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Supplemental Data

Genome-wide Linkage and Association Analyses

Implicate *FASN* in Predisposition to Uterine Leiomyomata

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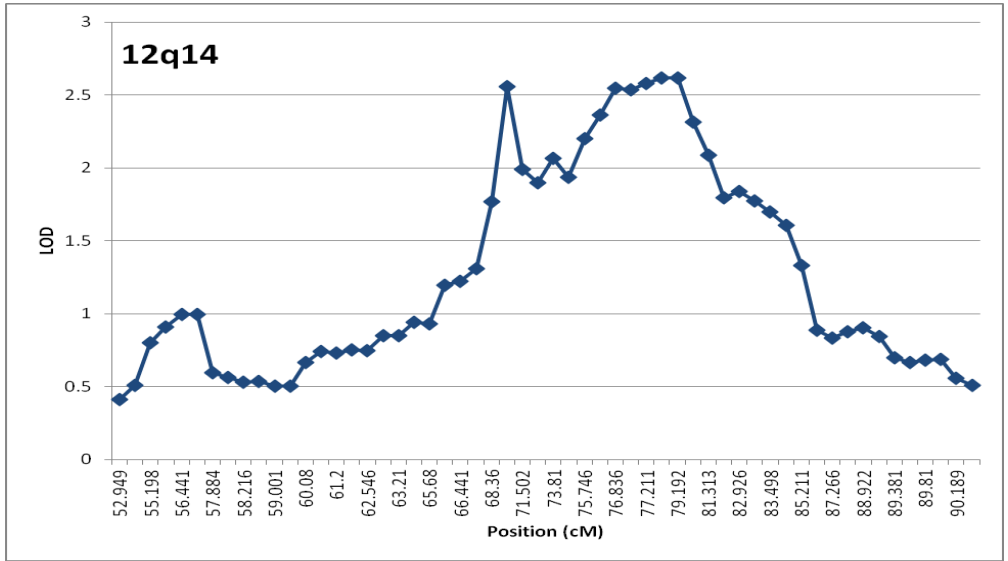
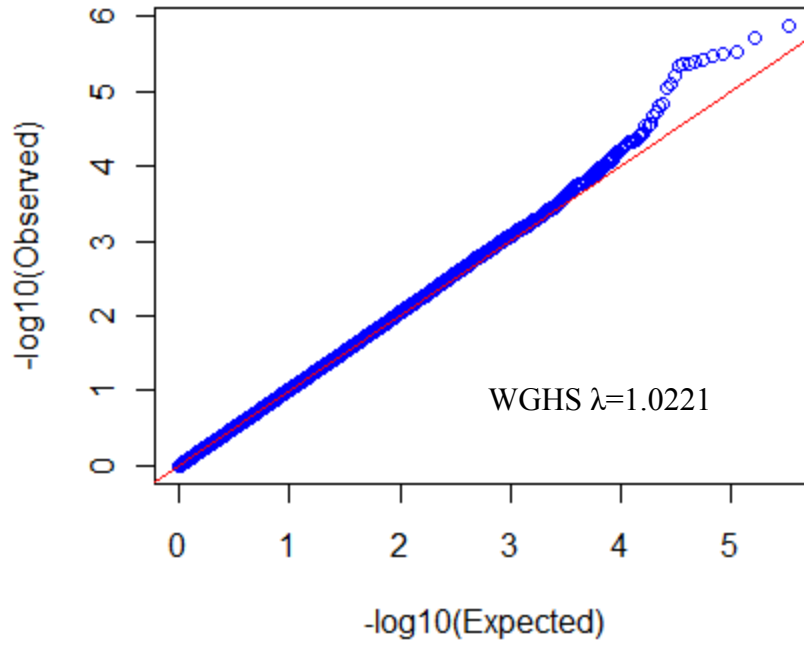


