

Materials List for:

Identifying Transcription Factor Olig2 Genomic Binding Sites in Acutely Purified PDGFR α + Cells by Low-cell Chromatin Immunoprecipitation Sequencing Analysis

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Materials

Name	Company	Catalog Number	Comments
Reagent/ Equipment			
Banderiaea simplicifolia lectin 1	Vector Laboratories	# L-1100	
Rat anti-PDGFR α antibody	BD Bioscience	# 558774	
Neural tissue dissociation Kit (P)	MACS Miltenyi Biotec	# 130-092-628	
Accutase	STEMCELL technologies	# 07920	
TRIzol	Thermo Fisher	# 15596026	
Anti-NG2 Chondroitin Sulfate Proteoglycan Antibody	Millipore	# AB5320	
Bioruptor Pico sonication device	Diagenode	# B01060001	
True MicroChIP kit	Diagenode	# C01010130	
Phenol:Chloroform:Isoamyl Alcohol (25:24:1, v/v)	Thermo Fisher	# 15593031	
NucleoSpin Gel and PCR Clean- Up kit	MACHEREY-NAGEL	# 740609	
Quant-iT PicoGreen dsDNA Assay Kit	Thermo Fisher	# P11496	
DNA SMART ChIP-Seq kit	Clontech Laboratories	# 634865	
Agencourt AMPure XP	Beckman Coulter	# A63880	
GlycoBlue	Thermo Fisher	# AM9516	
pico-green	Thermo Fisher	# P11496	
D-PBS	Thermo Fisher	# 14190-144	
SYBR Green master mix	Bio-Rad Laboratories	# 1725124	
DMEM/F12	Fisher Scientific	# 11-320-033	
Penicillin-Streptomycin (P/S)	Fisher Scientific	# 15140122	
N-2 Supplement	Fisher Scientific	# 17502048	
B-27 Supplement	Fisher Scientific	# 17504044	
insulin	Sigma	# I6634	Prepare 0.5 mg/ml insulin solution by dissolving 5 mg insulin in 10 ml water and 50 μ l of 1 N HCl.
Bovine Serum Albumin, suitable for cell culture (BSA)	Sigma	# A4161	Prepare 4% BSA solution by dissolving 4 g BSA in 100 ml D-PBS and adjust the pH to 7.4
Fibroblast Growth Factor basic Protein, Human recombinant (bFGF)	EMD Millipore	# GF003	
HUMAN PDGF-AA	VWR	# 102061-188	

poly-D-lysine	VWR	# IC15017510	Prepare 1 mg/ml poly-D-lysine solution by dissolving 10 mg poly-D-lysine in 10 ml water and dilute 100 times when using.
Falcon Disposable Petri Dishes, Sterile, Corning, 100x15mm	VWR	# 25373-100	
Falcon Disposable Petri Dishes, Sterile, Corning, 150x15mm	VWR	# 25373-187	
HBSS, 10X, no Calcium, no Magnesium, no Phenol Red	Fisher Scientific	# 14185-052	
Trypan Blue	Stemcell Technologies	# 07050	
protease inhibitor cocktail	Sigma	# 11697498001	
Software			
FastQC	[10] http://www.bioinformatics.babraham.ac.uk/projects/fastqc/		Obtaining quality control metrics of raw and trimmed reads
Trimmomatic 0.33	[11] http://www.usadellab.org/cms/?page=trimmomatic		Trimming and filtering raw reads
GENCODE mm10	ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M15/GRCm38.primary_assembly.genome.fa.gz		Mouse reference genome
Bowtie2 2.2.4	[12] http://bowtie-bio.sourceforge.net/bowtie2/index.shtml		Aligning reads to a reference genome
SAMTools 1.5	[13] http://samtools.sourceforge.net/		Converting SAM file into BAM format
HOMER 4.9.1	[14] http://homer.ucsd.edu/homer/		Creating a tag directory and annotating enriched genomic regions with gene symbols
R 3.2.2	[15] https://www.R-project.org/		Programming scripts and running functions
SPP 1.13	[16] https://github.com/hms-dbmi/spp		Creating a strand cross-correlation plot
MACS2 2.2.4	[17] https://github.com/taoliu/MACS		Finding regions of ChIP enrichment over control
BEDTools 2.25	[18] http://bedtools.readthedocs.io/en/latest/		Genome arithmetics
bedGraphToBigWig	http://hgdownload.cse.ucsc.edu/admin/exe/		Converting bedGraph file into bigwig
IGV browser 2.3.58	[19] http://software.broadinstitute.org/software/igv/		Visualization and browsing of significant ChIP-seq peaks
Microsoft Excel			Spreadsheet program
ENCODE's blacklist	https://sites.google.com/site/anshulkundaje/projects/blacklists		Filtering peaks
mm10.chrom.sizes	http://hgdownload.cse.ucsc.edu/goldenPath/mm10/bigZips/mm10.chrom.sizes		Converting bedGraph file into bigwig
ENCODE's motif database	[25] http://compbio.mit.edu/encode-motifs/		Comprehensive motif database required for motif enrichment
MEME-ChIP	[20] http://meme-suite.org/index.html		Motif enrichment analysis and motif discovery
Primer names used for qPCR			Primer sequences used for qPCR
Mbp-F:			CTATAAATCGGCTCACAAGG

Mbp-R:			AGGCGGTTATATTAAGAAGC
Iba1-F:			ACTGCCAGCCTAAGACAACC
Iba1-R:			GCTTTTCCTCCCTGCAAATCC
Mog-F:			GGCTTCTTGGAGGAAGGGAC
Mog-R:			TGAATTGTCCTGCATAGCTGC
GAPDH-F			ATGACATCAAGAAGGTGGTG
GAPDH-R			CATACCAGGAAATGAGCTTG
Tuj1-F			TTTTCGTCTCTAGCCGCGTG
Tuj1-R			GATGACCTCCCAGAACTTGGC
PDGFR α -F			AGAGTTACACGTTTGAGCTGTC
PDGFR α -R			GTCCCTCCACGGTACTCCT