

Supplemental Information

Analysis of Dual Histone Modification-Binding Protein Interaction Network by Combining Mass Spectrometry with Isothermal Titration Calorimetry

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Figures

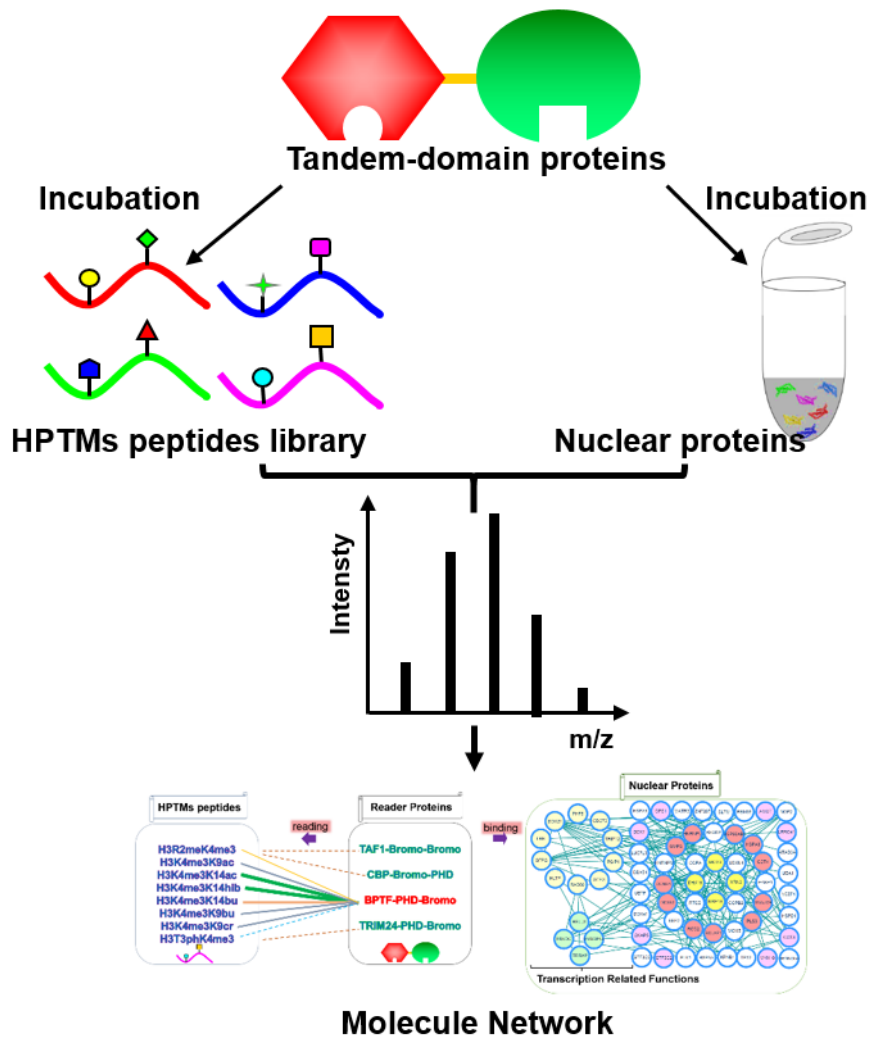


Fig S1. The schematic view of the approach.

First, the tandem-domain proteins were incubated with combinatorial HPTMs peptides and HEK293T nuclear extract separately. Then the enriched peptides or nuclear proteins were identified by MALDI-TOF MS or HPLC-MS/MS. Finally, the network of “HPTMs-reader proteins-binding proteins” was built.

