Supplementary results for Assemblathon 2 paper

Table S1: Different assembly IDs used in Assemblathon 2.

While the Assemblathon 2 entries were being assessed, an anonymous identifier was used to refer to all assemblies. This consisted of a species description followed by a 2–3 character code. These have since been replaced with more human-readable identifiers but as other publications may refer to the older identifiers we have included them here. Assembly names with a ‘C’ or ‘E’ suffix refer to ‘competition’ or ‘evaluation’ entries. For the newer assembly IDs, evaluation entries are indicated by the use of one or two asterisks appended to the assembly ID: one asterisk for the first, or only, evaluation entry and two asterisks to refer to the second evaluation entry.

Team name	New assembly ID prefixes	Old assembly IDs
ABL	ABL	bird 15C
ABySS	ABYSS	fish 7C, snake 9C
Allpaths	ALLP	bird 11C, fish 6C
BCM-HGSC	BCM	bird 2C, bird 3E, fish 1C, snake 1C
CBCB	CBCB	bird 9C
$CoBiG_2$	COBIG	bird 8C
CRACS	CRACS	snake 10C
CSHL	CSHL	fish 12C, fish 14E, fish 15E
CTD	CTD	fish 2E, fish 9C, fish 10E
Curtain	CURT	snake 3C
GAM	GAM	snake 4C
IOBUGA	IOB	fish 13C, fish 16E
MLK Group	MLK	bird 5C
Meraculous	MERAC	bird 6C, fish 8C, snake 6C

Newbler-454	NEWB	bird 7C
Phusion	PHUS	bird 1C, snake 5C
PRICE	PRICE	snake 12C
Ray	RAY	bird 4C, fish 4C, snake 2C
SGA	SGA	bird 10C, fish 3C, snake 7C
SOAPdenovo	SOAP	bird 12C, bird 13E, bird 14E, fish 11E, snake 11C
Symbiose	SYMB	fish 5C, snake 8C

Table S2: Details of principle assembly software and CPU/RAM requirements of different assembly pipelines.

Instructions to run assemblers are included in Supplementary Methods for some teams.

Team name	Principle Software Used	CPU/RAM requirements
ABL	HyDA	512 GB RAM machine with 48 cores. Runtime: 14 hours
ABySS	ABySS v1.3.0 and Anchor	ABySS: 48 core-cluster for the single-end stage, and 12 cores for the paired-and and scaffolding stages, each with 4 GB RAM. Runtime was ~4 hours for the single-end stage, and 13 hours for the paired-end stage, then another three days for the final scaffolding stage. Anchor: Same cluster as above, using 1–100 cores for the various stages. Total runtime was approximately 13 hours.
Allpaths	ALLPATHS-LG	48 core server with 512 GB RAM, with a runtime of ~151–215 hours (depending on species).
BCM-HGSC	SeqPrep (version: a1e1d38), KmerFreq, Quake (v0.2), BWA, Newbler (v2.3), ALLPATHS-LG (version: allpathslg-37405), Atlas-Link, Atlas-GapFill, Phrap, CrossMatch, Velvet, BLAST, and BLASR	Estimated max RAM: 300–500GB (depending on species). Estimated running time: 3.5 weeks; using a single node with 1TB RAM and 32 CPUs, as well as a cluster of 100 cores each with 16 GB RAM. Gap filling step used a cluster of 100–600 cores (depending on species), each with 16 GB RAM and required a run time of 90 hours.
CBCB	Celera assembler v7 and PacBio Corrected Reads (PBcR)	Runtime of 6.75 days for PacBio read correction and 9.5 days for assembly. Serial steps were executed on 32 core head node with 256 GB RAM. Parallel jobs were distributed across 60 nodes, with 16 cores and 32 GB RAM each.
$CoBiG_2$	4Pipe4 pipeline, Seqclean	DELL Power Edge R710, CPU: 2x Intel Xeon

	(version: 2011-02-22), Mira (v3.2.1), Bambus2	E5520, RAM: 64 GB, Runtime of 24 hours
CRACS	ABySS, SSPACE, Bowtie, and FASTX	Single 6-core AMD Opteron(tm) processor (2100MHz) with 128 GB of RAM. The approximate total amount of computation time required to generate the assembly was 300 hours.
CSHL	Metassembler, ALLPATHS, SOAPdenovo	Metassembler: <3 hours runtime and <50 GB RAM for the pairwise alignment. Computing the CE statistic required ~10 hours and 50 GB RAM, dominated by aligning the reads to the assemblies to determine placement. Evaluating the alignments and patching the assemblies required ~1 hour. ALLPATHS: 48 available CPUs, 945 hours of elapsed time, and 456 GB RAM memory usage peak SOAPdenovo: ~1 day, 100GB RAM, 48 cores for FLASH, and Quake ~1 day for the basic assembly ~1 day to align the mates, filter failed mates, remove PCR duplicates ~1 day to improve the assembly with the corrected mates
CTD	Unspecified	48 GB RAM
Curtain	SOAPdenovo (v1.05), fastx_toolkit (v0.0.6), bwa (v0.5.8a), samtools (v0.1.17), velvet (v1.1.06), curtain (v0.2.3-BETA)	14 hours on 1 machine with 170 GB RAM, plus 11 hours on 20 machines with 60 GB RAM
GAM	GAM, CLC and ABySS	CLC: one server, 8 cores, 128Gb RAM, half a day runtime. ABySS, cluster with 6 nodes, 8 cores per node, one day runtime. GAM: one server, 8 cores, 128Gb RAM, half a

		day runtime. SSPACE: single CPU, 1 hour runtime.
IOBUGA	ALLPATHS-LG (38293) and SOAPdenovo (1.05)	32 CPU machine, 512 GB RAM. Runtime: ~ 120 hours for ALLPATH-LG and 48 hours for SOAPdenovo.
MLK Group	ABySS	672 core cluster, 1.2 TB RAM distributed, non-parallel steps done on 256 GB RAM machine and single node. SGA steps done on local workstation with 36 GB RAM
Meraculous	meraculous	500 core cluster with 8 GB RAM per core. Runtime: 20 hours. Single core machine with ~100 GB RAM. Runtime 10 hours.
Newbler-454	Newbler (R&D version, post2.8_v20110815). Run with options "-large -scaffold -het -sio -cpu 12"	Shared memory machine, 12 cores used, 130 GB RAM, run time of 18 hours
Phusion	Phusion2, SOAPdenovo, SSPACE	160GB RAM for 72 hours, 100 cores with 4GB RAM for 2 hours
PRICE	PRICE	Run on various 8–64 core machines with 16–256 GB RAM.
Ray	Ray (version 1.7 with some modifications, see: https://github.com/sebhtml/assemblathon-2-ray)	Version: 32 computers, 8 cores per computer, 24 GB RAM per computer. Approx. running time: 36–72 hours (depending on species).
SGA	SGA	Total CPU time: 1000–1900 hours (depending on species). Total wall clock time: 174 hours. Peak memory usage: 34–50 GB RAM (depending on species).
SOAPdenovo	SOAPdenovo	110–150 GB RAM (peak), depending on species, 24–32 CPUs (depending on species). Runtime 48–72 hours (depending on species).
Symbiose	Monument (for paired-end assembly), SSPACE (for mate-pair scaffolding in snake), SuperScaffolder (for mate-pair scaffolding in fish), and	Computational resources: 40 cores on 5 nodes with 140 GB RAM (max RAM usage not recorded) Runtimes:

	GapCloser (for GapClosing)	Indexing: ~1 day (40 cores / 5 nodes). Paired-end assembly: ~1 day (16 cores / 1 node). Two rounds of scaffolding and gap-filling: ~1 day (8 cores / 1 node)

Table S3: Availability of software used for assemblies

Assembly software	URL	Reference (if published)
4Pipe4 pipeline	https://github.com/StuntsPT/4Pipe4/commit/a1808cecce7025a3fb90d64a337ccbe08619267a	
ABySS	http://www.bcgsc.ca/platform/bioinfo/software/abyss	[1]
ALLPATHS-LG	http://www.broadinstitute.org/software/allpaths-lg/blog/	[2]
Anchor	http://www.bcgsc.ca/platform/bioinfo/software/anchor	
Atlas-GapFill	https://www.hgsc.bcm.edu/content/atlas-gapfill	[3]
Atlas-Link	https://www.hgsc.bcm.edu/content/Atlas-Link	[4]
Bambus2	http://www.cbcb.umd.edu/software/bambus/	
BLASR	http://www.pacificbiosciences.com/products/software/algorithms/	[5]
BLAST	http://blast.ncbi.nlm.nih.gov/	[6]
Bowtie	http://bowtie-bio.sourceforge.net/index.shtml	[7]
BWA	http://bio-bwa.sourceforge.net/	[8]
Celera	http://wgs-assembler.sourceforge.net/	[9]
CLC Genomics Workbench de novo assembler	http://clcbio.com	
Curtain	http://code.google.com/p/curtain/	
FASTX	http://hannonlab.cshl.edu/fastx_toolkit/	
GAM (Genomic Assemblies Merger)	https://github.com/vice87/gam-ngs	[10]
HyDA	http://compbio.cs.wayne.edu/software/hyda/	
KmerFreq (part of SOAPdenovo)	http://soap.genomics.org.cn/soapdenovo.html	[11]
Meraculous	ftp://ftp.jgi-psf.org/pub/JGI_data/meraculous/	[12]

Metassembler	http://sourceforge.net/apps/mediawiki/metassembler/index.php?title=Metassembler	
MIRA	http://www.chevreux.org/projects_mira.html	
Monument		[13]
Newbler	http://454.com/products/analysis-software/index.asp	[14]
PBcR	http://www.cbcb.umd.edu/software/PBcR/	[15]
Phrap & Crossmatch	http://www.phrap.org/	
Phusion2	ftp://ftp.sanger.ac.uk/pub/zn1/phusion2/	[16]
PRICE	http://derisilab.ucsf.edu/software/price/	[17]
Quake	http://www.cbcb.umd.edu/software/quake/	[18]
Ray	http://denovoassembler.sourceforge.net	[19]
SAMtools	http://samtools.sourceforge.net/	[20]
Seqclean	http://sourceforge.net/projects/seqclean/files/seqclean-x86_64.tgz	
SeqPrep	https://github.com/jstjohn/SeqPrep	
SGA	http://github.com/jts/sga	[21]
SOAPdenovo	http://soap.genomics.org.cn/soapdenovo.html	[11]
SSPACE	http://www.baseclear.com/landingpages/sspacev12/	[22]
Velvet	http://www.ebi.ac.uk/~zerbino/velvet/	[23]

