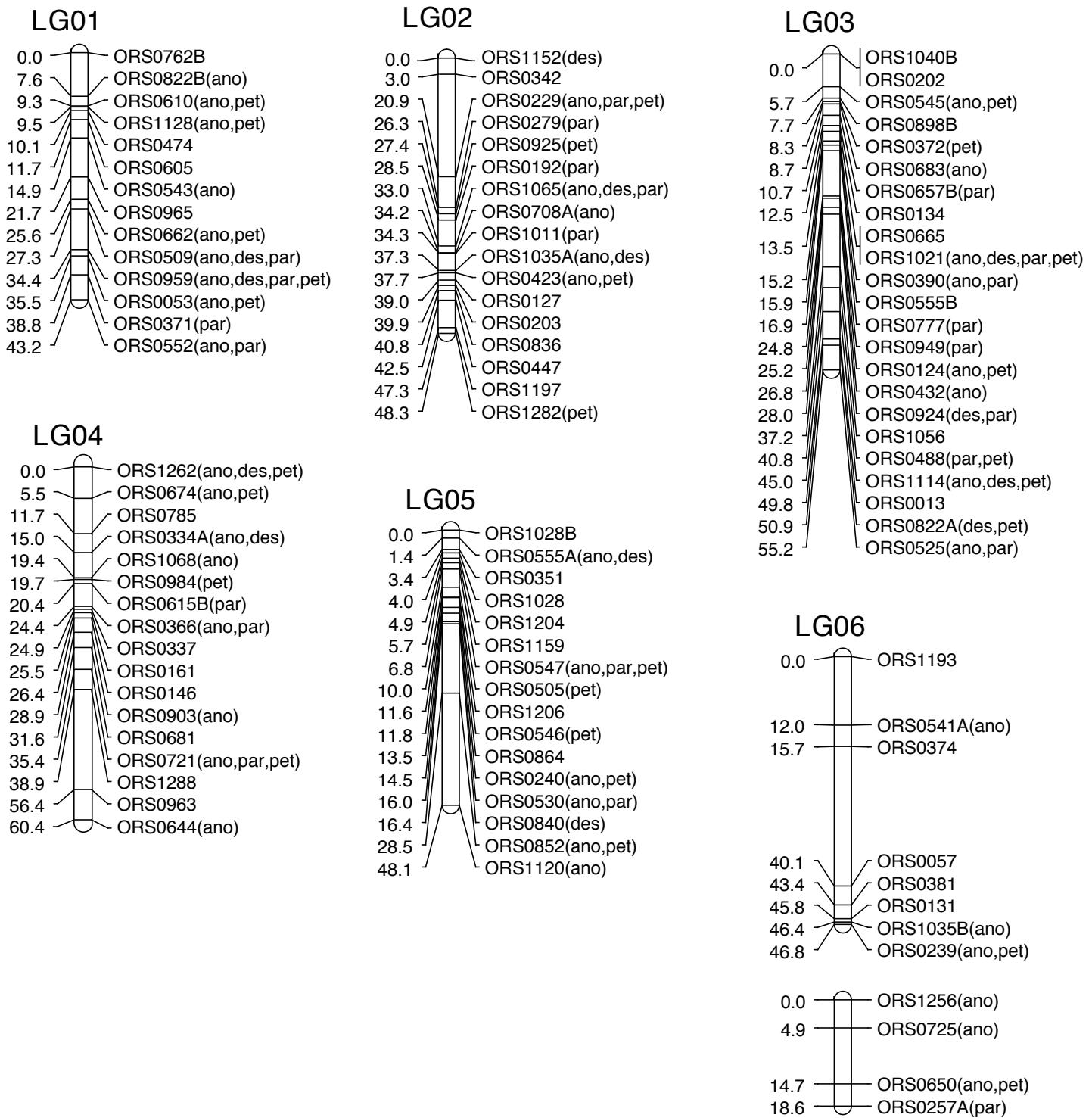
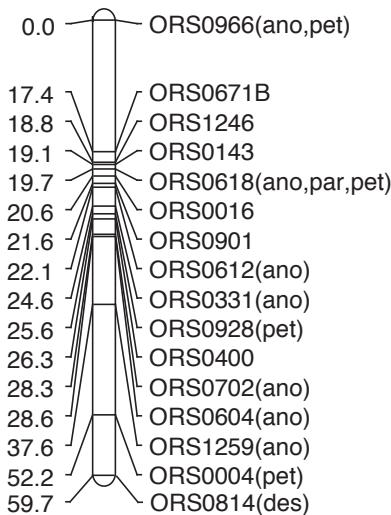
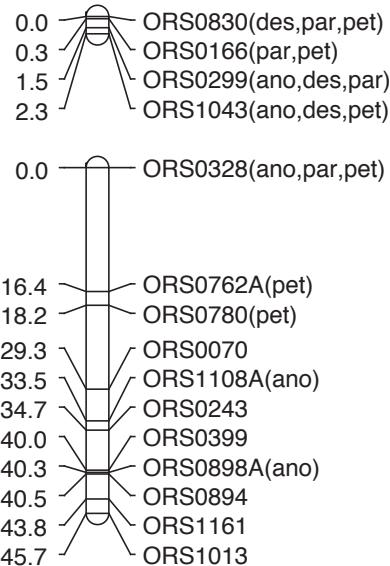
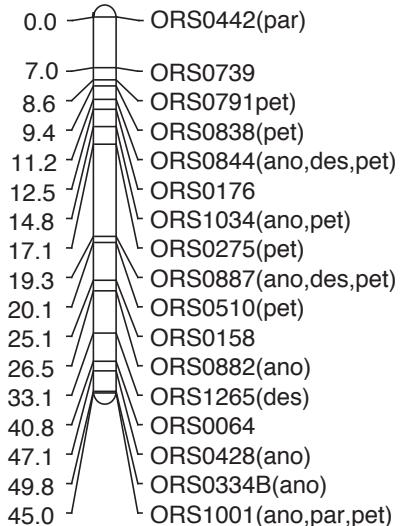
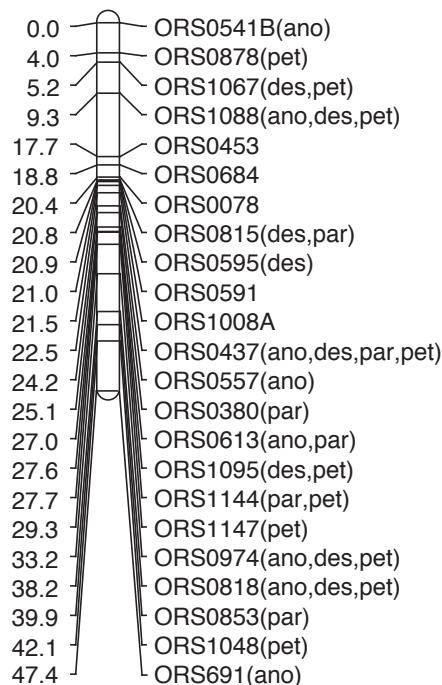
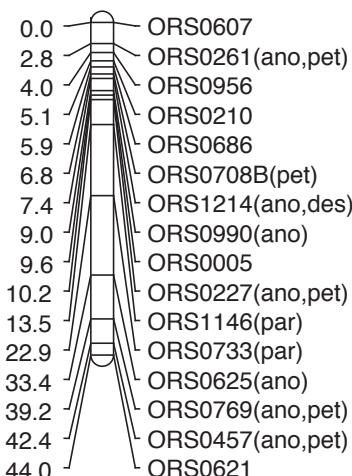
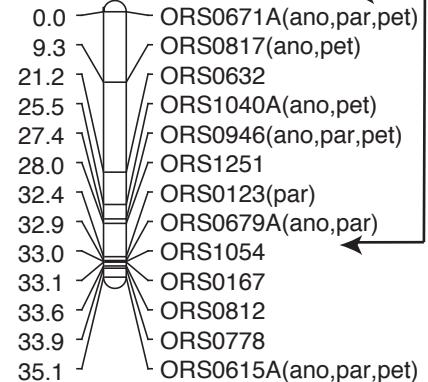
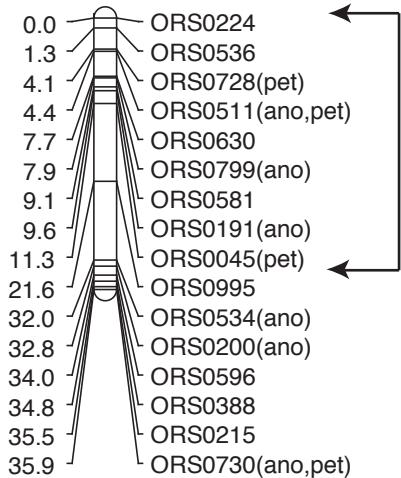
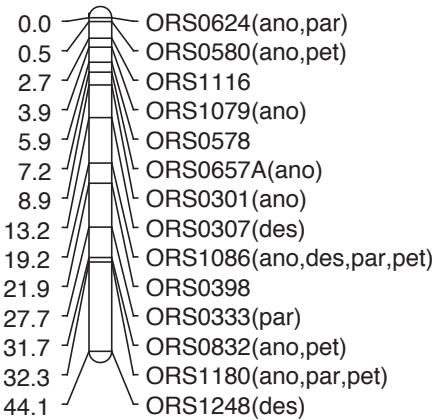
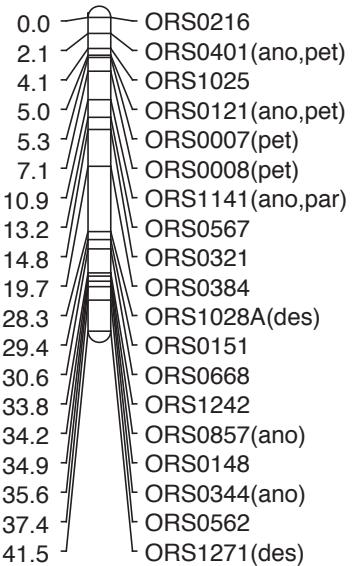
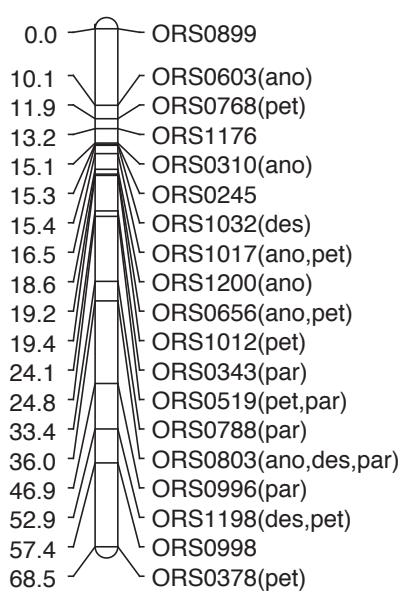
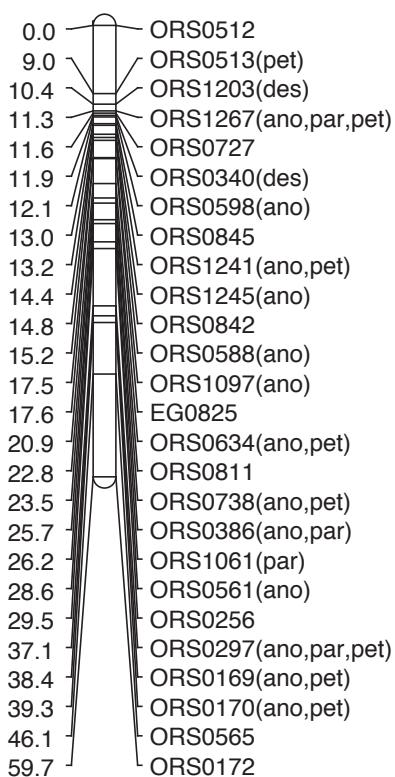


