

Supplementary table S1. Sequencing depth and coverage of all samples

Normal conditions				
Samples	No.reads	Mapped reads	Mean coverage(X)	Mean Mapping Quality
NC-Paternal	102,334,097	99.73%	32.9723	21.48
NC-Maternal	106,476,407	99.75%	34.2729	21.3
NC-offspring-1	113,240,333	99.81%	36.5216	21.52
NC-offspring-2	157,090,378	99.81%	50.654	21.49
NC-offspring-3	117,020,978	99.77%	37.6965	21.48
NC-offspring-4	121,410,039	99.81%	39.1693	21.57
NC-offspring-5	130,213,361	99.82%	41.9743	21.53
NC-offspring-6	135,843,883	99.80%	43.8225	21.57
NC-offspring-7	124,705,370	99.74%	40.1756	21.53
NC-offspring-8	97,341,821	99.82%	31.4037	21.58
NC-offspring-9	133,625,850	99.82%	43.0968	21.55
NC-offspring-10	102,744,542	99.73%	33.1089	21.58
NC-offspring-11	141,964,996	99.73%	45.7257	21.58
NC-offspring-12	118,854,098	99.79%	38.3124	21.52
NC-offspring-13	95,602,982	99.59%	30.6295	21.47
NC-offspring-14	138,901,831	99.82%	44.809	21.54
NC-offspring-15	115,422,424	99.77%	37.1748	21.52
NC-offspring-16	121,143,511	99.74%	38.9763	21.3
NC-offspring-17	110,462,424	99.79%	35.5785	21.3
NC-offspring-18	129,239,764	99.77%	41.6265	21.33
NC-offspring-19	130,208,024	99.73%	41.9198	21.31
NC-offspring-20	118,664,268	99.75%	38.1988	21.27
NC-offspring-21	134,638,604	99.51%	43.3233	21.25
NC-offspring-22	116,424,472	99.75%	37.5395	21.27
NC-offspring-23	143,429,685	99.76%	46.1688	21.25
NC-offspring-24	116,051,579	99.75%	37.368	21.25
NC-offspring-25	103,932,734	99.76%	33.5194	21.24
NC-offspring-26	128,354,485	99.73%	41.3713	21.26
NC-offspring-27	135,234,628	99.75%	43.5493	21.27
NC-offspring-28	136,149,869	99.74%	43.872	21.31
NC-offspring-29	113,064,167	99.78%	36.4006	21.26
NC-offspring-30	133,326,762	99.78%	42.9638	21.35

Low temperature				
Samples	No.reads	Mapped reads	Mean coverage(X)	Mean Mapping Quality
LT-Maternal	102,904,534	99.78%	33.2178	21.12
LT-Paternal	104,289,419	99.83%	33.7196	21.14
LT-offspring-1	83,989,840	99.81%	27.1266	21.14
LT-offspring-2	75,002,344	99.73%	24.1939	21.03
LT-offspring-3	83,596,507	99.76%	26.9958	20.72
LT-offspring-4	78,746,188	99.76%	25.4143	21.06
LT-offspring-5	92,966,203	99.84%	30.0389	20.94
LT-offspring-6	69,939,577	99.49%	22.5362	21.35
LT-offspring-7	87,804,757	99.86%	28.404	21.21
LT-offspring-8	78,887,093	99.86%	25.5083	21.32
LT-offspring-9	81,070,607	99.83%	26.2112	21.42
LT-offspring-10	73,645,332	99.80%	23.784	21.24

High temperature				
Samples	No.reads	Mapped reads	Mean coverage(X)	Mean Mapping Quality
HT-Maternal	94,687,253	99.79%	30.5639	21.02
HT-Paternal	108,112,620	99.73%	34.8955	21.27
HT-offspring-1	83,005,550	99.79%	26.8074	21
HT-offspring-2	84,024,521	99.82%	27.1427	20.84
HT-offspring-3	76,748,540	99.81%	24.7832	20.93
HT-offspring-4	77,410,675	99.84%	25.0004	21.03
HT-offspring-5	70,368,965	99.83%	22.737	20.8
HT-offspring-6	81,034,084	99.85%	26.183	21.28
HT-offspring-7	72,583,253	99.83%	23.443	21.24
HT-offspring-8	84,178,201	99.80%	27.1971	21.45
HT-offspring-9	85,732,489	99.84%	27.7105	21.26
HT-offspring-10	82,210,107	99.81%	26.5712	21.21

Supplementary table S2. The information of all *de novo* mutations.

