

# DNA Methylation Profiling of Blood Monocytes in Patients With Obesity Hypoventilation Syndrome

## Effect of Positive Airway Pressure Treatment

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**e-Appendix 1:** Detailed materials and methods used in this study

**Patient population and sample preparation.** Our inclusion criteria were age  $\geq 18$  and  $\leq 75$  years of age, diagnosis of OHS in the past 3 months but no initiation of PAP therapy, body mass index (BMI)  $\geq 30 \text{ kg/m}^2$ , daytime partial pressure of arterial CO<sub>2</sub> (PaCO<sub>2</sub>)  $\geq 45 \text{ mmHg}$  and daytime pH  $> 7.35$  from an arterial blood gas, presence of OSA with an apnea-hypopnea index (AHI)  $\geq 5$  events/h of sleep, and forced expiratory volume in 1 second (FEV<sub>1</sub>)/forced vital capacity (FVC)  $> 70\%$ . We excluded acutely ill and unstable patients, hospitalization for respiratory exacerbation  $< 6$  weeks prior to screening visit, and evidence of alkalosis (pH  $> 7.45$ ) on the arterial blood gas measurement. Between March 2012 and February 2014, 39 patients evaluated in the Sleep Disorders Clinic were referred to the University of Chicago research site for suspicion of OHS. Written informed consent was provided by all patients. Due to lack of hypercapnia on the screening baseline arterial blood gas (PaCO<sub>2</sub>  $< 45 \text{ mmHg}$ ) eighteen subjects were excluded. Of the remaining 21 participants, 6 did not agree to undergo two venipunctures. Therefore, the final analytic cohort consisted of 15 patients (6 male and 9 female) with OHS who underwent two venipunctures and two measurements of arterial blood gases 6 weeks apart after being prescribed PAP therapy.

All of these patients had OSA (14 patients with severe OSA as indicated by a apnea-hypopnea index (AHI) pre-treatment  $> 30$  events/hour total sleep time, and 1 patient with mild OSA: AHI pre-treatment= 8). All patients were clinically evaluated by sleep specialists in the Sleep Disorders Center of the University of Chicago. Each participant underwent three in-laboratory polysomnograms (PSG): baseline PSG, PAP titration PSG and PSG after 6 weeks of home PAP therapy. The final 6-week PSG was performed while the patient was wearing their home prescribed PAP device. Bedtimes were from 10:00 pm-12:00 am until 7:00 am-9:00 am. Each PSG included 8 hours of recording. PSG (Nihon Kohden, Foothill Ranch, CA) included recordings of six electroencephalographic channels, bilateral electro-oculograms, chin and tibialis electromyogram, electrocardiogram, airflow by nasal pressure transducer and oronasal thermocouples, chest and abdominal wall motion by respiratory inductance plethysmography belts, and oxygen saturation by finger pulse oximeter. Transcutaneous CO<sub>2</sub> monitoring was performed during baseline and 6-week PSG. All PSGs were staged and scored according to the 2007 American Academy of Sleep Medicine Manual for the Scoring of Sleep and Related Events <sup>1</sup>. Apneas were defined as a reduction of airflow of at least 90% on the oronasal thermistor for at least 10 seconds (obstructive if respiratory effort was present and central if respiratory effort was absent). Hypopneas were scored if the magnitude of the signal decreased by at least 30% of the baseline amplitude of the nasal pressure transducer for at least 10 seconds, and were associated with a 4% or greater drop in oxygen saturation as measured by finger pulse oximetry. The total AHI was defined as the number of apneas and hypopneas per hour of sleep. OSA was defined as AHI  $\geq 5$ . Severity of OSA was measured by the AHI. A subject was

considered to have mild OSA if the AHI was 5-14, moderate OSA if the AHI was 15-29, and severe OSA if the AHI was  $\geq 30$ . PAP titration was performed following the American Academy of Sleep Medicine recommendations<sup>2,3</sup>.

Adherence to the treatment was monitored using smart card technology embedded in the PAP machines (average adherence among the complete patient cohort:  $5.45 \pm 1.37$  days/week used;  $88.9 \pm 15.3\%$  of days used, with  $67.7 \pm 25.0\%$  of days used > 4 hours/night). In addition, co-existent diagnosis of hypertension (9/15 patients), T2DM (4/15 patients), congestive heart failure (4/15 patients) or dyslipidemia (3/15 patients) were also registered. Supplementary table S1 lists the demographic and clinical characteristics of these patients. All the participants provided written informed consent and the research protocol was approved by the research ethical board at the University of Chicago (protocol # 10-702-A-CR004). For each patient, blood was collected by venipuncture in the fasting state within 1 hour from awakening before start receiving PAP treatment (PRE- group), as well as after 6 weeks of treatment (POST-group). Both venipunctures were performed in the sleep laboratory after the patients awakened from the overnight in-laboratory polysomnogram. Peripheral blood mononuclear cells (PBMCs) were isolated using gradient centrifugation and the CD14+ monocytes fraction was isolated using the Miltenyi Biotec MACS magnetic cell separation system, as described elsewhere<sup>4</sup>. DNA was isolated from the isolated CD14+ monocytes using the DNeasy kit (Qiagen, Valencia, CA), according to manufacturer's instructions. DNA was quantified and quality assessed by absorbance measurement using Nanodrop (Thermo Scientific, Wilmington, DE) and DNA integrity was verified by agarose gel electrophoresis. Isolated DNA was stored at -20 °C until use.

**Microarray-based DNA profiling.** DNA methylation profiles before and after treatment for the patients exhibiting the highest POST/PRE AHI ratios (n=6) were assessed using a MeDIP-chip strategy. First, 1.5 µg of fragmented DNA was immunoprecipitated using an antibody against 5-methylcytosine (Eurogentec-AnaSpec, Inc. Freemont, CA) following the MeDIP protocol<sup>5</sup>. Immunoprecipitated DNA was amplified using an adaptor mediated PCR strategy, as described elsewhere<sup>6</sup> and subsequently fragmented, biotin-labeled, and hybridized on Affymetrix GeneChip Human Promoter Array 1.0R (Affymetrix, Santa Clara, CA) and scanned, according to manufacturer's protocol. The array consisted of over 4.6 million probes tiled to interrogate over 25,000 human promoter regions. Probes in the microarray were tiled at an average resolution of 35 base pairs, as measured from the central position of adjacent 25-mer oligos, leaving a gap of approximately 10 base pairs between probes. Each promoter region covered approximately 7.5 kb upstream through 2.5 kb downstream of 5' transcription start sites. The array interrogates regions proximal to transcription start sites, covering approximately 59 percent of the annotated CpG islands (NCBI Build 34/hg16)

**Microarray data analysis.** The data set(s) supporting the results of this article is available in the NCBI's Gene Expression Omnibus (GEO) repository (Accession number: GSE73053)

Microarray data was processed as previously described<sup>7</sup>. In brief, raw data (.cel files) was managed using the Partek® Genomic Suite® Software, version 6.6 (Partek Inc., St. Louis, MO, USA). Data pre-processing consisted of probe sequence adjustment, Robust Multichip Averaging (RMA)<sup>8</sup> background correction, quantile normalization and log2 transformation. The relationship between samples was examined by Multidimensional scaling (MDS) analysis. Normalized signals in the PRE and POST groups were compared using Analysis of Variance (ANOVA) and t-statistic were calculated for each probe. Regions of differential DNA methylation were identified using the Model-based Analysis of Tilling-arrays (MAT)<sup>9</sup> algorithm. A sliding window of fixed genomic length (500 bp) was applied and MAT score of each window was generated using the trimmed mean of probe t-statistics, which is calculated by taking the average of all probes within a window excluding 10% of the highest and lowest probes. Only regions containing more than 10 probes were considered for further analysis. Windows at p-value < 0.001 and absolute MAT scores >4 were considered as significant. Regions with positive and negative MAT scores represent hyper- and hypo-methylated regions in the POST group as compared to PRE, respectively. Regions supported by less than 80% of the probes were removed from further analysis. The probe locations were obtained from the array's annotation file and genome coordinates were updated to the GRCh37/hg19 build using the LiftOver tool at the UCSC genome browser. Promoter and gene associations were annotated comparing genomic coordinates against the RefSeq transcript annotation of human reference genome assembly. Networks and pathways significantly enriched in the genes of interest were identified through Ingenuity Pathways Analysis (IPA) (Ingenuity® Systems, [www.ingenuity.com](http://www.ingenuity.com)). Significance of the enrichment is calculated Fisher's exact test right-tailed, with a cutoff of p-value=0.05. Statistical analysis were further performed using R statistical environment (version 3.1.3)<sup>10</sup>.

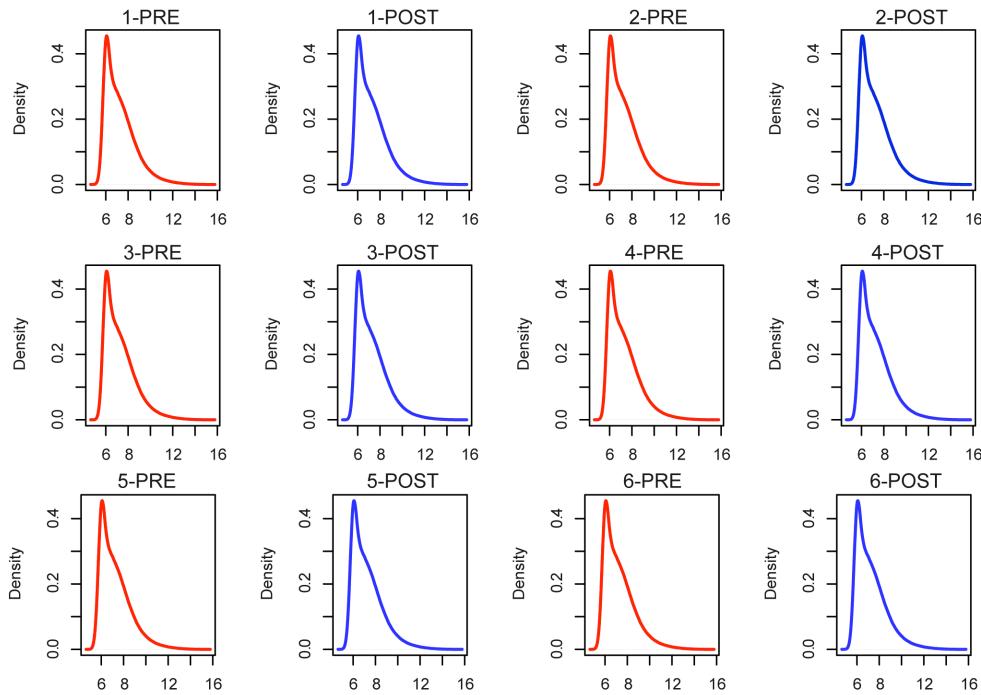
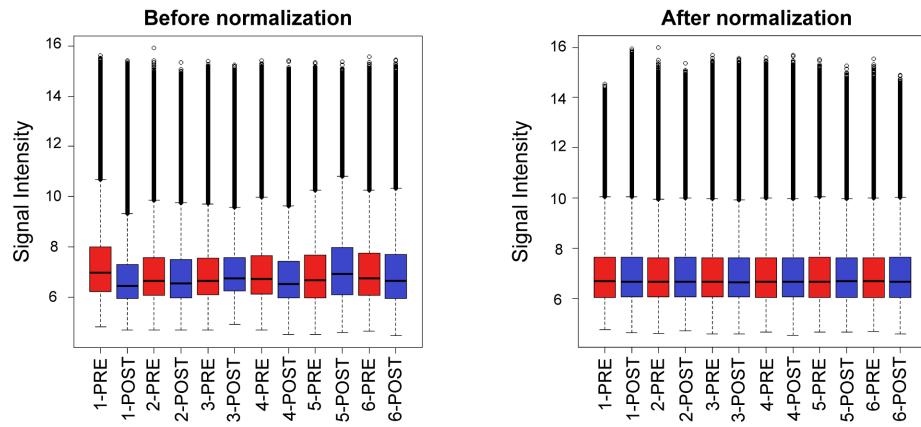
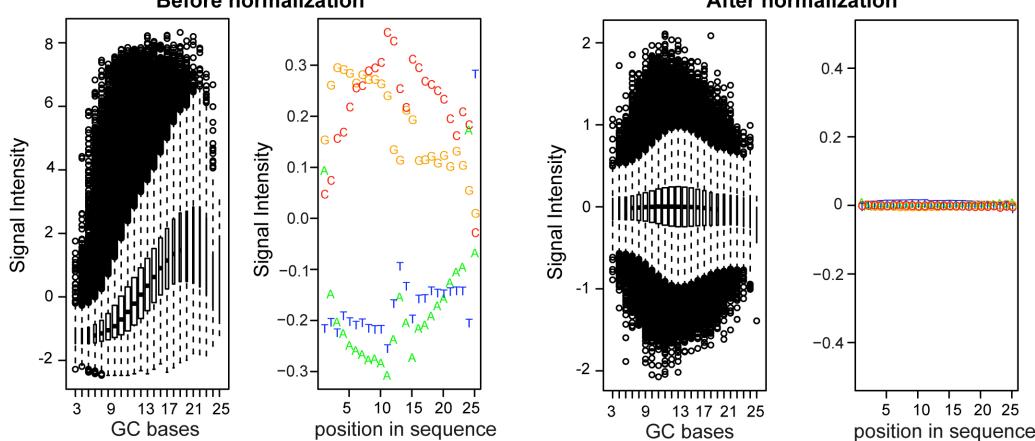
**Single-locus DNA methylation analysis.** Microarray data was verified by single locus analysis of 8 loci previously identified as PPAR targets using a SYBR-green based real-time PCR analysis of the MeDIP DNA for all samples in the study (n=15). We decided to focus our single locus analysis in this group of genes, since our DNA methylation arrays showed an enrichment on mechanisms of gene regulation by PPARs in both canonical pathways and gene network analyses, and given the widely-recognized role of PPARG in inflammation and macrophage biology<sup>11,12</sup>. The 8 PPAR response elements were selected from the literature on the base of being reported PPARG targets<sup>13-21</sup>. The location of the PPARE were identified either by experimental data reported from the literature and/or a computational approach (Dragon PPAR Response Element (PPRE) Spotter v.2.0 <http://www.cbrc.kaust.edu.sa/ppre/index.php>). The immunoprecipitated DNA methylation fraction (IP fraction) was diluted 1:20 in 1X low TE buffer containing

