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| Status | Public on Jun 09, 2017 |
| Title | Menin Enhances c-Myc-mediated Transcriptional Activity To Promote Cancer Progression |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Experiment type | Genome binding/occupancy profiling by high throughput sequencing Expression profiling by high throughput sequencing |
| Summary | MYC is a master regulator of transcription in growing cells. Menin is an enigmatic protein that displays unique ability to either suppress or promote tumorigenesis in a context dependent manner. It's interesting to ask is there any relationship between MYC and menin. **Here, we used RNA-seq to study global transcriptomic expression of MYC or MEN1 knockdown HT1080 cells** to investigate whether there are any correlations between MYC- and menin- regulated gene expression. Besides, we performed ChIP-seq assays for MYC and Menin binding sequences to address whether Menin and MYC share some common binding sites on chromatin. |
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| Overall design | Human fibrosarcoma HT1080 cells were transfected with MYC shRNAs, MEN1 shRNAs or non-targeting control shRNA followed by RNA extraction and sequenced on Illumina HiSeq 4000 (Homo sapiens). And also we performed MYC ChIP-seq and Menin ChIP-seq to address whether Menin and MYC share some common binding sites on chromatin.RNA Pol II ChIP-seq for NTC and shMEN1 HT1080 cell samples were used to study the effect of Menin on RNA Pol II-mediated elongation. |
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| Citation(s) | * Wu G, Yuan M, Shen S, Ma X et al. Menin enhances c-Myc-mediated transcription to promote cancer progression. *Nat Commun* 2017 May 5;8:15278. PMID: [28474697](https://www.ncbi.nlm.nih.gov/pubmed/28474697) |

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| Status | Public on May 24, 2016 |
| Title | HCT116 MYC 3' TBE1 (WT) and KO RNA-Seq |
| Organism | [Homo sapiens](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=9606) |
| Experiment type | Expression profiling by high throughput sequencing |
| Summary | mRNA was sequenced from HCT116 MYC 3' TBE1 (WT) and KO cells to identify genes differentially expressed after deletion of the MYC 3' TBE1 |
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| Overall design | mRNA levels from two biological replicates of HCT116 MYC 3' TBE1 (WT) and KO cells were examined |
|  |  |
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| Citation missing | *Has this study been published? Please*[*login*](https://www.ncbi.nlm.nih.gov/geo/submitter)*to update or*[*notify GEO*](mailto:geo@ncbi.nlm.nih.gov?subject=Citation%20for%20GSE70833%20%5Bnot%20logged%20in%5D&body=Thank%20you%20very%20much%20for%20helping%20to%20keep%20GEO%20citation%20links%20up-to-date.%20Please%20enter%20the%20PubMed%20ID%20(PMID)%20or%20full%20citation%20for%20GSE70833%20below,%20and%20we%20will%20update%20the%20record%20accordingly%20within%20the%20next%20day%20or%20two.%20The%20PubMed%20ID%20or%20citation%20is:)*.* |
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|  |  |
| Platforms (1) | |  |  | | --- | --- | | [GPL16791](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL16791) | Illumina HiSeq 2500 (Homo sapiens) | |
| Samples (4)  [[ess...](javascript:HandleVisibilityChangeL1227782303()) Less...](javascript:HandleVisibilityChangeL1227782303()) | |  |  | | --- | --- | | [GSM1820153](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM1820153) | HCT116 MYC 3' TBE1 (WT) - 1 | | [GSM1820154](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM1820154) | HCT116 MYC 3' TBE1 (WT) - 2 | | [GSM1820155](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM1820155) | HCT116 MYC 3' TBE1 (KO) - 1 |  |  |  | | --- | --- | | [GSM1820156](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM1820156) | HCT116 MYC 3' TBE1 (KO) - 2 | |