Figure S1. FGFF Linkage Peak at 12q14 with *HMGA2* Circled in Red

A



B

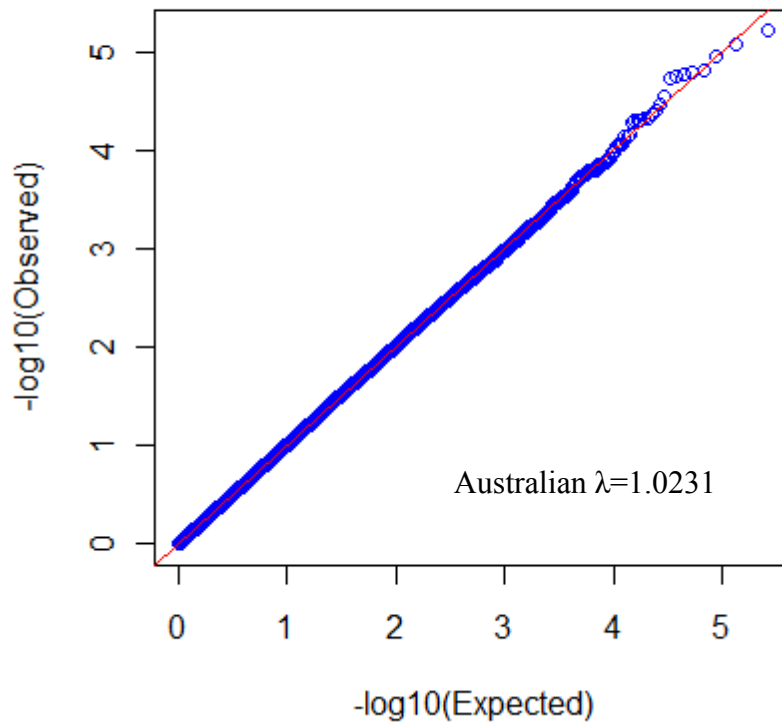


Figure S2. Quantile-Quantile Plot of (A) WGHS GWAS Results and (B) Australian GWAS Results

The p values observed in the studies are compared to the p values expected under the null hypothesis.

