**Supplementary Materials– Tables 1-7**

**Table S1.** shRNA sequences and CRISPR dCas9 gRNAs

| **Description** | **Location (bp upstream of the gene)** | **Sequence** |
|---|---|---|
| gRNA1 (617 in mass spec) | *Lhb* (-3676)-(-3657) | ATCCAGAGCTTCCTGCGGGC |
| gRNA3 (618 in mass spec) | *Lhb* (-3800)-(-3781) | CTCCCTAATGCCGGCATTAA |
| gRNA4 (p594) | *Lhb* (-3565)-(-3546) | TTAAAACTGGACCGTTGCTG |
| shRNA for eRNAs | | |
| #1 (p591) | *Lhb* (-3754)-(-3736) | AGAAGATAAATTCAAGGCG |
| #2 (p549) | *Lhb* (-4872)-(-4854) | TTCCCAAGCCTGGACCTCA |
| #3 (p544) | *Lhb* (2632)-(-2614) | CCAGGGGCAACGGTCACAA |
| #4 (p548) | *Lhb* (2632)-(-2614) | TTGTGACCGTTGCCCCTGG |
| shRNA for Hmgb2 | *Hmgb2* (+817)-(+835) exon2 | CCAAGAAATGCTCCGAGAG |

**Table S2.** U1 site mutations

| **LncRNA site** | **Sequence** | **Mutated sequence** |
|---|---|---|
| End of exon 1 | CAG GTGAGA | CAG CCGAGA |
| End of exon 2 | AAG GTAGGG | AAG CCAGGG |
| End of exon 3 | CAG GTAGAG | CAG CCAGAG |
| End of exon 4 | AAG GTGAGC | AAG CCGAGC |
| Mid intron 1 (-2330) | AAG GTGGAG | AAG CCGGAG |
| Mid intron 3 (-1473 | CAG GTAGGA | CAG CCAGGA |

**Table S3.** Primers

| **Primer #** | **Gene (*Lhb* unless noted) and position** | **Sequence (5' to 3')** |
|---|---|---|
| **Primers used for ChIP (many used also for PCR)** | | |
| 1490 | -5228F | GTGAGCTGGCAGTATGCGA |
| 1491 | -5086R | CGTCTCGAAGAAGTACTGAC |
| 596 | -5005F | GCTCTCAGAATGCAAGGCTA |
| 614 | -4796R | GGTCCTTTCAGCATCCAGCT |
| 595 | -4435F | CTCCATCCTGAACATCATAAAC |
| 1518 | -4326R | CAGACAAGGCTGGCTTCAAC |
| 594 | -4275F | TATGTACTGTAATCCTAATGCTTA |
| 613 | -4076R | CAGGTGGGACTTGTCTGGTG |
| 1583 | -3775F | TACATCACCACTGTGTGGCT |
| 1584 | -3705F | TGTATTATGCAGTCAGTGCTG |
| 1535 | -3662R | CAGGAAGCTCTGGATTCCAT |
| 1536 | -3638R | TTCAGATGAGGGAGCTCCTG |
| 1619 | -3610F | CCTTTCCAATGCTTTGGGAC |
| 1527 | -3567R | CCAGCCTGAGCTTGGTGAG |
| 1620 | -3533R | TTAAGGTCATCCTCAGCAAC |
| 546 | -3485F | TTGAGTGTTTTTGCCTGCATG |

