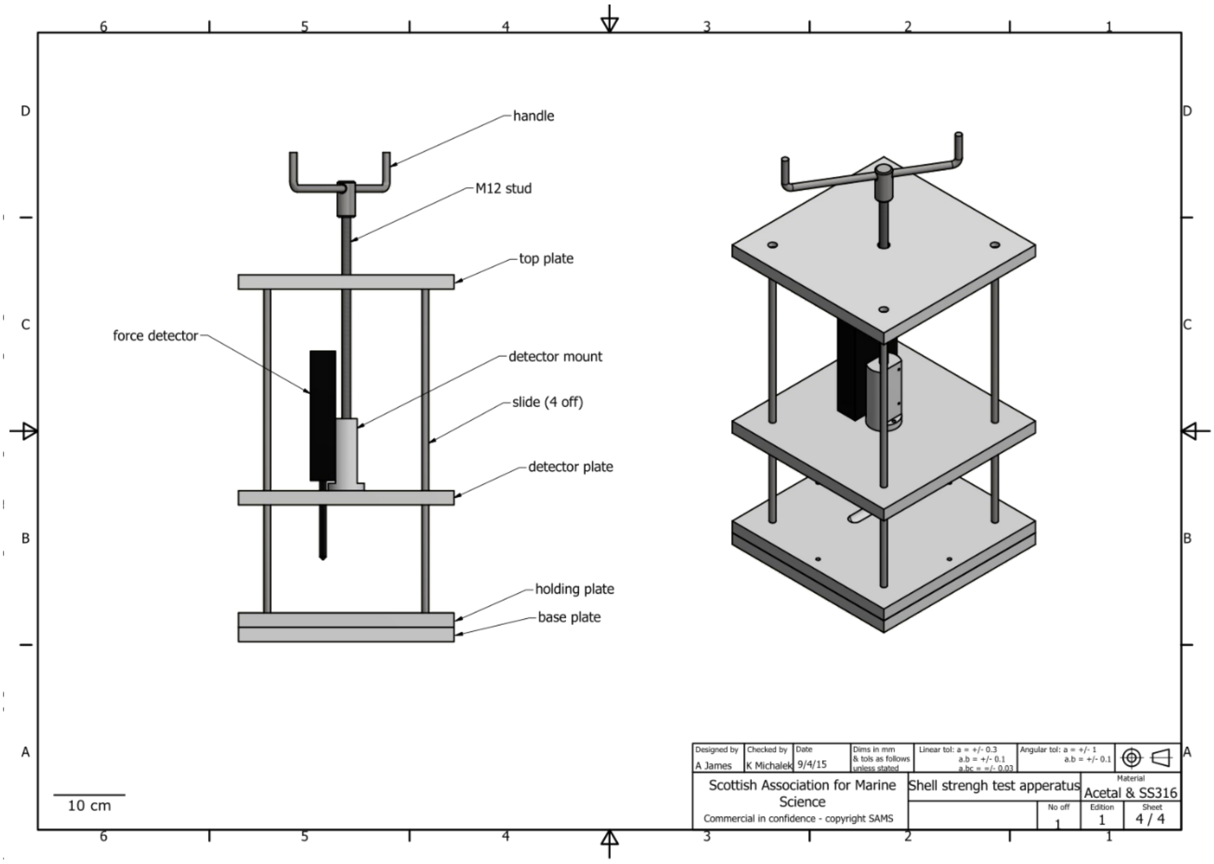
SUPPLEMENTARY MATERIAL

Figure S1 Custom-built device for quantitatively measuring shell strength in mussels. The design was adapted from Penney et al. (2007) and Beaumont et al. (2008) and the apparatus was manufactured in house (SAMS). See section 2.3 for a description of the mode of operation.



Designed by	Checked by	Date	Dims in mm & tols as follows unless stated	Linear tol: a = +/- 0.3 a.b = +/- 0.1 a.bc = =/- 0.03	Angular tol: a = +/- 1 a.b = +/- 0.1
A James	K Michalek	9/4/15			

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Shell strengh test apperatus

Material: Acetal & SS316
No off: 1
Edition: 1
Sheet: 4 / 4

Figure S2 PCA biplot of the SNP allele frequencies (*n* = 33 SNPs) in cultured mussel from Loch Leven, Scotland (*n* = 435 individuals); colour-coded by their depth of cultivation. PC1 captured most of the genetic variation, with three main clusters being observed and corresponding to the individuals carrying different relative proportions of *MT* alleles. *From left to right*: mussels with none or low, intermediate, and high *MT* allele frequencies (MT_{AF}), respectively.