Normal conditions														
Variant Number	Samples	Chromosome	Position	Ref	Alt	Read depth	Ref reads	Alt reads	Proportion of Alt read	Region	TE	Validation	Forward primer	Reverse primer
NC1	NC-offspring-9	Bomo Chr23	3722500	T	G	30	21	9	0.30	intergenic	OUT	F	CAGTTTTCCGGTGTGGTCCCT	GCATACAAAACCCGACAGC
NC2	NC-offspring-13	Bomo Chr17	13472593	A	G	36	25	11	0.31	intergenic	OUT	T	CCGGTACTCGAGACAGCATT	GTGGTTGTACCTACCCGTGC
NC3	NC-offspring-13	Bomo Chr21	14309584	G	A	26	18	8	0.31	intergenic	OUT	T	TCGTTGCCGGGTCTAAAGTC	CAACAGCATTACGTTGCGA
NC4	NC-offspring-6	Bomo Chr22	17131823	T	C	29	20	9	0.31	intergenic	OUT	T	GCCTCCGTCCTGAGAAGAAC	CTCCCCGATTACGATCAGC
NC5	NC-offspring-20	Bomo Chr28	10516179	A	T	32	22	10	0.31	intergenic	IN	T	CGTCCCCTCCTCTAATGCC	CTTTTTGGCGGAACACGAG
NC6	NC-offspring-7	Bomo Chr13	2692518	G	A	35	24	11	0.31	intergenic	OUT	T	CCACATCGGAGCTAACTGCT	AAGTGCACACGTCTTTGGA
NC7	NC-offspring-9	Bomo Chr11	14924852	T	A	38	26	12	0.32	intergenic	IN	T	GACGCTTTTTACCGGTGTGG	CGCGAAATGTACCCAGCTA
NC8	NC-offspring-27	Bomo Chr19	3738838	A	C	38	26	12	0.32	intergenic	IN	F	CAGCTTATCCTCGACTGCGT	AGCGGTTAGTGGCCTCAAT
NC9	NC-offspring-13	Bomo Chr4	17341932	A	G	25	17	8	0.32	intron	OUT	T	GGCTCGCTGACCAAAGTAGT	CATAGCCCGTTAGATGGCGT
NC10	NC-offspring-13	Bomo Chr15	8809936	G	A	24	16	8	0.33	intergenic	OUT	T	AGTTACGGCAAAAGTGTGGCT	ACAGTTGACAGATGACGGCTT
NC11	NC-offspring-24	Bomo Chr13	12343252	A	T	33	22	11	0.33	intergenic	OUT	T	CGGGCAACTAACTGTCAGGA	TGACACGACGACTGCGTTTAT
NC12	NC-offspring-21	Bomo Chr10	13566275	A	T	45	30	15	0.33	intergenic	OUT	T	GACTGTCCGTTGTTTTGCC	CCTACCGGTTTTTGCTCCT
NC13	NC-offspring-23	Bomo Chr17	10023	A	G	39	26	13	0.33	intergenic	OUT	F	TCTCGCAGAGTAGAGCACCT	TTTCCACGTCTCGATGGTG
NC14	NC-offspring-15	Bomo Chr24	16497379	T	G	44	29	15	0.34	intron	IN	T	GCCAAGGGGGAGATTTGGAA	TCGTAGGCTCGAAGGGGAG
NC15	NC-offspring-18	Bomo Chr19	6823092	C	G	35	23	12	0.34	intergenic	OUT	T	TGTTGCTCGTGAACCGTCTT	TAGGTGCTCGTGGCATAG
NC16	NC-offspring-12	Bomo Chr10	11685117	T	A	32	21	11	0.34	intergenic	OUT	T	GTCAAAGCGATCCGAGGCTA	TACATCGCCAACGGAACGAA
NC17	NC-offspring-24	Bomo Chr5	4669486	G	A	26	17	9	0.35	intergenic	OUT	T	GCGAGGGTTGAACGAAACTG	TGAACCGCTAATCTCAGGA
NC18	NC-offspring-16	Bomo Scaf010	93298	A	G	28	18	10	0.36	intergenic	IN	T	CGGGGCTAAGCGACAATAAC	CGGCCTTACTCTCAAAGGGT
NC19	NC-offspring-29	Bomo Chr10	10772046	C	A	53	34	19	0.36	intron	OUT	T	TCTGTGGGTCCAGTAACCA	AGTACCGCGAAAGGAAGTC
NC20	NC-offspring-13	Bomo Chr7	12904904	C	T	25	16	9	0.36	exon	OUT	T	TTGCGCTACTGGTGGTAGGA	GCACGATGTACACGAAGG
NC21	NC-offspring-22	Bomo Chr5	7531454	T	C	36	23	13	0.36	intron	OUT	T	TTGGGGCTCAACACTTTTCTCT	CGTACAGCGGCTTTGTTTCT
NC22	NC-offspring-30	Bomo Chr12	6965686	C	G	30	19	11	0.37	intron	OUT	T	AAGCGTACTGAAGGCCCAAA	GGCCTGGACACGCTTTAGTA
NC23	NC-offspring-28	Bomo Chr7	1064237	C	A	43	27	16	0.37	exon	OUT	T	GCACGATGATGTAGTCCCA	GCACGATAGGTACACCAACC