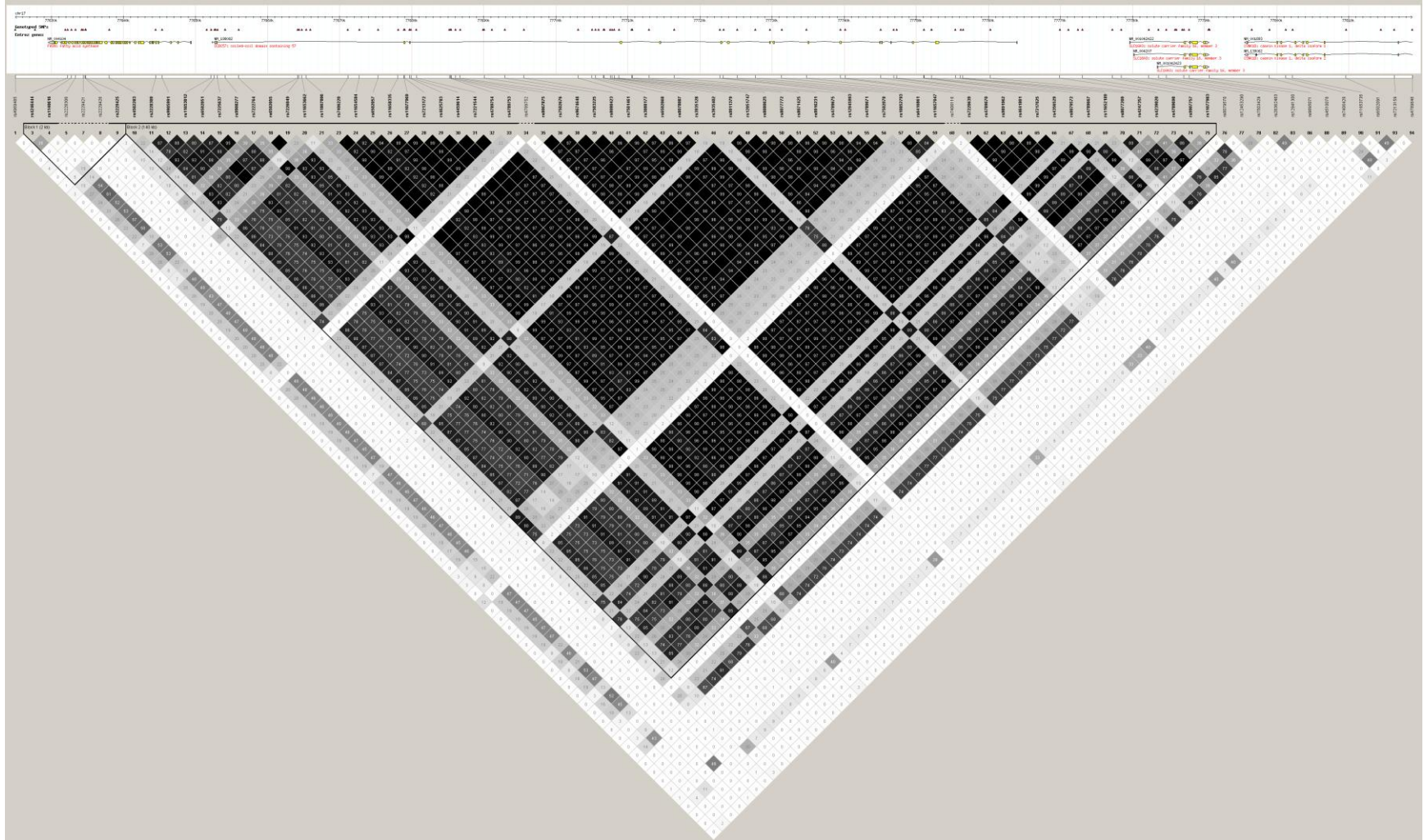


Figure S3. HapMap Generated LD Plot of Candidate Region