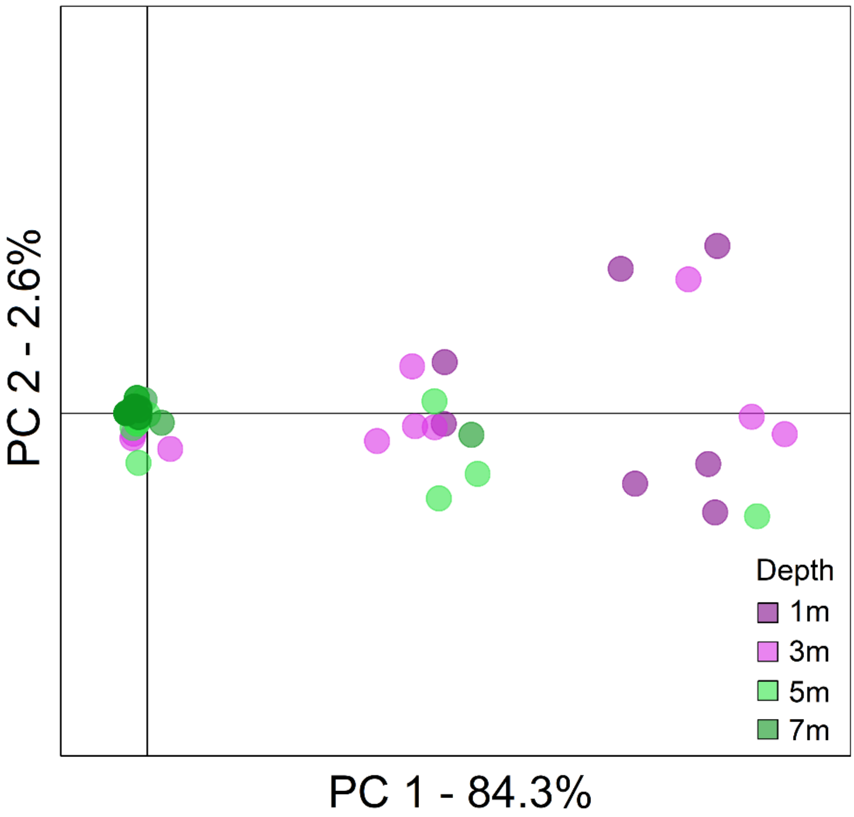

Figure S3 Overview of the first five principal components (PC1-5; 'shape variables') capturing more than 95 % of the variation in *Mytilus* shell shape. *From left to right* (for each PC): (a) The percentage of variance explained, the contribution to shell outline reconstruction with decreasing / increasing PC values (mean PC value ± 3 standard deviations), and to specific shell features. (b) The effect of selected predictors ('*SL*' shell length, in mm; 'MT_{AF}' frequency of *M. trossulus* alleles, 0 - 1; '*S*' salinity, in PSU) on each PC. Loess-smoothed curves to aid the visualisation of individual relationships. Univariate GLMs revealed significant effects of some predictor variables on each PC (*p*-value < .001 '***', < .01 '**', < .05 '*').