NC24	NC-offspring-23	Bomo Chr14	2192356	C	T	42	26	16	0.38	intron	OUT	F	GGGGATCGTTTGTAGTGGTG	TCGCATGGATCGTCTGGAAG
NC25	NC-offspring-19	Bomo Chr17	2432066	G	A	39	24	15	0.38	intergenic	OUT	T	TGGCGGAAGTGGACTTATGG	TTAGTACCTCGAAGGGCTG
NC26	NC-offspring-14	Bomo Chr6	16129500	A	T	39	24	15	0.38	intergenic	OUT	T	TTTACGACAACCACGGGGAG	TGACCACATCTCGGCTTC
NC27	NC-offspring-27	Bomo Chr12	16426416	A	G	36	22	14	0.39	intergenic	OUT	T	GAGAGACCGGAAACATGGCA	CGCTAAACCTCGAGAACGGC
NC28	NC-offspring-8	Bomo Chr13	14215074	C	A	33	20	13	0.39	intergenic	OUT	T	GGAGCGTAGGCTGGAATCTT	GAGAGCCGCAACATACGAGA
NC29	NC-offspring-24	Bomo Chr10	4254666	C	A	30	18	12	0.40	intron	OUT	T	CGAAAAACAGCATTCGGGCT	TCGTAGGCGTCATAAGGCAC
NC30	NC-offspring-14	Bomo Chr6	13935671	G	A	45	27	18	0.40	intron	OUT	T	CCACCTTCAAAACCGAAACG	TGACGGAGCTATCCTCGTGT
NC31	NC-offspring-11	Bomo Chr19	6370594	C	A	32	19	13	0.41	intergenic	OUT	T	TCGTAGCACTTTTGGCGGAGT	CGACAAGGGTGGTGTGATGGA
NC32	NC-offspring-17	Bomo Chr7	11757413	C	T	32	19	13	0.41	intergenic	OUT	T	GTCTAAGAAACCCAGCCCAAC	CAAGCAATGCCTGCACCAAT
NC33	NC-offspring-29	Bomo Chr4	5281848	C	T	27	16	11	0.41	intergenic	OUT	T	CCGTAACAGAGTTGTCTCCA	CGAGTACGACCACTCAAC
NC34	NC-offspring-6	Bomo Chr11	15169940	A	C	38	22	16	0.42	exon	OUT	T	CTTTGTCTGGGCGTGTTCG	GGGGACTTATAGCCGGGAGA
NC35	NC-offspring-21	Bomo Chr16	13183326	C	A	26	15	11	0.42	intron	OUT	T	GCGGTATGATGGCCCTGTAA	AGCTGTTTCCATCTCGTCCG
NC36	NC-offspring-14	Bomo Chr3	6656473	G	C	33	19	14	0.42	intergenic	IN	T	GACTTGGCTACGCTCCTTCT	AATTCAACCCACTGCCGTGA
NC37	NC-offspring-18	Bomo Chr1	4351349	A	T	14	8	6	0.43	intron	OUT	F	AAACCGTCGTTAAAGGCCCA	CTGCAAAAGAGTTCGACGTGC
NC38	NC-offspring-30	Bomo Chr13	11037414	C	T	37	21	16	0.43	intergenic	OUT	T	CCGATAAGCCTCCTTCGCAA	CGGCTTTGTACGCAAACTG
NC39	NC-offspring-12	Bomo Chr13	5314947	T	A	34	19	15	0.44	intron	OUT	T	TGGACACGGCTAGCTTAACG	CGCACAGACGATAATTGCGG
NC40	NC-offspring-1	Bomo Chr8	3492258	G	A	36	20	16	0.44	intergenic	OUT	T	GTCCAAAGAAAGGTTGAGGGTA	AGTAATGCTTCGCAGAACTGA
NC41	NC-offspring-29	Bomo Chr3	4134264	T	C	42	23	19	0.45	exon	OUT	T	TATTGGGCTTTGCTGAACCT	ATTGAGCGTGGCTTCATTTCT
NC42	NC-offspring-28	Bomo Chr6	4515432	A	T	50	27	23	0.46	intron	OUT	T	GACGTGTTAGGCTGGTCTCT	TCAGGTAATTACGGTGGGGCG
NC43	NC-offspring-17	Bomo Chr24	5135557	A	T	26	14	12	0.46	intergenic	OUT	T	ATTTGGTAGTGCTGTGGCTTAGA	GCTTCATCAGGACAGGTGGG
NC44	NC-offspring-15	Bomo Chr1	6410731	T	A	30	16	14	0.47	intron	OUT	T	TCGCTAACCGAGCACTAAGACC	CAGAGACTGATCTCGCTCGC
NC45	NC-offspring-13	Bomo Chr3	7194205	C	T	30	16	14	0.47	exon	OUT	T	CGTACACCACGACCATAGG	CTAAGACGGCGCTTCAATCA
NC46	NC-offspring-21	Bomo Chr8	14707532	T	A	47	25	22	0.47	intron	OUT	T	CCTAATATCGTACAAGAGCCTTCATC	ACAGGTGACCGCTTACACGAT
NC47	NC-offspring-9	Bomo Chr10	10266170	T	A	32	17	15	0.47	intergenic	IN	T	ACATTCGGACCACAAGGAGAC	CGATCGAGTCCGCTTCTAC
NC48	NC-offspring-12	Bomo Chr26	2681149	G	A	49	26	23	0.47	intergenic	OUT	T	GCCAGCAGCACTTACTAACTACCT	GAATGCCGTACGCCACCTC
