T7

CCGGCGGCAGCTGAGTGAGCAGAGCCTGTGAGCAAGGAGTGTCAACATTATCTTTATTCTCATCATTTTT  
TTCAGTTTCACAGTTTGGATTCCACCTTAGAATTTGGAGACAGTACTTCCGTTTTTACCTCATTGGTAACA  
GTGGATTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCTTTTTTTTTGGT  
TCAACAAATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTATTCCTCATTAAACATGCTTTTC  
TTATCTCCAGGTCAAGTTCTGGATCTGTATATGCAATGATATCAAACCTCCTCCGACCTTAAAAGGTCATC  
CAGCTATAGTGTACCTAATTGTCAAAGTTTTTTCCGGAGA

>Hec1B\_KMT2C\_M13

TCCTTTTTATTTCGATTCACTATAGGGTGTAAAACGACGGCCAGGTGAGTGAGCAGAAGCCTGTGAGCA  
AGGAGTGTCAACATTATTTTTATTTTCATCATTTTTTTCAGTTTCACATTTGGATTCCACCTTAGAATTTGG  
AGACAGTAATTCCGTTTTTACCTCATTGGTAACAGTGGATTTTTTTTTGTGGTGAATGTTTATCAGAGAGAA  
CCAGAGTTTTGTTTTTTGTTCTTTTTTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAAT  
TGGAAGGTCTAGTTCCTCATTAAACATGCTTTTCTTATCTCCCATGTCAAGTTCTGGATCTGTATATGCAA  
TGATATCAAACCTCCTGACTTAAAGAGGTCATCCCATGGTAGTTGGCCCC

>Hec59\_KMT2C\_T7

CAAGTTGGCAGCTGAGTGAGCAGAGCCTGTGAGCAAGGAGTGTCAACATTATCTTTATTCTCATCATTTTT  
TTTCAGTTTCACATTTGGATTCCACCTTAGAATTTGGAGACAGTACTTCCGTTTTTACCTCATTGGTAACA  
GTGGATTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCTTTTTTTTTGGT

TCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGTTCCTCATTAAACATGCTTTT  
CTTATCTCCCATGTCAAGTTCTGGATCTGTATATGCAATGATATCAAACCTCTCCTGACCTTAAGAGGTCAT  
CCAGCTATAGTGTACCTAAATGTCATAGCTGTTTCCGAAAG

>Hec59\_KMT2C\_M13

TTTTTAATACGACCCACTATAGGGTGTAAAACGACGGCCAGCTGAGTGAGCAGAAGCCTGTGAGCAAG  
GAGTGTCAACATTATCTTTATTCTCATCATTTTTTTTCAGTTTCACATTTGGATTCCACCTTAGAATTTGGAG  
ACAGTACTTCCGTTTTTACCTCATTGGTAACAGTGGATTTTTCTGTGGTGAATGTTTATCAGAGAGAACC  
AGAGTTTTGTTTTCTTGTTCTTTTTTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTG  
GAAGGTCTAGTTCCTCATTAAACATGCTTTTCTTATCTCCCATGTCAAGTTCTGGATCTGTATATGCAATG  
ATATCAAACCTCTCCTGACCTTAAGAGGTCATCCAGCTTAGCC

**Alignment\_result\_KMT2C\_MS\_region:**

HCT116_6_T7	GATTTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTTT	203
Hec1B_6_T7	GATTTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTTT	204
LoVo_6_T7	GATTTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTTT	206
Hec59_6_T7	GATTTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTTT	204
HCT116_6_M13	GATTTTTTTTGTGGGAAAGTTTATTAGAGAGAACCAGAGTTTTGTTTTTTTGTTCCTT-	236
KMT2C_reference	GATTTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTTT	204
LoVo_6_M13	GATTTTTTTTGTGGGAAATGTTTTCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTT-	238
Hec1B_6_M13	GATTTTTTTTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTTTTGTTCCTTT	238
Hec59_6_M13	GATTTTTTCTGTGGTGAATGTTTATCAGAGAGAACCAGAGTTTTGTTTTCTTGTTCCCTTT	235

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HCT116_6_T7	-TTTTTGGTTCAACAAATACCCACGGATAATCTAATTTATCACCATTTGAAAGGTCTATT	262
Hec1B_6_T7	TTTTTGGTTCAACAAATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTATT	264
LoVo_6_T7	-TTTTTGGTTCAACAGATACACACTGGTTATCTAACTTATCATCAATTGGAAGGGCTAGT	265
Hec59_6_T7	TTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGT	264
HCT116_6_M13	TTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGT	296
KMT2C_reference	TTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGT	264
LoVo_6_M13	TTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGT	298
Hec1B_6_M13	TTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGT	298
Hec59_6_M13	TTTTTGGTTCAACAGATACACACTGATTATCTAACTTATCATCAATTGGAAGGTCTAGT	295

\*\*\*\*\* \*\* \*\* \* \* \*\*\*\*\*

**Conclusion: HCT116, LoVo have MS-related deletion**

**XYLT2 MS locus analysis:**

>XYLT2\_reference

GGAAAAGCCGCAGGAGGCTGAGCTCTAGGCAGTGCTGAGGGGCCAGCCCCACCATGCCCTCTGGGGCT  
TCCAGAGCCCTTACCCCTTGCCTCTCCCACTCCAGCAAGTCTCCAGACCCACCTTCTCGCCCGGAAG  
TTCGAGTCGACTGTGAACCAGGAGGTGCTGGAAATCCTGGACTTCCACCTGTATGGCAGCTACCCCCC  
GGCAGGCCAGCCCTCAAGGCCTACTGGGAGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAG  
TGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCCTCAGCCTGCACCATGCCGCCACTGCTGCACCCC  
CAATGGGCACCCCACTCTGCAGGTGAGACCCCTTCTGACATACAGCAGGCCCT

>HCT116\_XYLT2\_T7

ACAACCTGCAGTGTAGCGCAGAGGCTGAGCTCTGCGCAGTGCTATAGGGGCCAGCCCCACCATGCCCTCT  
GGGGCTTCCAGAGCCCTTACCCCTTGCCTCTCCCACTCCAGCAAGTCTCCAGACCCACCTTCTCGCC  
CGGAAGTTCGAGTCGACTGTGAACCAGGAGGTGCTGGAAATCCTGGACTTCCACCTGTATGGCAGCTAC  
CCCCCGGCCCGGCCCTCAGGGCCTACGGGGAAACACCTACAACCCGCCTAAGGGCCCCGTTGGG  
CTCATTGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCCTCACCCGGCACCAAGGCCCCCCCTGCTGC  
ACCCCAAGGGGCACCCCACTTCTGCAGGTAAAACCCCTTCTAACATACAGCAGGCCCTATGGTGTCCACC  
TAATTTTCAAACTTTTCCGGAAGGTATCTCAACGGGAATTAACCTTTTCGCACATCTATTGTGTCCCTTC  
CATCCACTCTGGGTTTCTTCACTTCTTAGATACGGTGTGCCTTTAAACAACACTTCTCCAGCGACAA

ACCGCACGTGGGAGATTCTAATGTCTAGTCTGTACCCTCCTGATCTGGGCACTTCTGTCCCTACTAGAGA  
CCTCCAAAGATAAGCCTTCATTGAGCATGCTGGTTTGTATCTGTCTCCTCCCTGCACAGGTGTGTGCACA  
ATTCTGCTCGCTATTGTATCCCGTACTGATCTAAAATACAGAAGCCCCTATTCCGGGCGCCGAAATGGTTA  
ATTAATTCTTTGG

>HCT116\_XYLT2\_M13

CGTGGCCGTTTTCTTGAGACAACTCCATTTTTTTGAAGGTCTTTAGAAAGCAGCATGAGGCCGAGTTTT  
ATTTTTACTATACAAATGGTGGCGAAGGTGCAGAAGTTGAACAGGGGGTCCGTTTACTTCCAGTAAAA  
GAGCTAAGTGCAGTCAGCGTAGCGGTAAGCAGGTAATACTAATAAGGTATTCTCCAATGAAAATATCC  
GTCAAGTAGTCAATAATATTAATCGTATAACTTTTTATGTTGCTATACTTTATAAGACTCAATATAGGGT  
GTAAAAAGACGGCCAGTGAAAAGCCGCAGGAGGGTGAGCTTTTGGCAGTGGTGAGGGGCCAGCCCCA  
CCATGCCCTTTGGGGGTTCCAGAGCCCTTACCCTCCTTGCCTTTTCCAATCCAGCAAGTTTCCAGACCCA  
CCTTTTTTGGCCGAAATTCGAGTTGAATGTGAACCCGGAGGTGGTGAAATCCTGGAATCCACCTGTA  
TGGCAGGTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGGAGAACACCTACGACGCGGCTGATG  
GCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCCTCAGCCTGCACCATTA  
ATACAATGCTGCACCCGGCAATGGGCACCCCACTATGGCAAGTGCAGACCCCACTGCTGACATACAGCAG  
GCCCTATAACCCC

>LoVo\_XYLT2\_T7

GAGATGGCAGTGAAGCCGCAGAGGCTGAGGACTGCGCGTGCTATAGGGTCCCGCCCCTGTTGACCTCT  
GGGGCTTCCAGAGCCCTTACCCTCCTTGCCGCTCCCACTCCAGCAAGTCTCCAGACCCACCTTCTTCGCC  
CGGAAGTTCGAGTCGACTGTGAACCAGGAGGTGCTGGAAATCCTGGACTTCCACCTGTATGGCAGCTAC  
CCCCCGGCACGCCAGCCCTCAAGGCCTACTGGGAGAACACCTACAACGCGGCTGATGGCCCCAGTGG  
GCTCAGTGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCCTCAGCCTGCACCATGCCGCCACTGCT  
GCACCCCAATGGGCACCCCACTCTGCAGGTGAGACCCCTTCTGACATACAGCAGGCCCTATAGTGTA  
CCTAAATGTCATAGCTGTTTCCTAA

>LoVo\_XYLT2\_M13

CCTCCTAATACGACTCACTATAGGGTGTAACGACGGCCAGTGAAAAGCCGCAGGAGGCTGAGCTCTA  
GGCAGTGCTGAGGGGCCAGCCCCACCATGCCCTCTGGGGCTTCCAGAGCCCTTACCCTCCTTGCCTCTC  
CCACTCCAGCAAGTCTCCAGACCCACCTTCTTCGCCCCGGAAGTTCGAGTCGACTGTGAACCAGGAGGTG  
CTGGAAATCCTGGACTTCCACCTGTATGGCAGTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGG  
GAGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTTACACAGCC  
TTCGCCCCCTCAGCCTGCACCATTAATACGATGCTGCACTCGGCAGTAAACACCCCAACAGGCAAAAG  
CCACCCAGTCTGACATACAGCAGGCCGGGTAGCCCT

>Hec1B\_XYLT2\_T7

GCAACGGCAGTGAAGCGCAGAGGCTGAGGACTGCGCGCGCTATAGGGGCCCGCCCCTGTCGACCTCTG  
GGGCTTCAAGAGCCCTTACCCTCCTTGCCTCTCCCACTCCAGCAAGTCTCCAGACCCACCTTCTTCGCCC  
GGAAGTTCGAGTCGACTGTGAACCAGGAGGTGCTGGAAATCCTGGACTTCCACCTGTATGGCAGCTACC  
CCCCCGGCACGCCGCCCTCAAGGCCTACTGGGAGAACACCTACAACGCGGCTGATGGCCCCAGTGGGCT  
CAGTGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCCTCAGCCTGCACCATGCCGCCACTGCTGCA  
CCCCAATGGGCACCCCACTCTGCAGGTGAGACCCCTTCTGACATACAGCAGGCCCTATAGTGTCACCT  
AAATGTCATACTGTTTCTGAAAGTTTTCTTTTGGGCTTGACTGGCTTTAAGCTGAAGCCTTCGGTGAAT  
TCCAGGGCACACTGGCCTTCTTCATCTCCTTAAAGGTTGGGGGTGTGTCGTACAGACAGTTCGGAGG  
ACCTAGGTACTTGGGTGAGATTCTTGGCCATGCTAAGGAGGCAGAGATAAGGCAGGCGAGGGGGAG

>Hec1B\_XYLT2\_M13

TCTCCAATACGACTCACTTTAGGGTGTAACGACGGCCAGTGAAAAGCCGCAGGAGGCTGAGCTCTAG  
GCAGTGCTGAGGGGCCAGCCCCACCATGCCCTCTGGGGCTTCCAGAGCCCTTCACCCTCCTTGCCCTCC  
CACTCCAGCAAGTCTCCAGACCCACCTTCTTCGCCCCGGAAGTTCGAGTCGACTGTGAACCAGGAGGTGC  
TGAAATCCTGGACTTCCACCTGTATGGCAGTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG  
AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTTACACAGCCT  
TCGCCCCGCTCAGCCTGCACCATTTAATACGATGCTGCACTAGGCAGTGGACACCCACCAGGCAAAGC  
CACCCAGTCTGACATACAGCATACCTTTAAACC