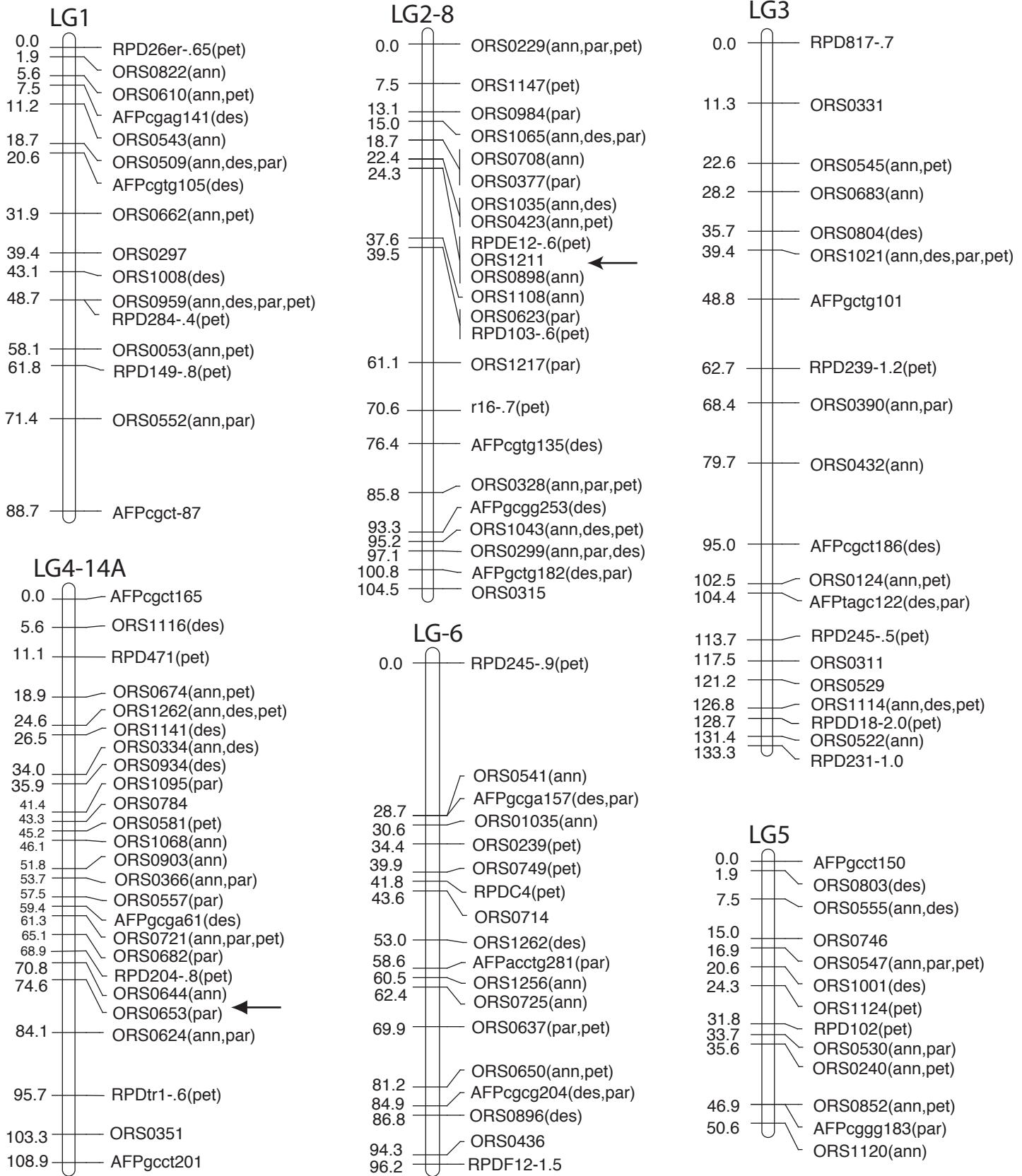
**Figure1S (Supplementary Information. Genetic map of *H. annuus*.** All markers are simple sequence repeats (SSRs). Markers followed by species names in parentheses (ano = *anomalus*, des = *deserticola*, par = *paradoxus*, and pet = *petiolaris*) are informative and map to the same linkage group in the listed species. Numbers to the left of each linkage group refer to genetic distance (cM). Double/bracketed arrows indicate the location of inferred chromosomal inversions that appear to be unique to *H. annuus*.