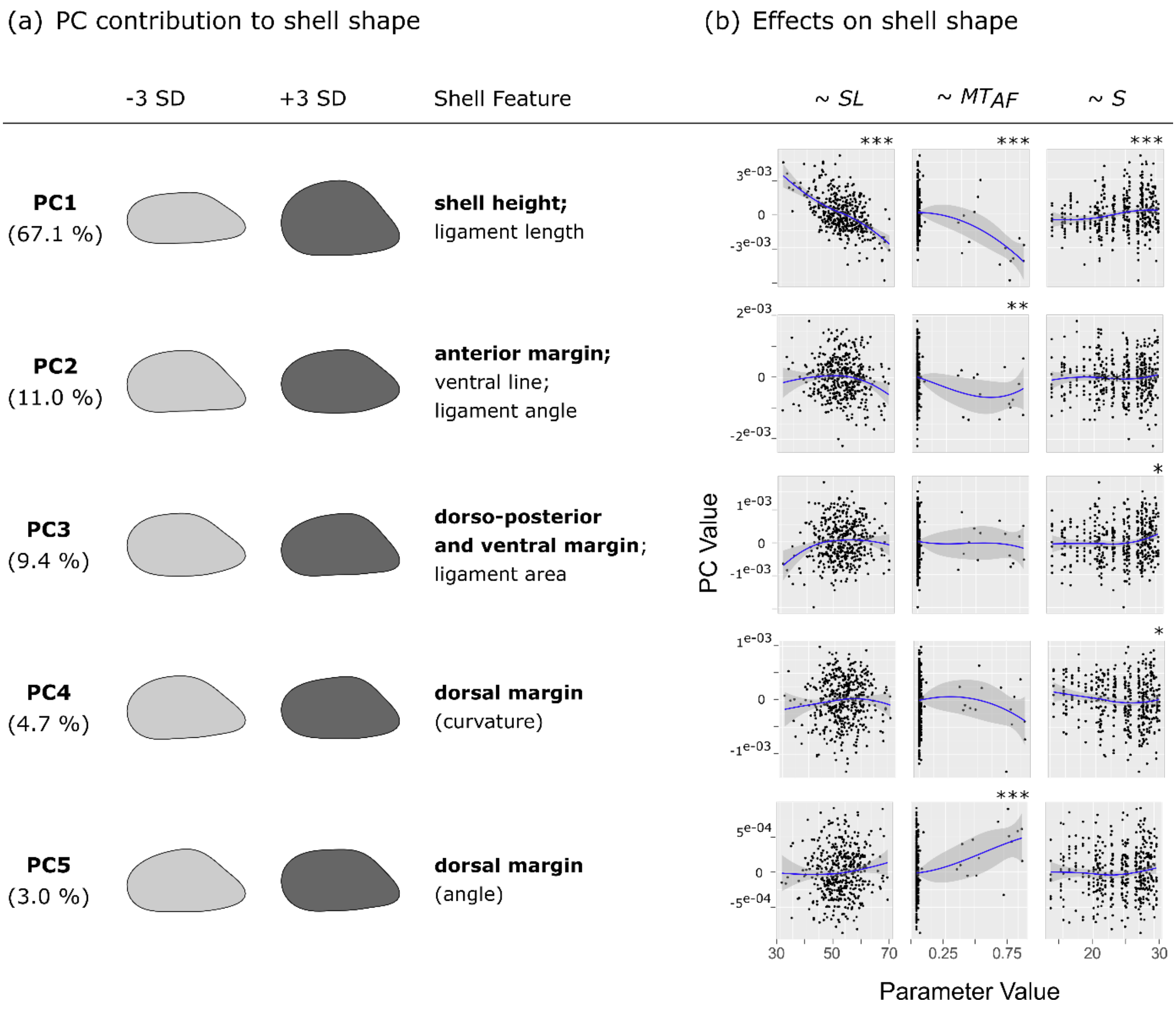

Table S1 SNP marker panel (n = 33) diagnostic for *Mytilus trossulus* (MT). Shown are the locus ID and reference, species-specific nucleotide call, and RAD sequence for each marker. The number of genotyped mussels (sample size, n) and the number of individuals showing alleles of MT (MT-positive), also expressed as proportion of the genotyped sample population, are shown for each marker, respectively.

