Supplementary Material

The original scaffolds are assembled by two different assemblers Velvet and Soap2. The genome S.aureus includes read dataset 1 and 2. The genome R.sphaeroides includes read dataset 3 and 4. The genome Human 14 includes read dataset 5. The detail information about the five datasets and original scaffolds are shown in the main text. The following tables show the evaluation results of gap-filled scaffolds by different gap filling tools.

Table S1. Evaluations of gap filling results on dataset 2 (Scaffolds are assembled by Velvet for S.aureus)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	248	135	124	11	0.919	0.5	0.648
	Relocation Gap	17	2376	570	538	32	0.944	0.226	0.365
	Normal Gap	97	31777	5547	5337	210	0.962	0.168	0.286
	All Gap	125	34401	6252	5999	253	0.96	0.174	0.295
GapFiller	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	238	0	0	0	–	–	–
	Relocation Gap	17	2246	62	59	3	0.952	0.026	0.051
	Normal Gap	97	31777	312	214	98	0.686	0.007	0.013
	All Gap	125	34261	374	273	101	0.73	0.008	0.016
Sealer	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	238	0	0	0	–	–	–
	Relocation Gap	17	2687	543	469	74	0.864	0.175	0.29
	Normal Gap	97	31777	2316	2185	131	0.943	0.069	0.128
	All Gap	125	34702	2859	2654	205	0.928	0.076	0.141
Gap2Seq	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	235	135	121	14	0.896	0.515	0.654
	Relocation Gap	17	2246	82	78	4	0.951	0.035	0.067
	Normal Gap	97	31777	1543	1444	99	0.936	0.045	0.087
	All Gap	125	34258	1760	1643	117	0.934	0.048	0.091

Table S2. Evaluations of gap filling results on dataset 2 (Scaffolds are assembled by SOAP2 for S.aureus)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	2	3940	130	122	8	0.938	0.031	0.06
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	1	488	488	255	233	0.523	0.523	0.523
	Normal Gap	6	702	66	49	17	0.742	0.07	0.128
	All Gap	9	5130	684	426	258	0.623	0.083	0.147
GapFiller	Missing Gap	2	3940	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	1	488	488	255	233	0.523	0.523	0.523
	Normal Gap	6	702	48	46	2	0.958	0.066	0.123
	All Gap	9	5130	536	301	235	0.562	0.059	0.106
Sealer	Missing Gap	2	3940	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	1	488	488	255	233	0.523	0.523	0.523
	Normal Gap	6	702	115	84	31	0.73	0.12	0.206
	All Gap	9	5130	603	339	264	0.562	0.066	0.118
Gap2Seq	Missing Gap	2	3940	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	1	488	488	255	233	0.523	0.523	0.523
	Normal Gap	6	702	80	80	0	1	0.114	0.205
	All Gap	9	5130	568	335	233	0.59	0.065	0.118

Table S3. Evaluations of gap filling results on dataset 1 and 2 (Scaffolds are assembled by Velvet for S.aureus)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	155	145	141	4	0.972	0.91	0.94
	Relocation Gap	17	2680	1245	1150	95	0.924	0.429	0.586
	Normal Gap	97	31777	13114	12611	503	0.962	0.397	0.562
	All Gap	125	34612	14504	13902	602	0.958	0.402	0.566
GapFiller	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	1668	1661	1429	232	0.86	0.857	0.859
	Relocation Gap	17	3714	2080	1845	235	0.887	0.497	0.637
	Normal Gap	97	31777	9579	8970	609	0.936	0.282	0.434
	All Gap	125	37159	13320	12244	1076	0.919	0.33	0.485
Sealer	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	238	0	0	0	–	–	–
	Relocation Gap	17	2738	829	729	100	0.879	0.266	0.409
	Normal Gap	97	31777	3266	3027	239	0.927	0.095	0.173
	All Gap	125	34753	4095	3756	339	0.917	0.108	0.193
Gap2Seq	Missing Gap	0	0	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	11	241	141	116	25	0.823	0.481	0.607
	Relocation Gap	17	2806	2461	2366	95	0.961	0.843	0.898
	Normal Gap	97	31777	17460	16620	840	0.952	0.523	0.675
	All Gap	125	34824	20062	19102	960	0.952	0.549	0.696

