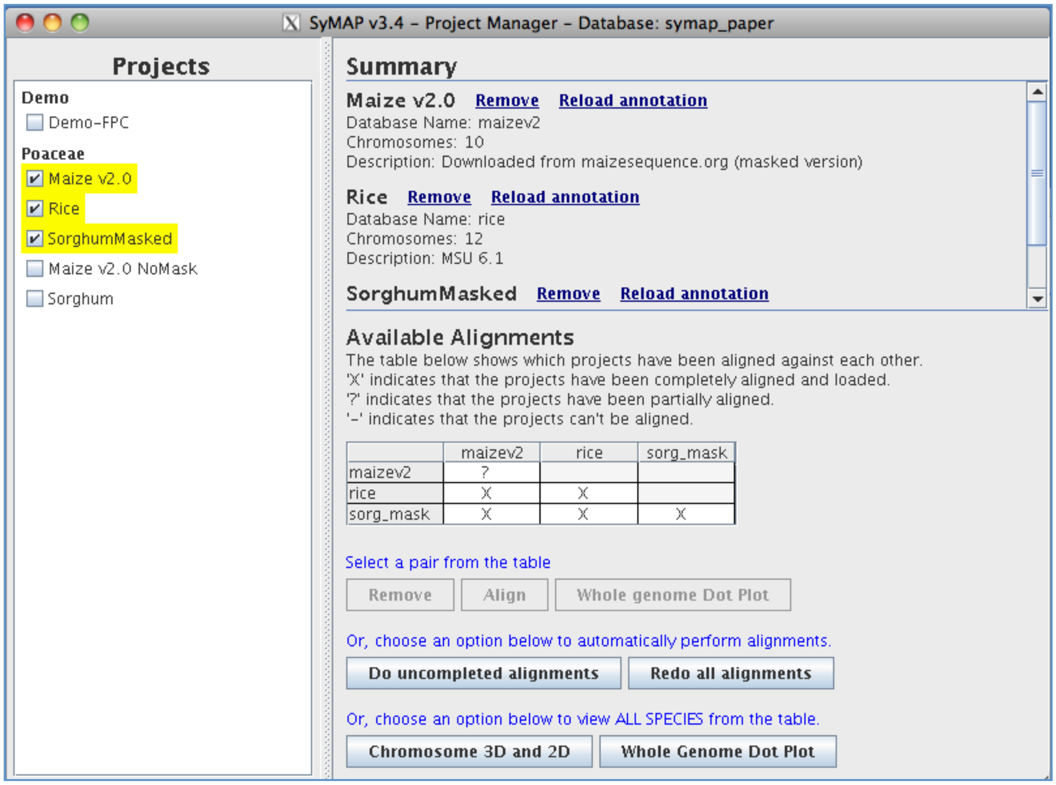
Additional material for SyMAP v3.4: Figures S1-S3



Projects

Demo

☐ Demo-FPC

Poaceae

☑ Maize v2.0

☑ Rice

☑ SorghumMasked

☐ Maize v2.0 NoMask

☐ Sorghum

Summary

Maize v2.0 Remove Reload annotation

Database Name: maizev2
Chromosomes: 10
Description: Downloaded from maizesequence.org (masked version)

Rice Remove Reload annotation

Database Name: rice
Chromosomes: 12
Description: MSU 6.1

SorghumMasked Remove Reload annotation

Available Alignments

The table below shows which projects have been aligned against each other.
'X' indicates that the projects have been completely aligned and loaded.
'?' indicates that the projects have been partially aligned.
'–' indicates that the projects can't be aligned.