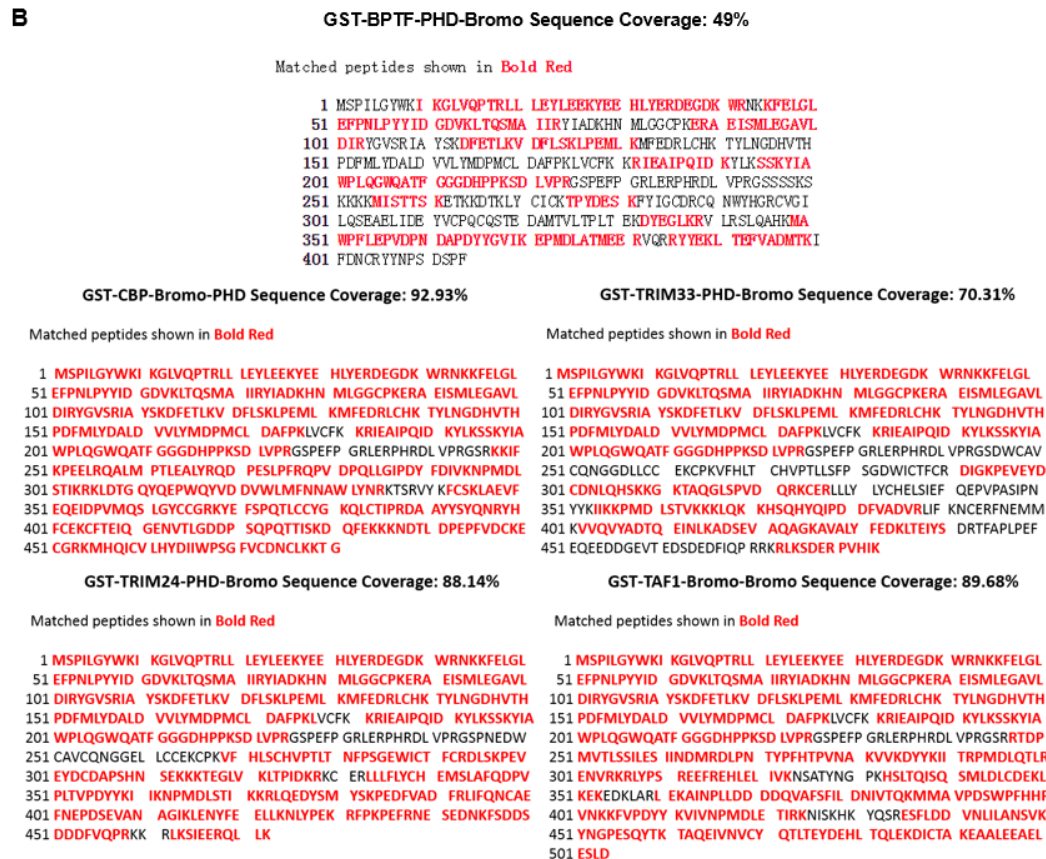
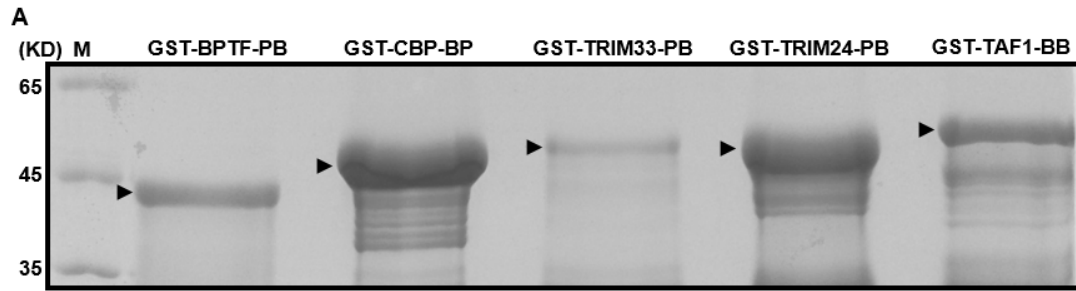


Fig S2. The identification of the tandem-domain proteins (BPTF-PB, CBP-BP, TRIM24-PB, TRIM33-PB and TAF1-BB) by HPLC-MS/MS.

A). The SDS-PAGE gel of the GST tagged tandem-domain proteins (BPTF-PB, CBP-BP, TRIM24-PB, TRIM33-PB and TAF1-BB); B) The identification of these proteins by HPLC-MS/MS.

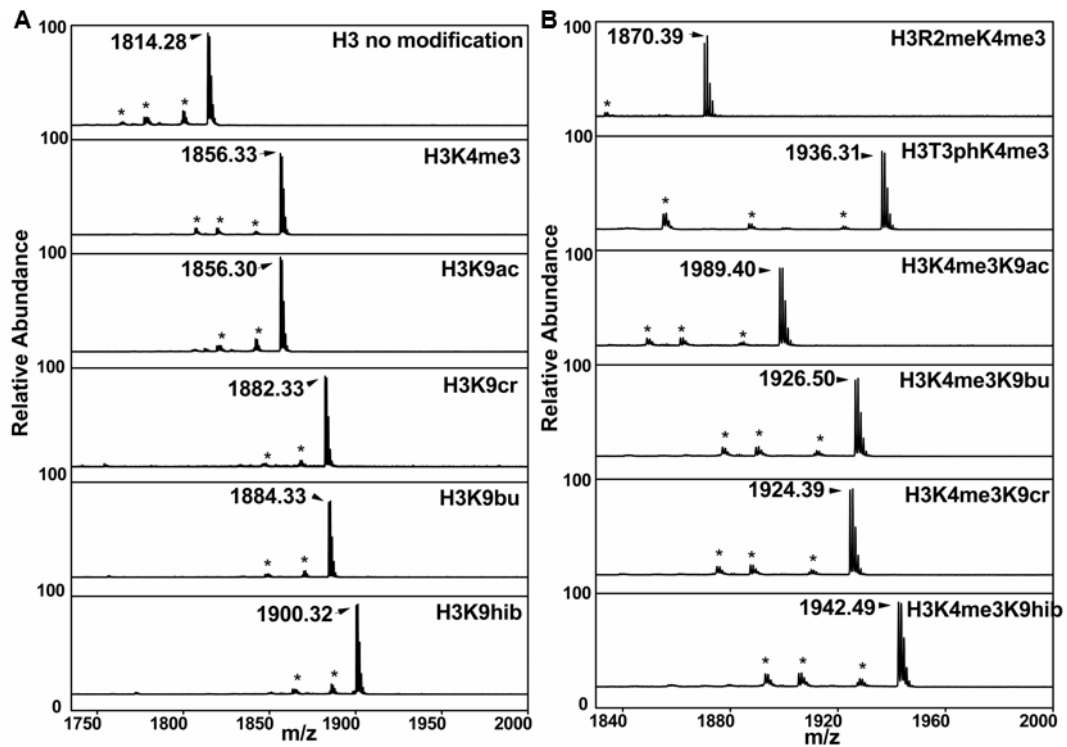


Fig S3. The identification of HPTMs peptides by MALDI-TOF MS.

A). The identification of single HPTMs peptides by MALDI-TOF MS; B). The identification of combinatorial HPTMs peptides by MALDI-TOF MS. The arrow points to the target peptide. While, the asterisk points to the false positive peptides.