NC49	NC-offspring-18	Bomo Chr21	1687204	C	T	36	19	17	0.47	intron	OUT	T	GGGGCATCTTCCGATACGTT	TTTCCGATCGCTACCATCG
NC50	NC-offspring-18	Bomo Chr13	9471056	T	C	40	21	19	0.48	intergenic	OUT	T	AACTCATTCGTCTGCGACT	TTTAAGGCTCACACCGGACG
NC51	NC-offspring-27	Bomo Chr16	11790607	A	G	40	21	19	0.48	intergenic	OUT	T	CCACTACTGTTAGGTACGCGG	TCTGGACCGACTCTCAAAGA
NC52	NC-offspring-19	Bomo Chr20	854321	C	T	44	23	21	0.48	intergenic	OUT	T	GACGCCCAAGAAATAGGCAGA	CACCGTTAGTGGATCGAGGG
NC53	NC-offspring-18	Bomo Chr8	15166412	G	A	25	13	12	0.48	intergenic	OUT	T	TTTGGACACTGGAATCGGCA	CAGTGCTCCATGACTTGGCT
NC54	NC-offspring-4	Bomo Chr11	3984547	T	C	27	14	13	0.48	intergenic	IN	T	ATAGTGTGCTGGTTGCGACA	GCCGGTGCATTGTTATCGAC
NC55	NC-offspring-12	Bomo Chr1	12012967	T	C	29	15	14	0.48	intergenic	OUT	T	TCGCAATGGAGACCAGAACA	GTGGGTTTACAGAACGAATGC
NC56	NC-offspring-1	Bomo Scaf001	260233	T	A	31	16	15	0.48	intron	OUT	T	TTCCCGATGGTGATTGGACA	GAGACGGCAACACACGAAAC
NC57	NC-offspring-16	Bomo Chr10	8935930	A	G	39	20	19	0.49	intron	OUT	T	AAGACTAAGGCAATAGACCCACT	ATGTAGCAACCATAGATCCCAAT
NC58	NC-offspring-4	Bomo Chr17	2768643	T	C	43	22	21	0.49	intergenic	OUT	T	CAGATCCAGACCATGCACCT	AAGTACGATACGACCCGTGC
NC59	NC-offspring-19	Bomo Chr2	885244	G	A	34	17	17	0.50	intergenic	OUT	T	ATTATCATAGGCGCGTCCCC	GCCTGTATGACCAAGGAAGGG
NC60	NC-offspring-1	Bomo Chr7	12194406	T	C	30	15	15	0.50	intergenic	OUT	T	TCTGCGCTCTACGATTACG	CGAGTCTTCGCCGACCATAA
NC61	NC-offspring-4	Bomo Chr25	12651239	G	A	38	19	19	0.50	intergenic	IN	T	GCGCTTATCATGCAAGAGATGG	CGAGGCAGTGGAGGAAAGT
NC62	NC-offspring-4	Bomo Chr21	6637923	C	A	36	18	18	0.50	intergenic	IN	T	AAACTCGGTACGAAACGGGC	GATTTCGCCGCGCTGACTATAA

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NC63	NC-offspring-10	Bomo Chr20	2502150	T	C	26	13	13	0.50	intron	OUT	T	GTTCTTCTCGTTGAGCCAGTT	GTAATAAGCGGTGCGTATCCC
NC64	NC-offspring-30	Bomo Chr14	2282655	G	C	35	17	18	0.51	intron	OUT	T	TGCCTCTTGTGTCGGAATGT	TTTGCGGAGACTCACGGTTA
NC65	NC-offspring-23	Bomo Chr8	15724617	T	C	31	15	16	0.52	intron	OUT	T	CTTTTCGTGCGCCGATCAAC	ATAGACACACACAGCGAGCC
NC66	NC-offspring-13	Bomo Chr28	3227528	T	C	25	12	13	0.52	intron	OUT	T	GAACACGTTCCGTCCAGTGT	ATCAAAGCCGGCAATGTGAC
NC67	NC-offspring-28	Bomo Chr2	791699	A	G	38	18	20	0.53	intergenic	IN	T	CGTTGCGTTTTTCGAGTCAGC	TTGGCGGTTTTTGAATGAGC
NC68	NC-offspring-2	Bomo Chr12	8870076	C	T	38	18	20	0.53	intergenic	IN	T	GTACTAGTGCACGCGACTT	ACATCAGCCGGACGCAATAC
NC69	NC-offspring-11	Bomo Chr12	4561504	G	A	26	12	14	0.54	intergenic	OUT	T	TATGCGTGCATGCGACATTG	AGCTTCGTCCATCTAAGCCG
NC70	NC-offspring-2	Bomo Chr21	3259305	C	T	73	33	40	0.55	intergenic	OUT	T	AGTAGGATTCGCGCTATTATCGTA	TCTACTGGTGATAGGACCTGTTGT
NC71	NC-offspring-8	Bomo Chr18	7981971	G	A	18	8	10	0.56	intergenic	IN	T	CGCCTCGTTGATAGTGGTTTG	AACTCGTATGACTGTTTCGCCTC
NC72	NC-offspring-4	Bomo Chr25	1203868	G	A	39	17	22	0.56	intergenic	OUT	T	GCTATGCCAGGTTTACCAAGT	AGCTTCCCACTTCGCATTCT
