

Supplemental Material

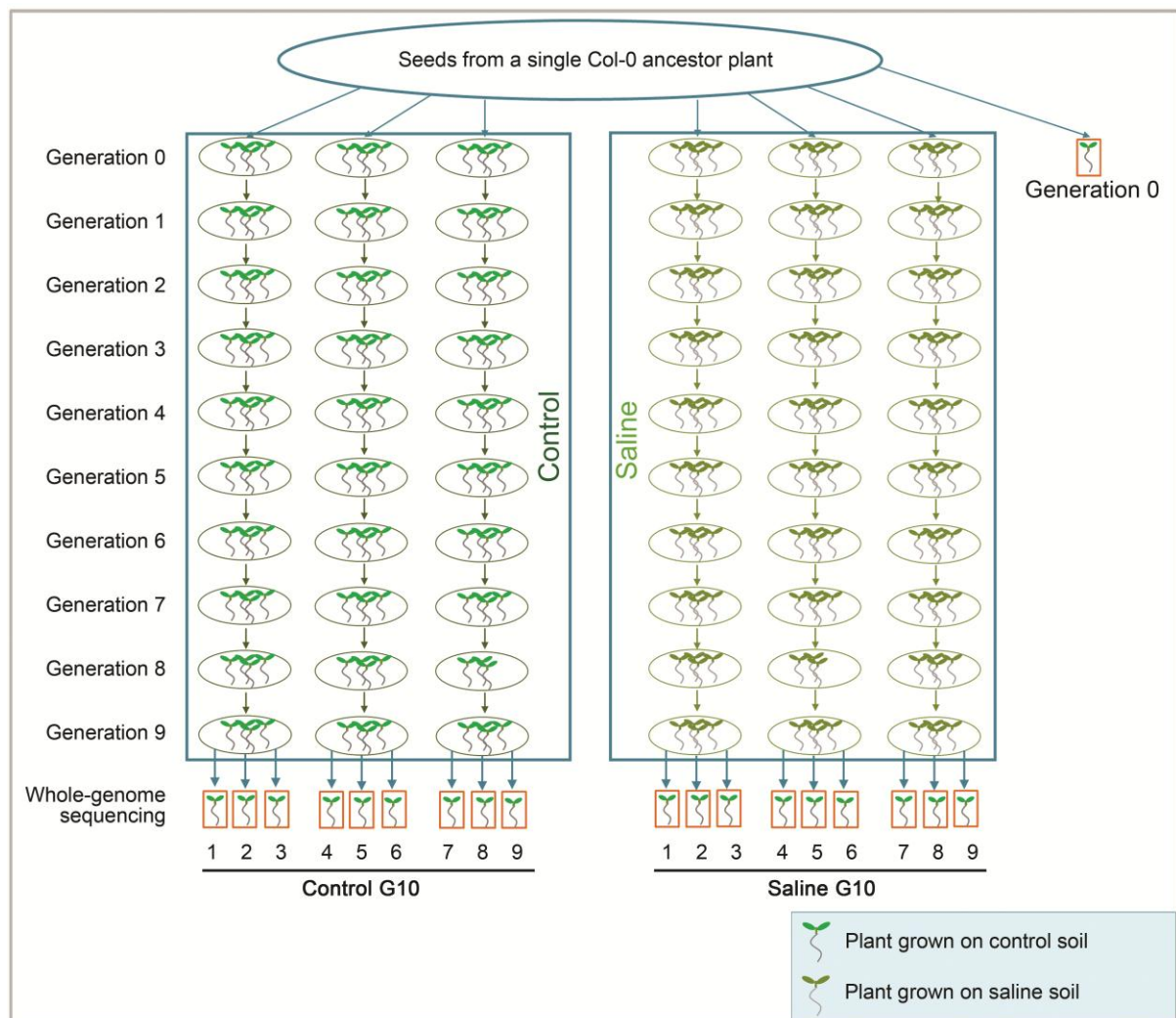


Figure S1. Schematic representation of *Arabidopsis thaliana* Mutation Accumulation (MA) lineages.

Seeds from a single *A. thaliana* Col-0 plant were divided into 6 sets and grown independently on either Control or Saline soil for 10 successive generations (see Materials and Methods). Three 10th generation (Generation 10; G10) plants from each lineage were then each randomly selected for individual whole-genome sequencing. A single Generation 0 (G0) plant was also sequenced to provide the progenitor (reference) control genome sequence. Genome-sequenced plants are highlighted in orange boxes.

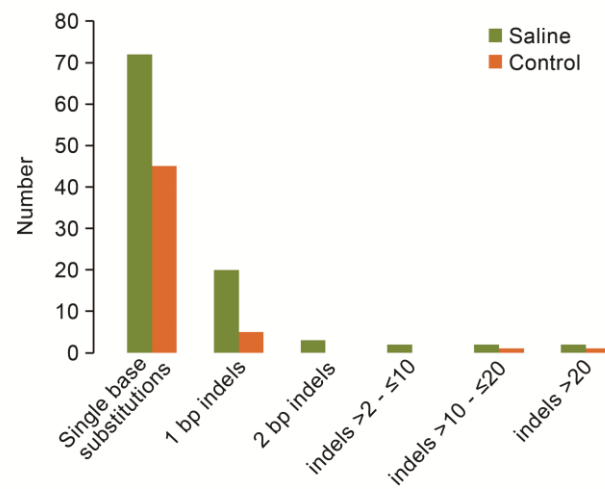


Figure S2. Frequencies and categories of DNA sequence mutations identified in genomes of G10 plants from saline-soil (Saline) and control MA lineages.