>Hec59\_XYLT2\_T7

CAGCGGCAGTGAGCCGCAGAGGCTGAGCTCTGCGCGCGCTATAGGGGCCCGCCCCACCATGCCCTCTG  
GGGCGAAAGAGCCCTTCACCCTCCTTGCCCTCCCACTCCAGCAAGTCTCCAGACCCACCTTCTTCGCCCC  
GAAGTTCGAGTCGACTGTGAACCAGGAGGTGCTGGAAATCCTGGACTTCCACCTGTACGGCAGCTACCC  
CCCCGGCACGCCAGCCCTCAAGGCCTACTGGGAGAACACCTACGACGCGGCTGATGGCCCCAGTGGGC  
TCAGTGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCGCTCAGCCTGCACCATGCCGCCACTGCTGC  
ACCCCCAATGGGCACCCCACTCTGCAGGTGAGACCCCTTCTGACATACAGCAGGCCCTATAGTGTCCACC  
TAAATGTCATAGCTGTTCCGGGAATTTTTGTGGGAGGGAAAGTGAGGATGTAGGCACGAAGCAGTGT  
GTCGTTCTGCCTCTCTGACGTTGCTTGTTCCTTTAAAAGGGAGAAGTATTATGGATGAGAGACTTC  
GAAAGACAATCCACTTGGCTGAAATTAGATGGTGTGGACTGGGGCTCCTAATCTGTTGAACTTTTGTACA  
ACT

>Hec59\_XYLT2\_M13

AGAAATCTTGAACCTGGAGGGCTCGAGTGCCAATTATCTGTTAATAAACCTATTCACTCCATACTTGTCT  
ACAGAGTGAGAGTCTCTGTGAAAAGCTAAAAAGAACCAAAAGAACCTGTCCATTTCTCACTTAGATAG  
AAAAACACTCCGTGTGTCTCAGTTTTTTTTACAAGCTTCTTGAGACCGTTACAATTGTTTTAAATCACAAG  
GGGTTGGGAAAATCAGCAATCTAAAGATGGGGGATCAGAGATTCACCAAAGAGTAAAAACAAGTAT  
TCAAGGTCACCGGAACGAAAAAATTCTATTACGGCAAACCCTCCATTGAAACGACATTTTGTGCCCAAA  
CAAAAAAAAAACAAAAGAACCTGGGGAGGCAGCTTTAATACGACTCACTATAGGGTGTAACGACGG  
CCAGTGAAAAGCCGCAGGAGGCTGAGCTCTAGGCAGTGCTGAGGGGCCAGCCCCACCATGCCCTCTGG  
GGCTCCAGAGCCCTTCACCCTCCTTGCCCTCCCACTCCAGCAAGTCTCCAGACCCACCTTCTTCGCCCCG  
GAAGTTCGAGTCGACTGTGAACCCGGAGGTGCTGGAAATCCTGGACTTCCACCTGTACGGCAGCTACCC  
CCCCGGCACGCCAGCCCTCAAGGCCTACTGGGAGAACACCTACGACGCGGCTGATGGCCCCAGTGGGC  
TCAGTGATGTCATGCTCACTGCTTACACAGCCTTCGCCCCGCTCAGCCTGCACCATTTAATACGATGCTGC  
ACCCGGCAGTGGGCACCCACCAGGAAAAGAGACCCCACTGCTGACATACAGCAGCCGATAGCC

**Alignment\_result\_KMT2C\_MS\_region:**

HCT116_9_T7	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	183
HCT116_9_M13	GACCCACCTTTTTTTCGCCCGAAATTCGAGTTGAATGTGAACCCGAGGTGGTGGAAATCC	471
Hec59_9_M13	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCGAGGTGCTGGAAATCC	597
LoVo_9_M13	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	218
Hec1B_9_M13	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	217
LoVo_9_T7	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	182
Hec1B_9_T7	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	181
XYLT2_reference	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	176
Hec59_9_T7	GACCCACCTTCTTCGCCCGGAAGTTCGAGTCGACTGTGAACCCAGGAGGTGCTGGAAATCC	180
	***** ** ***** ***** ** ***** ***** ***** *****	
HCT116_9_T7	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCCCGCCCTCAGGGCTACGGGG	243
HCT116_9_M13	TGGAAATCCACCTGTATGGCAGGTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	531
Hec59_9_M13	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	657
LoVo_9_M13	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	278
Hec1B_9_M13	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	277
LoVo_9_T7	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	242
Hec1B_9_T7	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCACGC-CGCCCTCAAGGCCTACTGGG	240
XYLT2_reference	TGGACTTCCACCTGTATGGCAGCTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	236
Hec59_9_T7	TGGACTTCCACCTGTACGGCAGCTACCCCCCGGCACGCCAGCCCTCAAGGCCTACTGGG	240
	*** ***** ***** ***** * * ***** ***** **	
HCT116_9_T7	AAAACACCTACAACCCGCTAAGGGCCCCGTTGGGCTCATTGATGTCATGCTCACTGCTT	303
HCT116_9_M13	AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	591
Hec59_9_M13	AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	717
LoVo_9_M13	AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	338
Hec1B_9_M13	AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	337
LoVo_9_T7	AGAACACCTACAACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	302
Hec1B_9_T7	AGAACACCTACAACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	300
XYLT2_reference	AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	296
Hec59_9_T7	AGAACACCTACGACGCGGCTGATGGCCCCAGTGGGCTCAGTGATGTCATGCTCACTGCTT	300
	* ***** ** ** * ***** ***** ***** *****	

## Conclusion: HCT116 has MS-related deletion

### COBLL1 MS locus analysis:

>COBLL1\_reference

TCATCAGTTTTTCAACAAGGGGTTGTGGAACAGAGTGAGGCATTTTACTTAAGGGAGAAAGAGTCTGC  
TCCGGAGAAGGCAGCATATCCCTTCTGCCTCTTTATTTGTCAGTTCTTTGGAGCAGGATTAGGGGCAG  
CATGGACACTCTTGGCAGCTGCAGATGTCACATAGTGACCCGATACTCTTCTGCATCTGCAAAAAAA  
AGAGCTGGGTTTGGCCTGGGCATTTGAAGCCCGAGATTTAAATTTTGATTCCAAAATATTGTTTATTTCTT  
CCAAATTTGGTGCAAAAGGAGCTGTGCCAGTGTCTTGTCAATTTGGGAGCAGGTTTCAGAGGACTAA  
CCATGGCATCATCAGGTGAGCTCACAGAACTGGGCACTTGATGCTCTGTTCT

>LoVo\_COBLL1\_T7

ACAGCGCAATGTACAGTTTGAAGTCAGGAGGATTTAAGGACAATGATGCTAGTGTTACTTTTCTGACT  
TTTCTGGACCTGGAGATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTTGAAG  
ACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTGT  
AAGTTATCCAGTTAGCTTTTCAATTTGAAATTTCAATAAAACACTTTTTCAGAGGAATTATTTATCTCTGCAC  
ATTTCTCTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTACACAGGATATTCTAGAGTTCTAGAGGCT  
GTGTCACCTAAATGTCATAGCTGTTTCTAAAGAA

>LoVo\_COBLL1\_M13

TTCCCTTTAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAGTCAGGAGGA  
TTTTAATGAAAATGATTTATTTACTTTTCTACTTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGA  
GGAGGAAATTGGCCAGCATCCATCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCC  
TGTTTTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCAATTTGAAATTTCAATAA

AACACTTTTCAGAGGAATTATTTTTATTTGCACTCTTCTCTTTGTTTAAACAGGTATTTTAGGAAGCTGATCG  
TCAACTCAGGATATTCTAGATTTTCAGAGGGTATCCTC

>Hec1B\_COBLL1\_T7

ACCGGCGGCAGTGTACAGTTTGAGTCAGGAGATATCTATAATGTTTCATATGAAGTGTCTATTGTTCACTC  
TTTCTGACTTTTCTGGACCCGGAATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATC  
TCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGGCCTGTTTTAAGAGATTATTGGCAGAA  
ACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACACTTTTCAGAGGAATTATTTA  
TCTCTGCACATTTCTTTCTTCTGCAAGTATTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTC  
TAGAGGCTGTGTCACCTAAATGTCATAGCTGTTTCCTGGGAGAA

>Hec1B\_COBLL1\_M13

TCTCCTTTAATACGATTTTTATAGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATT  
TTAATGAAAATGATTTATTTTACTTTTCTTACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAG  
GAGGAAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGGCCT  
GTTTTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAA  
ACACTTTTCAGAGGAATTATTTTATTTGGACTCTTCTTTGGTGTAAAGATGGCTCAGTGAACCTGATCT  
TCAACTCAGGATATTCTAGATTCCCGGCGTCTAACCCC

>Hec59\_COBLL1\_T7

CCAGAAGCCCTTAACCGGGGGGGGGCTGAAGAGTGTTTAAAGTTCAAGAGTTATTTGCCTTTTCTGACT  
TTTCAGGAAAGAAAAGGATTCTGTGGCCGTTTTAGGAGAAATTTCCAGCATCCATCTCTTGAAGACCTG  
CCAGAAGGTGTTGGGCATAAAAAAATAGGCCTGGGTTTGGAGATTTTGGCGAAAACCTGCTGGAAGTT  
ATCCAATAGCGGTTCAATTTGAAATCCAATCAAGAACTTTTCAGAGGAATTATTTATCTCTGCACATTTCTC  
TTTCTTCTGCAAGTATTTTCTGTAATGTGATCTTCACACAGGATATTATAGAGTTCTAGGGGCTGTGTCAC  
CTAAATGTCAGGGCTGTTTTAATAGT

>Hec59\_COBLL1\_M13

TCTTTTTAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATT  
TAATGAAAATGATTTATTTTACTTTTCTTACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGG  
AGGAAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGT  
TTTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAAC  
ACTTTTCAGAGGAATTATCTTCTTTGCACATTTCTTTGTTCTACAAGTATTTTCAGGAAGCTGTGCGAACT  
ACAGGATTTCCAGATTCCATTTCCCA

>HCT116\_COBLL1\_T7

ACCGGGGCAGTGTACAGTTTGAGTCAGGAGATATCTTAAGGTCTATGAGGCTAGTGTTACCTTTCTGA  
CTTTTCTGGATCCGTAGATGAATACATGTTGCCATTTGAGGAGGAAATTGGCCAGCATCCATCTCTTGA  
GACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTTTTAAGAGATTATTGGCAGAAACATGCTG  
TAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAACACTTTTCAGAGGAATTATTTATCTCTGCAC  
ATTTCTCTTTCTTCTGCAAGTATTTTCTGGAAGGTGATCTTCACACAGGATATTCTAGAGTTCTAGAGGCT  
GTGTCACCTAAATGTCATAGCTGTTTCCTAAAGA

>HCT116\_COBLL1\_M13

CTTTTTAATACGACTCACTATAGGGTGTAAACGACGGCCAGTGTACCAGTTTGAAAGTCAGGAGGATTT  
AATGAAAATGATTTATTTTACTTTTCTTACTTTTCAGGACCTGTAGATGAATACATGTTGCCATTTGAGGA  
GGAAATTGGCCAGCATCCATCTCTTGAAGACATGCAGGAAGTTGTTGTGCATAAAAAAAGAGGCCTGTT  
TTAAGAGATTATTGGCAGAAACATGCTGTAAGTTATCCAGTTAGCTTTTCATTTGAAATTCCAATAAAAC  
ACTTTTCAGAGGAATTATTTTATTAGGACTCTTCTATTTGGTGTAAACAGATGGCTCAGTGAACGCAGATC  
TGACAACTCAGGATATCTAGAGTCAGAGGGTAGCCCT

**Alignment\_result\_COBLL1\_MS\_region:**

COBLL1_reference	GTCACATAGTGACCCGATACTCTTCTGCATCTGCAAAAAAAAAAGAGCTGGGTTTGGCC	225
Hec59_3_T7	CTCTTGAAGACCTGCCAGAAGTGTGGGCATA-----AAAAAATAGGCC-TGGGTTTGG	179
Hec1B_3_T7	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAAAAGAGGCCTGTTTTAAG	194
LoVo_3_T7	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAA-AAGAGGCCTGTTTTAAG	184
HCT116_3_T7	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAA-AAGAGGCCTGTTTTAAG	185
Hec1B_3_M13	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAAAAGAGGCCTGTTTTAAG	218
HCT116_3_M13	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAA-AAGAGGCCTGTTTTAAG	215
LoVo_3_M13	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAA-AAGAGGCCTGTTTTAAG	218
Hec59_3_M13	CTCTTGAAGACATGCAGGAAGTGTGTGCATA-----AAAA-AAGAGGCCTGTTTTAAG	216
	**    **    *    *    *    **    ****    **** *    *    *    *	