Figure S1: Contig NG50 length for all competitive assemblies

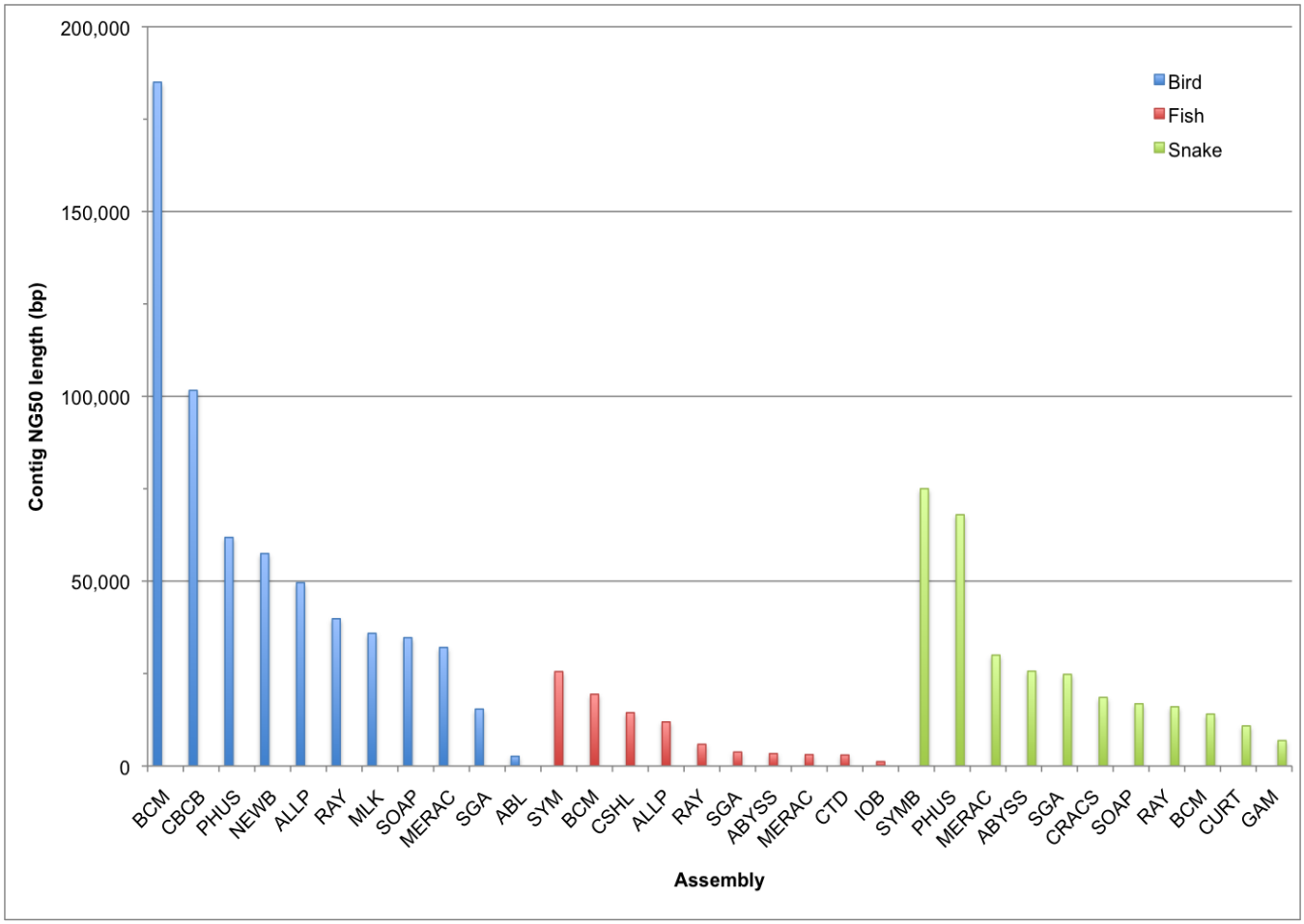


Figure S2: Relationship between scaffold NG50 length and contig NG50 length.

P-values from correlation coefficients: bird: $P = 0.0587$, fish: $P = 0.0039$, snake: $P = 0.0398$

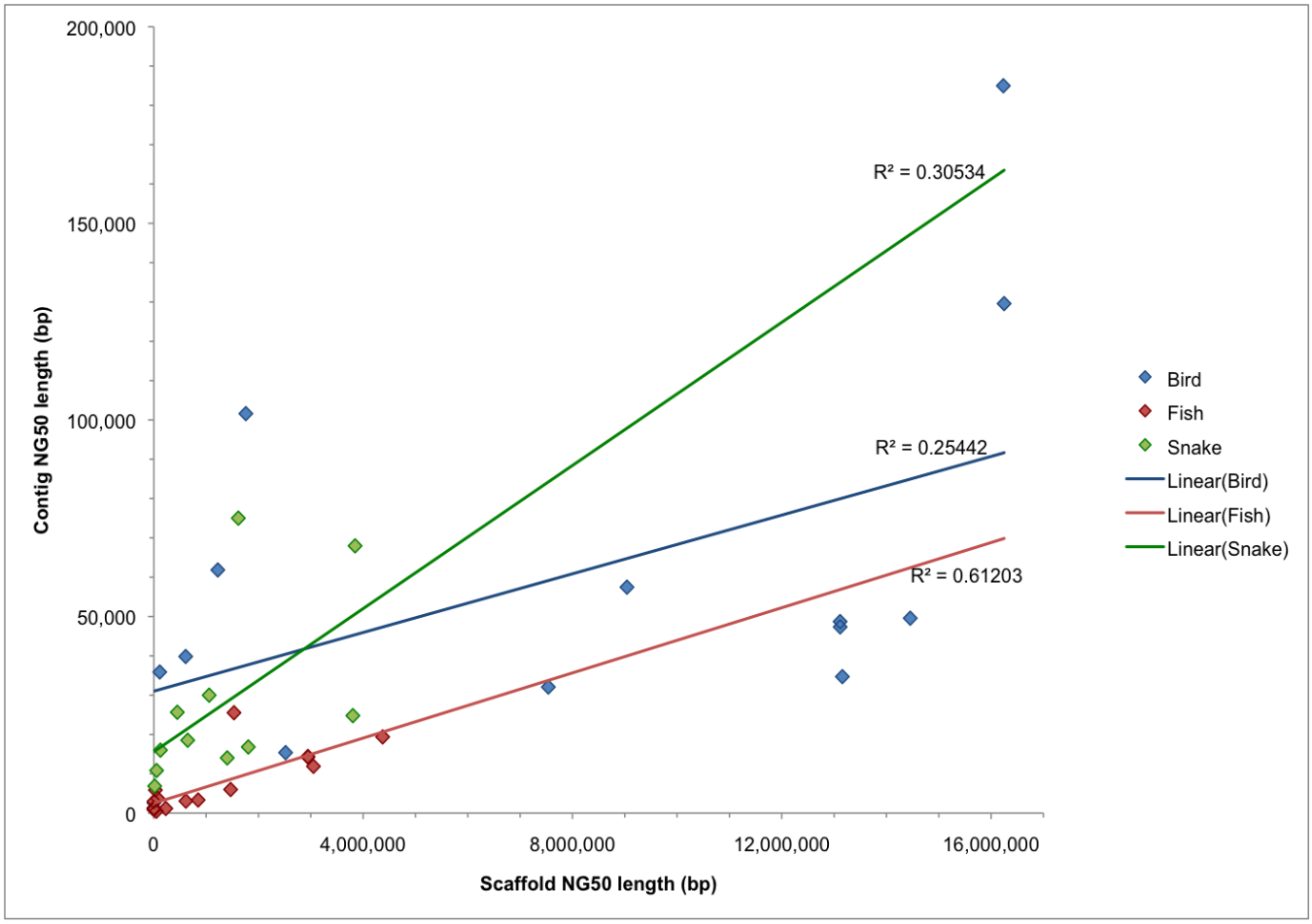


Figure S3: NG50 scaffold length distribution in bird assemblies and the fraction of the fish genome represented by gene-sized scaffolds.

Primary Y-axis (red) shows NG50 length for fish assemblies: the N50 scaffold length that captures 50% of the estimated genome size (~1.6 Gbp). Secondary Y-axis (blue) shows percentage of estimated genome size that is represented by scaffolds >= 25 Kbp (the average length of a vertebrate gene).

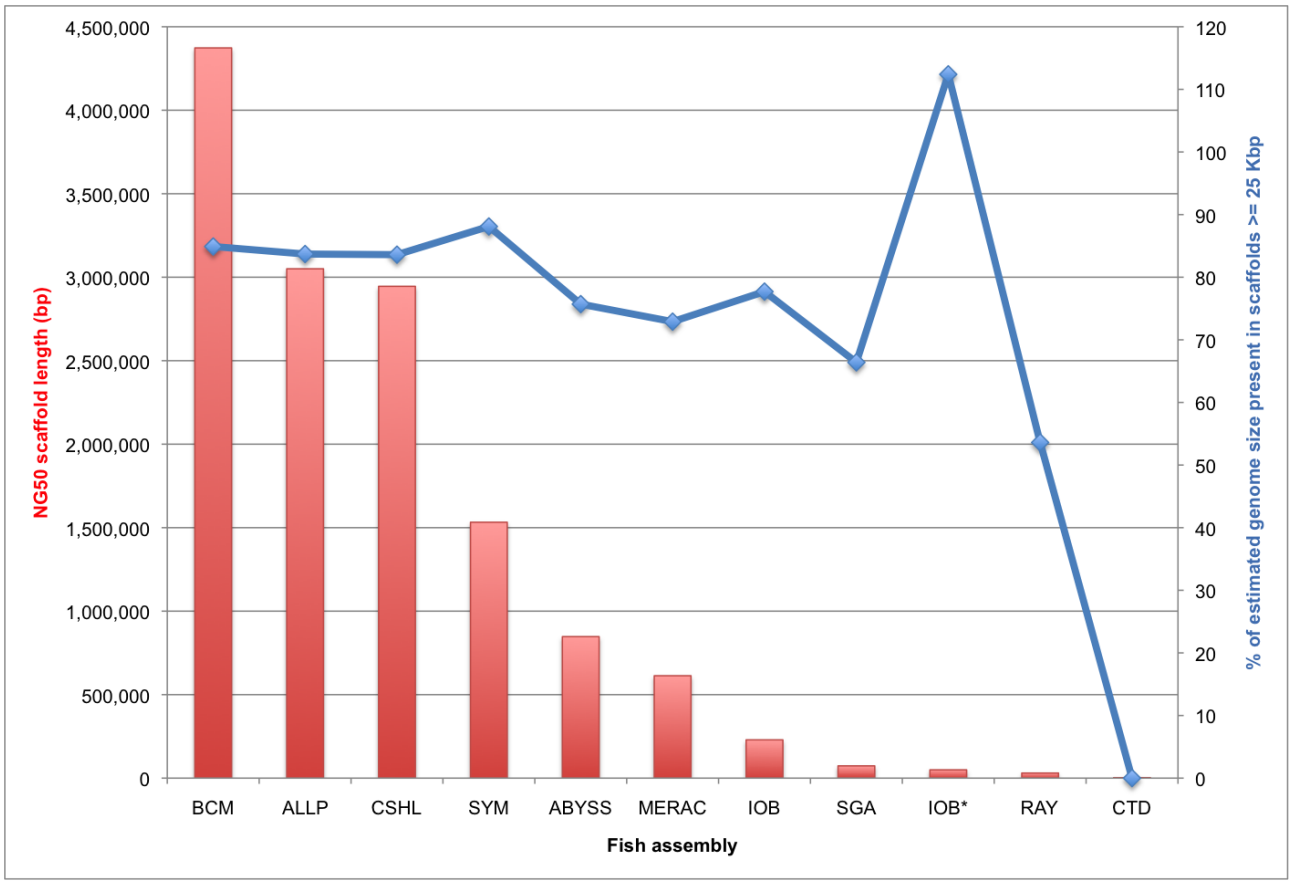


Figure S4: NG50 scaffold length distribution in bird assemblies and the fraction of the snake genome represented by gene-sized scaffolds.