on Chromosome 17

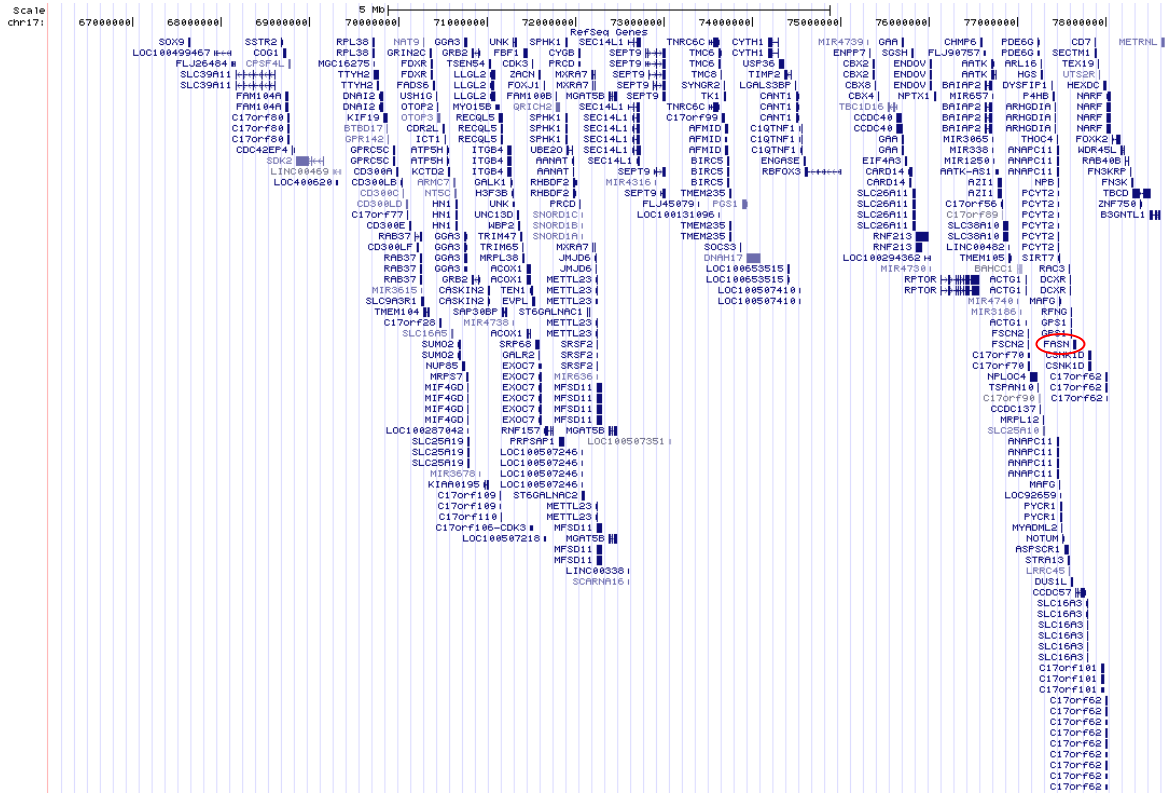
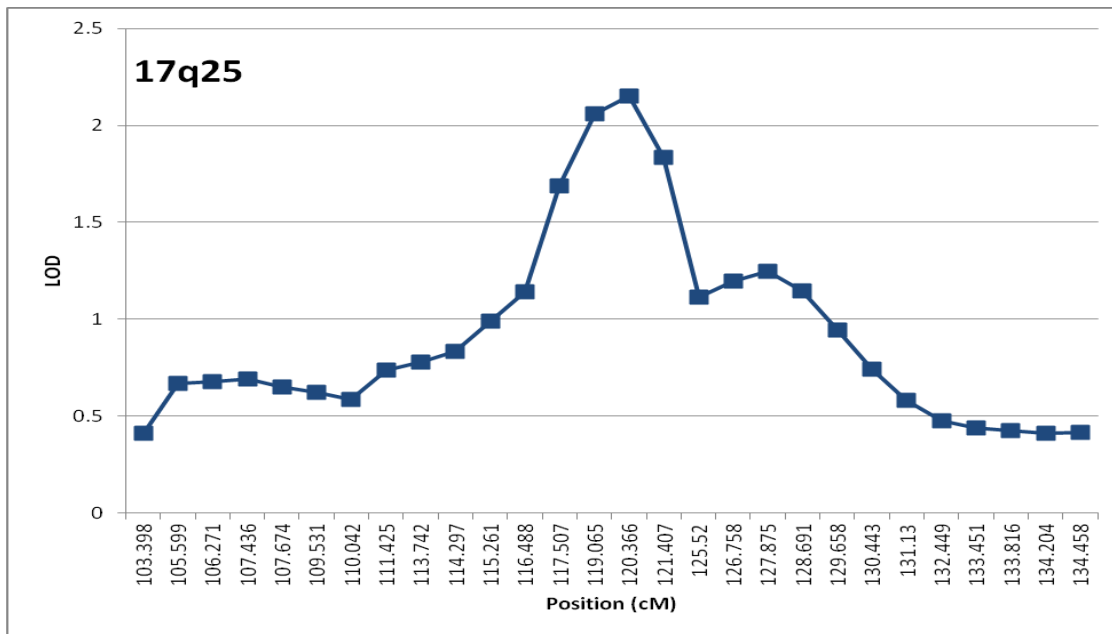