| | | |
|---|---|---|
| 1521 | -3458F | GGGTCTTCATGCATGGGTGT |
| 612 | -3286R | TGATCTACTCTACTCGCACAC |
| 450 | -3257F | CCTCCTTGGTGTTGGAGAAA |
| 451 | -3102R | GAGAGTGGGAGGTGGCTAGA |
| 1384 | -2802F | TGTATTCCCTCACCTCACCT |
| 1385 | -2633R | TAACAGAACCTGCCCACTCT |
| 572 | -2432F | TCTGCCTACTCTCCAGGTGA |
| 548 | -2255F | CTGATCTATGCGCCTTCACA |
| 112 | -2196R | TTTCGAGACTGCAGGCAGGG |
| 562 | -2096R | TGGGGTCCTTGTGCTCTGGT |
| 1943 | -635F | GGCCTACTGCACTGAGAATT |
| 907 | -520F | GACACACCCCTTACTTCCAGAG |
| 1944 | -474R | GATCAGTAAATTGCGCCTGG |
| 909 | -424F | ATCCTGATTAGGGGCTGGGAG |
| 908 | -421R | GGATGCCTGGATTGGGTCCAA |
| 910 | -325R | GGCACAGCTTCAACCTTAGGTT |
| 913 | -235F | CTCCCCTTTACCTTGTTTCCCGT |
| 1937 | -225F | CCTTGTTTCCCGTGCTTCCA |
| 915 | -141F | TCCCTGGCTTCCCTGACCTTG |
| 914 | -136R | CAGGGACTAGCTCCAGTGTC |
| 1938 | -79R | TGGGTAACCTAGACACTAATC |
| 1935 | -68F | CACTACTTAGTGGCCTTGCC |
| 917 | -44F | CCACAACCCGCAGGTATAA |
| 916 | -42R | TGGGGGTGGCAAGGCCACTA |
| 919 | +51F | AATCCCACCAAACCCATAGATG |
| 918 | +54R | GATTGGGAAGTACCCTGGG |
| 1936 | +61R | TGGTGGGATTGGGAAGTACC |
| 1939 | +62F | AACCCATAGATGGACAGCCT |
| 955 | +106F | AGAGGAGGGGGTCTCCTA |
| 920 | +150R | GTTTATCTCCTGTTTGAAGTCCAC |
| 1940 | +250R | TCACTCTACCCCTGACCTG |
| 966 | +271R | CCCTGGGACATAGCCAGTG |
| 286 | *Atoh*F | CCCTCACTCAGGTCGCCTG |
| 287 | *Atoh*R | CGTGCGAGGAGCCAATCA |
| 382 | mCga -5139R | GCGTTCACAATAACTTGTAACC |
| 440 | mCga -5377F | TTGGGAACCTTTGTTTTTGACACTTT |
| 3093 | G4 positiveF Cga intron1 | TGGCAATAGGGGAATTTCCAG |
| 3094 | G4 positiveR Cga intron1 | TAACCGGATCTGTTTGCAATC |
| 3124 | G4 negative | CTGAAGTTCATTATGCAATGTTTG |
| 3123 | G4 negative | CCCCTATATCAGTTGTTATATTC |
| 1959 | mZnrf2F intron | AGATTGGATGCTCCTGTAGG |

| | | |
|---|---|---|
| 1960 | mZnrf2R intron | CCTGAGAACAAAGCCACAGC |
| **3C Primers** | | |
| 598 | -6005F | CCAGCAGCCAAGTCAGTCTC |
| 597 | -5105F | GTCAGTACTTCTTCGAGACG |
| 596 | -5005F | GCTCTCAGAATGCAAGGCTA |
| 595 | -4435F | CTCCATCCTGAACATCATAAAC |
| 594 | -4275F | TATGTACTGTAATCCTAATGCTTA |
| 546 | -3485F | TTGAGTGTTTTTGCCTGCATG |
| 111 | -2513F | GGTACTTGGAACCTGGCCCA |
| 593 | -2375F | ACTTGTGTGCCAGGAGGAAA |
| 59 | -1991F | GAATCTTTGGGCTCCCTTC |
| 549 | -1355F | CCACTAAGTGTTTGGATAGG |
| 545 | +379F | TCTGCCCAGTCTGCATCACC |
| 44 | +344F | GCCTGTCAACGCAACTCTGG |
| **UMI-4C primers** | | |
| *Lhb* downstream (nested) | | GTCCAAAAATAGGTGTGGTTTCAGC |
| *Lhb* upstream (outer) | | CCCTAATCAGGATGCCTGGA |
| **Additional Primers for eRNA and lncRNA characterization** | | |
| 1387 | -4856R | CCCAAGCCTGGACCTCAG |
| 563 | -2825F | AGCCTGTCTGTCTCTGTGTC |
| 564 | -2606R | CCGGCTTGTTGTGACCGTTG |
| 1424 | -2655F | TTCAGAGTGGGCAGGTTCTG |
| 2276 | -2575F | ATGGCAGGTCGAACCCTAGC |
| 2286 | -2152R | GGGGTGTATGTAGACTGTGA |
| 2278 | -2232F | TCTATGGTCAAGGCACCCCT |
| 2279 | -2061R | CTTTTCTGCCAAAGACTTGATG |
| 2280 | -1966F | CTAAGAAGACATGAGGGACG |
| 2281 | -1803R | CTGAGAAGGTCCCCCGCGA |
| 60 | -1743R | CAGGCTCCTTCCTGCAGTGC |
| 2282 | -1235F | GCCCTCATCCCCTGGACGA |
| 2283 | -1117R | CTTGTGAAGTCACTTGCAGTA |
| 55 | -952F | ATCTGAACTCTGCTGCACTT |
| 2284 | -903F | GAACGTGTCTGGATATCCCC |
| 2285 | -582R | TCACAGCAGCTCCGCCCTG |
| 367 | -394R | GCACCACCGTCTCCCAGCCC |
| 181 | -151R | GTGTCCCAGTGAATTGGCCTCA |
| 2311 | -863R | GCCCATCACCGGTTTCTGGT |
| 2312 | -2593F | CAGAGAAGGTGAGGACCATG |
| 2313 | -2611F | AGCCGGTTTCTTGGCTTCC |
| 2314 | -1106R | CACAGGCTCACCTTGTGAA |
| 2315 | -1088R | TCACCAGCGCCTGCTGGG |
| 2316 | -880R | GGTGGGGATATCCAGACAC |
| 2324 | -814R | CTCGGTAAACTTGCCCGATC |