Locus	**Reference** (Primer; Assay)	**Allele**			**RADseq marker sequence**	**Sample Size**	**MT-positive**	
		ME	MG	MT		n	n	% Pop
1	100173_B GTA0189062	{TT}	{TT}	{AA}	TGCAGTTTCTTGATAAGCAAATAGTTGATATGACTG[AT]ATTTCTGCATGATTTTTAGCAATATAGGTCATATTCCATGATAAAACAATGCCTAC	435	19	4.37
2	117000_B GTA0189052	{TT}	{TT}	{GG}	TGCAGAGAAGTTAAAGTTTTGTCCAGGTGGAGAAGTCATTGA[GT]GCTGAATGTGCAACCAAAGATGGCATGCCTTATGATGGTACTGGTGAGAT	434	19	4.38
3	24411_A GTA0189075	{AA}	{AA}	{GG}	TGCAGCTTTCAAAAAGGAATCTGGTTTATTCGATTCA[AG]TGAATGTTACCCCTACTATATGACTGCTATGGTTTGCTCAATATTTTGTTATTTA	434	23	5.30
4	39506_A GTA0189092	{AA}	{AA}	{TT}	TGCAGATGCAAAAGATAGAGCAAAAAGAATATTGGCAGGTTGTAGAGGAGG[AT]AGTATTGGGTCTTACACTGCTAGCCCTGGTGTTGAGGTTAT	435	19	4.37
5	76606_B GTA0189093	{TT}	{TT}	{AA}	TGCAGATCTGGTTAGTAACACAAGGG[AT]TTTACAAAGCAAACATTTAGCTATATTAATTATATTTGTTTGAAGAGAAAACCATGAAATTGACAA	435	19	4.37
6	100259_A GTA0189097	{AA}	{AA}	{GG}	TGCAGCCGAATTAGAAACTATTAAAAAGAAAATGGA[AG]GGAGAGAATGATGAGCTCAAGAAAGATATAGAAGATTTAGAAAGTTCTCTTGCAAA	435	23	5.29
7	123343_A GTA0189068	{GG}	{GG}	{AA}	TGCAGCTTCAGCTTCTTCACGTTTCTTCTTTTCTTCCTCTTCCTGGTCCAATTCTTTGAT[AG]CTTTCTTCTAAAACATTGGGCCAGAAATCTCC	435	22	5.06
8	141978_A GTA0189090	{GG}	{GG}	{AA}	TGCAGATTAAACGCCAACCAAAACAGAAATTAAAGCCAAA[AG]CGTTATTGTCTCATTATTGGAATTAATCAGGATTTTATTAAAATATAAATAT	435	23	5.29
9	212387_A GTA0189078	{AA}	{AA}	{CC}	TGCAGATTACATAATATCTCTGCACTTGATGTAACCCATAAAACATT[AC]AAATGAACCCTGTCATTACTGCTCTGACATTTATATAGCCCTCCT	434	37	8.53
10	123488_A GTA0189044	{AA}	{AA}	{CC}	TGCAGCAGCCTCGTTTCCATATGG[AC]ATACCCTCTGCAAATTCTAGTCCATTTAATGTATACTCACAAATGGGCATCCAAAGACCAACAAACAA	432	14	3.24
11	26598_A GTA0189045	{AA}	{AA}	{TT}	TGCAGACTGTATGTAATGTTAACTGGAAGAAAAAATATC[AT]GAGTCCATTTATAAGTAATATATACATGTATGTTTAAACAGGAAATATTTTTT	433	17	3.93
12	53148_A GTA0189071	{CC}	{CC}	{TT}	TGCAGCATCATAATCATATAAAACTCTAGC[CT]TGTTTTTTCTCTGTACTAGGTGTTGCAGCTGTGATGTGTATCATAGGGGGTGCACTTGGCTG	435	19	4.37
13	8289_B GTA0189070	{AA}	{AA}	{AC, CC}	TGCAGATTGACCAGCTATTGTTATAGAATTTGGATTCCCTCCAAAACTTTCAATATTGTCATG[AC]ACCCATTTAATCGCCATTTGTTGGTCCCA	434	20	4.61

