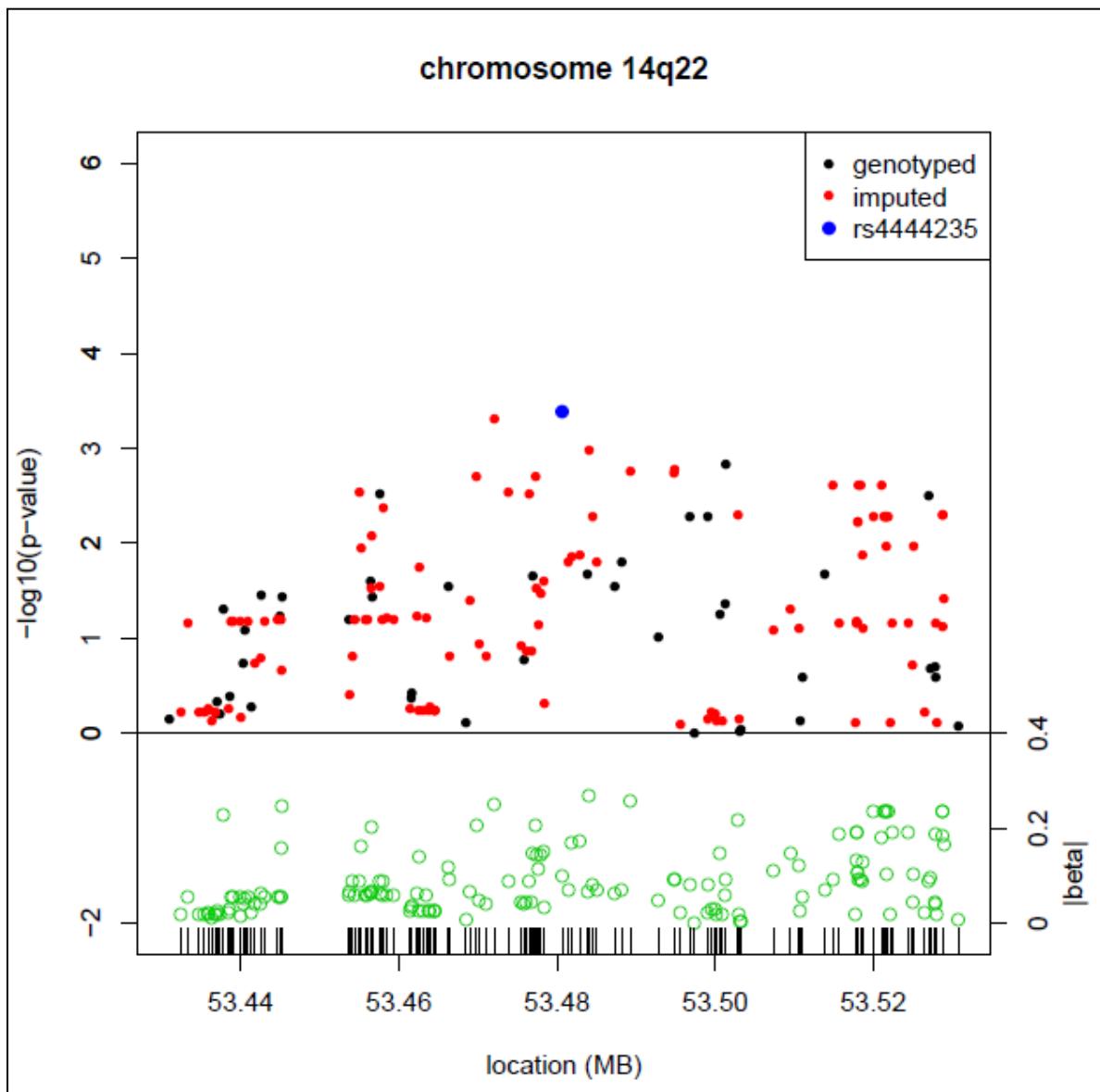


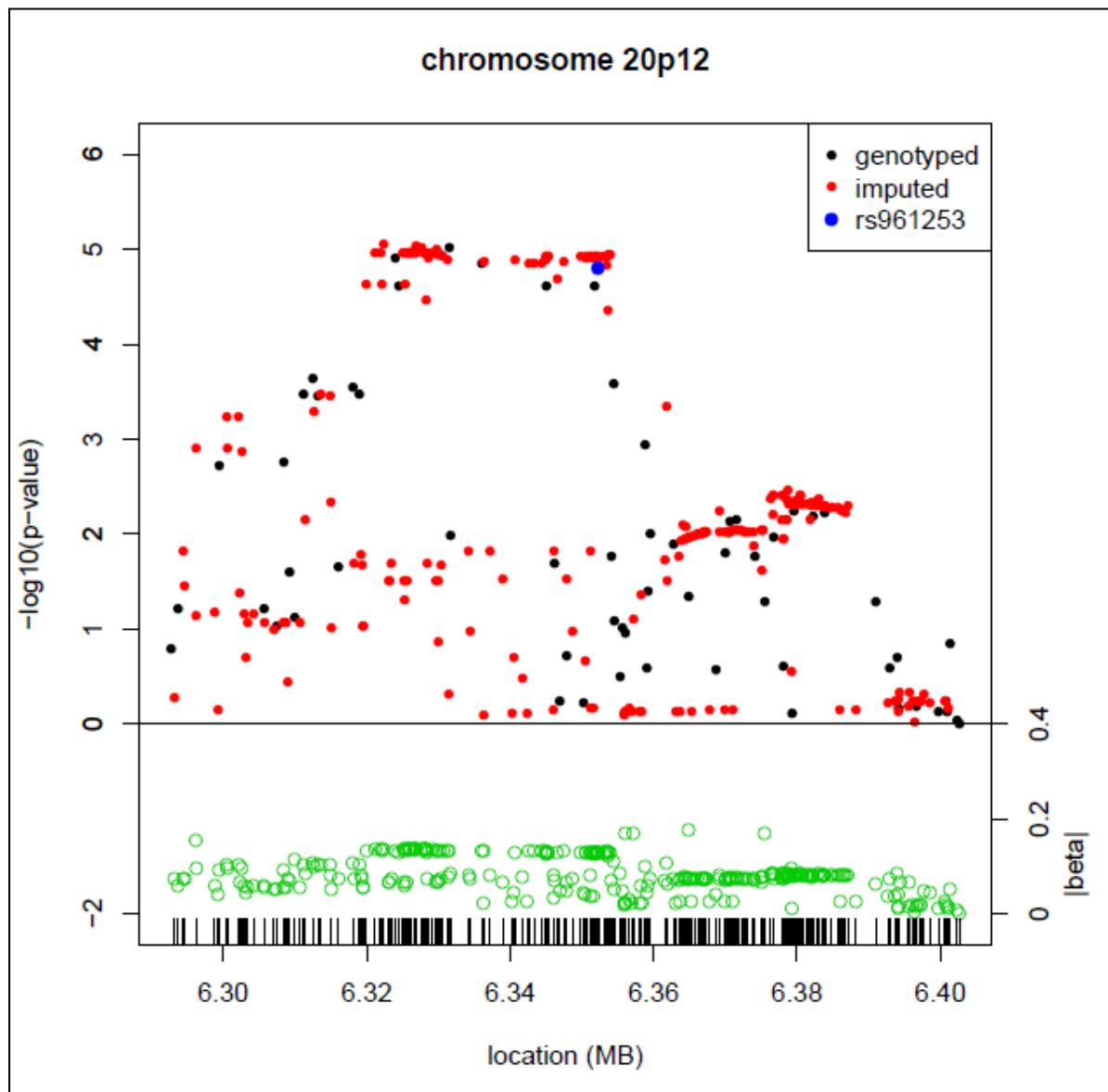
Supplemental Figure 1. Fine mapping around the known CRC risk SNPs close to (a) BMP4 (14q22) and (b) BMP2 (20p12).

Results for meta-analysis of UK2 and Scotland2 are shown. Both significance of association ($-\log_{10}(P)$) and effect size (β) are presented. The original CRC-associated tagSNPs are shown in blue. Near *BMP4*, the strongest signal is at the original tagSNP, rs4444235. rs961253, the original tagSNP near *BMP2*, lies