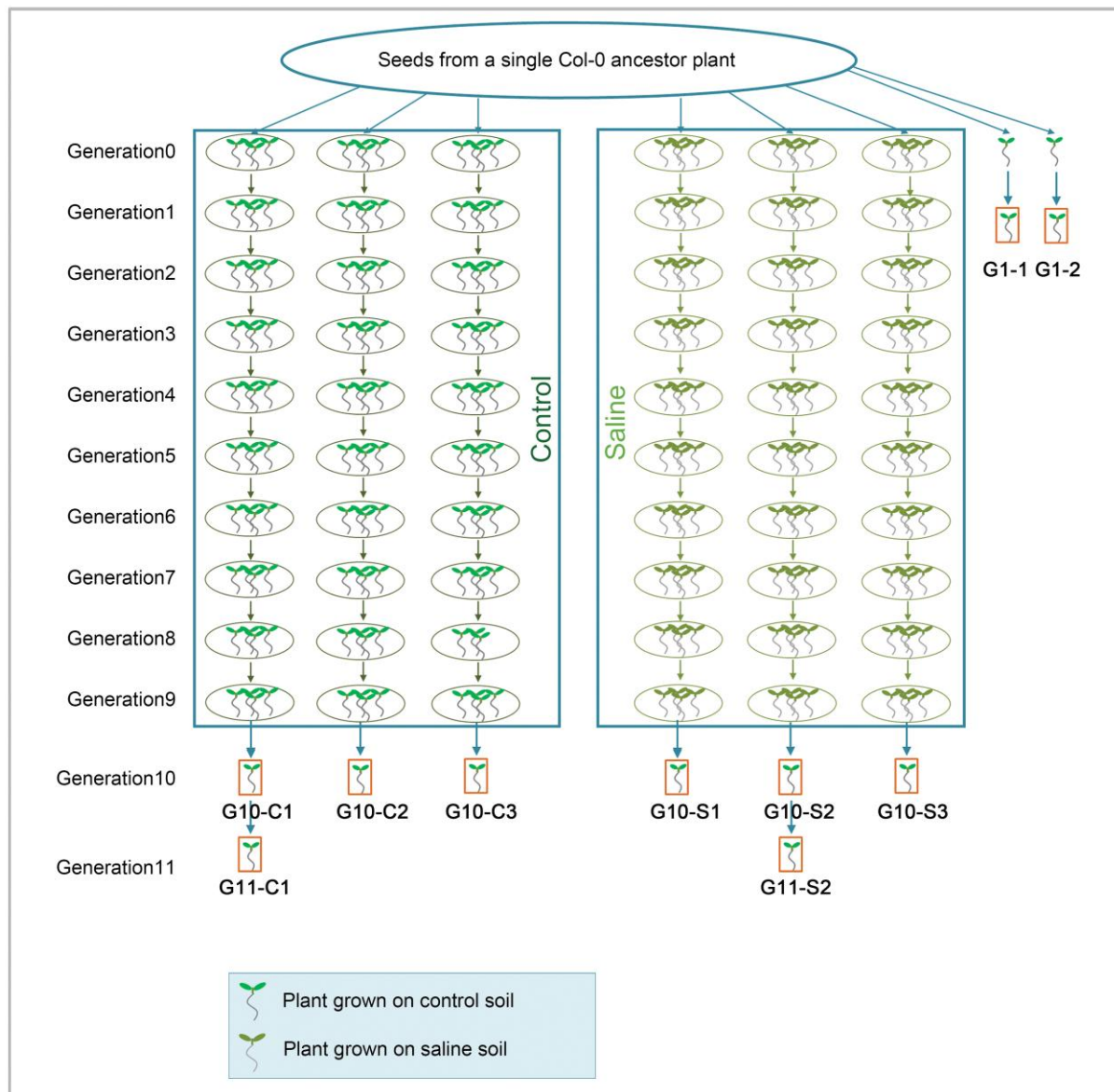


Figure S3. Whole-genome bisulphite sequencing of *Arabidopsis thaliana* MA lineages and bulked samples.

Control and Saline-Soil MA lineages were established as shown in Figure S1. Single G10 plants from each of the six MA lineages were randomly selected for individual whole-genome bisulphite sequencing. Two 1st generation plants (G1-1 and G1-2) were also sequenced to provide progenitor controls, together with 11th generation plant G11-C1 and G11-S2. Bisulphite-sequenced plants/samples are highlighted in orange boxes.

