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## Series GSE128242

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Status	Public on Jan 01, 2020
Title	Altered chromatin landscape and enhancer engagement underlie transcriptional dysregulation in MED12 mutant uterine leiomyomas
Organism	<a href="#">Homo sapiens</a>
Experiment type	Expression profiling by high throughput sequencing Genome binding/occupancy profiling by high throughput sequencing Other
Summary	This SuperSeries is composed of the SubSeries listed below.
Overall design	Refer to individual Series
Citation(s)	Moyo MB, Parker JB, Chakravarti D. Altered chromatin landscape and enhancer engagement underlie transcriptional dysregulation in MED12 mutant uterine leiomyomas. <i>Nat Commun</i> 2020 Feb 24;11(1):1019. PMID: <a href="#">32094355</a>
Submission date	Mar 13, 2019
Last update date	Mar 09, 2020
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ZIP/Postal code	60611
Country	USA
Platforms (1)	<a href="#">GPL18573</a> Illumina NextSeq 500 (Homo sapiens)
Samples (142)	<a href="#">GSM3667569</a> MYO-PT354 <a href="#">GSM3667570</a> MYO-PT563 <a href="#">GSM3667571</a> MYO_PT728

This SuperSeries is composed of the following SubSeries:

[More...](#)

[GSE128229](#) Profiling of Myometrium and Leiomyoma transcriptomes in 15 leiomyoma (MED12 G44 mutant) and 15 matched normal myometrium (WT) patient tissue samples.

[GSE128230](#) Genome-wide maps of chromatin state, transcription factor and cofactor occupancy

9/7/2020

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in 5 leiomyoma (MED12 G44 mutant) and 5 matched normal myometrium (WT) patient tissue samples.

GSE128234

Genome-wide chromatin interaction maps of enhancer-promoter and promoter-promoter contacts in 5 leiomyoma (MED12 G44 mutant) and 5 matched normal myometrium (WT) patient tissue samples.

Relations

BioProjectPRJNA526890

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Series Matrix File(s)

Format

SOFT

MINiML

TXT

Supplementary file	Size	Download	File type/resource
GSE128242_RAW.tar	21.1 Gb	(http)(custom)	TAR (of BED, BW, TXT)

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