**Conclusion: LoVo, HCT116, Hec59 has MS-related deletion.**

**ZBTB20\_MS locus analysis:**

>ZBTB20\_reference

TTTTTTGTTGTTGTTTTGTTTGTTCATAAGAAAGAGAGAAAGATACTACTTATCCGTCAGACACATGCAT  
CCTCATGTGGTCGTTGAACTGCTCGATTTGGTCAAACCTTGGCTGGGCAGACGGAGCAGACGTAAGTGGT  
CCCCTCCGTGCAGGCCACCACGCCTGGGGGGCCAGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGG  
GTCCCATTGCTGGCACTGTGCAGGGCCACGTGTGCTCCAGGAGGGTCTTGTGAGAGAACTTCTTTTTG  
CAGATGTAGCACTCGTAGGACTTCTCTCCCCGGTGGAGGCGCATGTGCACGTTGAGGGAGCTCTTCTGG  
GTGAAGCGCTTGTTCAGATACTACTGGTATGCCCTCACTCCTGTGTGTGTGCAC

>HCT116\_ZBTB20\_T7

ACGGCTAGAAGTCTACTTATCCGTCAGTACACATTGCTATTCGCTCATAGTGGTCGTTGAACTGCTCAGA  
TTTGTGTCAGGCTTTGCTGGGCAGACGGAGCAGACGTAAGTGGTCCCCTCCGTGCAGGCCACCACGCCT  
GGGGGGCCAGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAGGG  
CCACGTGTGCTCCAGGAGGGTCTTGTGAGAGAACTTCTTTTTGCAGATGTAGCACTCGTAGGACTTCTC  
TCCCCGGTGGAGGCGCATGTGCACGTTGAGGGAGCTCTTCTGGGTGAAGCGCTTGTTCAGATACTACA  
CTGGTATGCCCTCACTCCTGTGTGTGCTATAGTGTACCTAAATGTCATACTTGTTCCTGAA

>HCT116\_ZBTB20\_M13

TTTAATACGACTCACTATAGGGTGTAAAACGACGAGAGAAAGATACTACTTATCCGTCAGACACATGCAT  
CCTCATGTGGTCGTTGAACTGCTCGATTTGGTCAAACCTTGGCTGGGCAGACGGAGCAGACGTAAGTGGT  
CCCCTCCGTGCAGGCCACCACGCCTGGGGGGCCAGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGG  
GTCCCATTGCTGGCACTGTGCAGGGCCACGTGTGCTCCAGGAGGGTCTTGTGAGAGAACTTCTTTTTG  
CAGATGTAGCACTCGTAGGACTTCTCTCCCCGGTGGAGGCGCATGTGCACGTTTGTGGGAGCTCTTCATG  
GGGAAGACAAATTGATCGCAGGTAATACACTGGTATGCCCTCACTCCTGGTGCCTTAGCCTG

>LoVo\_ZBTB20\_T7

ACAATAAGAGAGGTCTACTTATCCGTCAGTACACAGTTGCTATTCGCTCATAGTGGTCGTTGAACTGCT  
CGATTTGTGTCAGGCTTTGCTGGGCAGACGGAGCAGACGTAAGTGGTCCCCTCCGTGCAGGCCACCACG  
CCTGGGGGGCCAGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCA  
GGGCCACGTGTGCTCCAGGAGGGTCTTGTGAGAGAACTTCTTTTTGCAGATGTAGCACTCGTAGGACT  
TCTCTCCCCGGTGGAGGCGCATGTGCACGTTGAGGGAGCTCTTCTGGGTGAAGCGCTTGTTCAGATA  
TACTGGTATGCCCTCACTCCTGTGTGTGCTATAGTGTACCTAAATGTCATAGCTGTTTCCTGGG

>LoVo\_ZBTB20\_M13

AAACCGGGACTCACTTAGGGTTAAAATGACGAGAGAAAGATAGTACTTATCCGTCAGACACATGCATCC  
TCATGTGGTCGTTGAACTGCTCGATTTGGTCAAACCTTGGCTGGGCAGACGGAGCAGACGTAAGTGGTCC  
CCTCCGTGCAGGCCACCACGCCTGGGGGGCCAGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGGT  
CCCATTGCTGGCACTGTGCAGGGCCACGTGTGCTCCAGGAGGGTCTTGTGAGAGAACTTCTTTTTGCA

GATGTAGCACTCGTAGGACTTCTCTCCCCGGTGGAGGCGCATGTGCATTTTGAGGGAGCTTCTGGGT  
GAAGCGCTTGTTGACATACTACTGGTATGCCCTCACTCTCTGGTTGGCTATTAACC

>Hec1B\_ZBTB20\_T7

ACCACCAAAGGAGGTCTACTTATCCGTCAGTACACAGTGCTATTCGCTCATAGTGGTTCGTTGAACTGCTC  
GATTTGTTTACAGGCTTTGCTGGGCAGACGGAGCAGACGTAAGTGGTCCCCTCCGTCAGGGCCACCATGCC  
TGGGGGGCCAGCGCGGGGACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAAGG  
CCACGTGTCCCTCCCGGAAGGTCTTGTGAAAAAATCTTTTTGCAGATGTAACACTCCTAAGAATTCTCT  
CCCCGGTGGAAAGCGCATGTGCACGTTGAAGGAATCTTCTGGGTGAAACGCTTGTTGCAAATACTACAC  
TGGTATGCCCTCACTCCTGTGTGTCTATAATGGTACCTTCTTCGGGGGTGTTTACCGGCCGA

>Hec1B\_ZBTB20\_M13

TATTAGGATTCATTATAGGGTGTAAAAGGAGGAGAGAAAGATATTATTTTCCTTCAGACACATGCATCT  
TCATGTGGTCGTTGAATTGTTGGATTGGTCAAACTTTCTGGGCAGACGGAGCAGACGTAAGTGTTC  
CTTCCGTGCAGGCCACCATCCCTGGGGGGCCAGCGGGGGACCCGGGGGGTGTGCCTCCAGGGGGGTCTC  
CCATTGCTGGCACTGTGCAGGGCCACGTGTCCCTCCAGGAGGGTCTTGTGAGAGAACTTCTTTTTGCAG  
ATGTAGCACTCGTAGGACTTCTCTCCCCGGTGGAGGCGCATGTGCACGTTGAGGGAGCTTCTGGGGG  
AAGCAAATTGTCGAGATAATACTGGTATCCCTCACTCCTGTGTTGCCATAATC

>Hec59\_ZBTB20\_T7

GGAATCTTGGAGAGATCTACTTATCCGTCAGTACACATTGCTATTCGCTCATTAGTGGTCGTTAGA  
GCATCAGATTTGTGTCAAAGCATTGCTGGGCAGACGGAGCAGACGTAAGTGGTCCCCTCCGTCAGGG  
CACCACGCCTGGGGGGCCAGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGGTCCCTTGGTGGGAC  
TGGGGCAGGGCCCCTTGCCTTCCGGAAGGGCCTGGGAAAAAATTTCTTTTTGCAAATTTACCATCTA  
AGAATTTCTCCCCCGGGGAAGGCCAGTCCCCTTTAAGGAACCTTCTCCGGGTTAAACCCTTGGTGGCA  
AATCCAACCCGGGAAGGCCCCCATCCCGGGGGGGGCAAATGCCCCCAAATGGTCAAAGTGTTCCTCC  
GGAAA

**Alignment\_result\_ZBTB20\_MS\_region:**

Hec59_10_T7	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCCTTGGTGGGACTGGGGCAGGGC	217
Hec1B_10_T7	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGG-GGTCCCATTGCTGGCACTGTGCAAGGC	207
Hct116_10_T7	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAAGGC	207
LoVo_10_T7	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAAGGC	210
Hec1B_10_M13	AGCGGGGGCACCCGGGGGTGTGCCTCCAG-GGGGTCCCATTGCTGGCACTGTGCAAGGC	229
Hct116_10_M13	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAAGGC	232
ZBTB20_reference	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAAGGC	233
LoVo_10_M13	AGCGCGGGCACCTGGGGGTGTGCCTGCAGGGGGGTCCCATTGCTGGCACTGTGCAAGGC	229
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**Conclusion: Hec59B and Hec1B have MS-related deletion**

**BMPR2\_MS locus analysis:**

>BMPR2\_reference

TCATAAATGTACGTTCTCAATGTGATACTTTTTTCTTTCTTTAAGCAACCTGTCACATAATAGGCGTGTGC  
CAAAAATTGGTCCTTATCCAGATTATTCTTCTCCTCATAATTGAAGACTCTATCCATCATACTGACAGC  
ATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGGGAAAAAACCGAA  
ATTCAATTAATACTATGAACGACAGCAAGCAAGCTCGAATCCCCAGCCCTGAAACAAGTGTACCCAGCCT  
CTCCACCAACAACAACCACAAACACCACAGGACTCACGCCAAGTACTGGCATGACTACTATATCTGAG  
ATGCCATACCAGATGAAACAAATCTGCATACCACAAATGTTGCACAG

>HCT116\_BMPR2\_T7



CCAGCTGCACTGTCCATAAGAGGCGTGTGCCAAAATTGGTCCTTATCCAGATTATTCTTCCGCCTCATACA  
TTGAAGACTCTATCCATCATACTGACAGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACA  
CCTTTGACTATAGGGGAAAAAACCAGAAATTTCAATTAATTTAAAGAACGCCAGCCCCAACCCAAACCC  
CCGCCCTGGAACCAAGTTGCCCCACCTCCCCCAACCCCAACCCCAACCCCAACCCCAACCCCAAGGATCCAGGCC  
AGGAATGGCCTGGCCACCAATTTCTAAAATGCCTAACCCGAATAAACCAATTTTCCAAACCAAAAAGGTG  
CCAAACTTTTGTGGCCCCAAATTTTCACTTTTTTTTCTGGGACTAAAGCGTGGCAGCTTAGATCGCAGCA  
TAGAGGCAGGTATACAGGGAACCTTAACAGAAGGGGGGGGGTGGGAGAG

>HCT116\_ Bmpr2\_M13

ATGTCCTGTGTGCAGAGAGGTAGATGTTACGCAGCATTATCTAGATACAATTGTCATGCGCTCACGACT  
ATCCAGCATTACCGCTTGCCAAGCCAGAAGGCACCATGACCTCATACATGCGTCATTGGCAGACCAT  
CTTCACGAAGCTGCCTTCATAGGGGCAGTGCTGACCACTTTTTTATTTGACCAACAATGGGGTAAAAAG  
GCGGCCCCACCTGTTAACTTATTGGGGGGGGGCAAAAATTGTCCTTATTCCGGATAATTTTTCTTCTTCT  
ACCATGAAGGATTTTTTCTTATTATGGAAGGATTGGGAAGGATTATTTCTTTGAACCTTTTAAAGTTCAAC  
AAACCTTTGAATATTGGGGAAAAAACCAGAAATTCATTAACTATGAACGACAGCAAGCACAAGCTCGA  
ATCCCCAGCCCTGAAACAAGTGTACCAGCCTCTCCACCAACACAACAACCACAAACACCACAGGACTCA  
CGCCAAGTACTGGCATGACTATTATATCTGAGATGCCATACCCAGATGAAACAAATCTGCATACCACAAA  
TGTGCACAGCTAGCCC

>LoVo\_ Bmpr2\_T7

ACGGCCTGCCACTGTCCATAATAGGCGTGTGCCAAAATTGGTCCTTATCCAGATTATTCTTCTCCTCAT  
ACATTGAAGACTCTATCCATCATACTGACAGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGC  
ACACCTTTGACTATAGGGGAAAAAACCAGAAATTTCAATTAATAAAGAACGCCAGCCCCAACCCAAA  
CCCCCGCCCTGGAACCAAGTGGTCACCGCCCCCTCCCCACCCACCACCCCAACCCCAAGGATTCAG  
CCCAGTTATGGGCTGGACAACAATTTTTAAAAGGCCTAACCCGAATAAACCAATTCTCCAAACAAAAAG  
GTGGCAAACTTTTGTGGCCACCAATGTTCAAACCTTTTTTCCGGGAA

>Hec1B\_ Bmpr2\_T7

ACACAATTGCCACCTGTCACATATGATGCACAGTGCCAAATAGTTCGCGCTCACTTATTCCAGATTATTCT  
TCCGCCTCATACATTGAAGACTCTATCCATCATACTGACAGCATCGTGAAGAATATTTCTCTGAGCATTCT  
TATGTCCAGCACACCTTTGACTATAGGGGAAAAAACCAGAAATTCATTAACTATGAACGACAGCAAGC  
ACAAGCTCGAATCCCAGCCCTGAAACAAGTGTACCAGCCTCTCCACCAACACAACAACCACAAACACC  
ACAGGACTCACGCCAAGTACTGGCATGACTACTATATCTGAGATGCCATACCCAGATGAAACAAATCTG  
CATACCACAAATGTTGCACAGCTATAGTGTACCTAAATGTCATACCTGTTTTCCGAGAA

>Hec1B\_ Bmpr2\_M13

TTCCTTTCTCCCGCATCACTATAGGGTGTAACGACGGCCCAACCTGTACATAATAGGCGTGTGCC  
AAAAATTGGTCCTTATCCAGATTATTCTTCTCCTCATACATTGAAGACTCTATCCATCATACTGACAGCAT  
CGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGGGAAAAAACCAGAAAT  
TCAATTAACTATGAACGACAGCAAGCACAAGCTCGAATCCCAGCCCTGAAACAAGTGTACCAGCCTCT  
CCACCAACACAACAACCACAAACACCACAGGACTCACGCCAAGTACTGGCATGACTTTTATATGTGAGAT  
GCCATACCCAGATGAAACAAATCTGCATACCACAAATGTGCACCACGCAATAACCCCC