250 ng/µL salmon sperm DNA and 5 µL of this dilution were subjected to real-time PCR. The reaction consisted of 1× ABI master mix containing Taq polymerase, dNTPs, SYBR green dye and ROX as passive dye (Life Technologies, Carlsbad, CA, USA) and 200 nM of specific primers (Supplementary Material Table S5). The PCR program started with a Taq polymerase activation step (10 min at 95°C) followed by 40 cycles at 95°C for 15 s, 60°C for 1 min and 95°C for 15 s. Data analyses were performed using the 7500 System SDS software version 1.4 (Applied Biosystems). An aliquot (10 %) of the input material in the MeDIP analysis (IN fraction) was used as reference and the % of Input fraction recovery was calculated as: % recovery=100\*(2<sup>((Ct<sub>IN</sub>-3.32)-Ct<sub>IP</sub>)</sup>). Fold changes between the POST and PRE groups was calculated as the ratio of % recovery between the two groups.

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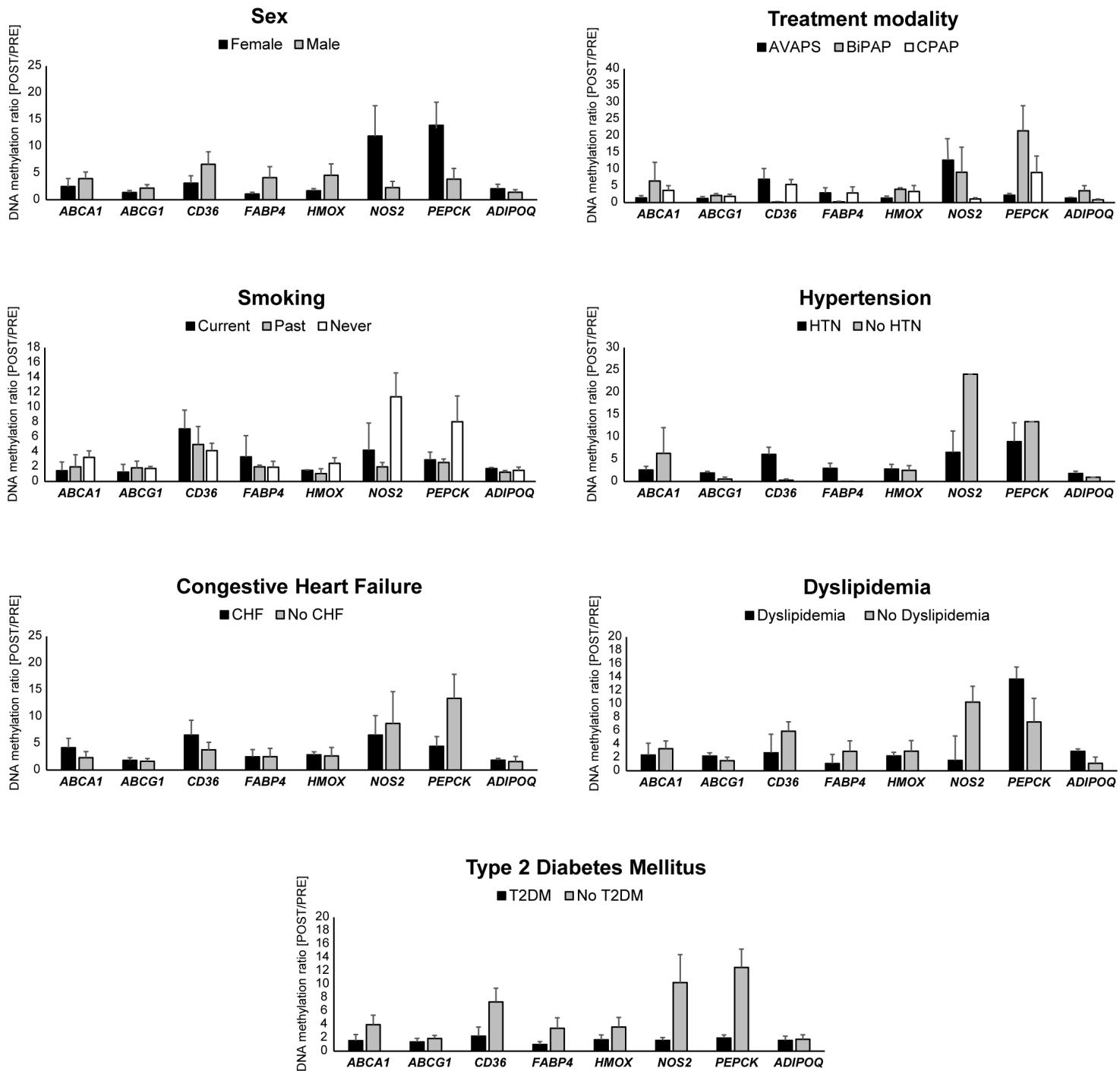
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**e-Figure 1.**
**A**

**B**

**C**


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**e-Figure 2.**



**e-Table 1:** Primer sequences for MeDIP-qPCR assays for PPAR-targeted genes.

Gene Symbol	Gene Name	Primer 1 sequence	Primer 2 sequence	Size [bp]
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	AAAAAGGAAGGAATCACCGA	AAGGACACAATGTAGCAGTT	119
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	TCTCCTTCTCTCCTTCGAT	AAGGAGGCACAGCTTTAT	101
ADIPOQ	adiponectin	taggaagttctccgtcaga	cccttatttgccctctaca	103
CD36	CD36 molecule (thrombospondin receptor)	ttagcaagtgcaggcccttt	ttctggtaagaccattac	114
FABP4	fatty acid binding protein 4, adipocyte	TGACGAAAATCCTCTCTCAC	TGCAGCAGAACGAAATAACAT	115
HMOX	heme oxygenase 1	AGGTCAGTTGAGGGATGAA	CTCCTCACACCCCTTTAAA	103
NOS2	nitric oxide synthase 2, inducible	catccctccatcactacaga	cagttcaggtaaacagcactc	119
PEPCK	phosphoenolpyruvate carboxykinase 1 (soluble)	TCTTAGGTAGAGAGGCTTCC	CTTGCTGGAGTTGGAGAA	105

**e-Table 2:** Demographic and clinical data for the patients in the study.

Demographics				
Sample ID	Microarray	Age	Sex	Ethnicity
1	YES	60	Female	African American
2	YES	65	Female	African American
3	YES	45	Male	African American
4	YES	54	Female	African American
5	YES	41	Female	African American
6	YES	49	Female	African American
7	NO	51	Male	African American
8	NO	59	Female	African American
9	NO	36	Male	African American
10	NO	73	Female	African American
11	NO	48	Male	African American
12	NO	56	Male	African American
13	NO	33	Male	Hispanic
14	NO	47	Female	African American
15	NO	47	Female	African American


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<b>Treatment details</b>				
<b>ID</b>	<b>Modality</b>	<b>PAP adherence (mean all days used)</b>	<b>PAP adherence (% days used)</b>	<b>PAP adherence (% days used above 4 hours)</b>
1	CPAP	6.4	100	97.1
2	BiPAP	6.6	100	86.8
3	CPAP	6.02	94	84
4	AVAPS	3.82	90.7	46.5
5	BiPAP	6.37	100	88.6
6	CPAP	6.18	100	83.3
7	BiPAP	3.1	93.2	27.3
8	AVAPS	5.27	84	72
9	AVAPS	2.7	64.3	32.1
10	CPAP	6.82	96.2	67.3
11	AVAPS	3.95	88	48
12	AVAPS	6.02	97.7	86
13	CPAP	6.77	90.7	86
14	AVAPS	6.9	93	90.7
15	CPAP	4.9	42	20

<b>Pre-Post treatment physiological values</b>									
<b>ID</b>	<b>AHI (events/hour total sleep time)</b>			<b>4% ODI (/hrTST)</b>			<b>T90 (minutes)</b>		
	<b>pre</b>	<b>post</b>	<b>diff</b>	<b>pre</b>	<b>post</b>	<b>diff</b>	<b>pre</b>	<b>post</b>	<b>diff</b>
1	118.1	2.9	115.2	117.5	4.6	112.9	257.6	7.2	250.4
2	65.3	5.9	59.4	65.5	9.3	56.2	65.5	7.2	58.3
3	81.9	1.5	80.4	74.1	1.2	72.9	217.3	1.3	216
4	118.3	1.4	116.9	117.5	1.9	115.6	327.6	1.6	326
5	52.5	1.5	51	114.5	0	114.5	204.5	0	204.5
6	110.2	9.6	100.6	160.2	9.6	150.6	257.1	25.7	231.4
7	91.3	3.9	87.4	97.6	8.9	88.7	290.7	15.9	274.8
8	103.8	31.3	72.5	127.9	32.5	95.4	200.8	70.7	130.1
9	103.6	35.7	67.9	111	47	64	252.9	115.8	137.1
10	65.2	24.3	40.9	76.6	25.8	50.8	224.8	88.1	136.7
11	54	26.2	27.8	58	24.8	33.2	81	80.4	0.6
12	95.1	11.3	83.8	80.4	11	69.4	274.4	49.6	224.8
13	89.7	10.6	79.1	98.1	2.5	95.6	292.4	1.5	290.9
14	117.6	3.5	114.1	127.2	5	122.2	356	14.5	341.5
15	8.4	0.6	7.8	9.8	1.5	8.3	6.6	2.1	4.5


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**Pre-Post treatment physiological values (continued)**

ID	SpO <sub>2</sub> nadir (%)			PaCO <sub>2</sub> * (mmHg)			BMI (kg/m <sup>2</sup> )		
	pre	post	diff	pre	post	diff	pre	post	diff
1	64.4	82.9	-18.5	49.3	46.9	2.4	48.1	46.2	1.9
2	58.9	83.9	-25	51.1	44.3	6.8	37.3	37.4	-0.1
3	56.8	88.6	-31.8	44.5	35.2	9.3	42	44.5	-2.5
4	61.2	88.1	-26.9	46.7	35.6	11.1	44.1	43.1	1
5	55.3	93.6	-38.3	48	42.9	5.1	77.1	66.7	10.4
6	50.1	63.6	-13.5	50.5	41.3	9.2	55.6	55.9	-0.3
7	55	83.5	-28.5	71.6	63.8	7.8	52	48.2	3.8
8	54.8	70	-15.2	45.8	40.2	5.6	38.3	38.7	-0.4
9	55.9	59	-3.1	51.1	42.8	8.3	53.2	52.9	0.3
10	53.7	63.8	-10.1	53.6	43.4	10.2	57.2	55.8	1.4
11	50.6	65.9	-15.3	44.7	41.1	3.6	48.9	48.26	0.6
12	51.8	78.5	-26.7	52	35.2	16.8	40	40	0
13	50.1	88.9	-38.8	62.4	44.7	17.7	40.1	41.1	-1
14	51.5	82.6	-31.1	44	44.1	-0.1	61.2	61.5	-0.3
15	83.4	89.3	-5.9	48.4	40.8	7.6	45.6	45.1	0.5

\*: PaCO<sub>2</sub>= Partial pressure of CO<sub>2</sub> in the arterial blood obtained at 6 weeks after initiating PAP therapy.

