Supplementary Figures

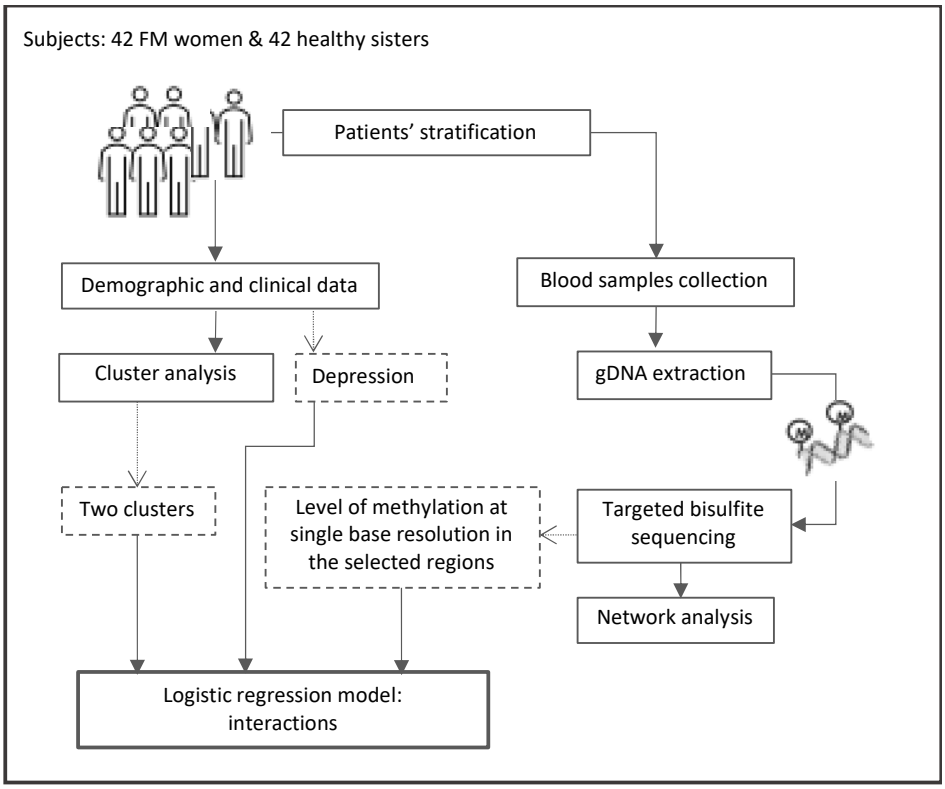


Figure S1. Study design.

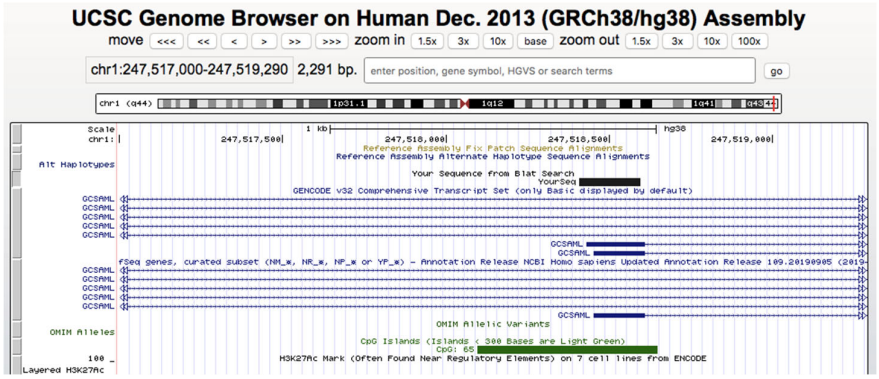


Figure S2. The sequence analyzed related to the *GCSAML* gene: the region is on the first exon in a CpG region of the gene that has multiple transcripts.

Supplementary Tables

Table S1. Data collected for each female participant (C1-C42: healthy controls; P1-P42: Fibromyalgia patients): age, diagnosis code, Fibromyalgia Impact Questionnaire (FIQ), Widespread Pain Index (WPI), Symptom Severity scale (SSS), Fibromyalgia Severity (FS) score (the sum of the WPI and SSS), Visual Analog Scale (VAS) for main FM symptoms, Pittsburgh Sleep Quality Inventory (PSQI) and Beck Depression Inventory (BDI) scores. Average (AVER) and standard deviation (STDEV) are reported for the collected data.

