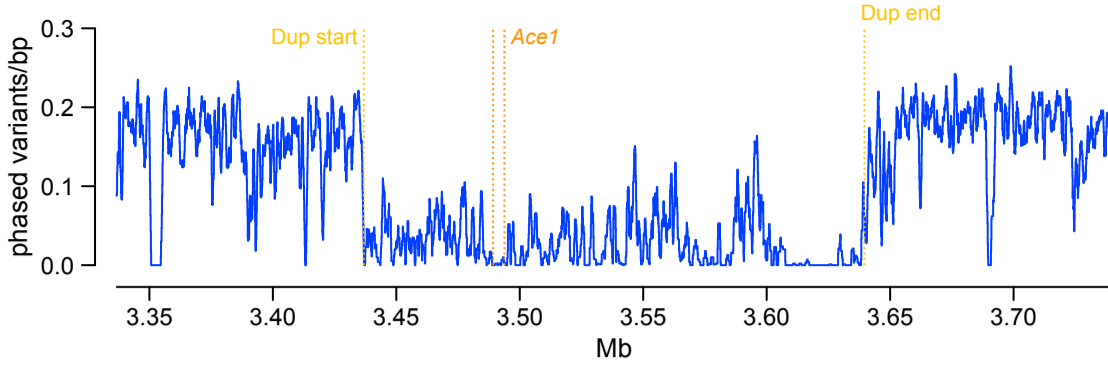
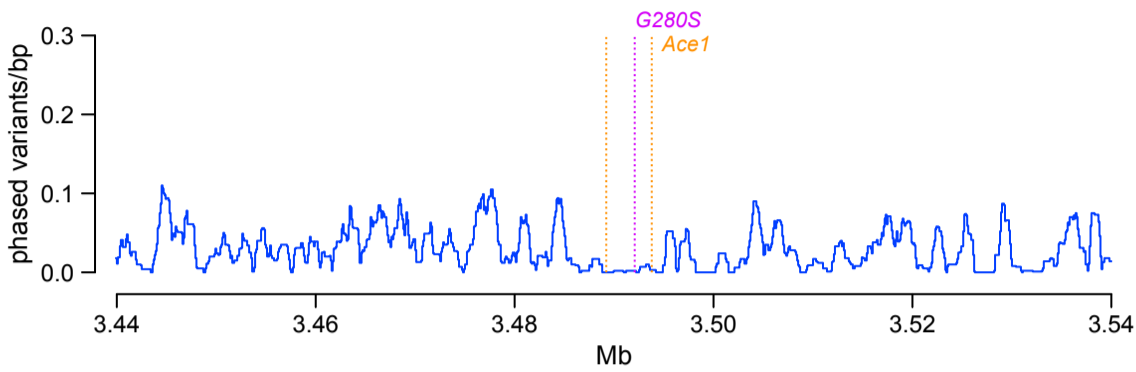


Supplementary Material SM9

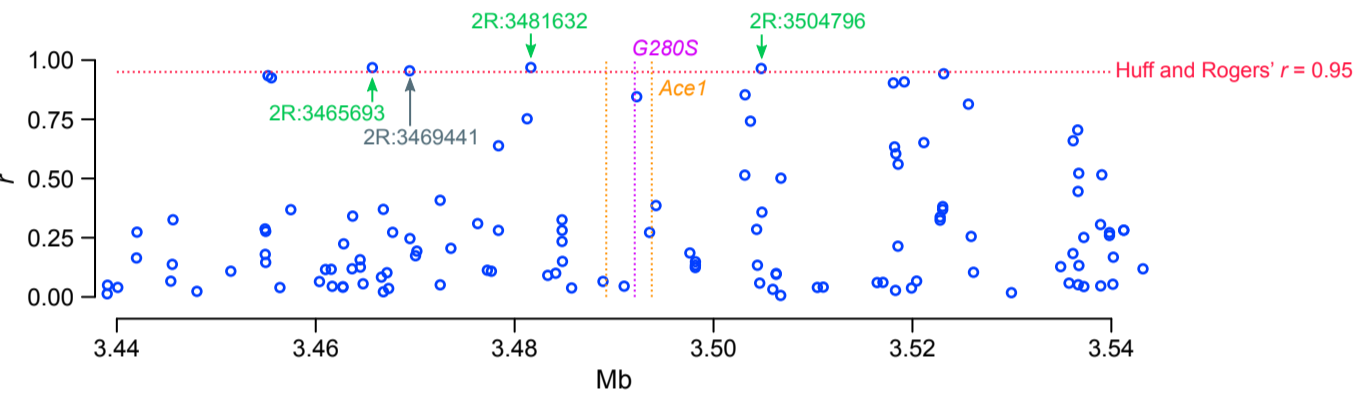
A) Density of phased variants around *Ace1* duplication region