Figure S4. FGFF Linkage Peak at 17q25 with *FASN* Circled in Red

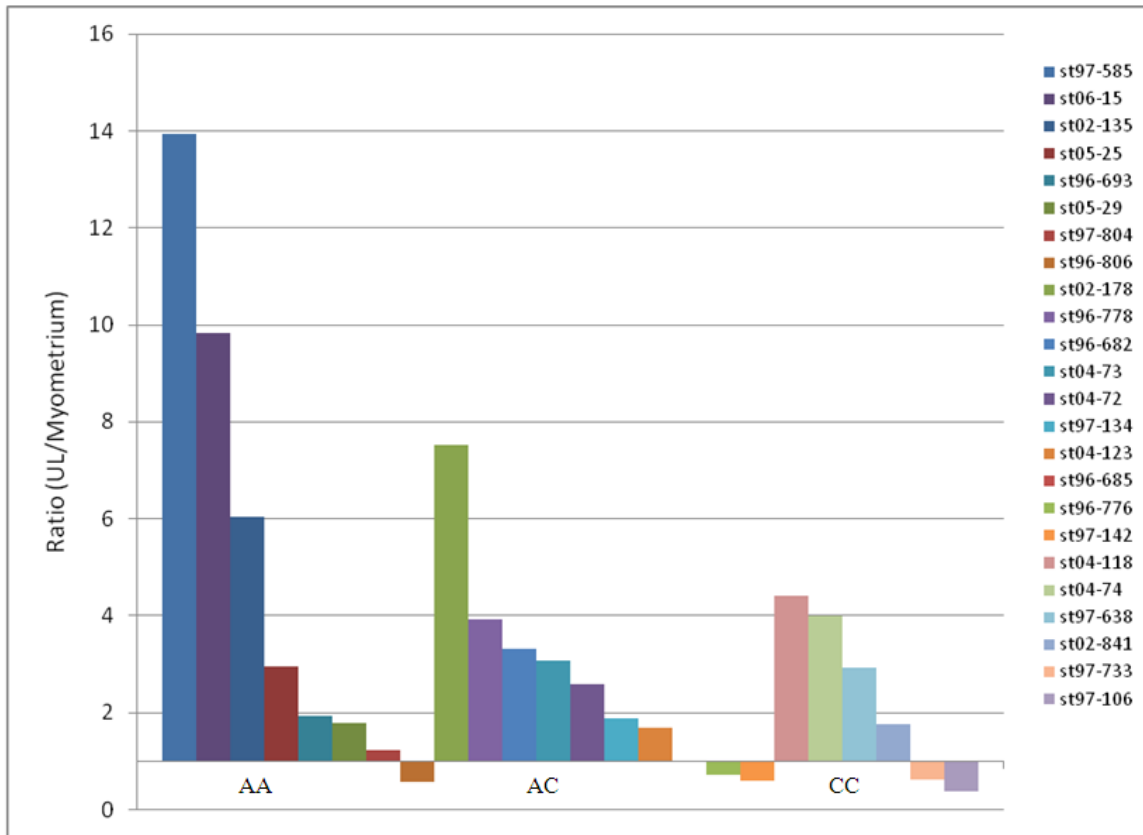


Figure S5. Ratio of FAS Protein Expression in Matched UL/Myometrium Samples Grouped by rs4247357 Genotype

Each bar represents the ratio from one woman.