Table S4. Evaluations of gap filling results on dataset 1 and 2 (Scaffolds are assembled by SOAP2 for S.aureus)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	2	3264	1441	1126	315	0.781	0.345	0.479
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	1	671	671	357	314	0.532	0.532	0.532
	Normal Gap	6	702	131	104	27	0.794	0.148	0.25
	All Gap	9	4637	2243	1587	656	0.708	0.342	0.461
GapFiller	Missing Gap	2	3940	492	492	0	1	0.125	0.222
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	1	488	488	255	233	0.523	0.523	0.523
	Normal Gap	6	702	147	147	0	1	0.209	0.346
	All Gap	9	5130	1127	894	233	0.793	0.174	0.286
Sealer	Missing Gap	2	3940	0	0	0	-	-	-
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	1	488	488	255	233	0.523	0.523	0.523
	Normal Gap	6	702	108	91	17	0.843	0.13	0.225
	All Gap	9	5130	596	346	250	0.581	0.067	0.121
Gap2Seq	Missing Gap	2	4047	4047	2942	1105	0.727	0.727	0.727
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	1	622	622	325	297	0.523	0.523	0.523
	Normal Gap	6	702	134	100	34	0.746	0.142	0.239
	All Gap	9	5371	4803	3367	1436	0.701	0.627	0.662

Table S5. Evaluations of gap filling results on dataset 3 (Scaffolds are assembled by Velvet for R.sphaeroides)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	2	21	11	10	1	0.909	0.476	0.625
	Translocation Gap	20	19040	2349	1852	497	0.788	0.097	0.173
	Inversion Gap	11	195	92	89	3	0.967	0.456	0.62
	Relocation Gap	15	3866	150	145	5	0.967	0.038	0.072
	Normal Gap	377	85875	8332	7771	561	0.933	0.09	0.165
	All Gap	425	108997	10934	9867	1067	0.902	0.091	0.165
GapFiller	Missing Gap	2	272	271	219	52	0.808	0.805	0.807
	Translocation Gap	20	20843	1891	1788	103	0.946	0.086	0.157
	Inversion Gap	11	740	646	645	1	0.998	0.872	0.931
	Relocation Gap	15	4724	1032	901	131	0.873	0.191	0.313
	Normal Gap	377	85875	8135	7914	221	0.973	0.092	0.168
	All Gap	425	112454	11975	11467	508	0.958	0.102	0.184
Sealer	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	20045	313	308	5	0.984	0.015	0.03
	Inversion Gap	11	189	0	0	0	–	–	–
	Relocation Gap	15	3856	2	2	0	1	0.001	0.001
	Normal Gap	377	85875	3086	2538	548	0.822	0.03	0.057
	All Gap	425	109985	3401	2848	553	0.837	0.026	0.05
Gap2Seq	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	20038	10495	10224	271	0.974	0.51	0.67
	Inversion Gap	11	379	279	272	7	0.975	0.718	0.827
	Relocation Gap	15	4117	4007	3899	108	0.973	0.947	0.96
	Normal Gap	377	85875	30131	28252	1879	0.938	0.329	0.487
	All Gap	425	110429	44912	42647	2265	0.95	0.386	0.549

Table S6. Evaluations of gap filling results on dataset 3 (Scaffolds are assembled by SOAP2 for R.sphaeroides)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	4	2193	145	132	13	0.91	0.06	0.113
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	0	0	0	0	0	-	-	-
	Normal Gap	34	9511	621	483	138	0.778	0.051	0.095
	All Gap	38	11704	766	615	151	0.803	0.053	0.099
GapFiller	Missing Gap	4	2193	151	145	6	0.96	0.066	0.124
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	0	0	0	0	0	-	-	-
	Normal Gap	34	9511	124	104	20	0.839	0.011	0.022
	All Gap	38	11704	275	249	26	0.905	0.021	0.042
Sealer	Missing Gap	4	2193	0	0	0	-	-	-
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	0	0	0	0	0	-	-	-
	Normal Gap	34	9511	90	81	9	0.9	0.009	0.017
	All Gap	38	11704	90	81	9	0.9	0.007	0.014
Gap2Seq	Missing Gap	4	2193	0	0	0	-	-	-
	Translocation Gap	0	0	0	0	0	-	-	-
	Inversion Gap	0	0	0	0	0	-	-	-
	Relocation Gap	0	0	0	0	0	-	-	-
	Normal Gap	34	9511	90	89	1	0.989	0.009	0.019
	All Gap	38	11704	90	89	1	0.989	0.008	0.015

