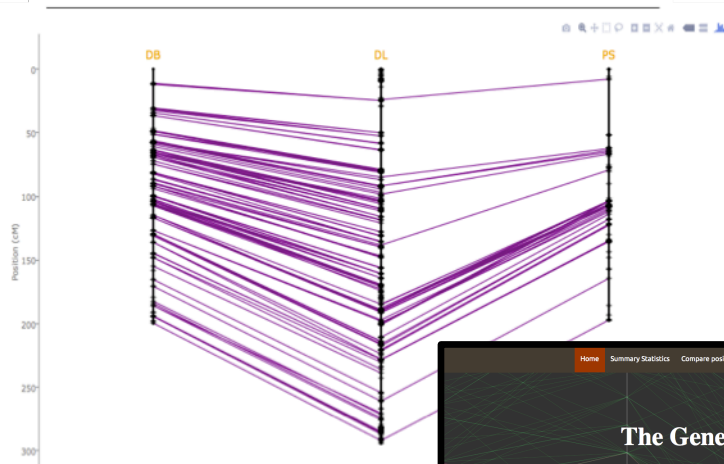
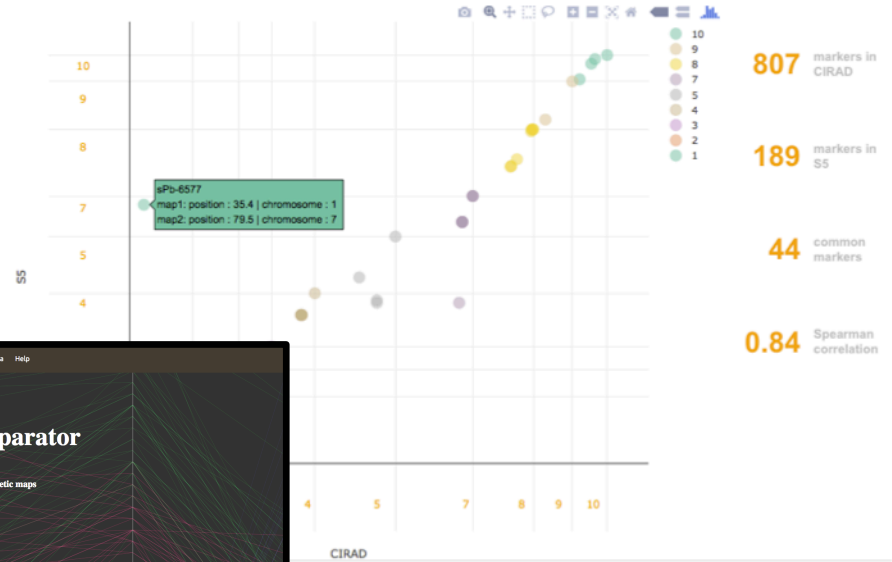


- Comparison of marker positions -



- Interchromosomal Analysis -



- Key statistics

Here you can compare various maps through five key statistics:

1. their number of genetic markers,
2. their overall size (in cM),
3. size of their biggest gap (cM) and the number of unique positions.

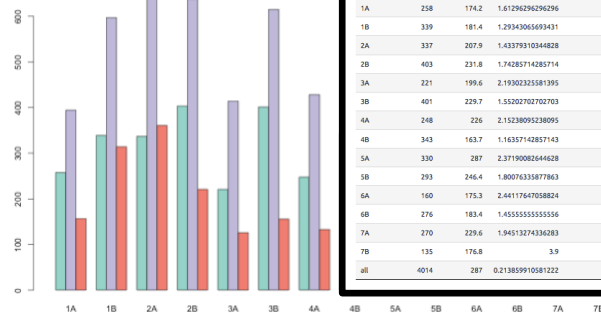
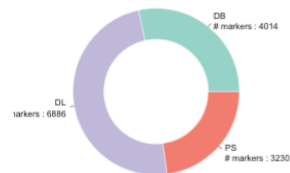
The donut plot (on the left) summarizes the selected statistics for every chromosome.

Select some maps:

☒ DB ☒ DL ☒ PS

Select one feature:

- ☒ # markers
- ☐ map size
- ☐ average gap size
- ☐ biggest gap size
- ☐ # unique positions



Chr.	#markers	map_size	average_gap_size	biggest_gap_size	#unique_positions
1A	258	174.2	1.61296296296296	22.5	109
1B	339	181.4	1.29343065693431	11.9	138
2A	337	207.9	1.43379310344828	19.2	146
2B	403	231.8	1.74283714285714	13.5	134
3A	221	199.6	2.1930232581395	18.5	87
3B	401	223.7	1.55202702702703	16.4	149
4A	248	226	2.15238095238095	41.3	106
4B	343	163.7	1.16357142857143	20.1	141
5A	330	287	2.37190082444628	16.1	122
5B	293	246.4	1.80074335877863	21.7	132
6A	160	175.3	2.44117647058824	13	69
6B	276	183.4	1.45555555555556	36.4	127
7A	270	229.6	1.94513274336283	20.1	114
7B	135	176.8	3.9	24.1	45
all	4014	287	0.213859910581222	14.6	1619

- Marker density

Here is a description of marker density along chromosomes. This figure allows to visualize chromosome lengths variation among maps, and to identified regions with unusually low/high genetic marker density.

Select some chromosomes:

☒ 1 ☒ 2 ☒ 3 ☒ 4 ☒ 5 ☒ 6 ☒ 7 ☒ 8 ☒ 9 ☒ 10 ☒ 9.1 ☒ 9.2