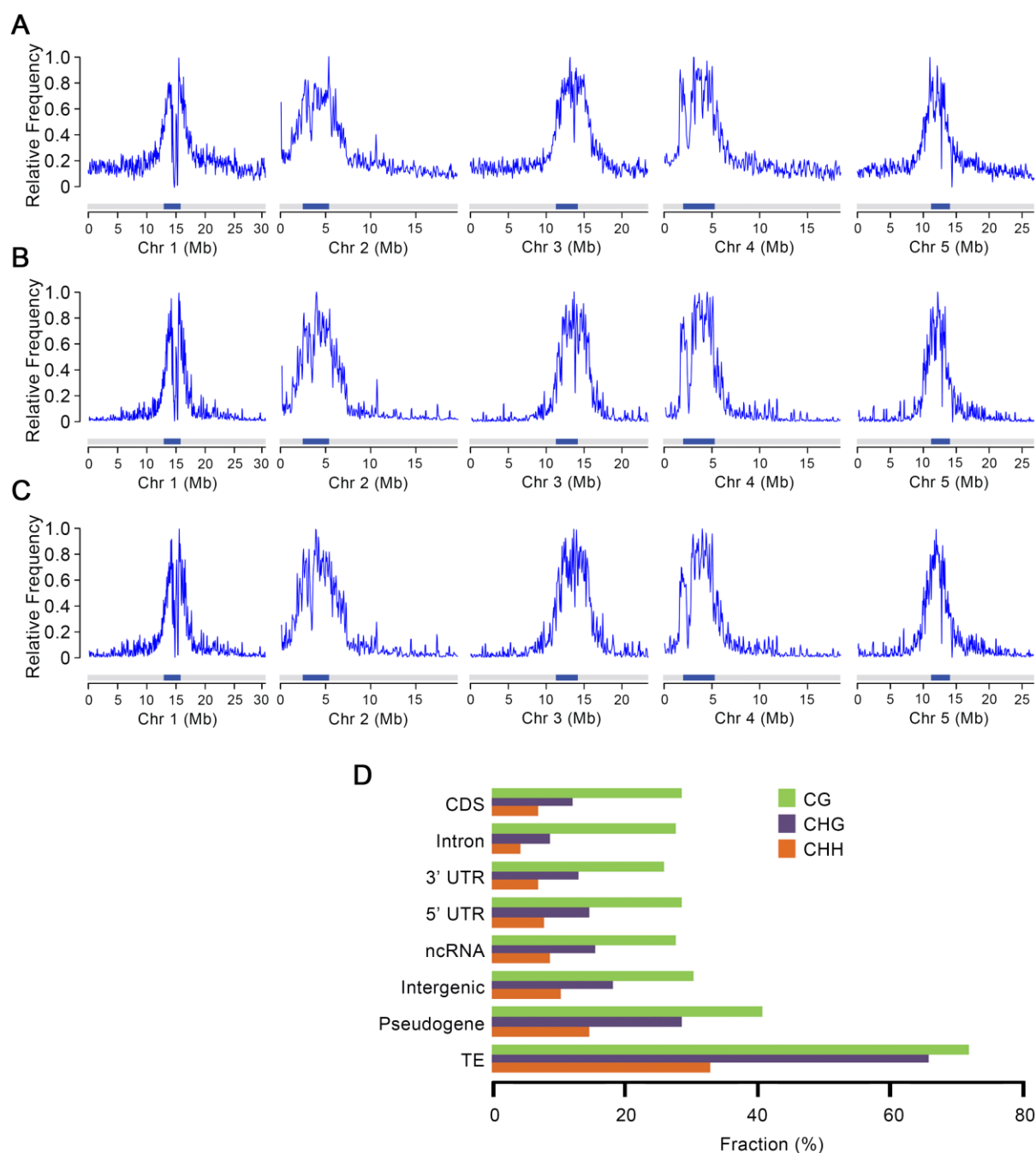


Figure S4. Genome-wide distribution of cytosine methylation in *A. thaliana* MA lineages.

(A-C) Distribution along individual chromosomes (Chr 1, Chr 2, etc.) of methylated cytosines in CG (A), CHG (B), and CHH (C) positions (methylation detected in at least one of six G10 and two G1 samples, see main text). Data were normalized to the highest value for each chromosome. Dark blue bars indicate centromeres. (D) Fraction of methylated (versus non-methylated) cytosines in all G10 and G1 samples (at CG, CHG and CHH positions) in genomic regional categories as determined by genome sequence annotation: CDS, coding sequence; ncRNA, non-coding RNA; TE, transposable element.

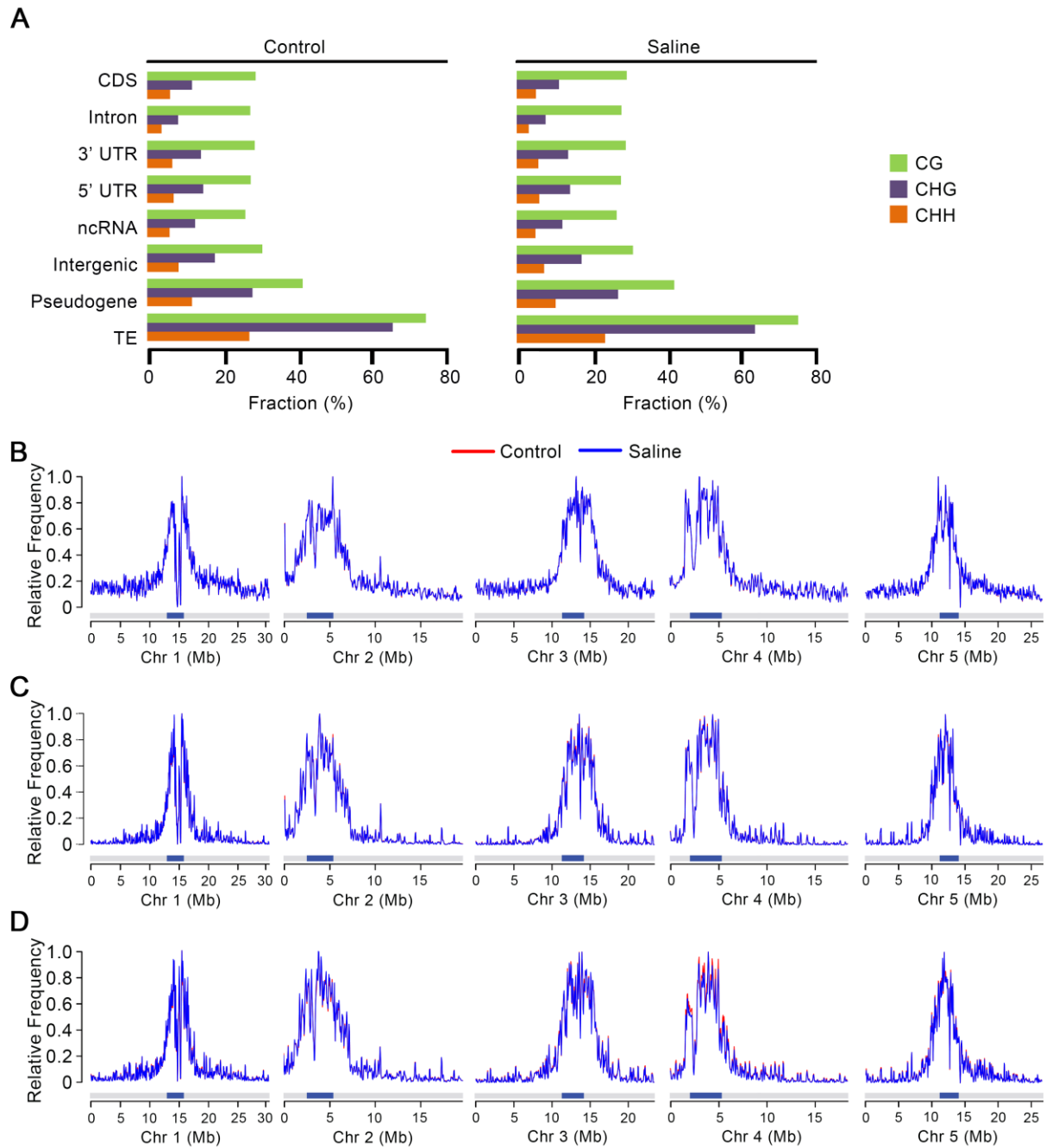


Figure S5. Distribution of cytosine methylation in G10 Control and G10 saline-soil MA plants