Table S7. Evaluations of gap filling results on dataset 4 (Scaffolds are assembled by Velvet for R.sphaeroides)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	2	21	17	17	0	1	0.81	0.895
	Translocation Gap	20	19903	560	532	28	0.95	0.027	0.052
	Inversion Gap	11	196	123	110	13	0.894	0.561	0.69
	Relocation Gap	15	3874	120	117	3	0.975	0.03	0.059
	Normal Gap	377	85875	3593	3203	390	0.891	0.037	0.072
	All Gap	425	109869	4413	3979	434	0.902	0.036	0.07
GapFiller	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	20015	243	236	7	0.971	0.012	0.023
	Inversion Gap	11	189	0	0	0	–	–	–
	Relocation Gap	15	3929	75	75	0	1	0.019	0.037
	Normal Gap	377	85875	989	933	56	0.943	0.011	0.021
	All Gap	425	110028	1307	1244	63	0.952	0.011	0.022
Sealer	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	19895	143	138	5	0.965	0.007	0.014
	Inversion Gap	11	189	0	0	0	–	–	–
	Relocation Gap	15	3864	0	0	0	–	–	–
	Normal Gap	377	85875	1096	1063	33	0.97	0.012	0.024
	All Gap	425	109843	1239	1201	38	0.969	0.011	0.022
Gap2Seq	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	20425	693	671	22	0.968	0.033	0.064
	Inversion Gap	11	189	0	0	0	–	–	–
	Relocation Gap	15	3864	0	0	0	–	–	–
	Normal Gap	377	85875	1913	1879	34	0.982	0.022	0.043
	All Gap	425	110373	2606	2550	56	0.979	0.023	0.045

Table S8. Evaluations of gap filling results on dataset 4 (Scaffolds are assembled by SOAP2 for R.sphaeroides)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	4	2193	55	52	3	0.945	0.024	0.046
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	868	440	428	0.507	0.046	0.085
	All Gap	38	11704	923	492	431	0.533	0.042	0.078
GapFiller	Missing Gap	4	2193	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	0	0	0	–	–	–
	All Gap	38	11704	0	0	0	–	–	–
Sealer	Missing Gap	4	2193	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	100	91	9	0.91	0.01	0.019
	All Gap	38	11704	100	91	9	0.91	0.008	0.015
Gap2Seq	Missing Gap	4	2193	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	100	96	4	0.96	0.01	0.02
	All Gap	38	11704	100	96	4	0.96	0.008	0.016

Table S9. Evaluations of gap filling results on dataset 3 and 4 (Scaffolds are assembled by Velvet for R.sphaeroides)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	2	21	11	3	8	0.273	0.143	0.187
	Translocation Gap	20	20053	630	613	17	0.973	0.031	0.059
	Inversion Gap	11	197	98	94	4	0.959	0.477	0.637
	Relocation Gap	15	3867	148	141	7	0.953	0.036	0.07
	Normal Gap	377	85875	7393	6811	582	0.921	0.079	0.146
	All Gap	425	110013	8280	7662	618	0.925	0.07	0.13
GapFiller	Missing Gap	2	272	271	219	52	0.808	0.805	0.807
	Translocation Gap	20	20843	1891	1788	103	0.946	0.086	0.157
	Inversion Gap	11	740	646	645	1	0.998	0.872	0.931
	Relocation Gap	15	4724	1032	901	131	0.873	0.191	0.313
	Normal Gap	377	85875	8135	7914	221	0.973	0.092	0.168
	All Gap	425	112454	11975	11467	508	0.958	0.102	0.184
Sealer	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	20045	313	294	19	0.939	0.015	0.029
	Inversion Gap	11	189	0	0	0	–	–	–
	Relocation Gap	15	3856	2	2	0	1	0.001	0.001
	Normal Gap	377	85875	4074	3665	409	0.9	0.043	0.081
	All Gap	425	109985	4389	3961	428	0.902	0.036	0.069
Gap2Seq	Missing Gap	2	20	0	0	0	–	–	–
	Translocation Gap	20	20887	3255	3116	139	0.957	0.149	0.258
	Inversion Gap	11	379	279	271	8	0.971	0.715	0.824
	Relocation Gap	15	4259	1735	1659	76	0.956	0.39	0.554
	Normal Gap	377	85875	13802	12870	932	0.932	0.15	0.258
	All Gap	425	111420	19071	17916	1155	0.939	0.161	0.275