Primary Y-axis (red) shows NG50 length for snake assemblies: the N50 scaffold length that captures 50% of the estimated genome size (~1.0 Gbp). Secondary Y-axis (blue) shows percentage of estimated genome size that is represented by scaffolds >= 25 Kbp (the average length of a vertebrate gene).

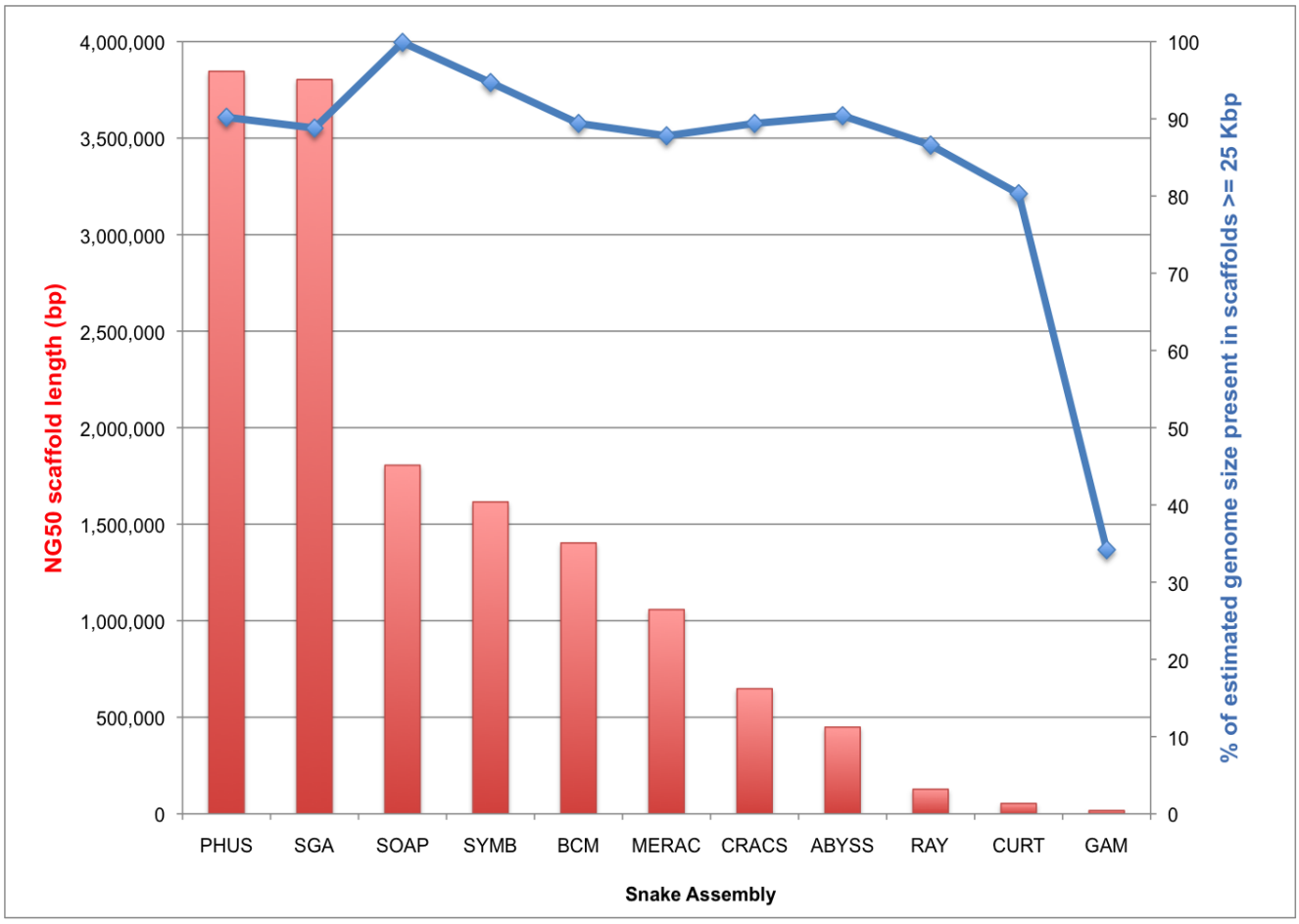


Table S3: Summary of available transcript and RefSeq data for bird, fish, and snake.

Numbers in parentheses indicate partial length mRNAs. Data taken from release 192.0 of GenBank, accessed from: http://www.ncbi.nlm.nih.gov/nucleotide/

Species	Number of mRNAs	Number of RefSeq entries
Bird (*Melopsittacus undulatus*)	26 (15)	1
Fish (*Maylandia zebra*)	27 (22)	0
Snake (*Boa constrictor constrictor*)	0	0

Figure S5: Alignment of snake predicted CEGMA proteins for the core gene family KOG3372.

Alignment made using T-COFFEE program with default parameters. The initial set of proteins predicted by CEGMA are aligned to the underlying HMMER profile for each core gene, and only those that span at least 70% of the alignment are considered ‘full-length’ and retained.

```
CLUSTAL FORMAT for T-COFFEE Version_5.31 [http://www.tcoffee.org], CPU=3.13
sec, SCORE=96, Nseq=11, Len=205

ABYSS           MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
BCM             MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
CRACS           MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
CURT            MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
GAM             MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVMLFYEVRKIKNVED
MERAC           MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
PHUS            MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
RAY             MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
SGA             MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
SYMB            MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVMLFYEVRKIKNVED
SOAP            MNTVLTRANSLFAFSLSVMAALTFGCFITTAFKERTVPVSIAVSRVML-------KNVED
                ********************************************       *****

ABYSS           FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
BCM             FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
CRACS           FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
CURT            FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
GAM             FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNNLPHTHI
MERAC           FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
PHUS            FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
RAY             FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
SGA             FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
SYMB            FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
SOAP            FTGPGERSDLGIITFNISANILYYKHSSLFPNIFDWNVKQLFLYLSAEYSTKNN------
                **************************************************

ABYSS           ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
BCM             ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
CRACS           ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
CURT            ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
GAM             YGHALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLK------------------
MERAC           ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
PHUS            ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
RAY             ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
SGA             ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
SYMB            ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
SOAP            ---ALNQVVLWDKIILRGDDPNLLLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAG
                   ************************************
```

```
ABYSS           ILPLVTGAGHISVPFPDTYKMTKSY
BCM             ILPLVTGAGHISVPFPDTYKMTKSY
CRACS           ILPLVTGAGHISVPFPDTYKMTKSY
CURT            ILPLVTGAGHISVPFPDTYKMTKSY
GAM             -------------------------
```

Table S4: CEGMA bird results: total number of all CEGs present in all bird assemblies.

Results in 3rd column reflect the numbers in the 2nd column as a percentage of the 442 CEGs that were found across all bird assemblies. Final column shows results for a subset of 248 CEGs which are the most highly conserved CEGs, and which tend to occur as single copy genes.

Assembly	Number of 458 CEGs present in assembly	% of 442 CEGs present across all bird assemblies	Number of 248 highly conserved CEGs present
PHUS	391	88.5%	176
BCM	420	95.0%	197
BCM*	420	95.0%	197
RAY	404	91.4%	190
MLK	401	90.7%	181
MERAC	393	88.9%	189
NEWB	380	86.0%	179
CBCB	403	91.2%	197
SGA	371	83.9%	169
ALLP	408	92.3%	199
SOAP	416	94.1%	202
SOAP*	415	93.9%	202
SOAP**	412	93.2%	201
ABL	229	51.8%	61

Table S5: CEGMA fish results: total number of all CEGs present in all fish assemblies.

Results in 3rd column reflect the numbers in the 2nd column as a percentage **o**f the 455 CEGs that were found across all fish assemblies. Final column shows results for a subset of 248 CEGs which are the most highly conserved CEGs, and which tend to occur as single copy genes.

Assembly	**Number of 458 CEGs present in assembly**	**% of 455 CEGs present across all fish assemblies**	**Number of 248 highly conserved CEGs present**
BCM	434	95.4%	228
CTD*	169	37.1%	25
SGA	423	94.9%	207
RAY	435	95.6%	210
SYM	428	94.1%	221
ALLP	430	94.5%	225
ABYSS	431	94.7%	224
MERAC	426	93.6%	216
CTD	350	76.9%	103
CTD**	207	45.5%	41
SOAP*	436	95.8%	225
CSHL	436	95.8%	227
IOB	387	85.1%	163
CSHL*	436	95.8%	227
CSHL**	307	67.5%	86
IOB*	83	18.2%	16

Table S6: CEGMA snake results: total number of all CEGs present in all snake assemblies.

Results in 3rd column reflect the numbers in the 2nd column as a percentage of the 454 CEGs that were found across all snake assemblies. Final column shows results for a subset of 248 CEGs which are the most highly conserved CEGs, and which tend to occur as single copy genes.

Assembly	Number of 458 CEGs present in assembly	% of 454 CEGs present across all snake assemblies	Number of 248 highly conserved CEGs present
BCM	434	95.6%	214
RAY	422	93.0%	194
CURT	360	79.3%	91
GAM	415	91.4%	157
PHUS	435	95.8%	214
MERAC	430	94.7%	217
SGA	433	95.4%	218
SYMB	436	96.0%	209
ABYSS	429	94.5%	208
CRACS	438	96.5%	211
SOAP	428	94.3%	209

Figure S6: Correlation between use of two different Core Eukaryotic Genes (CEGs) datasets.

Assemblies which contain more full-length core genes from the set of 458 CEGs, also contain more full-length core genes from the set of 248 CEGs which represent the most highly-conserved, least-paralogous CEGs. All correlations are highly statistically significant ($P < 0.000001$).