**Comorbidities**

ID	Smoking	Hypertension	Type 2 diabetes mellitus	Congestive heart failure	Dyslipidemia
1	current	no	yes	no	no
2	never	yes	no	no	yes
3	never	yes	no	no	no
4	past	yes	no	no	no
5	never	no	no	yes	no
6	never	yes	no	no	no
7	never	yes	yes	yes	yes
8	past	yes	yes	no	no
9	current	yes	no	yes	no
10	past	yes	yes	yes	yes
11	never	yes	no	yes	no
12	never	yes	yes	no	yes
13	never	yes	no	no	no
14	current	yes	no	yes	no
15	never	yes	no	no	no

**e-Table 3:** Differentially DNA methylated regions between PRE and POST groups.

<b>Coordinates</b>	<b>Length</b>	<b># probes</b>	<b>p-value</b>	<b>MAT-score</b>	<b>Transcript type</b>	<b>Gene symbol</b>	<b>Distance to TSS</b>
chr10:1372012-1373260	1249	33	8.08E-06	7.22	RefSeq	ADARB2	396411
chr13:113510138-113512001	1864	48	8.08E-06	6.36	RefSeq	LINC00452	3867
chr18:75725595-75727061	1467	40	8.08E-06	6.34	RefSeq	KCNG2	939
chr17:77701017-77702693	1677	46	8.08E-06	6.29	RefSeq	CCDC57	61286
chr11:111248820-111249661	842	24	8.08E-06	6.1	RefSeq	ALG9	-1304
chr17:77910324-77911148	825	18	8.08E-06	6.04	RefSeq	TEX19	0
chr7:100388396-100389290	895	26	8.08E-06	6.02	RefSeq	MUC3A	3408
chr15:81010226-81010914	689	21	8.08E-06	5.75	RefSeq	CPEB1	26715
chr22:48948622-48949878	1257	34	8.08E-06	5.52	RefSeq	PANX2	-1409
chr1:112969380-112970190	811	23	8.08E-06	5.43	RefSeq	CAPZA1	5782
chr18:70381919-70382707	789	22	8.08E-06	5.39	RefSeq	CNDP1	29247
chr9:72218932-72219646	715	20	8.08E-06	5.35	RefSeq	KLF9	0
chr1:55277778-55278666	889	22	8.08E-06	5.31	RefSeq	PCSK9	41
chr19:7008172-7009009	838	25	8.08E-06	5.3	RefSeq	MBD3L3	637
chr12:13038273-13039025	753	19	8.08E-06	5.29	RefSeq	HEBP1	5486
chr11:2881744-2882577	834	19	8.08E-06	5.23	RefSeq	SLC22A18	1656
chr8:67673216-67673873	658	19	8.08E-06	5.22	RefSeq	MYBL1	14166
chr17:35097485-35098366	882	25	8.08E-06	5.21	RefSeq	ERBB2	0
chr6:546547-547487	941	20	8.08E-06	5.2	RefSeq	EXOC2	90655
chr3:171195493-171196125	633	17	8.08E-06	5.19	RefSeq	SEC62	28219
chr16:69255066-69255914	849	23	8.08E-06	5.19	RefSeq	MTSS1L	21542
chr12:113329046-113329897	852	24	8.08E-06	5.11	RefSeq	TBX5	734
chr2:72997421-72998042	622	17	8.08E-06	5.11	RefSeq	EMX1	-70
chr5:176230640-176232948	2309	60	8.08E-06	5.1	RefSeq	UNC5A	60474
chr21:37300697-37301276	580	16	8.08E-06	5.09	RefSeq	RIPPLY3	0
chr15:98914126-98916379	2254	59	8.08E-06	5.07	ncRNA	PRKXP1	633
chr16:65531324-65532117	794	22	8.08E-06	5.07	RefSeq	CES2	5476
chr7:151566456-151567147	692	20	8.08E-06	5.06	RefSeq	KMT2C	196877
chr7:157845745-157846960	1216	35	8.08E-06	5.05	RefSeq	PTPRN2	226284
chr19:6168037-6168807	771	23	8.08E-06	5.04	RefSeq	MLLT1	62153
chr8:347618-348380	763	22	8.08E-06	5.04	RefSeq	FBXO25	810
chr9:139186433-139187221	789	20	8.08E-06	5.04	RefSeq	TMEM210	-113
chr11:133293153-133293964	812	22	8.08E-06	5.04	RefSeq	IGSF9B	37896
chr1:199446299-199447161	863	23	8.08E-06	5.02	RefSeq	IGFN1	19723
chr5:52127026-52127685	660	19	8.08E-06	5.01	RefSeq	PELO	7495
chr7:27172252-27172907	656	19	8.08E-06	5.01	RefSeq	HOXA9	-577


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chr16:55038657-55039439	783	22	8.08E-06	5.01	RefSeq	NUDT21	3324
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chr19:58387162-58387770	609	18	2.42E-05	4.74	RefSeq	ZNF665	662
chr10:44817627-44818496	870	25	2.42E-05	4.73	RefSeq	C10orf25	-1150
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chr17:52345523-52346023	501	14	3.23E-05	4.71	RefSeq	TRIM25	386
chr5:55564379-55564956	578	16	4.04E-05	4.69	RefSeq	ANKRD55	0
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chr5:147422468-147423134	667	18	4.04E-05	4.68	RefSeq	SPINK5	-594
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chr15:32180417-32181036	620	18	4.85E-05	4.67	RefSeq	EMC7	310
chr1:34054131-34054683	553	11	5.65E-05	4.65	RefSeq	CSMD2	348780
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chr11:124485958-124486529	572	16	5.65E-05	4.63	RefSeq	TMEM218	286
chr5:14195580-14196164	585	16	5.65E-05	4.62	RefSeq	TRIO	-665
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chr19:42644345-42645053	709	20	9.69E-05	4.53	RefSeq	ZNF569	5127
chr20:62266436-62267027	592	17	1.05E-04	4.52	RefSeq	MYT1	165
chr13:45523147-45523702	556	16	1.05E-04	4.51	RefSeq	ZC3H13	1196

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chr4:167016214-167016764	551	15	1.13E-04	4.49	RefSeq	TLL1	2354
chr8:125532040-125532675	636	18	1.13E-04	4.49	RefSeq	TRMT12	0
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chr6:35803227-35803838	612	18	1.13E-04	4.49	RefSeq	FKBP5	501
chrX:48724856-48725345	490	15	1.13E-04	4.49	RefSeq	GRIPAP1	18275
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chr7:65343708-65344349	642	13	1.29E-04	4.45	RefSeq	TPST1	36014
chr14:102869868-102870386	519	14	1.29E-04	4.45	RefSeq	EIF5	0
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chr8:42867849-42868347	499	12	1.29E-04	4.42	RefSeq	RNF170	2677
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chr8:131019094-131019923	830	23	1.37E-04	4.41	RefSeq	FAM49B	1378
chr16:46049083-46049586	504	14	1.37E-04	4.4	RefSeq	ITFG1	2931
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chr7:92949643-92950198	556	16	1.37E-04	4.39	RefSeq	CALCR	91781

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chr1:173230492-173230997	506	14	2.02E-04	4.32	RefSeq	RABGAP1L	29964

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chr3:173488546-173489098	553	16	4.85E-04	4.04	RefSeq	FNDC3B	247508
chr5:176800864-176801496	633	18	4.85E-04	4.04	RefSeq	GRK6	14571
chr12:48221186-48221832	647	15	4.85E-04	4.04	RefSeq	KCNH3	1979
chr2:3720674-3721218	545	16	4.85E-04	4.04	RefSeq	ALLC	37013
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chr8:17564747-17565162	416	12	4.85E-04	4.04	RefSeq	MTUS1	137545
chr3:157756232-157756728	497	14	4.93E-04	4.04	RefSeq	SSR3	-564
chr1:42393011-42393457	447	13	4.93E-04	4.04	RefSeq	GUCA2B	1332
chr19:5792072-5792581	510	15	4.93E-04	4.04	RefSeq	FUT6	-1329
chr1:115124422-115124978	557	15	4.93E-04	4.04	RefSeq	SIKE1	0
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chr8:86537708-86538216	509	15	4.93E-04	4.04	RefSeq	CA3	-92
chr7:77165053-77165642	590	17	4.93E-04	4.04	RefSeq	RSBN1L	1374
chr9:93161853-93162571	719	20	4.93E-04	4.03	RefSeq	AUH	1457

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chr13:102515003-102515510	508	15	5.09E-04	4.03	RefSeq	SLC10A2	1688
chr6:138580215-138580753	539	14	5.09E-04	4.03	RefSeq	KIAA1244	55469
chr10:22672333-22672958	626	18	5.09E-04	4.03	RefSeq	SPAG6	-1422
chr15:33626709-33627262	554	14	5.09E-04	4.03	RefSeq	DPH6	-1012
chr5:34071598-34072206	609	17	5.09E-04	4.03	RefSeq	C1QTNF3	6923
chr6:27886132-27886664	533	15	5.09E-04	4.03	RefSeq	HIST1H3H	311
chr3:59934750-59935537	788	23	5.09E-04	4.03	RefSeq	FHIT	1276637
chr12:5023488-5024237	750	22	5.09E-04	4.03	RefSeq	KCNA5	142
chr16:4334038-4334616	579	16	5.09E-04	4.03	RefSeq	CORO7-PAM16	72348
chr11:65117483-65118334	852	20	5.09E-04	4.03	RefSeq	KCNK7	1710
chr9:6002721-6003432	712	20	5.09E-04	4.03	RefSeq	RANBP6	2209
chr15:20636683-20637176	494	15	5.09E-04	4.03	RefSeq	NIPA1	1109
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chr8:67253002-67253504	503	12	5.33E-04	4.02	RefSeq	CRH	0
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chr14:63744645-63745136	492	14	5.33E-04	4.01	RefSeq	SYNE2	355209

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chr13:34955033-34955639	607	18	5.33E-04	4.01	RefSeq	NBEA	6147
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chr4:2785482-2786107	626	17	5.33E-04	4.01	RefSeq	SH3BP2	20934
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chr7:141013875-141014435	561	17	5.33E-04	4.01	RefSeq	KIAA1147	33988
chr2:180160155-180160725	571	16	5.33E-04	4.01	RefSeq	ZNF385B	158290
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chr3:102048858-102049347	490	14	5.33E-04	4.01	RefSeq	ABI3BP	145678
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chr6:65677902-65678411	510	14	5.33E-04	4.01	RefSeq	EYS	795429
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chr1:115012116-115012649	534	15	5.49E-04	4	RefSeq	DENND2C	1607
chr11:71501658-71502156	499	14	5.57E-04	4	RefSeq	ANAPC15	-187
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chr12:45201641-45202652	1012	29	5.74E-04	4	ncRNA	LOC100288798	137915

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chr11:64173467-64173959	493	13	5.98E-04	3.99	RefSeq	NRXN2	73278
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chr12:51623450-51624142	693	15	6.06E-04	3.99	RefSeq	KRT8	5776
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chr19:14390838-14391370	533	15	6.54E-04	3.96	RefSeq	DDX39A	0
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chr5:37238305-37238648	344	10	6.54E-04	3.96	RefSeq	C5orf42	46640
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chr4:123594655-123595129	475	11	6.54E-04	3.96	RefSeq	IL2	1972
chr1:204709637-204710154	518	16	6.54E-04	3.96	RefSeq	IKBKE	-55
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chr2:111206459-111206971	513	12	6.54E-04	3.95	RefSeq	ACOXL	0


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chr14:57833435-57833923	489	14	6.95E-04	3.95	RefSeq	ARID4A	-1052
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chr7:127737908-127738398	491	14	7.19E-04	3.94	RefSeq	RBM28	32801
chr1:160304829-160305314	486	14	7.19E-04	3.94	RefSeq	NOS1AP	-891
chr3:48646920-48647425	506	14	7.19E-04	3.94	RefSeq	SLC26A6	-636
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chr6:64088492-64089063	572	16	7.51E-04	3.93	RefSeq	LGSN	-650
chr13:102290206-102290698	493	15	7.51E-04	3.93	RefSeq	BIVM	40806
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chrX:6156368-6156933	566	16	8.16E-04	3.9	RefSeq	NLGN4X	0
chr18:69964365-69964904	540	15	8.16E-04	3.9	RefSeq	FBXO15	1177
chr4:115045570-115046083	514	14	8.16E-04	3.9	RefSeq	ARSJ	74245
chr22:34965592-34966081	490	11	8.32E-04	3.9	RefSeq	APOL2	0