>Hec59\_ Bmpr2\_T7

GGGGGGTGGCCACTGTCAATAAGAGGCGTGTGCCAAAATTGGTCCTTATCCAGATTATTCTTCTCCTCCTC  
ATACATTGAAGACTCTATCCATCATACTGACAGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCA  
GCACACCTTTGACTATAGGGGAAAAAACCAGAAATTCATTAACTATGAACGACAGCAAGCACAAGCTC  
GAATCCCAGCCCTGAAACAAGTGTACCAGCCTCTCCACCAACACAACAACCACAAACACCACAGGACT

CACGCCAAGTACTGGCATGACTACTATATCTGAGATGCCATACCCAGATGAAACAAATCTGCATACCACA  
AATGTTGCACAGCTATAGTGTACCTAAATGTCATACCTGTTTTCTAAGA

>Hec59\_BMP2\_M13

CACGCCAAGAGGAACCCGCCAGGGGTCGACCAAGTGGGGATGGTCCCCTGCTGGCAGAGAGGGCAG  
CAGGGGGCCAGCAGCCCTCCGCAAGCACGTGTCATCAACCAAGACTCATCTGCAACGACCTGCTA  
TTCAAGTCCAGAAACGCACCCCCACCTCATATTTGGTCTCTCGCGCACAGCCCATTACAGGAAGCTGCC  
CCTCCGTGCAGCGAAATCTTTTTTAATACGACTCACTATAGGGTGAAAACGACGGCCCAACCTGTCA  
CATAATAGGCGTGTGCCAAAAATTGGTCCTTATCCAGATTATTCTTCTCCTCATACATTGAAGACTCTAT  
CCATCATACTGACAGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAG  
GGGAAAAAACCGAAATTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGCCCTGAA  
CAAGTGTACCAGCCTCTCCACCAACACAACAACCACAACACCACAGGACTCACGCCAAGTACTGGCAT  
GACTACTATATCTGAGATGCCATACCCAGATGAAACAAATCTGCATACCACAAATGTGCACAGGCTTTAA  
CCT

### Alignment\_result\_BMP2\_MS\_region:

HCT116_11_T7	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	157
LoVo_11_T7	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	160
HCT116_11_M13	AGGATTTGGGAAGGATTATTTCTTTGAACCTTTAAGTTCAACAAACCTTTGAATATTGGG	370
Hec1B_11_T7	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	170
Hec59_11_T7	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	161
BMP2_reference	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	200
Hec1B_11_M13	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	197
Hec59_11_M13	AGCATCGTGAAGAATATTTCTCTGAGCATTCTATGTCCAGCACACCTTTGACTATAGGG	420
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HCT116_11_T7	GAAAAAACCGAAATTTCAATTAATTTAAAGAACGCCAGCCCCAACCCAAACCCCGCC	217
LoVo_11_T7	GAAAAAACCGAAATTTCAATTAATTTAAAGAACGCCAGCCCCAACCCAAACCCCGCC	220
HCT116_11_M13	GAAAAAACCGAAATTTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGC	430
Hec1B_11_T7	GAAAAAACCGAAATTTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGC	230
Hec59_11_T7	GAAAAAACCGAAATTTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGC	221
BMP2_reference	GAAAAAACCGAAATTTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGC	260
Hec1B_11_M13	GAAAAAACCGAAATTTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGC	257
Hec59_11_M13	GAAAAAACCGAAATTTCAATTAACCTATGAACGACAGCAAGCACAAGCTCGAATCCCAGC	480
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**Conclusion: HCT116 and LoVo have MS-related deletions**

### CCDC168\_MS locus analysis:

>CCDC168\_reference

GTAATGTCAGCTATGAAAAACGGTAGTAAGGGACCCCGAGAGCGACCCCAACAACCTTTTGGAGGAACT  
CCATATATTTCAAGAATTGAAATCTTTGCCACTAGGGGAATTCTGAAGTTTCTTTTCTTAAGGTTTTCAG  
GGGAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCCAAAAAAA  
AAGGGCCGTTTTTTTTTTTTCTTTTCAAGAATAGAAGTTGATATCGTCATGATGAGTTTTGATGCTGATTAT  
GTTTGCTTTGGAAACAATCCAATCTTTTCTGACTCATAATCATACACTCTTCTTTTCTGTCCAGTTTCCCTT  
GCTGTGTGTACAACCTGTAATCGTGGTCCCAATGACTGCTGTTCTTCTTAA

>HCT116\_CCDC168\_T7

ACAGTTAGTACAGCTATGATACGGTAGTAAGGGACCCCGAGAGCGACCCCAACAACCTTTTGGAGGAACT  
CCATATATTTCAAGAAGTTGAAATCTTTGCCACTAGGGGAATTCTGAAGTTTCTTTTCTTAAGGTTTTCAG  
GGGAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCCAAAAAAA  
AGGGGCGTTTTTTTTTTTTTTTTTCAAATAAAAATTATATCTCCTCGTGAAGAGTTGAGACGCATATTTGTG  
TTTGTGTTTTGAACTCCCTCTTTTGAACACTCAAACACACTCTTCTCTTTCTCTCGTTTTCCCTTTG

GTGTGTGCAACTGTGTACTCGGGCCCCCTGAGAGCGGCGCTATTGTGTCCCAATGTGTCAATGTTTTTC  
CAGGAAAGA

>HCT116\_ CCDC168\_M13

CTTTTTTTAATGAGACACAATAGGGGGTAAAAAGAGTAAAGTGTGATCTGAAAAAGGTGTTATAGGG  
GCCCCAGAGAGAGCCCCAAAAATTTGGGGGAAATCTCCATATTTACAAAAACGAAATATTTGCCCCA  
AGGGGAAATTTGAAAAATTTTTCTCTAAAGGGTCTCGGGGGGTATTCCCCAGAAAGGGGTTGGGGATA  
ACACCCACAGAGTGTGCCCTACACACGCAAAAAAAAAGGGCCGTTTTGTTTTCTTTCAGAATAGAAG  
TTGATATCGTCATGATGAGGTTTTGATGCTGATTTATGTTTGCTTTGGAAACAATCCAATCTTCTGACTC  
ATAATCATACTCTCTTCTTCTGTACGTTTCCCTTGCTGTGTGTACAACCTGTAATCGTGGTCCCAATGA  
CTGCGCTTAGCCC

>LoVo\_ CCDC168\_T7

CCAAGTATATGTCAGCTATGAAACGGTAGTAAGGGACCCCGAGAGCGACCCCACTTTTTGGAGGAA  
CTCCATATATCCAAGAAGTTGAAATCTTGGCCACTAGGGGAATTCTGAAGTTTCTTTCCCTAAGGTTTC  
AGGGGGAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAAAAA  
AAAGGGCCGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTTTTGATGCTGATTTA  
TGTTTGCTTTGGAAACAATCCAATCTTCTGACTCATAATCATACTCTCTTCTTCTGTACGTTTCCCTT  
TGCTGTGTGTACAACCTGTAATCGTGGTCCCAATGACTGCTGCTATAGTGTACCTAAATGTCATAGCTGT  
TTCCTAAAGG

>LoVo\_ CCDC168\_M13

TCTTTTTAATACGACTCACTATAGGGTGTAAAACGAGTAATGTCAGCTATGAAAAACGGTAGTAAGGG  
ACCCCGAGAGCGACCCCACTTTTTGGAGGAACTCCATATATCCAAGAAGTTGAAATCTTTGCCAC  
TAGGGGAATTCTGAAGTTTCTTTCCCTAAGGTTTCAGGGGGAATAGTCCAGCGAATGGTTTTGGGTATA  
ACCTCCAGTGAGTCTGCCGGTACACAGGCAAAAAAAAAGGGCCGTTTTGTTTTCTTTCAGAATAGAAGT  
TGATATCGTCATGATGAGGTTTTGATGCTGATTTATGTTTGCTTTGGAAACAATCCAATCTTCTGACTCA  
TAATCATACTCTCTTCTTCTGTACGTTTCCCTTGCTGTGTGTACAACCTGTAATCGTGTCCCAATGACG  
CGGCTTTTTCCCCC

>Hec1B\_ CCDC168\_T7

ACAATTTAGTCACTATGAAACGGTAGTAAGGGACCCCGAGAGCGACCCCACTTTTTGGAGGAAAC  
TCCATATATCCAAGAAGTTGAAATCTTTGCCACTAGGGGAATTCTGAAGTTTCTTTCCCTAAGGTTTCA  
GGGGGAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAAAAA  
AAAGGGCCGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTTTTGATGCTGATTTA  
TGTTTGCTTTGGAAACAATCCAATCTTCTGACTCATAATCATACTCTCTTCTTCTGTACGTTTCCCTT  
TGCTGTGTGTACAACCTGTAATCGTGGTCCCAATGACTGCTGCTATAGTGTACCTAAATGTCATAGATGT  
TTCCGAAAGG

>Hec1B\_ CCDC168\_M13

TCTTTTTTATACGACTTACTATAGGGTGTAAAACGAGTAATGTCAGCTATGAAAAACGGTAGTAAGGGA  
CCCCGAGAGCGACCCCACTTTTTGGAGGAACTCCATATATCCAAGAAGTTGAAATCTTTGCCACT  
AGGGGAATTCTGAAGTTTCTTTCCCTAAGGTTTCAGGGGGAATAGTCCAGCGAATGGTTTTGGGTATA  
ACCTCCAGTGAGTCTGCCGGTACACAGGCAAAAAAAAAGGGCCGTTTTGTTTTCTTTCAGAATAGAAG  
TTGATATCGTCATGATGAGGTTTTGATGCTGATTTATGTTTGCTTTGGAAACAATCCAATCTTCTGACTC  
ATAATCATACTCTCTTCTTCTGTACGTTTCCCTTGCTGTGTGTACAACCTGTAATCGTGGTCCCAAGACT  
GCCGCTTCAAGCCC

>Hec59\_ CCDC168\_T7

AGGATATAGGGTGGCCTTTGTGAACGGTAGGTAAGGGACCCCGAGAGCGATCCCAACAACCTTATAGA  
AGAACTCCATATATACAAAAACATAAAATCTTTGCCACTAGGGGAATTCTGAAGTTTCATTTCTTAAG  
GTTTCAGGGTGAATAGTCCAACGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCT  
AAAAAAAAGGGCCGGTTTTGTTTCCTTTGAAATAAAAGTGGAATCGTCTTCTAAAGTTTAAAGGGGA  
ATTTATTTGTGCTCCGAAAAATCAATATTTTTACACATGGTCAAACTCCTCGTTTTACAGGCCACTTT  
TCCCTCAGCTGGCCGGGGTTTTACATTCTACCTGGTTGGAAGTAAAGAATAAAA

>Hec59\_CCDC168\_M13

TTCTTTTTATAAGACCCACTATAGGGTGTAAAACGAGTAAAGTTAGGTTTGAAAAACGGTAGTAAGGG  
ACCCCGAGAGGGACCCCAACAATTTTTGGAGGAAATCCATATATTTCCAGAACTTGAAATTTTTGCCCC  
TAGGGGAATTTGAAGTTTTTTTTCTTAAGTTTCAGGGGAATAGTCCAGCGAATGGTTTTGGGTATA  
ACCTCCCGTGAGTTTGCCGGTACACCGGCAAAAAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGT  
TGATATCGTCATGATGAGGTTTTGATGCTGATTTATGTTTGCTTTGGAAACAATCCAATCTTCTGACTCA  
TAATCATACACTCTCTTCTTCTGTCACGTTTCCCTTGCTGTGTGTACAATCGTGTCCTCAAGAC  
GGTGCCAATGCCCC

