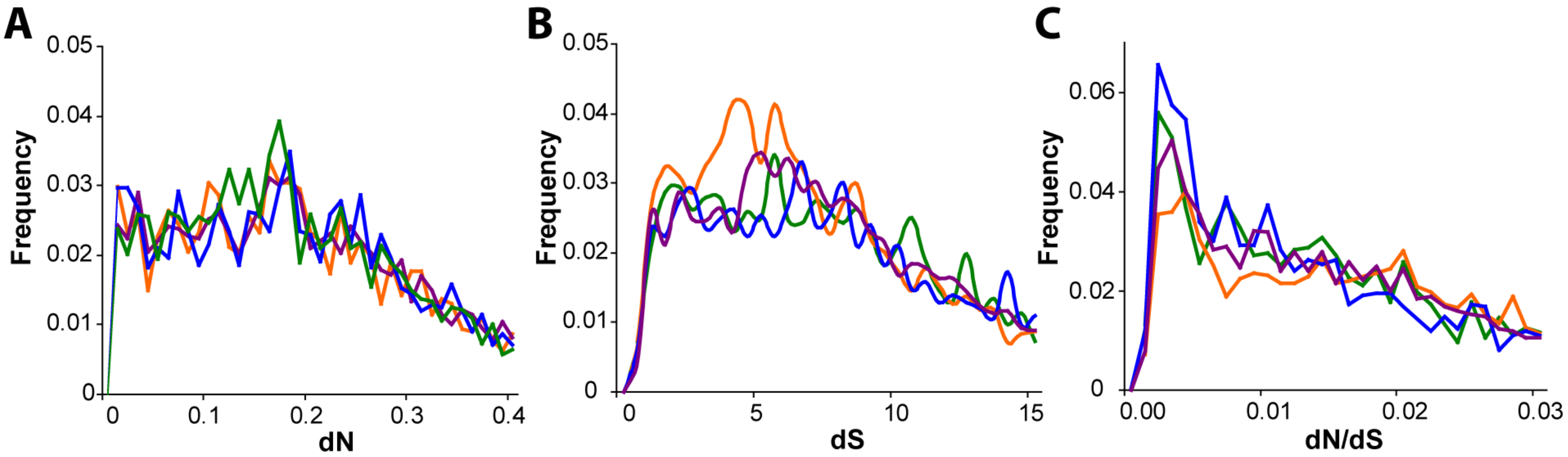

Figure S1 Distributions of dN (A), dS (B), and dN/dS (C) among intermediate WGD duplicates. Green = intermediate WGD duplicates within *biaurelia*, orange = intermediate WGD duplicates within *tetraurelia*, blue = intermediate WGD duplicates within *sexaurelia*, purple = intermediate WGD duplicates between *tetraurelia* and *sexaurelia*.

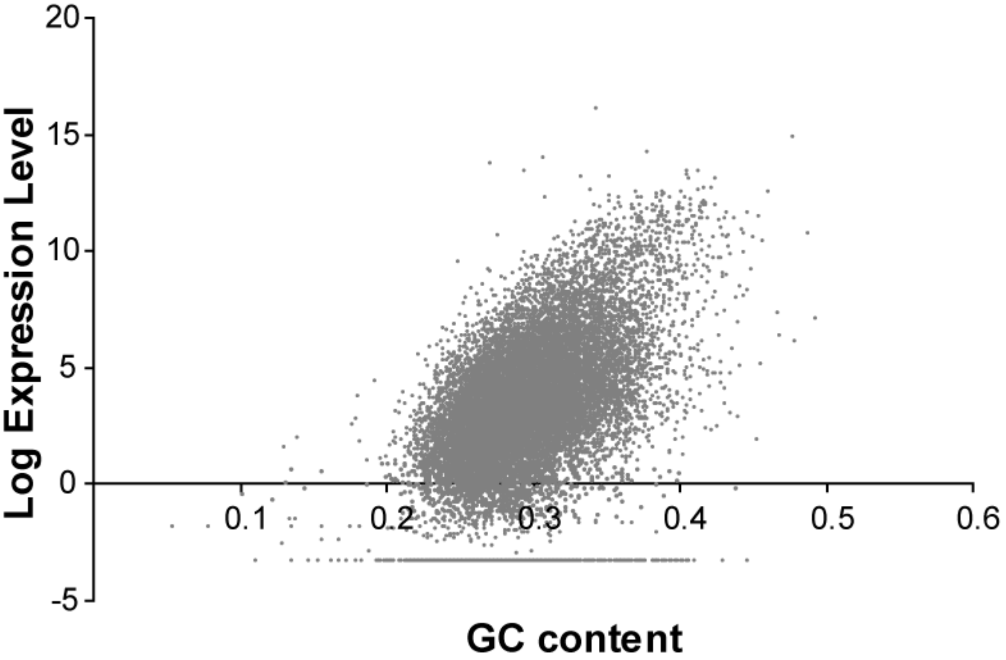

Figure S2 Relationship between log expression level and GC content of *caudatum* genes. R^2=0.23

