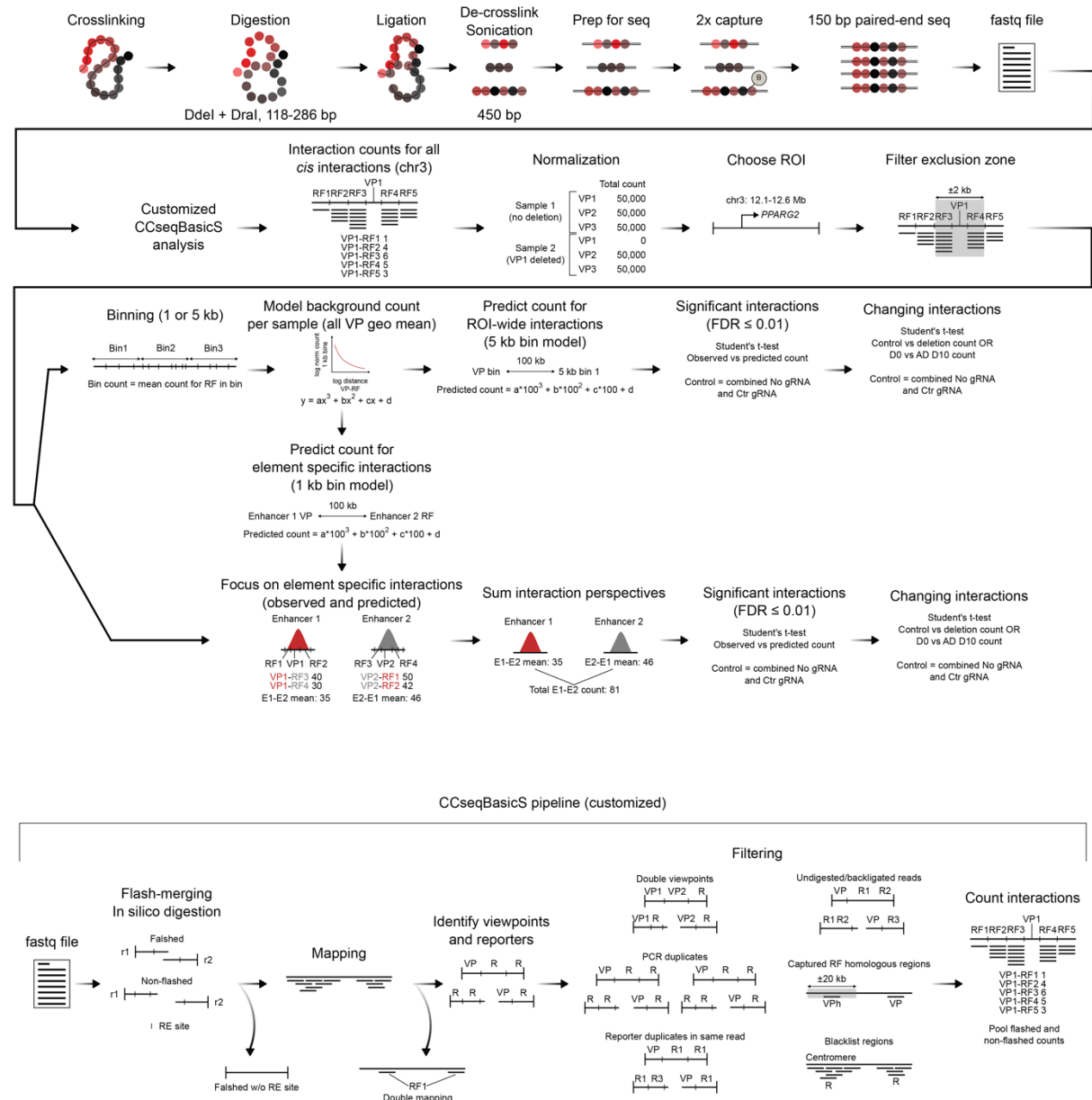


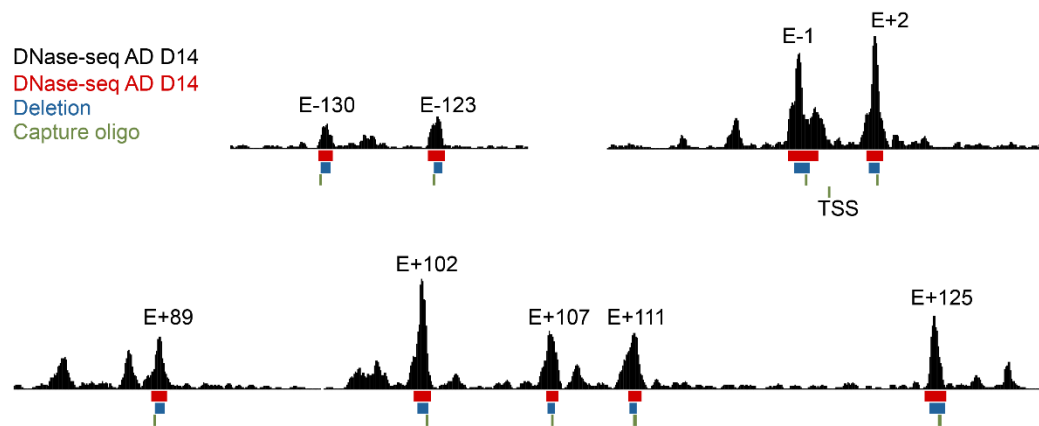
Supplementary Information

Supplementary Figure 1 - related to Figure 2b, 2c and 4



Supplementary Fig. 1: Overview of Capture-C workflow. See methods for details. E1/2: Enhancer 1/2; r1/2: Read 1/2; FDR: False discovery rate; Geo mean: Geometric mean; R: reporter; RE site: Restriction enzyme cut site; RF: Restriction fragment; ROI: Region of interest; VP(h): Viewpoint (homologous); w/o: Without.

Supplementary Figure 2 - related to Extended Data Table 3



Supplementary Fig. 2: Overview of enhancer deletions and capture oligos, related to Table S8. UCSC genome browser screenshots showing DNase-seq signal at the *PPARG* community enhancers at day 14 of adipogenesis in hMSC-TERT4, the span of the called DNase-sequencing peak, the expected enhancer deletion, and the capture oligo used for Capture-C. Total track heights are identical. $n=2$ biological replicate.

Supplementary Table 1: Enformer queries

Experiment type	Enformer experiment/ tissue index	Enformer experiment/tissue name
Enhancer	1481	H3K27ac subcutaneous abdominal adipose tissue nuclear fraction female adult 49 years
	1700	H3K27ac Adipose tissue male adult 34 years
	1456	H3K27ac muscle layer of colon female adult
	1778	H3K27ac peripheral blood mononuclear cell male adult
	1468	H3K9Aac MSC originated from adipose
	1448	H3K27ac cardiac muscle cell [used as control]
	363	DNASE adipocyte
CAGE	4678	CAGE Adipose tissue adult pool1
	4751	CAGE MSC adipose
	4810	CAGE Preadipocyte subcutaneous depot
	4811	CAGE Preadipocyte visceral depot
	4893	CAGE MSC adipose
	4902	CAGE Adipocyte subcutaneous depot
	5121	CAGE MSC adipose
	5143	CAGE Mature adipocyte
	5278	CAGE Adipose
	4805	CAGE Whole blood [used as control]

