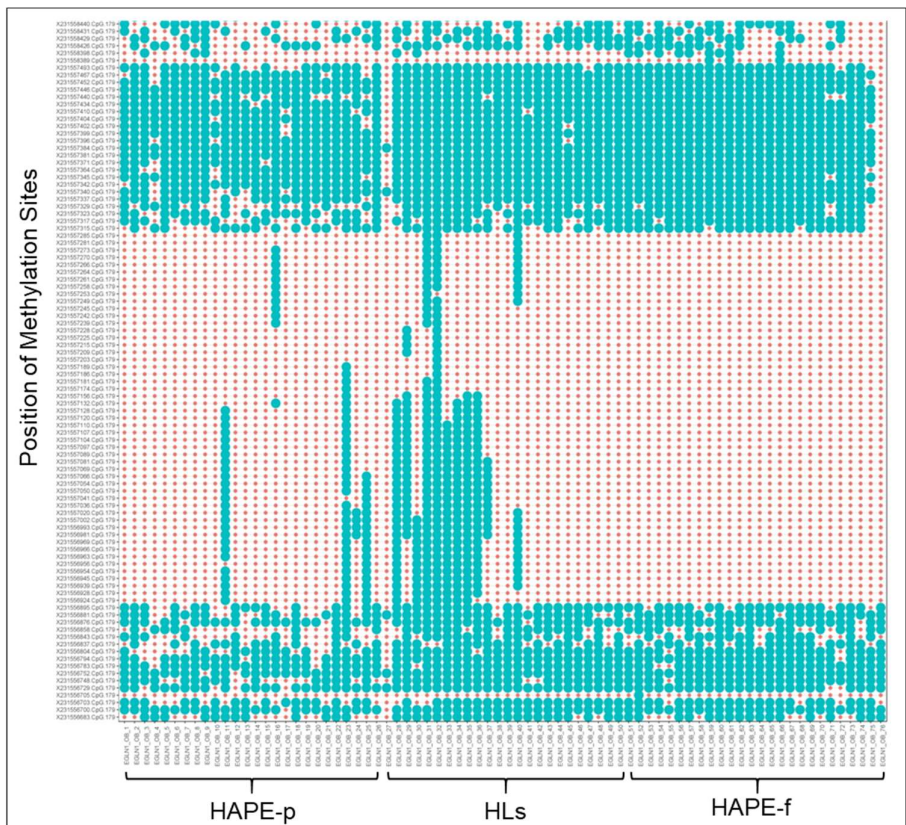
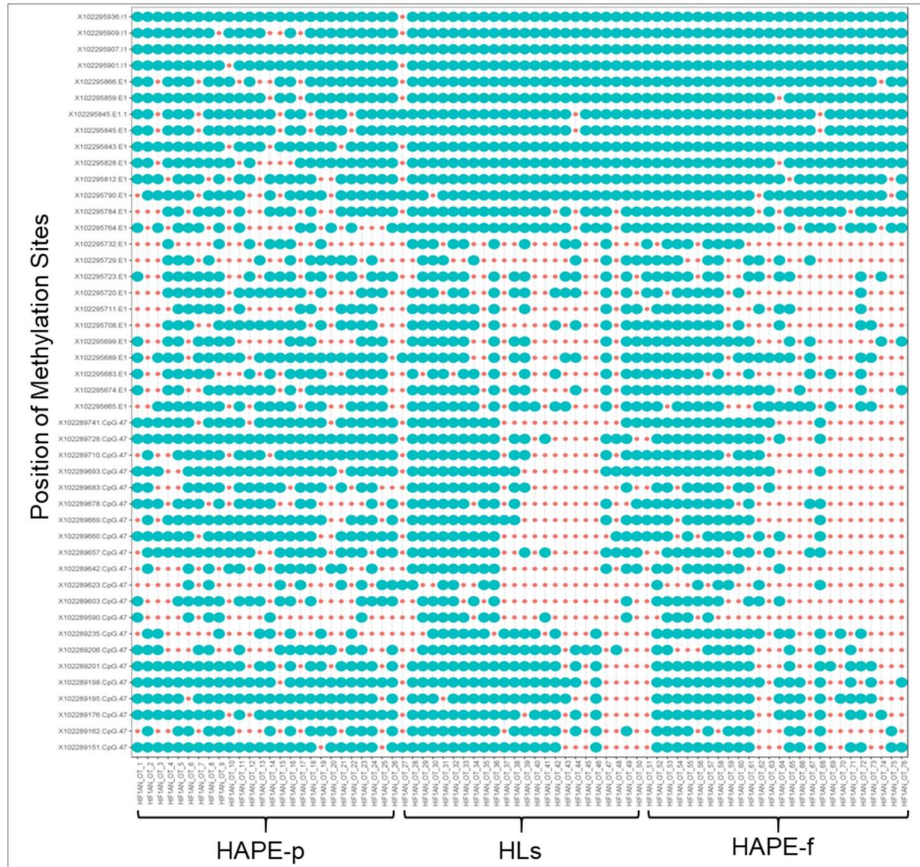


Supplementary Figure 1. Levels of SpO₂% in HAPE-p, HAPE-f and HLs. SpO₂: Blood arterial oxygen saturation level; NS: Not significant



SupplementaryFigure 2. Dot plot of CpG methylation in *EGLN1* in the three study groups i.e. HAPE-p, HLs and HAPE-f. It revealed 97 CpG sites in *EGLN1* CpGisland 179.

