

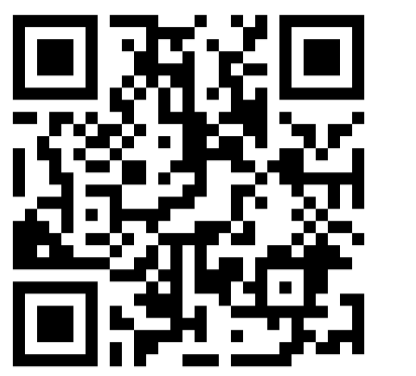
Do methane traits have the same genetic background?

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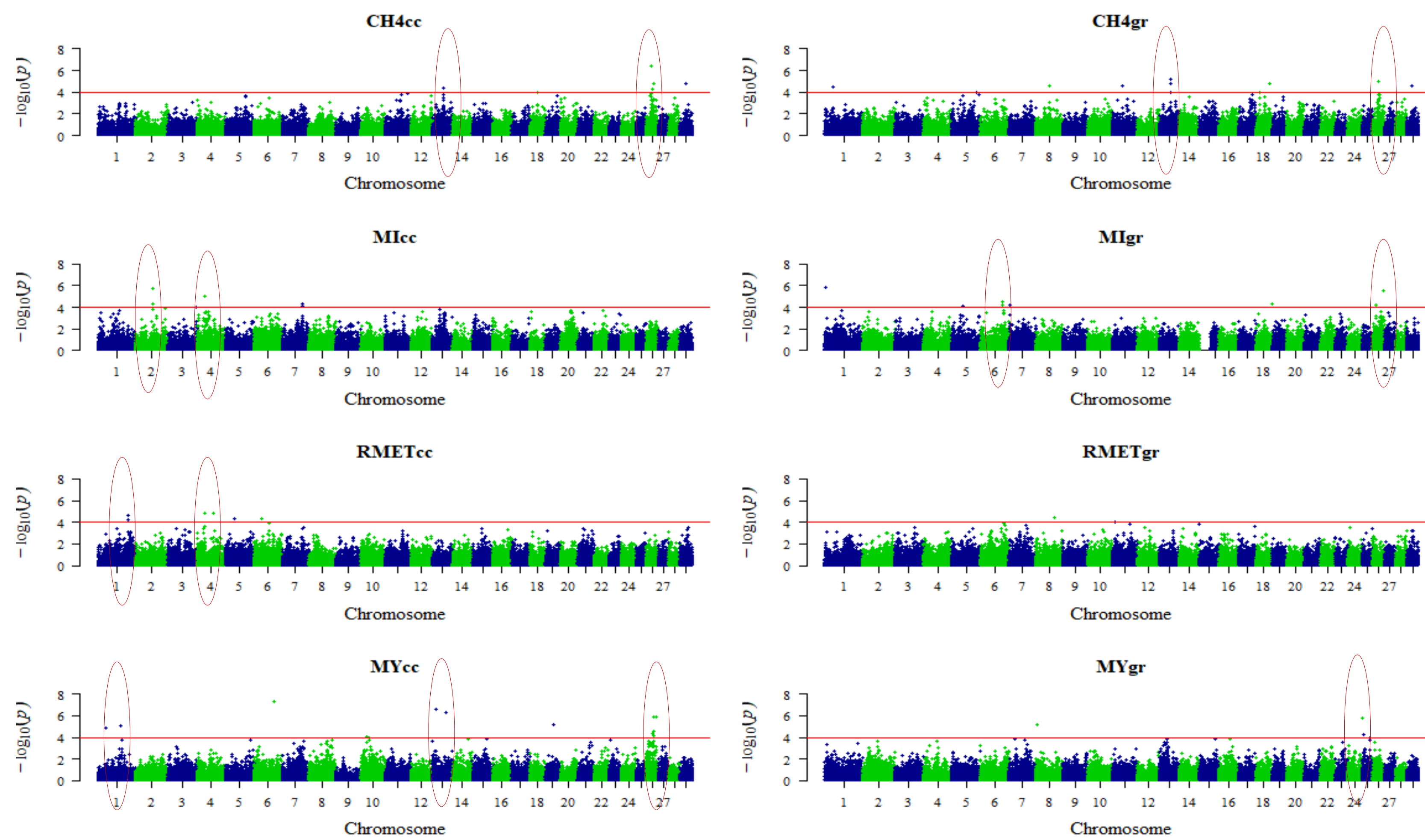
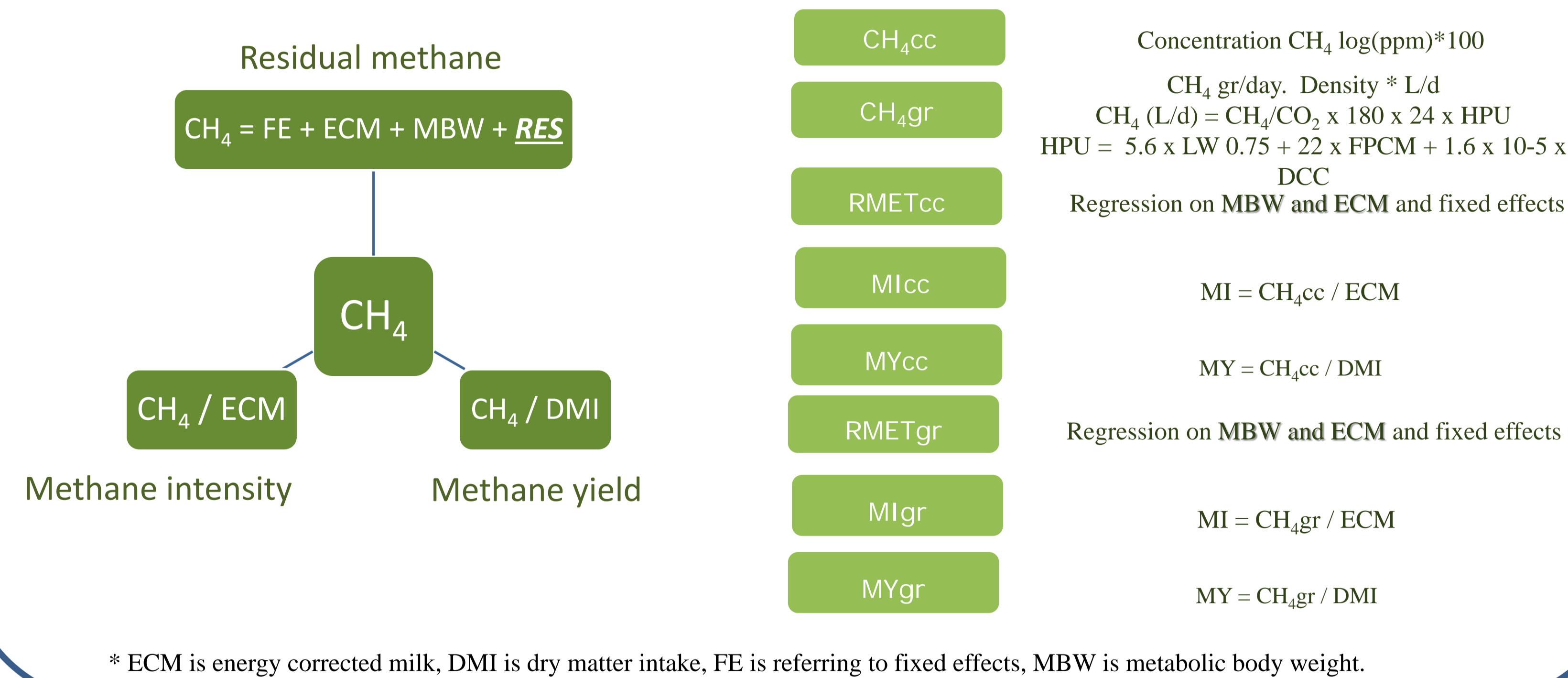


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Identify SNP associated with eight CH₄ traits in Danish Holstein cattle and determine if there are SNP in common controlling these methane traits

Materials and Methods



Segments of 1mbp significantly associated to each trait (**diagonal; P < 0.01 / P < 0.001**) and between traits (P < 0.01 below the diagonal, P < 0.001 above the diagonal).

