Supplementary Table S1. Sequencing and alignment statistics for the Brazilian White Leghorn lineage

Samples	Depth	bp Sequenced	Breadth (bp Sequenced/depth)	% of the *Gal.gal* genome v.5.0
7015_MeD1	31.7	295408723	9312189.4	0.87
7016_MeD2	25.6	832172066	32458414.1	3.02
7020_MeD1	25.2	189546154	7530578.0	0.70
7021_MeD2	27.8	1003311203	36121385.0	3.36
7022_MeD1	33.8	1225330777	36247027.9	3.37
7023_MeD2	25.4	192182531	7554879.3	0.70
7027_MeD1	32.6	1304734864	39971045.4	3.72
7028_MeD2	29.6	393804620	13301603.7	1.24
7032_MeD1	28.8	984802938	34171765.3	3.18
7033_MeD2	30.5	459302304	15078966.5	1.40
7034_MeD1	25.0	720493706	28793488.6	2.68
7035_MeD2	29.0	441295599	15194193.5	1.41
7037_MeD1	34.1	479456188	14069747.4	1.31
7038_MeD2	28.5	575777754	20228777.2	1.88
7041_MeD1	35.3	445276355	12625971.7	1.17
7042_MeD2	31.2	470414147	15060771.0	1.40
7046_MeD1	31.6	1191563338	37753937.2	3.51
7047_MeD2	29.6	433131327	14610307.3	1.36
7053_MeD1	33.9	462793117	13641975.8	1.27
7054_MeD2	26.3	780340135	29679642.7	2.76
7055_MeD1	29.2	368092791	12605097.3	1.17
7056_MeD2	31.6	384803020	12183633.9	1.13
7058_MeD1	23.1	634030676	27451969.0	2.55
7059_MeD2	27.9	1024884425	36795402.6	3.42
7060_MeD1	33.1	427452168	12922669.0	1.20
7061_MeD2	32.6	430368078	13182307.9	1.23
7069_MeD1	31.6	526618575	16650075.4	1.55
7070_MeD2	34.1	493849470	14489867.8	1.35
7078_MeD1	30.8	491468744	15978150.8	1.49
7079_MeD2	32.3	553372862	17120148.9	1.59
7080_MeD1	31.7	462173602	14600334.9	1.36
7081_MeD2	32.4	436780887	13474029.8	1.25
7015_input1	24.3	768825540	31633053.1	2.94
7016_input2	26.7	928586824	34751070.3	3.23
7020_input1	24.5	824291960	33598902.7	3.13
7021_input2	22.0	777816462	35301378.9	3.28
7022_input1	26.4	914468705	34669696.1	3.23
7023_input2	25.2	844495123	33468812.7	3.11
7027_input1	23.6	666364228	28274590.0	2.63

7028_input2	23.1	724726481	31338032.8	2.92
7032_input1	19.0	535820492	28134148.9	2.62
7033_input2	18.3	554995745	30405227.8	2.83
7034_input1	19.5	581623116	29859442.2	2.78
7035_input2	22.9	694511191	30283302.0	2.82
7037_input1	22.0	643137379	29246412.2	2.72
7038_input2	32.2	1279677373	39686933.0	3.69
7041_input1	22.4	680844300	30403793.1	2.83
7042_input2	20.8	659574765	31657056.2	2.94
7046_input1	20.7	691598186	33434930.1	3.11
7047_input2	22.1	760937592	34360822.4	3.20
7053_input1	19.3	488638882	25365653.8	2.36
7054_input2	20.4	587823560	28878441.3	2.69
7055_input1	19.2	535161417	27916464.5	2.60
7056_input2	21.1	715608621	33993721.1	3.16
7058_input1	33.7	1389053102	41215380.0	3.83
7059_input2	22.5	701101585	31178223.1	2.90
7060_input1	21.5	726590471	33771344.2	3.14
7061_input2	23.3	678911047	29189050.6	2.72
7069_input1	23.1	743286547	32217771.8	3.00
7070_input2	23.1	739180764	32011362.1	2.98
7078_input1	20.8	686583876	33069573.7	3.08
7079_input2	21.7	656157576	30249106.9	2.81
7080_input1	26.5	815248418	30744136.6	2.86
7081_input2	22.9	733997562	31999893.7	2.98
TotalAverage	25.8	662218637.7	26479622.2	2.46
TotalSD	5.2	248211623	9150209	0.85
MeDIPAverage	30.2	597344785.8	20026886.1	1.86
MeDIPSD	3.1	294204155.2	10085067.7	0.94
InputAverage	23.0	741551215	31947116.0	2.97
InputSD	3.4	186608136	3230589.0	0.30

*MeD means that individuals were subjected to GBS+MeDIP approach, and input means that individuals were subjected to GBS approach only. The numbers 1 and 2 represent control and isolated groups, respectively.