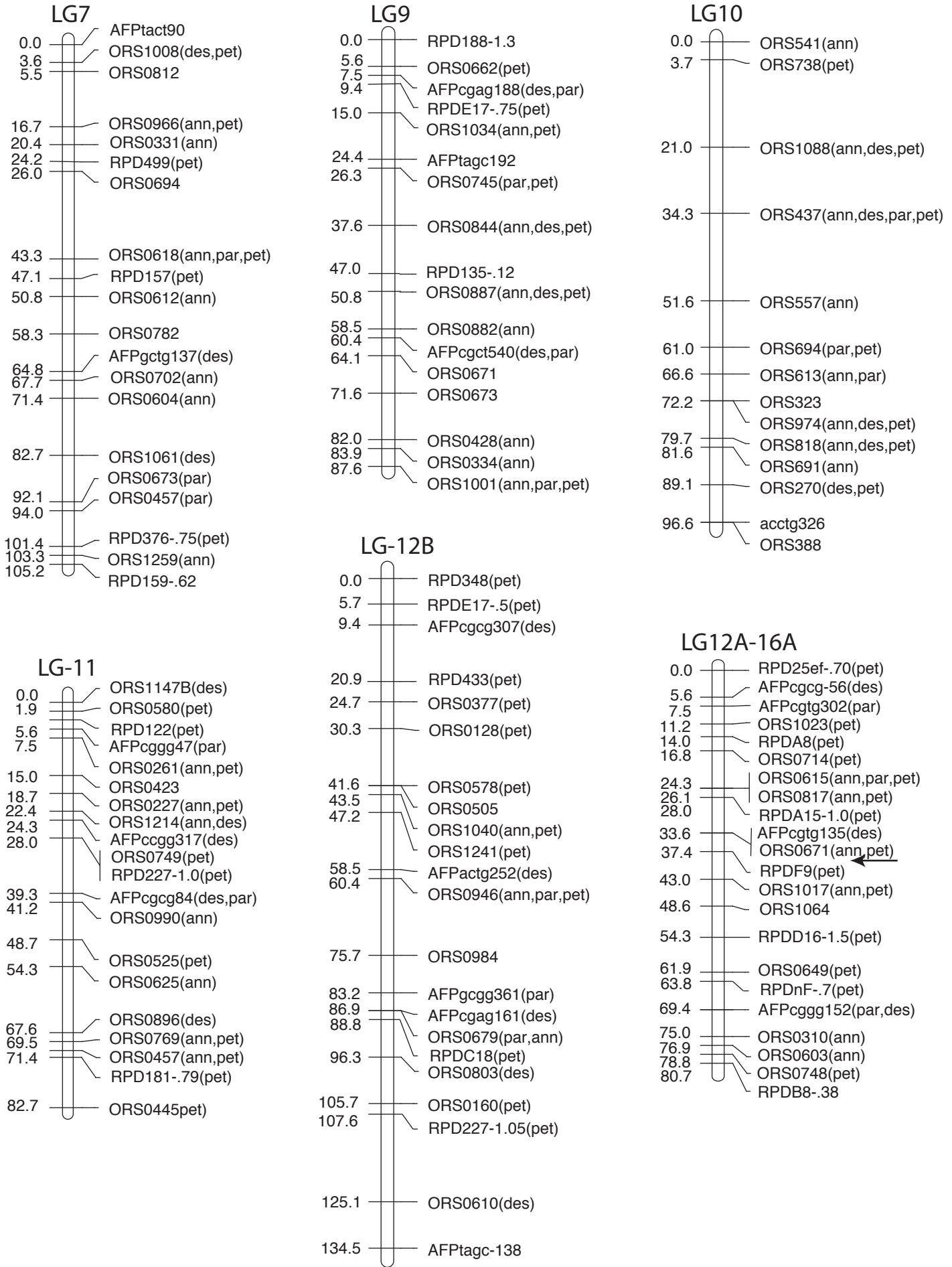


**LG07****LG08****LG09****LG10****LG11****LG12**

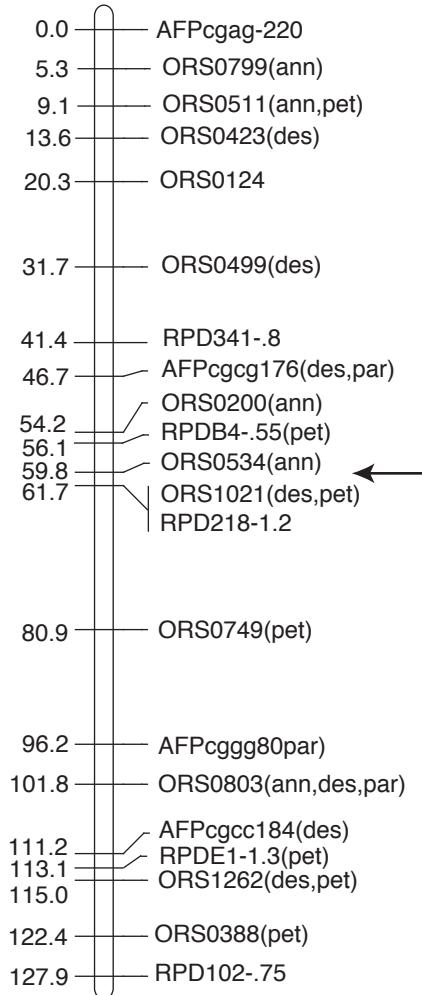
**LG13****LG14****LG15****LG16****LG17**

**Figure 2S (Supplementary Information. Genetic map of *H. anomalous*.** Markers beginning with ORS are simple sequence repeats (SSRs), those beginning with AFP are AFLPs, and those beginning with RPD are RAPDs. Markers followed by species names in parentheses (ann = *annuus*, des = *deserticola*, par = *paradoxus*, and pet = *petiolaris*) are informative and map to the same linkage group in the listed species. Numbers to the left of each linkage group refer to genetic distance (cM). Single arrows indicate the location of inferred chromosomal breakages/fusions that are necessary to account for the account for differences between this map and that of *H. annuus* (Figure 1S). Letters (A,B,C) following some linkage groups indicate fragmented linkage groups, with fragments homologous to the top of the *H. annuus* linkage group designated "A", the next highest fragment labeled "B", and so forth.