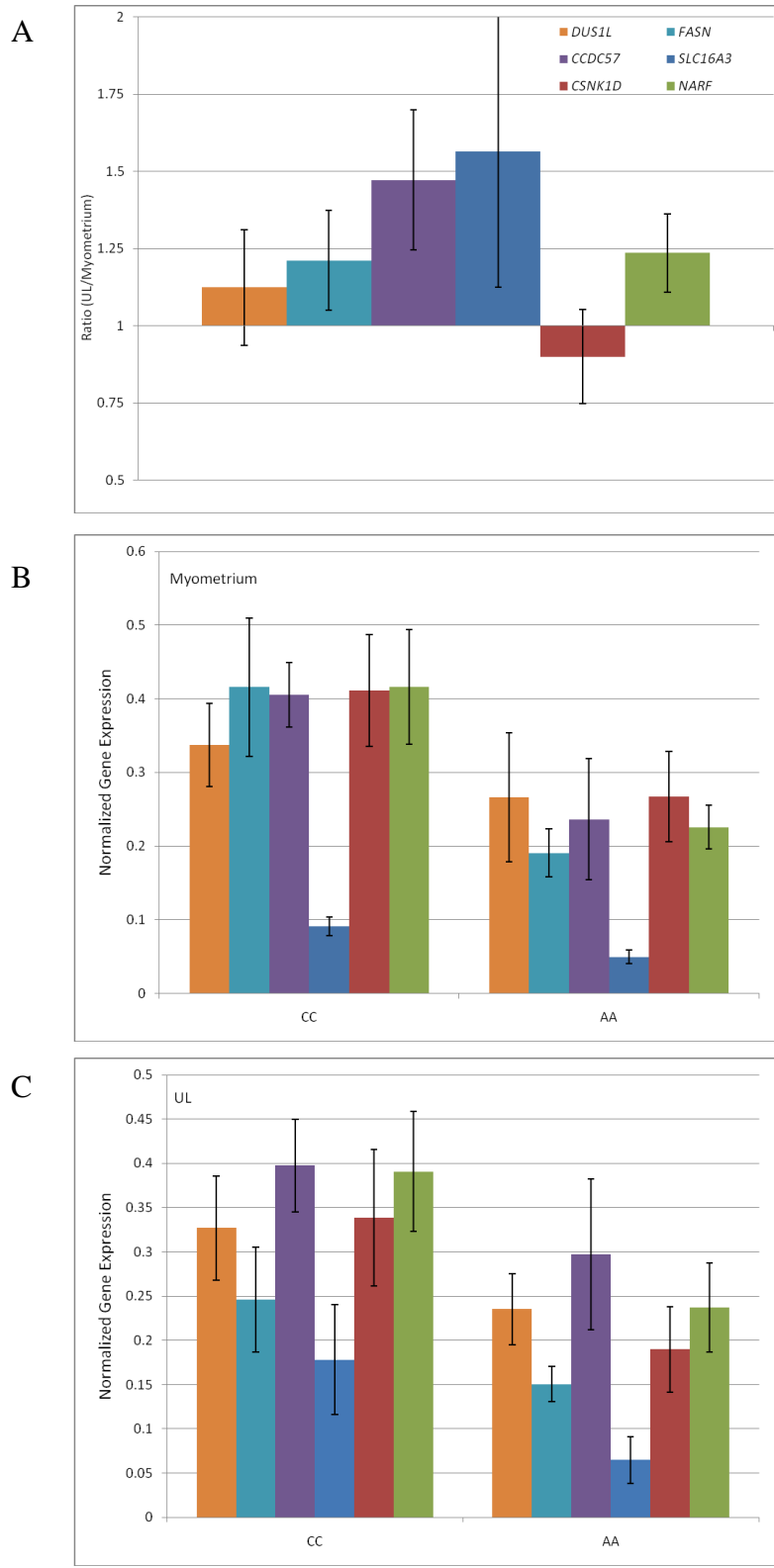


Figure S6. mRNA Expression by qPCR of *FASN*, *CCDC57*, *SLC16A3*, and Three Genes in Direct Proximity (*DUS1L*, *CSNK1D*, *NARF*) in (A) Myometrium and Matched UL Samples (B) Myometrium with the Major (CC) and Minor (AA) Allele of rs4247357 and (C) UL with the Major (CC) and Minor (AA) Allele of rs4247357

Table S1. Demographics of the FGFF, WGHS, and Australian Cohorts

		WGHS All (5,233)	WGHS Cases (746)	WGHS Controls (4487)	p Value	Australian All (1,094)	Australian Cases (484)	Australian Controls (610)	p Value	FGFF Sisters (522)
Age in years (yrs)	Yrs Median (IQR)	52.9 (48.9-59.0)	52.3 (48.8-56.9)	52.5 (48.7-58.0)	0.0038	41.0 (34.0-50.0)	44.0 (37.0-51.0)	39.0 (34.0-48.0)	0.0001	47.0 (41.0-53.0)
BMI	kg/m ² Median (IQR)	24.8 (22.3-28.3)	25.0 (22.6-28.2)	24.2 (22.0-27.4)	0.1595	23.6 (21.5-27.1)	24.8 (22.3-28.3)*	23.4 (21.3-26.5)	0.0019	24.1 (22.0-27.4)**
Height	Inches Median (IQR)	65.0 (63.0-66.0)	64.0 (63.0-66.0)	65.0 (63.0-66.0)	0.0528	63.8 (61.8-65.4)	63.4 (61.8-65.4)*	63.8 (61.8-65.7)	0.0195	65.0 (63.0-66.75)
Age at menarche	Yr Median (IQR)	12.0 (12.0-13.0)	12.0 (11.0-13.0)	12.0 (12.0-13.0)	2.82E-05	13.0 (12.0-14.0)	13.0 (12.0-14.0)	13.0 (12.0-14.0)	0.0069	12.0 (12.0-13.0)
Hysterectomy history	Hysterectomy N (%)					312 (28.5%)	263 (56.1%)	49 (8.3%)	3.77E-28	165 (30.1%)

*BMI and height were only available for 175 Australian cases.

