- Pipeline components:
  - minimap2 was used to align one assembly to another;
  - blat chain/net tools were used to process alignment resuls and build synteny chains/nets;
  - bcftools and GATK4 were used to call variants;
  - snpEff was used to evaluate variant effects on sytenic genes
- whole genome synteny plots
  - Mo17 vs B73
  - W22 vs B73
  - PH207 vs B73
  - PHB47 vs B73
- Table 1. Whole genome alignment statistics.

| | Mo17 vs B73 | | | | W22 vs B73 | | | | PH207 vs B73 | | | | PHB47 vs B73 | | | |
| | Mo17 | | B73 | | W22 | | B73 | | PH207 | | B73 | | PHB47 | | B73 | |
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
genome space	2,204,525,176	100.0%	2,137,643,061	100.0%	2,133,882,028	100.0%	2,137,643,061	100.0%	2,372,587,326	100.0%	2,137,643,061	100.0%	2,164,788,649	100.0%	2,137,643,061	100.0%
gap-free space	2,147,450,341	97.4%	2,104,350,193	98.4%	2,093,255,169	98.1%	2,104,350,193	98.4%	1,714,072,453	72.2%	2,104,350,193	98.4%	2,126,513,527	98.2%	2,104,350,193	98.4%
in synteny	1,232,534,653	57.4%	1,232,534,653	58.6%	1,253,067,639	59.9%	1,253,067,639	59.5%	1,091,867,114	63.7%	1,091,867,114	51.9%	1,320,582,689	62.1%	1,320,582,689	62.8%
genic space	156,283,135	7.1%	164,588,349	7.7%	174,277,885	8.2%	164,588,349	7.7%	243,071,285	10.2%	164,588,349	7.7%	158,226,649	7.3%	164,588,349	7.7%
genic space in synteny	125,160,600	80.1%	130,489,534	79.3%	135,146,791	77.5%	130,983,423	79.6%	152,879,810	62.9%	125,238,677	76.1%	131,905,386	83.4%	132,930,266	80.8%
total genes	38,620		46,117		40,690		46,117		40,557		46,117		36,988		46,117	
genes w. >=75% covered in synteny	30,621	79.3%	35,959	78.0%	31,861	78.3%	36,093	78.3%	28,803	71.0%	33,429	72.5%	30,231	81.7%	36,675	79.5%

- Table 2. Summary of variants called by synteny comparison.

| | size | Mo17 vs B73 | | | | W22 vs B73 | | | | PH207 vs B73 | | | | PHB47 vs B73 | | | |
		#events	%events	#bases	%bases	#events	%events	#bases	%bases	#events	%events	#bases	%bases	#events	%events	#bases	%bases
SNP		9,162,131		9,162,131		8,528,915		8,528,915		7,951,915		7,951,915		7,978,260		7,978,260	
Insertion		603,210		743,374		570,985		740,415		547,733		754,883		528,952		650,232	
	0-10bp	509,418	84.5%	509,418	68.5%	464,973	81.4%	464,973	62.8%	415,587	75.9%	415,587	55.1%	447,793	84.7%	447,793	68.9%
	10-100bp	66,558	11.0%	133,116	17.9%	62,300	10.9%	124,600	16.8%	73,174	13.4%	146,348	19.4%	57,763	10.9%	115,526	17.8%
	100bp-1kb	15,404	2.6%	46,212	6.2%	30,275	5.3%	90,825	12.3%	48,637	8.9%	145,911	19.3%	13,089	2.5%	39,267	6.0%
	1-5kb	4,522	0.7%	18,088	2.4%	7,168	1.3%	28,672	3.9%	4,638	0.8%	18,552	2.5%	3,889	0.7%	15,556	2.4%
	5-10kb	7,308	1.2%	36,540	4.9%	6,269	1.1%	31,345	4.2%	5,697	1.0%	28,485	3.8%	6,418	1.2%	32,090	4.9%
Deletion		720,933		856,324		539,399		672,667		529,120		700,874		496,874		614,928	
	0-10bp	629,897	87.4%	629,897	73.6%	449,716	83.4%	449,716	66.9%	412,161	77.9%	412,161	58.8%	417,715	84.1%	417,715	67.9%
	10-100bp	64,984	9.0%	129,968	15.2%	63,082	11.7%	126,164	18.8%	78,789	14.9%	157,578	22.5%	56,517	11.4%	113,034	18.4%
	100bp-1kb	14,788	2.1%	44,364	5.2%	16,087	3.0%	48,261	7.2%	27,415	5.2%	82,245	11.7%	12,657	2.5%	37,971	6.2%
	1-5kb	4,225	0.6%	16,900	2.0%	4,044	0.7%	16,176	2.4%	4,885	0.9%	19,540	2.8%	3,717	0.7%	14,868	2.4%
	5-10kb	7,039	1.0%	35,195	4.1%	6,470	1.2%	32,350	4.8%	5,870	1.1%	29,350	4.2%	6,268	1.3%	31,340	5.1%
Mixed		14,859		28,129,289		23,118		35,050,545		126,434		153,928,948		12,251		22,605,984	

- plot of synteny content and variant density
- Table 3. Summary of variant effects on syntenic genes.

