

Table S1. TaqMan™ probe sequences. Sequences of custom TaqMan™ probes used for validation of novel miRNA candidates and sequences of two known miRNAs used as the reference.

Novel miRNA candidate ID / reference miRNA name	TaqMan™ probe sequence 5' -> 3'	Consensus mature miRNA sequence 5' -> 3'
2_nv_chr2_212678788	uuugcacugcacauccuuu	uuugcacugcacauccuu
3_nv_chr5_168090507	ugucucaugcaugguacucucu	ugucucaugcaugguacucucu
1_nv_chr6_1475207	cauggcauacuacugagcagu	cauggcauacuacugagcagu
6_nv_chr6_149118294	uuggggcagugagggucugugu	uuggggcagugagggucugugu
7_nv_chr7_9978163	auuugcuucugugauaacauga	auuugcuucugugauaacauga
4_nv_chr19_6613612	uuacauugggauuagagacaag	uacauugggauuagagacaaga
hsa-miR-191-5p (reference, validation of NGS experiment)	caacggaaucccaaaagcagcug	caacggaaucccaaaagcagcug
hsa-miR-361-5p (reference, validation of NGS experiment)	uuaucagaauccaggguac	uuaucagaauccaggguac
hsa-miR-423-3p (reference, validation of novel miRNAs biogenesis)	agcucggucugaggcccucagu	agcucggucugaggcccucagu

Table S2. *TENM2* expression primers. Primer sequences used for *TENM2* mRNA expression analysis.

Gene	Primer F 5' -> 3'	Primer R 5' -> 3'
<i>TENM2</i>	TCCCTTAGCACAGGGTCTGA	GAGCTAGGCAGCTGAGCAGA
<i>ACTB</i>	CACCACACCTTCTACAATG	TAGCACAGCCTGGATAG
<i>GAPDH</i>	GTCGGAGTCAACGGATT	CCTGGAAGATGGTGATGG

Table S3. Amplified sequences used in functional analysis. Genomic locations of amplified regions (GRCh38) and primer sequences used for amplification of two novel miRNA genes. The amplicons were used in further functional analysis. Detailed information about the amplified regions: whole amplified sequence, miRNA precursor sequence (green), mature miRNA sequence (highlighted in yellow) is presented below the table.

Novel miRNA gene	Primer F 5' -> 3'	Primer R 5' -> 3'	Genomic location of amplified region (GRCh38)	Genomic location of novel miRNA precursor sequence (GRCh38)	Genomic location of novel miRNA mature sequence (GRCh38)
2_nv_chr2_212678788	TGCAAAGTTTCATCCTTCCAG	GTGAAATCTGTGAACTGAAAATCA	chr2:212678556-212679130	chr2:212678788-212678849	chr2:212678791-212678810
3_nv_chr5_168090507	CCATCATTGTAGAAGGCCAGA	ACAAGAGATTGTGGCCTAGAGT	chr5:168090330-168090728	chr5:168090507-168090561	chr5:168090539-168090560

>chr2:212678556-212679130; 2_nv_chr2_212678788; (GRCh38)

TGCAAAGTTTCATCCTTCCAGATTCCCTACATCTAACTTCCTTTTACTGTAAATAACTCGGGTGGTGTAAATAGTCCGTTCTTATGCTGCTATAAAACAACCTCCCAAGACTGGGTAATTCATAAAG
AAAAGAAGTTCAGTTGACTCGCAGTTCTGCAGGGTTAGGGAAGCCTCAGGAACTTACAATCATGGTGGAAAGGGAAGCAAACACATCCTTCTTCACGTGGCAACAGAAAGGAGATGTGCAG
TGCAAATGGAGGGGGCATGGGGGCCATTTTCACTGCACTTCTCCTTCTGTTGCCATGTATAAAACCATCAGACCTCATGAGAACTCACTTACTGTATGAGAACAGCATGGGGGAACCGCTGCC
ATGATCTGTGCGCTCCCGTGAGGTTCTCCCCAACACATGGGGATTACAATTGGGATTACAATTCAAGATGAGATTTGGGTGGGGATACAGAGCCAAACCATATCTTCCACTTCTGACCAAA
TTAACTTATACATGAAGCAAATCCTCAAACATTCAAACAACAATTCAGATAATGATTTTCAGTTCACAGATTTTAC

>chr5:168090330-168090728; 3_nv_chr5_168090507; (GRCh38)

ACAAGAGATTGTGGCCTAGAGTAATAAAAGTATTAATAGTAGCAATAATTATAAAGCATAATAAATAATGACTGTTATTATTGTTACACATTTTGC GGCTCTTGT TTTCTGGATAAGTTCATAGC
AAAATGTGCTACAAAAAAGGTCTTTCTCCATTAACAAATGGGTTCTGGGGGGAGAGTACCAGGTATGGGACCACATCCACACCTTGTCTCATGCATGGTACTCTCTCTCCTTTTCCAGTATGACT
TCATGGAACGTCTGGACGGGAAGGAGAAGTGGAGTGTGGTTGAGTCTCCAGGGAACGCCGGAGCATACAGACCTTGTTTCAGAATGAAGCCGTGTTGTGCAGTACCTGGATGTGGGCCTG
TGGCATCTGGCCTTCTACAATGATGG

