

compare the effective number of tests (m_{eff}) according to each correction method. The ‘n_prune’ column gives the number of SNPs in the region after pruning all SNPs with $r^2 > 0.2$.

Table 1: Maternal SNPs

region	n	n_prune	Nyholt_2004	Li_Ji_2005	Gao_2008	Galwey_2009
chr1 r1	61	8	48	12	14	9
chr2 r2/3	53	8	44	19	32	17
chr3 r4	70	11	47	12	21	9
chr3 r5	87	14	69	15	27	13
chr5 r6	42	6	30	11	17	9
chr6 r7	51	5	44	16	22	13
chr10 r8	53	12	42	16	21	13
chr10 r9	61	5	36	9	8	5
chr13 r10	75	11	63	22	30	17
chr14 r11	42	7	31	8	8	5
chr14 r12	88	8	22	8	7	3
chr17 r13	80	8	65	18	25	13
chr19 r14	50	9	39	11	16	9

Table 2: Parent origin SNPs

region	n	n_prune	Nyholt_2004	Li_Ji_2005	Gao_2008	Galwey_2009
chr1 r1	94	11	46	8	7	4
chr1 r2	35	3	22	8	9	5
chr1 r3	39	5	26	7	6	4
chr1 r4	68	6	40	12	13	7
chr2 r5	32	5	25	11	19	11
chr4 r6/7	29	6	21	8	10	6
chr5 r8	132	15	83	14	21	9
chr6 r9	51	6	41	12	18	11
chr8 r10	143	25	126	33	62	30
chr9 r11	53	5	41	14	27	13
chr9 r12	34	3	25	9	13	7
chr12 r13	68	8	53	11	16	9
chr14 r14	66	10	52	17	29	15
chr14	36	10	28	13	23	13
r15/16						
chr16 r17	52	16	44	20	31	19