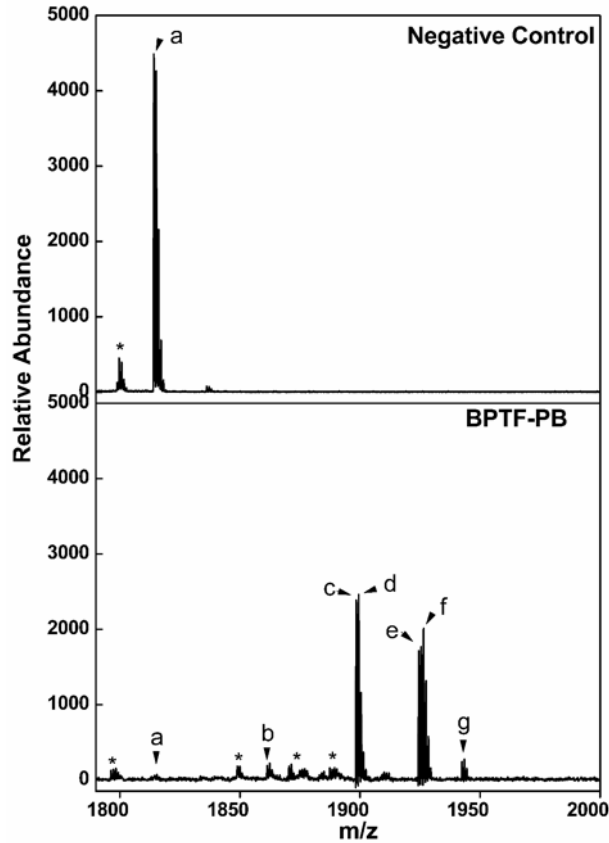


Fig S4. The identification of peptides enriched by GST beads and BPTF-PB by MALDI-TOF MS.

The peptide mixture incubated only with GST beads were set as negative control. Except control peptide (a), all peptides could be enriched by tandem-domain protein BPTF-PB instead of GST beads by peptide pull-down.

a, control, H3(1-17), peptide with no modification (1814.39 Dalton), b, H3R2meK4me3 (1870.39 Dalton), c, H3K4me3K9ac (1898.40 Dalton), d, H3K4me3K14ac (1898.65 Dalton), e, H3K4me3K9cr (1924.39 Dalton), f, H3K4me3K9bu (1926.50 Dalton), h, H3K4me3K9hib (1942.49 Dalton). The asterisk points to the false positive peptides.

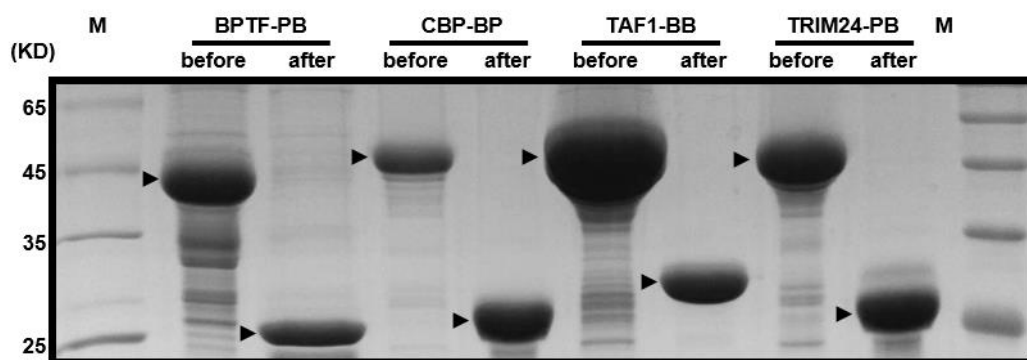


Fig S5. The SDS-PAGE of the tandem-domain proteins during ITC array.

To remove the GST tag, the tandem-domain proteins (GST-BPTF-PB, GST-CBP-BP, GST-TRIM24-PB and GST-TAF1-BB) were digested by thrombin proteases. (“before” refer to before enzyme digestion; “after” refer to after enzyme digestion) Then the tandem-domain proteins were titrated by peptides during ITC array.