(A) Fraction of methylated (versus non-methylated) cytosines in G10 Control and G10 saline-soil samples (at CG, CHG and CHH positions) in genomic regional categories as determined by genome sequence annotation: CDS, coding sequence; ncRNA, non-coding RNA; TE, transposable element. (B-D) Distribution of methylated CG (B) CHG (C) and CHH (D) sites along each chromosome in G10 samples from control (red) and saline-soil (blue) MA lineages. Data from each group (control or saline-soil) were combined and normalized to the highest value for each chromosome. Dark blue bars indicate centromeres.

Table S1. Depth of whole-genome sequencing of genomic DNA samples.

	Mapped reads	Uniquely mapped reads	Sequencing depth (×)
Progenitor G0	56,264,110	41,387,516	27.1
Control G10-1	39,201,650	31,923,055	23.9
Control G10-2	39,060,106	32,217,156	24.2
Control G10-3	39,158,782	32,104,535	24.1
Control G10-4	39,394,966	32,353,820	24.3
Control G10-5	39,267,778	32,545,657	24.4
Control G10-6	38,911,914	32,268,122	24.2
Control G10-7	39,226,372	32,340,108	24.3
Control G10-8	39,112,786	31,250,354	23.4
Control G10-9	38,599,868	31,280,949	23.5
Saline G10-1	38,425,952	31,718,984	23.8
Saline G10-2	36,857,984	29,426,467	22.1
Saline G10-3	36,881,896	30,489,506	22.9
Saline G10-4	38,460,644	31,677,261	23.8
Saline G10-5	38,183,746	31,048,621	23.3
Saline G10-6	33,053,026	26,651,195	20.0
Saline G10-7	38,227,070	31,434,879	23.6
Saline G10-8	38,888,390	31,852,179	23.9
Saline G10-9	38,939,832	32,090,617	24.1

Table S2. Number of DNA sequence mutations identified in Saline Soil and Control G10 samples (see Figure S1).

Saline G10											
Sample	1	2	3	4	5	6	7	8	9	Total	Mean
Total	8	16	11	9	13	11	12	14	8	102	11.33
SBSs	6	11	6	7	9	9	10	8	6	72	8.00
Ts	5	7	3	3	7	2	6	5	4	42	4.67
Tv	1	4	3	4	2	7	4	3	2	30	3.33
indels	2	5	5	2	4	2	2	6	2	30	3.33

Control G10											
Sample	1	2	3	4	5	6	7	8	9	Total	Mean
Total	4	6	5	9	8	6	8	3	3	52	5.78
SBSs	4	5	4	8	6	5	7	3	3	45	5.00
Ts	4	2	3	5	6	3	2	3	3	31	3.44
Tv	0	3	1	3	0	2	5	0	0	14	1.56
indels	0	1	1	1	2	1	1	0	0	7	0.78

Table S3. List of individual DNA sequence mutations identified in Saline Soil and Control G10 samples (see Figure S1).

Sample	Position	Mutation*	Context	Gene ID	Gene annotation
Saline G10-1	Chr1:12166925	G to A	intergenic		
Saline G10-1	Chr2:11056465	del G	intergenic		
Saline G10-1	Chr2:17106972	T to C	intergenic		
Saline G10-1	Chr2:6414749	del T	intergenic		
Saline G10-1	Chr3:13702924	C to G	intergenic		
Saline G10-1	Chr3:19284780	C to T	nonsynonymous	AT3G51970	ACYL-COA STEROL ACYL TRANSFERASE 1
Saline G10-1	Chr3:8850734	C to T	transposable		
Saline G10-1	Chr5:13624311	C to T	intergenic		
Saline G10-2	Chr1:19104356	C to T	intron		
Saline G10-2	Chr1:2236379	CGAC to TTGAG	intergenic		
Saline G10-2	Chr1:29018984	del C	nonsynonymous	AT1G77240	ACYL ACTIVATING ENZYME 2 protein
Saline G10-2	Chr1:9723821	226 bp del	nonsynonymous	AT1G27910	U-BOX 45
Saline G10-2	Chr2:1814465	T to C	transposable		
Saline G10-2	Chr2:2390619	A to T	intergenic		
Saline G10-2	Chr2:2824464	T to C	intergenic		
Saline G10-2	Chr2:338742	T to A	intron		
Saline G10-2	Chr2:5154998	C to T	transposable		
Saline G10-2	Chr2:6321157	G to A	intergenic		
Saline G10-2	Chr2:9237549	T to C	UTR		
Saline G10-2	Chr3:20378945	A to C	intergenic		
Saline G10-2	Chr3:20378946	A to C	intergenic		
Saline G10-2	Chr3:23019074	del A	intergenic		
Saline G10-2	Chr3:3791810	C to T	intron		
Saline G10-2	Chr5:12531351	ins AT	intron		
Saline G10-2	Chr5:24647408	del AT	intergenic		
Saline G10-3	Chr1:24640163	G to T	nonsynonymous	AT1G66170	MALE MEIOCYTE DEATH 1
Saline G10-3	Chr1:7059442	4 bp ins	intergenic		
Saline G10-3	Chr2:15253629	T to A	intergenic		
Saline G10-3	Chr2:19006443	G to T	synonymous		
Saline G10-3	Chr2:8764428	13 bp del	intergenic		
Saline G10-3	Chr3:12316905	T to C	intergenic		
Saline G10-3	Chr3:14013828	C to T	intergenic		