Supplementary Table 2: qPCR primers

Primer name	Forward 5'-3'	Reverse 5'-3'
PPP1R12C_intron1_int1	AGGAACCCCTGTAGGGAAGG	TCTGGGTTTGAGTCCTTGGC
E130_int2	ACTCCCGTTGACTCTCCAGT	GGAGCGAGCAGTTCTTGTCT
E123_int2	TCAACCTCAAGTGGGTTTCTGG	GGTCAAATTTTGCTGATGGATTGC
E1_int1	TCTCCTTGCCAAAAGGGCA	TACGCTGTAGGTTGGCGAG
E2_int2	ACCTCATGCTGGCTCTGAAA	TGGCACTAAAAGCAGGAGGC
E89_int1	GAGGAGCCGGCGTGTATC	GCTTTTCCAGGGCAGCTTTC
E102_int1	CTGCCTCCATGTTCCCCATT	TCCCATGGCCTTATCCTGA
E107_int2	GATGAAATGCGTCTGTTGGGG	GTGTGGCGAATGGAGCAACT
E111_int1	CAGAGCATTGTGGTCTCTTTC	GACTTGCAAAACACTATGGCATT
E125_int1	GGGGCATTATTCTGTTTGC	TGCTTGCCTGGGTACATCTG
NoGene2	GGTCCGTTCTGCCACTACTC	ATTCGCTGTGGCAGGAATAC
PPARG background	CCATCGAGCTGGTGCACCTA	TGAAATCTCTGCGTGGAGGG
ZRANB3 promoter	CGCTCCAGGCCGAAAAGAGCA	CATGTGGGGCGAAGTGAGGCA
hPPARG2_mRNA	CGGATTGATCTTTTGCTAGATAGA	TGCTGTAATTCACACTGATATTTTG
hSYN2 mRNA	GAGACCCCTAACAACCCAGC	GAGGTGGGGTCTTGCTTGAG
hTIMP4_mRNA	AACTGTGGCTGCCAAATCAC	GCTTTCGTTCCAACAGCCAG
hTSEN2_mRNA	ACTGTTGCTAAATGGAAAGATATG	TGCCCACTCAACACTATGCT
hTAMM41_mRNA	TGGCGCTGGAGTTTACTACAAT	TGAGGAGATCTTCAATCAGAACG
hMKRN2_mRNA	AAGCTTTCAAACAGGGGATGGG	TCGGGGTAAGCATGGCGATA
hRAF1_mRNA	ACAACCTACTGGCTCTGTCC	AGGAGTAGACATCCGACTGGAA
pSico LTR	TGGCTAACTAGGGAACCCACTGCT	TCACACAACAGACGGGCACACAC

Supplementary Table 3: End-point PCR primer

Primer name	Forward 5'-3'	Reverse 5'-3'
PPP1R12C_intron1	ACCCTAAGAACTTGGGAAC	CTTTGGCTCTTCACCTTTC
E130	GGTGCTGCACTGAAAATAC	TGGCAGTGCCTTTATATCC
E123	GATCAAAACAAGCACACTC	TCTAAGACGCTTATTCACG
E1	CTTAATGGCACAGTTGCTC	TGGGCAAAGTTTTCTTTCG
E2	AATGTGAGCTCCTAAAGGC	ATGGCGTGCTTAAATTCAC
E89	TCATCTAGTTGGCGAAGTC	ACTTGGTGCTGGAGAATAC
E102	GTGATGGAACCTAGATTGG	TCTCACAGTGATCCACAAC
E107	TTGTCCAACCAACCATAG	AGATGCATACGTAGCACAG
E111	TATTGACTCACGACAGACC	CCAAGCTCTCAGGATTAAG
E125	TTCTTGGGCAGGTTTAGAG	TTTCCCACTCTTCGATTCC

Supplementary Table 4: crRNA spacer sequences

crRNA name	Spacer sequence 5'-3'	Strand
PPP1R12C_intron1_L1	CTTGGCAAACCTCACTCTTCG	-
PPP1R12C_intron1_R1	CAGGTAAAACTGACGCACGG	+
E130_L2	AAAAGGTAGCATGTATCCAC	+
E130_R2	TTTTGACTGAATGAATGAGC	+
E123_L2	AAAAGCTGGAACCTGAAGCT	+
E123_R1	ACAGAGATGTATGTTATGTG	-
E1_L2	AACATCACGGAATAAAGTGG	-
E1_R1	TGATACCAACGTTTAAACTA	+
E2_L2	CTTAGCCACTATGCCCAAAG	+
E2_R2	AGCAAATATGTGGCCAACAA	-
E89_L1	CAGAGAACACAGGCCTCCGA	-
E89_R1	GGAGAATACTTGCTATCGTG	-
E102_L2	ATCTACGCCCCTACCAATGG	+
E102_R2	CACAACACCCCTTATAGATG	+
E107_L2	ATGGCAGAGAGACGCTGCTG	+
E107_R2	TGTACACCCATGTCTACTCA	+
E111_L1	CCATCCATAAAACAAACCCC	+
E111_R2	ATCAAAATTTCTTTGTCCAC	-
E125_L1	CAAATCCTCACGTGTTCCAG	-
E125_R1	TACATCAAATGCATCAACAT	+