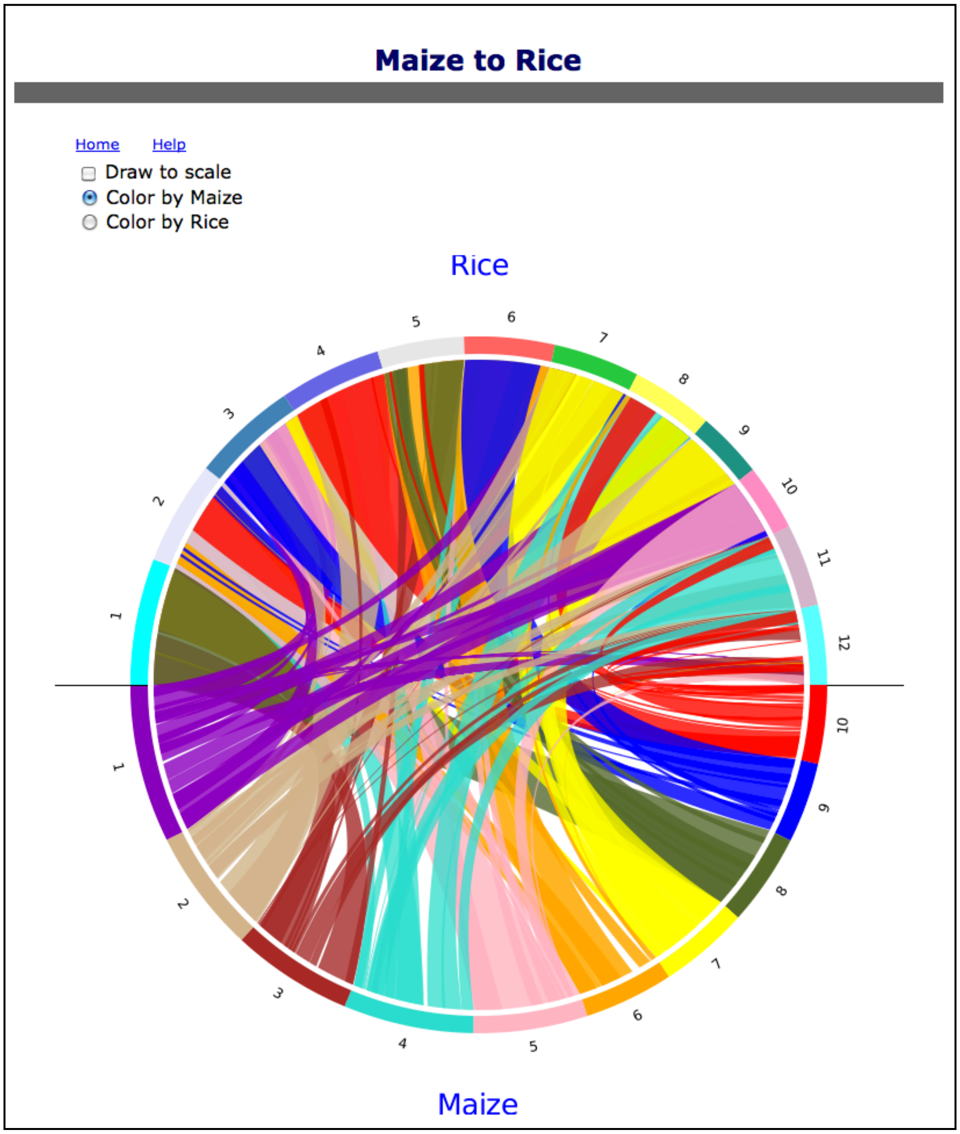
	maizev2	rice	sorg_mask
maizev2	?		
rice	X	X	
sorg_mask	X	X	X

Select a pair from the table

Or, choose an option below to automatically perform alignments.

Or, choose an option below to view ALL SPECIES from the table.

Figure S1: The SyMAP project manager. The ‘X’ in each cell of the matrix indicates that the genome pair have been aligned. Selecting a cell allows the pair to be removed, re-aligned or displayed. Selecting the “3D” or “Dot Plot” shows all projects in the respective view. If there is not an ‘X’ in a cell, it can be selected to be aligned.