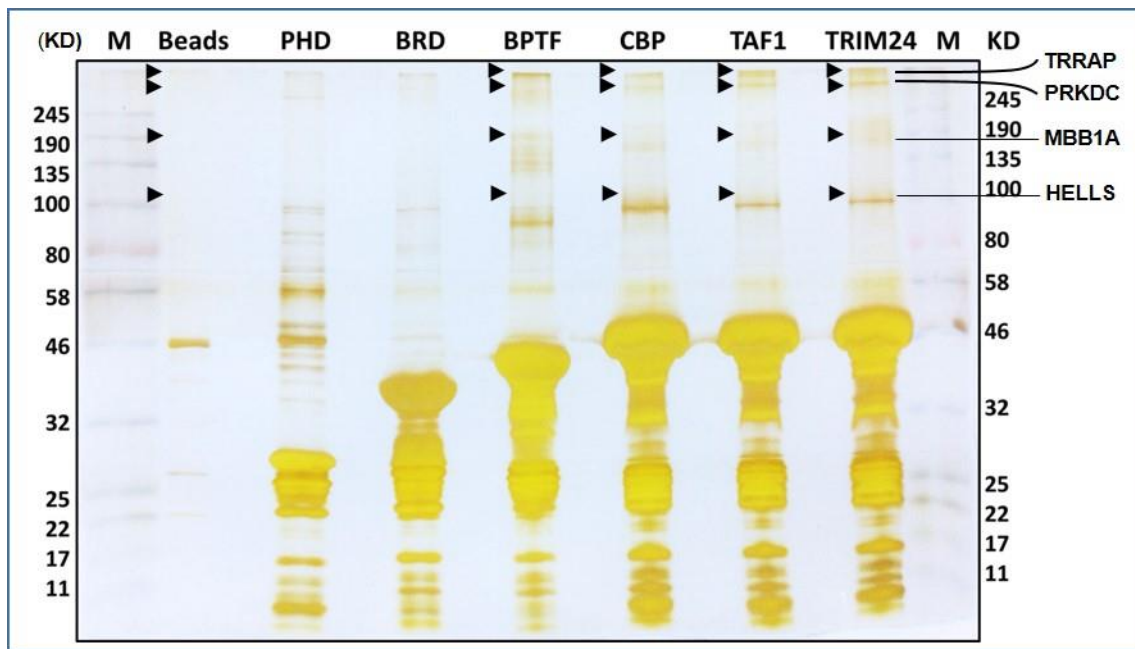


Fig S6. The proteins (MBB1A, HELLS, PRKDC and TRRAP) were pointed out in silver stain gel.

The enriched nuclear proteins were separated by silver dye gradient gel. The proteins in each electrophoresis lane were cut and digested in gel by trypsin, and finally identified by HPLC-MS/MS. The four screened proteins (MBB1A, HELLS, PRKDC and TRRAP) were pointed out in the gel. (MBB1A, 149KD, HELLS, 97KD, PRKDC, 469KD, TRRAP, 437.6KD).

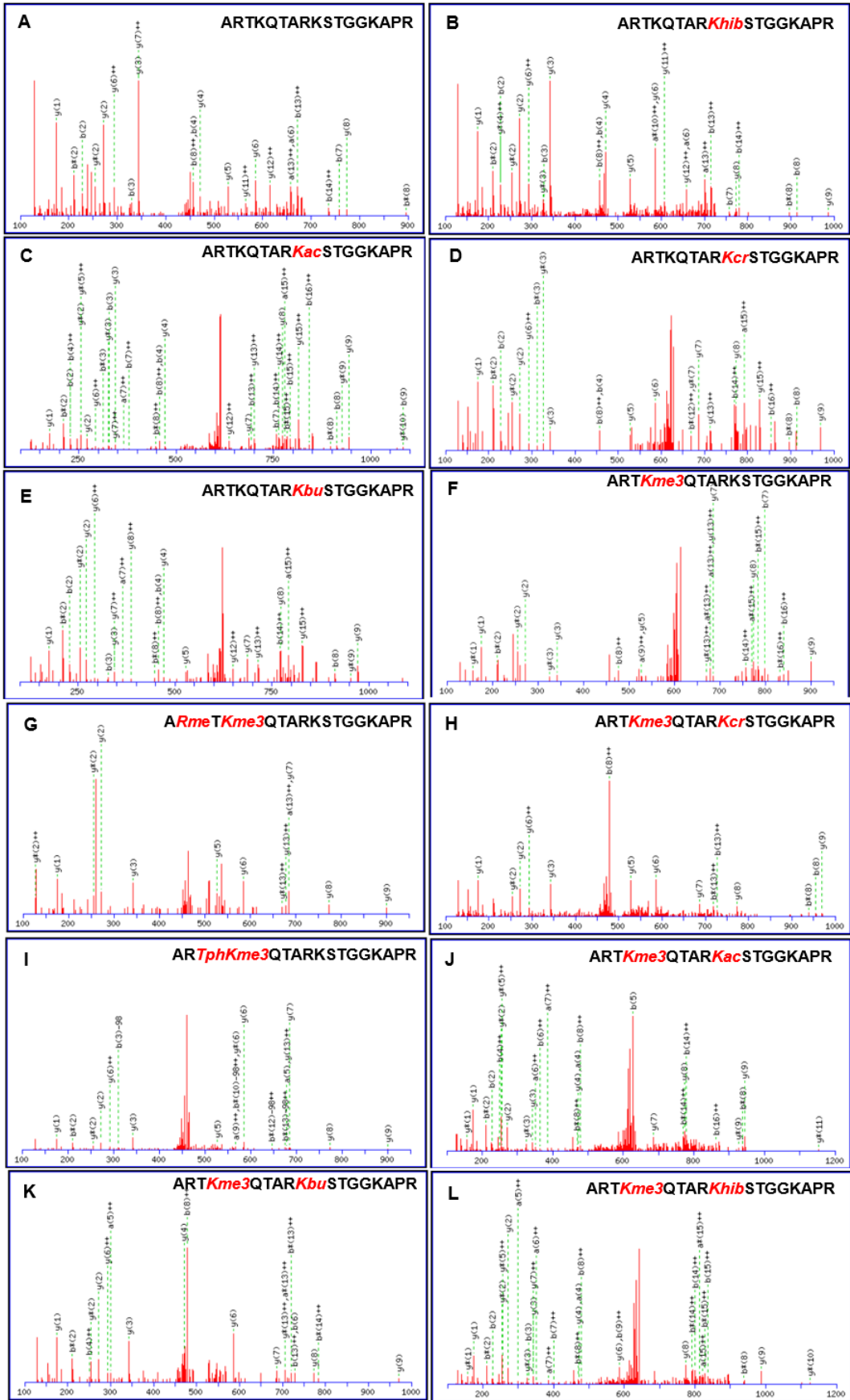


Fig S7. The sequence identification of HPTMs peptides by MS/MS.