Traits	CH ₄ cc	CH ₄ gr	MIcc	MIgr	RMETcc	RMETgr	MYcc	MYgr
CH ₄ cc	248 / 34	17	1	1	0	0	5	1
CH ₄ gr	145	362 / 54	1	2	0	0	3	0
MIcc	34	48	301 / 54	4	4	1	2	0
MIgr	40	65	89	316 / 37	0	0	5	1
RMETcc	26	47	39	35	299 / 35	1	3	1
RMETgr	34	45	35	39	36	299 / 37	0	1
MYcc	37	53	39	52	38	39	280 / 52	1
MYgr	58	70	55	55	37	34	58	308 / 33

■ Significant segments in common within trait pairs (RMET, MI, MY).

Genetic correlations between trait pairs

$CH_{4gr} - CH_{4cc} = 0.82$ $MIgr - MIcc = 0.43^*$
 $RMETgr - RMETcc = 0.65^*$ $MYgr - MYcc = 0.78^*$
 *SE between 0.14 to 0.23

SNP significantly associated to two traits (P < 0.001), chromosome and position (bp)

SNP	Chromosome	Position	Trait 1	Trait 2
ARS-BFGL-NGS-93180	1	138832098	RMETcc	MYgr
ARS-BFGL-NGS-24888	4	3583133	CH ₄ cc	CH ₄ gr
Hapmap59221-rs29014908	4	35939871	MIcc	MIgr
Hapmap44201-BTA-114510	4	36842170	MIcc	MIgr
Hapmap51046-BTA-75812	6	61984747	CH ₄ cc	CH ₄ gr
Hapmap52436-rs29009653	6	99732094	MIcc	MIgr
ARS-BFGL-NGS-47330	11	44562022	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-12929	11	64313748	CH ₄ cc	CH ₄ gr
Hapmap26463-BTA-159947	11	92086008	CH ₄ cc	CH ₄ gr
Hapmap49571-BTA-32781	13	47583553	CH ₄ cc	CH ₄ gr
BTB-00525367	13	47915618	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-70206	13	48622655	CH ₄ cc	CH ₄ gr
BTA-115847-no-rs	13	48826815	CH ₄ cc	CH ₄ gr
BTA-37116-no-rs	15	57228610	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-32691	18	34159637	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-54767	18	7605307	MIcc	MIgr
UA-IFASA-7562	19	49438164	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-103202	24	61455723	MYcc	MYgr
Hapmap33073-BTA-162864	26	21180893	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-2180	26	24477962	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-1092	26	24531763	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-18194	26	24575207	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-81009	26	26491674	CH ₄ cc	CH ₄ gr
Hapmap38478-BTA-20824	26	28723721	CH ₄ cc	CH ₄ gr
Hapmap40449-BTA-61103	26	31213256	CH ₄ cc	CH ₄ gr
Hapmap19519-rs29022379	27	19017466	MIgr	MYcc
ARS-BFGL-NGS-60192	28	25609489	CH ₄ cc	CH ₄ gr
ARS-BFGL-NGS-24205	29	25325889	CH ₄ cc	CH ₄ gr

Main findings



CH₄cc and CH₄gr had the highest number of significant segments and SNP in common



Given its genetic correlation CH₄cc is closer related to CH₄gr than the other trait pairs



RMET, MI, and MY seem to be different traits and they can not be used interchangeable

Figure 1. Genome-wide association plots (-log₁₀(P)) of methane concentration (CH₄gr), methane grams (CH₄cc), methane intensity concentration (MIcc), methane intensity grams (MIgr), residual methane concentration (RMETcc), residual methane grams (RMETgr), methane yield concentration (MYcc), methane yield grams (MYgr) performed on 1,900 animals with repeated records. The genomewide significance level is set at 10 × 10⁻⁵ and is plotted as the red line.