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chr19:47073610-47074115	506	13	8.32E-04	3.9	RefSeq	CD79A	580
chr6:75970437-75970923	487	14	8.32E-04	3.9	RefSeq	COL12A1	1421
chr17:21257637-21258077	441	13	8.32E-04	3.9	RefSeq	KCNJ18	8596
chr17:38185408-38185898	491	14	8.32E-04	3.89	RefSeq	WNK4	-277
chr5:140281679-140282496	818	22	8.32E-04	3.89	RefSeq	PCDHA1	135774
chr1:234371274-234371814	541	15	8.40E-04	3.89	RefSeq	GPR137B	-641
chr2:211124122-211124631	510	15	8.40E-04	3.89	RefSeq	CPS1	73471
chr1:145481293-145481821	529	15	8.40E-04	3.89	RefSeq	BCL9	1398
chr19:7651476-7651964	489	13	8.56E-04	3.89	RefSeq	TRAPP5	0
chr3:49138017-49138532	516	15	8.56E-04	3.89	RefSeq	LAMB2	7072
chr1:93578538-93579028	491	14	8.56E-04	3.89	ncRNA	LOC100131564	4929
chr16:63601447-63601935	489	14	8.56E-04	3.89	RefSeq	CDH11	111486
chr19:2187563-2188105	543	16	8.56E-04	3.89	RefSeq	PLEKHJ1	-210
chr3:127683701-127684257	557	16	8.56E-04	3.89	RefSeq	UROC1	35050
chr11:193868-194369	502	15	8.56E-04	3.89	RefSeq	BET1L	3054
chr2:178643902-178644391	490	14	8.56E-04	3.89	RefSeq	PDE11A	36922
chr15:42616163-42616670	508	13	8.56E-04	3.89	RefSeq	EIF3J	0
chrX:53580353-53580847	495	14	8.56E-04	3.89	RefSeq	HUWE1	149553
chr4:9392797-9393296	500	14	8.56E-04	3.89	RefSeq	DRD5	441
chr11:67133360-67133925	566	16	8.64E-04	3.89	RefSeq	NDUFV1	2461
chr2:174820613-174821130	518	14	8.64E-04	3.89	RefSeq	OLA1	482
chr6:31789251-31789731	481	13	8.64E-04	3.89	RefSeq	LY6G6D	-1381
chr12:7234299-7234800	502	13	8.64E-04	3.89	RefSeq	PEX5	74
chr11:47473889-47474397	509	14	8.64E-04	3.89	RefSeq	CELF1	27720
chr16:30916660-30917179	520	15	8.64E-04	3.88	RefSeq	STX1B	12152
chr12:94709025-94709534	510	15	8.64E-04	3.88	RefSeq	NTN4	-357
chr9:111559-112108	550	15	8.64E-04	3.88	RefSeq	CBWD1	56968
chr5:149345398-149345917	520	15	8.64E-04	3.88	RefSeq	SLC26A2	24905
chr22:22529542-22530313	772	21	8.64E-04	3.88	RefSeq	SLC2A11	652
chr11:111604028-111604635	608	17	8.64E-04	3.88	RefSeq	PTS	1730
chr22:36533025-36533570	546	14	8.64E-04	3.88	RefSeq	GCAT	-288
chr2:160277672-160278187	516	14	8.64E-04	3.88	RefSeq	42070	458
chr1:54642116-54642615	500	14	8.64E-04	3.88	RefSeq	SSBP3	2042
chr16:29738772-29739280	509	14	8.64E-04	3.88	RefSeq	MVP	0
chr11:9067379-9067858	480	13	8.64E-04	3.88	RefSeq	SCUBE2	1869
chr1:205105202-205105695	494	14	8.64E-04	3.88	RefSeq	IL20	-82
chr1:176330522-176331016	495	14	8.64E-04	3.88	RefSeq	RASAL2	1035
chr2:232497302-232497790	489	14	8.64E-04	3.88	RefSeq	NPPC	1493
chr1:6502137-6502737	601	17	8.64E-04	3.88	RefSeq	PLEKHG5	0

chr15:64370982-64371463	482	14	8.64E-04	3.88	RefSeq	DIS3L	-1224
chr7:91703882-91704225	344	10	8.72E-04	3.88	RefSeq	KRIT1	8940
chr7:93041425-93041968	544	16	8.72E-04	3.88	RefSeq	CALCR	11
chr5:137534620-137535137	518	15	8.81E-04	3.87	RefSeq	BRD8	7121
chr18:46598683-46599116	434	12	8.89E-04	3.87	RefSeq	MRO	6637
chr5:149771301-149771681	381	10	8.89E-04	3.87	RefSeq	CD74	1012
chr5:38630890-38631376	487	14	8.89E-04	3.87	RefSeq	LIFR	0
chrX:106964191-106964666	476	14	8.89E-04	3.87	RefSeq	MID2	8451
chr14:67253535-67254041	507	10	8.89E-04	3.87	RefSeq	RDH12	15179
chr7:142885066-142885588	523	15	8.89E-04	3.87	RefSeq	TAS2R41	0
chr18:3438403-3438903	501	14	8.89E-04	3.87	RefSeq	TGIF1	-508
chr3:150856235-150856746	512	14	8.89E-04	3.87	RefSeq	WWTR1	47005
chr6:97352540-97353100	561	15	8.89E-04	3.87	RefSeq	GPR63	38975
chr7:21549101-21549833	733	20	8.89E-04	3.87	RefSeq	DNAH11	0
chr11:133319933-133320424	492	15	8.97E-04	3.87	RefSeq	IGSF9B	11436
chr11:386148-386650	503	15	8.97E-04	3.87	RefSeq	PKP3	1931
chr9:14187941-14188455	515	16	8.97E-04	3.87	RefSeq	NFIB	115591
chr16:1522502-1523000	499	14	8.97E-04	3.87	RefSeq	TMEM204	3759
chr3:110153051-110153570	520	15	8.97E-04	3.87	RefSeq	GUCA1C	1798
chr13:43908340-43908843	504	14	8.97E-04	3.87	RefSeq	TSC22D1	548
chr11:6999867-7000520	654	15	8.97E-04	3.87	RefSeq	NLRP14	1591
chrX:40393985-40394512	528	14	8.97E-04	3.87	RefSeq	MED14	85237
chrX:53586837-53587354	518	15	8.97E-04	3.87	RefSeq	HUWE1	143046
chr1:144291496-144291831	336	10	8.97E-04	3.87	RefSeq	PIAS3	4151
chr1:151280226-151280732	507	14	8.97E-04	3.87	RefSeq	SPRR2D	-7
chr7:149195545-149196058	514	15	8.97E-04	3.87	ncRNA	ATP6V0E2-AS1	5827
chr1:2312574-2313069	496	14	8.97E-04	3.87	RefSeq	MORN1	0
chr2:96873743-96874241	499	15	8.97E-04	3.86	RefSeq	ANKRD23	-257
chr12:50912549-50913051	503	14	8.97E-04	3.86	RefSeq	KRT7	-170
chr6:116956402-116956898	497	14	8.97E-04	3.86	RefSeq	TRAPPC3L	16569
chr12:25600974-25601458	485	14	8.97E-04	3.86	RefSeq	LMNTD1	91306
chr8:31616162-31616651	490	14	8.97E-04	3.86	RefSeq	NRG1	-159
chr5:172025260-172025763	504	15	8.97E-04	3.86	RefSeq	NEURL1B	24379
chr6:47956295-47956957	663	19	8.97E-04	3.86	RefSeq	PTCHD4	187428
chr7:96471707-96472271	565	16	8.97E-04	3.86	RefSeq	DLX6	-955
chr5:108112094-108112696	603	16	8.97E-04	3.86	RefSeq	FER	672
chr2:108432367-108432901	535	15	8.97E-04	3.86	RefSeq	GCC2	358
chr18:2836389-2836874	486	14	8.97E-04	3.86	RefSeq	EMILIN2	-154
chr15:19335082-19335586	505	15	8.97E-04	3.86	RefSeq	POTEB2	748


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chr1:39565935-39566433	499	15	8.97E-04	3.86	RefSeq	MACF1	243509
chr17:370607-371098	492	14	8.97E-04	3.86	RefSeq	VPS53	193749
chrX:148428203-148428711	509	15	8.97E-04	3.86	ncRNA	LINC00893	493
chr1:199444904-199445555	652	18	8.97E-04	3.86	RefSeq	IGFN1	18328
chr2:229843261-229843754	494	13	8.97E-04	3.86	RefSeq	PID1	548
chr14:69428506-69428976	471	13	8.97E-04	3.86	RefSeq	SMOC1	12639
chr17:36646583-36647133	551	16	8.97E-04	3.86	RefSeq	KRTAP9-8	-663
chr3:155422330-155422841	512	10	8.97E-04	3.85	RefSeq	ARHGEF26	100848
chrX:33137168-33137663	496	13	8.97E-04	3.85	RefSeq	DMD	129985
chr1:58931446-58932073	628	18	9.05E-04	3.85	RefSeq	MYSM1	6263
chr19:54670343-54670844	502	14	9.05E-04	3.85	RefSeq	FLT3LG	1065
chr20:35589429-35589919	491	12	9.05E-04	3.85	RefSeq	BLCAP	0
chr15:87945600-87945987	388	11	9.05E-04	3.85	RefSeq	TICRR	25778
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chr12:11231693-11232179	487	14	9.05E-04	3.85	RefSeq	TAS2R42	-882
chr7:122091532-122092026	495	14	9.05E-04	3.85	RefSeq	CADPS2	222024
chr4:153550616-153551097	482	14	9.05E-04	3.85	RefSeq	FBXW7	124539
chr1:43596750-43597242	493	13	9.05E-04	3.85	RefSeq	CDC20	0
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chr1:103840890-103841396	507	14	9.05E-04	3.85	RefSeq	LOC101928436	-196
chr20:31723001-31723392	392	12	9.05E-04	3.84	RefSeq	NECAB3	2534
chr11:1559805-1560304	500	14	9.05E-04	3.84	ncRNA	KRTAP5-AS1	9258
chr13:44936801-44937297	497	13	9.05E-04	3.84	RefSeq	COG3	0
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chr6:32246807-32247323	517	14	9.13E-04	3.84	RefSeq	AGPAT1	4572
chr7:93470065-93470583	519	15	9.21E-04	3.84	RefSeq	BET1	1044
chr10:12275121-12275639	519	15	9.29E-04	3.84	RefSeq	NUDT5	2511
chr9:127714252-127714765	514	15	9.37E-04	3.84	RefSeq	PBX3	163953
chr17:61492878-61493397	520	13	9.37E-04	3.84	RefSeq	CEP112	125278
chr11:93772509-93773024	516	15	9.37E-04	3.84	RefSeq	GPR83	1210
chr7:153375798-153376311	514	14	9.37E-04	3.84	RefSeq	DPP6	160683
chr15:20256205-20256719	515	15	9.45E-04	3.84	ncRNA	GOLGA8DP	10374
chr17:77609056-77609570	515	15	9.45E-04	3.83	RefSeq	DUS1L	7417
chr18:64654002-64654534	533	15	9.45E-04	3.83	RefSeq	CCDC102B	120531
chr15:86981971-86982460	490	13	9.45E-04	3.83	RefSeq	ISG20	-583
chr2:168704978-168705577	600	17	9.45E-04	3.83	RefSeq	STK39	106775
chr4:39454280-39454788	509	15	9.45E-04	3.83	RefSeq	UBE2K	78221
chr10:111961946-111962291	346	10	9.45E-04	3.83	RefSeq	MXI1	1967
chr3:44975511-44976002	492	14	9.45E-04	3.83	RefSeq	ZDHHC3	16677

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chr15:80552459-80552977	519	14	9.45E-04	3.83	RefSeq	GOLGA6L10	262277
chr10:62429733-62430216	484	14	9.53E-04	3.83	ncRNA	RHOBTB1	527
chr2:218791684-218792290	607	18	9.53E-04	3.83	RefSeq	ARPC2	1319
chr5:170746738-170747255	518	15	9.53E-04	3.83	RefSeq	NPM1	-58
chr5:94442050-94442544	495	14	9.53E-04	3.83	RefSeq	MCTP1	783
chr19:51899821-51900334	514	14	9.53E-04	3.83	RefSeq	PRKD2	11891
chr17:25111247-25111735	489	14	9.53E-04	3.83	RefSeq	SSH2	169638
chr3:157493520-157494045	526	15	9.53E-04	3.83	RefSeq	KCNAB1	150075
chr6:31656497-31657033	537	15	9.53E-04	3.83	RefSeq	LTB	1149
chr12:50490780-50491495	716	21	9.53E-04	3.83	RefSeq	SCN8A	219493
chr4:71098131-71098647	517	14	9.53E-04	3.83	RefSeq	ODAM	1298
chr6:53626135-53626751	617	15	9.53E-04	3.83	RefSeq	KLHL31	11715
chr2:48702331-48702817	487	14	9.53E-04	3.83	RefSeq	GTF2A1L	3908
chr6:53765913-53766417	505	14	9.53E-04	3.83	RefSeq	LRRC1	-1320
chr2:207511513-207511998	486	14	9.53E-04	3.83	RefSeq	CPO	-525
chr6:105958161-105958652	492	14	9.53E-04	3.83	RefSeq	PREP	-468
chr14:60022360-60022844	485	14	9.53E-04	3.83	RefSeq	C14orf39	0
chr22:29421871-29422322	452	13	9.53E-04	3.83	RefSeq	OSBP2	2102
chr1:16959293-16959778	486	13	9.53E-04	3.82	RefSeq	MST1L	3785
chr19:993789-994284	496	14	9.53E-04	3.82	RefSeq	ABCA7	2687
chr1:166170227-166170720	494	14	9.53E-04	3.82	RefSeq	MPC2	2212
chr20:56157836-56158413	578	16	9.53E-04	3.82	RefSeq	C20orf85	-976
chr10:22674496-22674996	501	14	9.53E-04	3.82	RefSeq	SPAG6	116
chr6:42123700-42124281	582	17	9.53E-04	3.82	RefSeq	CCND3	330
chr4:77125835-77126269	435	13	9.53E-04	3.82	RefSeq	SDAD1	4871
chr10:30695199-30695687	489	14	9.61E-04	3.82	ncRNA	GOLGA2P6	5156
chrX:101281865-101282379	515	15	9.61E-04	3.82	RefSeq	TCEAL6	1666
chr15:61672306-61672818	513	13	9.61E-04	3.82	RefSeq	USP3	88543
chr16:18479726-18480239	514	14	9.61E-04	3.82	RefSeq	NOMO2	697
chr4:123389562-123390192	631	18	9.61E-04	3.82	RefSeq	KIAA1109	78354
chr12:55130284-55130800	517	15	9.61E-04	3.82	RefSeq	TIMELESS	-816
chr21:42793705-42794222	518	15	9.61E-04	3.82	RefSeq	SLC37A1	894
chr8:57244153-57244645	493	14	9.61E-04	3.82	RefSeq	PLAG1	41769
chr10:16601835-16602498	664	16	9.61E-04	3.82	RefSeq	C1QL3	1513
chr17:34814743-34815257	515	14	9.69E-04	3.82	RefSeq	MED1	45797
chr16:65062244-65062756	513	15	9.69E-04	3.82	RefSeq	BEAN1	43543
chr18:32022968-32023475	508	14	9.69E-04	3.82	RefSeq	MOCOS	1490
chrX:119576711-119577211	501	14	9.77E-04	3.81	RefSeq	CUL4B	1635
chr19:45553660-45554187	528	16	9.77E-04	3.81	RefSeq	PLD3	7488