							VAS scales								
CTRL	**AGE**	**DIAG**	**S-FIQ TOTAL**	**WPI**	**SSS**	**FS**	**PAIN**	**HEALTH**	**RIGIDITY**	**FATIGUE**	**MOOD**	**HEAD ACHE**	**SLEEP**	**PSQI**	**BDI**
C1	39	1	28.720	2	7	9	1.782	2.376	1.782	2.376	3.762	0.297	4.455	10	19
C2	61	2	40.478	2	7	9	4.700	4.700	0.000	0.100	0.000	0.000	10.000	17	10
C3	48	1	7.000	6	3	9	1.400	1.100	1.400	1.300	1.100	1.100	4.000	12	2
C4	41	1		4	3	7									
C5	72	2	45.000	3	5	8	5.500	8.100	1.000	6.100	5.100	7.900	3.300	2	14
C6	44	1	7.000	2	2	4	1.400	1.200	5.100	4.500	2.200	0.100	1.000	6	1
C7	47	2	12.000	3	1	4	4.900	1.500	1.000	0.500	1.800	3.000	2.900	3	14
C8	51	1	6.529	1	0	1	0.200	0.200	0.300	0.200	0.400	0.300	0.200		5
C9		1	23.811	4	2	6	1.300	2.400	4.200	4.400	3.500	6.500	7.500		
C10	52	1	2.430	0	1	1	0.800	1.500	0.000	1.400	0.000	0.000	0.000	6	2
C11		1		3	6	9									
C12	40	1	20.430	4	6	10	2.500	2.300	1.500	4.900	3.000	2.400	8.400	16	10
C13	58	1	2.860	3	1	4	1.600	0.300	0.300	0.200	0.300	0.300	4.900	4	3
C14	33	1	7.000	2	1	3	0.300	0.000	0.000	0.700	0.000	0.700	7.600	11	5
C15	42	1	20.860	1	3	4	0.000	0.316	0.000	2.000	2.526	0.000	3.053	10	18
C16	44	1		0	3	3	0.211	0.947	0.000	0.211	0.737	0.105	0.526	7	12
C17	68	2	32.287	6	4	10	4.105	3.474	3.053	0.105	4.526	1.474	7.895	16	8
C18	44	1	3.430	2	2	4	0.211	0.211	0.211	0.105	0.105	0.105	0.211	4	2
C19	44	2	16.010	5	3	8	3.158	0.421	1.474	0.000	4.842	0.000	4.211	12	12
C20	59	2	46.720	3	8	11									
C21	39	1	11.816	2	5	7	1.474	2.737	0.105	4.421	4.526	6.842	2.632	3	6
C22	29	1	8.000	5	3	8	1.789	0.000	0.000	0.000	0.632	4.947	1.368		4
C23	53	2	63.768	3	5	8	6.737	6.632	4.316	4.421	4.421	2.737	5.895	13	12

