

Table S5 Summary of synteny testing different distance parameters

Distance ^a	Duplicated Regions ^b	Expected Triplets ^c	Observed Triplets	Max Genes /Block	Average genes per block	Average size per block (kb)	Genomic coverage (%)
10,000	174	32	0	8	3.9	5	10.8
20,000	256	47	3	9	4.7	57	12.2
30,000	273	50	10	16	4.7	57	16.9
40,000	291	54	20	16	4.8	64	20.3
50,000	303	56	26	16	4.9	81	21.7

^aThe distance between two neighboring homologous gene pairs that share the same order and orientation in two genomic locations;

^bThe genomic regions that contain at least three homologous gene pairs with another genomic region;

^cThe expected triplets according to a Poisson distribution.