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chr7:44051506-44052006	501	14	9.77E-04	3.81	RefSeq	DBNL	742
chr21:42606451-42606959	509	14	9.77E-04	3.81	RefSeq	TFF3	1817
chr11:102217478-102217980	503	14	9.77E-04	3.81	RefSeq	MMP3	1573
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chr5:122400470-122400955	486	13	9.77E-04	3.81	RefSeq	PPIC	-145
chr5:112099479-112099966	488	14	9.77E-04	3.81	RefSeq	APC	-1489
chr22:29694641-29695222	582	15	9.77E-04	3.81	RefSeq	MORC2	-453
chr6:35419497-35419997	501	14	9.86E-04	3.81	RefSeq	PPARD	1184
chr3:153496691-153497205	515	15	9.86E-04	3.81	RefSeq	MBNL1	28172
chrY:9298041-9298555	515	15	9.86E-04	3.81	RefSeq	TSPY3	2011
chr5:159785285-159785626	342	10	9.86E-04	3.81	RefSeq	PTTG1	3790
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chr2:105727200-105727590	391	11	9.94E-04	3.81	RefSeq	NCK2	-362
chr22:36682710-36683195	486	14	9.94E-04	-3.57	RefSeq	POLR2F	3094
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chr3:180272616-180273081	466	14	9.86E-04	-3.57	RefSeq	ZMAT3	-265
chr6:161333876-161334374	499	15	9.86E-04	-3.57	RefSeq	MAP3K4	1127
chr11:64642623-64643094	472	14	9.86E-04	-3.57	RefSeq	ZNHIT2	-876
chr1:32436811-32437308	498	15	9.86E-04	-3.57	RefSeq	CCDC28B	-1266
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chr21:44956800-44957318	519	12	9.86E-04	-3.57	RefSeq	TSPEAR	-876
chr17:24013178-24013749	572	17	9.86E-04	-3.57	RefSeq	SUPT6H	0
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chr9:134922064-134922572	509	15	9.86E-04	-3.57	RefSeq	GTF3C5	26181
chr6:165915440-165915932	493	14	9.77E-04	-3.57	RefSeq	PDE10A	79647
chr22:23797280-23797882	603	16	9.77E-04	-3.57	RefSeq	KIAA1671	43339
chr2:203444893-203445472	580	16	9.77E-04	-3.57	RefSeq	ICA1L	0
chr17:20192014-20192525	512	15	9.77E-04	-3.58	ncRNA	CCDC144CP	26935
chr5:141976303-141976797	495	12	9.77E-04	-3.58	RefSeq	FGF1	69448
chr12:52964507-52965002	496	14	9.77E-04	-3.58	RefSeq	HNRNPA1	3752
chr6:88237982-88238482	501	14	9.77E-04	-3.58	RefSeq	SLC35A1	-880
chr12:130005749-130006259	511	15	9.69E-04	-3.58	RefSeq	GPR133	1344
chr9:134448368-134448940	573	17	9.69E-04	-3.58	RefSeq	BARHL1	554
chr17:4096155-4096645	491	14	9.69E-04	-3.58	RefSeq	ANKFY1	17247
chr22:29103039-29103645	607	17	9.69E-04	-3.58	ncRNA	KIAA1656	250
chrX:48640438-48640940	503	14	9.61E-04	-3.58	RefSeq	PQBP1	299
chr1:113419374-113419783	410	12	9.61E-04	-3.58	RefSeq	LRIG2	2020
chr14:104430309-104430811	503	15	9.61E-04	-3.58	RefSeq	CEP170B	27614
chr1:117016052-117016414	363	10	9.61E-04	-3.58	ncRNA	MIR320B1	158

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chr1:778629-779174	546	16	9.61E-04	-3.58	ncRNA	LINC01128	25795
chr16:21378824-21379274	451	13	9.61E-04	-3.58	ncRNA	SMG1P3	41830
chr15:40539629-40540052	424	13	9.61E-04	-3.58	RefSeq	ZNF106	30636
chr13:107671715-107672163	449	13	9.61E-04	-3.58	RefSeq	ABHD13	2951
chr15:28484259-28484777	519	14	9.61E-04	-3.58	RefSeq	GOLGA8R	8979
chr7:5886023-5886534	512	15	9.61E-04	-3.58	RefSeq	OCM	-421
chr1:167825940-167826442	503	14	9.61E-04	-3.58	RefSeq	SELP	39560
chr19:41194157-41194539	383	10	9.61E-04	-3.58	RefSeq	ALKBH6	2447
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chr4:9707730-9708224	495	14	9.61E-04	-3.58	RefSeq	WDR1	19448
chr16:30680078-30680570	493	15	9.61E-04	-3.58	RefSeq	C16orf93	497
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chr5:34714661-34715157	497	14	9.61E-04	-3.59	RefSeq	RAI14	22308
chr1:111479818-111480328	511	15	9.61E-04	-3.59	RefSeq	DRAM2	4034
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chr16:24476134-24476650	517	12	9.53E-04	-3.59	RefSeq	RBBP6	17725
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chr6_cox_hap1:3946684-3947200	517	12	9.53E-04	-3.59	RefSeq	HLA-DRB1	861
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chr17:3515214-3515718	505	11	7.59E-04	-3.66	RefSeq	TAX1BP3	3005
chr10:101364412-101364800	389	12	7.59E-04	-3.67	RefSeq	SLC25A28	5412
chr16:561640-562256	617	18	7.59E-04	-3.67	RefSeq	PIGQ	1671
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chrX:100525325-100525879	555	16	7.51E-04	-3.67	RefSeq	BTK	1990
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chr6:150111658-150112209	552	15	7.43E-04	-3.67	RefSeq	PCMT1	-315


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chr18:42955263-42955764	502	14	7.43E-04	-3.68	RefSeq	IER3IP1	980
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chr11:71487902-71488417	516	15	7.03E-04	-3.69	RefSeq	LRTOMT	18877

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chr17:41946669-41947193	525	15	5.33E-04	-3.81	RefSeq	LRRC37A2	1277

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chr8:22477686-22478261	576	14	2.26E-04	-4.08	RefSeq	SORBS3	-863
chr10:75125201-75125744	544	15	2.26E-04	-4.08	RefSeq	AGAP5	1817
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chr11:4585566-4586084	519	14	2.26E-04	-4.1	RefSeq	TRIM68	0
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chr9:666419-667039	621	18	1.29E-04	-4.33	RefSeq	KANK1	206125
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chr3:185498339-185498882	544	11	1.29E-04	-4.35	RefSeq	PSMD2	-698
chr17:37275062-37275600	539	11	1.29E-04	-4.35	RefSeq	KLHL11	0
chr19:9296370-9296810	441	13	1.13E-04	-4.36	RefSeq	ZNF559-ZNF177	468
chr11:63147912-63148405	494	14	1.13E-04	-4.36	RefSeq	ATL3	47618
chr3:49288273-49288805	533	15	1.13E-04	-4.36	RefSeq	C3orf62	708
chr2:118560844-118561362	519	15	1.13E-04	-4.36	RefSeq	INSIG2	-1158
chr7:73965741-73966367	627	18	1.13E-04	-4.36	ncRNA	PMS2P5	20918
chr20:61021825-61022381	557	16	1.13E-04	-4.36	RefSeq	DIDO1	5968
chr5:138241341-138241910	570	17	1.13E-04	-4.37	RefSeq	CTNNA1	124357
chrX:49070584-49071222	639	18	1.13E-04	-4.37	RefSeq	GAGE12J	5131
chr17:70912220-70912828	609	18	1.13E-04	-4.38	RefSeq	GRB2	557
chr7:47984028-47984519	492	14	1.13E-04	-4.38	RefSeq	HUS1	1229
chr1:160800082-160800446	365	11	1.13E-04	-4.38	RefSeq	UAP1	2162
chrX:49216646-49217224	579	17	1.13E-04	-4.38	RefSeq	GAGE12F	4291
chr9:108666353-108666925	573	15	1.13E-04	-4.38	RefSeq	ZNF462	1154
chrX:118582497-118583065	569	16	1.05E-04	-4.41	RefSeq	CXorf56	336
chr11:104279583-104280106	524	15	9.69E-05	-4.41	ncRNA	LOC643733	14007
chr5:176624406-176625238	833	22	9.69E-05	-4.41	RefSeq	NSD1	130967
chr11:123314848-123316000	1153	31	9.69E-05	-4.41	RefSeq	OR4D5	0
chr19:54707350-54707824	475	14	9.69E-05	-4.41	RefSeq	FCGRT	2
chr16:87751547-87752765	1219	35	9.69E-05	-4.42	ncRNA	LINC00304	-364
chr16:3082705-3083232	528	15	9.69E-05	-4.42	RefSeq	ZSCAN10	6088
chr1:166150157-166150783	627	18	9.69E-05	-4.42	RefSeq	ADCY10	-68
chr9:114104044-114104657	614	18	8.89E-05	-4.43	RefSeq	PTBP3	31109
chr3:47597637-47598207	571	16	8.89E-05	-4.45	RefSeq	CSPG5	-902
chr2:110648093-110648678	586	16	8.89E-05	-4.45	ncRNA	LIMS3-LOC440895	16512
chr19:46635988-46636823	836	19	8.89E-05	-4.46	RefSeq	ATP5SL	499
chr10:127579635-127580276	642	18	8.89E-05	-4.47	RefSeq	FANK1	4537
chr17:43370440-43371383	944	23	8.89E-05	-4.47	ncRNA	LOC100506325	2387
chr3:154364367-154364940	574	15	8.89E-05	-4.47	RefSeq	RAP2B	1676
chr14:65004279-65004834	556	15	8.89E-05	-4.47	RefSeq	FUT8	57216
chr7:101894663-101895288	626	17	8.89E-05	-4.47	RefSeq	LRWD1	2268
chr19:2232043-2232934	892	25	8.89E-05	-4.48	RefSeq	C19orf35	248
chr5:140166141-140166739	599	17	8.89E-05	-4.48	RefSeq	PCDHA1	20236
chr17:36235869-36236547	679	18	8.89E-05	-4.49	RefSeq	TMEM99	6906

chr2:51113197-51113869	673	19	8.89E-05	-4.5	RefSeq	NRXN1	-18
chr11:67109561-67110281	721	19	8.89E-05	-4.5	RefSeq	GSTP1	1919
chr10:76539876-76540427	552	16	8.89E-05	-4.5	RefSeq	DUSP13	-899
chr17:2181816-2182469	654	19	8.89E-05	-4.5	RefSeq	TSR1	4960
chr1:149486845-149487432	588	18	8.08E-05	-4.52	RefSeq	PIP5K1A	49200
chr10:48579108-48579736	629	18	8.08E-05	-4.52	ncRNA	GLUD1P7	6510
chr5:56147540-56148357	818	21	8.08E-05	-4.52	RefSeq	MAP3K1	883
chrX:227522-228210	689	19	8.08E-05	-4.53	RefSeq	PPP2R3B	39481
chr1:153288690-153289229	540	16	8.08E-05	-4.53	RefSeq	DCST1	15784
chr7:151568623-151569198	576	16	8.08E-05	-4.53	RefSeq	KMT2C	194826
chr5:43073035-43073731	697	19	8.08E-05	-4.54	ncRNA	LOC648987	29568
chr1:144022706-144023543	838	23	7.27E-05	-4.54	RefSeq	NBPF12	717754
chr7:44008532-44009145	614	17	6.46E-05	-4.56	RefSeq	SPDYE1	1518
chr8:70569455-70569985	531	11	6.46E-05	-4.56	RefSeq	SULF1	28042
chr16:3871392-3871948	557	16	6.46E-05	-4.56	RefSeq	CREBBP	-1269
chr10:7783971-7784425	455	14	6.46E-05	-4.56	RefSeq	ITIH2	-817
chr19:46952491-46953026	536	16	5.65E-05	-4.57	RefSeq	CEACAM6	1223
chrX:119903990-119904472	483	14	5.65E-05	-4.57	RefSeq	CT47A10	-435
chr7:73963431-73964056	626	18	5.65E-05	-4.57	ncRNA	PMS2P5	18608
chr1:226889574-226890257	684	18	5.65E-05	-4.58	ncRNA	RHOU	42557
chr3:33680724-33681298	575	16	5.65E-05	-4.58	RefSeq	CLASP2	53412
chr22:16616330-16616982	653	18	5.65E-05	-4.58	RefSeq	BID	20280
chr10:70675364-70675892	529	15	5.65E-05	-4.6	RefSeq	HKDC1	25299
chr16:28671193-28671704	512	14	5.65E-05	-4.61	RefSeq	NPIPB9	0
chr19:2724299-2724924	626	17	5.65E-05	-4.61	RefSeq	SGTA	9431
chr22:49334801-49335387	587	16	5.65E-05	-4.61	RefSeq	KLHDC7B	1473
chr16:15380013-15380485	473	14	5.65E-05	-4.62	RefSeq	NPIPA5	-360
chr9:129255804-129256600	797	23	5.65E-05	-4.62	RefSeq	LRSAM1	2218
chr16:65814915-65815488	574	15	5.65E-05	-4.63	RefSeq	LRRC29	2915
chr5_h2_hap1:1006229-1006797	569	17	5.65E-05	-4.63	RefSeq	GTF2H2C_2	-936
chr16:30159356-30159831	476	14	4.85E-05	-4.64	ncRNA	LOC613037	4603
chr5:40871178-40871754	577	15	4.85E-05	-4.64	RefSeq	RPL37	-33
chr7:97830572-97831143	572	17	4.85E-05	-4.65	RefSeq	BAIAP2L1	37221
chr1:1658133-1658879	747	16	4.85E-05	-4.65	RefSeq	SLC35E2	8420
chr7:72139293-72139801	509	15	4.85E-05	-4.65	ncRNA	SPDYE8P	-1047
chr1:27574429-27574860	432	12	4.85E-05	-4.66	RefSeq	FCN3	-526
chr14:34656993-34657515	523	15	4.85E-05	-4.66	RefSeq	PPP2R3C	3756
chr1:27093219-27093906	688	20	4.85E-05	-4.67	RefSeq	GPATCH3	5644
chrX:152516355-152516757	403	12	4.85E-05	-4.67	RefSeq	FAM58A	1070