**Alignment\_result\_CCDC168\_MS\_region:**

HCT116_12_M13	GGGTATTCGCCAGAAGGGTTGGGGATAACACCCACAGAGTGTGCCCTACACAGGCAA	239
CCDC168_reference	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	203
LoVo_12_T7	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	205
Hec1B_12_T7	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	204
LoVo_12_M13	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	240
Hec1B_12_M13	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	240
Hec59_12_M13	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCCGTGAGTTGCCGGTACACCGGCAA	240
	* ** *** ** *	
HCT116_12_M13	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	299
CCDC168_reference	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	263
LoVo_12_T7	AAAA-AAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	264
Hec1B_12_T7	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	264
LoVo_12_M13	AAAA-AAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	299
Hec1B_12_M13	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	300
Hec59_12_M13	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	300
	**** *	
Hec59_12_T7	GAATAGTCCAACGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCTA	208
HCT116_12_T7	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	203
HCT116_12_M13	GGGTATTCGCCAGAAGGGTTGGGGATAACACCCACAGAGTGTGCCCTACACAGGCAA	239
CCDC168_reference	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	203
LoVo_12_T7	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	205
Hec1B_12_T7	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	204
LoVo_12_M13	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	240
Hec1B_12_M13	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCAGTGAGTCTGCCGGTACACAGGCAA	240
Hec59_12_M13	GAATAGTCCAGCGAATGGTTTTGGGTATAACCTCCCGTGAGTTGCCGGTACACCGGCAA	240
	* ** *** ** *	
Hec59_12_T7	AAAAAAGGGCCGGTTTTGTTTCCTTTGAAATAAAAGTGGAATCGTCTTCTAAAGTT	268
HCT116_12_T7	AAAAAAGGGCCGGTTTTTTTTTTTTTTTTCAAAATAAAATTATATCTCCTCGTGAAGAGGTT	263
HCT116_12_M13	AAAAAAGGGCCGGTTTTGTTTCCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	299
CCDC168_reference	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	263
LoVo_12_T7	AAAA-AAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	264
Hec1B_12_T7	AAAAAAGGGCCGGTTTTGTTTCCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	264
LoVo_12_M13	AAAA-AAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	299
Hec1B_12_M13	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	300
Hec59_12_M13	AAAAAAGGGCCGGTTTTGTTTTCTTTCAGAATAGAAGTTGATATCGTCATGATGAGGTT	300
	**** *	

**Conclusion: indel in HCT116, LoVo have MS-related deletions**

**EIF2B3\_MS locus analysis:**

>EIF2B3\_reference

ACATTAAAGAATCTAATCAATAGTTCTAAGCATTTTCCATTCAGGGACTGTGTCTTATTTGACTTTATGTC  
ATCAACTCCTAGCACAGAATCTGTGATGTATAGTAGATTCTTAATAAATGTTTTTTCAGGGAAAGCATGA  
GTGAGAATAATAATTACGAAAACCTCAACAAACAAAACAACTCCAATCTTCCTTACCTGCTTTTTTTTTCC  
CCTTTTGACCGGGAACAGGTTCTATGCTATCTTGGCCTTTTCTCATCAACATAGCAAGTGATGCATCATAA  
GCTCTAAACAGGTCCACAACCTCATGTAAGGCAACGTCTGTTATCAGATCACAGCTCAGCACCAGCACAT  
CTGTCTGTAAATGGAGATGGGAAAAGTCAATATCATAAAGGACAATG

>HCT116\_ EIF2B3\_T7

GCGGACTGCATCACTCCTAGCACAGAATCTGTGATGTATAGTAGATTCTTAATAAATGTTTTTTCAGGGA  
AAGCATGAGTGAGAATAATAATTACGAAAACCTCAACAAACAAAACAACTCCAATCTTCCTTACCTGCTT  
TTTTTCCCCTTTTAAACCGGAAACAGGTCCAATCCTTTTTGGCCCTTTTCCCACCACCTAACCAAGTGGAGG  
CACCAAAACCCCTAACCGGGTCCCAACCCCAGGTAAGGCACCTCCGGTAATCAAATCAAACCTAACCCAC  
CACCCCTCCTTTCGTTAAATGGAAAATGGAAAATTCATAATAAAAAGGAACATTGGCCCCCAAATTTTC  
AACTTTTTTCCGGGAAAA

>HCT116\_ EIF2B3\_M13

TTTTTTATTTGGCTCCACATTGGGGGGAAAAAGGCGGCCCTTAAATTCTTGCCCCGGATTTTTGAAGG  
TTTGAGGTTTTTAAAAAGGTTTTCCGGGAAAGCCTGGAGGGGGATTATAAATTAGGAAAATTAAC  
CAACAAAACCAAATTCCATTTTCTTACCTGGTTTTTTTTTCCCCTTTTGACCGGGAACAGGTTCTATGCTA  
TCTTGGCCTTTTCTCATCAACATAGCAAGTGATGCATCATAAGCTCTAACAGGTCCACAACCTCATGTAA  
GGCAACGTCTGTTATCAGATCACAGCTCAGCACCAGCACATCTGTCTGTAAATGGAGATGGAAAAGTC  
AATATCATAATGACCATCCC

>LoVo\_ EIF2B3\_T7

ACGGCCCCGCCAATCAACTCCTAGCACAGAATCTGTGATGTATAGTAGATTCTTAATAAATGTTTTTCA  
GGGAAAGCATGAGTGAGAATAATAATTACGAAAACCTCAACAAACAAAACAACTCCAATCTTCCTTACC  
TGCTTTTTTTTTCCCCTTTTGACCGGGAACAGGTTCTATGCTATCTTGGCCTTTTCTCATCAACATAGCAAG  
TGATGCATCATAAGCTCTAACAGGTCCACAACCTCATGTAAGGCAACGTCTGTTATCAGATCACAGCTC  
AGCACCAGCACATCTGTCTGTAAATGGAGATGGGAAAAGTCAATATCATAAAGGACAATTGTCACCTA  
AATGTCATAGCTGTTTCCTGGGAAA

>LoVo\_ EIF2B3\_M13

TTTCTTTATACGACTCACTATAGGGTGTAAAACGACGGCCCATCAACTCCTAGCACAGAATCTGTGATGT  
ATAGTAGATTCTTAATAAATGTTTTTTCAGGGAAAGCATGAGTGAGAATAATAATTACGAAAACCTCAACA  
AACAAAACAACTCCAATCTTCCTTACCTGCTTTTTTTTTCCCCTTTTGACCGGGAACAGGTTCTATGCTAT  
CTTGGCCTTTTCTCATCAACATAGCAAGTGATGCATCATAAGCTCTAACAGGTCCACAACCTCATGTAA  
GGCAACGTCTGTTATCAGATCACAGCTCAGCACCAGCACATCTGTCTGTTTAAATGGAGATGGAAAAGT  
CAATATCCAAAAGGGACCCCTACCCCC

>Hec1B\_ EIF2B3\_T7

ACCCAGCGGGCATCACTCCTAGCACAGATCTGTGATAGTATAGTAGATTCTTAATAAATGTTTTTTCAGG  
GAAAGCATGAGTGAGAATAATAATGACGAAAACCTCAACAAACAAAACAACTCCAATCTTCCTTACCTG  
CTTTTTTTTTCCCCTTTTGACCGGGAACAGGTTCTATGCTATCTTGGCCTTTTCTCATCAACATAGCAGGTG  
ATGCATCAAAGCTCTAACAGGTCCACAACCTCAGGTAAGGCAACGTCTGTTATCAAATCACAGCTCA  
CCACCAGCACATCTTCTGTAAATGGAAAAGTCAATATCATAAAGGACAATTGTCACCTAAA  
TGTCAAAGCTGTTTCCGGGGAAA

>Hec1B\_ EIF2B3\_M13

TTTTTTTTATATTTTTTCACTATAGGGTGTAACGACGGCCCATCAACTCCTAGCACAGAATTTGTGAAG  
TATAGTAGATTTTTAATAAATGTTTTTTCAGGGAAAGCCTGAGTGAGAATAATAATTACGAAAACCTCAAC  
AAACAAAACAACTCCAATTTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGCTA  
TCTTGGCCTTTTCTCATCAACATAGCAAGTGATGCATCATAAGCTCTAACAGGTCCACAACCTCATGTAA  
GGCAACGTCTGTTATCAGATCACAGCTCAGCACCAGCACATCTGTCTGTTAAATGGAGATGGAAAAGT  
CAATTCATAAAGGACCTATTCT

>Hec59\_EIF2B3\_T7

AGGCGAGTCGAAGACCCTAGCAAGAGCTGGTGATGTATAGTAGATTCTTAATAAATGTTTTTTCAGGGA  
AAGCATCGAGTGAGAATAATAATTACGAAAACCTCAACAAAACAAAACAACTCCAATCTTCTTACCTGCT  
TTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGCTATCTTGGCCTTTTCTCATCAACATAGCAAGTGAT  
GCATCATAAGCTCTAACAGGTCCACAACCTCATGTAAGGCAACGTCTGTTATCAGATCACAGCTCAGCA  
CCAGCACATCTGTCTGTTAAATGGAGATGGGAAAAGTCAATATCATAAAGGACAATTGTCACCTAAATG  
TCATAGCTGTTTCTGAAGAAA

>Hec59\_EIF2B3\_M13

TTTTTAATACGACTCACTATAGGGTGTAACGACGGCCCATCAACTCCTAGCACAGAATCTGTGATGT  
ATAGTAGATTCTTAATAAATGTTTTTTCAGGGAAAGCATGAGTGAGAATAATAATTACGAAAACCTCAACA  
AACAAAACAACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGCTAT  
CTTGGCCTTTTCTCATCAACATAGCAAGTGATGCATCATAAGCTCTAACAGGTCCACAACCTCATGTAA  
GGCAACGTCTGTTATCAGATCACAGCTCAGCACCAGCACATCTGTCTGTTAAATGGAGATGGAAAAGTC  
AAATATCCAAAAAAGG

**Alignment\_result\_EIF2B3\_MS\_region:**

HCT116_13_T7	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTAAACCGGAACAGGTCCAATCC	176
HCT116_13_M13	AAATTCATTTTTCTTACCTGGTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	209
Hec59_13_T7	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	176
LoVo_13_T7	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	180
Hec1B_13_T7	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	178
EIF2B3_reference	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	239
Hec1B_13_M13	AACTCCAATTTTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	211
LoVo_13_M13	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	209
Hec59_13_M13	AACTCCAATCTTCTTACCTGCTTTTTTTTTCCCTTTTGACCGGGAACAGGTTCTATGC	209

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**Conclusion: MS-related deletion in HCT116**

**SLAMF1\_MS locus analysis:**

>SLAMF1\_reference

AACACTGACGTTTAGTGACTTTAGGAGAACTCTTGTTCTTGACTCCTGTTCCCTACCTTCTCTGCTCTGG  
ATGGAAAACGTGAATGTCCAACAGGCAAGGTAGACTGGCCAGGAATACTCTAGGAAACATGACAGGT  
TCATCTCAAACAAAATATAGAACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCTTTTTTTTT  
CCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTGAAAAGAAACCATAATGTTATCTCCCTCTGGTCCC  
CAGCAGGAGCTCCTTACTCAGACCTGGTCTTACTGTCCTTGCATACCCACTTCCCAAGGGCACAATG  
GAAACAAAGCCCTGAGTCCCAGCCCCCTGCACATTTGTCATATTGTCT

>HCT116\_SLAMF1\_T7

ACAGCTGCATGACGTTTAGTGACTTTAGGAGACTCTTGTTCTTGACTCCGTTCCCTACCTTCTCTGCTCT  
GGATGGAAAACGTGAATGTCCAAGAGGCAAGGTAGACTGGCCAGGAATACTCTAGGAAACATGACAG  
GTTTCATCTCAAACAAAATATAGAACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCTTTTTTT  
TCCCTGGTTGTCGGGAAAGGGTTCTTTTTACCGGGGAAAAAAAACCATAAGGGTTATCTCCCTCTGGT

CCCCACCAGAACCTCCTTACTCAAACCGGGCCTTTACGGTCCTTTGCATACCCCCTTTCCCAAGGGCACA  
AGGAAAACAAACCCCGGCTATATTGTCACCAAATTGTCAAAGTTTTTTCCGGAAGA

>HCT116\_SLAMF1\_M13

TTTTTTTATTAGAATCCCCTTTGGGTTTAAAAGGCGGCCCCACGACGTTTAGGGAATTTAGGGGAAATT  
TTGTTTTTGAATCCTGTTCCCTACCTTTCTTTGGTTTGGGAGGAAAACCTGTGAAAGTTCAACCGGCAAGG  
TTGGATGGCCCGGAATAATTTTGAAACCTGACCGGTTTATTTCAAACCAAAAATAGAAATTACCCCTGG  
TTTTTGAATTGGGCATAGATTGTAAGGGTTTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTG  
GTGAAAAGAAACCATAATGGTTATCTCCCTCTTATACCCAGCAGGATAGGGGGTATAAGGCCGGGCCAT  
AGACTCTTAGGCACACTCATGAGTCGTCATAGGCACAATGAAACAAAGTCTGCTTAGCCTTT

>LoVo\_SLAMF1\_T7

AAAGATGCACTGACGTTTAGTGACTTTAGGAGACTCTTGTTCTTGACTCCAGTTCCTACCTTCCTCTGCT  
CTGGATGGAAAACCTGTGAATGTCCAAGAGGCAAGGTAGACTGGCCAGGAATACTCTAGGAAACATGAC  
AGTTTCATCTCAAACAAAATATAGAACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCTTTT  
TTTTCCCTGGTTGCCGGGAATGGTTCCTTTTTACTGGTGAACAAAAACCCTAAAGTTTACCCCTCCGG  
GCCCCACAAGAACTCCCTAATCCAACTGGTCCTAATGGCCTTTTGATAACCCCTTTTCCCAAGGCAC  
CATGGAAACCAAACCCTGGTAAAATGGCCACCAAATGGCCAACTTGTCTGAGGGAA