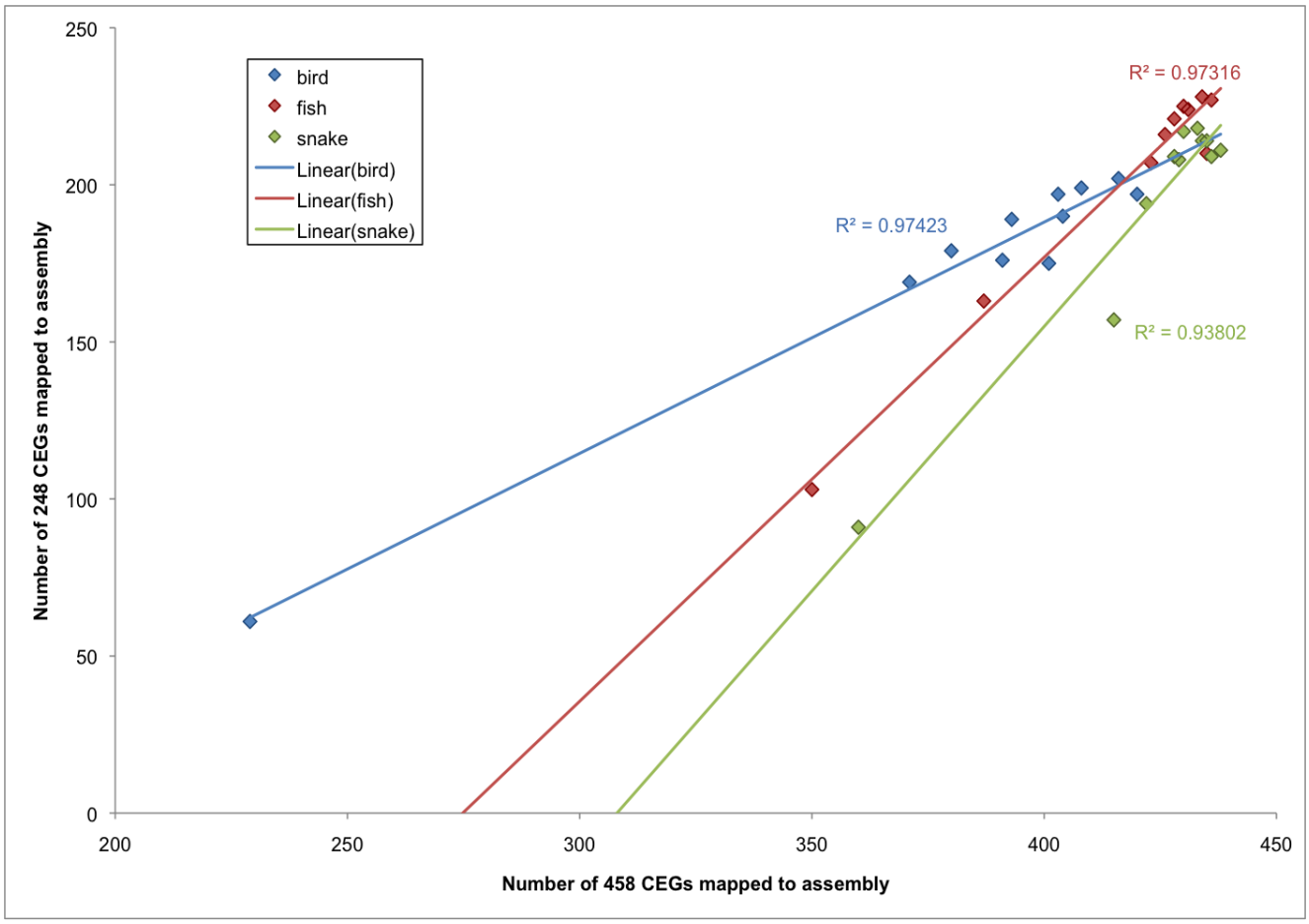


Figure S7: Some core genes are present as partial matches in assemblies.

Results from the CEGMA analysis of the 248 Core Eukaryotic Genes (CEGs) dataset includes details of how many CEGs match at full-length or only partially. The fraction of the alignment of a predicted protein to the HMMER profile can range from 20–100%. If this fraction exceeds 70% the protein is classed as a full-length CEG, otherwise it is classified as partial. In both cases, the predicted protein must also exceed a pre-determined cut-off score (see[24]).

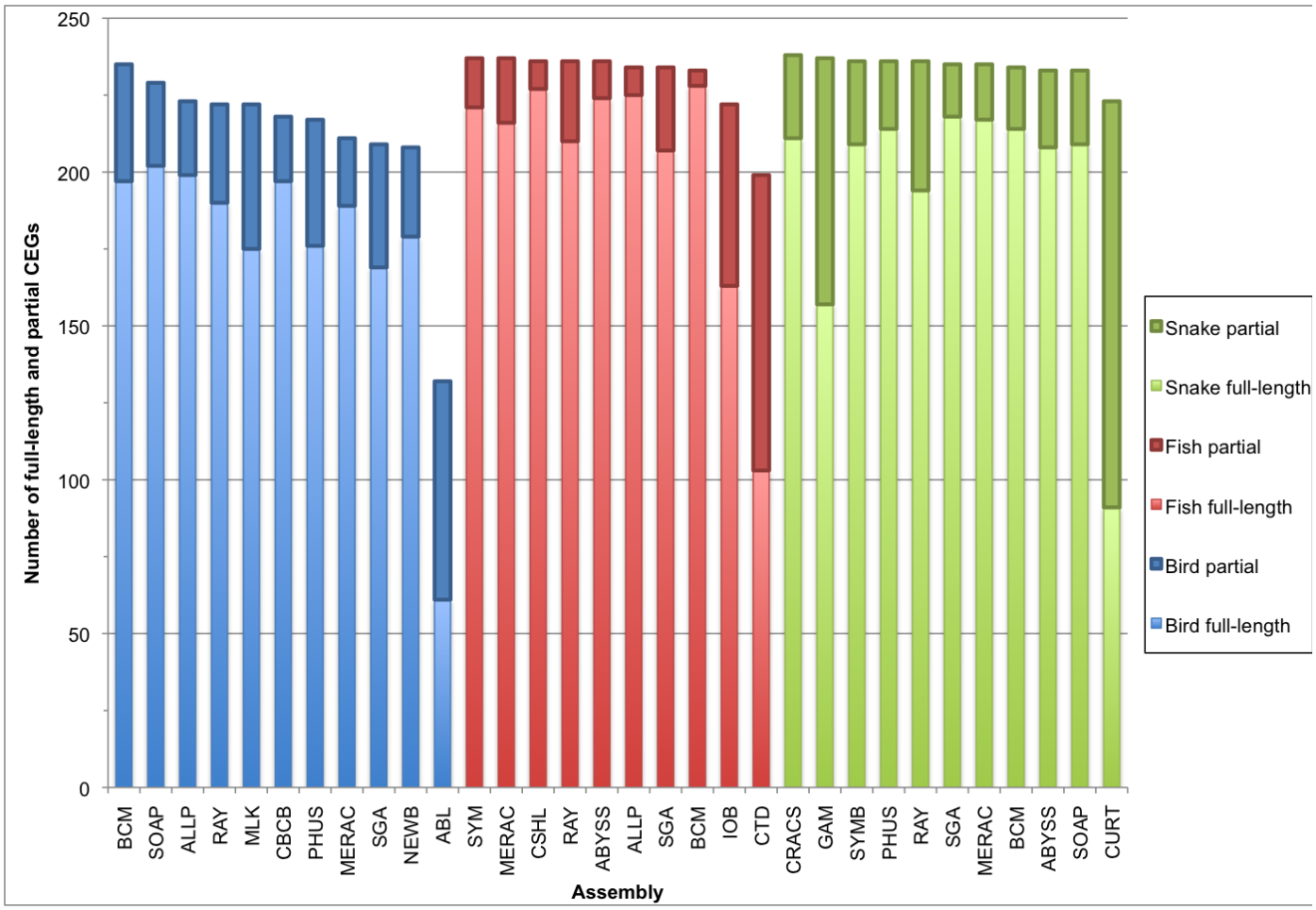


Figure S8: Relationship between assembly size and Fosmid coverage in bird and snake assemblies.

Coverage calculated using COMPASS tool.

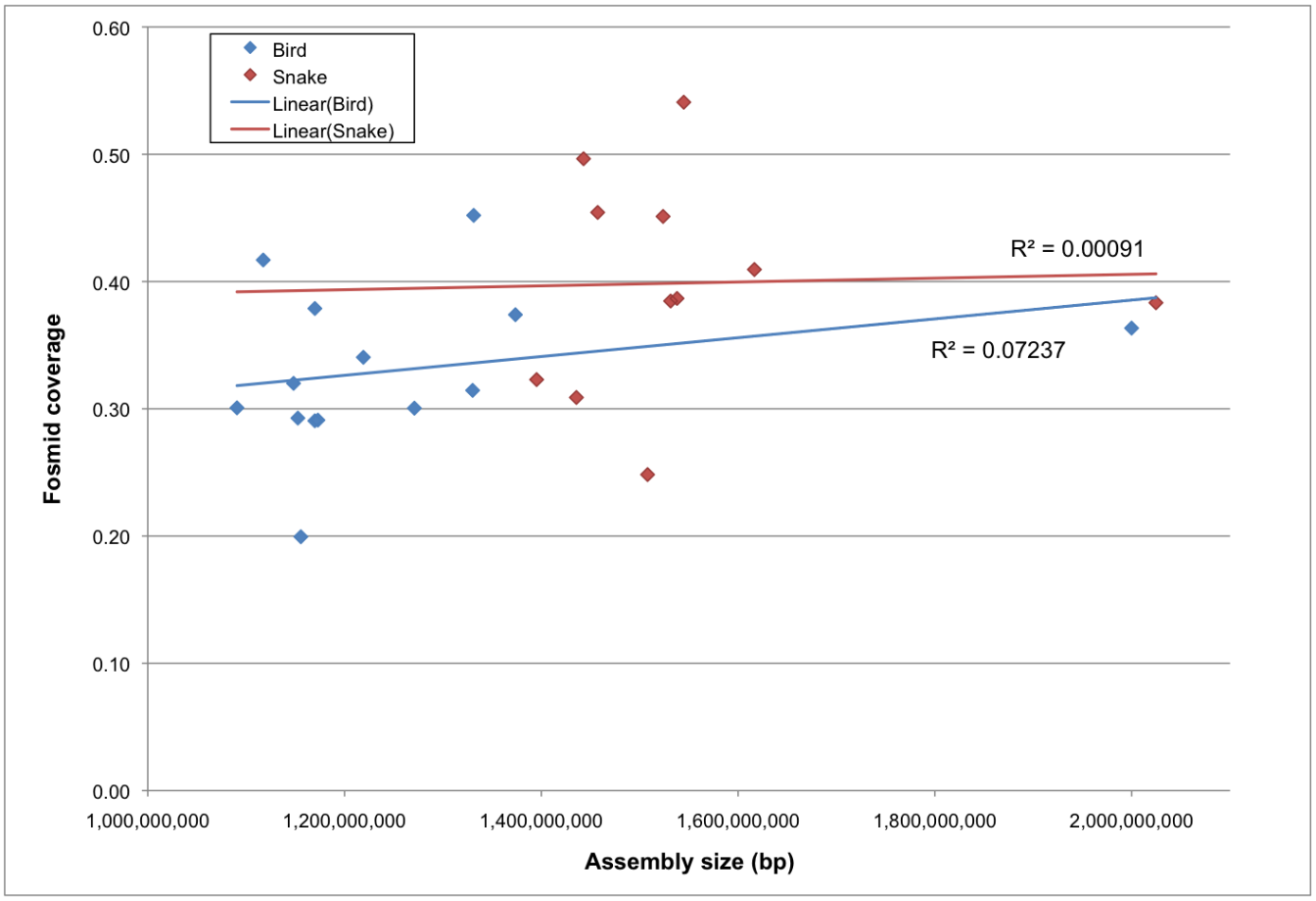


Table S5: Using validated fosmid regions (VFRs) to assess short-range accuracy in bird assemblies.