**BMI is only available for 491 FGFF sisters.

Table S2. WGHS Genome-wide Association Analysis Results ($p < 10^{-4}$)

CHR	SNP	Position (bp)	F_A	F_U	A2	CHISQ	p Value
1	rs2268179	22287371	0.2091	0.1588	C	23.37	1.34E-06
17	rs4247357	77760277	0.467	0.4014	C	22.64	1.95E-06
17	rs6502057	77675348	0.4628	0.3977	G	21.78	3.06E-06
15	rs2903332	78340261	0.3124	0.2542	G	21.75	3.10E-06
17	rs11077969	77678921	0.4655	0.4017	G	21.31	3.91E-06
17	rs7502078	77725167	0.4678	0.4044	C	21.24	4.04E-06
17	rs7213172	77678991	0.4657	0.4023	A	21.16	4.23E-06
17	rs8080423	77695567	0.4672	0.4039	A	21.1	4.36E-06
17	rs7406163	77679677	0.4772	0.4128	A	21.06	4.46E-06
17	rs7221544	77680625	0.4664	0.4042	A	20.41	6.26E-06
9	rs11139665	84451020	0.05295	0.03042	A	19.98	7.84E-06
22	rs732110	26345321	0.1166	0.08168	A	19.73	8.90E-06
5	rs30523	132138941	0.1516	0.1125	G	18.71	1.52E-05
1	rs6693503	19859880	0.4135	0.3555	G	18.61	1.61E-05
14	rs1951054	25147247	0.3004	0.3575	A	18.33	1.86E-05
1	rs2012235	68685342	0.2332	0.2866	A	18.11	2.09E-05
4	rs2333255	176819759	0.4289	0.4874	C	17.55	2.80E-05
1	rs12563321	26539088	0.2554	0.2074	G	17.5	2.87E-05
1	rs9729637	5468038	0.09182	0.06265	C	17.45	2.95E-05
14	rs1257670	98562725	0.3394	0.2867	A	17.06	3.63E-05
1	rs12117956	27370168	0.305	0.3598	A	16.89	3.97E-05
9	rs7855598	137454075	0.2262	0.1813	A	16.84	4.06E-05
1	rs4846689	219444057	0.1156	0.0832	A	16.71	4.36E-05
6	rs6903101	138567539	0.04625	0.02687	A	16.69	4.39E-05
17	rs917538	14975565	0.4538	0.3978	C	16.6	4.61E-05
1	rs6687674	27409687	0.362	0.4182	G	16.58	4.67E-05
14	rs2284230	77085649	0.175	0.2217	G	16.5	4.88E-05
10	rs3824700	26395911	0.4953	0.4388	A	16.48	4.92E-05
11	rs7945105	131162979	0.3653	0.4212	G	16.48	4.93E-05
10	rs1521032	26393597	0.4946	0.4385	A	16.3	5.41E-05
1	rs10902742	26548843	0.2372	0.1923	C	16.13	5.91E-05
10	rs11593128	26392957	0.4946	0.4385	A	16.09	6.04E-05
10	rs3936497	28619974	0.1034	0.0734	A	16	6.34E-05
1	rs1454356	189400411	0.3495	0.4044	A	15.97	6.42E-05
9	rs1556047	112083819	0.5121	0.4565	A	15.86	6.83E-05
2	rs12692335	7524145	0.2483	0.203	G	15.84	6.90E-05
8	rs10955841	119015721	0.3718	0.3198	A	15.67	7.52E-05
1	rs9786944	5471098	0.08914	0.06186	G	15.5	8.24E-05

6	rs6926282	112968480	0.128	0.09509	G	15.43	8.55E-05
21	rs13049184	21818485	0.4448	0.4998	G	15.4	8.70E-05
12	rs12579612	93189923	0.2426	0.1984	A	15.39	8.75E-05
10	rs1521033	26422356	0.494	0.4395	G	15.36	8.89E-05
6	rs627240	81042603	0.3834	0.4387	C	15.33	9.04E-05
15	rs11636483	96937674	0.2507	0.206	A	15.25	9.44E-05
16	rs16953111	78954425	0.09987	0.07114	G	15.17	9.83E-05

Table S3. Australian Genome-wide Association Analysis Results ($p < 10^{-4}$)