B) Density of phased variants within *Ace1* duplication region

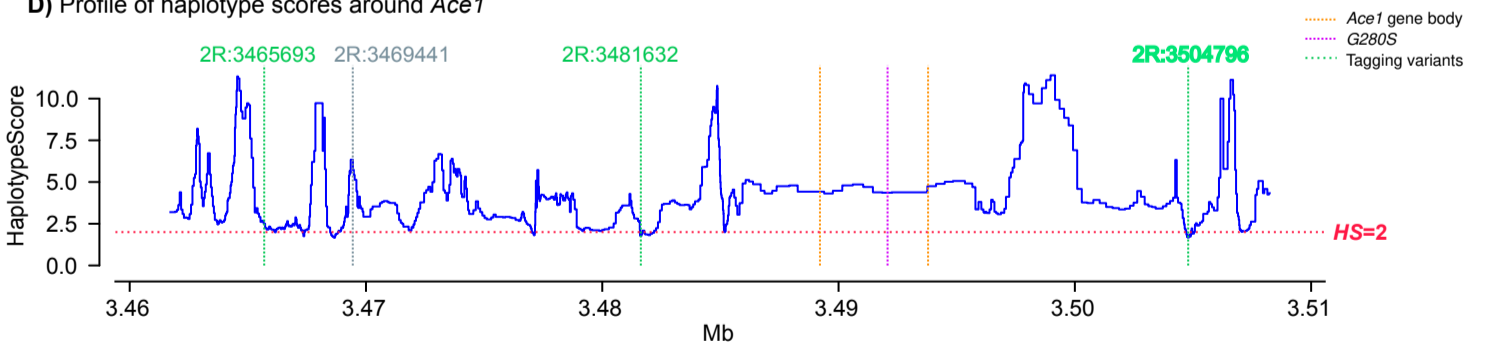


C) Linkage disequilibrium between *GG280S* and nearby phased variants

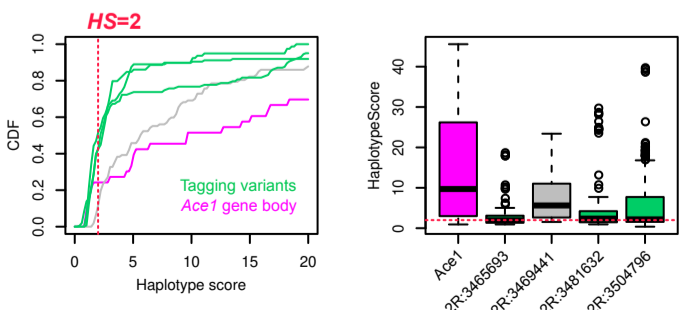


chrom	pos	LD with G280S	Freq C col	Phased?
2R	3444618	0.97264516	0.4366	0
2R	3445910	0.9504605	0.4366	0
2R	3447556	0.96361303	0.4366	0
2R	3456166	0.9675373	0.4366	0
2R	3456937	0.97637683	0.4366	0
2R	3459582	0.9591772	0.4366	0
2R	3464705	0.96810204	0.4366	0
2R	3465693	0.96810204	0.4366	1 ***
2R	3466268	0.9719312	0.4366	0
2R	3469441	0.95479333	0.4366	1
2R	3469672	0.96308875	0.4366	0
2R	3475119	0.9658597	0.4366	0
2R	3477809	0.98811066	0.4366	0
2R	3478595	1.0	0.4366	0
2R	3479474	0.98421353	0.4366	0
2R	3480330	1.0	0.4366	0
2R	3480406	0.98421353	0.4366	0
2R	3481632	0.96864766	0.4295	1 ***
2R	3482092	0.9716037	0.4154	0
2R	3483376	0.99236995	0.4366	0
2R	3483539	1.0	0.4366	0
2R	3486607	0.9959919	0.4366	0
2R	3487859	1.0	0.4366	0
2R	3496635	0.98388374	0.4366	0
2R	3498622	0.96866876	0.4366	0
2R	3498740	0.97213244	0.4366	0
2R	3504796	0.96453327	0.4436	1 ***
2R	3507961	0.97605	0.4507	0

D) Profile of haplotype scores around *Ace1*



E) Haplotype score in *Ace1* and the tagging variants (± 300 bp)



F) Sequencing depth in *Ace1* and the tagging variants (across samples)