Saline G10-3	Chr4:7943909	C to T	intergenic		
Saline G10-3	Chr5:26117786	del A	intergenic		
Saline G10-3	Chr5:547840	ins A	UTR		
Saline G10-4	Chr2:1811038	C to T	intergenic		
Saline G10-4	Chr2:4474918	A to T	intergenic		
Saline G10-4	Chr2:5320772	del T	intergenic		
Saline G10-4	Chr3:12739345	T to G	intergenic		
Saline G10-4	Chr3:13423391	del C	intergenic		
Saline G10-4	Chr5:14780917	T to G	intergenic		
Saline G10-4	Chr5:17951087	T to A	intergenic		
Saline G10-4	Chr5:20019821	G to A	intergenic		
Saline G10-4	Chr5:9024461	T to C	intergenic		
Saline G10-5	Chr1:13386362	C to T	intergenic		
Saline G10-5	Chr1:27313317	7 bp del	intron		
Saline G10-5	Chr1:9960525	T to A	intergenic		
Saline G10-5	Chr2:12087610	ins C	intron		
Saline G10-5	Chr3:13491919	G to A	nonsynonymous	AT3G32940	RNA-binding KH domain-containing protein
Saline G10-5	Chr3:16445583	del A	intergenic		
Saline G10-5	Chr3:16659016	A to G	nonsynonymous	AT3G45420	L-TYPE LECTIN RECEPTOR KINASE I.4
Saline G10-5	Chr4:13828476	14 bp del	UTR		
Saline G10-5	Chr4:8030661	G to A	nonsynonymous	AT4G13885	Polynucleotidyl transferase
Saline G10-5	Chr5:16276026	C to T	intergenic		
Saline G10-5	Chr5:20651877	C to G	intron		
Saline G10-5	Chr5:5962121	C to T	intergenic		
Saline G10-5	Chr5:912366	T to C	intergenic		
Saline G10-6	Chr1:24411983	C to A	intergenic		
Saline G10-6	Chr1:27684348	del T	intergenic		
Saline G10-6	Chr2:10657257	T to G	synonymous		
Saline G10-6	Chr2:4331945	A to T	intergenic		
Saline G10-6	Chr4:1531901	C to T	intergenic		
Saline G10-6	Chr4:2483913	del GA	intergenic		
Saline G10-6	Chr4:2483916	G to T	intergenic		
Saline G10-6	Chr4:2888020	A to T	transposable		
Saline G10-6	Chr4:2888180	A to C	transposable		
Saline G10-6	Chr4:2888185	C to T	transposable		
Saline G10-6	Chr4:508364	A to T	nonsynonymous	AT4G01210	glycosyl transferase family 1 protein

Saline G10-7	Chr1:15641547	T to A	intergenic
Saline G10-7	Chr1:15817964	del T	transposable
Saline G10-7	Chr1:16030593	G to A	transposable
Saline G10-7	Chr1:28857076	T to A	intergenic
Saline G10-7	Chr2:12327957	del T	intergenic
Saline G10-7	Chr2:202514	C to T	intron
Saline G10-7	Chr3:3252893	T to G	intergenic
Saline G10-7	Chr4:5297169	G to A	intergenic
Saline G10-7	Chr4:9489904	C to G	intergenic
Saline G10-7	Chr5:13975401	G to A	transposable
Saline G10-7	Chr5:14078050	G to A	intergenic
Saline G10-7	Chr5:15437838	C to T	intergenic
Saline G10-8	Chr1:10891650	del G	intergenic
Saline G10-8	Chr1:5353791	C to T	transposable
Saline G10-8	Chr1:6140622	G to A	intergenic
Saline G10-8	Chr2:17437518	C to T	intergenic
Saline G10-8	Chr2:9183999	ins A	intergenic
Saline G10-8	Chr3:13648097	C to T	intergenic
Saline G10-8	Chr3:14775750	del G	intergenic
Saline G10-8	Chr4:2552478	G to A	intergenic
Saline G10-8	Chr5:10019377	C to G	intron
Saline G10-8	Chr5:14974875	del A	intron
Saline G10-8	Chr5:15938556	ins T	intergenic
Saline G10-8	Chr5:18648466	C to G	intergenic
Saline G10-8	Chr5:24728612	T to G	intergenic
Saline G10-8	Chr5:4200148	ins A	intergenic
Saline G10-9	Chr1:13529028	22 bp deletion	intron
Saline G10-9	Chr1:18341983	T to A	intergenic
Saline G10-9	Chr2:17726930	del T	intergenic
Saline G10-9	Chr2:2782639	C to T	transposable
Saline G10-9	Chr3:19533943	C to A	splicing
Saline G10-9	Chr4:4493346	G to A	intergenic
Saline G10-9	Chr5:15736267	A to G	synonymous
Saline G10-9	Chr5:26903394	A to T	UTR
Control G10-1	Chr1:19303909	C to T	intergenic
Control G10-1	Chr1:23092218	T to C	intergenic
Control G10-1	Chr3:11380111	C to T	intergenic
Control G10-1	Chr3:1572300	C to T	intergenic
Control G10-2	Chr1:13246457	C to T	intergenic
Control G10-2	Chr2:2616028	C to T	transposable