CHR	SNP	Position (bp)	F_A	F_U	A2	CHISQ	p Value
8	rs10504743	82951580	0.04752	0.09918	G	20.43	6.18E-06
1	rs10779614	212656537	0.1777	0.2574	G	19.84	8.43E-06
1	rs6703314	104976389	0.3244	0.2397	A	19.29	1.13E-05
12	rs6539579	80696724	0.2562	0.3418	A	18.7	1.53E-05
3	rs4128782	89320422	0.468	0.5607	G	18.57	1.64E-05
7	rs1829993	77698210	0.469	0.5615	G	18.49	1.71E-05
5	rs10515600	147316068	0.3089	0.3975	C	18.45	1.74E-05
17	rs11079098	49220927	0.3295	0.4189	A	18.28	1.90E-05
2	rs750132	218548607	0.1508	0.09262	G	17.52	2.84E-05
17	rs3785655	14189892	0.2996	0.3844	T	17.15	3.46E-05
6	rs9389508	137842904	0.1405	0.08525	C	16.87	4.00E-05
18	rs4542757	48452722	0.3068	0.391	T	16.72	4.32E-05
7	rs6967325	77678568	0.407	0.323	A	16.56	4.72E-05
10	rs2082988	128254551	0.3409	0.4262	G	16.54	4.77E-05
20	rs6116201	4033758	0.1498	0.218	A	16.47	4.93E-05
20	rs10485664	38064192	0.2293	0.1607	A	16.48	4.93E-05
17	rs1859906	14191413	0.3688	0.4549	G	16.47	4.95E-05
9	rs11144978	78415148	0.3089	0.232	A	16.36	5.25E-05
1	rs1808973	112289357	0.4122	0.4975	T	15.83	6.93E-05
7	rs798332	77746864	0.3946	0.3131	T	15.78	7.11E-05
3	rs7429534	89273999	0.3564	0.4402	C	15.74	7.28E-05
6	rs6570048	136240287	0.4287	0.5131	T	15.41	8.64E-05
1	rs3006009	242697070	0.3533	0.4361	T	15.41	8.65E-05
1	rs11120315	212653320	0.1126	0.1721	C	15.36	8.90E-05
12	rs12228394	19482075	0.01756	0.04836	C	15.27	9.32E-05

Table S4. mRNA of Genes Found to Be Upregulated or Downregulated in UL with the Major Allele of rs4247357 Compared to UL with the Minor Allele

Gene	Location	Fold Change	Direction	p Value
<i>MMS19</i>	10q24.1	1.558	up	7.45E-07
<i>SH3BP4</i>	2q37.2	1.804	down	8.42E-07
<i>TUBB2A</i>	6p25.2	2.658	down	1.86E-06
<i>NLN</i>	5q12.3	1.617	down	2.19E-06
<i>FAM126A/DRCTNNB1A</i>	7p15.3	1.699	down	6.49E-06
<i>STX7</i>	6q23.2	2.014	down	6.88E-06
<i>PDS5B/KIAA0979</i>	13q13.1	1.753	down	7.25E-06
<i>CR613961</i>	1p36.11	2.655	down	7.96E-06
<i>CR749816</i>	1p21.2	1.817	down	8.49E-06
<i>PMEPA1</i>	20q13.31	2.284	down	1.16E-05
<i>MAP3K7IP3</i>	Xp21.2	2.581	down	1.17E-05
<i>HOOK3</i>	8p11.21	1.650	down	1.46E-05
<i>C12orf47</i>	12q24.12	1.728	up	1.47E-05
<i>ANKRD27</i>	19q13.11	1.870	down	1.55E-05
<i>RAB6C</i>	2q21.1	1.407	down	1.71E-05
<i>C6orf162</i>	6q15	1.585	up	1.82E-05
<i>PICALM</i>	11q14.2	1.884	down	1.83E-05
<i>c3orf19</i>	3p25.1	1.310	up	2.07E-05
<i>ZSIG13/FZD4</i>	11q14.2	2.527	down	2.15E-05
<i>PIAS1</i>	15q23	1.685	up	2.36E-05
<i>FADS1</i>	11q12.2	1.948	down	2.38E-05
<i>PHF21A/KIAA1696</i>	11p11.2	1.343	up	2.45E-05
<i>RBM15</i>	1p13.3	1.810	down	2.65E-05
<i>DIS3</i>	13q22.1	1.565	down	2.78E-05