| | | |
|---|---|---|
| 2326 | -729R | GTGCACCAAGGGTCCGTAG |
| 2321 | -643R | ACACTGTAAAGGCCCAGCAC |
| 612 | -3286R | TGATCTACTCTACTCGCACAC |
| 2300 | -3685R | CAGCACTGACTGCATAATACA |
| 2317 | +691R | CCCGGTGGGCAGCCAGG |
| 493 | +572R | AAGCCCTCTTCTGAGTGTCC |
| **Gene expression levels PCR** | | |
| 46 | *Lhb* (+601)F | TGCCGGCTGCTTTGCCTCCT |
| 45 | *Lhb* (+796)R | CAGGCCATTGGTTGAGTCCT |
| 350 | *Lhb* ($2^{nd}$+$3^{rd}$) exon (+590)F | CTAGCATGGTCCGAGTACTG |
| 351 | *Lhb* $3^{rd}$ exon (+727)R | CTGAGGGCTACAGGAAAGGA |
| 184 | *Rplp0* F | GCGACCTGGAAGTCCAACTA |
| 185 | *Rplp0* R | ATCTGCTTGGAGCCCACAT |
| 1384 | eRNA1 F *Lhb* (-2802) | TGTATTCCCTCACCTCACCT |
| 1385 | eRNA1 R *Lhb* (-2633) | TAACAGAACCTGCCCACTCT |
| 1583 | eRNA1 F *Lhb* (-3775) | TACATCACCACTGTGTGGCT |
| 1534 | eRNA1 R *Lhb* (-3682) | CCCCAGCACTGACTGCATAA |
| 1961 | *Znrf2* F cDNA | ACAGGACTCAGTGCACAGC |
| 1962 | *Znrf2* R cDNA | TGAGCATACCGGGCACTTA |
| 1923 | *Hmgb2* F | CGACTCGTCGGTGAACTTCG |
| 1924 | *Hmgb2* R | CTTCGGAGCATTGGGGTCTT |
| 1672 | *Greb1* $3^{rd}$ exon F | GCCGAGCAGACAATGAGGAA |
| 1673 | *Greb1* $4^{th}$ exon R | CAGGCTGGGAGACTTAGCAC |

