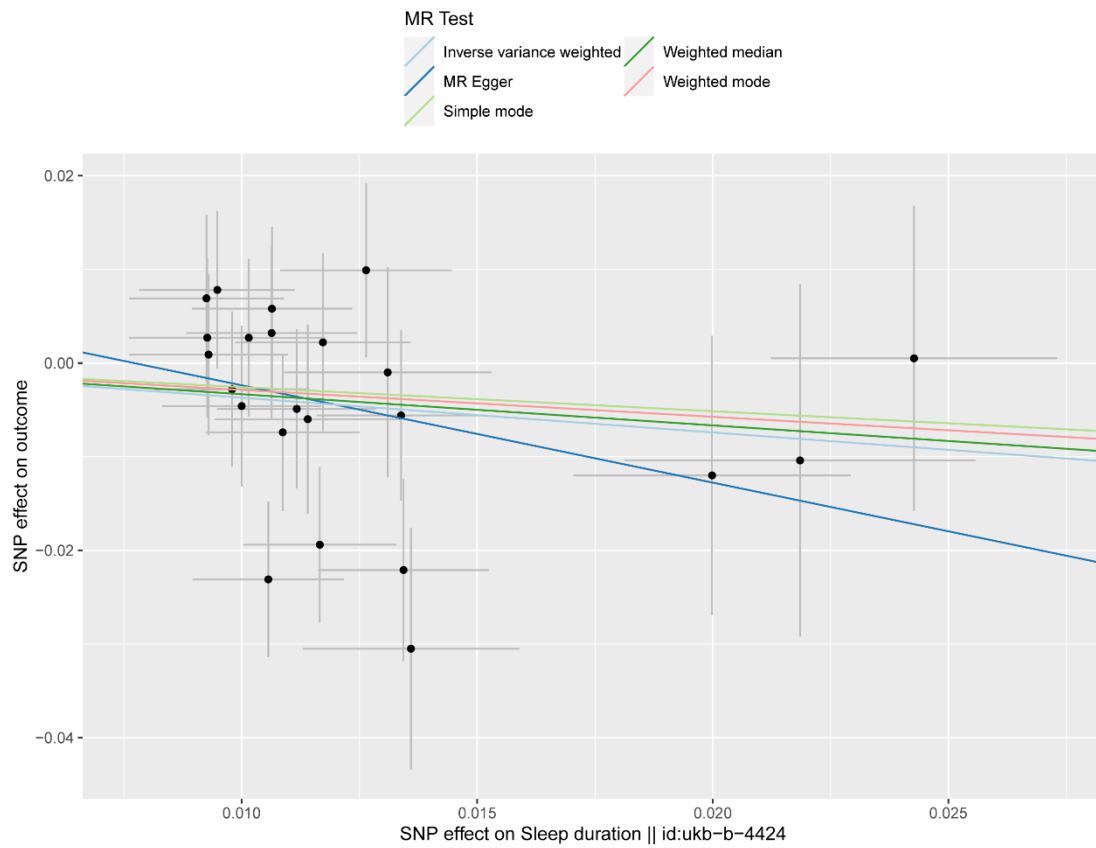
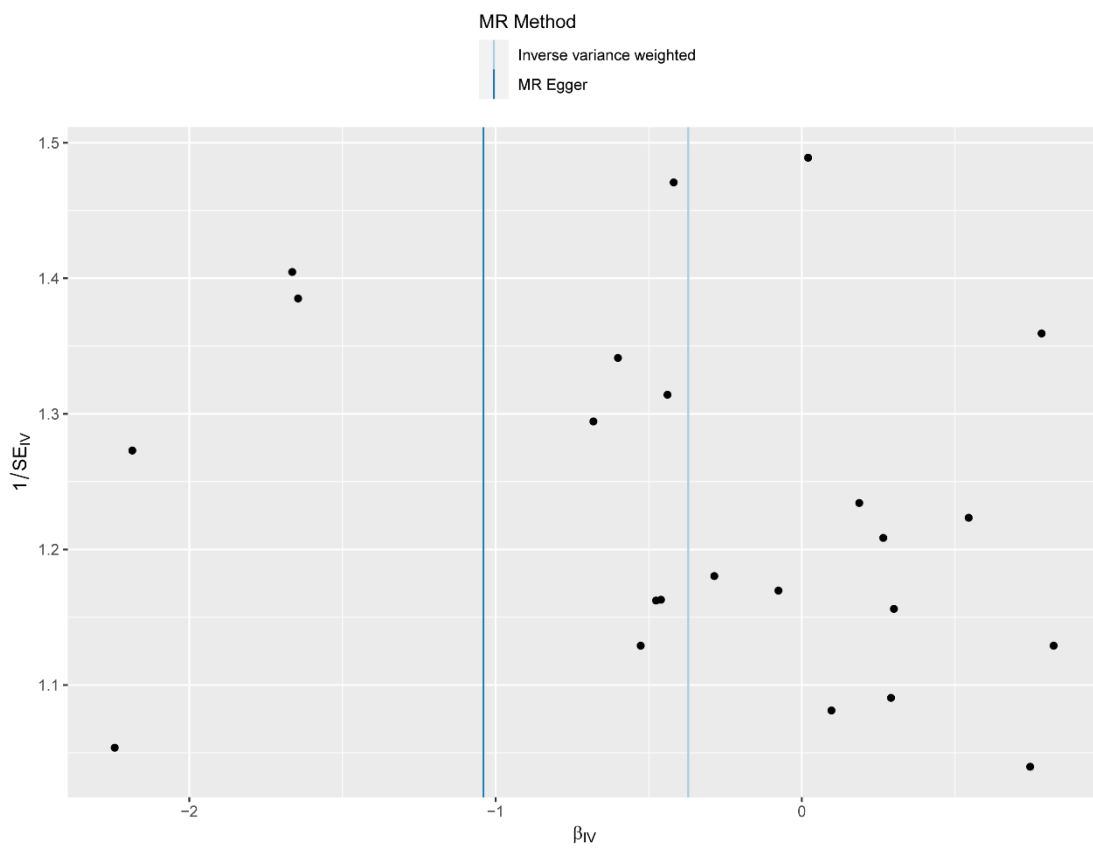


