	Target date	Mths from start	Objective	Description of milestone
1	31/10/09	7	Obj 3	1st VeGIN stakeholder meeting held
2	31/3/10	12	Obj 1b	384 C genome brassica SNPS mapped and made publicly available
3	31/3/10	12	Obj 1c	seed of ~120 Sal x Ice F8 RILs produced
4	31/3/10	12	Obj 1c	Lettuce TILLING population characterised for mutant load and made publicly available
5	31/3/10	12	Obj 1c	Sal x Ice linkage map anchored to integrated lettuce linkage map
6	31/3/10	12	Obj 1c	Lettuce diversity set of 96 accessions identified
7	31/3/10	12	Obj 2d	Polymorphic ESTs of genes causing discolouration in lettuce mapped
8	30/9/10	18	Obj 1b	Review of technologies available for identifying SNPs completed
9	31/3/11	24	Obj 3	2nd VeGIN stakeholder meeting held
10	31/3/11	24	Obj 4a	Re-Sequencing of parental lines A12, GD33, Mar34 and Iceberg
11	31/3/11	24	Obj 1b	A minimum of an additional 768 C genome brassica SNPs mapped and made available
12	31/3/11	24	Obj 2a	QTL analysis completed for N content variation in Brassica
13	31/3/11	24	Obj 2a	QTL for N metabolism/transport/accumulation in lettuce fine mapped
14	31/3/11	24	Obj 2b	Lettuce diversity set assayed for resistance to Nasonovia ribis- nigri
15	31/3/11	24	Obj 4b	Sequencing of transcriptome of 70 (minimum) wild DFFS S1 accessions
16	31/7/11	28	Obj 4c	Sequencing of transcriptome of 48 (minimum) B oleracea DFFS S1 accessions
17	30/9/11	30	Obj 1b	Identification of wider panel of SNP's (approx 1000) from transcriptome data for public release thru VeGIN we
18	31/3/12	36	Obj 3	3rd VeGIN stakeholder meeting held
19	31/3/12	36	Obj 1a	B oleracea and C genome diversity sets screened with 768 mapped C genome SNPs
20	31/3/12	36	Obj 1b	A minimum of an additional 500 brassica C genome SNPs identified, mapped and made publicly available
21	31/3/12	36	Obj 2a	Analysis of trial for N content of contrasting Brassica mapping population lines completed -QTL verified
22	31/3/12	36	Obj 2a	Additional polymorphic ESTs associated with nitrogen metabolism/transport/accumulation mapped
23	31/3/12	36	Obj 2a	Sequence homology identified between plant gene databases and lettuce ESTs fine mapped to nitrate and posthavest
24	31/3/12	36	Obj 2b	Potential sources of resistance to Diamond Back moth in brassica C genome identified
25	31/3/12	36	Obj 2c	Diversity for TuMV and TuYV resistance in brassica C genome assayed- potential sources of resistance identified
26	31/3/12	36	Obj 2c	C genome diversity sets 'assayed' for for TuRB01 like genes
27	31/12/12	45	Obj 1a	Fixed lines of brassica oleracea diversity set bulked up
28	31/12/12	45	Obj 1a	Fixing of C genome diversity set completed
29	31/12/12	45	Draft	Draft Final Report submitted