Supplementary Table 5: Capture oligo sequences

Capture oligo name	Forward 5'-3'	Reverse 5'-3'	Oligo length in bp
E130	ATTCCTAATTGTTTTCATGGCATAAGGATCTTATAGGAGTTGTTA AAAAGAGTTTAAGGTAAGAAAGAAAAATCCAGTCCTTTAATG ACTTACAGGTTTTTCAGCACATCCTAGTCTTTT	AAAGAACTAGGATGTGCTGAAAACCTGTAAGTCATTAAGGA CTGGAATTTTCTTTCTTACCTTAAACTCTTTTAAACAACCTCTA TAAGATCCTTATGCCATGAAAACAATTAGGAAT	120
E123	TGAATTCCTCCAGAGTCACAGAGCTGGGTAATAGTGACAAAAGC TGGAAGTTGAAGCTAGGTCTTTGATTGAGAAAGCTTGGTACTC TGCCACATAACCACTGAATTCCTTTTACTTTCT	AGAAAGTAAAAGGAATTCAGTGGTTATGTGGCAGAGTACCAA GCTTTCTGAATCAAGAGACCTAGCTTCAAGTTCCAGCTTTTGT CACTATTACCCAGCTCTGTGACTCTGGGGAATTCA	120
E1	CAATTGATGTTCAACATCAGCTGGTGTAACATTGCTGCAGTTG CTATTGATGGATAAGCTGAAGTTTTTAAGAAAGCAAACCCGATG TATAAAATTGAAACCATATCAAACCTTCTTTC	GAAGAAGGGTTTGATATGGTTTCAATTTTATACATCGGGTTTG CTTTCTTAAAACTTCAGCTTATCCATCAATAGCAACTGCAGCA ATGTTACACCAGCTGATGTTTGAACATCAATTG	120
E2	GGAGTGAGTGATTGATTGCATGCCATTTTATTGAGGGATACCT AATCTGTGGTTACATATCTCCAGGCAACTGTATATTGAGAAACAT TTAG ATAACTGACCAAAGTTTTACCTTTCC	GGAAAGGTGAAAACCTTTGGTCAGTTATCTAAATGTTTCTGAAT ATACAGTTGCCTGGAGATATGAACACAGATTAAAGTATCCCTC AATAAAATGGCATGCAATCAATCACTCACTCC	120
E89	GAAAGAGCCCTCTCTGGCTGACCTCGGAGGCTGTGTTCTCT GCTGCCTGTGCTTGCAATTCAGCCCTCCTAGCGACCTAGGCCCTGG ACCAGGCAACAGCCAGCACTTATTAAAGGCCTG	CAGGCCTTTAATAAGTGCTGGCTGTTGCCTGGTCCAGGCCTA GGTCGCTAGGAGGGCTGAATGCAAGCACAGGCAGCAGAGA ACACAGGCCTCCGAGGGTCAGCCAGAGAGGGGCTCTTTC	120
E102	TTAGATACCAACACAACAAGTTTTTGTGGGTGTGTCCATAGAG TGGCAGCCCCGAGACAGGACATTGAAATAGACATTATTTTCATAT GGTCACAACACCCCTTATAGATGAGGAAAC	GTTTCCTCATCTATAAGGGGTGTTGTGACCATATGAAATAATGT CTATTTCAATGTCTGTCTCGGGGCTGCCACTCTATGGACACA CCCAACAAAACTTGTGTGTTGGTATCTAA	118
E107	TTGGGGACCTGTTGGGAAATCCTGAACTGGGAGGAAGGAAC AGCCCTGCGGGGTCGGAGGCTACTTGAGCAAGTCCCCAGCAG TTGCTCCATTGCGCACACGGGGTGATGATGCCAGG	CCTGGGCATCATCACCCTGTGGCGAATGGAGCAACTGCTG GGGACTTGCTCAAGTAGCCTCCGACCCCGAGGGCTGTTCTCT TCCTCCAGTTTCAGGATTTCCCAACAGGTCCCCAA	120
E111	CATTGTGGTCTCTTTGCCTTGTCACAATAGTTCTGTTGCAAAAAC CTCTCTTAATGCCATAGTGTGTTGCAAGTCATTTGCCATGTCAGT GAGGAAAATATTGCCATCTCCAGAGGCCTG	CAGGCCTCTGGAGATGGCAATATTTCTCTACTGACATGGCAA ATGACTTGCAAAACACTATGGCATTAAAGAGAGGTTTTTGCAAC AGAACTATTGTGACAAGGCAAGAGACCACAATG	120
E125	TGAGGCAGATGTACCCAGGCAAGCAGGAAAGCCAGGTTTGGG CCATGTTCCGGCTCTTCTCCGTATCTTTGTGAGGAGACCAGA GTTTTTCAGCCACCCAGGAAATTAATAATC	GAATTTTAATTTCTGGGTGGCTGAAAACTCTGGTCTCTCTCA CAAGAGATACGGAAGAAGAGGCCGAACATGGCCCAAACCTG GCTTTCCTGCTTGCTGGGTACATCTGCCTCA	116
PPARG2 TSS	TGTTTCAGAACCTTAAAAAAGGAAACCTAACCTAATCTATTTATC TCTGTGCATGGCTCCCATTTCTGAATTTAAGCATTAAGGTAT AGT TATATCCAAAAACAATCCTGTTTCATTT	AAATGAACAGGATTGTTTTTGGATATAACTATACCTTTAATGCT TAAATTCAGGAAATGGGAGCCATGCACAGAGATAAAATAGA TTAGGTTAGGTTTCTCTTTTAAAGTTTCTGAACA	120