Control G10-2	Chr3:12731695	A to T	intergenic		
Control G10-2	Chr3:12731696	T to A	intergenic		
Control G10-2	Chr3:7865779	ins TA	intergenic		
Control G10-2	Chr4:3725952	G to C	intergenic		
Control G10-3	Chr1:17259876	G to A	transposable		
Control G10-3	Chr2:12871754	T to C	intergenic		
Control G10-3	Chr2:9544710	T to A	nonsynonymous	AT2G22475	GL2- EXPRESSION MODULATOR
Control G10-3	Chr3:11982679	G to A	intergenic		
Control G10-4	Chr4:3524909	del T	intergenic		
Control G10-4	Chr1:23317569	14 bp deletion	nonsynonymous	AT1G62950	leucine-rich repeat transmembrane protein kinase family protein
Control G10-4	Chr1:28009290	T to C	UTR		
Control G10-4	Chr2:14556005	A to T	intergenic		
Control G10-4	Chr2:7720666	C to T	intergenic		
Control G10-4	Chr3:13246990	C to T	transposable		
Control G10-4	Chr4:4384297	G to T	transposable		
Control G10-4	Chr4:4384298	G to C	transposable		
Control G10-3	Chr4:4999291	C to T	transposable		
Control G10-5	Chr2:5344615	G to A	transposable		
Control G10-5	Chr4:12526327	C to T	synonymous		
Control G10-5	Chr4:12561492	G to A	intergenic		
Control G10-5	Chr4:14333749	G to A	nonsynonymous	AT4G29090	Ribonuclease H-like superfamily protein
Control G10-5	Chr4:6791140	C to T	intergenic		
Control G10-5	Chr4:894129	G to A	intron		
Control G10-5	Chr5:6962879	del A	intergenic		
Control G10-5	Chr5:8027197	del T	intergenic		
Control G10-6	Chr2:4717423	C to T	transposable		
Control G10-6	Chr2:9328692	G to A	intergenic		
Control G10-6	Chr3:12820312	C to T	transposable		
Control G10-6	Chr3:14797211	G to T	transposable		
Control G10-6	Chr4:12274335	T to G	intergenic		
Control G10-6	Chr5:8698953	del A	intergenic		
Control G10-7	Chr1:16649726	G to T	intergenic		
Control G10-7	Chr1:16804632	T to G	intergenic		
Control G10-7	Chr1:1972314	66bp deletion	intron		
Control G10-7	Chr2:122208	G to A	intergenic		

Control G10-7	Chr2:2595696	C to G	transposable
Control G10-7	Chr4:3857987	C to A	intergenic
Control G10-7	Chr5:14601987	C to T	intergenic
Control G10-7	Chr5:7508063	G to C	intergenic
Control G10-8	Chr3:17358243	C to T	intergenic
Control G10-8	Chr4:9675492	T to C	intergenic
Control G10-8	Chr5:18172140	G to A	intergenic
Control G10-9	Chr1:15803484	G to A	transposable
Control G10-9	Chr2:575128	G to A	intergenic
Control G10-9	Chr3:14782790	G to A	intergenic

* del refers to deletion; ins refers to insertion.

Table S4. Depth of whole-genome bisulphite sequencing of genomic DNA samples.

	All reads	Uniquely mapped reads	Conversion rate* (%)	Sequencing depth (×)
G1-1	71,726,428	47,267,716	99.7	70.9
G1-2	72,616,980	48,725,994	99.65	73.1
G10-C1	78,856,452	57,801,780	99.67	86.7
G10-C2	78,034,956	57,745,868	99.67	86.6
G10-C3	75,760,526	58,562,886	99.71	87.8
G10-S1	66,982,446	50,973,642	99.63	76.7
G10-S2	75,055,548	57,117,272	99.64	85.7
G10-S3	67,160,488	50,437,526	99.63	75.7
G11-S2	72,911,068	46,517,262	99.68	69.8
Control [†]	75,101,058	50,993,618	99.68	76.5
Salinity [‡]	73,201,664	52,778,400	99.64	79.2

* Conversation rate were calculated based on the data from unmethylated lambda phage DNA spiked in each sample.

[†] Control refers to the bulk genomic DNA sample from inflorescence tissue of ~30 plants grown under control soil.

[‡] Salinity refers to the bulk genomic DNA sample from inflorescence tissue ~30 plants grown under salinity soil.

Table S5. Number of covered and methylated cytosine positions in genomic DNA samples.

	Covered cytosine sites (Coverage $\geq$ 3)				Methylated cytosine sites (Coverage $\geq$ 3)			
	CG	CHG	CHH	Total	CG	CHG	CHH	Total
G1-1	5,317,928	5,843,182	29,159,418	40,320,528	1,483,967	773,396	1,395,278	3,652,641
G1-2	5,321,010	5,844,093	29,136,912	40,302,015	1,480,703	800,948	1,555,982	3,837,633
G10-C1	5,400,758	5,932,103	30,004,046	41,336,907	1,501,788	820,979	1,584,234	3,907,001
G10-C2	5,376,697	5,924,502	30,256,769	41,557,968	1,462,692	661,831	1,051,311	3,175,834
G10-C3	5,410,559	5,946,159	30,234,469	41,591,187	1,495,991	792,752	1,475,333	3,764,076
G10-S1	5,351,427	5,903,617	30,054,516	41,309,560	1,466,036	676,367	1,121,428	3,263,831
G10-S2	5,404,917	5,944,730	30,276,130	41,625,777	1,487,109	753,476	1,279,776	3,520,361
G10-S3	5,379,781	5,925,606	30,183,261	41,488,648	1,474,384	698,414	1,128,333	3,301,131
G11-S2	5,311,288	5,832,457	29,060,701	40,204,446	1,599,421	844,448	1,506,276	3,950,145
Control	5,352,242	5,878,880	29,466,857	40,697,979	1,681,989	953,779	1,235,529	3,871,297
Salinity	5,349,065	5,873,781	29,411,831	40,634,677	1,690,990	979,379	1,395,316	4,065,685

Table S6. Number of differentially methylated positions (DMPs) identified in G10 samples. (A) Total covered cytosines and methylated positions. (B) Distribution of differentially methylated positions (DMPs).

Table S6A

Context	Covered cytosine sites ($200 \geq \text{coverage} \geq 3$ in all G10 MA and G1 progenitor lineages)	Methylated cytosine sites (methylation count ≥ 3 in at least one G10 MA or G1 progenitor lineages)	Fraction of Methylated sites (%)
CG	5,036,474	1,617,696	32.12
CHG	5,598,032	973,021	17.38
CHH	27,515,415	2,631,594	9.56

Table S6B

	Sequence Context	DMP	Percentage (%)
Total G10 control sample	CHG	102	0.51
	CHH	106	0.43
	CpG	19,808	98.96
	Total	20,016	100
Total G10 saline sample	CHG	178	0.62
	CHH	108	0.37
	CpG	28,598	99.01
	Total	28,884	100
Shared between any Control and saline MA lineages	CHG	20	
	CHH	46	
	CpG	3,877	
	Total	3,943	

Table S7. Frequency of DMPs among the G10 control or saline MA lineages.