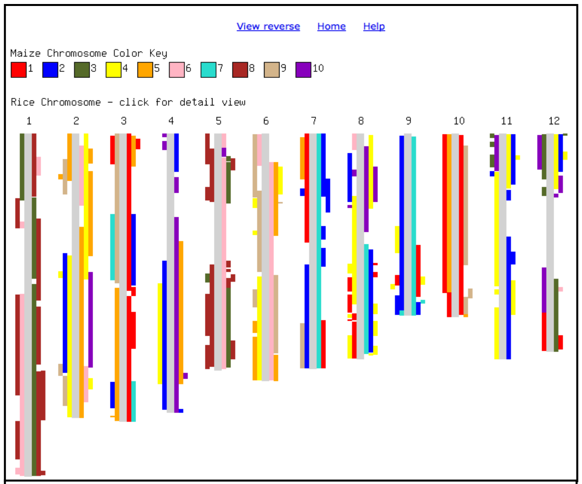


Maize to Rice

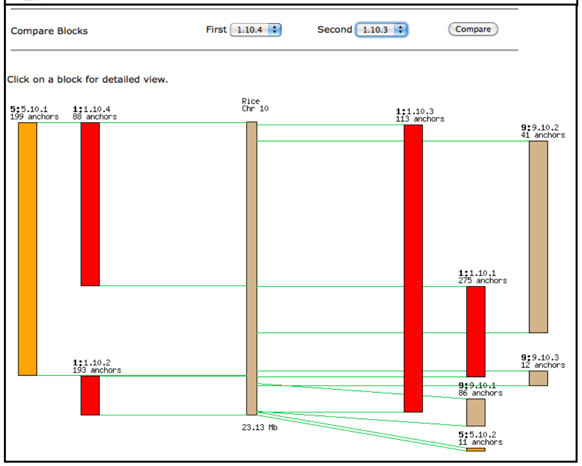
Home Help

☐ Draw to scale
● Color by Maize
○ Color by Rice

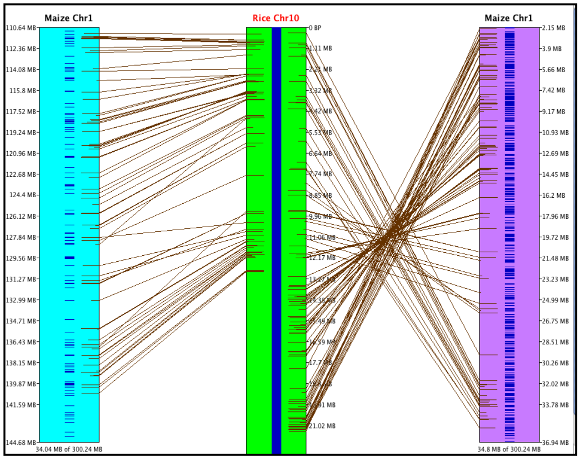
Figure S2. SyMAP Perl/CGI views. (A) Whole genome circle view



Block view of two genomes. This shows the alignment of all the maize blocks to the rice chromosomes.