Results from 86 VFRs, producing 988 VFR fragments of 1,000 nt and 988 pairs of VFR 'tags' (the end 100 nt of each fragment). Expected distance between start coordinates of VFR tags = 900 nt. Tag pairs are deemed to have mapped correctly if the distance between them is 898–902 nt.

Assembly	Number of pairs of VFR tags that both map to the same scaffold	Number of pairs of VFR tags that map uniquely at correct distance apart (898–902 nt)	% of uniquely mapped tag pairs that map at correct distance apart	Extremes of mismapping (lowest and highest distances in nt)
PHUS	815	557	89.1%	702–41,949
BCM	890	713	92.6%	882–2,780
RAY	896	699	91.6%	746–4,175
MLK	857	544	93.8%	804–2,780
MERAC	840	746	91.9%	800–7,815
NEWB	849	733	91.2%	871–2,780
CBCB	897	744	91.4%	855–8,002
SGA	795	709	91.6%	713–34,915
ALLP	881	758	92.6%	875–43,292
SOAP	876	720	90.1%	709–4,805
ABL	337	332	98.5%	893–952

Table S6: Using validated fosmid regions (VFRs) to assess short-range accuracy in snake assemblies.

Results from 56 VFRs, producing 350 VFR fragments of 1,000 nt and 988 pairs of VFR 'tags' (the end 100 nt of each fragment). Expected distance between start coordinates of VFR tags = 900 nt. Tag pairs are deemed to have mapped correctly if the distance between them is 898–902 nt.

Assembly	Number of pairs of VFR tags that both map to the same scaffold	Number of pairs of VFR tags that map uniquely at correct distance apart (898–902 nt)	% of uniquely mapped tag pairs that map at correct distance apart	Extremes of mismapping (lowest and highest distances in nt)
BCM	278	240	90.2%	835–1,864
RAY	311	253	95.5%	860–2,973
CURT	272	220	87.6%	835–46,813
GAM	236	200	88.9%	815–1,022
PHUS	336	247	89.2%	653–2,070
MERAC	319	263	95.3%	875–912
SGA	323	265	94.3%	860–920
SYMB	300	211	87.9%	673–1,364
ABYSS	323	267	94.7%	878–2,206
CRACS	304	253	90.7%	855–3,472
SOAP	334	227	90.4%	830–4,858

Figure S9: Average rank of bird assemblies when assessed by ten key metrics.

Each assembly was ranked by ten different key metrics and then an average rank was calculated. Positive and negative error bars reflect the best and worst average rank that could be achieved if any one key metric was omitted from the analysis. Assemblies in red represent evaluation entries.

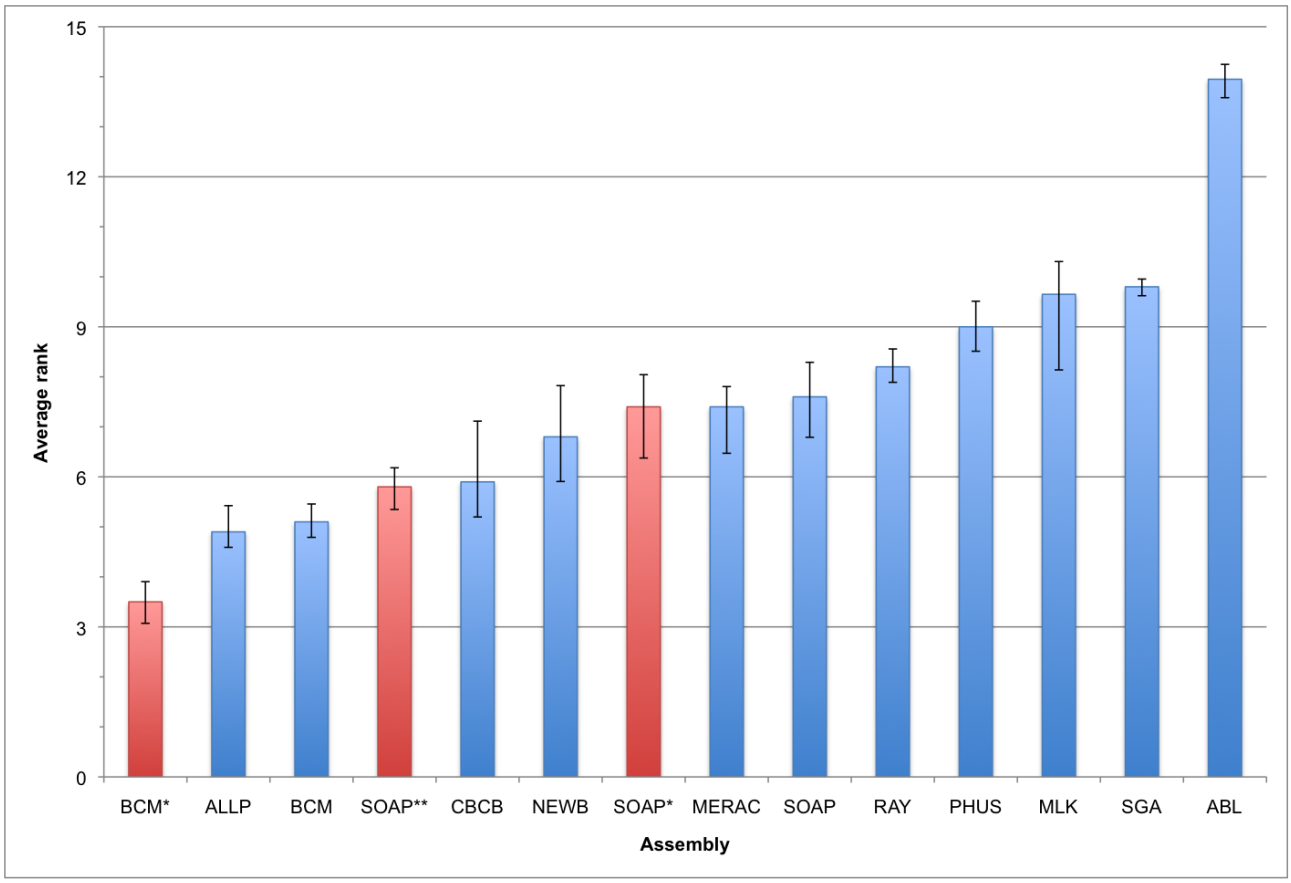


Figure S10: Average rank of fish assemblies when assessed by seven key metrics.

Each assembly was ranked by seven different key metrics and then an average rank was calculated. Positive and negative error bars reflect the best and worst average rank that could be achieved if any one key metric was omitted from the analysis. Assemblies in red represent evaluation entries.

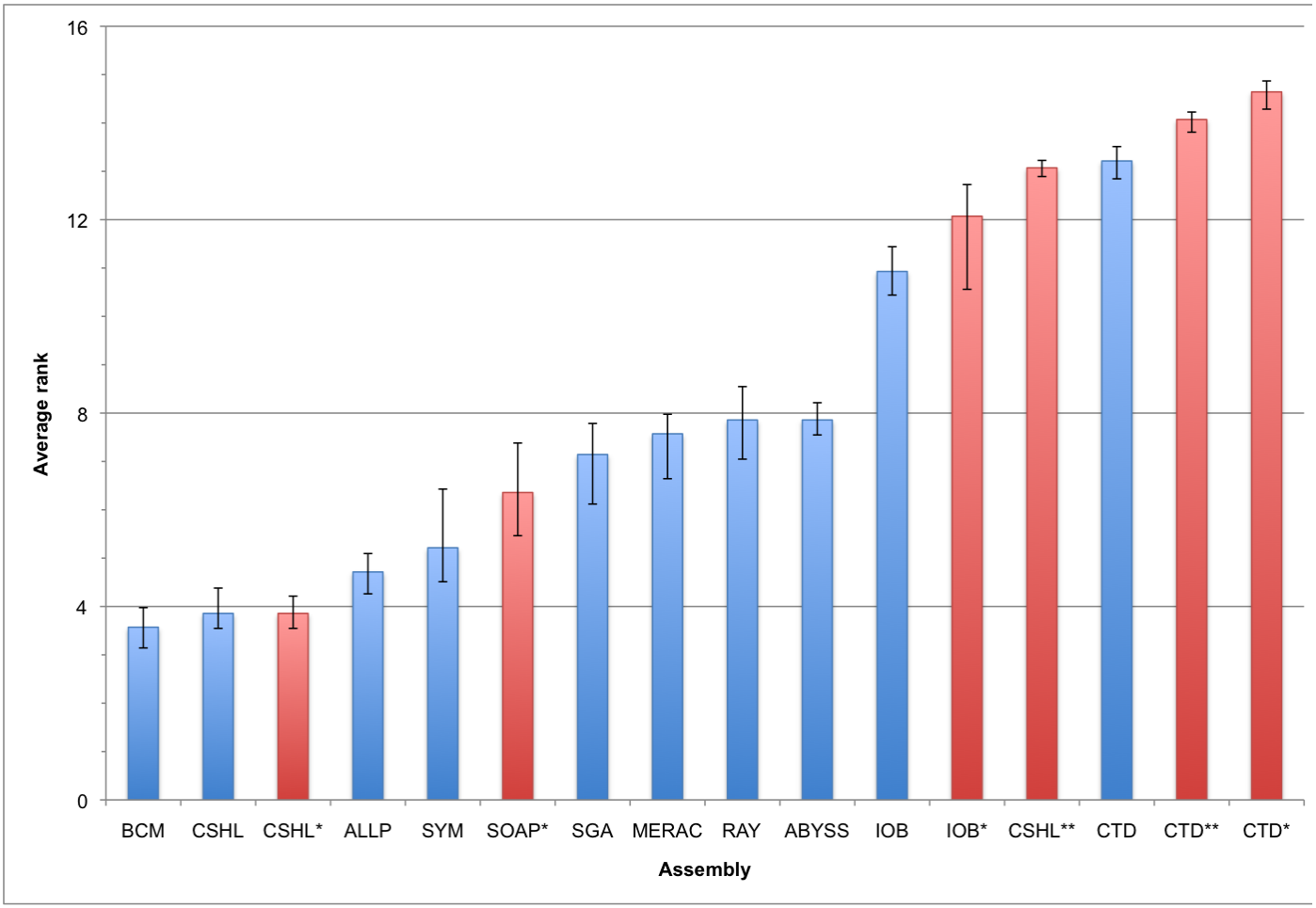


Figure S11: Average rank of snake assemblies when assessed by ten key metrics.

Each assembly was ranked by ten different key metrics and then an average rank was calculated. Positive and negative error bars reflect the best and worst average rank that could be achieved if any one key metric was omitted from the analysis.