Supplementary Table 6: TFModISco-derived CWM for PPAR γ ChIP AD D10 in hMSC-TERT4

pattern	num seqlets	MoDisco CWM forward	MoDisco CWM reverse	top match	q-value	JASPAR match logo
pos pattern 0	2192			MA0065.2 MA0065.2.Pparg::Rxra	1.304980e-10	
pos pattern 1	1816			MA0102.4 MA0102.4.CEBPA	4.821020e-03	
pos pattern 2	815			MA0065.2 MA0065.2.Pparg::Rxra	2.586570e-02	
pos pattern 3	777			MA1643.1 MA1643.1.NFIB	7.411890e-02	
pos pattern 4	601			MA1637.1 MA1637.1.EBF3	4.907850e-02	
pos pattern 5	378			MA0670.1 MA0670.1.NFIA	1.000000e+00	
pos pattern 6	328			MA0655.1 MA0655.1.JDP2	1.902770e-04	
pos pattern 7	209			MA0681.2 MA0681.2.PHOX2B	9.834870e-03	
pos pattern 8	177			MA0838.1 MA0838.1.CEBPG	4.443880e-02	
pos pattern 9	172			MA1148.1 MA1148.1.PPARA::RXRA	2.405930e-02	
pos pattern 10	83			MA0679.2 MA0679.2.ONECUT1	1.906230e-03	
pos pattern 11	54			MA0727.1 MA0727.1.NR3C2	9.221710e-03	
pos pattern 12	49			MA0484.2 MA0484.2.HNF4G	1.784360e-01	
pos pattern 13	43			MA0727.1 MA0727.1.NR3C2	4.539350e-01	
pos pattern 14	31			MA0065.2 MA0065.2.Pparg::Rxra	5.850090e-03	
pos pattern 15	26			MA1633.2 MA1633.2.BACH1	7.752080e-02	
pos pattern 16	26			MA0836.2 MA0836.2.CEBPD	3.133300e-02	
neg pattern 0	175			MA0679.2 MA0679.2.ONECUT1	9.586530e-02	
neg pattern 1	139			MA1125.1 MA1125.1.ZNF384	6.798420e-02	
neg pattern 2	102			MA0601.1 MA0601.1.Arid3b	1.733070e-01	
neg pattern 3	95			MA0681.2 MA0681.2.PHOX2B	1.041410e-01	
neg pattern 4	75			MA1978.1 MA1978.1.ZNF354A	2.456890e-01	
neg pattern 5	70			MA0679.2 MA0679.2.ONECUT1	2.044660e-01	
neg pattern 6	59			MA0681.2 MA0681.2.PHOX2B	6.435720e-02	
neg pattern 7	58			MA0680.2 MA0680.2.Pax7	4.639900e-02	