- ,Un-methylated site; ● ,Methylated site.



Supplementary Figure 3. Dot plot of CpG methylation in *HIF1AN* in the three study groups i.e. HAPE-f, HAPE-p and HLs. It revealed 46 CpG sites in *HIF1AN* CpGisland 47.

- ,Un-methylated site; ● ,Methylated site.

Supplementary Table 1. Methylation distribution of CpG sites of *EGLN1* and *HIF1AN* in each subject of the three study groups i.e., HAPE-f, HAPE-p and HLs.

Subjects	<i>EGLN1</i> 5mC sites			<i>HIF1AN</i> 5mC sites		
	HAPE-f	HAPE-p	HLs	HAPE-f	HAPE-p	HLs
1	42.27	36.08	5.15	65.22	67.39	17.39
2	42.27	39.18	65.98	93.48	65.22	86.96
3	38.14	35.05	67.01	93.48	52.17	93.48
4	40.21	19.59	50.52	86.96	69.57	95.65
5	37.11	35.05	87.63	93.48	82.61	93.48
6	41.24	34.02	93.81	84.78	82.61	95.65
7	43.30	35.05	67.01	95.65	67.39	93.48
8	39.18	40.21	71.13	95.65	86.96	82.61
9	41.24	38.14	71.13	71.74	86.96	73.91
10	44.33	23.71	70.10	80.43	54.35	95.65
11	41.24	58.76	53.61	80.43	76.09	50.00
12	43.30	31.96	34.02	58.70	63.04	73.91
13	40.21	26.80	40.21	45.65	65.22	73.91
14	37.11	29.90	64.95	52.17	67.39	50.00
15	40.21	31.96	31.96	56.52	63.04	52.17
16	44.33	46.39	36.08	43.48	84.78	54.35
17	42.27	23.71	40.21	45.65	69.57	45.65
18	36.08	35.05	41.24	60.87	82.61	47.83
19	38.14	31.96	40.21	36.96	73.91	32.61
20	36.08	29.90	39.18	32.61	52.17	47.83
21	32.99	28.87	40.21	41.30	67.39	69.57
22	35.05	40.21	40.21	58.70	76.09	36.96

23	38.14	70.10	40.21	43.48	84.78	78.26
24	36.08	36.08	41.24	32.61	84.78	65.22
25	27.84	47.42		30.43	65.22	
26	13.40	40.21		39.13	69.57	
Mean	38.14	36.36	51.37	62.29	71.57	66.94
Std Dev	6.3	10.6	20.1	22.7	10.6	23.0

Supplementary Table 2. Real-time PCR conditions for *EGLN1* and *HIF1AN*.

Gene	Primer sequence	Cycling conditions	Product size (bp)
<i>EGLN1</i>	F 5'- GCT ACA AGG TAC GCA ATA ACT G-3'	I94°C 10', D94°C 15",	154
	R 5'- TGG ATC AAA GGC TCT AGA AGA C -3'	A60°C 60", 40 cy	
<i>HIF1AN</i>	F 5'- TGA GTT CGT TGA GAA ACT GC -3'	I94°C 10', D94°C 15",	211
	R 5'- TGT CAC ATT TCC TTC CAT GC-3'	A60°C 60", 40 cy	

F: forward; R: reverse; I: initial denaturation; D: denaturation; A: annealing; cy: cycles.

Supplementary Table 3. Sodium bisulfite-conversion-based methylation PCR Primers and conditions for *EGLN1* and *HIF1AN*.