Table S4. Bisulfite DNA pyrosequencing primers. Genomic locations of amplified regions (GRCh38) and primer sequences used for bisulfite DNA pyrosequencing (DNA methylation analysis) of three regions corresponding to the two novel miRNA candidates.

miRNA candidate	Tested region/assay	Primer F 5' -> 3'	Primer R 5' -> 3'	Sequencing primer	Genomic location of amplified region (GRCh38)
2_nv_chr2_212678788	I	ATGTGTAGTGTAATGGAGGGGTAT	ATATCCCCACCCAAATCTCATCTT	AGAATAGTATGGGGGAA	chr2:212678797-212679018
3_nv_chr5_168090507	I	AGTTAGGTTTGAGTTTGGTATT	ATACAAAATAACCAAACTACATATTC	GTTTTAGTTTGGATTATGTTTT	chr5:167284647-167284800
	II	TGTGATTAATGGGATATGGGGTAGAGA	ACCAAAAAATAACAACCATTTTATTAAATACCTA	TTTGAGAAATGGAGAAAATTTTA	chr5:168088403-168088609

Table S5. pGEM[®]-T Easy Vector primer sequences. pGEM[®]-T Easy Vector primer sequences used for amplification and Sanger sequencing of nv_chr2_212678788 and 3_nv_chr5_168090507 novel miRNA sequences.

	M13 Forward	M13 Reverse
Primer sequence 5' -> 3'	GTAAAACGACGGCCAG	CAGGAAACAGCTATGAC

Table S7. Functional enrichment analysis results. Functional enrichments found in the group of 45 genes that are the putative targets of the novel 2_nv_chr2_212678788 miRNA expressed in cHL cell lines (STRING, GO Consortium).

List of 45 genes used in functional enrichment analysis (putative targets of novel 2_nv_chr2_212678788)	<i>KCNN3, TEAD1, TECPR2, RBMS3, CLOCK, SPRED1, RORA, AKAP5, PDE10A, LRCH1, FNBP1L, JOSD1, DCAF6, FNIP1, FPGT, GABRA4, ZFHX3, BCL11A, GATA6, IKZF2, PDZD2, KLHL14, JAZF1, TMEM56, CDK6, MYCBP2, IDH1, ST8SIA1, AMMECR1L, NCOA2, PTAR1, DYRK1A, C1orf174, ZNF681, CCDC93, UNKL, NUDT16, SLC38A2, BRWD1, TEF, GTF2H1, FANCI, GRHL1, HIPK3, SLC17A6</i>
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Biological process	Term ID	FDR STRING	FDR GO Consortium
Regulation of transcription by RNA polymerase II	GO:0006357	0.0130	2,55E-02
Circadian rhythm	GO:0007623	0.0130	7,14E-03
Positive regulation of gene expression	GO:0010628	0.0130	4,09E-02
Circadian regulation of gene expression	GO:0032922	0.0130	6,86E-03
Positive regulation of transcription, DNA-templated	GO:0045893	0.0130	3,52E-02
Positive regulation of nucleobase-containing compound metabolic process	GO:0045935	0.0130	2,92E-02
Rhythmic process	GO:0048511	0.0130	1,23E-02
Positive regulation of RNA metabolic process	GO:0051254	0.0130	3,35E-02
Positive regulation of macromolecule biosynthetic process	GO:0010557	0.0130	5,05E-02
Positive regulation of nitrogen compound metabolic process	GO:0051173	0.0152	3,64E-02
Regulation of RNA metabolic process	GO:0051252	0.0152	4,16E-02
Positive regulation of cellular metabolic process	GO:0031325	0.0152	4,26E-02
Positive regulation of macromolecule metabolic process	GO:0010604	0.0152	3,38E-02