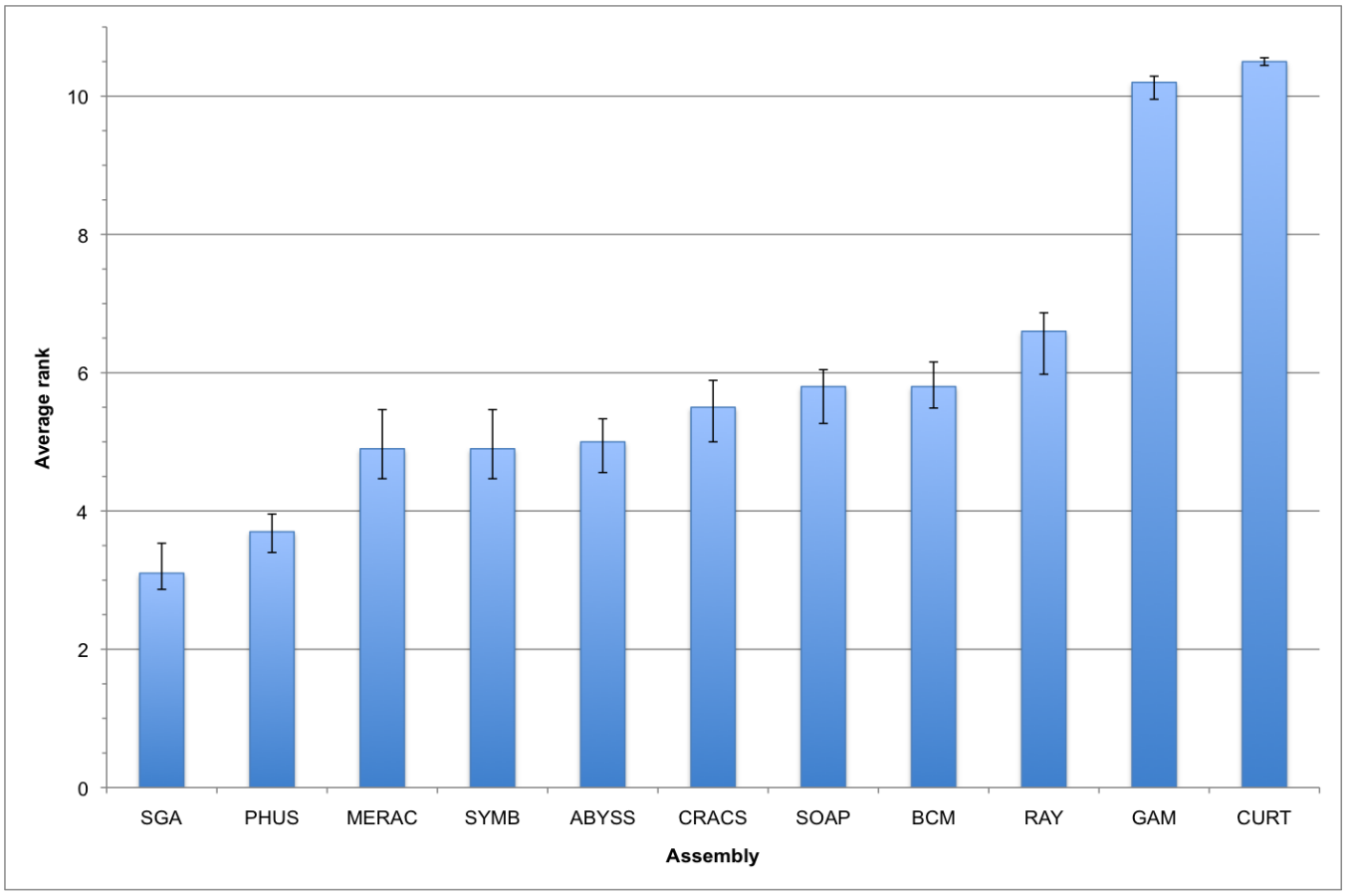


Figure S12: Correlation between key metrics in bird.

Pairwise Pearson's correlation matrix. Above the diagonals are Pearson's R correlations with significance (Bonferroni corrected) indicated as: *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$. Below the diagonal shows the scatterplot of the intersecting row and column key metrics with a simple linear regression drawn in red. Key metrics are CEGMA (number of 458 core eukaryotic genes present); COVERAGE and VALIDITY (of Validated Fosmid Regions, calculated using COMPASS tool); OPTICAL MAP 1 and OPTICAL MAP 1-3 (coverage of optical maps at level 1 or at all levels); VFRT SCORE (summary score of Validated Fosmid Region Tag analysis), GENE-SIZED (the fraction of an assembly's scaffolds that are 25 Kbp or longer); SCAFFOLD NG50 and CONTIG NG50 (the lengths of the scaffold or contig that takes the sum length of all scaffolds/contigs past 50% of the estimated genome size); REAPR SCORE (summary score of scaffolds from REAPR tool).

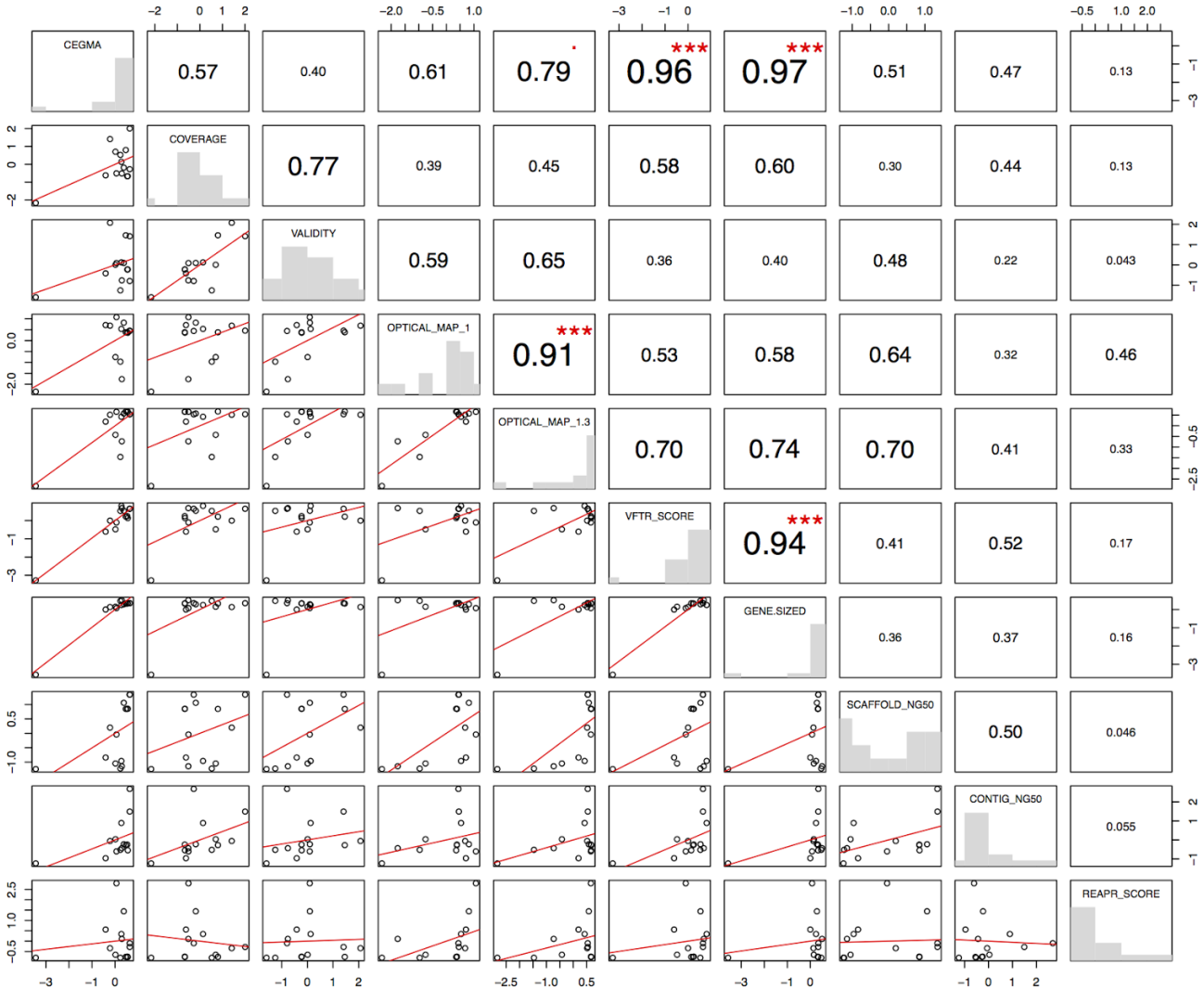


Figure S13: Correlation between key metrics in fish.

Pairwise Pearson's correlation matrix. Above the diagonals are Pearson's R correlations with significance (Bonferroni corrected) indicated as: *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$. Below the diagonal shows the scatterplot of the intersecting row and column key metrics with a simple linear regression drawn in red. Key metrics are CEGMA (number of 458 core eukaryotic genes present); COVERAGE and VALIDITY (of Validated Fosmid Regions, calculated using COMPASS tool); OPTICAL MAP 1 and OPTICAL MAP 1-3 (coverage of optical maps at level 1 or at all levels); VFRT SCORE (summary score of Validated Fosmid Region Tag analysis), GENE-SIZED (the fraction of an assembly's scaffolds that are 25 Kbp or longer); SCAFFOLD NG50 and CONTIG NG50 (the lengths of the scaffold or contig that takes the sum length of all scaffolds/contigs past 50% of the estimated genome size); REAPR SCORE (summary score of scaffolds from REAPR tool).

