# SR2C: A Novel Structurally Redundant Short Reads Collapser for Optimizing Genomic Sequencing Data Compression: Supplementary Materials

# S1 Experimental datasets

Eight real datasets from the NCBI open-source database (<a href="https://www.ncbi.nlm.nih.gov">https://www.ncbi.nlm.nih.gov</a>) were used for the experimental evaluation. The datasets were downloaded using the sra-tools tool, whose script configuration can be found at: <a href="https://github.com/ncbi/sra-tools">https://github.com/ncbi/sra-tools</a>.

### **Dataset 1: C.arietinum**

URL: https://www.ebi.ac.uk/ena/browser/view/SRR13556216

### **Download Script:**

cd SR2C/data

prefetch SRR13556216

fastq-dump SRR13556216

rm -rf SRR13556216 SRR13556216\_2.fastq

### Dataset 2: Human

URL: https://www.ebi.ac.uk/ena/browser/view/SRR16553126

### **Download Script:**

prefetch SRR16553126

fastq-dump SRR16553126

rm -rf SRR16553126 SRR16553126 2.fastq

### Datasets 3&4: M.fascicularis

URL: https://www.ebi.ac.uk/ena/browser/view/SRR8386204

# **Download Script:**

prefetch SRR8386204

fastq-dump SRR8386204

rm -rf SRR8386204

### Datasets 5&6: Mouse.tumor

**URL:** https://www.ebi.ac.uk/ena/browser/view/SRR17794741

### **Download Script:**

prefetch SRR17794741

fastq-dump --split-files SRR17794741

rm -rf SRR17794741

# Dataset 7: S.fontinalis-1

URL: https://www.ebi.ac.uk/ena/browser/view/SRR11995278

# **Download Script:**

prefetch SRR11995278

fastq-dump SRR11995278

rm -rf SRR11995278

# **Dataset 8: S.fontinalis-2**

URL: https://www.ebi.ac.uk/ena/browser/view/SRR11994956

# **Download Script:**

prefetch SRR11994956 fastq-dump SRR11994956 rm -rf SRR11994956

# S2 Supplementary experimental results

Table S1 The number of remaining reads obtained by running algorithms Minirmd and SR2C

Datasets	NMis = 0		NMis = 1		NMis = 2		NMis = 3	
Datasets	Minirmd	SR2C	Minirmd	SR2C	Minirmd	SR2C	Minirmd	SR2C
C.arietinum	27674276	25538394	25122345	23712805	23146415	22014323	21613589	20624364
Human	1134534	1102078	1020979	1017296	982487	980033	961736	959526
M.fascicularis-1	2330651	2321698	1213087	1205610	970240	962876	802288	794989
M.fascicularis-2	2270237	2261396	1260967	1253703	1020431	1013267	889445	882339
Mouse.tumor-1	416097	411960	204643	204506	106609	106516	66036	65947
Mouse.tumor-2	459250	455642	231544	231292	121670	121500	75559	75404
S.fontinalis-1	679936	679731	630201	630072	590035	589932	556059	555965
S.fontinalis-2	3392223	3344524	2990103	2989442	2728974	2728446	2515730	2515288
Total	38357204	36115423	32673869	31244726	29666861	28516893	27480442	26473822

Table S2 Memory overhead obtained by running the algorithms Minirmd and SR2C on 8 datasets (units: KB)

Datasets	NMis = 0		NMis = 1		NMis = 2		NMis = 3	
Datasets	Minirmd	SR2C	Minirmd	SR2C	Minirmd	SR2C	Minirmd	SR2C
C.arietinum	13330652	8540788	18001044	7850524	18578944	7278204	19739192	6824548
Human	1324260	343900	2108904	307072	2206368	296568	2401484	290532
M.fascicularis-1	4953592	716720	7560836	372956	7887288	292516	8538700	244796
M.fascicularis-2	4953300	697284	7560860	385708	7886788	306784	8538580	268436
Mouse.tumor-1	888316	143540	1325736	71888	1381732	38276	1494224	24796
Mouse.tumor-2	888876	157748	1331868	80812	1385460	43268	1494312	27952
S.fontinalis-1	735724	217376	1123732	201684	1172236	189896	1269204	179628
S.fontinalis-2	5592384	1064112	7882296	947280	8165280	867704	8731848	802712
Average	4083388	1485184	5861910	1277241	6083012	1164152	6525943	802712

Table S3 Time overhead obtained by running the algorithms Minirmd and SR2C on 8 datasets (units: HH:MM:SS)