in a region of about 40kb in which SNPs are in strong LD and thus show very similar signals of association.

(a)

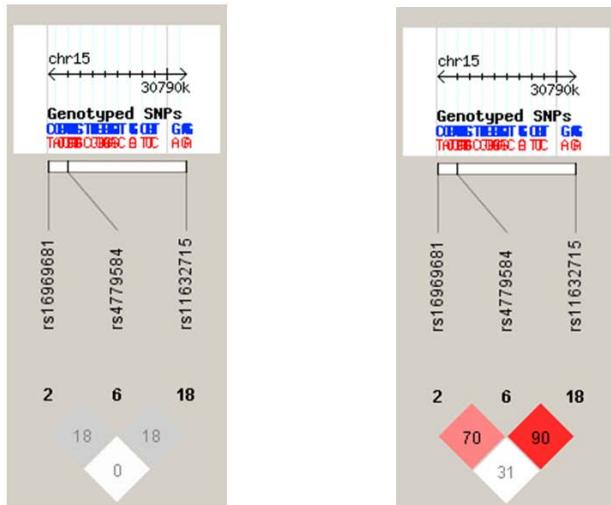


(b)

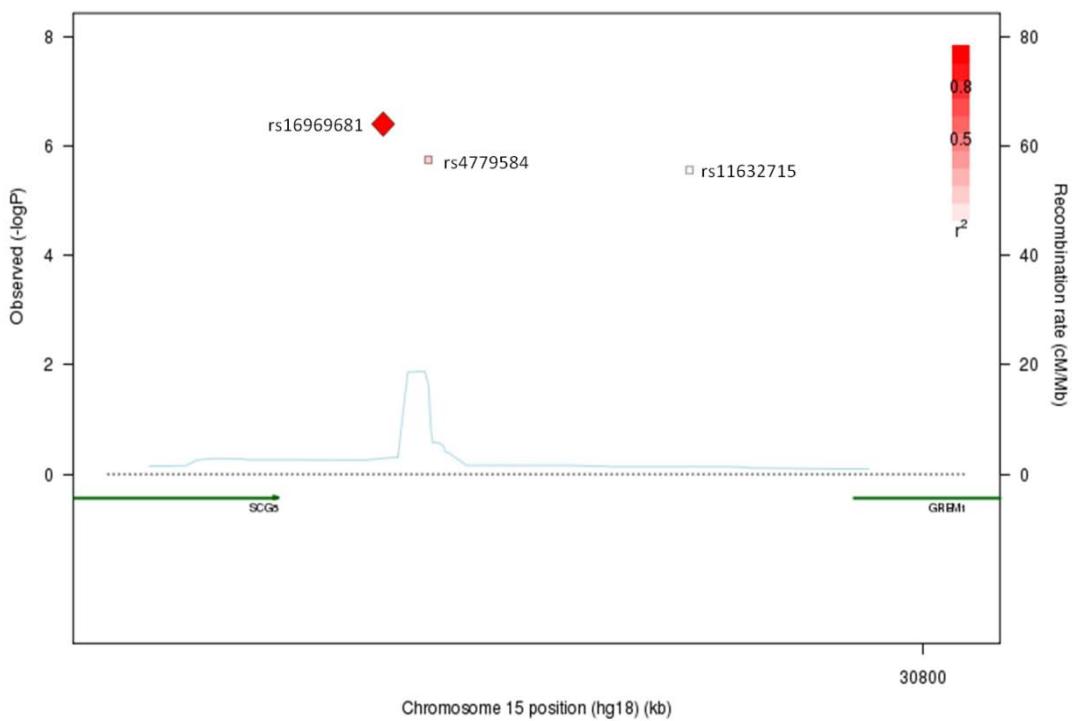


Supplemental Figure 2. Pairwise linkage disequilibrium between rs4779584, rs16969681 and rs11632715 near GREM1 (upper) and position of recombination hotspot (lower).

r^2 is shown left and D', right. Data are from HapMap 2 CEU. Standard Haploview colour schemes are used (<http://www.haploview.org/>).