Locus	**Reference** (Primer; Assay)	**Allele**			**RADseq marker sequence**	**Sample Size**	**MT-positive**	
		ME	MG	MT		n	n	% Pop
14	10704_A GTA0189058	{CC}	{CC}	{TT}	TGCAGATCATATTTTCACTATTAAAACTTTGATAAATAAATATTTACA[CT]AAATTAAAAAAGCCTATTTTTGCTTGTTTTGTAGATCTCTCTAA	434	15	3.46
15	33513_A GTA0189101	{TT}	{TT}	{GG}	TGCAGATGCAATTACTTCTAAATGTGGATGCCACACAAAGATAATT[GT]CACACAACATCCCTAATTAATTTTGTTTTCTCTTGTAGAACATGCT	434	18	4.15
16	84029_A GTA0189049	{CC}	{CC}	{TT}	TGCAGGCAGGGGATGGTATCCTATT[CT]ATTAACAATGCCAACACAGATCAGCTATCACATGAACAAGCTAAAATGGAGATGATCAGATCTGGCA	435	21	4.83
17	108748_B GTA0189082	{CC}	{CC}	{TT}	TGCAGTAATGGACCTTGCTTCCTTTGCCGCTTCCATTGCAAA[CT]GATACTGCTAATTTAACGCAAATGACAATATCTCCTACAAATTTGGATGC	434	21	4.84
18	131765_A GTA0189100	{TT}	{TT}	{GG}	TGCAGGATGCACTTGATATAGAAAACATGTCTCGTTAGGTTATAATCTATGTA[GT]AATCCAAATAACGTGGAATCAACATGCATATACGCAAAA	435	18	4.14
19	187177_A GTA0189085	{GG}	{GG}	{TT}	TGCAGATGGGTTTGAATACTGGA[GT]TATCTTTGTCATTTCCTGTGCTGTTTTGTGCACTGTGAATATATTGTCCTGACCGAGAACTACGAAATC	434	15	3.46
20	34117_A GTA0189050	{AA}	{AA}	{TT}	TGCAGGACAAGTCTTTTCCCAATCATCAGAACTCATTTTCTT[AT]ATCCAGGATAAATAAACAATTAGGAATCCTGCTATTCCAATATTGATCAA	434	18	4.15
21	58876_A GTA0189053	{GG}	{GG}	{AA}	TGCAGCAGTGTTTTCCATTTGCAGTGGTGTTCTCAATGAATATTTAGGAAGAAA[AG]CTTACAATTATAATTGGGAGTTTTGTGTTCACAGCTGG	433	11	2.54
22	109335_A GTA0189077	{TT}	{TT}	{GG}	TGCAGCTGCTGAGGGGACTGAACAACAGAGGTCAAGGGTGATGCAGATGTTGTTGGGATA[GT]TCGAGGTAGTCGGGTCAAGGGTCAAATTCTTA	435	20	4.60
23	158786_B GTA0189054	{AA}	{AA}	{GG}	TGCAGAACTAATGTCTGACCAAGTCC[AG]ACCGTCTGCTAGTAATTCCCCTCCATCAAGAGATCATAGATTATTATCTCCAATGAATAGATCAAG	435	10	2.30
24	188312_A GTA0189046	{AA}	{AA}	{TT}	TGCAGCCAACTTGTGTCCATTT[AT]ATTCTTTGCACATTTAGAATATGATCAATTGACTGTGAAGACCTTTTAAGAAATACCATTCTCATCTGTA	433	9	2.08
25	61387_A GTA0189065	{GG}	{GG}	{AA}	TGCAGTTCTCACCGACCGGTCGGATATACTAAATATTGAACG[AG]TACTGTTATTTGTTGACAATTATTTAGTGACAACAAAACATTCAATAGAC	435	19	4.37
26	116758_B GTA0189079	{AA}	{AA}	{GG}	TGCAGGAAACTGCATCAACTGATTC[AG]ATTACCATTCGCTACATGTCAATTTTCATGCATACAAAAACAAGATAAAGAAATGCATTAGATGAGA	435	16	3.68
27	138581_A GTA0189080	{AA}	{AA}	{CC}	TGCAGCATGGAATTGCATAAGAATTTGACCCTTGACCCGACTACCTCGA[AC]TATCCCAACAACATCTGCATCACCCTTGACCTCTGTTGTTCAG	435	19	4.37
28	93136_A GTA0189104	{TT}	{TT}	{CC}	TGCAGTTTTCTGTCTGTATGGTGCATTGTCTG[CT]GTGACAATTGACAACTATATTCGAATGTGTTATCCATCCATAGTTAATTTGTATTGTAAG	434	19	4.38
29	161905_A GTA0189048	{AA}	{AA}	{AG}	TGCAGACAAAGAAAATATGGATGTTTCAGATGA[AG]TCAACTAGTTTATCAGATATGAACAACAGTGCTATTGACCCAGTTACTCCTGGTAAGGG	435	13	2.99
30	202081_A GTA0189103	{TT}	{TT}	{CC}	TGCAGCAAGTCCACAGAGTTCTATTGA[CT]GAGTCCCAGGTTTTATCTCCAGAACAGGAAGCTAGTATCCCAGTGACAGTCTTGGATGAAATTGG	435	19	4.37

Locus	**Reference** (Primer; Assay)	**Allele**			**RADseq marker sequence**	**Sample Size**	**MT-positive**	
		ME	MG	MT		n	n	% Pop
31	239964_A GTA0189105	{TT}	{TT}	{CC}	TGCAGGGCGCACATGTCGTTCTATTTCTATTCATCGTCTGCATGTAA[CT]AGATTTTTCCATGTGGAATTCATTTACCTGTCGAAGTCATTAATT	434	17	3.92
32	37630_A GTA0189089	{CC}	{CC}	{TT}	TGCAGAGAAACTTGATCCTTTCTTCTGTAAAGGTTGTAATAACCTTGTACA[CT]AAACCATCAGCATCCTTTGTATAATGCTGAAAGATACAATT	434	17	3.92
33	7646_A GTA0189076	{GG}	{GG}	{AA}	TGCAGAACTTAAAAAGATTCTGGAATGCAGAGA[AG]GGAAAAGTAAATGTGAATTCATTTGACACTGAGGGACAAACGGCTTTGCATCAAAGTTG	435	22	5.06