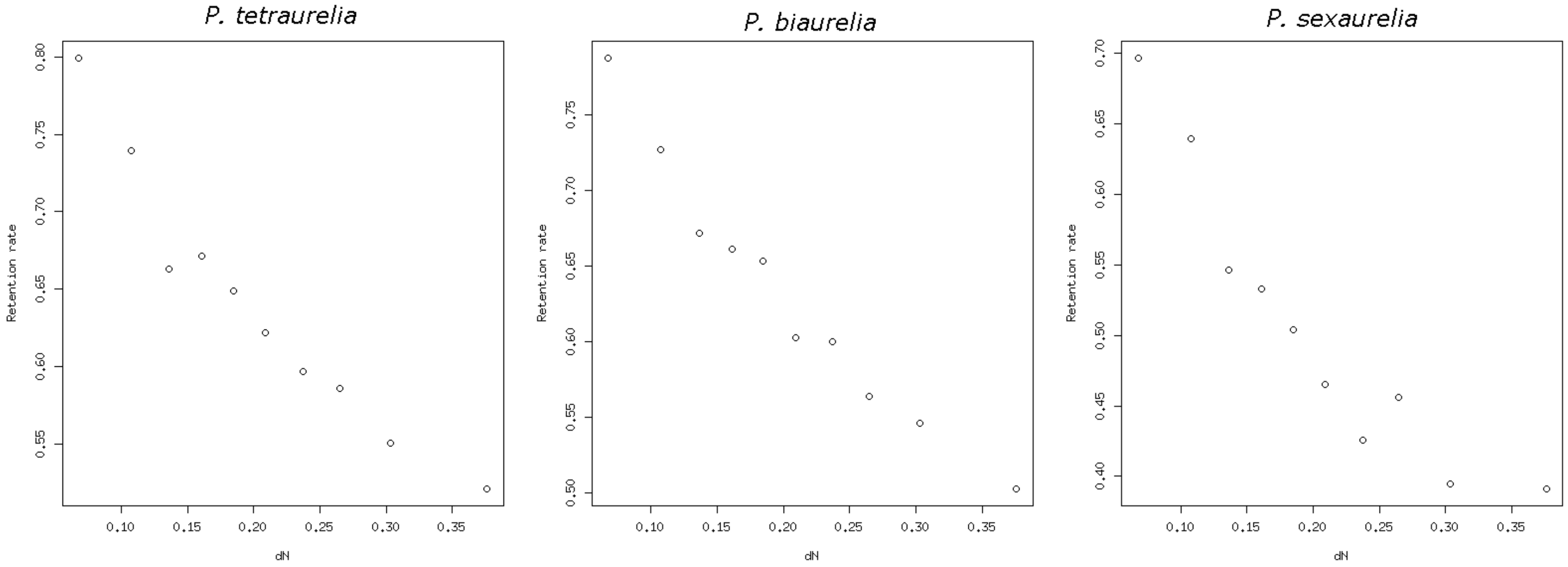

Figure S3 Relationship between evolutionary rate (dN computed between *P. caudatum* / *P. multimicronucleatum* orthologs) and post-recent-WGD retention rate in three *P. aurelia* species.

Files S1-S6

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.163287/-/DC1

File S1 Excel file containing orthologous blocks between *caudatum* genes and recreated pre-recent WGD *aurelia* segments. Cells where one gene has been lost from a scaffold contain a dot (“.”).

File S2 Excel file containing orthologous blocks between *caudatum* genes and recreated pre-intermediate WGD *aurelia* segments. Cells where one gene has been lost from a scaffold contain a dot (“.”).

File S3 Excel file containing number of intermediate WGD duplicates vs. single-copy genes in each GO term functional category and *P*-values.

File S4 Excel file containing candidates for neofunctionalization from *biaurelia*, *tetraurelia*, and *sexaurelia*.

File S5 Excel file containing paralogous blocks within *caudatum* from the ancient WGD.

File S6 Excel file containing number of ancient WGD duplicates vs. single-copy genes in each GO term functional category and *P*-values.

Table S1 Genome assembly and annotation statistics for *P. caudatum*, as compared to *biaurelia* (McGrath *et al*., submitted), *tetraurelia* (AURY *et al.* 2006) and *sexaurelia* (McGrath *et al.,* submitted).

	caudatum	*biaurelia*	*tetraurelia*	*sexaurelia*
Average coverage	186X	45X	13X	42X
Number of scaffolds (total)	1,202	2,362	N/A*	547
Number of scaffolds (> 2 kb)	274	1,426	697	230
Average scaffold length (>2 kb scaffolds)	109,242	53,140	103,448	294,183
Largest scaffold length	793,585	1,048,449	980,760	1,303,432
Number of gaps	1,412	1,459	419	1,298
Assembly length with gaps (all scaffolds)	30,525,943	76,976,592	72,102,941	68,020,722
Number of genes	18,509	39,242	39,521	34,939

* Only scaffolds > 2 kb are included in *tetraurelia* assembly

Table S2 Divergent resolutions of intermediate WGD duplicates between *aurelia* species.

Intermediate Duplicate 1 descendant(s)		Intermediate Duplicate 2 descendants (s)		Function (if known)
Divergent resolutions between *tetraurelia* and *sexaurelia*				
GSPATP00020634001	GSPATP00027241001	PSEXGNP07757	PSEXGNP11110	Serine/threonine protein kinase NEK
GSPATP00001449001	GSPATP00002598001	PSEXGNP12568	--	KH domain containing RNA binding protein
Divergent resolutions between *biaurelia* and *sexaurelia*				
PBIGNP32737	PBIGNP21940	PSEXGNP01107	PSEXGNP03977	Serine/threonine protein kinase-related
PBIGNP15479	PBIGNP27623	PSEXGNP17612	--	Ribosomal protein L15
PBIGNP00423	PBIGNP01848	PSEXGNP12568	--	KH domain containing RNA binding protein
PBIGNP00575	--	PSEXGNP18664	--	
Divergent resolutions between *biaurelia* and *tetraurelia*				
PBIGNP34817	--	GSPATP00027407001	--	
PBIGNP00237	--	GSPATP00004767001	--	Cabriolet-related

Table S3 Average GC content and log expression level for duplicated vs. single-copy *caudatum* genes from the ancient WGD.

	Duplicated	Single-copy	*P*-value
GC content	0.306	0.296	$<10^{-6}$
Log expression level	4.33	3.50	$<10^{-8}$