The plot from SNAP shows location of recombination hotspot (peak of blue line, right-hand Y-axis) between rs16969681 and rs11632715. Left-hand Y-axis shows single-SNP association $-\log_{10}(P)$ from logistic regression analysis based on samples genotyped for all 3 SNPs. X-axis shows physical distance.



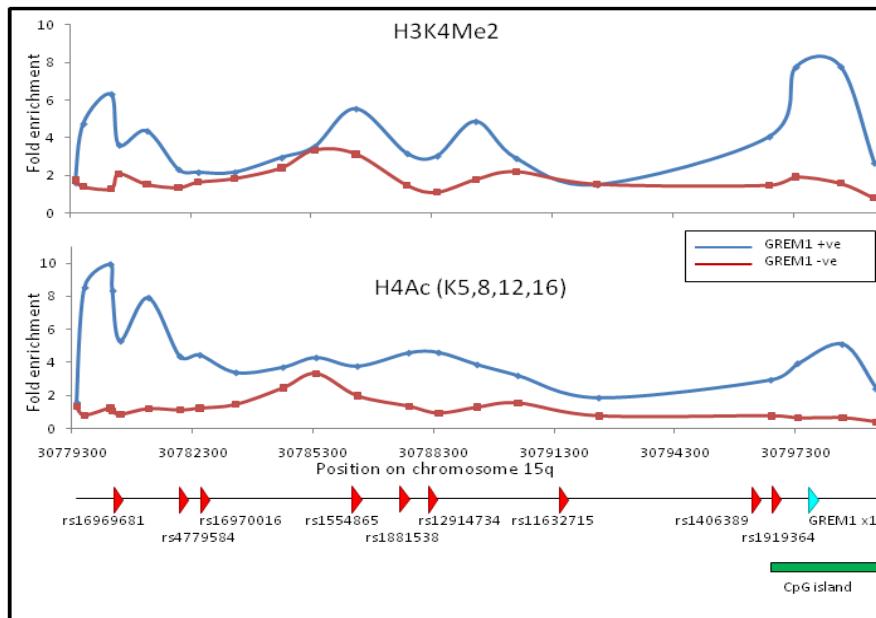
Supplemental Figure 3. Histone methylation and acetylation marks upstream of GREM1.

To search for possible regulatory elements tagged by SNPs in the 15q13.3 region, we carried out chromatin immunoprecipitation (ChIP) experiments to look for histone modifications between chr15:30,779,300 and the transcriptional start site of *GREM1*. Histone H4 acetylation; and histone H3 methylation at lysine 4 mark active chromatin and intergenic regions showing enrichment for such modifications may contain enhancer elements. We selected three CRC cell lines that express *GREM1* – LS180, C99 and HCC56 – and a control non-expressing cell line, SW48 and carried out ChIP on native chromatin using PCR assays spaced at ~1kb intervals.

ChIP experiments were carried out as previously described (9). Briefly, ~5 x10⁷ cells were collected from four colorectal cancer cell lines (LS180, C99, HCC56 and SW48) and washed in PBS. Nuclei were purified through a sucrose cushion and incubated with MNase to obtain fragments of one to five nucleosomes in length. Approximately 20 µg of native chromatin was incubated with 5-10 µg of antibody overnight at 4°C. The following antibodies were used: H3AcK1, 5, 9 and K14 (06-866) and H3K4me2 (07-030; Millipore). The antibody chromatin complexes were captured with Protein A magnetic beads (Invitrogen). After washing and elution DNA was extracted from the input chromatin, and bound fractions. Q-PCR analysis was carried out using Fast SYBR Green Master Mix using a 7900HT Fast Real-time PCR system (Applied Biosystems). Results were normalized to the Rhodopsin gene (a non-expressed control) and the relative enrichment of the bound fraction compared to the input was calculated using the $\Delta\Delta Ct$ method. Primer and probe sequences are available on request.