NC73	NC-offspring-22	Bomo Chr17	7615541	A	T	30	13	17	0.57	intron	OUT	T	AGTGTGACTGAAATGCCCTACCG	GGTGTGAGGAAGGGAAGGAGA
NC74	NC-offspring-1	Bomo Chr23	3610379	C	A	27	11	16	0.59	intergenic	OUT	T	CTATTCTCGGCTGCGTGGAT	CCGGAACATCAAGAGCACCT
NC75	NC-offspring-16	Bomo Chr24	6121645	A	T	30	12	18	0.60	intergenic	OUT	T	AGTACCCGGATTTCGAAGCG	CCGTGTGTCTCACCAAATG
NC76	NC-offspring-14	Bomo Chr9	14438522	T	A	48	19	29	0.60	intron	IN	T	CGTAGATGATACACGCAAGGC	TCTAGCCGAATTAAGTCTAAAGGA
NC77	NC-offspring-3	Bomo Chr7	12422408	T	A	32	12	20	0.63	intron	OUT	T	ATTGGGACCACAAATAGAGCG	CGAATACGAATCGGTAATAAGACA
NC78	NC-offspring-15	Bomo Chr18	13580932	G	A	34	12	22	0.65	intergenic	OUT	T	CGGCTGTACAGATACAAGTCC	TGGCCGAGCAGGCGAGC
NC79	NC-offspring-27	Bomo Chr4	7639783	C	T	40	14	26	0.65	intron	OUT	T	TCGTTAGTCCGCTACTGTCAT	AAAGTAGCCCTAGCTGCACC
NC80	NC-offspring-10	Bomo Chr3	4906455	T	A	26	9	17	0.65	intergenic	OUT	T	TGAATCAGCGCGGACCGAAA	GGAATTAGAGCACCACAACGG
NC81	NC-offspring-2	Bomo Chr27	7801770	A	C	38	13	25	0.66	intergenic	OUT	T	GGGCTGTGTATGTGGGCTAA	TACCCTCTCGGTTGAGTCC
NC82	NC-offspring-19	Bomo Chr1	16978349	T	A	21	7	14	0.67	intergenic	OUT	T	TGCGTGCCTAGATACCTGATTC	ACTATACTGCCAATCGTGAACCTGT
NC83	NC-offspring-3	Bomo Chr4	10820685	C	T	38	11	27	0.71	intron	OUT	T	TTAAGCTGATTGGCCGCGA	GATCGTTCTCAATTGCGTGCC
NC84	NC-offspring-13	Bomo Chr3	9909934	A	T	22	6	16	0.73	intron	OUT	T	ATCACTTTGAGAAGGCGGCA	ACGAGCCGGTCCCTAGTAAT
NC85	NC-offspring-11	Bomo Chr12	16123796	G	A	45	27	18	0.40	intergenic	IN	no band	GTACCACCGCCTTGCCCTATT	GCCTCGTATTCTCAGTGCCT
NC86	NC-offspring-18	Bomo Chr23	1606236	A	G	42	24	18	0.43	intergenic	OUT	no band	CTGTCGTGTTGTGTTTCGGG	CCTTCTCAGTGAGTCGCGTT
NC87	NC-offspring-10	Bomo Chr9	15515750	C	A	22	12	10	0.45	intron	OUT	no band	AGCTCAGTAGCACCACGAAG	AGCTCAGTAGCACCACGAAG
NC88	NC-offspring-26	Bomo Chr5	16064276	T	A	51	26	25	0.49	intergenic	OUT	no band	CTTTCCACGCATGTGGGTTT	GCCTCCAAGGAGACCTTAAC
NC89	NC-offspring-26	Bomo Chr3	7669184	G	A	33	16	17	0.52	intron	OUT	no band	TTCTTGAGTCTGCACGGG	TTTCACTCTCCGTCGCGC
NC90	NC-offspring-1	Bomo Chr15	14236033	T	C	19	9	10	0.53	intron	IN	no band	TGCTTCGGACGCTTATCCG	AAGATTGAACCGTCGCGCT
NC91	NC-offspring-8	Bomo Chr17	2179918	A	G	34	16	18	0.53	intron	OUT	no band	TGACTATTGCGCTGAGGGTC	ACGGCCACCTGATGTTAAG
NC92	NC-offspring-2	Bomo Chr2	5285664	A	T	32	15	17	0.53	intergenic	IN	no band	TTGGGTGGGTGAGAAAGACG	AAGCAGCGAGCGAAGAAAC
NC93	NC-offspring-15	Bomo Chr17	287866	T	G	15	7	8	0.53	exon	IN	no band	GTACCTCGGCCTCATTCTGG	GGGGGACCCGAAACCTTAG
NC94	NC-offspring-25	Bomo Chr21	14217853	T	C	30	14	16	0.53	intergenic	OUT	no band	CCTCTGGTAGCCAATTAACACC	ACCGTGCTCCCTTCACTCTA
NC95	NC-offspring-17	Bomo Chr8	14489965	A	G	27	12	15	0.56	intron	OUT	no band	TGACCTCTTTGCCAGCAAT	CTACCATCAGGGCGTAGCTG
NC96	NC-offspring-11	Bomo Chr8	10770419	G	A	39	17	22	0.56	exon	OUT	no band	GACCCCTTGTGTAGTGACC	TGATGGGTGCGACACTCCTA