Gene	Primer sequence	Cycling conditions	Product (bp)
<i>EGLN1</i>			
HP1F HP1R	F5'-GGGAAAAAGGGTTATAGTTAAGTTATTT-3' R5'-AACTCCCACATAACCAAAAACATATTC-3'	I95°C 5', D95°C 30", A58°C 30", E72°C 30", 38cy, FE72°C 10'	212
HP2F2 HP2R2	F5'-TTATTTTATTGATTTTGAGGGGTTA-3' R5'-CACATAACCAAAAACATATTC-3'	I95°C 5', D95°C 30", A59.3°C 30", E72°C 30", 38cy, FE72°C 10'	244
HP3F3 HP3R3	F5'-TTTTTGGTTATGTGGGAGGTTAG-3' R5'-TATCCAAAAAATAAAATAAAAAATC-3'	I95°C 5', D95°C 30", A52.6°C 30", E72°C 30", 38cy, FE72°C 10'	206
HP4F4 HP4R4	F5'-GGGATGTTTTTTGTAGTTATTGGATT-3' R5'-AAACCTACCTAATTTCCCTTCTTC-3'	I95°C 5', D95°C 30", A60°C 30", E72°C 30", 38cy, FE72°C 10'	260
HP5F5 HP5R5	F5'-TTTGTAGTTATTGGATTTTAAGATTT R5'-AAACCTACCTAATTTCCCTTCTTC-3'	I95°C 5', D95°C 30", A59.3°C 30", E72°C 30", 38cy, FE72°C 10'	251
HP6F6 HP6R6	F5'-GTGGTTTTTTGGTTTTGGAGAGT-3' R5'-CCCTAATCTAAAACCCTACCAATCT-3'	I95°C 5', D95°C 30", A60°C 30", E72°C 30", 38cy, FE72°C 10'	259
HP7F7 HP7R7	F5'-TGGTTTTTTGGTTTTGGAGAGTT-3' R5'-CTTCCCATAAACCTAATCTAAAAC-3'	I95°C 5', D95°C 30", A59.3°C 30", E72°C 30", 38cy, FE72°C 10'	269
HP8F8 HP8R8	F5'-TAGTGGAGTTTAGGATGTAGAGTTGATAT-3' R5'-CAAAACCAAAAACCACAACCT-3'	I95°C 5', D95°C 30", A59.3°C 30", E72°C 30", 38cy, FE72°C 10'	250

<i>HIF1AN</i>			
EP1F1	F5'- TTTTTTTATTGTTGTAAGGAGTATTAG-3'	I95°C 5', D95°C 30", A60°C	231
EP1R1	R5'- CTTAACCTTTACTTTTCCCTTAACC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP2F2	F5'-TTTTTTTTATTGTTGTAAGGAGTATTAG-3'	I95°C 5', D95°C 30", A56°C	232
EP2R2	R5'-CTTAACCTTTACTTTTCCCTTAACC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP3F3	F5'- GGGAGTTTGATTTTTGGATTAGT-3'	I95°C 5', D95°C 30", A58°C	176
EP3R3	R5'-ATCATAACTACTCTTCCTCCAAACC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP4F4	F5'- GGGAGTTTGATTTTTGGATTAGT-3'	I95°C 5', D95°C 30", A60°C	177
EP4R4	R5'-AATCATAACTACTCTTCCTCCAAACC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP5F5	F5'- TGGGTTGTTTATGAGTAGTATGGA-3'	I95°C 5', D95°C 30", A59°C	171
EP5R5	R5'-CTTCTCAACCTAAACAATTTCAATC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP6F6	F5'-TTGGGTTGTTTATGAGTAGTATGGA-3'	I95°C 5', D95°C 30", A57°C	172
EP6R6	R5'-CTTCTCAACCTAAACAATTTCAATC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP7F7	F5'-TAGTTGGTTAGTTAGAAGAGTGATT-3'	I95°C 5', D95°C 30", A59°C	109
EP7R7	R5'-TACTCATAAACAACCCAATAATTC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP8F8	F5'-GTAGTTGGTTAGTTAGAAGAGTGATT-3'	I95°C 5', D95°C 30", A60°C	110
EP8R8	R5'-TACTCATAAACAACCCAATAATTC-3'	30", E72°C 30" , 38cy, FE72°C 10'	
EP9F9	F5'-CGTATATTCGCGTCGGTTTGGAG-3'	I95°C 5', D95°C 30", A55°C	291
EP9R9	R5'-CTACGCTCCTCCGCACTCGAC-3'	30", E72°C 30" , 38cy, FE72°C 10'	

EP10F	F5'-TTCGTTTCGTTATTCGTTTGCGG-3'	I 95°C 5', D 95°C 30", A 58.6°C 30", E 72°C 30", 38cy, FE 72°C 10'	222
EP10R	R5'-CGAAACCGAACCTCGACTTCTAC-3'		
EP11F	F5'-GTAGAAGTCGAGGTTTCGGTT-3'	I 95°C 5', D 95°C 30", A 54.2°C 30", E 72°C 30", 38cy, FE 72°C 10'	308
EP11R	R5'-ACCTATACGACGAATAACAACCTA-3'		
EP12F	F5'-AGGTTGTTATTCGTCGTATAGGTT-3'	I 95°C 5', D 95°C 30", A 51.7°C 30", E 72°C 30", 38cy, FE 72°C 10'	357
EP12R	R5'-ATTCTCCATCTCCCGCACAA-3'		
EP13F	F5'-AGGGTTCGGCGGTGGTTGTC-3'	I 95°C 5', D 95°C 30", A 60°C 30", E 72°C 30", 38cy, FE 72°C 10'	199
EP13R	R5'-CGACACGATATACTCGAACGCCAA-3'		
EP14F	F5'-GAGTATATCGTGTCGTGTATGAA-3'	I 95°C 5', D 95°C 30", A 60°C 30", E 72°C 30", 38cy, FE 72°C 10'	138
EP14R	R5'-TAACCAACTACCCGTCGGTA-3'		

F: forward; R: reverse; I: initial denaturation; D: denaturation; A: annealing; E: extension; FE: final extension; cy: cycles