Supplementary

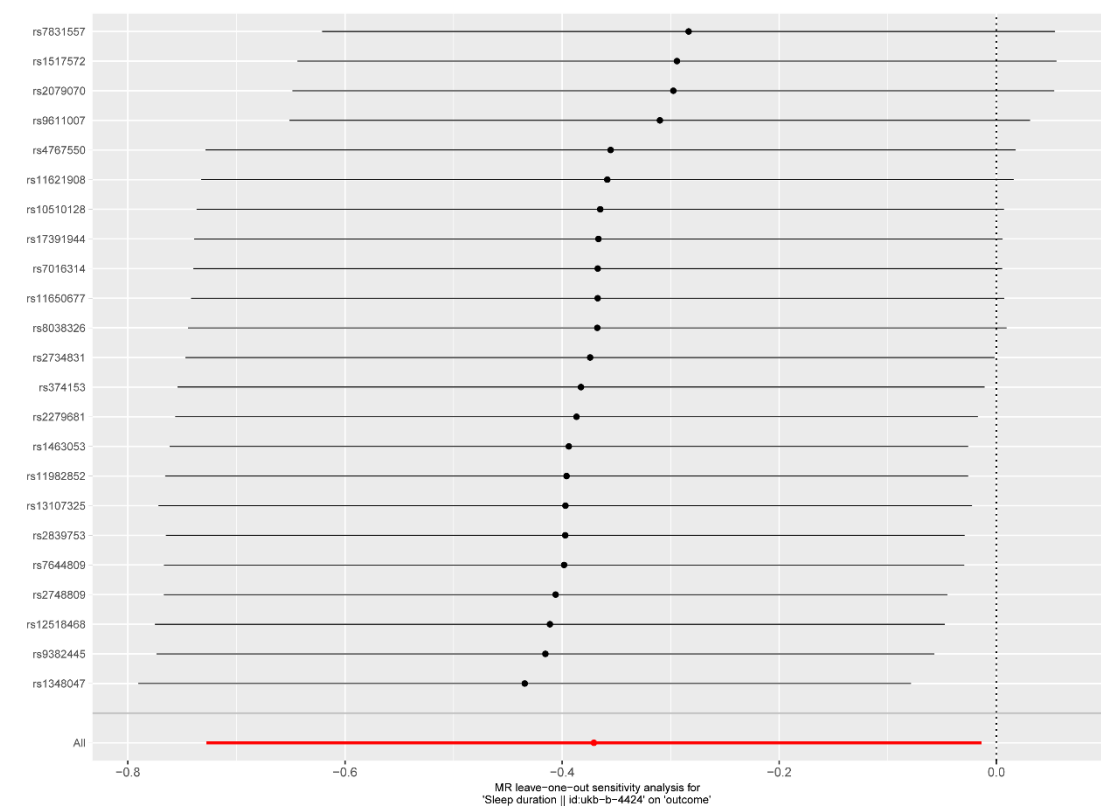
Supplementary Figure S1 Scatter plot of the effect of sleep duration on hip fracture in an MR analysis



Supplementary Figure S2 Funnel plot of the effect of sleep duration on hip fracture in an MR analysis