Datasets	NMis = 0		NMi.	NMis = 1		NMis = 2		NMis = 3	
Datasets	Minirmd	SR2C	Minirmd	SR2C	Minirmd	SR2C	Minirmd	SR2C	
C.arietinum	00:06:40	00:57:33	00:29:21	00:52:03	00:17:14	00:47:56	00:13:06	00:44:51	
Human	00:00:13	00:00:54	00:00:18	00:00:47	00:00:25	00:00:44	00:00:29	00:00:46	
M.fascicularis-1	00:00:44	00:02:11	00:01:47	00:01:00	00:01:50	00:00:49	00:02:04	00:00:38	
M.fascicularis-2	00:00:43	00:02:07	00:01:49	00:01:00	00:01:53	00:00:51	00:02:10	00:00:43	
Mouse.tumor-1	00:00:24	00:00:32	00:00:24	00:00:14	00:00:23	00:00:01	00:00:25	00:00:05	
Mouse.tumor-2	00:00:27	00:00:51	00:00:35	00:00:18	00:00:27	00:00:08	00:00:22	00:00:06	
S.fontinalis-1	00:00:11	00:00:43	00:00:28	00:00:41	00:00:24	00:00:34	00:00:26	00:00:31	
S.fontinalis-2	00:01:44	00:05:05	00:04:56	00:04:28	00:04:25	00:04:00	00:04:20	00:03:45	
Average	00:01:23	00:08:45	00:04:57	00:07:34	00:03:23	00:06:53	00:02:55	00:07:20	

Table S4 File sizes obtained by running SR2C cascading with the algorithms Pigz, PBzip2, XZ, and 7Z on 8 datasets (units: KB)

Datasets	Reads		Withou	t SR2C	With SR2C				
Datasets	(KB)	Pigz	PBzip2	XZ	7Z	Pigz	PBzip2	XZ	7Z
C.arietinum	3290620	861399	806193	535604	533003	758942	713971	555339	554035
Human	264860	31592	24917	24903	24695	33679	32998	24922	24963
M.fascicularis-1	1010380	298906	284658	97794	94049	119432	107110	86370	89656
M.fascicularis-2	1010380	298915	284688	98547	94854	118534	106243	86652	89881
Mouse.tumor-1	247098	35329	20419	10235	10195	16963	13557	8575	8639
Mouse.tumor-2	247098	35616	20835	10473	10432	17766	14157	8974	9041
S.fontinalis-1	166494	39403	34787	13857	13871	21502	19407	13899	13927
S.fontinalis-2	1384369	330651	292059	114968	113232	139508	125452	94255	93647
Average	952662	241476	221070	113298	111791	153291	141612	109873	110474

Table S5 Compression ratio improvements obtained by running SR2C cascading with the algorithms Pigz, PBzip2, XZ, and 7Z on 8 datasets (units: Ratio)

Datasets	Reads (KB)	Pigz	PBzip2	XZ	7Z	平均值
C.arietinum	3290620	13.500%	12.917%	-3.554%	-3.796%	4.767%
Human	264860	-6.197%	-24.489%	-0.076%	-1.074%	-7.959%
M.fascicularis-1	1010380	150.273%	165.762%	13.227%	4.900%	83.540%
M.fascicularis-2	1010380	100.473%	47.171%	16.704%	15.385%	44.933%
Mouse.tumor-1	247098	108.271%	50.616%	19.359%	18.011%	49.064%
Mouse.tumor-2	247098	100.473%	47.171%	16.704%	15.385%	44.933%
S.fontinalis-1	166494	83.253%	79.250%	-0.302%	-0.402%	40.450%
S.fontinalis-2	1384369	137.012%	132.805%	21.975%	20.914%	78.177%
Average	952662	92.345%	78.999%	10.132%	7.434%	47.228%

Table S6 Compression time overhead obtained by running SR2C cascading with the algorithms Pigz, PBzip2, XZ, and 7Z on 8 datasets (units: HH:MM:SS)

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Datasets	Reads		Withou	Without SR2C		With SR2C				
Datasets	(KB)	Pigz	PBzip2	XZ	7Z	Pigz	PBzip2	XZ	7Z	
C.arietinum	3290620	00:09:02	00:00:46	00:10:35	00:14:53	00:06:59	00:00:40	00:10:39	00:14:32	
Human	264860	00:00:14	00:00:07	00:02:07	00:02:25	00:00:12	00:00:02	00:02:02	00:01:15	
M.fascicularis-1	1010380	00:02:40	00:00:16	00:05:08	00:05:32	00:00:27	00:00:05	00:04:27	00:04:13	
M.fascicularis-2	1010380	00:02:33	00:00:16	00:05:39	00:05:18	00:00:32	00:00:05	00:04:54	00:04:22	
Mouse.tumor-1	247098	00:00:13	00:00:05	00:01:27	00:01:31	00:00:06	00:00:01	00:00:49	00:00:37	
Mouse.tumor-2	247098	00:00:19	00:00:05	00:01:25	00:01:33	00:00:07	00:00:01	00:00:48	00:00:40	
S.fontinalis-1	166494	00:00:16	00:00:03	00:02:20	00:02:17	00:00:10	00:00:01	00:01:15	00:00:54	
S.fontinalis-2	1384369	00:02:45	00:00:22	00:03:50	00:08:11	00:00:45	00:00:07	00:04:56	00:03:57	
Average	952662	00:02:15	00:00:15	00:04:04	00:05:12	00:01:10	00:00:08	00:03:44	00:03:49	

