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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 sequencingExpression 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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| Contributor(s) | [Wu G](https://www.ncbi.nlm.nih.gov/pubmed/?term=Wu%20G%5BAuthor%5D), [Shen S](https://www.ncbi.nlm.nih.gov/pubmed/?term=Shen%20S%5BAuthor%5D), [Zhang H](https://www.ncbi.nlm.nih.gov/pubmed/?term=Zhang%20H%5BAuthor%5D), [Gao P](https://www.ncbi.nlm.nih.gov/pubmed/?term=Gao%20P%5BAuthor%5D) |
| 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 |
|   |  |
| Contributor(s) | [Rennoll SA](https://www.ncbi.nlm.nih.gov/pubmed/?term=Rennoll%20SA%5BAuthor%5D), [Raup-Konsavage WM](https://www.ncbi.nlm.nih.gov/pubmed/?term=Raup-Konsavage%20WM%5BAuthor%5D), [Kawasawa YI](https://www.ncbi.nlm.nih.gov/pubmed/?term=Kawasawa%20YI%5BAuthor%5D), [Yochum GS](https://www.ncbi.nlm.nih.gov/pubmed/?term=Yochum%20GS%5BAuthor%5D) |
| Citation missing | *Has this study been published? Please*[*login*](https://www.ncbi.nlm.nih.gov/geo/submitter)*to update or**notify GEO**.* |
| Submission date | Jul 13, 2015 |
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| Platforms (1) |

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| [GPL16791](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL16791) | Illumina HiSeq 2500 (Homo sapiens) |

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| Samples (4)ess... Less...            |

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| [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 |

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| [GSM1820156](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM1820156) | HCT116 MYC 3' TBE1 (KO) - 2 |

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