

## Petition: make newbler open source

We, the signees of this petition, hereby ask Roche Applied Science to make the source code of GS De Novo Assembler, GS Reference Mapper and GS Amplicon Variant Analyzer, from here on collectively called 'Newbler', open source, at the latest when the 454 Life Sciences sequencing operations are shutdown.

We worry that after the 454 shutdown, Newbler will no longer be available, meaning that large swathes of the current scientific literature that relied for their analysis on the newbler software can no longer be recapitulated from the raw data. Also, long after the 454 shutdown, many researchers will have to process their 454 sequencing data, and many may still want to rely on Newbler for that purpose.

Additionally, Newbler represents a very valuable contribution to the field of genome assembly and mapping. Software developers can learn from the algorithms and implementations of the Newbler code, opening up for reusing these in other programs. Also, there is the hope that developers will improve upon the program, for example by adding support for other sequencing technologies, or assembling with longer reads.

	Name	Affiliation	Comments (Optional)
1	Lex Nederbragt	University of Oslo	
2	Guy Leonard	University of Exeter	
3	Filip Husnik	University of South Bohemia	
4	Tore Oldeide Elgvin	University of Oslo	
5	Pablo Balseiro	University of Bergen	Roche has an excellent opportunity of publicit their commitment with science making their fantastic product Newbler open-source
6	Nick Loman	University of Birmingham	
7	Albert Vilella	Illumina	
8	Ketil Malde	Institute of Marine Research	
9	Torsten Seemann	Monash university	It's the ethically right thing to do.
10	Roy Chaudhuri	University of Sheffield	
11	Karin Lagesen	Oslo University Hospital	
12	Martin Malmstrøm	University of Oslo	
13	Nathan Watson-Haigh	Australian Centre for Plant Functional Genomics (ACPFG)	
14	Bastiaan Star	University of Oslo	
15	Martin Hunt	Wellcome Trust Sanger Institute	
16	Andreas Leimbach	University of Münster, Germany	
17	Ole Kristian Tørresen	University of Oslo, Norway	
18	Shlomo Blum	Kimron Veterinary Institute	
19	Peter Cock	Open Bioinformatics Foundation	
20	Rodolfo Aramayo	Texas A&M University	
21	Jordi Durban	Sistemas Genómicos	
22	Jonathan Klassen	University of Connecticut	
23	Belynda Hicks	NCI	
24	Robert M Flight	Markey Cancer Center, University of Kentucky	
25	Ovidiu Rucker	IMG M Laboratories	
26	Jorge Langa	University of the Basque Country	
27	Ryo Koyanagi	Okinawa Institute of Science and Technology, Japan	I would like to runProject forever!
28	Lars Arvestad	Stockholm University	
29	Rayan Chikhi	PSU	
30	Mike Lelivelt	Life Technologies	Life Technologies would be happy to wrap Newbler as a Torrent Suite plug-in if the tool was available under a friendly open source license.
31	Jason Affourtit	my personal opinion	
32	Jim Hu	Texas A&M University	