>LoVo\_SLAMF1\_M13

GGGGTCTTTAGGAGAATTAAGTTTTGGATCCATGTTCCCTCCCTTCTTTGTTTGAAGGAAAACCTGG  
AAAGTTCAACCGGCCAGGGAGGCCGGCCAGAATTCTTTGGGAACCAGGCCGGGTTCTTTTAAAAAAA  
AAAAAGAAATTTCCCTGGGTTTTGGGACTGGGGCAAGGTTGTAAGGGTTTTTTTTTCCACTGTTGTCTG  
GTAATGGTTCGTTTTACCTGGTGAAGAAGGCATAATCCATTTCCCTCCTATCCCCATCAGGATAGGGG  
TAAAAGGCCGGGTACAGACTCTTAGTGACATTAGTGAGTCGCATGGGCACAATGAAACAAAGGCCCTT  
TTTTAAACC

>Hec1B\_SLAMF1\_T7

ACGGTGACATGACGTTTAGTGACTTTAGTGAATCTCATTATCTTGATGCTGTTCCCCCTTCTACTGCTCT  
CCATGGTGTCTATCTGTTTCTAAAGCACAATGGAAACAAAGCCCTGTTTTGTGGCCACCTAATGGTCTT  
ATTTGTTCCGGGGACAAAGGGAAAACAACCCCTGGCTAGGGGTCCCCTTATGGTCAAGCTTTTTCCGGG  
GCAAAAGAAAAAAAACCCCTTTTTTTGTTCCCTTAAATGTCCAATTTTTCCGGGGTCAATTTACAAACC  
CCGTTTTTTTTTTTAAAAAGTCCCAAG

>Hec1B\_SLAMF1\_M13

TGGCGTTTGAAGAATTATACCCGGGCTTTTTTCTTTTTCCCGGTAAAACCCCTCGCCATTTTGGGCA  
CATTTTTCGAGGGTGTCTCCTTTTTCTCGGAACACGTTTACACTTTTGGGGCCCCTTGCCCGGGGTTT  
TTTTCCCTTTCTTTTTGTTACAATAAGAACCTTAAGAAAAAGGCGGCACGGGGTGTTCCTTGTGCCTT  
TAATACGACTCAGTATAGGGAAAAAAGACGGGCCATAGACGCCTAGTGACGTTAGTGAGTCGTCCTA  
GGCACAATGAAACAAAGTCTTGCTTAACCC

>Hec59\_SLAMF1\_T7

GGAAAGGGCCAGGGCACTTTTTGTGGACTTTAGGAGAACTCTTGTTCTTGACTCCTGTTCCCTACCTTC  
CTCTGCTCTGCAAGGAAAACCTGTGAATGTCCAACAGGCAAGGTAGACTGGCCAGGAATACTCTAGGAAA  
CATGACAGGTTCTCAAACAAAATATAGAACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAG  
GCTTTTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTGAAGAAGAAACCATAATGGTTATCTC  
CCTCTGGTCCCCAGCAGGAGCTCCTTACTCAGACCTGGTCTTTACTGTCCTTTGCATACCCACTTTCCCA  
AGGGCACAATGGAAACAAAGCCCTGCTATAGTGTCACCTAAATGTCATAGCTGTTTCCTAAAG

>Hec59\_SLAMF1\_M13

TATTTTAATACGACCACTATAGGGTGTA AACGACGGCCCACTGACGTTTAGTGACTTTAGGAGAACTCT  
TGTTCTTGACTCCTGTTCCCTACCTCCTCTGCTCTGGATGGAAA ACTGTGAATGTCCAACAGGCAAGGTA  
GACTGGCCAGGAATACTCTAGGAAACATGACAGGTTTCATCTCAAACAAAATATAGA ACTTACACCTGGT  
TTCTGGACTTGGGCATAGATCGTAAGGCTTTTTTTTTTCCACTGTTGTCTGGTAATGGTTCTTTTACCTGG  
TGAAAAGAAACCATAATGGTTATCTCCCTTTTTCCCCAGCAGGAGCTCGGGAATAAGGCCGGGCCTTTA  
GACTCTTAGGCACACTCATGAGTCCCAAGGGCACAATGAAACAAAGTCATGCCAAAG

**Alignment\_result\_SLAMF1\_MS\_region:**

LoVo_16_M13	TTTTAAAAAAAAAAGAAATTTCCCTGGGTTTTGGGACTGGGGCAAGGTTGTAAGGGT	188
HCT116_16_M13	TTTCAAACAAAATAGAAATTACCCCTGGTTTTTGGAAATGGGCATAGATTGTAAGGGT	240
Hec59_16_M13	TCTCAAACAAAATATAGA ACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCT	239
LoVo_16_T7	TCTCAAACAAAATATAGA ACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCT	206
HCT116_16_T7	TCTCAAACAAAATATAGA ACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCT	204
SLAMF1_reference	TCTCAAACAAAATATAGA ACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCT	202
Hec59_16_T7	TCTCAAACAAAATATAGA ACTTACACCTGGTTTCTGGACTTGGGCATAGATCGTAAGGCT	212
	* * *** ** * **** * * * ***** ** ** * **** * * * ***** *	
LoVo_16_M13	TTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTAAAAGAAGGCATAATT	248
HCT116_16_M13	TTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTAAAAGAAGGCATAATT	300
Hec59_16_M13	TTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTAAAAGAAGGCATAATT	299
LoVo_16_T7	TTTTTTTTCCCTGGTTGCCGGGAATGGTTCCTT-TTFACTGGTAAAAAAAAACCCATAAG	265
HCT116_16_T7	TTTTTTTTCCCTGGTTGCCGGGAAGGTTCTTTTTACCGGGAAAAAAAAAACCCATAAG	264
SLAMF1_reference	TTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTAAAAGAAGGCATAATT	262
Hec59_16_T7	TTTTTTTTCCACTGTTGTCTGGTAATGGTTCGTTTTACCTGGTAAAAGAAGGCATAATT	272
	***** ** * **** *	

**Conclusion: MS\_related deletion in LoVo, HCT116**

**SLC35G2\_MS locus analysis:**

>SLC35G2\_reference  
AATTGATTATCTGAAGAAATGGATACTTCTCCCTCCAGAAAATATCCAGTTAAAAAACGGGTGAAAATAC  
ATCCAACACAGTGATGGTGAAATATACTTCTCATTATCCCCAGCCTGGCGATGATGGATATGAAGAAAT  
CAATGAAGGCTATGGAAATTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAAAAA  
AAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAATGATCAATGAGA  
TTGGACAATTCCAGAGCTTTGCAGAAAAAACATTTTTCAATCCCGAAAAATGTGGATAGTGCTGTTTGG  
ATCTGCTTTGGCTCATGGATGTGTAGCTCTTATCACTAGGCTTGTTCGATCG

>HCT116\_SLC35G2\_T7  
GCCGGTAAGCTGAGATGGATACTTCTCCCTCCGAAATATCCGTTAAAAAACGGGTGAAAATACATCCCA  
ACACGGTGATGGTGAAATATACTTCTCATTATCCCCAGCCTGGCGATGATGGATATGAAGAAATCAATG  
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AACTTTTTCTTTGAACCCTGGAAACCCCACTCCCCCAACAAAAACCCATGAATAATGAAATGGAAC  
ATTTCCGAACCTTTCCAAAAAAAACCTTTTTTCATCCCCAAAATGGGGAAATGTGGTTGTTGGAATTTCTT  
TGGGTCCAGGAAGTTTAACTTTTATCCCTAAGGCTGGTTCGTAATGGCCCCAAATGGCCAACCTTTTTTC  
CCGAGAAAA

>Hct116\_SLC35G2\_M13  
TTTTTTATTACGAACTCACATTGGGGGGTAAAAGGGGATATTCGGAGGAAAGGGTTATTTTTCTTCCGG  
AAAATTTCCGGTTAAAAAACGGGTGAAAATAATTCCACACCATGGATGTTGAATTTATTTTTCTTATTC  
CCCGCCCGGGGGTGGAGGGTTAGGAGGAATCCATGGAGGGTTAGGGAAATTTTAGGAGGGAAATTC  
AAGGAAAGTTTTGTGGATGGAAAGGAAAAAAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACC  
TCCACCAACAGAAGACCCAATGATCAATGAGATTGGACAATTCCAGAGCTTTGCAGAAAAAACATTTTT



CAATCCCGAAAAATGTGGATAGTGCTGTTGGATCTGCTTTGGCTCAGGATGTGTAGCTCTATCACTAGGC  
TTGTTACTTACCCC

>LoVo\_SLC35G2\_T7

CCAGGAAATCTGAGATGGATACTTCTCCCTCCGAAATATCCGTTAAAAAACGGGTGAAAATACATCCCAA  
CACGGTGATGGTGAATATACTTCTCATTATCCCCAGCCTGGCGATGATGGATATGAAGAAATCAATGA  
AGGCTATGGAAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAAATGAAAAAAAAAAGGGA  
GAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAATGATCAATGAGATTGGACA  
ATTCCAGAGCTTTGCAGAAAAAACATTTTTCAATCCCGAAAAATGTGGATAGTGCTGTTTGGATCTGCT  
TTGGCTCATGGATGTGTAGCTCTTATCACTAGGCTTGTCTGTAGTGTCACCTAAATGTCATACTGTTTC  
CTGG

>LOVO\_SLC35G2\_M13

TTCCCTCTTTTATTTTTCACTATAGGGTGTA AACGAGATTATCTGAAGAAATGGATACTTCTCCCTCCA  
GAAAATATCCAGTTAAAAAACGGGTGAAAATACATCCCAACACAGTGATGGTGAATATACTTCTCATT  
TCCCCAGCCTGGCGATGATGGATATGAAGAAATCAATGAAGGCTATGGAAATTTTATGGAGGAAAATCC  
AAAGAAAGGTCTGCTGAGTGAAATGAAAAAAAAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTAC  
CTCCACCAACAGAAGACCCAATGATCAATGAGATTGGACAATTCCAGAGCTTTGCAGAAAAAACATTTT  
TCAATCCCGAAAAATGTGGATAGTGCTGTTGGATCTGCTTTGGCTCAGGATGTGTAGCTCTTATCACTAG  
GCTTTTTTTGTTTTCTCC

>Hec1B\_SLC35G2\_T7

ACAGTTTATTCTGGAGATGGATACTTCTCCCTCCGAAATATCCGTTAAAAAACGGGTGAAAATACATCCC  
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GAAGGCTATGGGAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAAATGAAAAAAAAAAGG  
GAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAATGATCAATGAGATTGG  
ACAATTCCAGAGCTTTGCAGAAAAAACATTTTTCAATCCCGAAAAATGTGGATAGTGCTGTTTGGATCT  
GCTTTGGCTCATGGATGTGTAGCTCTTATCACTAGGCTTGTCTGTAGTGTCACCTAAATGTCATAGCAT  
GTTTCCTGGGGAAAAA

>Hec1B\_SLC35G2\_M13

TCTTTCTATACTCATCTTCTATAGGGTGTA AACGAGATTATCTGAAGAAATGGATACTTCTCCCTCCAGA  
AAATATCCAGTTAAAAAACGGGTGAAAATACATCCCAACACAGTGATGGTGAATATACTTCTCATTATC  
CCCAGCCTGGCGATGATGGATATGAAGAAATCAATGAAGGCTATGGGAATTTTATGGAGGAAAATCCA  
AAGAAAGGTCTGCTGAGTGAAATGAAAAAAAAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCT  
CCACCAACAGAAGACCCAATGATCAATGAGATTGGACAATTCCAGAGCTTTGCAGAAAAAACATTTTTC  
AATCCCGAAAAATGTGGATAGTGCTGTTTGGATCTGCTTTGGCTCAGGATGTGTAGCTCTTATCACCTT  
AGGTCTTTTTTCTTAACTACC

>Hec59\_SLC35G2\_T7

ACATTTATTTTCTGAGAATGGATACTTCTCCCTCCAGAAATATCCGTTAAAAAACGGGTGAAAATACATC  
CCAACACGGTGATGGTGAATATACTTCTCATTATCCCCAGCCTGGCGATGATGGATATGAAGAAATCA  
ATGAAGGCTATGGGAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAAATGAAAAAAAAA  
GGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAATGATCAATGAGATT  
GGACAATTCCAGAGCTTTGCAGAAAAAACATTTTTCAATCCCGAAAAATGTGGATAGTGCTGTTTGGAT  
CTGCTTTGGCTCATGGATGTGTAGCTCTTATCACTAGGCTTGTCTGTAGTGTCACCTAAATGTCATAGC  
TGTTTCCTGA

>Hec59\_SLC35G2\_M13

TTTTCTAATACGACTCACTATAGGGTGTAAAACGAGATTATCTGAAGAAATGGATACTTCTCCCTCCAGA  
 AAATATCCAGTTAAAAAACGGGTGAAAATACATCCCAACACAGTGATGGTGAATATACTTCTCATTATC  
 CCCAGCCTGGCGATGATGGATATGAAGAAATCAATGAAGGCTATGGGAATTTTATGGAGGAAAATCCA  
 AAGAAAGGTCTGCTGAGTGAATGAAAAAAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCT  
 CCACCAACAGAAGACCCAATGATCAATGAGATTGGACAATTCCAGAGCTTTGCAGAAAAAACATTTTTTC  
 AATCCCGAAAAATGTGGATAGTGCTGTTGGATCTGCTTTGGCTCAGGATGTGTAGCTCTACTAGGCT  
 GTTGCGTACCCC