C24	62	1	0.000	0	0	0	0.000	0.000	0.000	0.000	0.000	0.000	0.000	3	1
C25	34	1	9.990	0	0	0	0.000	0.000	0.000	0.000	0.000	1.765	4.471	3	0
C26	33	1	0.000	0	0	0	0.000	0.000	0.000	1.647	0.588	0.000	1.059	2	1
C27	38	1	36.010	3	1	4	2.235	2.471	0.235	0.824	6.471	0.706	2.588	9	18
C28	42	1	0.000	1	0	1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	3	0
C29	45	1	0.999	1	1	2	0.235	1.176	0.235	0.706	0.706	0.706	0.824	2	0
C30	43	2	12.860	4	1	5	6.471	1.647	0.118	0.118	0.118	10.000	0.118	7	5
C31	54	1	9.997	5	8	13	0.000	0.000	0.000	0.000	0.000	0.000	10.000	6	9
C32	33	1	4.000	1	5	6	0.000	0.000	0.000	4.706	0.118	0.000	4.941	10	4
C33	28	1	20.092	0	4	4	0.000	5.176	0.706	4.941	4.824	4.706	9.176	16	19
C34	60	1	0.740	8	3	11	2.471	1.294	7.294	4.471	1.882	0.588	6.471		2
C35	38	1	13.430	4	6	10	1.882	0.824	0.000	6.118	0.000	0.000	5.294	12	4
C36	56	2	34.072	6	8	14	3.176	4.118	4.471	6.588	7.882	1.176	10.000	15	18
C37	56	2	33.340	5	1	6	3.176	3.647	8.941	3.529	1.176	1.176	0.471		5
C38	51	1	16.720	0	6	6	1.412	7.882	8.706	7.412	1.176	2.235	1.412	7	6
C39	57	1	0.000	3	2	5	0.471	0.353	0.353	0.471	2.353	2.471	0.471	2	4
C40	56	1	5.291	2	3	5	0.353	0.588	0.471	0.471	1.412	0.824	0.353	1	10
C41	53	1	15.860	3	1	4	1.882	2.000	2.706	2.824	0.941	0.353	0.353	4	5
C42	46	1	2.000	2	0	2	0.118	0.235	0.000	0.000	0.000	0.000	0.000	1	0
AVER	**47.325**		**15.937**	**2.714**	**3.119**	**5.833**	**1.742**	**1.842**	**1.538**	**2.122**	**1.875**	**1.680**	**3.540**	**7.500**	**7.105**
STDEV	**10.577**		**15.570**	**1.979**	**2.491**	**3.602**	**1.896**	**2.179**	**2.451**	**2.326**	**2.103**	**2.479**	**3.321**	**5.041**	**6.004**
P1	46	5	70.340	14	11	25	6.931	7.030	10.000	7.129	1.386	7.723	9.307	12	21
P2	65	5	51.314	12	11	23	6.500	4.400	9.500	5.500	5.200	4.800	8.900	20	
P3	47	5	93.815	17	11	28	8.700	9.800	9.700	9.800	9.800	6.900	9.700	15	30
P4	67	5	78.628	14	11	25	9.100	7.200	9.700	8.100	9.900	8.000	8.500		
P5	49	5	16.665	8	3	11	2.300	1.300	4.900	5.000	0.000	0.000	0.800	2	4
P6	47	5	77.322	13	10	23	6.200	6.700	3.000	8.400	8.500	3.600	4.900	16	21
P7	42	5	72.800	9	10	19	9.300	9.500	9.400	9.500	9.900	0.300	5.400	8	40
P8	53	5	85.345	13	10	23	9.300	9.900	9.800	10.000	2.700	1.000	10.000	9	26
P9	52	5	72.434	10	11	21	5.400	5.600	10.000	7.400	7.500	4.600	7.800		
P10	49	5	57.628	10	9	19	4.400	4.700	10.000	9.900	0.200	0.200	6.400	13	12

P11	58	5	93.487	17	9	26								17	32
P12	46	5	67.909	15	11	26	8.200	8.500	9.800	8.400	9.000	9.800	9.200	18	34
P13	54	5	43.284	10	8	18	4.700	4.800	7.000	8.000	2.300	1.300	1.000	8	9
P14	53	5		14	10	24									
P15	43	5	86.962	17	10	27	8.316	7.368	10.000	10.000	10.000	6.316	10.000	18	27
P16	39	5	80.342	19	10	29	8.737	8.737	7.053	9.158	9.158	3.053	9.263		38
P17	58	5	52.382	13	8	21	6.211	6.526	4.211	7.263	7.474	8.105	7.579	15	35
P18	60	5	62.343	19	8	27	8.316	5.368	5.684	5.789	6.947	5.474	7.895		26
P19	54	5	50.772	14	9	23	9.684	9.579	9.684	5.789	9.684	4.632	9.684	16	14
P20	61	5	50.160	11	6	17	4.947	5.263	8.105	5.158	3.053	1.895	5.579	10	9
P21	36	5	71.531	15	9	24	8.842	8.632	10.000	8.632	3.368	6.211	8.842	13	20
P22	75	5	64.105	15	9	24	8.000	2.000	9.789	7.579	3.684	4.105	9.368	16	10
P23	51	5	52.675	10	7	17	7.895	7.895	1.684	7.579	1.789	3.158	2.947	11	12
P24	60	5	92.346	17	10	27	10.000	10.000	10.000	10.000	10.000	10.000	10.000	21	38
P25	47	5	41.149	10	5	15	8.353	7.882	2.824	6.941	3.647	8.588	5.765	11	11
P26	22	5	75.918	13	8	21	9.647	9.647	2.588	9.765	0.235	10.000	10.000	18	12
P27		5	92.681	9	10	19	9.529	8.941	10.000	9.529	10.000	9.647	10.000	14	46
P28	49	5	37.337	6	8	14	4.588	7.882	2.353	4.588	3.412	3.412	1.176	8	16
P29	34	5	65.411	9	9	18	5.412	3.765	6.118	6.706	1.176	2.941	5.294	10	15
P30	43	5	74.531	16	11	27	8.471	8.353	9.647	8.941	5.294	8.706	6.000	11	21
P31	57		85.433	19	12	31	9.647	9.412	9.294	9.176	9.412	9.412	9.647	20	35
P32	45	5	73.336	16	11	27								20	44
P33	40	5	79.723	12	10	22	6.000	8.824	8.706	9.647	9.647	0.000	9.882	17	22
P34	55	5	59.010	11	8	19	6.706	7.059	10.000	10.000	6.941	3.059	3.176	12	12
P35	55	5	91.860	11	10	21	9.059	7.176	10.000	10.000	7.882	3.059	8.471	16	26
P36	46	5	54.672	15	8	23	7.059	7.647	7.647	7.647	4.118	5.176	4.941	7	18
P37	43	5	65.142	16	10	26	10.000	10.000	10.000	10.000	0.588	10.000	10.000	20	17
P38	44	5	94.347	15	10	25	9.647	9.647	9.412	7.765	8.471	5.294	9.294	19	29
P39	59	5	71.487	14	9	23	6.353	6.235	2.000	6.588	5.059	4.235	9.176	17	21
P40	58	5		11	9	20	6.941	3.529	6.118	7.882	5.647	1.294	6.706	11	16
P41	56	5	64.342	16	9	25	7.882	7.765	8.588	7.647	7.647	8.000	8.235	17	12
P42	56	5	83.746	10	9	19		10.000	10.000	10.000	10.000		10.000	7	18
AVER	**50.585**		**68.868**	**13.214**	**9.214**	**22.429**	**7.560**	**7.296**	**7.803**	**8.126**	**5.916**	**5.105**	**7.457**	**13.865**	**22.342**
STDEV	**9.685**		**17.817**	**3.220**	**1.733**	**4.289**	**1.896**	**2.285**	**2.808**	**1.629**	**3.437**	**3.208**	**2.757**	**4.632**	**10.826**