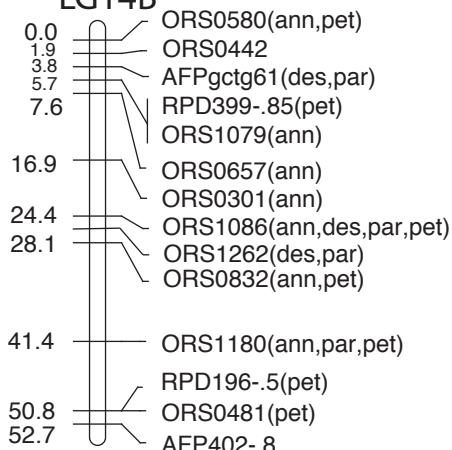




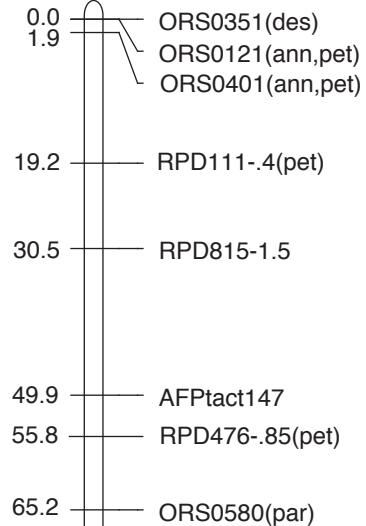
### LG13A-16C



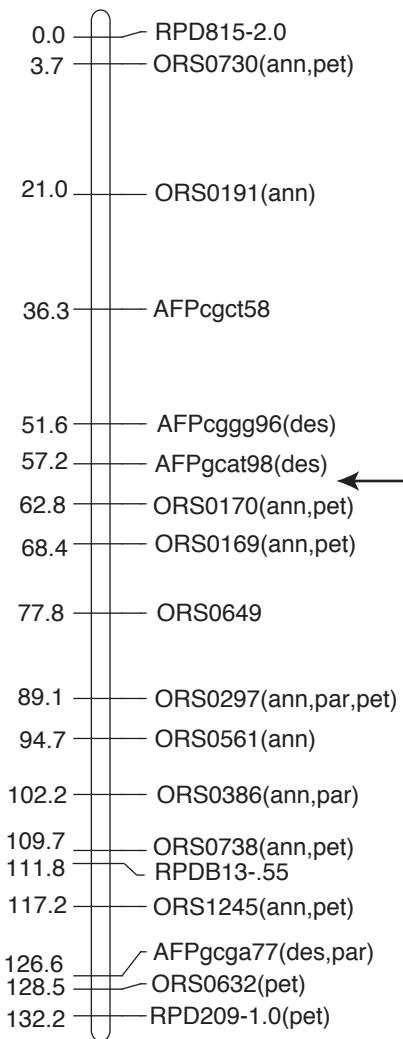
### LG14B



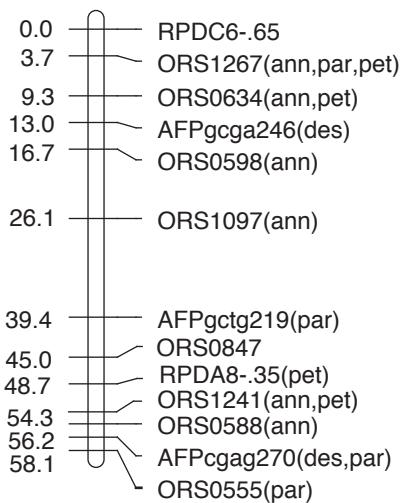
### LG15-16B



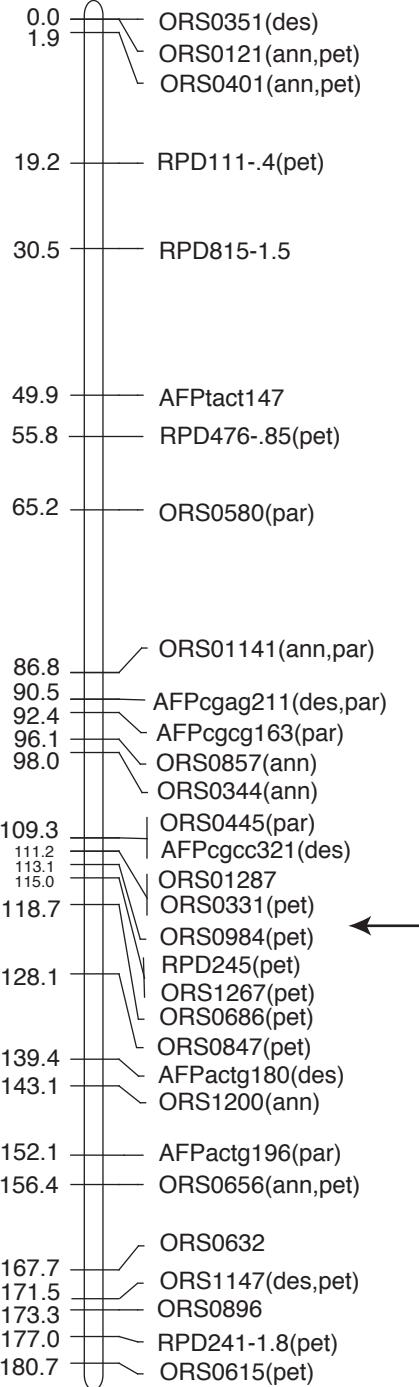
### LG13B-17B



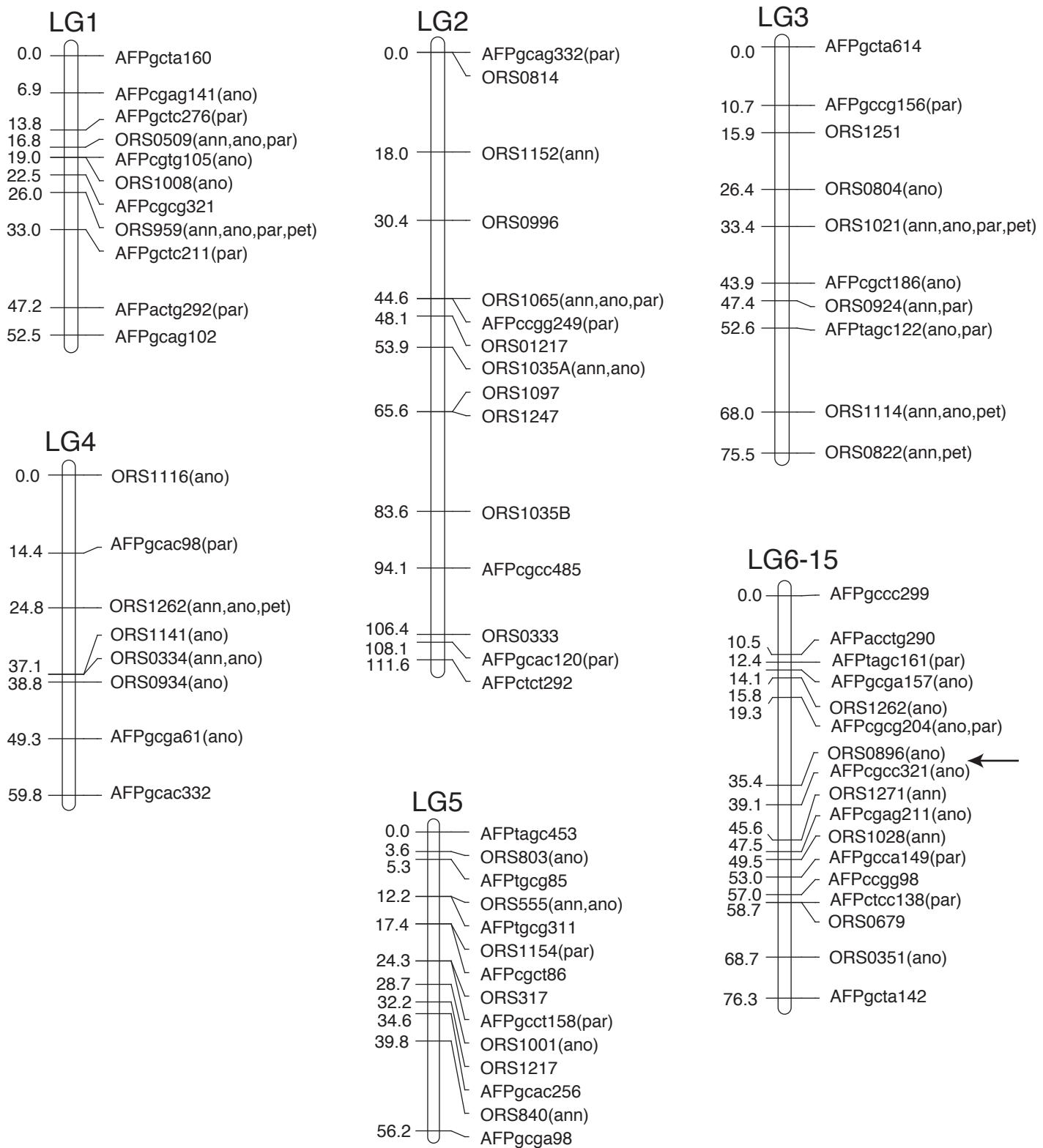
### LG-17A

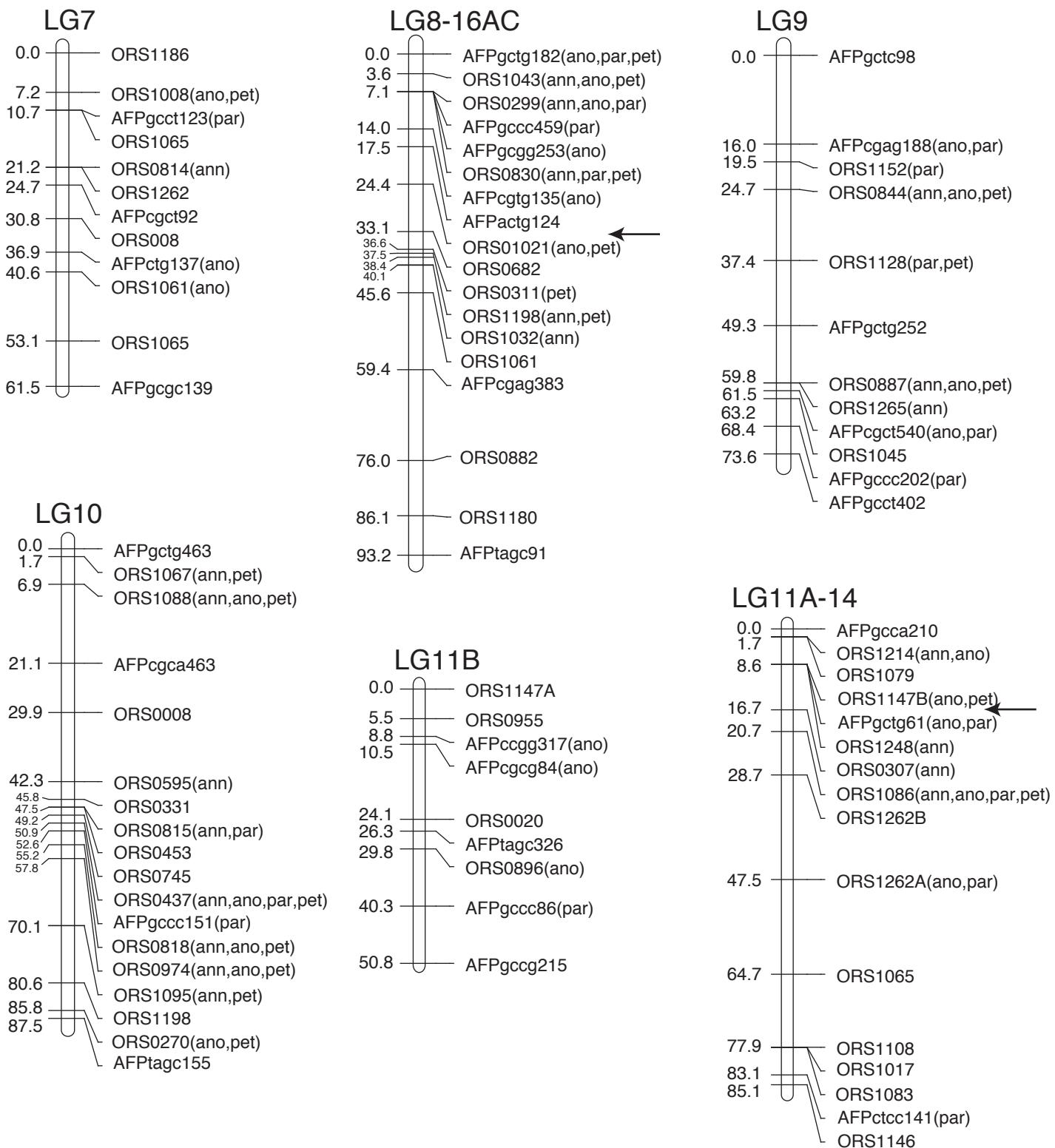


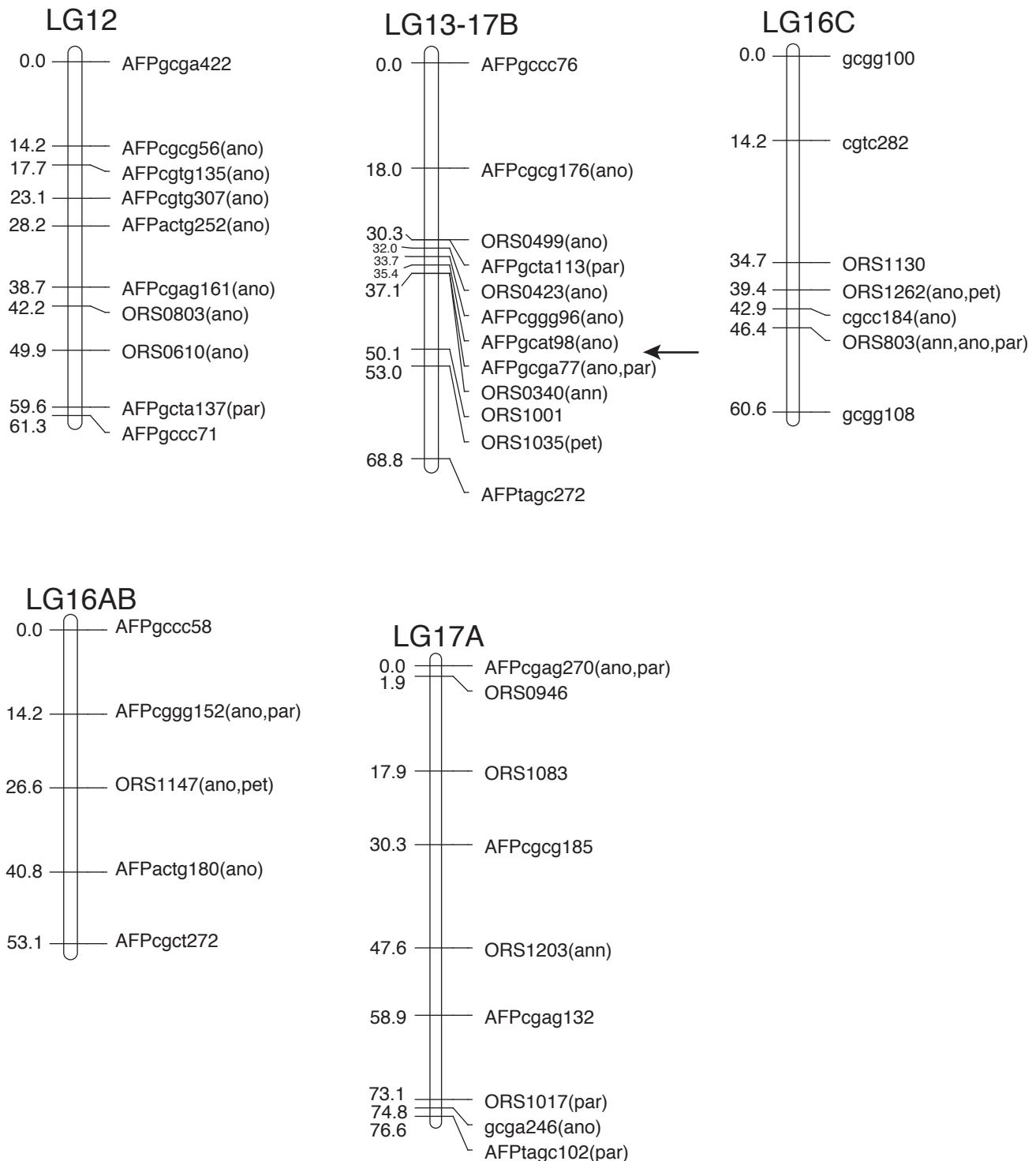
### LG15-16B



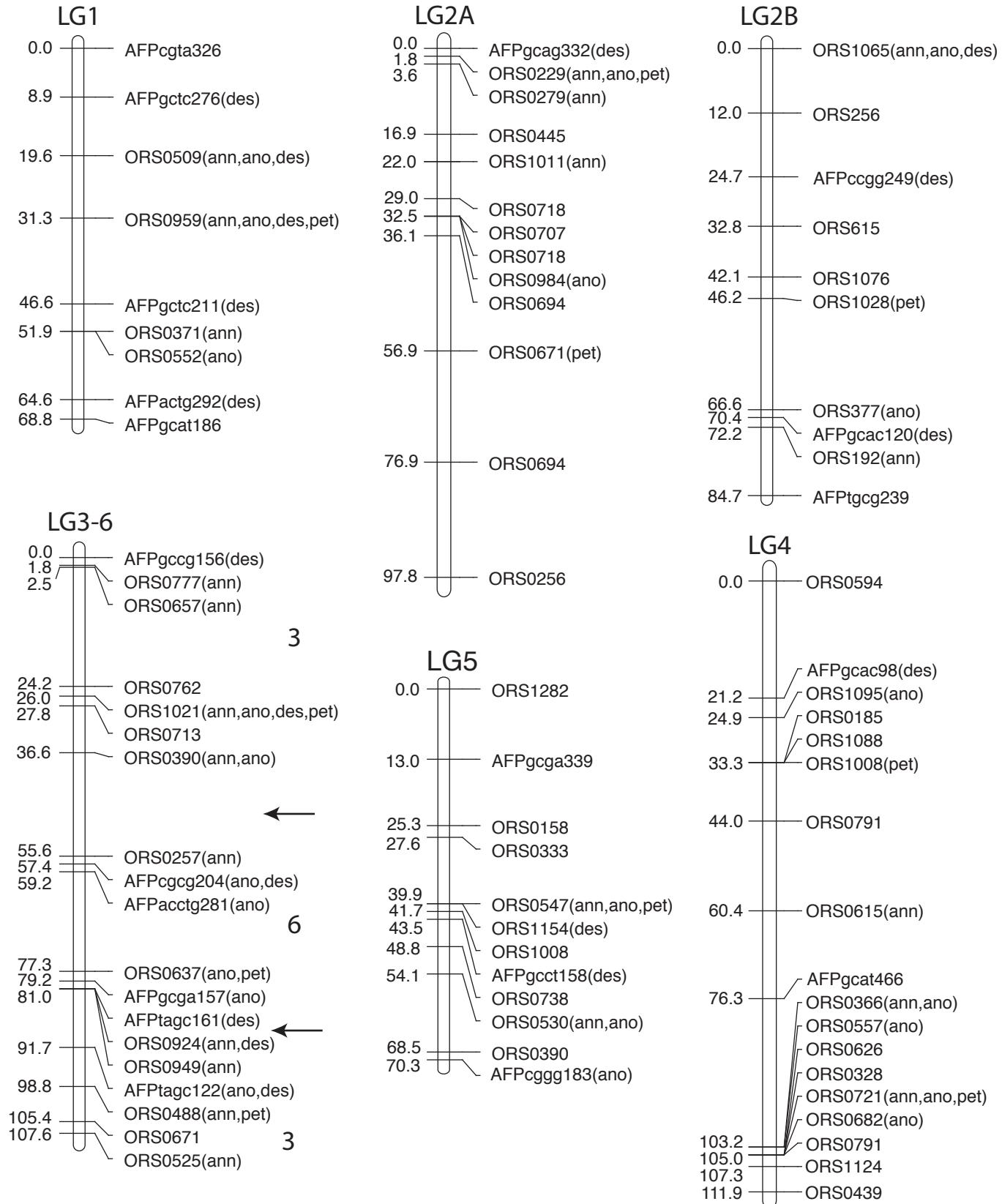
**Figure 3S (Supplementary Information. Genetic map of *H. deserticola*.** Markers beginning with ORS are simple sequence repeats (SSRs), those beginning with AFP are AFLPs, and those beginning with RPD are RAPDs. Markers followed by species names in parentheses (ann = *annuus*, ano = *anomalus*, par = *paradoxus*, and pet = *petiolaris*) are informative and map to the same linkage group in the listed species. Numbers to the left of each linkage group refer to genetic distance (cM). Single arrows indicate the location of inferred chromosomal breakages/fusions that are necessary to account for the account for differences between this map and that of *H. annuus* (Figure 1S). Letters (A,B,C) following some linkage groups indicate fragmented linkage groups, with fragments homologous to the top of the *H. annuus* linkage group designated "A", the next highest fragment labeled "B", and so forth.