- A. MS/MS Fragmentation of H3 (1-17) with no modification (ARTKQTARKSTGGKAPR);
- B. MS/MS Fragmentation of H3K9hib (ARTKQTAR*Khib*STGGKAPR);
- C. MS/MS Fragmentation of H3K9ac (ARTKQTAR*Kac*STGGKAPR);
- D. MS/MS Fragmentation of H3K9cr (ARTKQTAR*Kcr*STGGKAPR);
- E. MS/MS Fragmentation of H3K9bu (ARTKQTAR*Kbu*STGGKAPR);
- F. MS/MS Fragmentation of H3K4me3 (ART*Kme3*QTARKSTGGKAPR);
- G. MS/MS Fragmentation of H3R2meK4me3 (A*Rme*T*Kme3*QTARKSTGGKAPR);
- H. MS/MS Fragmentation of H3K4me3K9cr (ART*Kme3*QTAR*Kcr*STGGKAPR);
- I. MS/MS Fragmentation of H3T3phK4me3 (AR*Tph**Kme3*QTARKSTGGKAPR);
- J. MS/MS Fragmentation of H3K4me3K9ac (ART*Kme3*QTAR*Kac*STGGKAPR).

BPTF-PB

```
Query 1      TOCAGCTCAAAGTCCAAGAAAAAGAAAATGATCTCTACTACCTCAAAGGAAACTAAGAAG 60
             |||
Sbjct 8326   TOCAGCTCAAAGTCCAAGAAAAAGAAAATGATCTCTACTACCTCAAAGGAAACTAAGAAG 8385

Query 61     GACACAAAGCTTTACTGTATCTGTAAAACGCTTATGATGAATCTAAATTTTATATTGGC 120
             |||
Sbjct 8386   GACACAAAGCTTTACTGTATCTGTAAAACGCTTATGATGAATCTAAATTTTATATTGGC 8445

Query 121    TGTGATCGGTGTCAGAAATGGTACCATGGGCGCTGCGTTGGCATCTTGCAAAGTGAGGCA 180
             |||
Sbjct 8446   TGTGATCGGTGTCAGAAATGGTACCATGGGCGCTGCGTTGGCATCTTGCAAAGTGAGGCA 8505

Query 181    GAGCTCATTGATGAGTATGTCTGTCCACAGTGCCAGTCAACAGAGGATGCCATGACAGTG 240
             |||
Sbjct 8506   GAGCTCATTGATGAGTATGTCTGTCCACAGTGCCAGTCAACAGAGGATGCCATGACAGTG 8565

Query 241    CTCACGCCACTAACACAGAGAAGGATTATGAGGGGTTGAAGAGGGTGCTCCGTTCCCTTACAG 300
             |||
Sbjct 8566   CTCACGCCACTAACACAGAGAAGGATTATGAGGGGTTGAAGAGGGTGCTCCGTTCCCTTACAG 8625

Query 301    GOCCATAAGATGGCTGGCTTTCCCTTGAACCCAGTAGACCCCTAATGATGCACCAGATTAT 360
             |||
Sbjct 8626   GOCCATAAGATGGCTGGCTTTCCCTTGAACCCAGTAGACCCCTAATGATGCACCAGATTAT 8685

Query 361    TATGGTGTATTAAAGGAAOCTATGGACCTTGCCACCATGGAAGAAAAGAGTACAAAAGACGA 420
             |||
Sbjct 8686   TATGGTGTATTAAAGGAAOCTATGGACCTTGCCACCATGGAAGAAAAGAGTACAAAAGACGA 8745

Query 421    TATTATGAAAAGCTGACGGAATTTGTGGCAGATATGACCAAAATTTTGTATAACTGTCGT 480
             |||
Sbjct 8746   TATTATGAAAAGCTGACGGAATTTGTGGCAGATATGACCAAAATTTTGTATAACTGTCGT 8805

Query 481    TACTACAATCCAAGTGACTCCOCATTT 507
             |||
Sbjct 8806   TACTACAATCCAAGTGACTCCOCATTT 8832
```

Fig S8. The sequence alignment of the plasmid pGEX4T-BPTF-PB in GenBank

The sequence identity match of the plasmid pGEX4T-BPTF-PB was 100%, comparing to that of human sapiens bromodomain PHD finger transcription factor (BPTF) in GenBank.