Impact	Effect	Mo17 vs B73 B73 #	Mo17 vs B73 B73 %	Mo17 vs B73 Mo17 #	Mo17 vs B73 Mo17 %	W22 vs B73 B73 #	W22 vs B73 B73 %	W22 vs B73 W22 #	W22 vs B73 W22 %	PH207 vs B73 B73 #	PH207 vs B73 B73 %	PH207 vs B73 PH207 #	PH207 vs B73 PH207 %	PHB47 vs B73 B73 #	PHB47 vs B73 B73 %	PHB47 vs B73 PHB47 #	PHB47 vs B73 PHB47 %
high	exon_loss_variant	44	0.1%	56	0.1%	57	0.1%	89	0.2%	77	0.2%	206	0.5%	42	0.1%	32	0.1%
	frameshift_variant	2,871	6.2%	2,692	7.0%	2,631	5.7%	2,446	6.0%	6,386	13.8%	3,531	8.7%	2,323	5.0%	1,923	5.2%
	splice_acceptor_variant	475	1.0%	902	2.3%	469	1.0%	834	2.0%	476	1.0%	742	1.8%	380	0.8%	317	0.9%
	splice_donor_variant	596	1.3%	946	2.4%	588	1.3%	736	1.8%	691	1.5%	768	1.9%	490	1.1%	422	1.1%
	start_lost	222	0.5%	220	0.6%	255	0.6%	224	0.6%	796	1.7%	261	0.6%	194	0.4%	197	0.5%
	stop_gained	675	1.5%	536	1.4%	684	1.5%	1,395	3.4%	758	1.6%	558	1.4%	540	1.2%	360	1.0%
	stop_lost	219	0.5%	221	0.6%	225	0.5%	1,200	2.9%	266	0.6%	226	0.6%	197	0.4%	119	0.3%
	transcript_ablation													2	0.0%		
moderate	conservative_inframe_deletion	346	0.8%	320	0.8%	330	0.7%	290	0.7%	247	0.5%	401	1.0%	286	0.6%	305	0.8%
	conservative_inframe_insertion	493	1.1%	453	1.2%	512	1.1%	367	0.9%	660	1.4%	340	0.8%	422	0.9%	405	1.1%
	disruptive_inframe_deletion	630	1.4%	591	1.5%	692	1.5%	556	1.4%	446	1.0%	461	1.1%	533	1.2%	533	1.4%
	disruptive_inframe_insertion	530	1.1%	442	1.1%	510	1.1%	417	1.0%	566	1.2%	340	0.8%	418	0.9%	432	1.2%
	missense_variant	11,946	25.9%	10,754	27.8%	11,734	25.4%	10,521	25.9%	8,286	18.0%	8,959	22.1%	10,094	21.9%	9,817	26.5%
low	5_prime_UTR_premature_start_codon_gain_variant	62	0.1%	99	0.3%	65	0.1%	80	0.2%	36	0.1%	35	0.1%	51	0.1%	69	0.2%
	splice_region_variant	670	1.5%	590	1.5%	704	1.5%	497	1.2%	563	1.2%	640	1.6%	608	1.3%	657	1.8%
	stop_retained_variant	7	0.0%	6	0.0%	10	0.0%	9	0.0%	11	0.0%	6	0.0%	5	0.0%	6	0.0%
	synonymous_variant	2,016	4.4%	1,873	4.8%	2,068	4.5%	1,529	3.8%	1,428	3.1%	1,726	4.3%	1,819	3.9%	1,807	4.9%
modifier	3_prime_UTR_variant	663	1.4%	647	1.7%	622	1.3%	609	1.5%	455	1.0%	391	1.0%	588	1.3%	873	2.4%
	5_prime_UTR_variant	538	1.2%	538	1.4%	476	1.0%	473	1.2%	515	1.1%	230	0.6%	495	1.1%	604	1.6%
	intragenic_variant	1,089	2.4%			1,049	2.3%			975	2.1%	1	0.0%	913	2.0%	1	0.0%
	intron_variant	2,528	5.5%	2,163	5.6%	2,578	5.6%	2,551	6.3%	2,041	4.4%	3,602	8.9%	2,727	5.9%	2,671	7.2%
	non_coding_transcript_exon_variant	188	0.4%			165	0.4%			161	0.3%			175	0.4%		
no_change		9,151	19.8%	6,572	17.0%	9,669	21.0%	7,037	17.3%	7,589	16.5%	5,379	13.3%	13,373	29.0%	8,681	23.5%