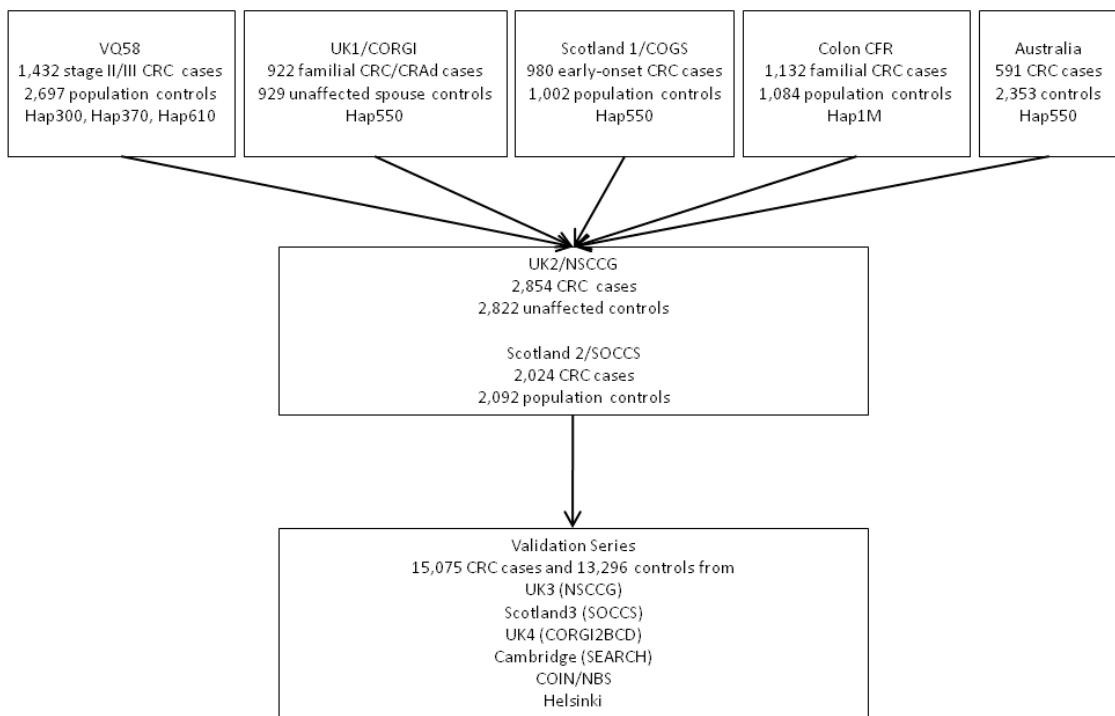
Plots show the enrichment of antibody bound chromatin relative to input chromatin plotted against the chromosome 15 co-ordinates for the average of the three *GREM1* expressing lines compared with the non-expressing line. The positions of selected SNPs are shown. Peaks were found, as expected, at the *GREM1* transcriptional start site, but there was a double peak of both acetylation and lysine 4 methylation centred on the region containing rs16969681. This peak was not seen in the control line. rs16969681 is therefore an excellent candidate functional SNP at the *GREM1* locus. The importance of the double-peak centred on rs1881538 is unclear given that it may also be present in the control. We tested rs1881538 in unconditional logistic regression analysis with rs16969681 and rs4779584 to determine whether it might be an association signal tagged by rs4779584 and independent of rs16969681. However, rs4779584 consistently captured more of the variation in disease risk than rs1881538 whether or not rs16969681 was included in the regression

model. rs11632715 was not associated with transcription control elements, whether from the ENCODE project or from our own data. It was, however, in LD with several SNPs in potential functionally important regions, including strong association with rs1919364 at the start of the *GREM1* promoter CpG island.

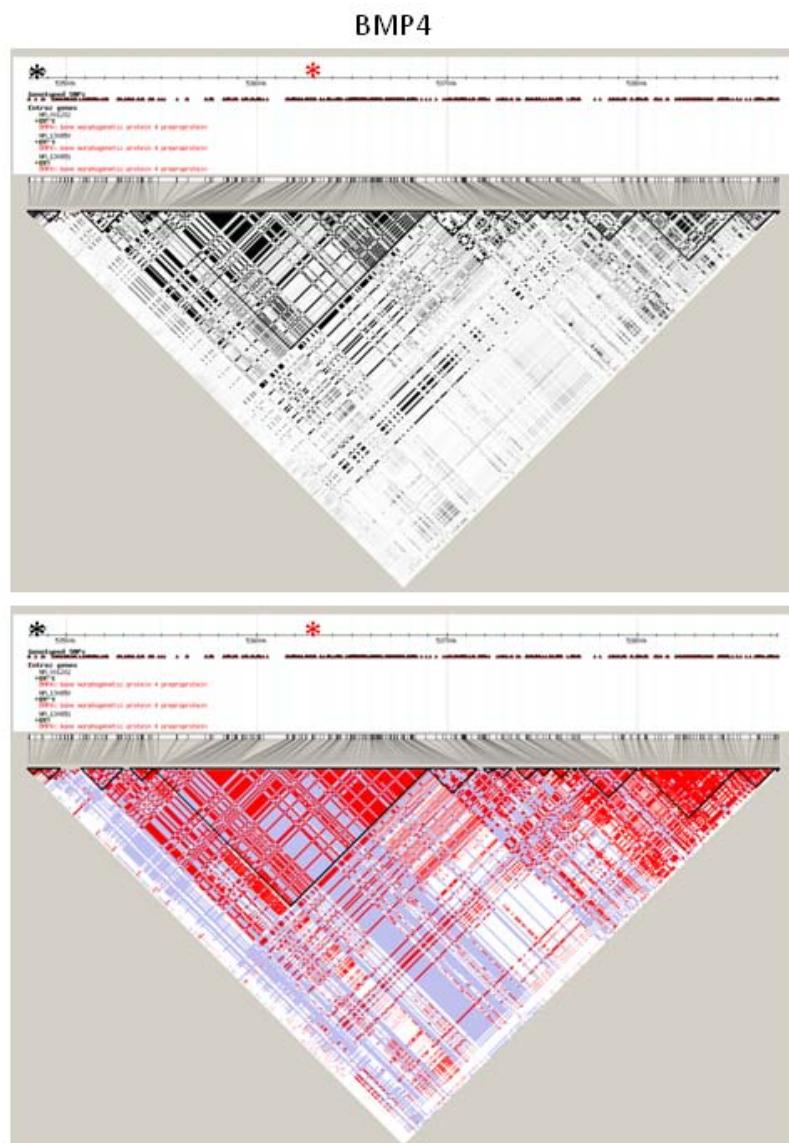


Supplemental Figure 4. Study design for discovery and validation phases.

