- 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.

		Mo17 vs B73				W22 vs B73				PH207 vs B73				PHB47 vs B73			
	size	#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
  - Mo17 vs B73
  - W22 vs B73
  - PH207 vs B73
  - PHB47 vs B73
- Table 3. Summary of variant effects on syntenic genes.

		Mo17 vs B73				W22 vs B73				PH207 vs B73				PHB47 vs B73			
		B73		Mo17		B73		W22		B73		PH207		B73		PHB47	
Impact	Effect	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
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%