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chr16:22386546-22387343	798	23	4.85E-05	-4.69	ncRNA	SMG1P1	30716
chr10:46321812-46322350	539	12	4.85E-05	-4.72	ncRNA	FAM35BP	4165
chr7:72134877-72135546	670	19	4.04E-05	-4.74	ncRNA	SPDYE8P	2700
chr3:64649742-64650549	808	20	3.23E-05	-4.75	RefSeq	ADAMTS9	-1336
chr8:92151917-92152588	672	19	3.23E-05	-4.76	RefSeq	OTUD6B	317
chr7:143679710-143680197	488	14	3.23E-05	-4.76	ncRNA	OR2A1-AS1	3548
chr5_h2_hap1:626640-627165	526	16	3.23E-05	-4.77	ncRNA	SMA4	5613
chr7:143526829-143527310	482	14	2.42E-05	-4.79	ncRNA	LOC101928605	3482
chr2:73867035-73867454	420	12	2.42E-05	-4.79	RefSeq	C2orf78	2211
chr3:190986694-190987593	900	20	2.42E-05	-4.85	RefSeq	TP63	154784
chr2:87589733-87590303	571	17	2.42E-05	-4.86	ncRNA	LINC00152	53644
chr17:36792212-36792764	553	16	2.42E-05	-4.86	RefSeq	KRT34	-49
chr16:28276611-28277085	475	14	2.42E-05	-4.88	RefSeq	NPIP6	4598
chr5:172253049-172253643	595	15	2.42E-05	-4.92	RefSeq	ERGIC1	59220
chr8:7871010-7871637	628	16	1.62E-05	-4.95	RefSeq	USP17L3	1281
chr7:77370775-77371396	622	14	8.08E-06	-4.98	RefSeq	PHTF2	63392
chr13:19621964-19622822	859	24	8.08E-06	-5	RefSeq	GJA3	10362
chr16:29368415-29368963	549	15	8.08E-06	-5.01	ncRNA	LOC606724	248
chr7:74805232-74805841	610	18	8.08E-06	-5.02	ncRNA	SPDYE8P	2736
chr9:32977690-32978461	772	21	8.08E-06	-5.03	RefSeq	APTX	13179
chr19:8951795-8952424	630	18	8.08E-06	-5.04	RefSeq	MUC16	595
chr12:52710794-52711458	665	19	8.08E-06	-5.04	RefSeq	HOXC6	2333
chr16:30160662-30161325	664	17	8.08E-06	-5.05	ncRNA	LOC613037	3109
chr16:70305676-70306366	691	19	8.08E-06	-5.05	RefSeq	PHLPP2	879
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chr11:4571383-4572309	927	26	8.08E-06	-5.08	RefSeq	OR52I1	0
chr17:26676990-26677490	501	14	8.08E-06	-5.11	RefSeq	NF1	230919
chr2:112957662-112958271	610	18	8.08E-06	-5.11	RefSeq	TTL	1448
chr21:43795398-43796193	796	22	8.08E-06	-5.12	RefSeq	HSF2BP	107610
chr17:3994012-3994804	793	20	8.08E-06	-5.12	RefSeq	CYB5D2	348
chr5:52893848-52894499	652	18	8.08E-06	-5.13	RefSeq	NDUFS4	1626
chr17:7540634-7541023	390	12	8.08E-06	-5.13	RefSeq	WRAP53	10520
chr4:8958574-8960106	1533	40	8.08E-06	-5.13	RefSeq	USP17L25	0
chr7:1084246-1085016	771	22	8.08E-06	-5.15	RefSeq	C7orf50	59404
chr11:122974772-122975365	594	17	8.08E-06	-5.16	RefSeq	GRAMD1B	73218
chr2:67479271-67480097	827	24	8.08E-06	-5.17	RefSeq	ETAA1	1325
chr4:8963612-8964816	1205	31	8.08E-06	-5.17	RefSeq	USP17L25	0
chr12:119036609-119037389	781	22	8.08E-06	-5.17	RefSeq	RAB35	1638
chr4:166426371-166426974	604	17	8.08E-06	-5.17	RefSeq	KLHL2	75750

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chr7:101981652-101982330	679	19	8.08E-06	-5.17	RefSeq	SPDYE2	2874
chrX:49207087-49207665	579	17	8.08E-06	-5.17	RefSeq	GAGE12F	4285
chr7:101588665-101589548	884	25	8.08E-06	-5.19	RefSeq	CUX1	342761
chr19:12049055-12049613	559	16	8.08E-06	-5.22	RefSeq	ZNF844	12509
chr16:14937943-14938425	483	14	8.08E-06	-5.22	RefSeq	NPIPA1	-376
chr3:195653574-195654080	507	15	8.08E-06	-5.23	RefSeq	ATP13A3	16178
chr9:44942433-44943477	1045	25	8.08E-06	-5.23	ncRNA	LOC102723709	1810
chr19:57996669-57997255	587	17	8.08E-06	-5.25	RefSeq	ZNF28	19480
chr2:224607729-224608251	523	15	8.08E-06	-5.26	RefSeq	SERPINE2	4030
chr16:1597053-1597638	586	17	8.08E-06	-5.27	RefSeq	IFT140	4473
chr4:8954158-8955180	1023	26	8.08E-06	-5.29	RefSeq	USP17L25	0
chr20:25728433-25729326	894	22	8.08E-06	-5.3	ncRNA	FAM182B	602
chr8:12474442-12475099	658	19	8.08E-06	-5.31	ncRNA	LOC729732	92393
chr15:19001513-19002108	596	14	8.08E-06	-5.31	RefSeq	GOLGA6L6	5021
chrX:49069698-49070274	577	17	8.08E-06	-5.35	RefSeq	GAGE12J	4245
chr20:3840550-3841296	747	21	8.08E-06	-5.38	RefSeq	PANK2	23064
chr16:30165093-30165926	834	24	8.08E-06	-5.38	ncRNA	LOC613037	-659
chr16:2529373-2530011	639	18	8.08E-06	-5.42	RefSeq	PDPK1	1407
chr7:74779567-74780409	843	24	8.08E-06	-5.43	ncRNA	SPDYE8P	5098
chr16:22446368-22446970	603	18	8.08E-06	-5.44	RefSeq	NPIP5	14023
chr15:48846611-48847254	644	19	8.08E-06	-5.44	RefSeq	SPPL2A	-1408
chr10:45411212-45411849	638	18	8.08E-06	-5.45	RefSeq	42071	-851
chr17:9507973-9508510	538	12	8.08E-06	-5.45	RefSeq	USP43	18394
chr8:27520073-27520407	335	10	8.08E-06	-5.46	RefSeq	CLU	7839
chr16:14751309-14751795	487	14	8.08E-06	-5.5	RefSeq	NPIPA3	-376
chr1:144016867-144017565	699	19	8.08E-06	-5.54	RefSeq	NBPF12	711915
chr16:30150024-30150672	649	19	8.08E-06	-5.55	ncRNA	LOC613037	13762
chr21:44661694-44662362	669	18	8.08E-06	-5.61	RefSeq	TRPM2	63782
chr19:11187013-11187745	733	21	8.08E-06	-5.65	RefSeq	DOCK6	46424
chr7:143620357-143621167	811	22	8.08E-06	-5.73	ncRNA	LOC101928605	97010
chr16:30145614-30146327	714	20	8.08E-06	-6.01	ncRNA	LOC613037	18107
chr1:93316250-93316886	637	18	8.08E-06	-6.06	RefSeq	MTF2	-494
chr1:244204571-244206821	2251	51	8.08E-06	-6.07	RefSeq	SMYD3	530447
chr16:22450720-22451359	640	18	8.08E-06	-6.07	RefSeq	NPIP5	18375
chr1:31121926-31122834	909	25	8.08E-06	-6.08	RefSeq	SDC3	31234
chr18:42807034-42807795	762	19	8.08E-06	-6.1	RefSeq	KATNAL2	26249
chr8:7178278-7179293	1016	26	8.08E-06	-6.13	RefSeq	USP17L1	959
chr5:69535062-69535636	575	13	8.08E-06	-6.14	ncRNA	SMA4	21743
chr1:144030100-144031194	1095	29	8.08E-06	-6.15	RefSeq	NBPF12	725148

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chr20:61981012-61982307	1296	36	8.08E-06	-6.17	RefSeq	TPD52L2	13987
chr7:99744290-99744954	665	19	8.08E-06	-6.18	RefSeq	SPDYE3	1029
chr5:69533183-69533708	526	16	8.08E-06	-6.22	ncRNA	SMA4	23671
chr4:8973243-8974307	1065	27	8.08E-06	-6.23	RefSeq	USP17L25	0
chr7:66383574-66384230	657	18	8.08E-06	-6.23	ncRNA	PMS2P4	20635
chr4:8970088-8971284	1197	32	8.08E-06	-6.32	RefSeq	USP17L10	881
chr5:70122606-70123134	529	15	8.08E-06	-6.42	ncRNA	SMA4	71091
chr16:16349723-16350468	746	21	8.08E-06	-7.14	ncRNA	PKD1P1	30756
chr18:42801111-42801880	770	19	8.08E-06	-7.26	RefSeq	KATNAL2	20326
chrX:49235747-49236325	579	17	8.08E-06	-7.48	RefSeq	GAGE12C	4251
chr4:8974870-8976030	1161	31	8.08E-06	-7.48	RefSeq	USP17L25	917
chr7:102082410-102083101	692	19	8.08E-06	-7.49	RefSeq	SPDYE2	4402
chr4:8960200-8961794	1595	43	8.08E-06	-7.65	RefSeq	USP17L25	483
chr22:45891632-45892379	748	21	8.08E-06	-7.97	RefSeq	TBC1D22A	354454
chr4:8955853-8957049	1197	32	8.08E-06	-8.06	RefSeq	USP17L25	881
chr4:8965343-8966539	1197	32	8.08E-06	-8.25	RefSeq	USP17L25	881
chr5:70120678-70121268	591	14	8.08E-06	-8.94	ncRNA	SMA4	69163


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**e-Table 4:** Gene-associated DMRs between PRE and POST groups.