**Alignment\_result\_SLC35G2\_MS\_region:**

Hct116_17_M13	AGGGTTAGGAAATTTTAGGAGGAAATCCAAAGAAAGTTTGTGGATGGAAAGGAAAA	237
HCT116_17_T7	AGGCTATGGAAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	199
Hec59_17_T7	AGGCTATGGGAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	203
LoVo_17_T7	AGGCTATGGAAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	199
Hec1B_17_T7	AGGCTATGGGAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	201
Hec1B_17_M13	AGGCTATGGGAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	238
SLC35G2_reference	AGGCTATGGAAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	206
LOV0_17_M13	AGGCTATGGAAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	240
Hec59_17_M13	AGGCTATGGGAATTTTATGGAGGAAAATCCAAAGAAAGGTCTGCTGAGTGAATGAAAA	237
	*** * ** ** ** * ** * ** * ** * ** * ** * ** *	
Hct116_17_M13	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	297
HCT116_17_T7	AAAAGGAAAACTTTTCTTTGAACCCTGGAAACCCCAA-CTCCCCCACCACAAAAACCCAT	258
Hec59_17_T7	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	263
LoVo_17_T7	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	259
Hec1B_17_T7	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	261
Hec1B_17_M13	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	298
SLC35G2_reference	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	266
LOV0_17_M13	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	300
Hec59_17_M13	AAAAGGGAGAGCTTTCTTTGGAACCATGGATACCCTACCTCCACCAACAGAAGACCCAAT	297
	***** * * ***** * ** * * *** * **** * ** ** * * ** *	

**Conclusion: HCT116 has MS-related deletion**

**TTK\_MS locus analysis:**

>TTK\_reference

TTTCCCAACTGTAAGAACAAGAGAGAAATAAATGTATTATATTTAGAATACATCAAATACATCTACTGA  
 TGTGACAGTACATTTAACTAAAAAATTGCAAAACAGATTTGTGTTTTTAAATTTTACAGACTTTTATATGAACA  
 CTATAGTGGTGGTGAAGTCATAATTCTTCATCCTCCAAGACTTTTGAACCAACAGAAGACCCAAT  
 ATTTGCAGTTATTCGTAATGTCAGATACCACCTATAAAATATATTGGACTGTTATACTCTTGAATCCCTGT  
 GGAAATCTACATTTGAAGACAACATCACTCTGAAGTGTTATCAGCAAAAAAATTTCAGTAGATTATCTTT  
 AAAAGAAAATGTAATAAGCAACCACTTATGGCACTGTATATATTGTA

>HCT116\_TTK\_T7

GCGACTCTGTAGACAGAGAGATAGCTGCCTCATATGTGCACTGAGTGTACCTACATGTCCAGCTGTTTC  
 CTACATGTAATAAAAAATTGCAAAACAGATTTGTGTTTTTAAATTTTACAGACTTTTATATGAACACTATAGT  
 GGTGGTGAAGTCATAATTCTTCATCCTCCAAGACTTTTGAACCAACAGAAGACCCAATGAATTTGCA  
 TTTTCTTAATGGCCAAATCCCCCAATAAAAAAATTGGAATGGTAACTCCTGAAACCCTGGGGAAATC  
 CTACTTTTAAAAACACCTCCCTCCTAAATGGTTACCACCAAAAAAATTTTATAAAATAACCTTTAAAAAA  
 ACTGGTAAAATAACAACCCCTTTTGGGCCTGGGGTCCCAATGGTCAAACCTGTTTCTGGGGA

>HCT116\_TTK\_M13

TTTTTTTATTAGGACCATATTGGGGGGTAAAGGCCCAACGTTAGAACCAAGGGGAAATAAAAGTTTT  
 ATTATTTGAATACCTTCAAAAACCTTTTATGGATAGGCCGGTCCATTAAATTAATAAAATGCCAAACCGGA  
 TTGGGTTTTTAAATTTTCGACTTATTTGGACCACATTGGGGGGGGGGAAGTTCTAATTTTTTCTTCTCC  
 AGGATTTTGGAAAAAAGGGGAAAAAATGATTTGCAGTTATTCGTAATGTCAGATACCACCTATAAA

ATATATTGGACTGTTATATCTCTTGAATCCCTGTGGAAATCTACATTTGAAGACAACATCACTTGATTAAT  
ACGACTCAAATAGGGTGCAAAGGACCTAACTGAAAGAACAAGATAGAAATAGCAACCACTATGCGC  
TGCCC

>LoVO\_TTK\_T7

CAGGTCAGTCTAGACAGAGAGAATAGCAGTCTTATTTGCAATGACTGTCACCTACATGTCCAGATGT  
TTTCTGCATTTAACTAAAAAATTGCAAACAGATTTGTGTTTTTTAATTTAGACTTTTATATGAACACTAT  
AGTGGTGGTCAAAGTCATAATTCTTCATCCTCCAAGACTTTTGAAGAAAAAAGGGAAAAAAGAATTT  
CCATTTTCTAATGGCCAATACCCCCAATAAAAAAATTGGAATGGTAAACTCCTGAATCCCTGGGGAA  
ATCCACCTTTAAAAACACCTCCCTCCTAAATGGTATCCACCAAAAAAATTCATAAATTAACCTTTAAAA  
AAAACTTTAAAAATTACCACCACTTTAGGGAACGGTGGTCCCAATGGCAAACCGTTTTCTGGGGAA  
AA

>LoVO\_TTK\_M13

TTTTTTTATTAGGATTCATTTGGGGGGTAAAAGGCCCAACGTTAGGACCAGGGGGGAAATAAATGTTT  
TTTATTTGGATTCCTTCAAATACTTTTATGGATGGGCCGTCCATTTAATTAATAAATTGCAAACAGAT  
TTGTGTTTTTTAATTTCCGACTTTTTAGGACCACAATGGGGGGGGGAAATTTCTAATTTTTCTTCTTCCA  
GGATTTTGGAAAAAAGGGGAAAAAATGATTTGCAGTTATTCGTAATGTCAGATACCACCTATAAAA  
TATATTGGACTGTTATACTCTTGAATCCCTGTGGAAATCTACATTTGAAGACAACATCACTTGTTAATAC  
GCCTCAAAAAAAGGTCAGAAGGACCAACTGAAAGAACAAGTGAAGAAATAGCAACCACTATGCCTTACCC

>Hec1B\_TTK\_T7

CCGTCTCTGCTAGACAGAGAGATAGCTGTCTTATATTGTACGATTACTGCCAAATACATGTCCAGATATG  
ACCGTGCATTTAACTAAAAAATTGCAAACAGATTTGTGTTTTTTAATTTAGACTTTTATATGAACACTAT  
AGTGGTGGTCAAAGTCATAATTCTTCATCCTCCAAGACTTTTGAAGAAAAAAGGGGAAAAAAGAATTT  
CCATTTATCCTAATGGCCAAAACCCCCAATAAAAAAATTGGAATGGTAAACCCCTGGAACCCCGGGGA  
AATCCACCTTTAAAAACACCTCCCTCCTAAATGGTTACCACCAAAAAAATTCATAAATAACCTTTAAA  
AAAACTGGTAAAATAACCACCCCTTAGGGCCTGGTGGCCCCCAATGGCCAACTGGTTTCCGGGGGA  
AA

>Hec1B\_TTK\_M13

TTTTTTTATTAGGTTTACATTGGGGGGTAAAAGGCCCAACGTTAGGACCAGGGGGGAAATTAAGTTTT  
ATTATTTGGATTCCTTCAAACCTTTTATGGTTTGGCCGTCCATTAATTAATAAATGCCAAAACAAAT  
TGGGTTTTTTAATTTCCGACTTATTAGGACCACATTGGGGGGGGGAAAGTTCTAATTTTTCTTCTTCCA  
GGATTTTGGAAAAAAGGGGAAAAAATGATTTGCAGTTATTCGTAATGTCAGATACCACCTATAAAA  
TATATTGGACTGTTATACTCTTGAATCCCTGTGGAAATCTACATTTGAAGACAACATCACTCTGTTTGTGT  
TATCAGCAAAAAAATTCAGTAGGTCATCACTAAAAGAAAAGTGAATAAATAGCAACCACTTATGCCTTA  
GCT

>Hec59\_TTK\_T7

ACAGCACTGTAGACAGAGAGAATAAATGTATTATATTTAGAAGACATCAAATACATCTACAGATGTGA  
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GTGGTGGTCAAAGTCATAATTCTTCATCCTCCAAGACTTTTGAAGAAAAAAGGGGAAAAAATGATTTG  
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TCTACATTTGAAGACAACATCACTCTGAAGTGTATCAGCAAAAAAATTCATTAAATAATCTTTAAAAAA  
AACTGTAAAAATACCAACCACTTAGGGCACTGGTGTACCTAAATGTCAAAGTTTTTTCCGGATA

>Hec59\_TTK\_M13

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ATTTAGAATACATCAAATACATTTAATGATGTGACCGTACATTTAATAAAAAAATTGCAAACAAAGATTT



TTTTTATTAGGATCCATTTTGGGTTTAAAACGGCGGGCGGGGAATTCAGCAAATTTTCCCCAGCCCAG  
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TATCCGGAATGGGAAGGAGGAGAAGTTATCCAGGAGGCCAGTTTGAAGGAGGCCGGGTCAAAGAA  
GTCCGGCCGGGTGGGAGGCCCAATGGAGAACCCCTTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGG  
ATCTGGTTGATGACTCGGTGAGCAGCCCCACCACCATCTCCAATGTTACCTCCACGAGCCTTGGCAATCG  
AATCCAGCTCATCAAAGAATATTAATACGACTCACTATAGGGTGTACAACGACGGCGCGAGGACTCATG  
CAAGCACTAACAAACAGATCTTAGCCCC

>LOVO\_VCP\_T7

CACCGAACTGGCCGAGATCATGCAGCACTAACCAAACACTCAGTGTAGTCTTCGGCTGCTCGCCTATGATGT  
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GTAGATGAGCTGATCAAGACGGCCAGGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAG  
CGCCAATGATGAACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGG  
TCAGCAACCCACCACCATCTCCAATGTTACCTCCACGAGCCTTGGCAATCCAATCCAGCTCATCAAAGA  
ATAGCACACAGGGGGCAGCTTGGCGGGCCTGTAGGAGGAATGGATTA

>LOVO\_VCP\_M13

CTTCCCCTTAATACGACTCACTATAGGGTGTAAAACGACGGCCGAGGACTCATGCAAGTCTCCCACAGCC  
CATGATCTTGACCTGCCTTGGCAAACGGGACTTGCAGGTTAGCCTTGAGGATGGCAACACGGGAC  
TTCTCATCAGGAAGTGGGATGTAGATGAGCTGATCAAGACGGCCAGGTCTGAGGATGGCAGGATCAAT  
GATGTCAGGCCGGTTGGTAGCGCCAATGATGAACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTC  
AGGATCTGGTTGATGACTCGGTGAGCAGCCCCACCACCATCTCCAATGTTACCTCCACGAGCCTTGGCAA  
TCGAATCCAGCTCATCAAAGAATTTAATACGACTCACATATAGGGTGTACAACGACGGCCGAGGACTC  
ATGCAAGCACTAACAAAACAGATTTGTTACT

>HEC1B\_VCP\_T7

ACAAGTGCAGATCATGCAGTCTCCCCAGACTATGTAGTCTCGCTGTCGCCTAAGTGTCTGGCTATTTCC  
TCAGGTTAGCCTTGAGGATGGCAACACGGGACTTCTCATCAGGAAGTGGGATGTAGATGAGCTGATCA  
AGACGGCCAGGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGAACAC  
ATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGTGAGCAGCCCCACCAC  
CATCTCCAATGTTACCTCCACGAGCCTTGGCAATCGAATCCAGCTCATCAAAGAATAGCACACAGGGGG  
CAGCTTGGCGGGCCTGTAGGAGGAATGGATTGATTCAAGCACTAACAAAACACTAGATGTCTCGTGTACC  
TAAATGTCATAGCTGTTTCCTAAGGGGAAATCGGAGGACA

>HEC1B\_VCP\_M13

GATTTCCCTTAATACGACTCATTATAGGGTGTAAAACGACGGCCGAGGACTCATGCAAGTCTCCCACAG  
CCCATGATCTTGACCTGCCTTGGCAAACGGGACTTGCAGGTTAGCCTTGAGGATGGCAACACGGG  
ACTTCTCATCAGGAAGTGGGATGTAGATGAGCTGATCAAGACGGCCAGGTCTGAGGATGGCAGGATCA  
ATGATGTCAGGCCGGTTGGTAGCGCCAATGATGAACACATTTTTTTTTTGTGGACATGCCATCCATTTCTG  
TCAGGATCTGGTTGATGACTCGGTGAGCAGCCCCACCACCATCTCCAATGTTACCTCCACGAGCCTTGGC  
AATCGAATCCAGCTCATCAAAGAATTTAATACGACTCGCATATAGGGTGTACAACGAGCGGGCGAGAG  
GACTCATGCAAGCACTAACAGAATCTATGAGGTTTTGGACCTA