NC97	NC-offspring-11	Bomo Chr1	229385	A	C	44	19	25	0.57	intron	OUT	no band	GCAAGCGTCACTTTGGGAGC	GATGGGTGCGACACTCTAC
NC98	NC-offspring-10	Bomo Chr20	10039975	T	A	21	9	12	0.57	intergenic	OUT	no band	AGGGCTCTCGAAATGTGGTG	CCGCGTGAAGCTGAAATAGC
NC99	NC-offspring-21	Bomo Chr21	4597013	G	T	33	14	19	0.58	intergenic	OUT	no band	CCACAAAGAGGCAACGCAAA	GCAACAGCTAGAGCCAAGA
NC100	NC-offspring-23	Bomo Chr1	5641333	G	A	17	7	10	0.59	intron	OUT	no band	GTGTGCGTCAAATGCATGGT	GATGACGACGGGTCCGCTAT
NC101	NC-offspring-2	Bomo Chr4	16350687	C	T	34	14	20	0.59	intergenic	IN	no band	CAATCTTGCTGTTTCCGCCG	GACCTTACCTCGCTGGTGAC
NC102	NC-offspring-18	Bomo Chr16	144208	T	C	37	15	22	0.59	intergenic	OUT	no band	CGACAAAGTCTGGCACAACG	GCGGCAACCTAAGGCGGATT
NC103	NC-offspring-4	Bomo Chr5	16878039	G	A	38	14	24	0.63	intergenic	IN	no band	GCAATCACAGCGATTGCGTT	TAGGTGGTATACGCGTTGCG
NC104	NC-offspring-23	Bomo Chr24	10406786	T	C	42	15	27	0.64	intergenic	IN	no band	GAATCGAACCCACGACCCTC	GCGAGCTGTTCACCACTTT
NC105	NC-offspring-21	Bomo Chr9	4004163	T	C	27	7	20	0.74	intergenic	OUT	no band	TGGTGGTCGAGCATTTGTT	TGGCCTTAGGTTTCGGCT
NC106	NC-offspring-23	Bomo Chr2	7047647	C	T	30	14	16	0.53	intron	OUT	\	\	\

High temperature

Variant Number	Sample	Chromosome	Position	Ref	Alt	Read depth	Ref reads	Alt reads	Proportion of Alt read	Region		Validation	Forward primer	Reverse primer
HT1	HT-offspring-6	Bomo Chr22	12045005	C	G	23	12	11	0.48	intergenic	OUT	T	GGTGGGATTCCAGTGTGGT	TATTCGTAGCGACACCTGCC
HT2	HT-offspring-8	Bomo Chr23	3704124	G	A	33	15	18	0.55	intergenic	OUT	T	AGAGCAGGAGCTAGGTGTCT	AACGGCTGATGGGGCTAAAA
HT3	HT-offspring-10	Bomo Chr23	19858453	G	T	29	18	11	0.38	intergenic	OUT	T	TGAGGATACGGGCCACCTAA	TTCGAACCCCATCACAGTCG
HT4	HT-offspring-10	Bomo Chr24	1666203	T	C	18	11	7	0.39	intergenic	OUT	T	TCCTTCGTTTTCACTAGGCC	ATGCGCTACACGGATCAAGT
HT5	HT-offspring-10	Bomo Chr26	6715071	G	C	29	11	18	0.62	intergenic	OUT	T	AAAACCCCGAGATGGGTGAC	GGCGCAATGTGGTTCTTT
HT6	HT-offspring-6	Bomo Chr27	10613054	T	G	17	5	12	0.71	intergenic	OUT	T	GAATGCTTTTTGGTCGGCG	TTGTTTGGTCTCGCTGCG
HT7	HT-offspring-3	Bomo Chr28	3126377	A	G	30	17	13	0.43	intergenic	IN	T	TAGACGAGCGGATCACACG	CGGTCAATGTCTGTGCGCT
HT8	HT-offspring-1	Bomo Chr4	7150454	C	G	11	6	5	0.45	intron	IN	T	ACACCCCTTTTTACCCGTGGT	GTTACAGCGGATCAGTGGCT
HT9	HT-offspring-8	Bomo Chr5	3600521	C	A	23	10	13	0.57	intergenic	OUT	T	GTGGCGTTGAAGAGTACCGA	TGGGTGAGGTGTTATGGGC
HT10	HT-offspring-10	Bomo Chr7	8771502	C	G	27	17	10	0.37	intergenic	OUT	T	CCCGCTCGCAATTCATACT	CCCTTGTGTTAAGCCGTCGC
HT11	HT-offspring-2	Bomo Chr7	11587262	C	T	24	13	11	0.46	intergenic	IN	T	TAAGCATGCAAGACCGACCG	TGCCACCTCGTATTGCTGT
HT12	HT-offspring-2	Bomo Chr9	16700363	G	A	22	14	8	0.36	intergenic	OUT	T	TGGAGGCACATCTAATGCGT	TAATTGCAGCGTCAAGTGC
HT13	HT-offspring-8	Bomo Chr11	20196424	C	T	22	12	10	0.45	intergenic	OUT	T	GTAACACCGCACGTTTACAG	GAGCCCGAGAAGCTAAGTCC