<b>Coordinates</b>	<b>Length</b>	<b># probes</b>	<b>p-value</b>	<b>MAT-score</b>	<b>Transcript type</b>	<b>Gene symbol</b>	<b>Distance to TSS</b>
chr18:75725595-75727061	1467	40	8.08E-06	6.34	RefSeq	KCNG2	939
chr11:111248820-111249661	842	24	8.08E-06	6.1	RefSeq	ALG9	-1304
chr17:77910324-77911148	825	18	8.08E-06	6.04	RefSeq	TEX19	0
chr22:48948622-48949878	1257	34	8.08E-06	5.52	RefSeq	PANX2	-1409
chr9:72218932-72219646	715	20	8.08E-06	5.35	RefSeq	KLF9	0
chr1:55277778-55278666	889	22	8.08E-06	5.31	RefSeq	PCSK9	41
chr19:7008172-7009009	838	25	8.08E-06	5.3	RefSeq	MBD3L3	637
chr11:2881744-2882577	834	19	8.08E-06	5.23	RefSeq	SLC22A18	1656
chr17:35097485-35098366	882	25	8.08E-06	5.21	RefSeq	ERBB2	0
chr12:113329046-113329897	852	24	8.08E-06	5.11	RefSeq	TBX5	734
chr2:72997421-72998042	622	17	8.08E-06	5.11	RefSeq	EMX1	-70
chr15:98914126-98916379	2254	59	8.08E-06	5.07	ncRNA	PRKXP1	633
chr8:347618-348380	763	22	8.08E-06	5.04	RefSeq	FBXO25	810
chr9:139186433-139187221	789	20	8.08E-06	5.04	RefSeq	TMEM210	-113
chr7:27172252-27172907	656	19	8.08E-06	5.01	RefSeq	HOXA9	-577
chr17:23901780-23902431	652	16	8.08E-06	5.01	RefSeq	UNC119	1343
chr2:46600411-46601179	769	22	1.62E-05	4.95	RefSeq	ATP6V1E2	0
chr3:46717877-46718651	775	22	1.62E-05	4.79	RefSeq	TMIE	50
chr19:58387162-58387770	609	18	2.42E-05	4.74	RefSeq	ZNF665	662
chr10:44817627-44818496	870	25	2.42E-05	4.73	RefSeq	C10orf25	-1150
chr4:104161782-104162598	817	23	3.23E-05	4.72	RefSeq	SLC9B1	-1436
chr17:52345523-52346023	501	14	3.23E-05	4.71	RefSeq	TRIM25	386
chr5:55564379-55564956	578	16	4.04E-05	4.69	RefSeq	ANKRD55	0
chr5:147422468-147423134	667	18	4.04E-05	4.68	RefSeq	SPINK5	-594
chr14:100362766-100363624	859	24	4.85E-05	4.67	ncRNA	MEG3	568
chr15:32180417-32181036	620	18	4.85E-05	4.67	RefSeq	EMC7	310
chr1:156230180-156230748	569	16	5.65E-05	4.65	RefSeq	KIRREL	493
chr6:50895875-50896502	628	16	5.65E-05	4.65	RefSeq	TFAP2B	1477
chr15:83325685-83326229	545	14	5.65E-05	4.64	RefSeq	PDE8A	937
chr11:124485958-124486529	572	16	5.65E-05	4.63	RefSeq	TMEM218	286
chr5:14195580-14196164	585	16	5.65E-05	4.62	RefSeq	TRIO	-665
chr14:24115524-24116329	806	23	6.46E-05	4.62	RefSeq	CTSG	-217
chr7:86617609-86618187	579	16	6.46E-05	4.61	RefSeq	DMTF1	-1426
chr17:18069275-18069786	512	11	6.46E-05	4.58	RefSeq	LLGL1	0
chrX:70280593-70281363	771	22	7.27E-05	4.57	RefSeq	NLGN3	-43
chr4:109312508-109313093	586	17	8.08E-05	4.56	ncRNA	LEF1-AS1	0

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chr19:10807192-10807762	571	16	9.69E-05	4.56	RefSeq	TMED1	222
chr17:37792928-37793757	830	23	9.69E-05	4.55	RefSeq	STAT3	283
chr20:62266436-62267027	592	17	1.05E-04	4.52	RefSeq	MYT1	165
chr13:45523147-45523702	556	16	1.05E-04	4.51	RefSeq	ZC3H13	1196
chr6:32481602-32482408	807	22	1.05E-04	4.51	RefSeq	BTNL2	471
chr8:125532040-125532675	636	18	1.13E-04	4.49	RefSeq	TRMT12	0
chr6:35803227-35803838	612	18	1.13E-04	4.49	RefSeq	FKBP5	501
chr12:16391275-16391910	636	18	1.29E-04	4.47	RefSeq	MGST1	0
chr20:13921702-13922422	721	20	1.29E-04	4.46	ncRNA	SEL1L2	1558
chr1:159367892-159368526	635	18	1.29E-04	4.44	RefSeq	DEDD	577
chr7:79978606-79979120	515	14	1.29E-04	4.43	RefSeq	GNAT3	59
chr3:127904943-127905653	711	20	1.29E-04	4.43	RefSeq	CHCHD6	-100
chr11:61315987-61316672	686	19	1.29E-04	4.43	RefSeq	FEN1	-13
chr3:130203764-130204448	685	20	1.29E-04	4.42	RefSeq	EFCC1	602
chr1:120415201-120415876	676	19	1.29E-04	4.42	RefSeq	NOTCH2	-1360
chr8:131019094-131019923	830	23	1.37E-04	4.41	RefSeq	FAM49B	1378
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chr12:116023515-116024039	525	15	1.37E-04	4.4	ncRNA	TESC-AS1	1860
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chr1:201587156-201587695	540	12	1.45E-04	4.39	RefSeq	FMOD	0
chr4:77152550-77153171	622	18	1.53E-04	4.38	RefSeq	ART3	1193
chr19:7647341-7647940	600	18	1.53E-04	4.37	RefSeq	MCEMP1	-3
chr3:125295211-125295823	613	14	1.70E-04	4.37	RefSeq	KALRN	-425
chr9:131636807-131637307	501	15	1.78E-04	4.36	RefSeq	USP20	-210
chr2:128284444-128284960	517	15	1.78E-04	4.36	RefSeq	WDR33	272
chr12:119117013-119117590	578	16	1.78E-04	4.36	RefSeq	GCN1L1	-116
chr3:44259790-44260366	577	16	1.86E-04	4.36	RefSeq	TOPAZ1	1408
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chr2:217205308-217205845	538	15	1.86E-04	4.36	RefSeq	IGFBP2	-527
chr19:53866440-53867202	763	21	2.02E-04	4.34	RefSeq	NTN5	875
chr4:141483934-141484580	647	15	2.02E-04	4.34	RefSeq	SCOC	0
chr10:74683255-74683882	628	18	2.02E-04	4.34	RefSeq	MRPS16	-797
chr11:101827602-101828261	660	19	2.02E-04	4.33	RefSeq	TMEM123	725
chr8:96351025-96351839	815	19	2.02E-04	4.33	RefSeq	C8orf37	-386
chr17:61731217-61731820	604	17	2.02E-04	4.33	RefSeq	PRKCA	1829
chr9:38413606-38414103	498	14	2.02E-04	4.33	RefSeq	IGFBPL1	342
chr10:70330227-70330907	681	14	2.02E-04	4.32	RefSeq	DDX50	-133

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chr2:3362888-3363402	515	11	2.02E-04	4.31	RefSeq	TRAPPC12	435
chr5:86742542-86743246	705	20	2.02E-04	4.31	RefSeq	CCNH	1232
chr3:8787041-8787708	668	16	2.02E-04	4.31	RefSeq	OXTR	-740
chr4:30330498-30331095	598	14	2.02E-04	4.31	RefSeq	PCDH7	-40
chr12:9776758-9777310	553	16	2.02E-04	4.3	RefSeq	CLECL1	0
chr6:168220260-168220775	516	14	2.02E-04	4.3	RefSeq	FRMD1	-864
chr1:158268658-158269224	567	13	2.02E-04	4.3	RefSeq	PIGM	-250
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chr19:14798232-14798886	655	18	2.10E-04	4.29	RefSeq	OR7A5	1391
chr11:626516-627152	637	17	2.10E-04	4.29	RefSeq	DRD4	-153
chrX:152792974-152793687	714	20	2.18E-04	4.29	RefSeq	L1CAM	1008
chr6:142508442-142508957	516	12	2.18E-04	4.28	RefSeq	VTA1	-1035
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chr2:20113420-20114124	705	20	2.42E-04	4.26	RefSeq	LAPTM4A	1147
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chr22:19697957-19698496	540	16	2.91E-04	4.23	RefSeq	P2RX6	-946
chr3:52064416-52064947	532	16	2.91E-04	4.23	RefSeq	DUSP7	555
chr7:139122919-139123416	498	15	2.91E-04	4.23	RefSeq	HIPK2	747
chrX:41433822-41434476	655	18	2.91E-04	4.23	RefSeq	GPR34	652

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chr19:40534735-40535226	492	13	3.15E-04	4.21	RefSeq	FFAR1	450
chr1:202448402-202448923	522	15	3.15E-04	4.21	RefSeq	GOLT1A	921
chr2:132890677-132891225	549	15	3.15E-04	4.21	RefSeq	GPR39	60
chr17:53759381-53760270	890	25	3.15E-04	4.2	RefSeq	BZRAP1	882
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chr18:28305386-28305864	479	12	3.15E-04	4.19	RefSeq	GAREM	-940
chr10:61571876-61572395	520	15	3.23E-04	4.19	RefSeq	ANK3	-1095
chr15:75499634-75500291	658	19	3.31E-04	4.19	RefSeq	HMG20A	-7
chr14:60517942-60518558	617	18	3.39E-04	4.19	RefSeq	SLC38A6	357
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chr5:172688513-172689023	511	14	3.47E-04	4.18	RefSeq	STC2	90
chr9:94471489-94472075	587	16	3.47E-04	4.18	RefSeq	IPPK	294
chr20:43029178-43029668	491	14	3.64E-04	4.17	RefSeq	STK4	644
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chr19:15612230-15612750	521	14	3.72E-04	4.15	RefSeq	CYP4F3	0
chr5:61735065-61735795	731	20	3.72E-04	4.15	RefSeq	DIMT1	0
chr20:33462295-33462958	664	14	3.72E-04	4.15	RefSeq	UQCC1	402
chrX:68317487-68318204	718	21	3.80E-04	4.15	ncRNA	LINC00269	1362
chr12:49705088-49705584	497	10	3.80E-04	4.15	RefSeq	SLC11A2	883
chr4:69851139-69851925	787	21	3.80E-04	4.15	RefSeq	UGT2A3	174
chr3:123034870-123035390	521	15	3.80E-04	4.15	RefSeq	IQCB1	1227
chr10:103103897-103104410	514	15	3.80E-04	4.14	RefSeq	BTRC	117


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chr8:144171620-144172275	656	19	3.88E-04	4.14	RefSeq	LY6E	343
chr14:44676764-44677252	489	14	3.88E-04	4.14	RefSeq	FANCM	1878
chr11:3211540-3212316	777	22	3.88E-04	4.14	RefSeq	MRGPRE	-1347
chr6:44234228-44235124	897	24	3.96E-04	4.14	RefSeq	CAPN11	0
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chr17:55325558-55326055	498	14	4.12E-04	4.1	RefSeq	TUBD1	-469
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chr19:6452143-6452682	540	16	4.28E-04	4.08	RefSeq	TUBB4A	1178
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chr15:39032271-39032798	528	14	4.28E-04	4.07	RefSeq	CHAC1	-130
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chr17:1567431-1567937	507	15	4.77E-04	4.05	RefSeq	WDR81	864
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chr13:102515003-102515510	508	15	5.09E-04	4.03	RefSeq	SLC10A2	1688
chr15:33626709-33627262	554	14	5.09E-04	4.03	RefSeq	DPH6	-1012
chr6:27886132-27886664	533	15	5.09E-04	4.03	RefSeq	HIST1H3H	311
chr12:5023488-5024237	750	22	5.09E-04	4.03	RefSeq	KCNA5	142
chr11:65117483-65118334	852	20	5.09E-04	4.03	RefSeq	KCNK7	1710
chr15:20636683-20637176	494	15	5.09E-04	4.03	RefSeq	NIPA1	1109
chr17:36348005-36348515	511	13	5.25E-04	4.02	RefSeq	KRT23	-583
chr3:145174164-145174690	527	15	5.25E-04	4.02	RefSeq	C3orf58	-167
chr5:147142755-147143369	615	17	5.33E-04	4.02	RefSeq	JAKMIP2	-150
chr1:66990317-66990800	484	14	5.33E-04	4.02	RefSeq	TCTEX1D1	0
chr11:47154987-47155532	546	15	5.33E-04	4.02	RefSeq	ARFGAP2	0
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chr5:179152284-179152771	488	14	5.33E-04	4.02	RefSeq	LTC4S	-821
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chr18:8706170-8706706	537	15	5.33E-04	4.01	RefSeq	MTCL1	-663
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chr8:19839014-19839547	534	15	5.41E-04	4	RefSeq	LPL	-1315
chr18:55718259-55718935	677	18	5.41E-04	4	RefSeq	PMAIP1	87
chr7:89712014-89712712	699	19	5.41E-04	4	RefSeq	CFAP69	0
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chr6:111910063-111910690	628	16	5.41E-04	4	RefSeq	REV3L	922
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chr12:120724462-120724974	513	14	5.49E-04	4	ncRNA	LINC01089	800
chr11:71501658-71502156	499	14	5.57E-04	4	RefSeq	ANAPC15	-187
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chr11:59804665-59805155	491	15	5.74E-04	3.99	RefSeq	MS4A4A	75