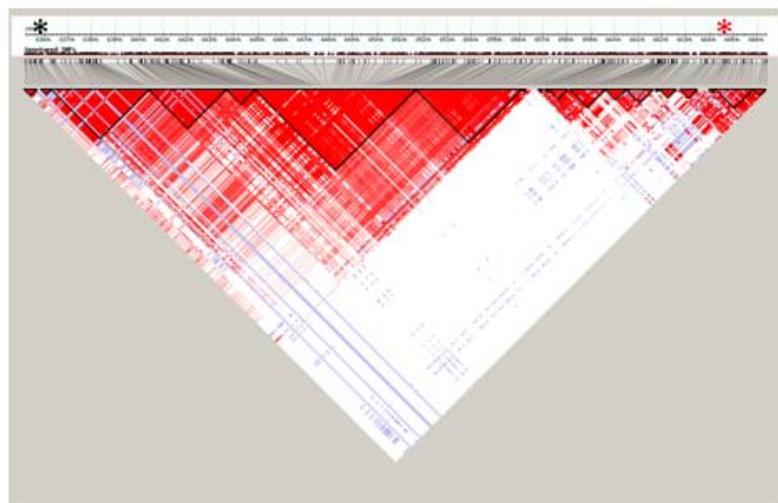
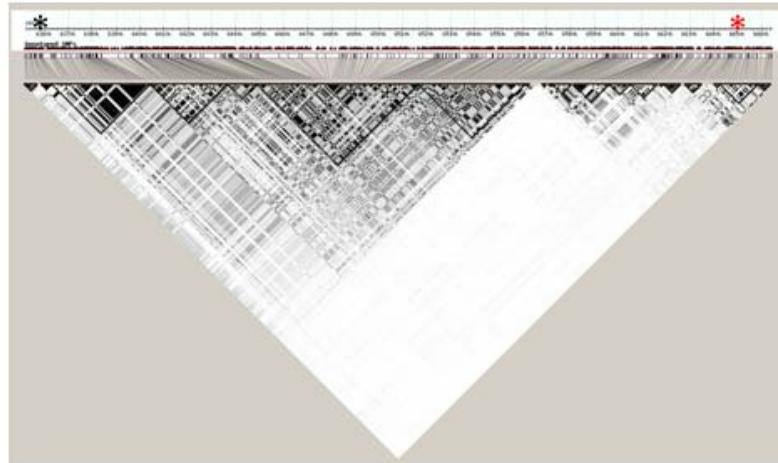
The proprietary Illumina arrays used for the 5 GWA studies are shown.



Supplemental Figure 5. Large-scale LD structure in regions around BMP4 and BMP2.
For each of *BMP2* and *BMP4*, the upper panel shows r^2 and the middle panel, D' (from SNAPData are from HapMap2 CEU samples in Haploview). In all cases, X-axes show physical distance. The original tagSNP is shown by a black star and the new signal by a red star.

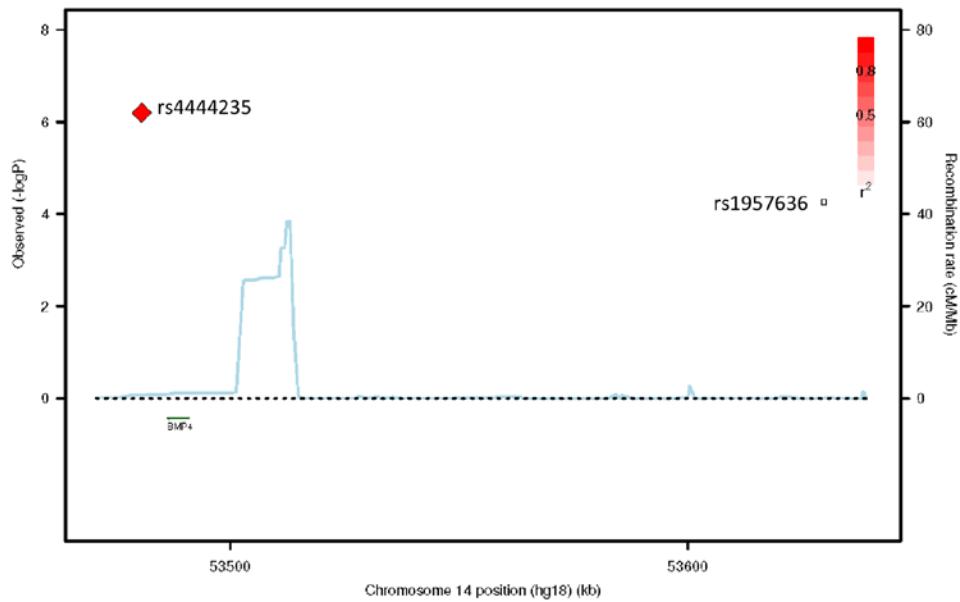


BMP2

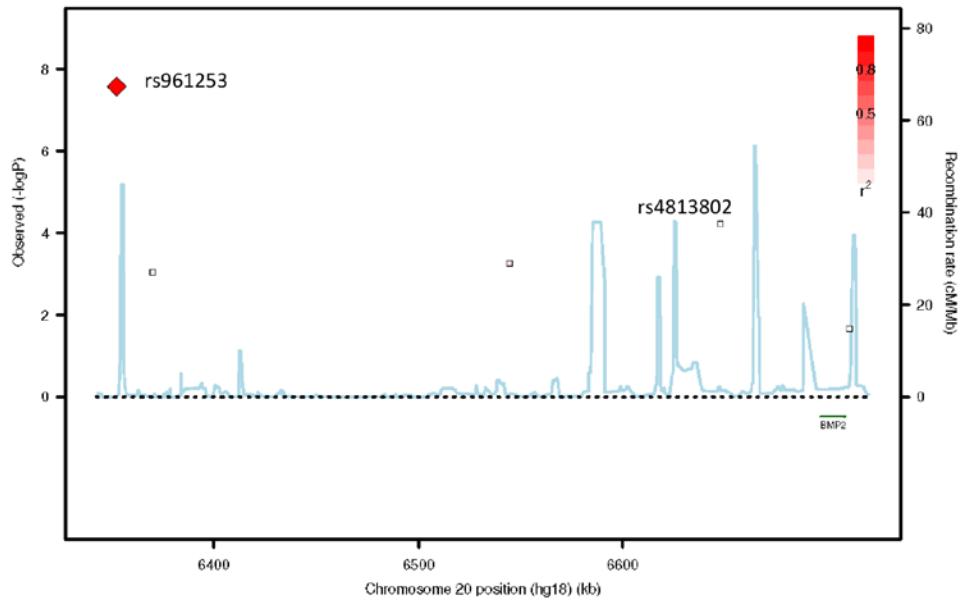


Supplemental Figure 6. Locations of recombination hotspots in regions around BMP4 and BMP2. The plots, from SNAP, show location of recombination hotspots (peaks of blue line, right-hand Y-axis) for the regions between the original tag SNPs near *BMP4* (rs4444235) and *BMP2* (rs961253) and the new signals (rs1957636 and rs4813802 respectively). X-axes show physical distance. Note the presence of hotspots between the locations of the pairs of SNPs.