Supplementary Table S2. Sequencing and alignment statistics for the Swedish White Leghorn lineage

Samples	Depth	bp Sequenced	Breadth (bp Sequenced/depth)	% of the *Gal.gal* genome v.5.0
9103_MeD2	58.6574	217291466	3704416.9	0.34
9104_MeD2	56.8586	228587592	4020281.8	0.37
9105_MeD2	66.9302	291254510	4351615.7	0.40
9109_MeD2	51.5768	386200724	7487876.8	0.70
9116_MeD2	45.8561	197302675	4302648.4	0.40
9117_MeD2	54.0269	438148433	8109820.0	0.75
9118_MeD2	52.6391	192624836	3659349.0	0.34
9120_MeD2	53.9478	260009946	4819658.0	0.45
9130_MeD1	58.4201	270670524	4633174.6	0.43
9132_MeD1	49.5792	282396940	5695875.3	0.53
9134_MeD1	50.4113	626865258	12435014.7	1.16
9136_MeD1	53.3895	207347664	3883678.7	0.36
9148_MeD1	56.6508	423679222	7478786.2	0.70
9154_MeD1	58.2284	326872583	5613628.1	0.52
MEDIPAverage	54.8	310660883.8	5728273.2	0.5
MEDIP SD	5.1	121917627.9	2441239.6	0.2

*MeD means that individuals were subjected to GBS+MeDIP approach. The numbers 1 and 2 represent control and isolated groups, respectively

Supplementary Table S3. Comparison between the enrichment of CpG in genomic regions covered by the set of sequenced *reads* (seq - White Leghorn line of Brazil) and reference genome (genome)

	seq / genome (nº of CpGs)		**seq / genome (relH)**		**seq / genome (GoGe)**		**enrichment.score (relH)**	**enrichment.score (GoGe)**	**% of CpGs from *Gal.gal* genome v.6.0**
Media Total	443891		1.78		0.28		1.59	1.07	**3.9**
Media (Inp1)	528605		1.68		0.27		1.50	1.04	**4.6**
Media (Inp2)	541815	/11403014	1.67	/1.116	0.27	/0.262	1.50	1.04	**4.8**
Media (Inp3)	510815		1.69		0.27		1.51	1.04	**4.5**
Media (MeD1)	346586		1.89		0.29		1.69	1.11	**3.0**
Media (MeD2)	320912		1.92		0.29		1.72	1.12	**2.8**

Legend: *relH* and *GoGe* show the relative frequency and the observed/expected CpG relation; enrichment.score.relH and enrichment.score.GoGe indicate the enrichment of CpGs within the regions sequenced in each experiment compared to a non-enriched reference genome, respectively

Supplementary Table S4. Comparison between the enrichment of CpG in genomic regions covered by the set of sequenced *reads* (seq - White Leghorn line of Sweden) and reference genome (genome)

	seq / genome (nº of CpGs)		**seq / genome (relH)**		**seq / genome (GoGe)**		**enrichment.score (relH)**	**enrichment.score (GoGe)**	**% of CpGs from *Gal.gal* genome v.6.0**
Media Total	132206		3.21		0.402		2.87	1.53	**1.2**
Media (MeD2)	112683	/11403014	3.24	/1.116	0.404	/0.262	2.90	1.54	**1.0**
Media (MeD1)	154997		3.16		0.399		2.83	1.52	**1.4**

Legend: *relH* and *GoGe* show the relative frequency and the observed/expected CpG relation; enrichment.score.relH and enrichment.score.GoGe indicate the enrichment of CpGs within the regions sequenced in each experiment compared to a non-enriched reference genome, respectively