HT14	HT-offspring-4	Bomo Chr12	6195345	C	T	31	12	19	0.61	intergenic	OUT	T	TGCCAATTCGGTGAAGTCA	GAAAGTTCCTTCGCGCTAT
HT15	HT-offspring-3	Bomo Chr16	13563717	A	T	23	7	16	0.70	intergenic	OUT	T	AAGCTGGTCCGACTTCTGTG	ACTTCTTTGTAGAAGCGCG
HT16	HT-offspring-3	Bomo Chr17	11294215	G	T	18	6	12	0.67	intergenic	OUT	T	ATGACTGTGGTCCCGAAAC	CTTTGTGTGGCCATTGCGA
HT17	HT-offspring-2	Bomo Chr18	11501635	C	T	25	14	11	0.44	intergenic	OUT	T	CGACCCGCATTTACTGACGA	ATTACACTTGTGGGGCTGGA
HT18	HT-offspring-1	Bomo Chr20	11157672	G	A	21	8	13	0.62	intron	OUT	T	GCTCGTCTGCCTACAAGTT	ATGCGAAGTGATGGAGGCA
HT19	HT-offspring-3	Bomo Chr22	9566002	T	C	24	12	12	0.50	exon	OUT	T	AGTCTTGTTCCGCCCGTTT	TTGGCAAGTACTCGTGTTCCT

Supplementary table S2 continue

HT20	HT-offspring-7	Bomo Chr22	12838456	G	A	18	11	7	0.39	intergenic	OUT	T	TGGGAAAGTGATACATCGGGC	GTGTTTGAACAGAGCGCGT
HT21	HT-offspring-4	Bomo Chr22	4397406	C	G	13	7	6	0.46	intron	OUT	\	\	\
HT22	HT-offspring-4	Bomo Chr15	15967075	T	C	26	14	12	0.46	intergenic	OUT	\	\	\
HT23	HT-offspring-7	Bomo Chr7	8002153	T	C	29	20	9	0.31	intergenic	OUT	\	\	\
HT24	HT-offspring-3	Bomo Chr8	15308025	G	A	16	11	5	0.31	intergenic	OUT	\	\	\
HT25	HT-offspring-3	Bomo Chr8	13704263	G	A	19	13	6	0.32	intergenic	IN	\	\	\
HT26	HT-offspring-1	Bomo Chr27	9944202	A	G	22	15	7	0.32	intergenic	OUT	\	\	\
HT27	HT-offspring-5	Bomo Chr11	18663809	C	T	18	12	6	0.33	intergenic	OUT	\	\	\
HT28	HT-offspring-4	Bomo Chr17	13226651	C	A	26	17	9	0.35	exon	OUT	\	\	\
HT29	HT-offspring-3	Bomo Chr3	2850560	G	T	23	15	8	0.35	intergenic	OUT	\	\	\
HT30	HT-offspring-8	Bomo Chr6	7705702	G	A	14	9	5	0.36	intron	OUT	\	\	\
HT31	HT-offspring-3	Bomo Chr9	11669641	C	T	21	13	8	0.38	intron	OUT	\	\	\
HT32	HT-offspring-5	Bomo Chr15	11572664	A	C	24	14	10	0.42	intron	OUT	\	\	\
HT33	HT-offspring-10	Bomo Chr4	11652949	A	T	24	14	10	0.42	intergenic	IN	\	\	\
HT34	HT-offspring-6	Bomo Chr15	1468256	A	C	21	12	9	0.43	intron	OUT	\	\	\
HT35	HT-offspring-8	Bomo Chr18	10055768	T	C	15	8	7	0.47	intron	OUT	\	\	\
HT36	HT-offspring-4	Bomo Chr11	13617206	T	G	15	8	7	0.47	intergenic	OUT	\	\	\
HT37	HT-offspring-9	Bomo Chr21	12202293	A	G	27	14	13	0.48	intergenic	OUT	\	\	\
HT38	HT-offspring-6	Bomo Chr13	1861996	T	C	29	15	14	0.48	intron	OUT	\	\	\
HT39	HT-offspring-2	Bomo Chr24	435531	A	T	6	3	3	0.50	intergenic	OUT	\	\	\
HT40	HT-offspring-7	Bomo Chr10	16014341	A	T	20	10	10	0.50	intron	OUT	\	\	\
HT41	HT-offspring-9	Bomo Chr10	11989876	G	A	21	10	11	0.52	intergenic	IN	\	\	\
HT42	HT-offspring-8	Bomo Chr8	14876585	G	A	28	13	15	0.54	intron	IN	\	\	\
HT43	HT-offspring-3	Bomo Chr23	10585292	A	G	18	8	10	0.56	intron	OUT	\	\	\
HT44	HT-offspring-7	Bomo Chr24	4246628	C	T	19	8	11	0.58	intergenic	OUT	\	\	\
HT45	HT-offspring-10	Bomo Chr13	3434412	G	T	17	7	10	0.59	intergenic	OUT	\	\	\
HT46	HT-offspring-8	Bomo Chr1	10411614	G	A	22	8	14	0.64	intergenic	IN	\	\	\
HT47	HT-offspring-8	Bomo Chr20	5765713	A	G	29	10	19	0.66	intergenic	OUT	\	\	\