BMP4 region



BMP2 region



Supplemental Table 1. SNPs genotyped directly or predicted by imputation in the fine mapping of the regions around rs4779584, rs4444235 and rs961253 in UK2 and Scotland2.

We undertook fine mapping of the genomic regions containing CRC-associated tag SNPs close to *GREM1* (15q13.3), *BMP4* (14q22.2) and *BMP2* (20p12.3). We identified all SNPs in the haplotype blocks and immediately flanking regions for rs4779584, rs4444235 and rs961253 from dbSNP (see Methods) and selected those with minor allele frequency >5%. After excluding SNPs that failed genotyping assay design or that fell below standard quality control (QC) thresholds, a total of 74, 113 and 255 SNPs in each region were successfully genotyped in the CRC cases and controls from the UK2 and Scotland2 sample sets. We then used 1000 Genomes and HapMap 3 reference genotypes to impute untyped SNPs mapping to these regions (1).

Region	Location	SNP ID	Imputed or Genotyped
15q13.3	30,733,560	rs12903437	Genotyped
15q13.3	30,734,914	rs11638385	Genotyped
15q13.3	30,734,931	rs11638089	Genotyped
15q13.3	30,735,171	rs7171657	Genotyped
15q13.3	30,735,386	rs12593101	Genotyped
15q13.3	30,737,358	rs55683307	Imputed
15q13.3	30,739,485	rs8023613	Genotyped
15q13.3	30,740,356	rs4238560	Genotyped
15q13.3	30,742,387	rs11071887	Genotyped
15q13.3	30,746,003	rs1406387	Genotyped
15q13.3	30,747,917	rs10083612	Genotyped
15q13.3	30,749,197	rs17228564	Genotyped
15q13.3	30,749,532	rs17228571	Imputed
15q13.3	30,749,742	rs11855680	Imputed
15q13.3	30,749,934	rs8041254	Genotyped
15q13.3	30,750,051	rs8037112	Imputed
15q13.3	30,750,497	rs16963973	Genotyped
15q13.3	30,751,048	rs16964074	Genotyped
15q13.3	30,752,649	rs12909871	Genotyped
15q13.3	30,752,922	rs11634086	Genotyped
15q13.3	30,753,521	rs11635362	Genotyped
15q13.3	30,755,075	rs62001857	Imputed
15q13.3	30,755,131	rs7161975	Genotyped
15q13.3	30,755,270	rs10775188	Genotyped
15q13.3	30,756,123	rs12148394	Genotyped
15q13.3	30,756,146	15-30756146	Imputed
15q13.3	30,756,215	rs7170561	Genotyped
15q13.3	30,756,749	rs10519737	Imputed
15q13.3	30,757,201	rs28688414	Imputed
15q13.3	30,757,349	rs7177176	Genotyped
15q13.3	30,757,435	rs6494576	Imputed
15q13.3	30,757,448	rs11633548	Genotyped
15q13.3	30,757,493	rs16965041	Imputed
15q13.3	30,757,554	rs6494577	Imputed
15q13.3	30,757,842	rs1881536	Genotyped
15q13.3	30,758,358	rs71462819	Imputed
15q13.3	30,758,440	rs11071897	Genotyped
15q13.3	30,758,464	rs34278216	Imputed
15q13.3	30,758,577	rs16965254	Imputed
15q13.3	30,758,627	rs35415313	Imputed
15q13.3	30,758,727	rs12102176	Imputed
15q13.3	30,759,050	rs3817592	Genotyped
15q13.3	30,759,226	rs7177843	Genotyped
15q13.3	30,759,546	15-30759546	Imputed

15q13.3 30,760,107	15-30760107	Imputed
15q13.3 30,760,231	rs12442397	Genotyped
15q13.3 30,760,289	rs12438604	Genotyped
15q13.3 30,760,617	15-30760617	Imputed
15q13.3 30,762,805	rs35703183	Imputed
15q13.3 30,762,980	rs12441136	Genotyped
15q13.3 30,763,009	rs12441140	Genotyped
15q13.3 30,763,347	rs17816224	Imputed
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15q13.3 30,764,833	rs11634570	Imputed
15q13.3 30,765,042	rs56338436	Imputed
15q13.3 30,766,061	rs7403093	Imputed
15q13.3 30,766,905	rs16966853	Genotyped
15q13.3 30,767,015	rs11638903	Genotyped
15q13.3 30,767,310	rs8043234	Genotyped
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15q13.3 30,768,217	rs4780033	Imputed
15q13.3 30,768,377	rs8039575	Imputed
15q13.3 30,768,468	15-30768468	Imputed
15q13.3 30,768,526	15-30768526	Imputed
15q13.3 30,768,620	rs7178316	Genotyped
15q13.3 30,768,935	rs6494587	Genotyped
15q13.3 30,769,270	rs8024160	Imputed
15q13.3 30,771,488	rs6494593	Imputed
15q13.3 30,772,597	rs17228585	Genotyped
15q13.3 30,772,770	rs12592208	Genotyped
15q13.3 30,773,082	rs28494912	Imputed
15q13.3 30,773,246	rs1997317	Genotyped
15q13.3 30,773,279	rs1997316	Genotyped
15q13.3 30,773,663	rs17228592	Genotyped
15q13.3 30,773,727	rs68050511	Imputed
15q13.3 30,774,389	rs16968154	Imputed
15q13.3 30,774,508	15-30774508	Imputed
15q13.3 30,774,799	15-30774799	Imputed
15q13.3 30,775,388	rs1406388	Genotyped
15q13.3 30,775,430	rs7494781	Genotyped
15q13.3 30,779,005	rs16969344	Genotyped
15q13.3 30,779,950	rs28399071	Imputed
15q13.3 30,780,036	rs8035130	Genotyped
15q13.3 30,780,128	rs12708491	Imputed
15q13.3 30,780,403	rs16969681	Genotyped
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15q13.3 30,781,293	rs16969862	Genotyped
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15q13.3 30,781,704	rs12592056	Genotyped
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15q13.3 30,782,069	rs4779585	Genotyped
15q13.3 30,782,135	rs9888701	Genotyped
15q13.3 30,782,465	rs11071915	Imputed
15q13.3 30,782,590	rs16970016	Genotyped
15q13.3 30,782,646	rs9888705	Imputed
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15q13.3 30,783,368	rs28663519	Imputed
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15q13.3 30,783,506	rs55659128	Imputed
15q13.3 30,783,535	rs28650777	Imputed
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15q13.3 30,784,442	rs3861195	Genotyped