Supplementary Figure S3 Leave-one-out plot of the effect of sleep duration on hip fracture in an MR analysis



Supplementary Table S1 SNPs site information for Mendelian randomization analysis was performed

SNP	pos.exp osure	chr.exp osure	effect_allele .exposure	other_allele. exposure	se.exp osure	beta.ex posure	pval.ex posure	samplesize. exposure	eaf.exp osure
rs9154 16	347319 84	1	G	C	0.0017 6	- 0.01273	4.80E- 13	460099	0.7090 6
rs2186 122	664702 06	1	T	A	0.0016 21	- 0.01083	2.30E- 11	460099	0.5599 11
rs2279 681	2.02E+ 08	1	G	C	0.0016 85	0.00929 9	3.40E- 08	460099	0.3417 85
rs7517 981	315550 56	1	C	T	0.0016 34	- 0.00997	1.10E- 09	460099	0.6014 98
rs1256 7114	985279 51	1	A	G	0.0017 94	0.01233 8	6.10E- 12	460099	0.2763 68
rs1463 053	870503 7	1	A	G	0.0016 61	0.00927	2.40E- 08	460099	0.6396 94
rs6681 755	717039 70	1	A	G	0.0020 05	0.01152 7	9.00E- 09	460099	0.1997 83
rs3741 53	403827 12	2	T	C	0.0021 97	-0.0131	2.50E- 09	460099	0.8425 67
rs2863 957	1.14E+ 08	2	A	C	0.0019 29	0.02890 4	9.60E- 51	460099	0.2205 37
rs1972 712	1.67E+ 08	2	C	T	0.0018 48	0.01179 6	1.70E- 10	460099	0.2494 55
rs7283 1782	1.04E+ 08	2	A	T	0.0018 44	- 0.01018	3.40E- 08	460099	0.2694 09
rs2683 630	580580 69	2	G	C	0.0016 56	0.01495 1	1.70E- 19	460099	0.6290 76
rs7553 9574	588716 58	2	C	A	0.0028 74	0.02366 5	1.80E- 16	460099	0.0857 74
rs3566 2245	1.48E+ 08	2	A	T	0.0016 91	0.01015 7	1.90E- 09	460099	0.3387 13
rs6783 516	1.79E+ 08	3	T	G	0.0016 31	- 0.00984	1.60E- 09	460099	0.5838 17
rs7625 8078	558238 90	3	G	A	0.0036 81	- 0.02169	3.80E- 09	460099	0.0499 94
rs1130 21516	1.36E+ 08	3	C	G	0.0016 97	0.01148 1	1.30E- 11	460099	0.3358 98
rs1773 2997	704708 34	3	G	C	0.0016 18	- 0.00884	4.60E- 08	460099	0.4296 79
rs9810 474	749611 96	3	T	C	0.0018 94	- 0.01115	3.90E- 09	460099	0.2321 84

rs7644 809	1.08E+ 08	3	C	T	0.0016 25	- 0.01015	4.10E- 10	460099	0.5760 33
rs1310 7325	1.03E+ 08	4	T	C	0.0030 39	- 0.02427	1.40E- 15	460099	0.0749 05
rs2192 528	183278 96	4	G	A	0.0016 01	- 0.00981	9.10E- 10	460099	0.5224 93
rs2839 753	822872 50	4	C	T	0.0018 12	- 0.01064	4.40E- 09	460099	0.2653 47
rs7711 696	1.35E+ 08	5	T	G	0.0017 35	- 0.00987	1.30E- 08	460099	0.3049 87
rs1251 8468	724969 6	5	C	T	0.0017 03	- 0.01064	4.10E- 10	460099	0.3286 85
rs3656 63	142888 3	5	G	A	0.0016 1	- 0.00928	8.10E- 09	460099	0.4549 5
rs6889 592	1.02E+ 08	5	A	G	0.0016 97	0.01176 6	4.10E- 12	460099	0.3326 08
rs1510 14368	1.77E+ 08	5	A	G	0.0019 88	0.01137 9	1.00E- 08	460099	0.2073 4
rs9382 445	549379 74	6	C	T	0.0016 49	- 0.00948	8.90E- 09	460099	0.3751 68
rs1131 13059	431603 75	6	C	T	0.0019 33	- 0.01113	8.60E- 09	460099	0.2198 34
rs7740 402	1.31E+ 08	6	G	T	0.0017 35	- 0.00951	4.10E- 08	460099	0.3061
rs9345 234	931626 39	6	C	A	0.0016 24	0.00919 2	1.50E- 08	460099	0.5778 6
rs3455 6183	285847 75	6	G	A	0.0017 82	- 0.01335	6.60E- 14	460099	0.2798 88
rs1198 2852	1.33E+ 08	7	T	C	0.0018 62	- 0.01173	3.10E- 10	460099	0.2438 58
rs6244 4917	210726 2	7	C	A	0.0019 26	0.01296 3	1.70E- 11	460099	0.2223 15
rs2079 070	1.14E+ 08	7	G	C	0.0018 11	- 0.01344	1.20E- 13	460099	0.7345 82
rs7831 557	102802 28	8	A	G	0.0016 01	- 0.01057	4.20E- 11	460099	0.5174 38
rs7016 314	140436 62	8	C	T	0.0016 88	0.01000 1	3.10E- 09	460099	0.6559 27
rs1739 1944	369014 94	9	G	T	0.0037 24	0.02185 2	4.40E- 09	460099	0.0498 6
rs1121 00783	705411 93	10	A	G	0.0045 49	- 0.02529	2.70E- 08	460099	0.0334 39
rs1051 0128	1.25E+ 08	10	A	G	0.0019 74	0.01140 3	7.70E- 09	460099	0.2079 51