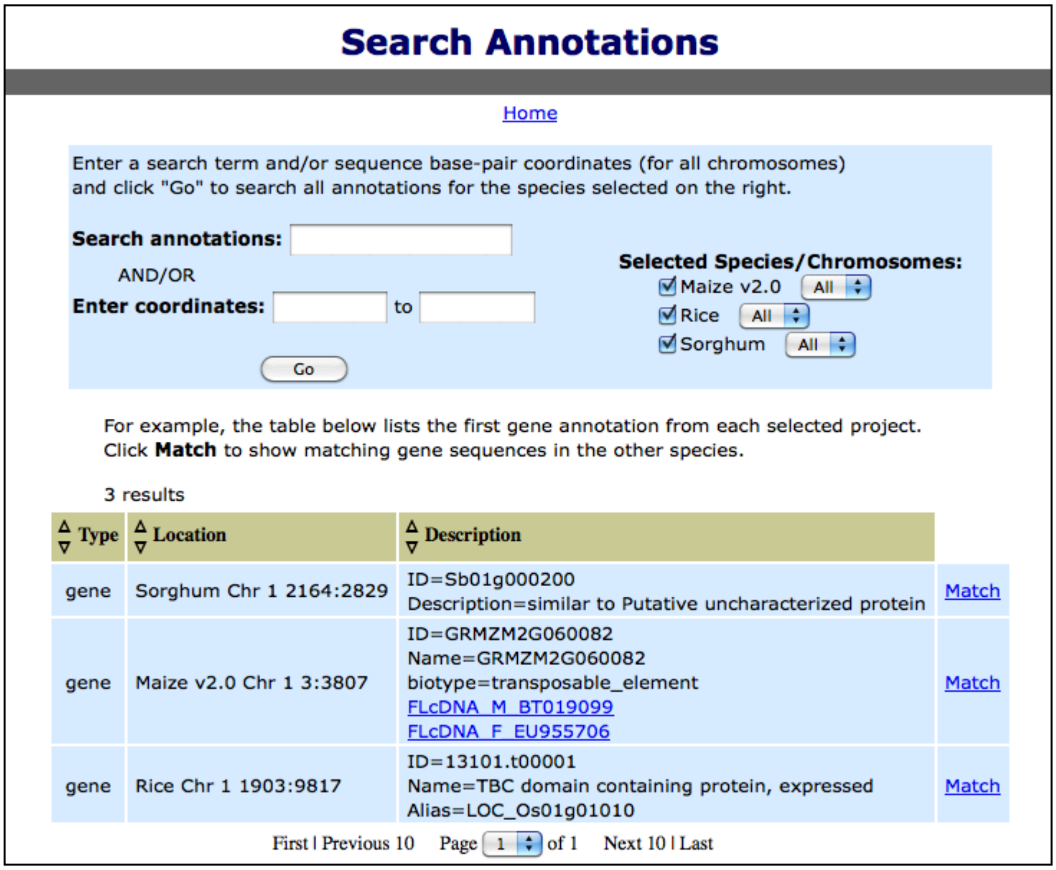


Block view for a chromosome. Rice-10 was selected from the above view, which displays this close-up of the blocks.



Java 2D of duplicated regions on the same chromosome. The blocks were selected from the above 'Compare', resulting in this view. The block on the left is from the lower part of maize-1 and the block on the right is from the top of maize-1.

(B) Block view and sub-views.



Enter a search term and/or sequence base-pair coordinates (for all chromosomes) and click "Go" to search all annotations for the species selected on the right.

Search annotations:

AND/OR

Enter coordinates: to

Selected Species/Chromosomes:

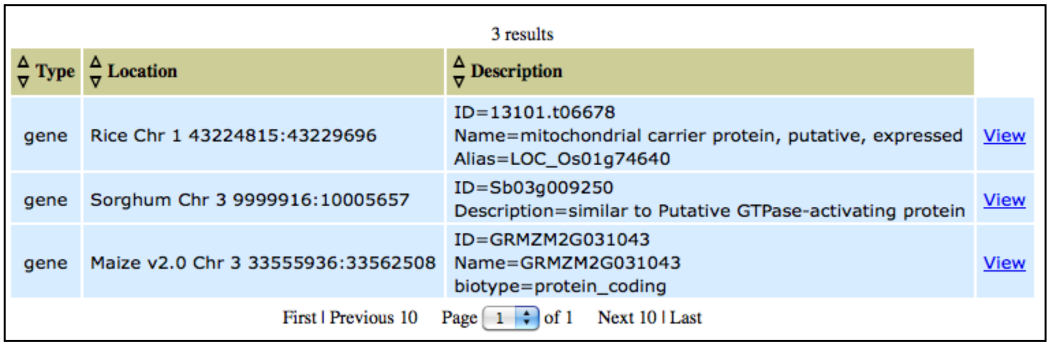
☑ Maize v2.0 All
☑ Rice All
☑ Sorghum All

For example, the table below lists the first gene annotation from each selected project.
Click **Match** to show matching gene sequences in the other species.

3 results

Type	Location	Description	
gene	Sorghum Chr 1 2164:2829	ID=Sb01g000200 Description=similar to Putative uncharacterized protein	Match
gene	Maize v2.0 Chr 1 3:3807	ID=GRMZM2G060082 Name=GRMZM2G060082 biotype=transposable_element FLcDNA_M_BT019099 FLcDNA_F_EU955706	Match
gene	Rice Chr 1 1903:9817	ID=13101.t00001 Name=TBC domain containing protein, expressed Alias=LOC_Os01g01010	Match

Search annotation and location. This searches all text from the attribute field of the GFF files; consequently, it is not dependent on which attributes have been set. Selecting 'Match' displays all (if any) anchors associated with the gene.