Table S10. Evaluations of gap filling results on dataset 3 and 4 (Scaffolds are assembled by SOAP2 for R.sphaeroides)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	4	2193	93	80	13	0.86	0.036	0.07
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	651	537	114	0.825	0.056	0.106
	All Gap	38	11704	744	617	127	0.829	0.053	0.099
GapFiller	Missing Gap	4	2193	151	145	6	0.96	0.066	0.124
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	124	104	20	0.839	0.011	0.022
	All Gap	38	11704	275	249	26	0.905	0.021	0.042
Sealer	Missing Gap	4	2193	0	0	0	–	–	–
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	100	91	9	0.91	0.01	0.019
	All Gap	38	11704	100	91	9	0.91	0.008	0.015
Gap2Seq	Missing Gap	4	2497	868	655	213	0.755	0.262	0.389
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	0	0	0	0	0	–	–	–
	Relocation Gap	0	0	0	0	0	–	–	–
	Normal Gap	34	9511	100	95	5	0.95	0.01	0.02
	All Gap	38	12008	968	750	218	0.775	0.062	0.116

Table S11. Evaluations of gap filling results on dataset 5 (Scaffolds are assembled by Velvet for Human 14)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	3473	2594853	224824	202183	22641	0.899	0.078	0.143
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	4875	3143932	187004	170268	16736	0.911	0.054	0.102
	Relocation Gap	6986	2749887	243958	220497	23461	0.904	0.08	0.147
	Normal Gap	32120	20250938	2015113	1794925	220188	0.891	0.089	0.161
	All Gap	47454	28739610	2670899	2387873	283026	0.894	0.083	0.152
GapFiller	Missing Gap	3473	2685810	85814	75806	10008	0.883	0.028	0.055
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	4875	3181647	90725	83238	7487	0.917	0.026	0.051
	Relocation Gap	6986	2843418	143928	130802	13126	0.909	0.046	0.088
	Normal Gap	32120	20250938	1021814	863965	157849	0.846	0.043	0.081
	All Gap	47454	28961813	1342281	1153811	188470	0.86	0.04	0.076
Sealer	Missing Gap	3473	2581395	110433	101457	8976	0.919	0.039	0.075
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	4875	3142167	47702	41729	5973	0.875	0.013	0.026
	Relocation Gap	6986	2750141	66700	57607	9093	0.864	0.021	0.041
	Normal Gap	32120	20250938	795852	757308	38544	0.952	0.037	0.072
	All Gap	47454	28724641	1020687	958101	62586	0.939	0.033	0.064
Gap2Seq	Missing Gap	*	*	*	*	*	*	*	*
	Translocation Gap	*	*	*	*	*	*	*	*
	Inversion Gap	*	*	*	*	*	*	*	*
	Relocation Gap	*	*	*	*	*	*	*	*
	Normal Gap	*	*	*	*	*	*	*	*
	All Gap	*	*	*	*	*	*	*	*

(Gap2Seq can not get the final gap filling results, so the metrics are represented by '*')

Table S12. Evaluations of gap filling results on dataset 5 (Scaffolds are assembled by Velvet for Human 14)

Tool	Gap Type	GC	RGL	GfL	MN	MmN	Pre	Rec	F1-score
GapCloser	Missing Gap	582	505549	35885	30328	5557	0.845	0.06	0.112
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	271	289728	21536	17497	4039	0.812	0.06	0.112
	Relocation Gap	359	352986	30715	24930	5785	0.812	0.071	0.13
	Normal Gap	7308	3853666	465018	275956	189062	0.593	0.072	0.128
	All Gap	8520	5001929	553154	348711	204443	0.63	0.07	0.126
Sealer	Missing Gap	582	522449	16361	13500	2861	0.825	0.026	0.05
GapFiller	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	271	288809	13930	8737	5193	0.627	0.03	0.058
	Relocation Gap	359	361890	16358	12288	4070	0.751	0.034	0.065
	Normal Gap	7308	3853666	290331	154288	136043	0.531	0.04	0.074
	All Gap	8520	5026814	336980	188813	148167	0.56	0.038	0.07
Sealer	Missing Gap	582	512281	6626	4417	2209	0.667	0.009	0.017
	Translocation Gap	0	0	0	0	0	–	–	–
	Inversion Gap	271	290551	6371	3792	2579	0.595	0.013	0.026
	Relocation Gap	359	355595	9384	5673	3711	0.605	0.016	0.031
	Normal Gap	7308	3853666	158447	58663	99784	0.37	0.015	0.029
	All Gap	8520	5012093	180828	72545	108283	0.401	0.014	0.028
Gap2Seq	Missing Gap	*	*	*	*	*	*	*	*
	Translocation Gap	*	*	*	*	*	*	*	*
	Inversion Gap	*	*	*	*	*	*	*	*
	Relocation Gap	*	*	*	*	*	*	*	*
	Normal Gap	*	*	*	*	*	*	*	*
	All Gap	*	*	*	*	*	*	*	*

(Gap2Seq can not get the final gap filling results, so the metrics are represented by '*')