rs2236 295	645648 92	10	T	G	0.0016 36	- 0.00908	2.90E- 08	460099	0.4030 43
rs1517 572	288298 82	11	C	A	0.0016 22	0.01165 9	6.50E- 13	460099	0.5812 56
rs7115 856	437692 87	11	C	A	0.0016 03	0.01081 9	1.50E- 11	460099	0.4612 73
rs1103 9216	474065 92	11	T	C	0.0016 04	- 0.01028	1.50E- 10	460099	0.5329 44
rs2734 831	1.13E+ 08	11	G	T	0.0016 39	-0.0098	2.20E- 09	460099	0.6068 81
rs1745 64	615883 05	11	G	A	0.0016 78	0.00974 5	6.30E- 09	460099	0.3486 02
rs1939 455	1.02E+ 08	11	T	G	0.0025 17	-0.0158	3.50E- 10	460099	0.1202 91
rs1553 132	882977 40	11	G	A	0.0018 25	0.01052 6	8.10E- 09	460099	0.2586 38
rs3435 4917	387645 59	12	A	C	0.0017 68	- 0.01002	1.40E- 08	460099	0.2886 25
rs4767 550	1.18E+ 08	12	G	A	0.0016 33	0.01087 3	2.70E- 11	460099	0.4131 71
rs6561 715	538885 26	13	A	T	0.0016 61	0.00978 2	3.90E- 09	460099	0.6306 36
rs5565 8675	655546 38	14	T	C	0.0016 75	- 0.00969	7.10E- 09	460099	0.3529 06
rs1162 1908	784957 61	14	T	C	0.0029 43	- 0.01999	1.10E- 11	460099	0.0828 07
rs2748 809	997352 33	14	C	T	0.0016 45	- 0.00925	1.90E- 08	460099	0.4292 58
rs8038 326	479897 99	15	G	A	0.0017 93	- 0.01338	8.40E- 14	460099	0.2731 69
rs5636 7859	654079 5	16	G	A	0.0016 36	0.01162 2	1.20E- 12	460099	0.3975 85
rs9302 680	562698 92	16	A	G	0.0016 11	0.01204 4	7.60E- 14	460099	0.4392 72
rs1164 3715	239095 38	16	G	C	0.0017 6	0.01094 9	5.00E- 10	460099	0.2926 25
rs8047 587	537986 22	16	T	G	0.0016 13	- 0.01102	8.30E- 12	460099	0.4395 14
rs7277 1082	200236 01	16	G	A	0.0019 36	0.01097 4	1.40E- 08	460099	0.2178 32
rs8074 498	799545 44	17	A	T	0.0016 34	- 0.00933	1.10E- 08	460099	0.5809 51
rs1165 0677	112315 13	17	A	G	0.0016 9	0.01117	3.80E- 11	460099	0.3391 85

rs9903 898	455753 54	17	T	C	0.0016 01	- 0.00945	3.60E- 09	460099	0.4888 83
rs8072 993	213356 27	17	G	T	0.0019 92	0.01092 2	4.20E- 08	460099	0.6356 77
rs1348 047	530500 58	18	T	G	0.0018 2	- 0.01264	3.80E- 12	460099	0.2672 53
rs3512 6035	349867 67	19	C	A	0.0016 44	-0.0092	2.20E- 08	460099	0.5583 3
rs3478 6000	994212 3	19	T	G	0.0016 28	0.01095 8	1.70E- 11	460099	0.5533 61
rs2072 727	435387 33	20	C	T	0.0016 14	- 0.00927	9.30E- 09	460099	0.5645 9
rs9611 007	390770 58	22	T	C	0.0022 97	- 0.01359	3.30E- 09	460099	0.1416 73