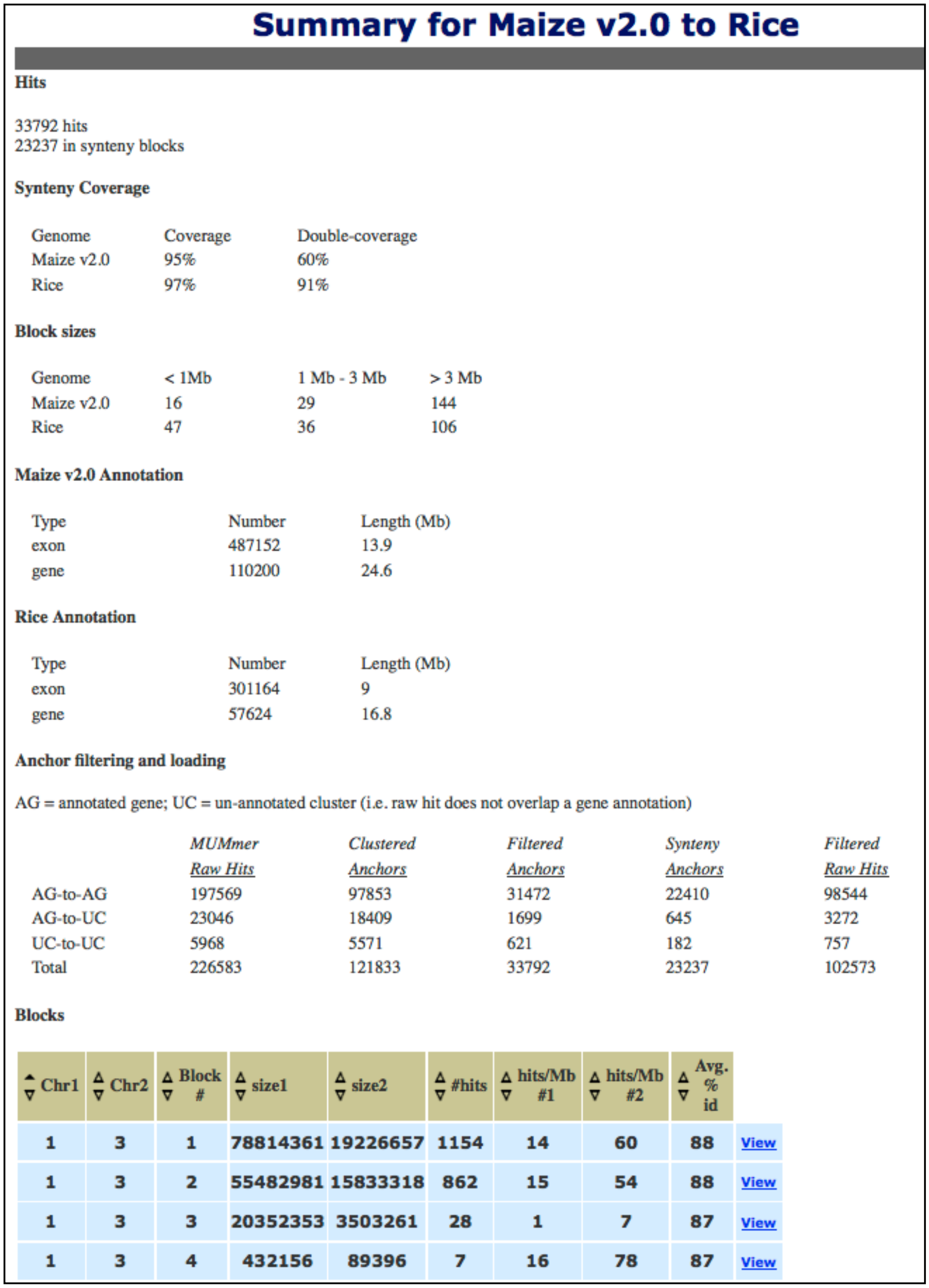


3 results

Type	Location	Description	
gene	Rice Chr 1 43224815:43229696	ID=13101.t06678 Name=mitochondrial carrier protein, putative, expressed Alias=LOC_Os01g74640	View
gene	Sorghum Chr 3 9999916:10005657	ID=Sb03g009250 Description=similar to Putative GTPase-activating protein	View
gene	Maize v2.0 Chr 3 33555936:33562508	ID=GRMZM2G031043 Name=GRMZM2G031043 biotype=protein_coding	View

Match view. The result of selecting the second 'Match' from the table. Selecting View shows the region in the Java 2D display.

(C) Gene Search and Match.