CBP-BP

```
Query 1 CGCaa aaaaaaTCTTTAAACCAGAGGAGTTACGCCAGGCCTCATGCCAACCCTAGAAGCA 60
      |||
Sbjct 4038 CGCAAAAAAATCTTTAAACCAGAGGAGTTACGCCAGGCCTCATGCCAACCCTAGAAGCA 4097

Query 61 CTGTATCGACAGGACCCAGAGTCATTACCTTTCCGGCAGCCTGTAGATCCCCAGCTCCTC 120
      |||
Sbjct 4098 CTGTATCGACAGGACCCAGAGTCATTACCTTTCCGGCAGCCTGTAGATCCCCAGCTCCTC 4157

Query 121 GGAATTCAGACTATTTTGACATCGTAAAGAATCCCATGGACCTCTCCACCATCAAGCGG 180
      |||
Sbjct 4158 GGAATTCAGACTATTTTGACATCGTAAAGAATCCCATGGACCTCTCCACCATCAAGCGG 4217

Query 181 AAGCTGGACACAGGGCAATACC AAGAGCCCTGGCAGTACGTGGACGACGTCTGGCTCATG 240
      |||
Sbjct 4218 AAGCTGGACACAGGGCAATACC AAGAGCCCTGGCAGTACGTGGACGACGTCTGGCTCATG 4277

Query 241 TTCAACAATGCCTGGCTCTATAATCGAAGACATCCCGAGTCTATAAGTTTTGCAGTAAG 300
      |||
Sbjct 4278 TTCAACAATGCCTGGCTCTATAATCGAAGACATCCCGAGTCTATAAGTTTTGCAGTAAG 4337

Query 301 CTTGCAGAGGTCTTTGAGCAGGAAATTGACCCTGTCATGCAGTCCCTTGGATATTGCTGT 360
      |||
Sbjct 4338 CTTGCAGAGGTCTTTGAGCAGGAAATTGACCCTGTCATGCAGTCCCTTGGATATTGCTGT 4397

Query 361 GGACGCAAGTATGAGTTTTCCCCACAGACTTTGTGCTGCTATGGGAAGCAGCTGTGTACC 420
      |||
Sbjct 4398 GGACGCAAGTATGAGTTTTCCCCACAGACTTTGTGCTGCTATGGGAAGCAGCTGTGTACC 4457

Query 421 ATTCCTCGCGATGCTGCCTACTACAGCTATCAGAATAGGTATCATTCTGTGAGAAGTGT 480
      |||
Sbjct 4458 ATTCCTCGCGATGCTGCCTACTACAGCTATCAGAATAGGTATCATTCTGTGAGAAGTGT 4517

Query 481 TTCACAGAGATCCAGGGCAGAAATGTGACCCTGGGTGACGACCCTTACAGCCCCAGACG 540
      |||
Sbjct 4518 TTCACAGAGATCCAGGGCAGAAATGTGACCCTGGGTGACGACCCTTACAGCCCCAGACG 4577

Query 541 ACAATTTCAAAGGATCAGTTTGAAGAAGAAAAATGATACCTTAGACCCCGAACCTTTC 600
      |||
Sbjct 4578 ACAATTTCAAAGGATCAGTTTGAAGAAGAAAAATGATACCTTAGACCCCGAACCTTTC 4637

Query 601 GTTGATTGCAAGGAGTGTGGCCGGAAGATGCATCAGATTTGCGTTCTGCACTATGACATC 660
      |||
Sbjct 4638 GTTGATTGCAAGGAGTGTGGCCGGAAGATGCATCAGATTTGCGTTCTGCACTATGACATC 4697

Query 661 ATTTGCCTTCAGGTTTTGTGTGCGACAAC TGCTTGAGAAAAC TGGC 708
      |||
Sbjct 4698 ATTTGCCTTCAGGTTTTGTGTGCGACAAC TGCTTGAGAAAAC TGGC 4745
```

Fig S9. The sequence alignment of the plasmid pGEX4T-CBP-BP in GenBank

The sequence identity match of the plasmid pGEX4T- CBP-BP was 100%, comparing to that of human sapiens CREB binding protein (CREBBP) in GenBank.

TRIM24-PB

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Query 1      CCCAATGAGGACTGGTGTGCAGTTTGTCAAACGGAGGGGAACTCCTCTGCTGTGAAAAG 60
            |||
Sbjct 2658   CCCAATGAGGACTGGTGTGCAGTTTGTCAAACGGAGGGGAACTCCTCTGCTGTGAAAAG 2717

Query 61     TGCCCCAAAGTATCCATCTTTCTGTGCATGTGCCACATTGACAAATTTTCCAAGTGA 120
            |||
Sbjct 2718   TGCCCCAAAGTATCCATCTTTCTGTGCATGTGCCACATTGACAAATTTTCCAAGTGA 2777

Query 121    GAGTGGATTGCACTTCTGCCGAGACTTATCTAAACCAGAAGTTGAATATGATTGTGAT 180
            |||
Sbjct 2778   GAGTGGATTGCACTTCTGCCGAGACTTATCTAAACCAGAAGTTGAATATGATTGTGAT 2837

Query 181    GCTCCAGTCACAACCTCAGaaaaaaaaGAAAACCTGAAGGCCTTGTTAAGTTAACACCTATA 240
            |||
Sbjct 2838   GCTCCAGTCACAACCTCAGAAAAAAAAAGAAAACCTGAAGGCCTTGTTAAGTTAACACCTATA 2897

Query 241    GATAAAAGGAAGTGTGAGCGCC TACTTTTATTTCTTTACTGCCATGAAATGAGCCTGGCT 300
            |||
Sbjct 2898   GATAAAAGGAAGTGTGAGCGCC TACTTTTATTTCTTTACTGCCATGAAATGAGCCTGGCT 2957

Query 301    TTTCAAGACCCGTTCCTCTAACTGTGCCTGATTATTACAAAATAATTA AAAATCCAATG 360
            |||
Sbjct 2958   TTTCAAGACCCGTTCCTCTAACTGTGCCTGATTATTACAAAATAATTA AAAATCCAATG 3017

Query 361    GATTTGTCAACCATCAAGAAAA GACTACAAGAAGATTATCCATGTACTCAAAACCTGAA 420
            |||
Sbjct 3018   GATTTGTCAACCATCAAGAAAA GACTACAAGAAGATTATCCATGTACTCAAAACCTGAA 3077

Query 421    GATTTGTAGCTGATTTTAGAT TGATCTTTCAAACCTGTGCTGAATCAATGAGCCTGAT 480
            |||
Sbjct 3078   GATTTGTAGCTGATTTTAGAT TGATCTTTCAAACCTGTGCTGAATCAATGAGCCTGAT 3137

Query 481    TCAGAAGTAGCCAATGCTGGTATAAACTT GAAAATTATTTGAAGA ACTTCTAAAGAAC 540
            |||
Sbjct 3138   TCAGAAGTAGCCAATGCTGGTATAAACTT GAAAATTATTTGAAGA ACTTCTAAAGAAC 3197