Table S2. Differentially methylated Cytosines (DMCs) test (Metilene output), including both significant and not significant p values: Metilene output reveals DNA methylation mean scores for patients (42 FM women) and controls (42 related healthy sisters) measured in FM related regions.

Chr	start	stop	q-value	mean methylation difference	#CpGs	pval (MWU)	pval (2D KS)	mean methyl control	mean methyl FM
chr1	247518407	247518408	1	-0.033329	1	0.44168	.	0.57261	0.60594
chr1	247518413	247518414	1	-0.064526	1	0.11537	.	0.57726	0.64178
chr1	247518422	247518423	1	-0.013254	1	0.60385	.	0.56487	0.57812
chr1	247518426	247518427	1	-0.067943	1	0.11537	.	0.47243	0.54038
chr1	247518435	247518436	1	-0.054567	1	0.25217	.	0.44734	0.50191
chr1	247518437	247518438	1	-0.036695	1	0.44701	.	0.29197	0.32867
chr1	247518439	247518440	1	-0.081927	1	0.085862	.	0.49216	0.57409
chr1	247518446	247518447	1	-0.065981	1	0.24848	.	0.47484	0.54083
chr1	247518454	247518455	1	0.014749	1	0.3295	.	0.017858	0.0031091
chr1	247518463	247518464	1	-0.045037	1	0.3295	.	0.57724	0.62228
chr1	247518478	247518479	1	-0.028706	1	0.74741	.	0.49835	0.52706
chr1	247518481	247518482	1	-0.027635	1	0.44168	.	0.55108	0.57872
chr1	247518498	247518499	1	0.015725	1	0.052222	.	0.016755	0.0010296
chr1	247518505	247518506	1	0.011128	1	0.1217	.	0.011128	2.38E-05
chr1	247518506	247518507	1	-0.011773	1	0.73389	.	0.59974	0.61152
chr1	247518520	247518521	1	0.014726	1	0.40542	.	0.017959	0.0032328
chr1	247518522	247518523	1	-0.014189	1	1	.	1.67E-03	0.01419
chr1	247518541	247518542	1	-0.068202	1	0.066663	.	0.57465	0.64285
chr1	247518550	247518551	1	0.020218	1	0.36151	.	0.66073	0.64051
chr1	247518553	247518554	1	0.015074	1	0.5549	.	0.026906	0.011832
chr1	247518554	247518555	1	-0.010049	1	0.77467	.	1.90E-03	0.010049
chr1	247518564	247518565	1	0.014635	1	0.29113	.	0.01883	0.0041948
chr1	247518566	247518567	1	-0.013171	1	0.95007	.	1.90E-03	0.013172
chr1	247518568	247518569	1	-0.052951	1	0.027755	.	0.66202	0.71497
chr3	51707199	51707200	1	-0.016213	1	0.48531	.	0.16117	0.17738
chr3	51707209	51707210	1	0.010693	1	0.66113	.	0.010693	1.67E-03
chr3	114178889	114178890	1	-0.026455	1	0.076507	.	0.11283	0.13929
chr3	114178938	114178939	1	-0.014882	1	0.025909	.	0.03726	0.052143
chr3	114179057	114179058	1	-0.018776	1	0.18254	.	0.095333	0.11411
chr8	72076045	72076046	1	0.016626	1	0.53705	.	0.51472	0.4981
chr11	4575858	4575859	1	0.019500	1	0.217	.	0.29905	0.27955
chr11	43581221	43581222	1	0.012045	1	0.021497	.	0.021129	0.0090842
chr11	43581242	43581243	1	0.013202	1	0.26346	.	0.020432	0.0072302
chr11	43581271	43581272	1	-0.015429	1	0.089178	.	0.012781	0.02821
chr11	43581296	43581297	1	-0.016972	1	0.049053	.	0.022165	0.039137
chr11	43581306	43581307	1	-0.011173	1	0.41559	.	0.0088797	0.020052
chr14	23372303	23372304	1	-0.010720	1	0.57303	.	0.87833	0.88905
chr17	16971852	16971853	1	-0.016130	1	0.11332	.	0.78101	0.79714