33	Christian	Biomatters	
34	Manabu Fujie	OIST	
35	Rebecca M Duar	University of Nebraska	
36	Daniel Udway	Warp Drive Bio	
37	Michael Schatz	Cold Spring Harbor Laboratory	
38	Anders Lanzen	Neiker	
39	Ivars	BMC	
40	Milton Tan	Auburn University	
41	Mary Krauland	University of Pittsburgh	Newbler source code is very valuable to the sequencing community. Roche will be doing a service to the scientific community by making the Newbler source code available after the 454 shutdown.
42	Martin Whittle	Genomic Engenharia Molecular	whittlemr@gmail.com
43	Mitchell Bekritsky	Cold Spring Harbor Laboratory	
44	Joseph Ryan	Whitney Laboratory for Marine Bioscience	make it open and rename it Rochembler
45	John Eppley	MIT	
46	Chad Harland	University of Liege	
47	Estefania Mancini	Fundacion Instituto Leloir	
48	Jonathan Jacobs	MRIGlobal	
49	Narayanan Raghupathy	Jackson Laboratory	
50	Laura Williams	US Dept of Agriculture	
51	Joke Reumers	Janssen R&D	
52	Keith Bradnam	UC Davis	
53	Shaun Jackman	University of British Columbia	
54	Sirisha Sunkara	Lawrence Berkeley National Lab	
55	Jeff Pummill	University of Arkansas	
56	Henk den Bakker	Cornell University	
57	Damien Marsic	University of Florida	
58	Joshua R. Herr	Ph.D. Department of Microbiology & Molecular Genetics, Michigan State University	
59	Keith Robison	Warp Drive Bio	Good will from making this OS is best value Roche can get for this code This is way overdue. James Knight has done wonderful work but Newbler may fall through the cracks if it is not opened up to the community.
60	Surya Saha	Cornell University	
61	Christopher Hill	UMD	
62	Ricardo Grøndahl-Rosado	Faculty of Veterinary Medicine and Biosciences, NMBU	
63	Jan van Haarst	Wageningen UR	
64	Jared Simpson	Ontario Institute for Cancer Research	
65	Russell Neches	UC Davis	newbler was always my favorite thing about 454. It deserves to live on. Newbler was the basis for contig assembly of MiSeq data for me. An excellent piece of software. S.Paterson@liv.ac.uk @scottishwormboy
66	Prof Steve Paterson	Centre for Genomic Research, University of Liverpool	
67	H van de Geest	Bsc	
68	Dan Fornika	Simon Fraser University	
69	Ruibang Luo	The Department of Computer Science, The University of Hong Kong	

70	Casey Bergman	University of Manchester	I strongly support this petition and note there is a precedent for a commercially-developed assembler to be made publicly available under an open source license - the Celera assembler - much to the benefit of the scientific community.
71	Sujai Kumar	University of Oxford	The Newbler suite has been remarkably useful and should continue to be so. I hope Jim Knight sees this and pushes for his creation to be made open source
72	Danny Miller	MD/PhD Student, University of Kansas Medical Center	
73	Daniel S. Standage	Indiana University	
74	Paul Flicek	EMBL European Bioinformatics Institute	
75	Jason Barbour	U Hawaii Manoa	
76	Leighton Pritchard	The James Hutton Institute	
77	Paul Johnston	Free University of Berlin	
78	Manoj Samanta	Systemix Institute	Call it 'oldbler' or whatever, but please make it open-source.
79	Dr. Colin Davenport	Hannover Medical School	
80	Nicholas Edgington	Southern Connecticut State University	
81	Ronny van Aerle	University of Exeter	
82	David Jenkins	GeneDx	
83	Ole Lund	DTU	
84	Nick Booher	Cornell University	
85	Sun Ho Cha	GenoTech	
86	Gaurav Sablok	Fondazione Edmund Mach, Italy	
87	Vincent Liu	New Zealand Forest Research Institute Limited	
88	yvan strahm	ous, oslo	
89	Bharani Kumar	IAEA-FAO	
90	Tom Kristensen	Dept. Biosciences, University of Oslo	
91	Helle Baalsrud	University of Oslo	
92	Ricardo Junqueira	FIOCRUZ	
93	Lei ZHANG	Logic Informatics Co.,Ltd.	
94	Laura Porturas	San Diego State University Alumni	
95	Yulong Niu	Sichuan University, China	
96	Soumitra Pal	IIT Bombay	
97	Andrew Yates	EMBL-EBI	Open source is a friend to science aiding reproducibility and allowing future developers to learn from existing work. Please do not limit science by preventing our access.
98	Joseph Hughes	CVR	
99	Juan Ugalde	Scripps Institution of Oceanography, UC San Diego	
100	Yannick Wurm	Queen Mary, University of London	
101	Georgia Tsagakogeorga	Queen Mary University of London	
102	Mark Chaisson	University of Washington	
103	Bastian Greshake	Department for Applied Bioinformatics, Goethe University, Frankfurt am Main, Germany	
104	Dag Ahren	Lund University	
105	Jeramia Ory	King's College, Wilkes-Barre, PA	
106	Andrew Warren	Virginia Bioinformatics Institute	
107	Bruno Miguel Pereira Vieira	Queen Mary, University of London	
108	Craig Anderson	Postdoc at CSIRO	
109	Juan Pascual-Anaya	RIKEN Center for Developmental Biology	