Table S7A: Frequency of DMPs among the G10 control MA lineages.

Frequency	Sequence Context	Number
G10-C1 only	CpG	5,862
G10-C2 only	CpG	5,910
G10-C3 only	CpG	6,105
G10-C1 and -C2	CpG	416
G10-C1 and -C3	CpG	568
G10-2 and -C3	CpG	599
G10-C1, -C2 and -C3	CpG	83

Table S7B: Frequency of DMPs among the G10 saline MA lineages.

Frequency	Sequence Context	Number
G10-S1 only	CpG	8,281
G10-S2 only	CpG	8,858
G10-S3 only	CpG	7,283
G10-S1 and -S2	CpG	977
G10-S1 and -S3	CpG	982
G10-S2 and -S3	CpG	949
G10-S1, -S2 and -S3	CpG	313

Supplementary Table 8. List of regions with losses and gains of methylation

Supplementary Table 8a. List of DMRs in 10th generation control samples.

Sample	Chromosome	Length (bp)	Loss or gain methylation	Context	Gene ID	Gene anotation
G10-C1	Chr2:11653428-11653443	16	gain	genic	AT2G27280	Coiled-coil domain-containing protein 55
G10-C2	Chr1:6132407-6132422	16	loss	genic	AT1G17820	Putative integral membrane protein
G10-C2	Chr1:9138940-9139042	103	loss	genic	At1g26140	unknown protein
G10-C2	Chr1:25323755-25323776	22	gain	genic	At1g67560	Lipoxtgbase 6
G10-C2	Chr2:7563388-7563413	26	gain	genic	AT2G17410	ARID/BRIGHT DNA-binding domain-containing protein
G10-C2	Chr2:7707776-7707818	43	loss	genic	AT2G17740	Cysteine/Histidine-rich C1 domain family protein
G10-C2	Chr2:12356980-12357041	62	loss	genic	AT2G28800	ALBINO3 family protein
G10-C2	Chr2:12733144-12733153	10	loss	genic	AT2G29840	NG/U-box superfamily protein
G10-C2	Chr3:8005374-8005418	45	loss	genic	AT3G22590	PLANT HOMOLOGOUS TO PARAFIBROMIN
G10-C3	Chr1:1211675-1211727	53	gain	genic	AT1G04470	unknown protein
G10-C3	Chr1:13127447-13127504	58	loss	intergenic		
G10-C3	Chr2:5398-5422	25	loss	intergenic		
G10-C3	Chr5:15949617-15949647	31	loss	intergenic		
G10-C3	Chr5:25502103-25502139	37	loss	genic	AT5G63710	Leucine-rich repeat protein kinase family protein
Average size		39				

Supplementary Table 8b. List of DMRs in 10th generation saline samples.

Sample	Chromosome	Length (bp)	Loss or gain methylation	Context	Gene ID	Gene anotation
G10-S1	Chr1:4469466-4469533	68	loss	genic	AT1G13120	unknown protein
G10-S1	Chr1:6693124-6693178	55	loss	genic	AT1G19370	unknown protein
G10-S1	Chr1:23034305-23034445	141	loss	intergenic		
G10-S1	Chr2:10897626-10897661	36	loss	genic	AT2G25600	STELAR OUTWARD RECTIFIER (AKT6) K+
G10-S1	Chr3:20559731-20559843	113	loss	genic	AT3G55450	PBS1-like (PBL1) 1
G10-S1	Chr3:693828-693871	44	loss	genic	AT3G03060	P-loop containing nucleoside triphosphate hydrolases superfamily protein
G10-S1	Chr3:1962098-1962142	45	loss	genic		
G10-S1	Chr3:6330449-6330476	28	loss	genic	AT3G18440	Encodes vacuolar channel a malate
G10-S1	Chr3:11809097-11809130	34	loss	intergenic		
G10-S1	Chr3:16067109-16067143	35	gain	intergenic		
G10-S1	Chr3:621920-621950	31	loss	genic	AT3G02850	SHAKER POLLEN INWARD CHANNEL (SKOR) K+
G10-S1	Chr4:2126464-2126494	31	loss	genic	AT4G04340	early-responsive to dehydration stress
G10-S2	Chr1:126219-126253	35	loss	genic	AT1G01320	Tetratricopeptide repeat (TPR)-like superfamily protein
G10-S2	Chr1:1196705-1196834	130	gain	intergenic		
G10-S2	Chr1:9768960-9768970	11	gain	genic	AT1G28020	Tetratricopeptide repeat (TPR)-like superfamily protein

G10-S2	Chr1:23533240-23533266	27	loss	genic	AT1G63450	Encodes xyloglucan-specific galacturonosyltransferase	a
G10-S2	Chr1:28515126-28515227	102	loss	intergenic			
G10-S2	Chr1:28515410-28515507	98	loss	intergenic			
G10-S2	Chr1:28515964-28516123	160	loss	intergenic			
G10-S2	Chr2:6963622-6963638	17	gain	intergenic			
G10-S2	Chr2:7151322-7151359	38	gain	genic	AT2G16500	ARGININE DECARBOXYLASE 1	
G10-S2	Chr2:14161150-14161174	25	gain	genic	AT2G33420	unknown protein	
G10-S2	Chr3:4130423-4130476	54	loss	genic	AT3G12940	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	
G10-S2	Chr3:8794625-8794714	90	loss	genic	AT3G24260	unknown protein	
G10-S2	Chr3:17015355-17015419	65	gain	genic	AT3G46290	Encodes HERCULES1 (HERK1)	
G10-S2	Chr3:18288998-18289007	10	loss	genic	AT3G49320	Metal-dependent protein hydrolase	
G10-S2	Chr3:19485799-19485852	54	loss	genic	AT3G52530	Protein kinase superfamily protein	
G10-S2	Chr3:19847547-19847558	12	gain	genic	AT3G53540	unknown protein	
G10-S2	Chr5:8285315-8285357	43	gain	genic	AT5G24320	Transducin/WD40 repeat-like superfamily protein	
G10-S3	Chr1:532526-532557	32	loss	genic	AT1G02530	P-glycoprotein 12	
G10-S3	Chr1:10425023-10425040	18	gain	genic	AT1G29770	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	