**Table S4** Oligonucleotides used for CD

| **Description** | **Sequence** |
|---|---|
| *Lhb* G-quadruplex | GGAAAGGTGGGGGTGGGGGTGGGGTGGGGTGGGG |
| *Lhb* G4 kill4 | GGAAAGGTGGTGGTGGTGGGGTGGAGTGGTG |
| *Lhb* G4 kill5 | GGAAAGGTGGTGGTGGTGGTGGTGTGGTGTGGTG |
| *Lhb* G4 kill7 | GGAAAGGTGGAGGTGGAGGTGGTGTGTGATGAGT |
| *Lhb* G-quadruplex mutated | GGAAAGGTGTTTGTGTTTGTGTTGTGTTGTGTTG |
| *c-MYC* G-quadruplex (human) | GGGGAGGGTGGGGAGGGTGGGGAAGGTGGGG |
| *Lhb* i-motif | CCCCACCCCACCCCACCCCCACCCCCACCTTTCC |
| *Lhb* i-M kill4 | CTCCACACCACCCCACCTCCACCTCCACCTTTCC |
| *Lhb* i-M kill7 | TCACAACTCACTCCACCACCACCACCACCTTTCC |
| *Lhb* i-motif mutated | CTTCACTTCACTTCACTTTCACTTTCACCTTTCC |
| *c-MYC* i-motif (human) | CCCCACCTTCCCCACCCTCCCCACCCTCCCC |

**Table S5** Constructs for protein pull down

| # | Description |
|---|---|
| 507 | Control construct, dCas9 without any gRNA |
| 617 | dCAS9 with gRNA1 (Table S3) targeting (-3676) -(3658) upstream of *Lhb* |
| 618 | dCAS9 with gRNA3 (Table S3) targeting (-3800) -(3781) upstream of *Lhb* |

**Table S6**. Sequences upstream of the *Lhb* gene predicted to form G-quadruplex (by both pqsfinder and G4 Hunter). All are shown 5' to 3'.

| Description | Strand of G4 | Putative G4 forming sequence | Pqsfinder score | G4 Hunter score |
|---|---|---|---|---|
| *Lhb* enhancer | (-) | GGGGGTGGGGGTGGGGTGGGGTGGGG | 115 | 3.385 |
| LncRNA promoter | (-) | GAGTGGGAGGTGGCTAGAGGGTGGG | 52 | 1.48 |
| | (-) | AACGGGGGAGGGGAGGGGGTATGGG | 94 | 2.56 |
| | (-) | TGGGTATGGGGGGCTGGGGAGACTG | 70 | 1.96 |
| LncRNA 1st intron | (+) | GGGTGGAGGGTGAGATAGGGAAAGGGGG | 57 | 1.76 |
| | (+) | GGGGTCTGGGAGCCTGGATACCAGGAGTTGGAGGAAG | 53 | 1.4 |
| LncRNA 3rd Exon | (-) | GGTGGTCAGCGAGCTCTGGGGGCTGGGGCTCTGCAAA GAGGGGGGCACTC | 81 | 1.84 |
| *Lhb* 1st intron | (-) | ATGGGTTTGGTGGGATTGGGAAGTACCCTGGG | 52 | 1.28 |
| | (+) | GGGGGTTGGAGGAGGGAGAGGAGGGGG | 103 | 2.16 |

**Table S7.** Proteins detected (≥3 peptides) following pull-down with both probes (617 and 618) and not with the control (507)

| | | | | | 507 | 617 | 618 |
|---|---|---|---|---|---|---|---|
| Gene names | ΣCoverage | Σ# Unique Peptides | Σ# Peptides | Σ# PSMs | A2: Area | B2: Area | C2: Area |
| Hmgb2 | 18.1 | 4 | 4 | 9 | 0.00E+00 | 2.59E+07 | 3.36E+06 |
| Afdn | 2.88 | 4 | 4 | 5 | 0.00E+00 | 4.53E+06 | 2.12E+06 |
| Gss | 6.33 | 3 | 3 | 4 | 0.00E+00 | 1.70E+07 | 2.11E+06 |
| Trove2 | 5.76 | 3 | 3 | 5 | 0.00E+00 | 1.29E+07 | 2.73E+06 |
| Stoml2 | 11.05 | 3 | 3 | 6 | 0.00E+00 | 3.50E+06 | 4.18E+06 |
| Tecr | 8.53 | 3 | 3 | 4 | 0.00E+00 | 3.90E+07 | 6.76E+06 |
| Camk2d | 25 | 3 | 3 | 5 | 0.00E+00 | 6.22E+06 | 1.95E+06 |

The peptides were filtered with high confidence and passed the 1% FDR threshold. Semi quantitation was performed by calculating the peak area of each peptide: the area is the average of the three most intense peptides from each protein.