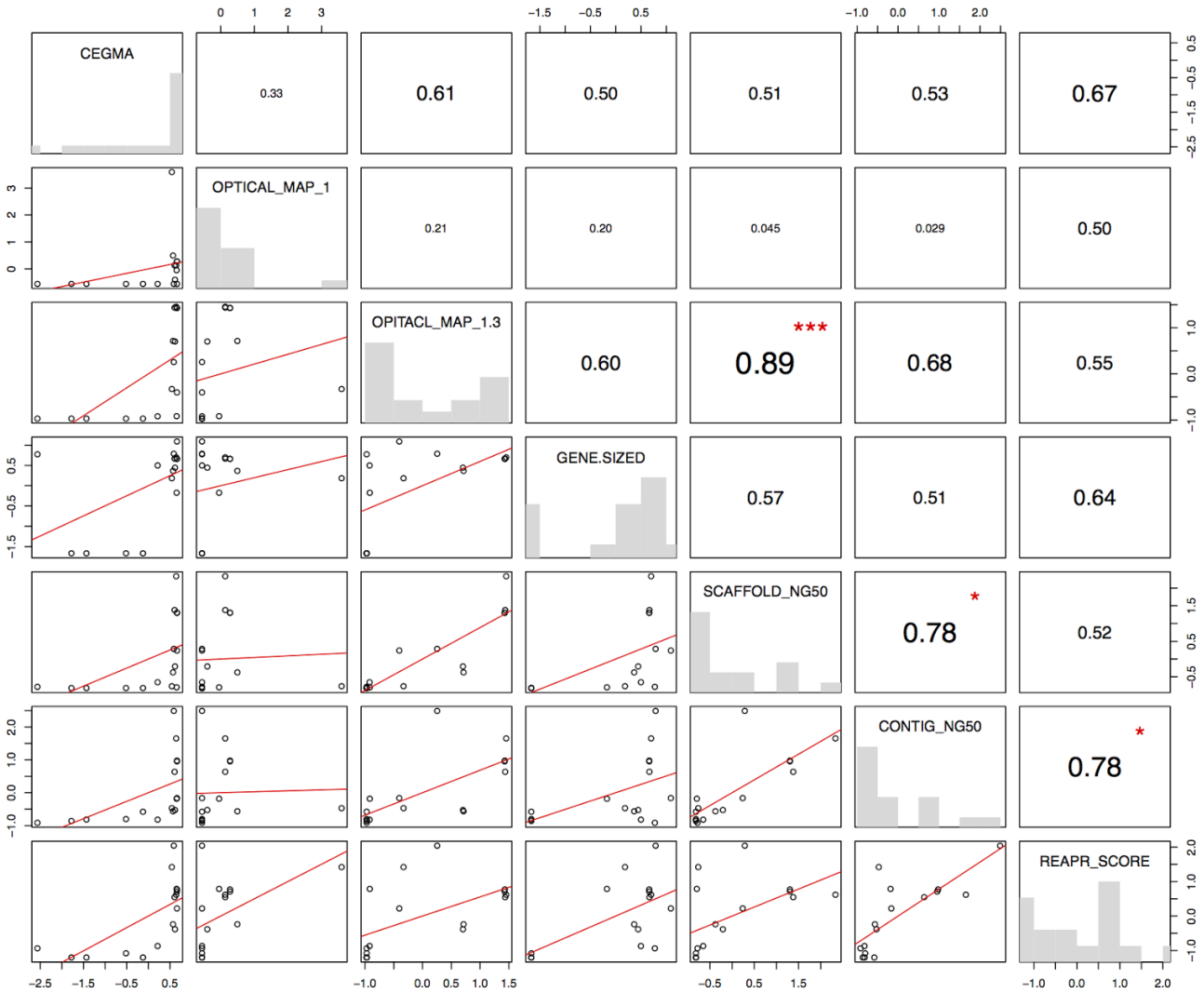


Figure S14: Correlation between key metrics in snake.

Pairwise Pearson's correlation matrix. Above the diagonals are Pearson's R correlations with significance (Bonferroni corrected) indicated as: *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$. Below the diagonal shows the scatterplot of the intersecting row and column key metrics with a simple linear regression drawn in red. Key metrics are CEGMA (number of 458 core eukaryotic genes present); COVERAGE and VALIDITY (of Validated Fosmid Regions, calculated using COMPASS tool); OPTICAL MAP 1 and OPTICAL MAP 1-3 (coverage of optical maps at level 1 or at all levels); VFRT SCORE (summary score of Validated Fosmid Region Tag analysis), GENE-SIZED (the fraction of an assembly's scaffolds that are 25 Kbp or longer); SCAFFOLD NG50 and CONTIG NG50 (the lengths of the scaffold or contig that takes the sum length of all scaffolds/contigs past 50% of the estimated genome size); REAPR SCORE (summary score of scaffolds from REAPR tool).

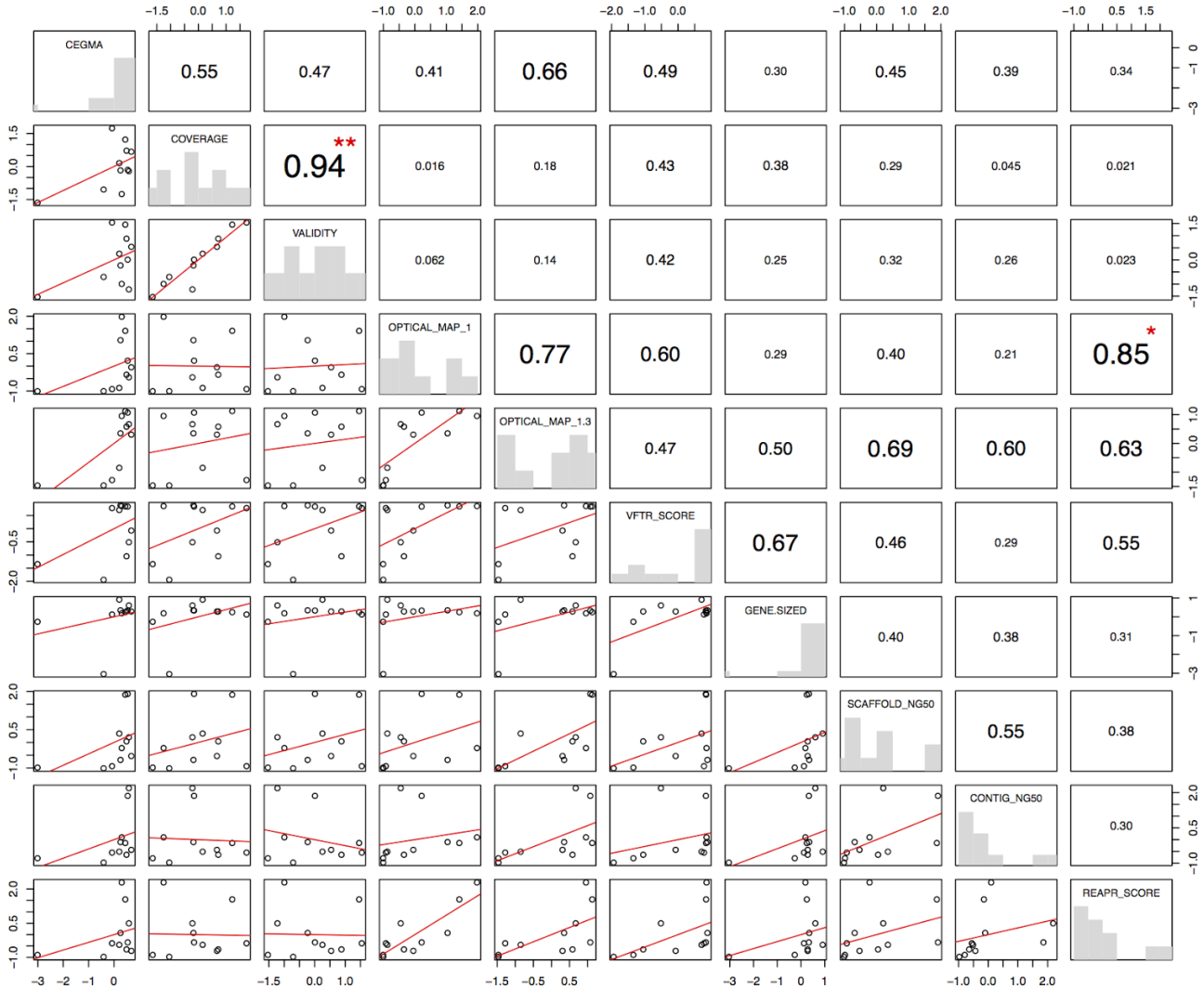


Figure S15: Correlation between key metrics in bird and snake.

Pairwise Pearson's correlation matrix from a combined dataset of z-score values from bird and snake. Above the diagonals are Pearson's R correlations with significance (Bonferroni corrected) indicated as: *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$. Below the diagonal shows the scatterplot of the intersecting row and column key metrics with a simple linear regression drawn in red. Key metrics are CEGMA (number of 458 core eukaryotic genes present); COVERAGE and VALIDITY (of Validated Fosmid Regions, calculated using COMPASS tool); OPTICAL MAP 1 and OPTICAL MAP 1-3 (coverage of optical maps at level 1 or at all levels); VFRT SCORE (summary score of Validated Fosmid Region Tag analysis), GENE-SIZED (the fraction of an assembly's scaffolds that are 25 Kbp or longer); SCAFFOLD NG50 and CONTIG NG50 (the lengths of the scaffold or contig that takes the sum length of all scaffolds/contigs past 50% of the estimated genome size); REAPR SCORE (summary score of scaffolds from REAPR tool).