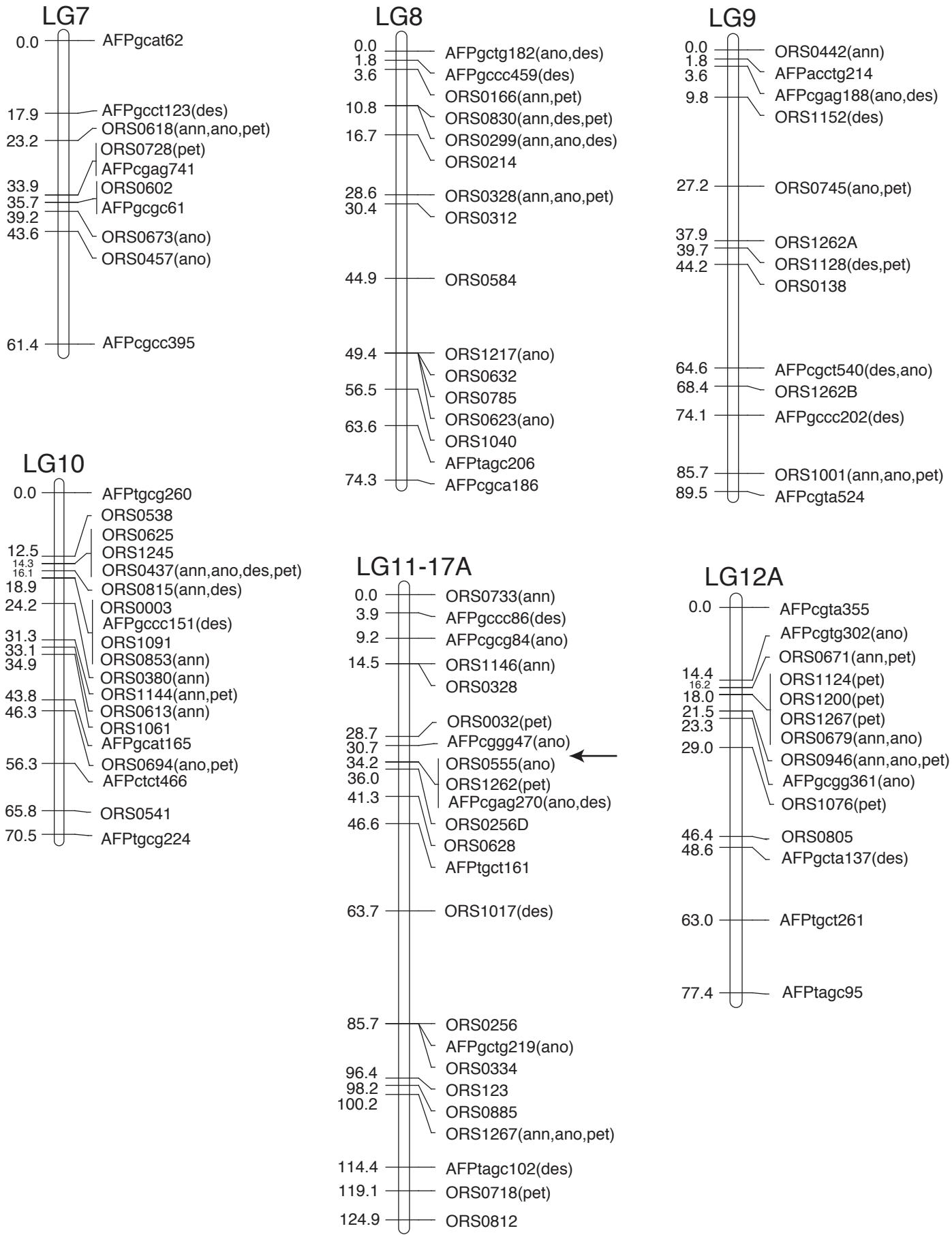


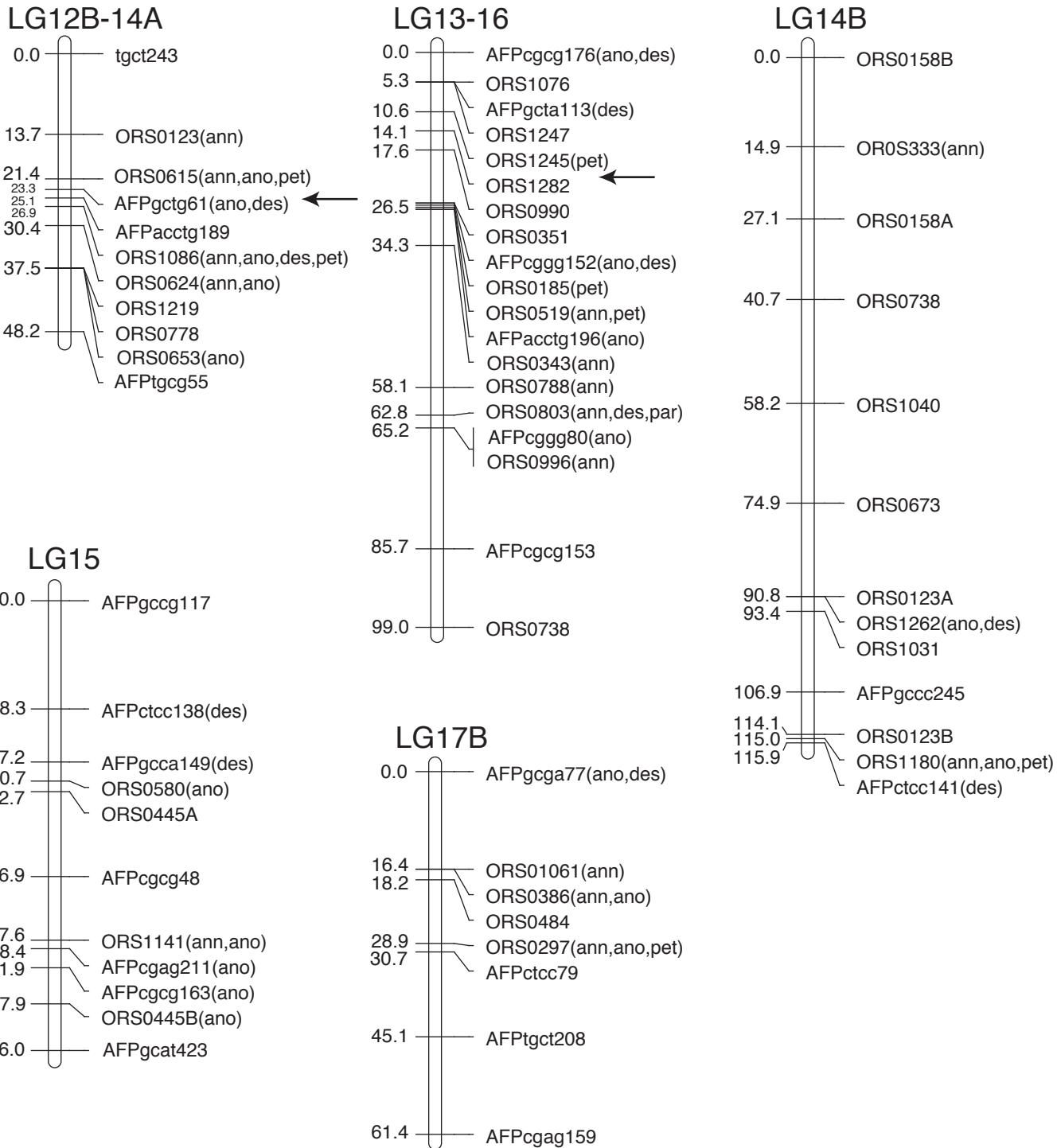




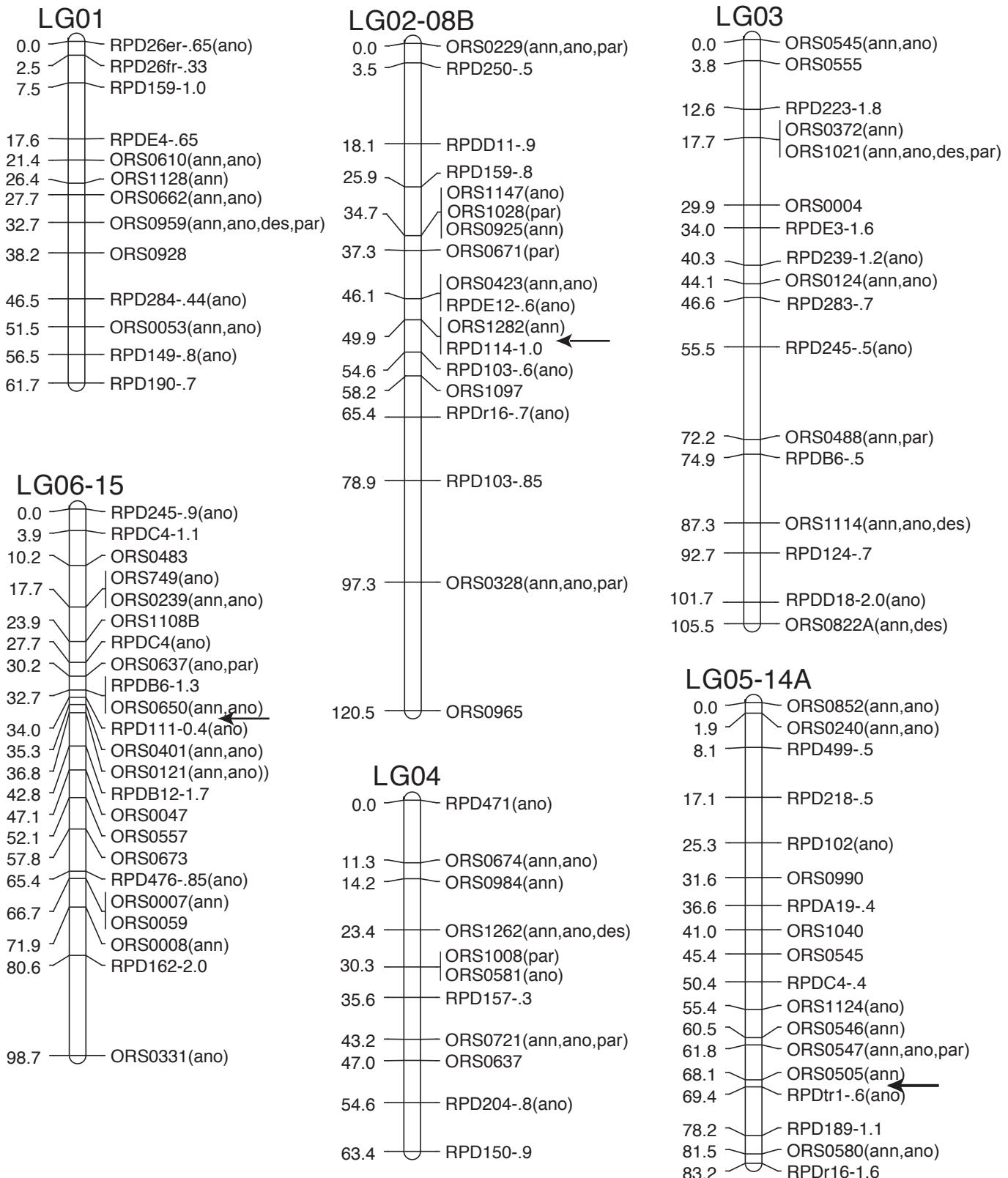
**Figure 4S (Supplementary Information. Genetic map of *H. paradoxus*.** Markers beginning with ORS are simple sequence repeats (SSRs), those beginning with AFP are AFLPs, and those beginning with RPD are RAPDs. Markers followed by species names in parentheses (ann = *annuus*, des = *deserticola*, par = *paradoxus*, and pet = *petiolaris*) are informative and map to the same linkage group in the listed species. Numbers to the left of each linkage group refer to genetic distance (cM). Single arrows indicate the location of inferred chromosomal breakages/fusions that are necessary to account for the account for differences between this map and that of *H. annuus* (Figure 1S). Letters (A,B,C) following some linkage groups indicate fragmented linkage groups, with fragments homologous to the top of the *H. annuus* linkage group designated "A", the next highest fragment labeled "B", and so forth.