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chr17:72787498-72788081	584	17	6.38E-04	3.97	RefSeq	42256	-1006
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chr4:87734175-87734842	668	19	8.08E-04	3.91	RefSeq	PTPN13	0
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chr9:44942433-44943477	1045	25	8.08E-06	-5.23	ncRNA	LOC102723709	1810
chr16:14937943-14938425	483	14	8.08E-06	-5.22	RefSeq	NPIPA1	-376
chr12:119036609-119037389	781	22	8.08E-06	-5.17	RefSeq	RAB35	1638
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chr5:52893848-52894499	652	18	8.08E-06	-5.13	RefSeq	NDUFS4	1626
chr17:3994012-3994804	793	20	8.08E-06	-5.12	RefSeq	CYB5D2	348
chr2:112957662-112958271	610	18	8.08E-06	-5.11	RefSeq	TTL	1448
chr11:4571383-4572309	927	26	8.08E-06	-5.08	RefSeq	OR52I1	0
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chr16:70305676-70306366	691	19	8.08E-06	-5.05	RefSeq	PHLPP2	879
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chr16:29368415-29368963	549	15	8.08E-06	-5.01	ncRNA	LOC606724	248
chr8:7871010-7871637	628	16	1.62E-05	-4.95	RefSeq	USP17L3	1281
chr17:36792212-36792764	553	16	2.42E-05	-4.86	RefSeq	KRT34	-49
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chr3:64649742-64650549	808	20	3.23E-05	-4.75	RefSeq	ADAMTS9	-1336
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chr1:27574429-27574860	432	12	4.85E-05	-4.66	RefSeq	FCN3	-526

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chr16:3871392-3871948	557	16	6.46E-05	-4.56	RefSeq	CREBBP	-1269
chr7:44008532-44009145	614	17	6.46E-05	-4.56	RefSeq	SPDYE1	1518
chr5:56147540-56148357	818	21	8.08E-05	-4.52	RefSeq	MAP3K1	883
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chr1:53302141-53302910	770	15	1.37E-04	-4.31	RefSeq	PODN	1829

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chr6:116705830-116706397	568	16	2.26E-04	-4.09	RefSeq	TSPYL1	1577
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chr2:46778352-46779141	790	18	2.67E-04	-4.03	RefSeq	SOCS5	-462
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chr19:63175394-63175947	554	16	5.41E-04	-3.79	RefSeq	C19orf18	1768
chr7:99411965-99412379	415	11	5.41E-04	-3.79	RefSeq	AZGP1	-293
chr1:161028937-161029421	485	14	5.41E-04	-3.79	RefSeq	HSD17B7	1817
chr4:145785391-145786012	622	17	5.41E-04	-3.79	RefSeq	HHIP	-586
chr3:120879261-120879681	421	12	5.49E-04	-3.78	RefSeq	COX17	-327
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chr8:124817785-124818243	459	13	5.57E-04	-3.78	RefSeq	ANXA13	586
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chrX:119938115-119938517	403	12	5.57E-04	-3.78	RefSeq	CT47A10	-515
chr1:245988345-245988882	538	15	5.57E-04	-3.78	RefSeq	OR1C1	-13
chr13:45324473-45325023	551	15	5.57E-04	-3.78	RefSeq	SIAH3	-625
chr8:119190751-119191292	542	14	5.57E-04	-3.77	RefSeq	EXT1	1948

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chr15:86964229-86964618	390	11	5.90E-04	-3.75	RefSeq	AEN	-913
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chr1:119757203-119757582	380	11	5.98E-04	-3.75	RefSeq	HSD3B2	-1495
chr21:45699363-45699945	583	17	5.98E-04	-3.75	RefSeq	COL18A1	0
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chr16:55218406-55218834	429	12	5.98E-04	-3.75	RefSeq	MT1E	1320
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chr1:35796754-35797154	401	12	6.14E-04	-3.74	RefSeq	NCDN	774
chr17:70768144-70768657	514	15	6.22E-04	-3.74	RefSeq	GGA3	1413
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chr6:44419869-44420401	533	15	6.30E-04	-3.73	RefSeq	SPATS1	1494
chrX:48214791-48215238	448	13	6.30E-04	-3.73	RefSeq	SLC38A5	-1202
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chr12:42436890-42437229	340	10	6.30E-04	-3.73	RefSeq	PUS7L	1615
chr15:39311282-39311682	401	12	6.38E-04	-3.73	RefSeq	EXD1	-1034
chr4:5071806-5072303	498	14	6.38E-04	-3.72	RefSeq	CYTL1	0
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chr6:49787877-49788377	501	15	6.54E-04	-3.72	RefSeq	CRISP2	886
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chr10:15171932-15172672	741	21	6.79E-04	-3.71	RefSeq	ACBD7	-1150
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chr19:9982912-9983263	352	11	6.79E-04	-3.7	RefSeq	COL5A3	-764
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chr9:42999421-43000119	699	18	6.79E-04	-3.7	ncRNA	GXYLT1P3	-1027
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chr11:5233896-5234337	442	10	7.11E-04	-3.69	RefSeq	HBG2	-1308
chr11:64404713-64405192	480	13	7.19E-04	-3.69	RefSeq	EHD1	-951


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chr16:55777631-55778134	504	13	7.35E-04	-3.68	RefSeq	FAM192A	-153
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chr2:37045791-37046306	516	14	7.35E-04	-3.68	RefSeq	STRN	814
chr15:32616255-32616781	527	14	7.43E-04	-3.68	RefSeq	GOLGA8B	-740
chr18:42955263-42955764	502	14	7.43E-04	-3.68	RefSeq	IER3IP1	980
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chr9:34600552-34601058	507	14	7.51E-04	-3.67	RefSeq	RPP25L	1053
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chr12:121752621-121753118	498	14	7.84E-04	-3.66	RefSeq	HCAR2	740
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chr11:64706738-64707233	496	14	7.84E-04	-3.65	RefSeq	CAPN1	1476
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chr19:9407970-9408441	472	13	8.00E-04	-3.65	RefSeq	ZNF266	-715
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chrX:47999303-47999834	532	15	8.00E-04	-3.65	RefSeq	SSX1	0

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chrX:100193722-100194255	534	15	8.40E-04	-3.63	RefSeq	TRMT2B	0
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chr13:77009775-77010226	452	13	8.97E-04	-3.61	RefSeq	SCEL	1965

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chr11:64642623-64643094	472	14	9.86E-04	-3.57	RefSeq	ZNHIT2	-876
chr6:161333876-161334374	499	15	9.86E-04	-3.57	RefSeq	MAP3K4	1127
chr3:156278868-156279433	566	15	9.86E-04	-3.57	RefSeq	MME	-697
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chr5:151044917-151045455	539	11	8.89E-04	-3.61	RefSeq	SPARC	1354
chr14:76914230-76914742	513	15	9.61E-04	-3.59	RefSeq	SAMD15	715
chrX:49065674-49066173	500	14	9.61E-04	-3.58	RefSeq	GAGE12J	221
chr3:125294404-125294909	506	14	9.61E-04	-3.58	RefSeq	KALRN	-1339
chr12:130005749-130006259	511	15	9.69E-04	-3.58	RefSeq	GPR133	1344
chr17:24013178-24013749	572	17	9.86E-04	-3.57	RefSeq	SUPT6H	0
chr21:44956800-44957318	519	12	9.86E-04	-3.57	RefSeq	TSPEAR	-876
chr3:180272616-180273081	466	14	9.86E-04	-3.57	RefSeq	ZMAT3	-265

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**e-Table 5:** Canonical pathways overrepresented in DMRS between PRE and POST groups.

<b>DMRs with higher DNA methylation in PRE group</b>		
<b>Pathway</b>	<b>-log(p-value)</b>	<b>Ratio</b>
RAR Activation	1.81E+00	4.21E-02
Biogenesis of Mitochondria	1.36E+00	1.00E-01
Xenobiotic Metabolism Signaling	1.23E+00	2.98E-02
Increases Glomerular Injury	1.22E+00	5.66E-02
Increases Renal Proliferation	1.10E+00	3.68E-02
Hepatic Fibrosis	1.07E+00	4.04E-02
Negative Acute Phase Response Proteins	8.97E-01	1.25E-01
Fatty Acid Metabolism	8.70E-01	3.42E-02
Renal Ischemic Resistance Panel (Rat)	8.07E-01	1.00E-01
Glutathione Depletion - CYP Induction and Reactive Metabolites	7.35E-01	8.33E-02
PPAR $\alpha$ /RXR $\alpha$ Activation	7.08E-01	2.73E-02
LPS/IL-1 Mediated Inhibition of RXR Function	6.05E-01	2.39E-02
Cytochrome P450 Panel - Substrate is a Xenobiotic (Human)	5.80E-01	5.56E-02
Aryl Hydrocarbon Receptor Signaling	5.42E-01	2.48E-02
Glutathione Depletion - Phase II Reactions	5.41E-01	5.00E-02
PXR/RXR Activation	5.07E-01	2.99E-02
Nongenotoxic Hepatocarcinogenicity Biomarker Panel	5.06E-01	4.55E-02
Mitochondrial Dysfunction	4.64E-01	2.27E-02
Cytochrome P450 Panel - Substrate is a Xenobiotic (Mouse)	4.61E-01	4.00E-02
Cytochrome P450 Panel - Substrate is a Xenobiotic (Rat)	4.48E-01	3.85E-02
Renal Proximal Tubule Toxicity Biomarker Panel (Rat)	4.35E-01	3.70E-02
Reversible Glomerulonephritis Biomarker Panel (Rat)	4.35E-01	3.70E-02
Increases Cardiac Dilation	4.22E-01	3.57E-02
CAR/RXR Activation	4.10E-01	3.45E-02
Increases Liver Steatosis	4.02E-01	2.47E-02
TGF- $\beta$ Signaling	3.48E-01	2.22E-02
Mechanism of Gene Regulation by Peroxisome Proliferators via PPAR $\alpha$	3.22E-01	2.11E-02
Hepatic Cholestasis	2.78E-01	1.82E-02
Increases Liver Damage	2.72E-01	1.89E-02
NRF2-mediated Oxidative Stress Response	2.55E-01	1.71E-02
Increases Renal Nephritis	2.48E-01	2.04E-02
Increases Liver Hepatitis	2.32E-01	1.92E-02
Decreases Transmembrane Potential of Mitochondria and Mitochondrial Membrane	2.30E-01	1.71E-02

<b>DMRs with higher DNA methylation in POST group</b>		
<b>Pathway</b>	<b>-log(p-value)</b>	<b>Ratio</b>
Renal Necrosis/Cell Death	2.22E+00	3.63E-02
Cell Cycle: G1/S Checkpoint Regulation	2.10E+00	7.58E-02
Cardiac Fibrosis	2.00E+00	4.71E-02

Increases Liver Hyperplasia/Hyperproliferation	1.95E+00	6.00E-02
VDR/RXR Activation	1.81E+00	6.41E-02
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.79E+00	7.69E-02
Mechanism of Gene Regulation by Peroxisome Proliferators via PPAR $\alpha$	1.48E+00	5.26E-02
Increases Cardiac Proliferation	1.24E+00	6.38E-02
Cardiac Necrosis/Cell Death	1.18E+00	3.36E-02
Increases Liver Hepatitis	1.13E+00	5.77E-02
Increases Heart Failure	1.13E+00	8.33E-02
Aryl Hydrocarbon Receptor Signaling	1.08E+00	3.73E-02
Increases Cardiac Dilatation	1.02E+00	7.14E-02
Renal Safety Biomarker Panel (PSTC)	9.70E-01	1.67E-01
Cytochrome P450 Panel - Substrate is an Eicosanoid (Human)	9.07E-01	1.43E-01
Liver Proliferation	8.69E-01	3.08E-02
Vasopressin-induced Genes in Inner Medullary Renal Collecting Duct Cells (Rat)	8.53E-01	1.25E-01
Cytochrome P450 Panel - Substrate is a Fatty Acid (Human)	7.64E-01	1.00E-01
Genes Upregulated in Response to Proteinuria-induced Oxidative Stress in Renal Proximal Tubule Cells (Human)	7.64E-01	1.00E-01
Cytochrome P450 Panel - Substrate is a Fatty Acid (Rat)	7.26E-01	9.09E-02
Glutathione Depletion - CYP Induction and Reactive Metabolites	6.93E-01	8.33E-02
Increases Bradycardia	6.07E-01	6.67E-02
Cytochrome P450 Panel - Substrate is a Fatty Acid (Mouse)	5.83E-01	6.25E-02
Hepatic Fibrosis	5.48E-01	3.03E-02
Increases Depolarization of Mitochondria and Mitochondrial Membrane	5.40E-01	5.56E-02
Oxidative Stress	5.39E-01	3.51E-02
Glutathione Depletion - Phase II Reactions	5.02E-01	5.00E-02
Increases Liver Damage	4.96E-01	2.83E-02
Acute Renal Failure Panel (Rat)	4.90E-01	3.23E-02
Decreases Depolarization of Mitochondria and Mitochondrial Membrane	4.38E-01	4.17E-02
Hepatic Cholestasis	4.28E-01	2.42E-02
Renal Proximal Tubule Toxicity Biomarker Panel (Rat)	3.98E-01	3.70E-02
Increases Renal Damage	3.47E-01	2.47E-02
Increases Renal Proliferation	3.28E-01	2.21E-02
Hepatic Stellate Cell Activation	3.15E-01	2.86E-02
TGF- $\beta$ Signaling	2.97E-01	2.22E-02
Pro-Apoptosis	2.61E-01	2.38E-02
p53 Signaling	2.55E-01	2.02E-02
Increases Renal Nephritis	2.19E-01	2.04E-02