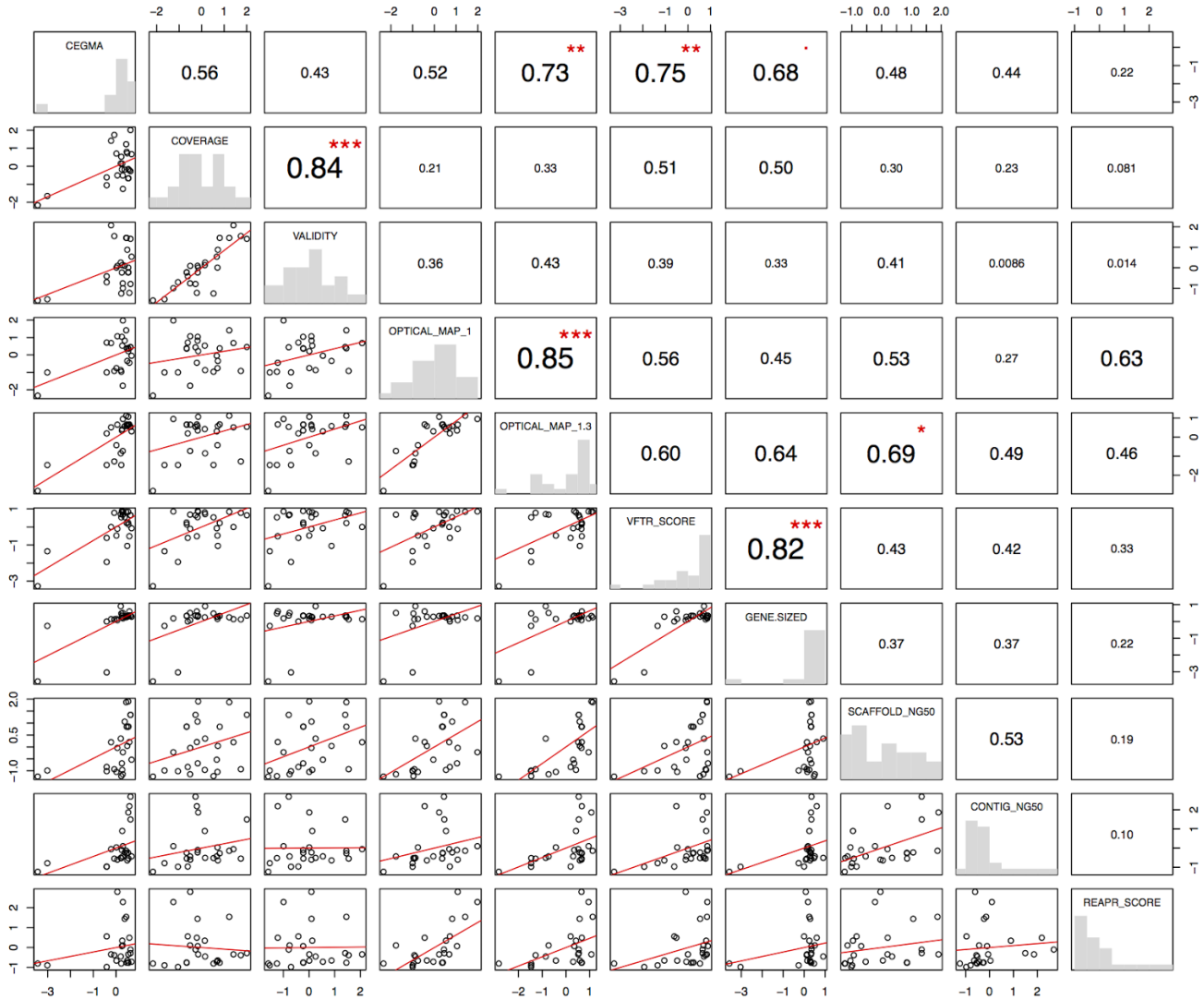
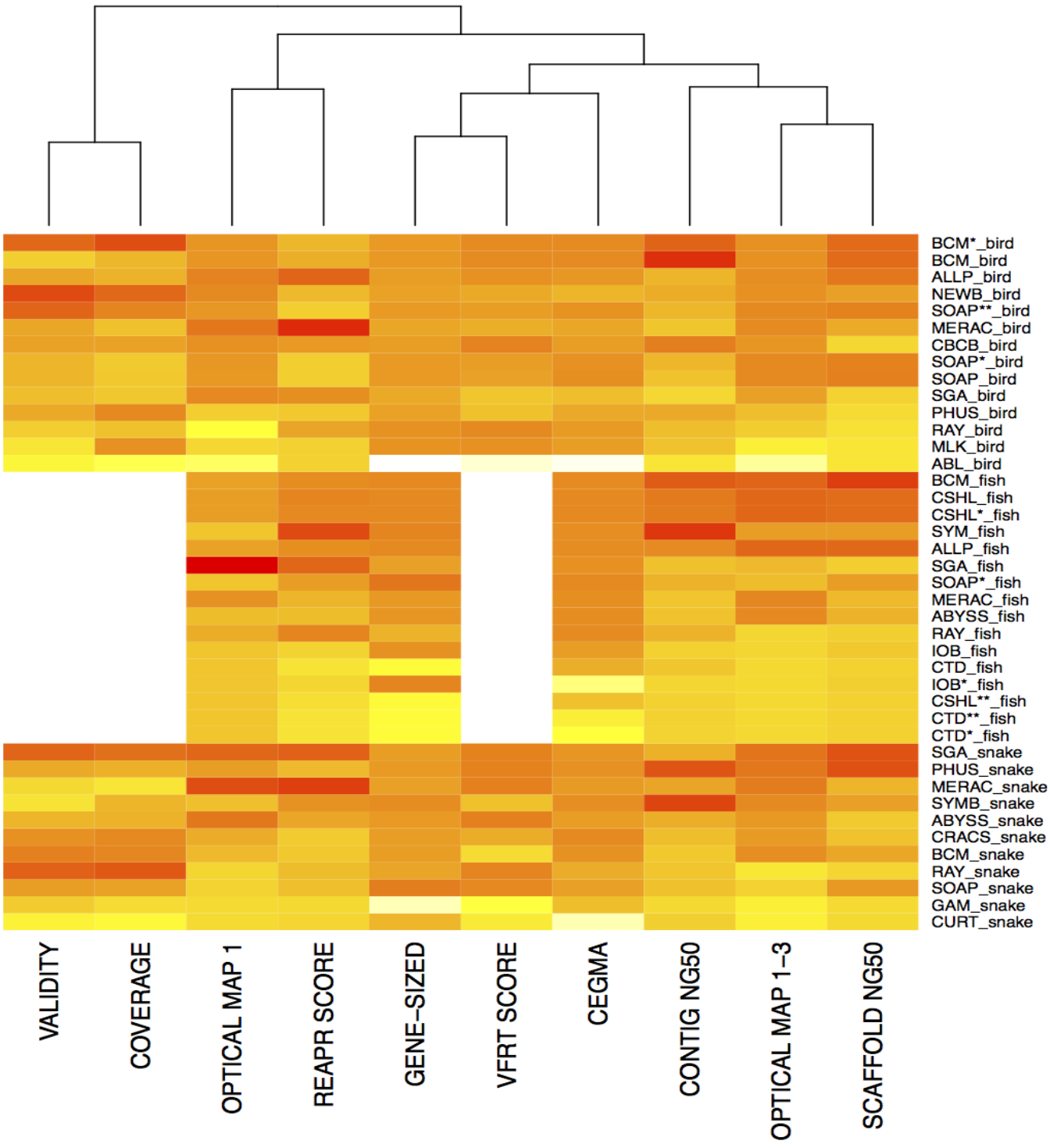


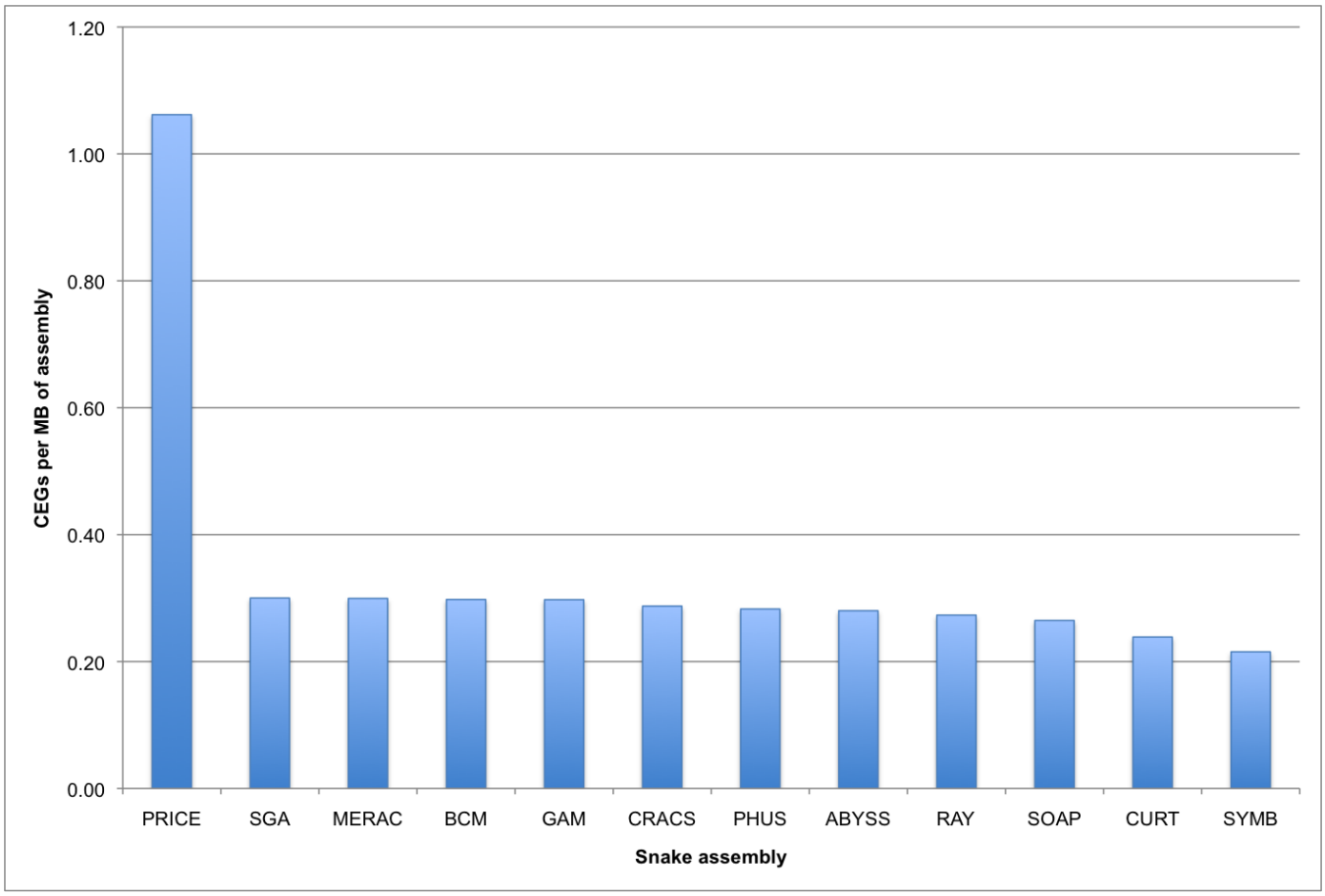
Figure S16: Heat map showing performance of all assemblies as assessed by z-scores from all key metrics.

Assemblies arranged in order of their sum z-score (after separating by species). Red and yellow colors indicate higher and lower z-score values respectively. Three key metrics were not computable for fish assemblies and have been left blank. Key metrics are CEGMA (number of 458 core eukaryotic genes present); COVERAGE and VALIDITY (of Validated Fosmid Regions, calculated using COMPASS tool); OPTICAL MAP 1 and OPTICAL MAP 1-3 (coverage of optical maps at level 1 or at all levels); VFRT SCORE (summary score of Validated Fosmid Region Tag analysis), GENE-SIZED (the fraction of an assembly's scaffolds that are 25 Kbp or longer); SCAFFOLD NG50 and CONTIG NG50 (the lengths of the scaffold or contig that takes the sum length of all scaffolds/contigs past 50% of the estimated genome size); REAPR SCORE (summary score of scaffolds from REAPR tool).


BCM*_bird
BCM_bird
ALLP_bird
NEWB_bird
SOAP**_bird
MERAC_bird
CBCB_bird
SOAP*_bird
SOAP_bird
SGA_bird
PHUS_bird
RAY_bird
MLK_bird
ABL_bird
BCM_fish
CSHL_fish
CSHL*_fish
SYM_fish
ALLP_fish
SGA_fish
SOAP*_fish
MERAC_fish
ABYSS_fish
RAY_fish
IOB_fish
CTD_fish
IOB*_fish
CSHL**_fish
CTD**_fish
CTD*_fish
SGA_snake
PHUS_snake
MERAC_snake
SYMB_snake
ABYSS_snake
CRACS_snake
BCM_snake
RAY_snake
SOAP_snake
GAM_snake
CURT_snake
VALIDITY
COVERAGE
OPTICAL MAP 1
REAPR SCORE
GENE−SIZED
VFRT SCORE
CEGMA
CONTIG NG50
OPTICAL MAP 1−3
SCAFFOLD NG50

Supplementary Figure 17. Performance of all snake assemblies when assessed in terms of 'number of core eukaryotic genes (CEGs) per Mbp of submitted assembly'.

PRICE assembly (first data point) was excluded from full analysis in the Assemblathon 2 contest because the total assembly size comprised <25% of the estimated genome size.



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