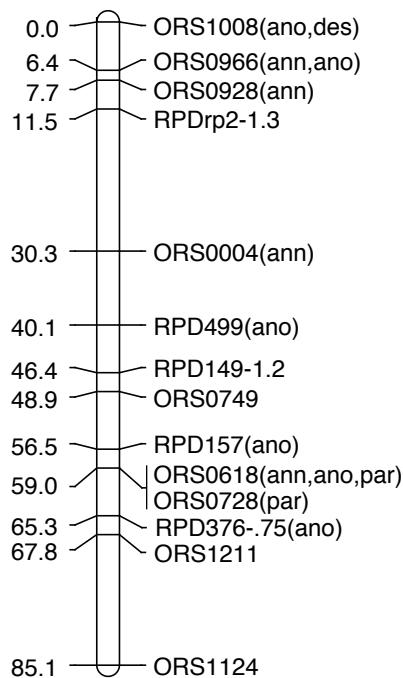
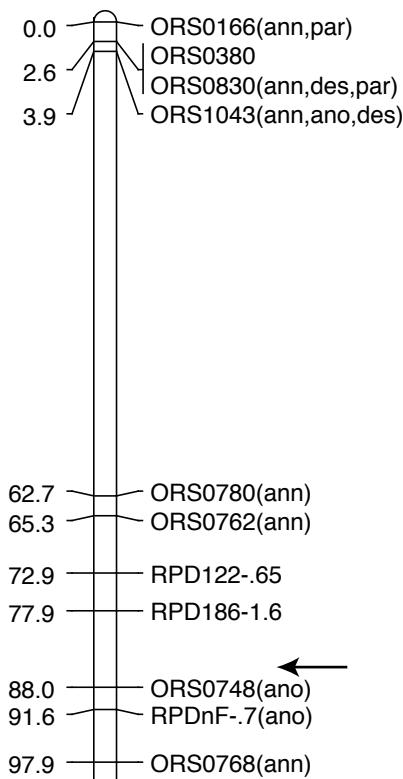
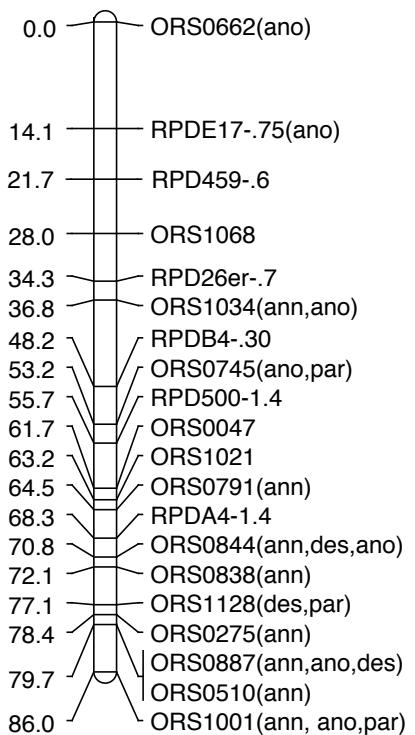
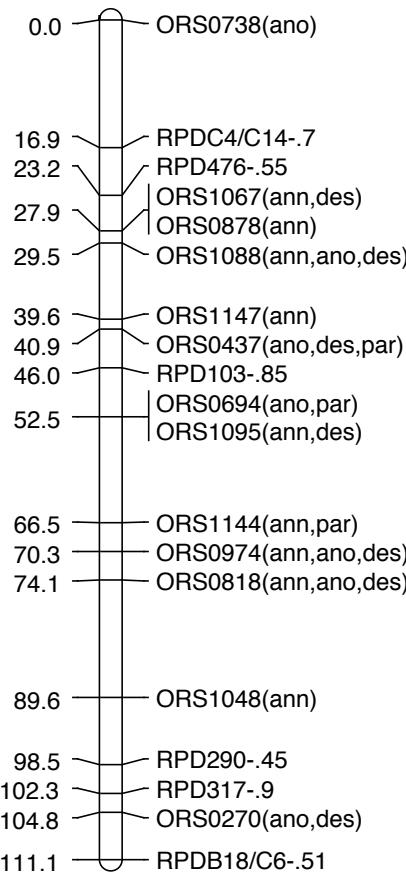
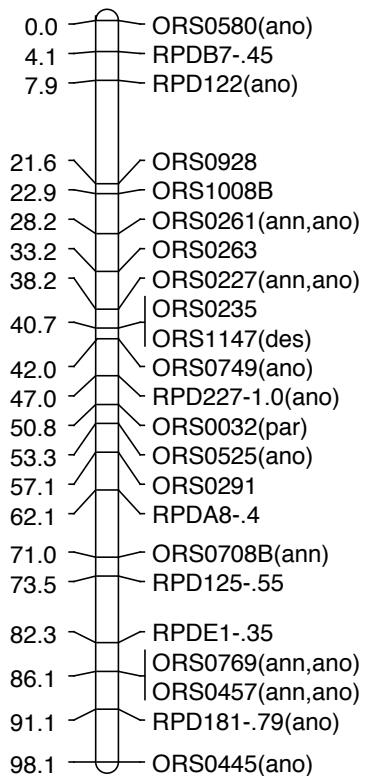




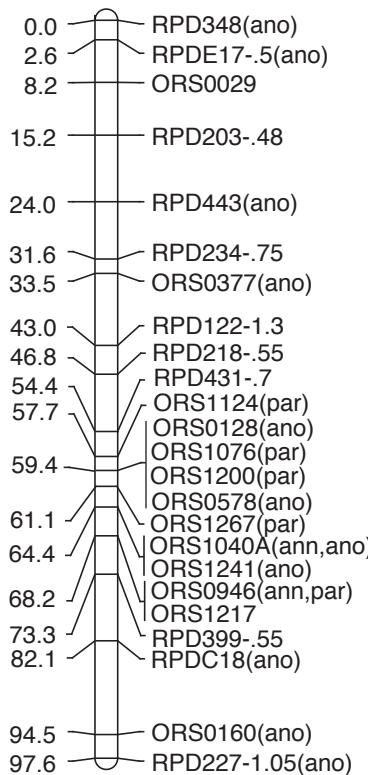


**Figure 5S (Supplementary Information. Genetic map of *H. petiolaris*.** Markers beginning with ORS are simple sequence repeats (SSRs), those beginning with AFP are AFLPs, and those beginning with RPD are RAPDs. Markers followed by species names in parentheses (ann = *annuus*, ano = *anomalus*, par = *paradoxus*, and pet = *petiolaris*) are informative and map to the same linkage group in the listed species. Numbers to the left of each linkage group refer to genetic distance (cM). Single arrows indicate the location of inferred chromosomal breakages/fusions that are necessary to account for the account for differences between this map and that of *H. annuus* (Figure 1S). Double/bracketed arrows indicate the location of inferred chromosomal inversions that appear to be unique to *H. petiolaris*. Letters (A,B,C) following some linkage groups indicate fragmented linkage groups, with fragments homologous to the top of the *H. annuus* linkage group designated "A", the next highest fragment labeled "B", and so forth.

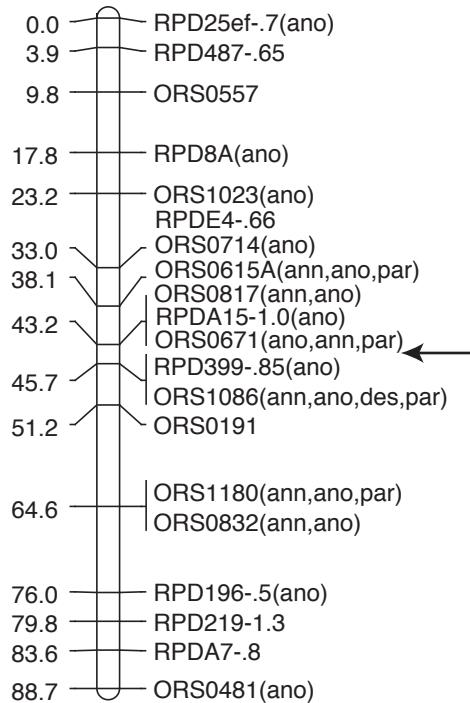


**LG07****LG08A-16A****LG09****LG10****LG11**

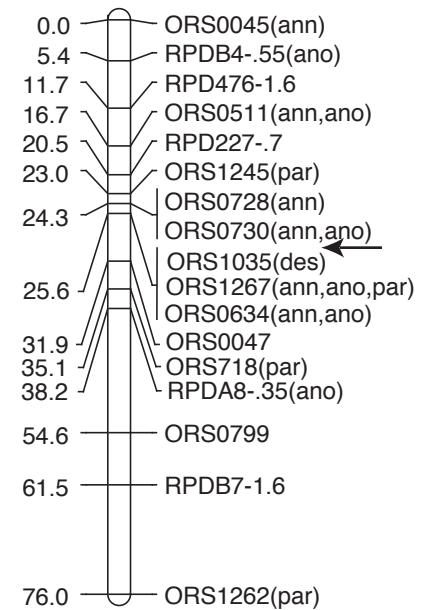
### LG12B



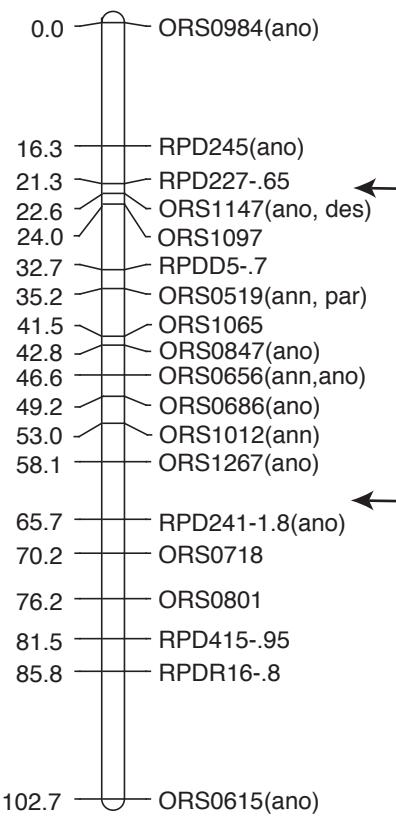
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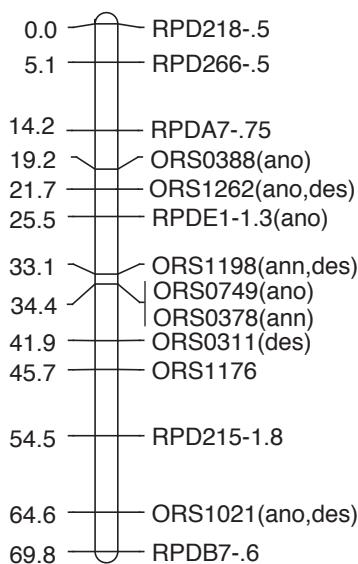
### LG13-17AB



### LG16B



### LG16C



### LG17AB