Query 541    CTCTATCCAGAAAAAAGGTTTCCCAAACCGAATTCAGGAATGAATCAGAAGATAATAAA 600
            |||
Sbjct 3198   CTCTATCCAGAAAAAAGGTTTCCCAAACCGAATTCAGGAATGAATCAGAAGATAATAAA 3257

Query 601    TTTAGTGATGATT CAGATGATGACTTTGTACAGCCCCGGAAGAAACGCCTCAAAA GCATT 660
            |||
Sbjct 3258   TTTAGTGATGATT CAGATGATGACTTTGTACAGCCCCGGAAGAAACGCCTCAAAA GCATT 3317

Query 661    GAAGAACGCCAGTTGCTTAAAT AA 684
            |||
Sbjct 3318   GAAGAACGCCAGTTGCTTAAAT AA 3341
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Fig S10. The sequence alignment of the plasmid pGEX4T-TRIM24-PB in GenBank. The sequence identity match of the plasmid pGEX4T- TRIM24-PB was 100%, comparing to that of human sapiens tripartite motif containing 24 (TRIM24) in GenBank.

TRIM33-PB

```
Query 1 GACTGGTGTGCTGTCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGTCCAAAG 60
      |||
Sbjct 2789 GACTGGTGTGCTGTCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGTCCAAAG 2848

Query 61 GTCTTTCATCTAACTTGTTCATGTTCCAACACTACTTAGCTTCCAAGTGGGGACTGGATA 120
      |||
Sbjct 2849 GTCTTTCATCTAACTTGTTCATGTTCCAACACTACTTAGCTTCCAAGTGGGGACTGGATA 2908

Query 121 TGCACATTTTGTAGAGATATTGAAAAGCCAGAAGTTGAATATGATTGTGATAATTTGCAA 180
      |||
Sbjct 2909 TGCACATTTTGTAGAGATATTGAAAAGCCAGAAGTTGAATATGATTGTGATAATTTGCAA 2968

Query 181 CATAGTAAGAAGGGGAAAACCTGCGCAGGGGTTAAGCCCGTGGACCAAGGAAATGTGAA 240
      |||
Sbjct 2969 CATAGTAAGAAGGGGAAAACCTGCGCAGGGGTTAAGCCCGTGGACCAAGGAAATGTGAA 3028

Query 241 CGTCTTCTGCTTTACCTCTATTGCCATGAATTAAGTATGAATTCAGGAGCCTGTTCCCT 300
      |||
Sbjct 3029 CGTCTTCTGCTTTACCTCTATTGCCATGAATTAAGTATGAATTCAGGAGCCTGTTCCCT 3088

Query 301 GCTTCGATACCAAACACTACTATAAAATTATAAAGAAACC AATGGATTTATCCACCGTGAAA 360
      |||
Sbjct 3089 GCTTCGATACCAAACACTACTATAAAATTATAAAGAAACC AATGGATTTATCCACCGTGAAA 3148

Query 361 AAGAAGCTTCAGAAAAACATTCCCAACACTACCAAATCCCGGATGACTTTGTGGCCGAT 420
      |||
Sbjct 3149 AAGAAGCTTCAGAAAAACATTCCCAACACTACCAAATCCCGGATGACTTTGTGGCCGAT 3208

Query 421 GTCCGTTTGATCTTCAAGAACTGTGAAAGGTTTAAATGAAATGATGAAAGTTGTTCAAGTT 480
      |||
Sbjct 3209 GTCCGTTTGATCTTCAAGAACTGTGAAAGGTTTAAATGAAATGATGAAAGTTGTTCAAGTT 3268

Query 481 TATGCAGACACAC AAGAGATTAATTTGAAGGCTGATTCAGAAGTAGCTCAGGCAGGGAAA 540
      |||
Sbjct 3269 TATGCAGACACAC AAGAGATTAATTTGAAGGCTGATTCAGAAGTAGCTCAGGCAGGGAAA 3328

Query 541 GCAGTTGCATTGTACTTTGAAGATAAACTCACAGAGATCTACTCAGACAGGACCTTCGCA 600
      |||
Sbjct 3329 GCAGTTGCATTGTACTTTGAAGATAAACTCACAGAGATCTACTCAGACAGGACCTTCGCA 3388

Query 601 CCTTTGCCAGAGTTGAGCAGGAAGAGGATGATGGTGAGGTAAGTGAAGGACTCTGATGAA 660
      |||
Sbjct 3389 CCTTTGCCAGAGTTGAGCAGGAAGAGGATGATGGTGAGGTAAGTGAAGGACTCTGATGAA 3448

Query 661 GACTTTATACAGCCCCGCAGAAAACGCCTAAAGTCAGATGAGAGACCAGTACATATAAAG 720
      |||
Sbjct 3449 GACTTTATACAGCCCCGCAGAAAACGCCTAAAGTCAGATGAGAGACCAGTACATATAAAG 3508

Query 721 TAA 723
      |||
Sbjct 3509 TAA 3511
```

Fig S11. The sequence alignment of the plasmid pGEX4T-TRIM33-PB in GenBank. The sequence identity match of the plasmid pGEX4T- TRIM33-PB was 100%, comparing to that of human sapiens tripartite motif containing 33 (TRIM33) in GenBank.

