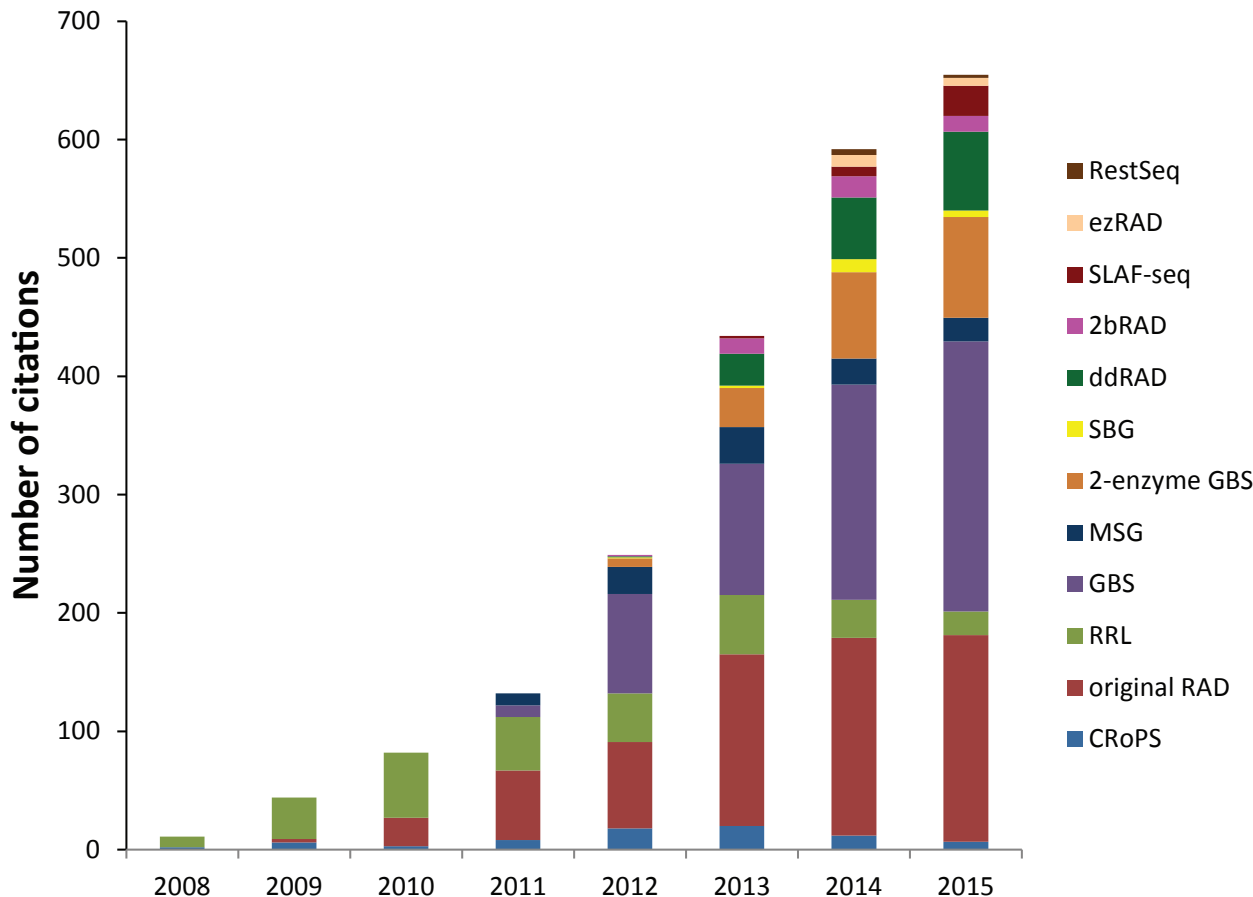**Supplementary figure S1.** Numbers of articles citing the original papers describing each type of RADseq protocol over time. Data (see table) generated using Web of Science. Data for 2015 are extrapolated using numbers of articles cited from January through September 2015. Protocols are arranged by order of first appearance in the literature. CRoPS, complexity reduction of polymorphic sequences; original RAD, original restriction-site associated-DNA; RRL, reduced representation library; GBS, genotyping by sequencing; MSG, multiplexed shotgun genotyping; SBG, sequence-based genotyping; ddRAD, double-digest restriction-site-associated DNA; SLAF-seq, specific-locus amplified fragment sequencing; RestSeq, restriction fragment sequencing.

Table. Data from Web of Science on the numbers of articles citing the original papers describing each RADseq protocol over time; used to produce supplementary figure S1.

	2008	2009	2010	2011	2012	2013	2014	2015	REF.
CRoPS	2	6	3	8	18	20	12	6.67	1
original RAD	0	3	24	59	73	145	167	175	2,3
RRL	9	35	55	45	41	50	32	20.0	4,5
GBS	0	0	0	10	84	111	182	228	6
MSG	0	0	0	10	23	31	22	20.0	7
2-enzyme GBS	0	0	0	0	7	33	73	85.3	8
SBG	0	0	0	0	1	2	11	5.33	9
ddRAD	0	0	0	0	1	27	52	66.7	10
2bRAD	0	0	0	0	1	13	18	13.3	11,12
SLAF-seq	0	0	0	0	0	2	8	25.3	13
ezRAD	0	0	0	0	0	0	10	6.67	14
RestSeq	0	0	0	0	0	0	5	2.67	15

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