>HEC59\_VCP\_t7

CCGACGTGCCGAGGATCATGCAGTCTCCCCAAACTATGTATTCTCGCTGTCGCCTAAGTCTCATGAGCTA  
CTTTCCGAGGTTAGCCTTGAGGATGGCAACACGGGACTTCTCATCAGGAAGTGGGATGTAGATGAGCT  
GATCAAGACGGCCAGGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATG  
AACACATTTTTTTTTTGTGGACTTGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGTCAACACCC  
ACCACCATCTCCAATGTTACCTCCCCAAGCCTTGGCAATCGAATCCAGCTCATCAAAGAATAGCACACAG

GGGGCAGCTGGGCGGGCCTGTAGGAGGAATGGATTGATTCAAGCACTAACAAAATAAATGTCTCGTG  
 TCACCTAAATGTCATACCTTTTTCCGGAAAAAGGTCAAGATCTAGTAAAATGAAAACCAGAACTTCACC  
 AGACTGTCTCCAGCCACGTGTGTGGTTAATTTCTCTGCTAAATTGCTACACATAAAGCTTTTATTGGTCTG  
 CCACGCTTTGTTAGTCTTCCTGATGCTGGACAAATTCAGCACTAACAAAATAAGATGTCTCGTGTCCAC  
 TAAATGTCATAGCTGTTTCTGAGAGGAGAAGTGGG

>HEC59\_VCP\_M13

GGCCGAGGACTCATGCAAGTCTCCCATCAAGGCCCCCAAGTGCTGGGATTATATGAGCCACTGTCTC  
 TATCCCAGACAGCTTTCTAATTACTGGTTCTATATCCAAATTATGTTTAACTAAGAAATGAAGTAGCCTT  
 GAGAAGTTACACAAGCATTCCACGCATTATACCTTGTTTATTCGACTCACTATAGGGTGTAAAACGACGG  
 CCGAGGAATCATGCAAGTTTCCACCGCCCCTGATTTTGCACCTGCCTTGGCAAATGGGGACTTGCGCAG  
 GTTAGCCTTGAGGATGGCAACACGGGACTTCTCATCAGGAAGTGGGATGTAGGTGAGGTGATCAAGAC  
 GGCCAGGTTTGAGGATGGCAGGATCAATGATGTCAGGCCGTTGGTAGCGCCAATGATGAACACATTT  
 TTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGTGAGCAGCCCCACCACCATC  
 TCCAATGTTACCTCCACGAGCCTTGGCAATCGAATCCAGCTCATCAAAGAATATTAATACGAGGGCGCAGA  
 TAGGGTGGACACAGGACGGCGCAGATGGACTCATGCAAGCACTAACAAAATAAGATTCTAAGCC

**Alignment\_result\_VCP\_MS\_region:**

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Hct116_19_M13      GGCCAGTTTGAAGGAGGCCGGTCAAAGAAGTCCGGCCGGTGGGAGGCCAATGGAGA 235
HEC59_19_M13      GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 408
LOV0_19_M13      GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 239
HEC1B_19_M13     GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 241
HCT116_19_T7     GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 201
LOV0_19_T7       GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 219
HEC59_19_t7      GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 208
VCP_reference     GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 196
HEC1B_19_T7      GGCCAGTCTGAGGATGGCAGGATCAATGATGTCAGGCCGGTTGGTAGCGCCAATGATGA 202
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Hct116_19_M13     ACCCTTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 295
HEC59_19_M13     ACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 468
LOV0_19_M13     ACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 299
HEC1B_19_M13     ACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 301
HCT116_19_T7     ACACATTTTTTTTTTGGGAACCTCCCTTTTTTTTTTTCAGGATTGGGTTAAGAATTCGTC 261
LOV0_19_T7       ACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 279
HEC59_19_t7      ACACATTTTTTTTTTGTGGACTTGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 268
VCP_reference     ACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 256
HEC1B_19_T7      ACACATTTTTTTTTTGTGGACATGCCATCCATTTCTGTCAGGATCTGGTTGATGACTCGGT 262
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**Conclusion: HCT116 has MS-related deletion**

**DCAF13\_MS locus analysis:**

>DCAF13\_reference

GTAATGAAAAAATCCTCTTAACCTTTTTGCTTTAAAGACAGTGTATACTGGGATTGATCATCACTGGA  
 AAGAAGCTGTTTTGCCACATGTGGACAGCAAGTAGACATTTGGGATGAACAAAGAATAATCCTATAT  
 GTTCAATGACCTGGGGATTTGACAGTATAAGTAGTGTTAAATTTAACCCAATTGAGGTAATGTTTTTTTT  
 AAGTATGTTTTACTTATTATGGCTTAATAATTTAGTTCTGTTTAAAACTTTGAATGTATGATAGAAA  
 CTTCTGAATTTAATGGTGTTTTGGCATTGTCAGTTTTCCCGATTGTAAATGAGTTCTGATACCTTTGCT  
 CAAATCCCAACATGTTTCCAGCAGTTTAGTCCAGATACTAGAGTTA

>HCT116\_DCAF13\_T7

ACAGACTGCAGTGTAACTGGGATTGATCATCACTGGAAGAAGCTGTTTTGCCACATGTGGACAGCAA  
 GTAGACATTTGGGATGAACAAAGAATAATCCTATATGTTCAATGACCTGGGGATTTGACAGTATAAGT

AGTGTTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTTACTTATTATGGCTTAATAATTT  
CAGTTCTGTTTAGAAAACCTTTGAATGTATGATAGAAAACCTTCTGAATTTAATGGTGTTTTGGCATTGTTGT  
CAGTTTTCCCGATTGTAATGAGTTCTGATACCTTTGCTCAAATCCCAACATGTTCCAGCAGTTTAGTC  
CCAGATACTAGAGTAGTGTCACCTAAATGTCATACTTGTTCCTAAAGAAC

>HCt116\_DCAF13\_M13

TTCCTGTTTTAATATCGTCTCACTATAGGGTGTAACGACGGCCAGTGTATACTGGGATTGATCATCA  
CTGGAAAGAAGCTGTTTTGCCACATGTGGACAGCAAGTAGACATTTGGGATGAACAAAGAATAATCC  
TATATGTTCAATGACCTGGGGATTGACAGTATAAGTAGTGTTAAATTTAACCCAATTGAGGTAATGTTT  
TTTTTAAGTATGTTTTACTTATTATGGCTTAATAATTTAGTTCTGTTTAGAAAACCTTTGAATGTATGAT  
AGAAAACCTTCTGAATTTAATGGTGTTTTGGCATTGTTGTCAGTTTTCCCGATTGTAATGAGTTCTGATACC  
TTTGCTCAAATCCCAACATGTTCCAGCAGTTTATCCAGAACAGAGGTACCCCT

>LOVO\_DCAF13\_T7

ACGGGCGGGCAGTGTAACGGGGATTGATCATCACTGGAAGAAGCTGTTTTGCCACATGTGGACAGCA  
AGTAGACATTTGGGATGAACAAAGAATAATCCTATATGTTCAATGACCTGGGGATTGACAGTATAAG  
TAGTGTTAAATTTAACCCAATTGAGGTAATGTTTTTTTTAAATTAGTTTTTATTAATAAGGGTTAATAATTT  
TCATTTGTTTAAAAAATTTTGAAGGAAGAAAAAACCTTCGAAATTTAAAGGGGGTTTGGCCTTTTG  
GCCATTTCCCAATGGAAATGAATCCGAAACCTTGCCCAATCCCACTGGTTCCCAACCATTTAAT  
CCCAAAACCAAAATAATGGCCCCAAATGGCCAAACTTTTTCCAGAGGAA

>LOVO\_DCAF13\_M13

TTCCTTTTTAATTAGGACCCACATTGGGGGTTAAAAGGAGGCCCGGGGTTTATGGGGATTATTCTCCACG  
GAAAGGAGGTGTTTTGCCCCAGGGGGCCGCAAGGTGGCCTTTGGGGAGGACCAAGAAATTATTCCA  
TTATTTCAATGACCCGGGGGTTTGGCCGTTTAGTTGGTTTAAAATTAACCCAATGGGGTAAAGGTTTT  
TTTTAAGTATGTTTTACTTATTATGGCTTAATAATTTAGTTCTGTTTAGAAAACCTTTGAATGTATGATAG  
AAACTTCTGAATTTAATGGTGTTTTGGCATTGTTGTCAGTTTTCCCGATTGTAATGAGTTATGATACCTCT  
GCTCAAATCCCAACATGTTCCAGCAGTTAGTCCAGAACAGAGGTAGCCCT

>HEC1B\_DCAF13\_T7

GCGGGCCTGCAGATGTATACTGGGATTGATCATCACTGGAAGAAGCTGTTTTGCCACATGTGGACAGC  
AAGTAGACATTTGGGATGAACAAAGAATAATCCTATATGTTCAATGACCTGGGGATTGACAGTATAA  
GTAGTGTTAAATTTAACCCAATTGAGGTAATGTTTTTTTTAAGTATGTTTTACTTATTATGGCTTAATAAT  
TTCAGTTCTGTTAATAAACTTTTGAATGCAGGATAAAAACCTTCGGAATTTAAAGATGTTATGACTTTTT  
TTTGGACCCCAATGCTTCTTGATGGCTCTAAGGGGCAACAGCTTCTTTCCGTGTTGCTCATCCCTT  
AGTAAAAACATCCTAAAGTTTTGTCCCCTTTTTTCACTGTTTCAGACACGCC

>HEC1B\_DCAF13\_M13

TCCCTGATTTTATATCGACTCACTATAGGGTGTAACGACGGCCAGTGTATACTGGGATTGATCATCAC  
TGAAAGAAGCTGTTTTGCCACATGTGGACAGCAAGTAGACATTTGGGATGAACAAAGAATAATCCT  
ATATGTTCAATGACCTGGGGATTGACAGTATAAGTAGTGTTAAATTTAACCCAATTGAGGTAATGTTTT  
TTTTAAGTATGTTTTACTTATTATGGCTTAATAATTTAGTTCTGTTTAGAAAACCTTTGAATGTATGATA  
GAACTTCTGAATTTAATGGTGTTTTGGCATTGTTGTCAGTTTTCCCGATTGTAATGAGTTCTGATACCT  
TTGCTCAAATCCCAACATGTTCCAGCAGTTTAGTACCAGATTATTTGCATTTACCC

>HEC59\_DCAF13\_T7

ACGAATGCAGTGTAACGGGATTGATCATCACTGGAAGAAGCTGTTTTGCCACATGTGGACAGCAAGT  
AGACATTTGGGATGAACAAAGAATAATCCTATATGTTCAATGACCTGGGGATTGACAGTATAAGTAG  
TGTTAAATTTAACCCAATTGAGGTAATGTTTTTTTTAAGTATGTTTTACTTATTATGGCTTAATAATTTCA  
GTTCTGTTTAAAAAATTTTGAATGTATGAAAAAATCTCTGAATTTAATGGGGTTTTGGCATTGTTGTC

GTTTTCCCGATTGGAAATGAATTCTGAAACCTTTGCTCAAATCCCAACATGTTTCCCAGCAATTTAATCCC  
AAATACTAAAGTAATGTCACCTAAATGTCAAACTTTTTCCGGGATA

>HEC59\_DCAF13\_M13

TTTTTTTTTTGGAACCACAATAGGGTGTAAAACGACGGCCAGTGTTTACTGGGATTGATCATCACGGGAA  
AGAAGCTGTTTTGCCACATGTGGACAGCAAGTAGACATTTGGGATGAACAAAGAATTAATCCAATATG  
TTCAATGACCTGGGGATTTGACGGTATAAGTAGTGTTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTA  
AGTATGTTTTACTTATTATGGCTTAATAATTTAGTTCTGTTTAGAAAACTTTTGAATGTATGATAGAAAC  
TTCTGAATTTAATGGTGTTTGGCATTGTCAGTTTTCCCGATTGTAATGAGTTCTGATACCTTTGCTC  
AAATCCCAACATGTTCCCAGCAGTTTAGTCCCAGAACAGAGAAGCCC

**Alignment\_result\_DCAF13\_MS\_region:**

HEC1B_20_T7	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	204
LOVO_20_M13	TTAAATTTAACCCAATGGGGTAAAGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	237
LOVO_20_T7	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	202
HEC1B_20_M13	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	239
Hct116_20_M13	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	240
HEC59_20_M13	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	234
DCAF13_reference	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	235
HCT116_20_T7	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	202
HEC59_20_T7	TTAAATTTAACCCAATTGAGGTAATGTTTTTTTTTAAGTATGTTTACTTATTATGGCTT	200

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**Conclusion: LOVO has MS-related deletion**