G10-S3	Chr1:17559469-17559530	62	gain	genic	AT1G47710	Serine protease inhibitor (SERPIN) family protein
G10-S3	Chr1:23825659-23825676	18	gain	genic	AT1G64190	6-phosphogluconate dehydrogenase family protein
G10-S3	Chr2:7333066-7333125	60	loss	genic	AT2G16910	basic helix-loop helix transcription factor
G10-S3	Chr2:8947975-8948073	99	loss	genic	AT2G20780	Major facilitator superfamily protein
G10-S3	Chr3:2658533-2658550	18	loss	genic	AT3G08760	osmotic stress-inducible kinase
G10-S3	Chr3:4302181-4302199	19	gain	genic	AT3G13290	VARICOSE-RELATED (VCR)
G10-S3	Chr3:10133450-10133486	37	loss	genic	AT3G27930	unknown protein
G10-S3	Chr3:15525290-15525327	38	loss	intergenic		
G10-S3	Chr3:15525395-15525525	131	loss	retrotransposon	AT3G43620	
G10-S3	Chr3:15526183-15526245	63	loss	intergenic		
G10-S3	Chr4:2478108-2478176	69	gain	genic	AT4G04890	PROTODERMAL FACTOR 2 (PDF2)
G10-S3	Chr5:2640323-2640375	53	loss	genic	AT5G08200	peptidoglycan-binding LysM domain-containing protein
G10-S3	Chr5:7492827-7492844	18	gain	genic	AT5G22560	unknown protein
G10-S3	Chr5:21284097-21284122	26	loss	genic	AT5G52430	hydroxyproline-rich glycoprotein family protein
G10-S3	Chr5:21723617-21723670	54	gain	genic	AT5G53490	Thylakoid lumenal 17.4 kDa protein
Average size		53				

Supplementary Table 9. Validation of mutations detected in G10-S3 and G10-S6 by capillary (“Sanger”) DNA sequencing.

Samples	Position	Mutation	Forward primer	Reverse primer	Sequencing primer	Sequencing Results
Saline G10-3	Chr1:24640163	G to T	agagaggaggagtcacagga	ggacttttgggatcggcttt	agagaggaggagtcacagga	Confirmed
Saline G10-3	Chr1:7059442	4bp ins	ggtttgaatacccagagcc	ccctcacaagtcacaaatcgt	ggtttgaatacccagagcc	Confirmed
Saline G10-3	Chr2:15253629	T to A	gtggacagcttttcacagg	acagaaaagtaggggtcaagcc	gtggacagcttttcacagg	Confirmed
Saline G10-3	Chr2:19006443	G to T	atgcatcttgaccacctcca	gcaaagcagctgatgactct	gggtcacaaggaggccatta	Confirmed
Saline G10-3	Chr2:8764428	13 bp del	ggaagaatgtagcgcgtgag	tccgagtcacccgatattatgct	ggaagaatgtagcgcgtgag	Confirmed
Saline G10-3	Chr3:12316905	T to C	agggaagacgaaaggtgtct	tcagggaagacgaaaggttg		PCR failure
Saline G10-3	Chr3:14013828	C to T	ccagcactcccctccatta	tccttgcatcatccaagt	ccagcactcccctccatta	Confirmed
Saline G10-3	Chr4:7943909	C to T	tctgatgaagacggcgaaat	tgcaattgacctttagtgtgc	tctgatgaagacggcgaaat	Confirmed
Saline G10-3	Chr5:26117786	del A	aagggtttgatgatgtgtct	gtgctaccatcatcatcggtg	aagggtttgatgatgtgtct	Confirmed
Saline G10-3	Chr5:547840	ins A	ttcttactgtggaaccgct	cccaaatccagatctccca	ttcttactgtggaaccgct	Confirmed
Saline G10-6	Chr1:24411983	C to A	tggcacctggatccaatagt	tgcattgcagttactttcgga	tggcacctggatccaatagt	Confirmed
Saline G10-6	Chr1:27684348	del T	gcacaagaaacaagaaagcgt	gcgtatactcgttcgtcgt	gcacaagaaacaagaaagcgt	Confirmed
Saline G10-6	Chr2:10657257	T to G	gtggaggcagaggagaagat	gaggattttgtctcgtccgc		PCR failure
Saline G10-6	Chr2:4331945	A to T	ttcttctccataaactcttggt	tggttgagatgaatttggaatcg	ttcttctccataaactcttggt	Confirmed
Saline G10-6	Chr4:1531901	C to T	cgtgtaaagctgtcgttgga	ggctacgagaagaaaggcct	cgtgtaaagctgtcgttgga	Confirmed
Saline G10-6	Chr4:2483913	del GA	aataccgccgtacagcatct	tggctcatgatccttgcaaa	aataccgccgtacagcatct	Confirmed
Saline G10-6	Chr4:2483916	G to T	aataccgccgtacagcatct	tggctcatgatccttgcaaa	aataccgccgtacagcatct	Confirmed
Saline G10-6	Chr4:2888020	A to T	aagctgtccacttcacta	gaaagtgtcgccctgttctg	aagctgtccacttcacta	Confirmed
Saline G10-6	Chr4:2888180	A to C	aagctgtccacttcacta	gaaagtgtcgccctgttctg	aagctgtccacttcacta	Confirmed
Saline G10-6	Chr4:2888185	C to T	aagctgtccacttcacta	gaaagtgtcgccctgttctg	aagctgtccacttcacta	Confirmed
Saline G10-6	Chr4:508364	A to T	acggtttgttcgatgatgct	acttggaactattgccacca	acggtttgttcgatgatgct	Confirmed