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15q13.3 30,789,764	rs11071922	Imputed
15q13.3 30,789,986	rs34054489	Imputed
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15q13.3 30,790,143	15-30790143	Imputed
15q13.3 30,790,156	15-30790156	Imputed
15q13.3 30,790,171	15-30790171	Imputed
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15q13.3 30,793,696	rs12591802	Genotyped
15q13.3 30,793,707	rs12594148	Imputed
15q13.3 30,793,800	rs12592288	Genotyped
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15q13.3 30,794,643	rs28473724	Imputed
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15q13.3 30,796,866	rs1919364	Imputed
15q13.3 30,797,704	rs2293582	Imputed
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15q13.3 30,799,794	rs73376930	Imputed
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15q13.3 30,802,498	rs1528734	Genotyped
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Region	Location	SNP ID	Imputed or Genotyped
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14q22.2	53,434,718	rs56132091	Imputed
14q22.2	53,435,381	rs4901464	Imputed
14q22.2	53,435,871	rs7140284	Imputed
14q22.2	53,435,915	rs7140441	Imputed
14q22.2	53,436,318	rs4901465	Imputed
14q22.2	53,436,788	rs10144601	Imputed
14q22.2	53,436,952	rs4898817	Genotyped
14q22.2	53,437,038	rs1957847	Genotyped
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14q22.2	53,438,458	rs12433303	Imputed
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14q22.2	53,439,923	rs2181734	Imputed
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14q22.2 53,464,481	rs4901469	Imputed
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14q22.2 53,511,069	rs12895262	Genotyped
14q22.2 53,513,874	rs12892252	Genotyped
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14q22.2 53,530,761 rs17127134 Genotyped

Region	Location	SNP ID	Imputed or Genotyped
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20p12.3 6,356,114	rs6077000	Imputed
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20p12.3 6,376,764	rs4815900	Genotyped
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20p12.3 6,377,964	rs6117263	Imputed
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20p12.3 6,379,393	rs6054265	Imputed
20p12.3 6,379,457	rs6054266	Imputed
20p12.3 6,379,569	rs6054267	Genotyped
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20p12.3 6,380,618	rs6054272	Imputed
20p12.3 6,380,735	rs2876033	Imputed
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20p12.3 6,385,981	rs6054282	Imputed
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20p12.3 6,386,553	rs2183450	Imputed
20p12.3 6,386,797	rs6038514	Imputed
20p12.3 6,387,088	rs6054284	Imputed
20p12.3 6,388,258	rs7509140	Imputed
20p12.3 6,390,961	rs6077004	Genotyped
20p12.3 6,392,659	rs13036856	Imputed
20p12.3 6,392,931	rs7269050	Genotyped
20p12.3 6,393,632	rs62199997	Imputed
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20p12.3 6,395,663	rs12626134	Imputed
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20p12.3 6,397,281	rs6085566	Imputed
20p12.3 6,397,722	rs62199999	Imputed
20p12.3 6,398,549	rs990123	Imputed
20p12.3 6,399,752	rs2326787	Genotyped
20p12.3 6,400,601	rs6054290	Imputed
20p12.3 6,400,773	rs6054291	Genotyped
20p12.3 6,400,982	rs6085568	Genotyped
20p12.3 6,401,105	rs6085569	Imputed
20p12.3 6,401,324	rs4815903	Genotyped
20p12.3 6,402,309	rs6077007	Genotyped
20p12.3 6,402,661	rs6054292	Genotyped

Supplemental Table 2. Haplotype risk analysis at rs16969681 and rs4779584.

Haplovew (<http://www.haplovew.org/>) was used to estimate haplotype frequencies in our data at SNPs close to rs16969681 and rs4779584. We then used PLINK to perform haplotype association analysis at rs16969681 and rs4779584.

LOCUS	HAPLOTYPE	F_A	F_U	CHISQ	DF	P	SNPs
WIN1	OMNIBUS	NA	NA	24.91	3	1.609x10 ⁻⁵	rs16969681 rs4779584
WIN1	TT	0.0632	0.0525	16.01	1	6.29x10 ⁻⁵	rs16969681 rs4779584
WIN1	CT	0.1470	0.1380	4.938	1	0.02628	rs16969681 rs4779584
WIN1	TC	0.0326	0.0306	1.008	1	0.3154	rs16969681 rs4779584
WIN1	CC	0.7571	0.7789	19.94	1	7.974x10 ⁻⁶	rs16969681 rs4779584

Supplemental Table 3. Logistic regression model analysis of CRC risk and genotypes at rs4779584, rs16969681 and rs11632715.

Samples typed for all 3 SNPs are included. The best fitting model (minimum Akaike Information Criterion) included rs16969681 and rs11632715. Inclusion of rs4779584 did not improve the fit of the model. When all 3 SNPs were included in the logistic regression model: for rs11632715, P=1.36x10⁻⁵; for rs16969681, P=3.96x10⁻⁵; and for rs4779584, P=0.14.