TAF1-BB

```
Query 1 AGAAAATCTCTGGTTCTCAAGTTTCCTAAACAGCAGCTTCCTCCAAAAGAAGAAACGGCGA 60
|||
Sbjct 4033 AGAAAATCTCTGGTTCTCAAGTTTCCTAAACAGCAGCTTCCTCCAAAAGAAGAAACGGCGA 4092

Query 61 GTTGAACCACTGTTCACTGTGACTATTTG AATAGACCTCATAAGTCCATCCACC GGCGC 120
|||
Sbjct 4093 GTTGAACCACTGTTCACTGTGACTATTTG AATAGACCTCATAAGTCCATCCACC GGCGC 4152

Query 121 CGCACAGACCCTATGGTGACGCTGTCGTCC ATCTTGGAGTCTATCATCAATGACATGAGA 180
|||
Sbjct 4153 CGCACAGACCCTATGGTGACGCTGTCGTCC ATCTTGGAGTCTATCATCAATGACATGAGA 4212

Query 181 GATCTTCCAAATACATACCCTTCCACACTCCAGTCAATGCAAAGGTGTAAAGGACTAC 240
|||
Sbjct 4213 GATCTTCCAAATACATACCCTTCCACACTCCAGTCAATGCAAAGGTGTAAAGGACTAC 4272

Query 241 TACAAATCATCACTCGGCCAATGGACCTACAAACTCCGCGAAAACGTGCGTAAACGC 300
|||
Sbjct 4273 TACAAATCATCACTCGGCCAATGGACCTACAAACTCCGCGAAAACGTGCGTAAACGC 4332

Query 301 CTCTACCCATCTCGGGAAGAGTTCAGAGAGCATCTGGAGCTAATTGTGAAAAATAGTGCA 360
|||
Sbjct 4333 CTCTACCCATCTCGGGAAGAGTTCAGAGAGCATCTGGAGCTAATTGTGAAAAATAGTGCA 4392

Query 361 ACCTACAATGGGCCAAAACACTCATTGACTCAGATCTCTCAATCCATGCTGGATCTCTGT 420
|||
Sbjct 4393 ACCTACAATGGGCCAAAACACTCATTGACTCAGATCTCTCAATCCATGCTGGATCTCTGT 4452

Query 421 GATGAAAACTCA AAGAGAAAAG AAGACAAATTAGCTCGCTTAGAGAAAGCTATCAACCCC 480
|||
Sbjct 4453 GATGAAAACTCA AAGAGAAAAG AAGACAAATTAGCTCGCTTAGAGAAAGCTATCAACCCC 4512

Query 481 TTGCTGGATGATGATGACCAAGTGGCGTTT TCTTTCATCTGGACAACATTGTCACCCAG 540
|||
Sbjct 4513 TTGCTGGATGATGATGACCAAGTGGCGTTT TCTTTCATCTGGACAACATTGTCACCCAG 4572

Query 541 AAAATGATGGCAGTTCCAGATTCTTGGCCATTTATCACCAGTTAATAAGAAATTTGTT 600
|||
Sbjct 4573 AAAATGATGGCAGTTCCAGATTCTTGGCCATTTATCACCAGTTAATAAGAAATTTGTT 4632

Query 601 CCAGATTATTACA AAGTGATTGTCAATCCAATGGATTTAGAGACCATACGTAAGAACATC 660
|||
Sbjct 4633 CCAGATTATTACA AAGTGATTGTCAATCCAATGGATTTAGAGACCATACGTAAGAACATC 4692

Query 661 TCCAAGCAC AAGTATCAGAGTCGGGAGAGCTTTCTGGATGATGTAAACCTTATTC TGGCC 720
|||
Sbjct 4693 TCCAAGCAC AAGTATCAGAGTCGGGAGAGCTTTCTGGATGATGTAAACCTTATTC TGGCC 4752

Query 721 AACAGTGTTAAGTATAATGGACCTGAGAGTCAGTATAC TAAGACTGCCAGGAGATTGTG 780
|||
Sbjct 4753 AACAGTGTTAAGTATAATGGACCTGAGAGTCAGTATAC TAAGACTGCCAGGAGATTGTG 4812

Query 781 AACGTCTGTTACCAGACATTGACTGAGTATGATGAACATTTGACTCAACTTGAGAAGGAT 840
|||
Sbjct 4813 AACGTCTGTTACCAGACATTGACTGAGTATGATGAACATTTGACTCAACTTGAGAAGGAT 4872

Query 841 ATTTGACTGCTAAAGAAGCAGCTTTGGAGGAAGCA 876
|||
Sbjct 4873 ATTTGACTGCTAAAGAAGCAGCTTTGGAGGAAGCA 4908
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Fig S12. The sequence alignment of the plasmid pGEX4T-TAF1-BB in GenBank

The sequence identity match of the plasmid pGEX4T- TAF1-BB was 100%, comparing to that of human sapiens TATA-box binding protein associated factor 1 (TAF1) in GenBank.

Table S4 The relevant parameters of the ITC titration

protein	peptide	KA (M ⁻¹)	ΔH (cal/mol)	ΔS (cal/mol/deg)
BPTF-PB	H3R2meK4me3	7.69E4±5.61E3	-7312±215.9	-2.17
BPTF-PB	H3K4me3K9ac	6.34E4±3.38E3	-8976±220.9	-8.13
BPTF-PB	H3K4me3K9bu	3.62E4±3.64E3	-7863±1054	-5.51
BPTF-PB	H3K4me3K9cr	5.72E4±1.00E3	-8549±76.15	-6.91
BPTF-PB	H3K4me3K9hib	7.07E4±2.49E3	-7936±109.7	-4.43