Summary for Maize v2.0 to Rice

Hits

33792 hits
23237 in synteny blocks

Synteny Coverage

Genome	Coverage	Double-coverage
Maize v2.0	95%	60%
Rice	97%	91%

Block sizes

Genome	< 1Mb	1 Mb - 3 Mb	> 3 Mb
Maize v2.0	16	29	144
Rice	47	36	106

Maize v2.0 Annotation

Type	Number	Length (Mb)
exon	487152	13.9
gene	110200	24.6

Rice Annotation

Type	Number	Length (Mb)
exon	301164	9
gene	57624	16.8

Anchor filtering and loading

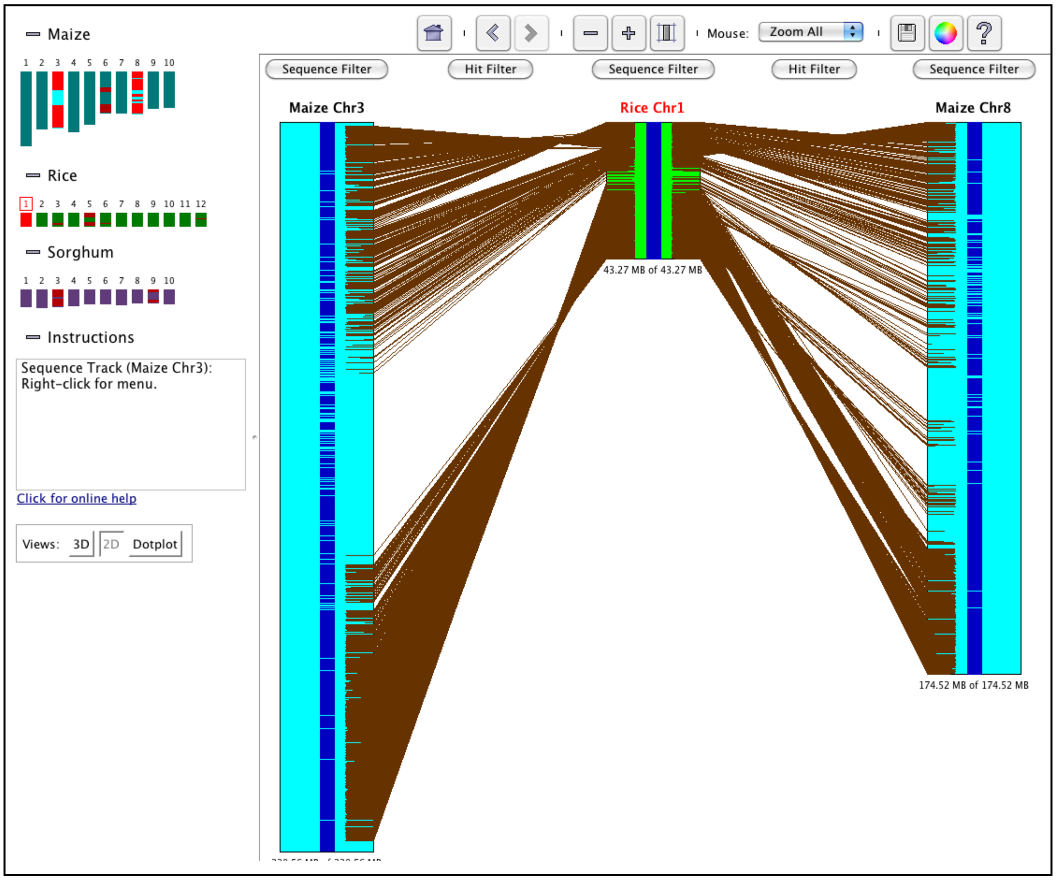
AG = annotated gene; UC = un-annotated cluster (i.e. raw hit does not overlap a gene annotation)

	MUMmer Raw Hits	*Clustered Anchors*	*Filtered Anchors*	*Synteny Anchors*	*Filtered Raw Hits*
AG-to-AG	197569	97853	31472	22410	98544
AG-to-UC	23046	18409	1699	645	3272
UC-to-UC	5968	5571	621	182	757
Total	226583	121833	33792	23237	102573

Blocks

Chr1	Chr2	Block #	size1	size2	#hits	hits/Mb #1	hits/Mb #2	Avg. % id	
1	3	1	78814361	19226657	1154	14	60	88	View
1	3	2	55482981	15833318	862	15	54	88	View
1	3	3	20352353	3503261	28	1	7	87	View
1	3	4	432156	89396	7	16	78	87	View

(D) Summary table. Selecting ‘View’ displays the corresponding synteny block in the Java 2D view.



Sequence Track (Maize Chr3):
Right-click for menu.

Figure S3: Drawn to scale. This is the same as Figure 3A, but drawn to scale by selecting the SyMAP scale button (next to the + at the top)