chr17	16972244	16972245	1	0.015841	1	0.23062	.	0.8706	0.85476
chr20	3071396	3071397	1	0.024708	1	0.51372	.	0.65995	0.63524
chr20	3071418	3071419	1	-0.028115	1	0.99286	.	0.0055438	0.033659
chr20	3071453	3071454	1	0.026037	1	0.32508	.	0.66122	0.63518
chr20	3071606	3071607	1	-0.039032	1	0.13056	.	0.58464	0.62367
chr20	3071615	3071616	1	0.026128	1	0.25589	.	0.79303	0.7669
chr20	3071627	3071628	1	-0.017024	1	0.5195	.	0.40155	0.41857
chr20	3071643	3071644	1	-0.018169	1	0.36623	.	0.41897	0.43714
chr20	3071649	3071650	1	-0.035845	1	0.33396	.	0.30344	0.33929
chr20	3071660	3071661	1	-0.018483	1	0.39044	.	0.17675	0.19524
chr20	3071672	3071673	1	-0.046248	1	0.1054	.	0.23066	0.2769
chr20	3071698	3071699	1	-0.021525	1	0.25966	.	0.23427	0.2558
chr20	3072579	3072580	1	0.026709	1	0.062775	.	0.83985	0.81314
chr20	3072581	3072582	1	-0.020724	1	0.35217	.	0.86304	0.88377
chr20	3072657	3072658	1	-0.019683	1	0.10349	.	0.65244	0.67213
chrX	139692245	139692246	1	-0.023783	1	0.72717	.	0.13689	0.16067
chrX	139692250	139692251	1	-0.011196	1	0.81607	.	0.26235	0.27355
chrX	139692253	139692254	1	-0.032995	1	0.44701	.	0.28068	0.31368
chrX	139692271	139692272	1	-0.013257	1	0.35682	.	0.0021758	0.015433
chrX	139692274	139692275	1	-0.067809	1	0.027128	.	0.45756	0.52536
chrX	139692285	139692286	1	-0.012456	1	0.82303	.	0.011681	0.024137
chrX	139692291	139692292	1	-0.027269	1	0.1093	.	0.019267	0.046536
chrX	139692297	139692298	1	-0.057321	1	0.11332	.	0.24152	0.29884
chrX	139692312	139692313	1	-0.056372	1	0.014961	.	0.3033	0.35967
chrX	139692315	139692316	1	-0.036593	1	0.13518	.	0.28335	0.31995
chrX	139692317	139692318	1	-0.044408	1	0.13753	.	0.34278	0.38719
chrX	139692321	139692322	1	-0.011993	1	0.57913	.	0.22928	0.24128
chrX	139692332	139692333	1	-0.029140	1	0.17963	.	0.37614	0.40528