<u>SNPs included in model</u>	AIC
rs4779584+rs16969681+rs11632715	25541
rs4779584+rs16969681	25558
rs4779584+rs11632715	25556
rs16969681+rs11632715	25541
rs4779584	25570
rs16969681	25565
rs11632715	25564

Although the data for the SNPs near *GREM1* are by far most compatible with 2 independent CRC variants at or tagged by rs16969681 and rs11632715, we cannot entirely exclude the remote possibility of the signals at rs16969681 and rs11632715 capturing a single very rare disease variant on a haplotype which we estimate to have a frequency of ~1%. However, no such variant was evident on imputation using 1000 genomes project data as a reference (see above). Moreover, such a variant might have a sufficiently large effect size that it would be detectable by linkage screens, and no evidence of a such a linkage signal at *GREM1* has emerged from linkage studies of CRC in white northern European populations (2-7). It is also highly implausible that these SNPs are reporting the effects of the high-penetrance *HMPSP/CRAC1* gene found in Ashkenazim (8), since HMPSP families are generally large, have distinct phenotypes and tumour histology. Moreover, the *HMPSP/CRAC1* ancestral mutation resides on a haplotype that does not include the risk allele at rs16969681 or rs11632715.

Supplemental Table 4. TagSNPs around GREM1, BMP4 and BMP2 analysed for new associations.

CHR	BP	SNP
15q13.3	30,775,388	rs1406388
15q13.3	30,775,430	rs7494781
15q13.3	30,779,005	rs16969344
15q13.3	30,779,779	rs12708490
15q13.3	30,780,036	rs8035130
15q13.3	30,780,403	rs16969681
15q13.3	30,780,937	rs16969816
15q13.3	30,781,293	rs16969862
15q13.3	30,781,348	rs12591992
15q13.3	30,781,704	rs12592056
15q13.3	30,781,917	rs12594722
15q13.3	30,782,048	rs4779584
15q13.3	30,782,135	rs9888701
15q13.3	30,782,198	rs7172208
15q13.3	30,782,590	rs16970016
15q13.3	30,782,673	rs7166282
15q13.3	30,784,442	rs3861195
15q13.3	30,784,874	rs11853552
15q13.3	30,785,128	rs11857997
15q13.3	30,787,098	rs1554865
15q13.3	30,788,001	rs1881538
15q13.3	30,788,556	rs12914734
15q13.3	30,788,858	rs7182252
15q13.3	30,791,354	rs11638007
15q13.3	30,791,539	rs11632715
15q13.3	30,793,167	rs1534594
15q13.3	30,793,800	rs12592288
15q13.3	30,796,770	rs1406389
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15q13.3	30,811,747	rs7162202
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15q13.3	30,813,959	rs1129456
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15q13.3	30,826,590	rs17816285
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15q13.3	30,828,074	rs10519740
15q13.3	30,828,286	rs12439770
15q13.3	30,829,630	rs16958114
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15q13.3	30,830,747	rs1919360
15q13.3	30,830,949	rs1919362
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15q13.3	30,850,518	rs1979168
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14q22.2	52,701,921	rs4901357
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14q22.2	52,730,313	rs2552400
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14q22.2	52,776,759	rs763328
14q22.2	52,801,683	rs7146135
14q22.2	52,810,756	rs7151631
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14q22.2	52,823,675	rs8013473

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14q22.2	52,833,496	rs4901392
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14q22.2	52,867,043	rs17126346
14q22.2	52,867,898	rs1424838
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14q22.2	52,873,879	rs4901408
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14q22.2	52,886,214	rs17126390
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14q22.2	52,889,727	rs1255309
14q22.2	52,892,776	rs877018
14q22.2	52,896,997	rs1255288
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14q22.2	52,912,225	rs17831927
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14q22.2	52,918,686	rs4901416
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14q22.2	53,237,867	rs964254
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14q22.2	53,242,605	rs7151053
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20p12.3	6,037,552	rs6085405
20p12.3	6,037,797	rs6085406
20p12.3	6,041,090	rs2326719
20p12.3	6,041,177	rs16991866
20p12.3	6,044,695	rs2295435
20p12.3	6,059,569	rs6038366
20p12.3	6,062,257	rs6053925
20p12.3	6,063,581	rs6053929
20p12.3	6,066,980	rs2144936
20p12.3	6,072,113	rs1774885
20p12.3	6,074,302	rs11087720
20p12.3	6,076,201	rs947465
20p12.3	6,076,223	rs1774886
20p12.3	6,076,868	rs1778777
20p12.3	6,076,868	rs6053941
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20p12.3	6,078,577	rs1342347
20p12.3	6,085,310	rs6076954
20p12.3	6,091,379	rs3844457
20p12.3	6,092,454	rs3852936
20p12.3	6,104,745	rs7270088
20p12.3	6,110,015	rs6085425
20p12.3	6,114,488	rs6133296
20p12.3	6,124,595	rs6053959
20p12.3	6,124,793	rs6053961
20p12.3	6,128,089	rs6085432
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20p12.3 7,821,112	rs2423322
20p12.3 7,821,818	rs6133511
20p12.3 7,824,255	rs6117980
20p12.3 7,825,416	rs1569454

Supplemental Table 5. Additional BMP pathway genes around which tagSNP associations with CRC were analysed.

BMPR1A
BMPR1B
BMPR2
GREM1
GREM2
NOG
CER1
DAND5/GREM3
NBL1
CHRD
FST
FSTL1
FSTL3
FSTL4
FSTL5
BMP2
BMP3
BMP4
BMP5
BMP6
BMP7
BMP8A
BMP8B
BMP9/GDF2
BMP10
BMP11/GDF11
SMAD1
SMAD5
SMAD9 (SMAD8)
SMAD4
SMAD6
SMAD7
BAMBI
SMURF1
SYCP1
SYCP2
SYCP3

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