110	Livio Antonielli	AIT-Austrian Institute of Technology	
111	Andreas Bremges	Bielefeld University	
112	David McKean	University of Colorado	
113	Luke hickey	Pacific Biosciences	
114	Brian Walenz	J. Craig Venter Institute	
115	Volker Haring	CSIRO Animal, Food and Health Sciences	
116	Andrew Severin	Iowa State University	My opinions are my own. this is important to the field of bioinformatics.
117	Robert Tyx	US CDC	
118	Jarle Pahr	N/A	
119	Anton Korobeynikov	Algorithmic Biology Lab	
120	Torben Lüders	University of Oslo	
			Dear Roche,
			The newbler is great assemblers for paired end data. Please make it opensource, and I would be happy to contribute to it's development. 454/Roche user since 2006...
121	Markiyany Samborskyy	University of Cambridge	-- Best Regards, Markiyany.
122	Brant Faircloth	University of California, Los Angeles	
123	Brad Chapman	Harvard School of Public Health	
124	bert hubert	Delft University of Technology	We could possibly help with the actual open sourcing & IPR screening.
125	J Koval	Ramaciotti Centre for Genomics - UNSW Australia	
126	Markus Grohme	Max Planck Institute for Molecular Cell Biology and Genetics	
127	Valentin Loux	INRA (French National Institute for Agricultural Research)	
128	Torfinn Nome	The Norwegian University of Life Sciences	
129	Sara calabrese	University of Bergen	
130	Michel Abanto Marin	Oswaldo Cruz Intitute	
			Newbler is my favourite assembler! Since 2008 (454 sequencer FLX start in our lab) I'm using it for de novo assembly of bacterial genomes. ContigGraph.txt - I'm loving it!! Best wishes for all Newbler users!
131	Jan Gawor	IBB PAS Poland	
132	Robert Gromadka	DNA Sequencing Laboratory Institute of Biochemistry and Biophysics PAS, Warsaw Poland	
133	Zachary Charlop-Powers	The Rockefeller University	
134	Mikael Huss	SciLifeLab / Stockholm University	
135	David Eccles	Gringene Bioinformatics	
136	Thomas H.A. Haverkamp	University of Oslo, Department of Biosciences	
137	Thomas Källman	Uppsala UNIVERSITY	
138	Ana Gomes	University of Bergen	
139	Cindy Pedrosa	Uni Research	
140	Andreas Sjödin	Swedish Defence Research Agency	
141	Robert Davey	The Genome Analysis Centre, UK	
142	Evan Ernst	CSHL	
143	Peter Fields	University of Virginia	
144	Vince Forgetta	McGill University	
145	Le bras	cnrs	

146	Darek Kedra	CRG, Barcelona, SPAIN
147	Paul McAdam	The Roslin Institute
148	Neil hall	University of liverpool
149	Philip Ashton	Public Health England
150	Karthi Sivaraman	H3Me Life Sciences
151	Mick Watson	The Roslin Institute
152	Peter Chines	NHGRI
153	Aye Wollam	The Genome Institute Washington University
154	Derek Albracht	The Genome Institute (Washington University in St. Louis)
155	Blake Stamps	University of Oklahoma
156	Alistair Darby	University of Liverpool
157	Kym Pepin	The Genome Insitute
158	Christopher J. Grassa	University of British Columbia
159	Tony Håndstad	Oslo University Hospital
160	Tony Brooks	University College London
161	Milinn Kremitzki	The Genome Institute
162	Lee Trani	Genome Institute

Open-source Newbler!

I have used the various versions of newbler for the first day of getting our 454 in liverpool it has been a valuable tools and without equal for 454 assembly. The magic that Jim has captured in this software need to be released, as software developers should learn from the algorithms and implementations of the Newbler code.