Table S7 Compression memory overhead obtained by running SR2C cascading with the algorithms Pigz, PBzip2, XZ, and 7Z on 8 datasets (units: KB)

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Detecate	Reads		Wi	thout SR2C		With SR2C			
Datasets	(KB)	Pigz	PBzip2	XZ	7Z	Pigz	PBzip2	XZ	7Z
C.arietinum	3290620	6172	72116	7599220	3601116	6688	75328	7500016	3672028
Human	264860	5768	69628	1467600	697100	6636	79500	757996	697172
M.fascicularis-1	1010380	6340	73648	4238156	3461328	6544	73812	1656040	1523060
M.fascicularis-2	1010380	6224	73508	4238928	3461552	6524	74052	1653292	1495948
Mouse.tumor-1	247098	5896	69384	1279856	697220	6500	77576	647592	643532
Mouse.tumor-2	247098	5888	69524	1280128	697156	6512	79336	673248	664456
S.fontinalis-1	166494	6024	71408	800936	697072	6560	75448	687652	669464
S.fontinalis-2	1384369	6040	73136	5831548	3520396	6396	74600	2180468	1720896
Average	952662	6044	71544	3342047	2104118	6545	76207	1969538	1385820

 $Table \ S8 \ Decompression \ time \ overhead \ obtained \ by \ running \ SR2C \ cascading \ with \ the \ algorithms \ Pigz,$ 

PBzip2, XZ, and 7Z on 8 datasets (units: HH:MM:SS)

Datasets	Reads		Withou	t SR2C		With SR2C			
Datasets	(KB)	Pigz	PBzip2	XZ	7Z	Pigz	PBzip2	XZ	7Z
C.arietinum	3290620	00:00:13	00:00:16	00:00:49	00:00:08	00:00:15	00:00:19	00:00:49	00:00:10
Human	264860	00:00:01	00:00:01	00:00:03	00:00:02	00:00:01	00:00:01	00:00:03	00:00:02
M.fascicularis-1	1010380	00:00:05	00:00:07	00:00:11	00:00:04	00:00:02	00:00:03	00:00:10	00:00:06
M.fascicularis-2	1010380	00:00:05	00:00:07	00:00:11	00:00:06	00:00:02	00:00:03	00:00:10	00:00:06
Mouse.tumor-1	247098	00:00:01	00:00:01	00:00:02	00:00:01	00:00:01	00:00:01	00:00:01	00:00:01
Mouse.tumor-2	247098	00:00:01	00:00:01	00:00:02	00:00:01	00:00:01	00:00:01	00:00:01	00:00:01
S.fontinalis-1	166494	00:00:01	00:00:01	00:00:02	00:00:01	00:00:01	00:00:01	00:00:02	00:00:01
S.fontinalis-2	1384369	00:00:07	00:00:08	00:00:14	00:00:04	00:00:03	00:00:03	00:00:11	00:00:06
Average	952662	00:00:04	00:00:05	00:00:12	00:00:03	00:00:03	00:00:04	00:00:11	00:00:04

Table S9 Decompression memory overhead obtained by running SR2C cascading with the algorithms Pigz,

PBzip2, XZ, and 7Z on 8 datasets (units: HH:MM:SS)

Datasets	Reads		Wit	hout SR2C		With SR2C				
Datasets	(KB)	Pigz	PBzip2	XZ	7Z	Pigz	PBzip2	XZ	7Z	
C.arietinum	3290620	992	54896	66564	2445572	988	59492	66552	2541752	
Human	264860	1012	48068	66560	284252	1008	53212	66560	131920	
M.fascicularis-1	1010380	1012	55232	66564	1081688	1008	51992	66560	408480	
M.fascicularis-2	1010380	1000	51280	66564	1082336	1012	50924	66560	405908	
Mouse.tumor-1	247098	1008	48856	66560	252568	1008	48180	64492	73048	
Mouse.tumor-2	247098	1008	49912	66564	252836	1008	48388	66564	77800	
S.fontinalis-1	166494	1012	47676	66564	177528	1008	48532	66564	87836	
S.fontinalis-2	1384369	1008	55588	66564	1466436	1008	53136	66564	532024	
Average	952662	1007	51439	66563	880402	1006	51732	66302	532346	