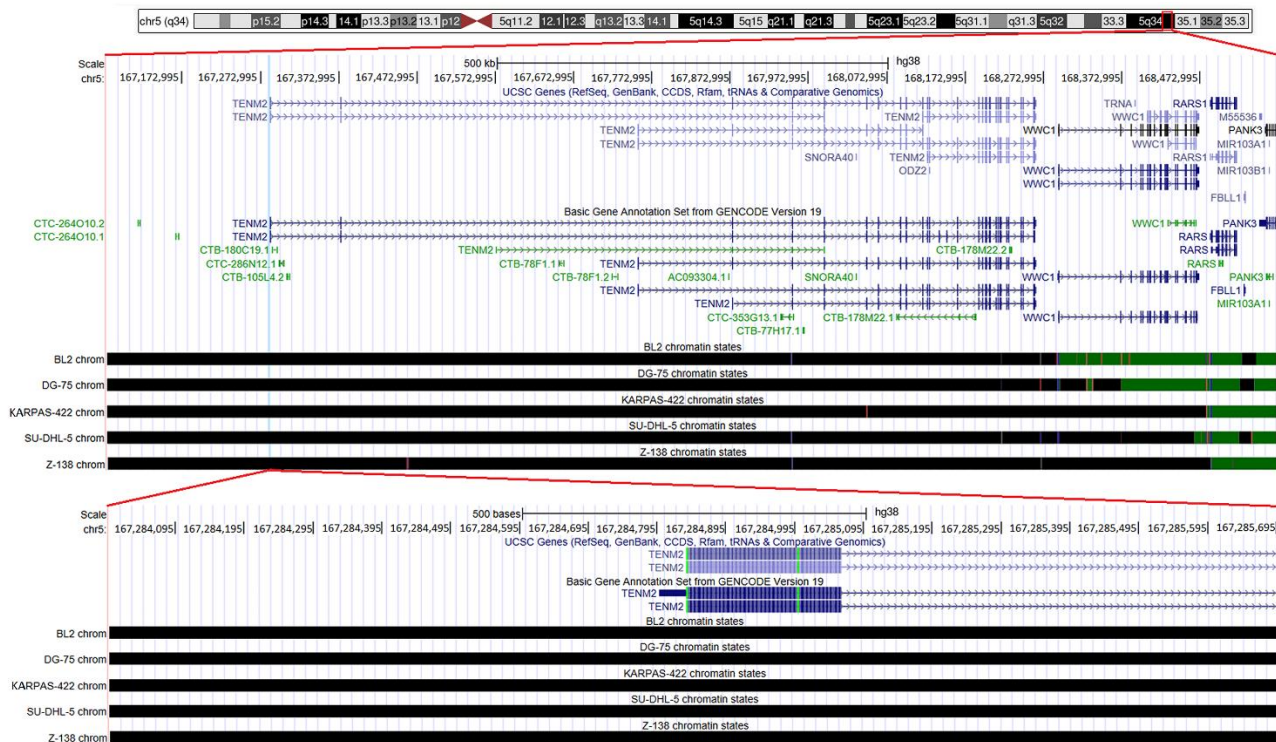


Fig S1. *TENM2* chromatin activity profile. The visualisation (UCSC) of data from BLUEPRINT project (<https://www.blueprint-epigenome.eu/index.cfm?p=3D6C68FA-3048-9110-625D850E3E055A84>) regarding chromatin activity of *TENM2* promoter region (vertical blue bar showed on upper panel). The ChIP-seq (H3K27ac) experiment was performed on 5 NHL cell lines. The horizontal bars near particular cell line name represent chromatin state. Black colour of the bar indicates inactive heterochromatin region, whereas other colours are showing active states of chromatin. The 27th lysine acetylation for *TENM2* promoter region shows fully closed chromatin regions in all NHL cell lines.

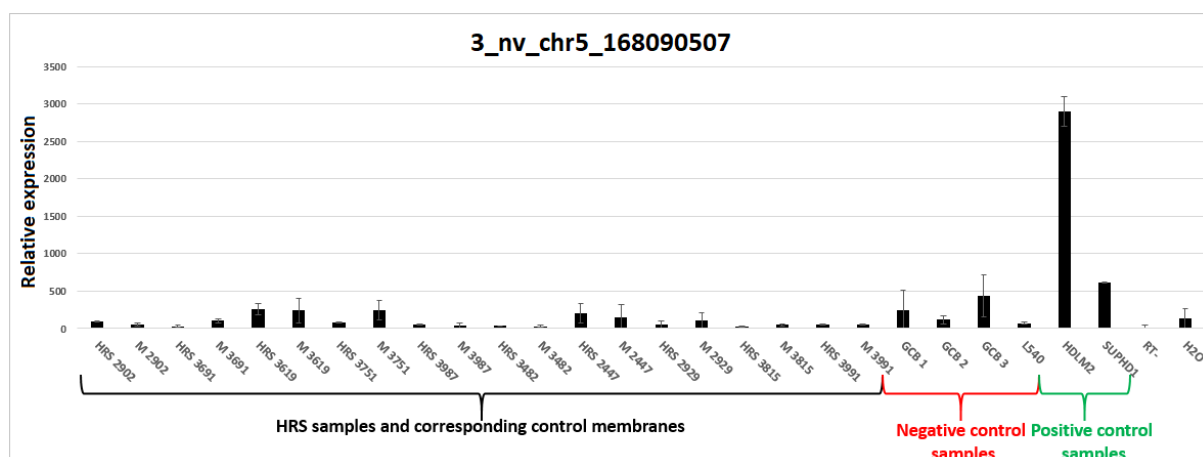


Fig S2. Novel miRNA expression in HRS cells. Expression of 3_nv_chr5_168090507 novel miRNA in 10 primary microdissected HRS cell pools with corresponding membrane negative controls. (cHL cell lines (green) and GC B cells (red) are shown as positive and negative controls, respectively.