HT48	HT-offspring-5	Bomo Chr10	7468077	A	G	20	3	17	0.85	exon	OUT	\	\	\

Low temperature

Variant Number	Sample	Chromosome	Position	Ref	Alt	Read depth	Ref reads	Alt reads	Proportion of Alt read	Region		Validation	Forward primer	Reverse primer
LT1	LT-offspring-5	Bomo Chr25	2452472	A	C	20	11	9	0.45	intergenic	OUT	T	GACGGCGCATGTTTAGTGCA	GTAAAGAGTGCAGGGGAGTCG
LT2	LT-offspring-8	Bomo Chr5	17207321	C	A	23	12	11	0.48	intergenic	OUT	T	ACATTACCGCCATTAGGGCA	TGAAAGCTGCCGCTCCTTAT
LT3	LT-offspring-7	Bomo Chr28	8706402	G	A	25	13	12	0.48	intergenic	IN	T	CCTCCTGAAGCCAGATGGTG	CATCACCTATCCTCCCTCG
LT4	LT-offspring-6	Bomo Chr26	11333293	G	T	20	10	10	0.50	intergenic	OUT	T	GCGACAAGGTTTCAGAACTC	GGTTTCGTTCCCAACCCTCT
LT5	LT-offspring-8	Bomo Chr14	3421776	C	T	25	12	13	0.52	intergenic	OUT	T	GGGGAACCCCTCTGCCT	TCCGCCAAAAAGTCCCTG
LT6	LT-offspring-6	Bomo Chr4	7550538	T	A	23	11	12	0.52	intergenic	OUT	T	CCGTATGCTGGTTCGTCGT	TGCTGGTTATTCGTGACCGA
LT7	LT-offspring-2	Bomo Chr21	10057248	G	T	27	12	15	0.56	intergenic	OUT	T	GCTTGCCGGTCATTTTACCC	GCCTGTCTGAATACTTCG
LT8	LT-offspring-5	Bomo Chr17	10028944	G	A	40	17	23	0.58	intron	IN	T	CGGGGTGATCACACATTCCA	TGTGGGCGGTATGTAACTGC
LT9	LT-offspring-9	Bomo Chr15	4949810	A	G	27	11	16	0.59	intergenic	OUT	T	GGTCCGTTGGCAGATACCTC	GTGCTGAAAGCATAGCGGC
LT10	LT-offspring-6	Bomo Chr11	11830078	G	A	20	8	12	0.60	exon	OUT	T	CGGAGTACAGTTAGCGCAGG	GAAGTGTTCGCACTGCTATTC
LT11	LT-offspring-7	Bomo Chr16	5281095	C	T	22	5	17	0.77	intergenic	OUT	T	CGTTTCAGAAGCTCCAGTGC	CGGCTTATCTGATGTTCCGT
LT12	LT-offspring-3	Bomo Chr17	14176597	G	T	17	11	6	0.35	intron	OUT	T	GTGTGGTGACATCGAGACGA	GCCATCTTAGCATCGACGTG
LT13	LT-offspring-8	Bomo Chr20	6457627	G	T	25	16	9	0.36	intron	OUT	T	ACTGCGGGGTGTTCTTATG	GCTTCCAGAGCCCAATCCT
LT14	LT-offspring-8	Bomo Chr11	17195085	C	G	22	14	8	0.36	intron	OUT	T	TACCACAAGCATCGTCTCTG	CGTCATTAAGTCCGCACACG
LT15	LT-offspring-1	Bomo Chr25	9833409	G	A	13	8	5	0.38	intron	OUT	T	ATCAGCGAGCCTTGAGTACG	GTTCCGAAGATCATGTCCG
LT16	LT-offspring-1	Bomo Chr23	13500367	A	T	13	8	5	0.38	intergenic	IN	T	TCTGTGGGCGCATTTCTAAG	CGCTTGGGTAAGCATCAACG
LT17	LT-offspring-10	Bomo Chr10	11837225	G	A	18	11	7	0.39	intergenic	OUT	T	CTAGTCAAACCCGGCCCACT	TTGGTTCCAGGAGTCGCATC
LT18	LT-offspring-8	Bomo Chr25	2872459	C	A	23	14	9	0.39	intergenic	OUT	T	GAGGATCGTTTATTGGCGGA	CGGCTTAATTGTACGGCAC
LT19	LT-offspring-1	Bomo Chr15	16941965	T	G	22	13	9	0.41	intron	OUT	T	AAAGGCGGACTGCCATTACT	TTCCACGCGCTTAATAGCCA
LT20	LT-offspring-4	Bomo Chr10	15881638	T	C	29	17	12	0.41	exon	OUT	T	ACTAACCTGAAGCCGAAGC	CTCGGACACCTCGTCGTATG
LT21	LT-offspring-6	Bomo Chr13	1457891	C	T	12	7	5	0.42	intergenic	IN	\	\	\
LT22	LT-offspring-1	Bomo Chr12	7528199	G	A	30	17	13	0.43	intergenic	OUT	\	\	\
LT23	LT-offspring-5	Bomo Chr3	212920	A	T	20	14	6	0.30	intergenic	OUT	\	\	\
LT24	LT-offspring-6	Bomo Chr4	17564731	C	T	20	14	6	0.30	intergenic	OUT	\	\	\
LT25	LT-offspring-2	Bomo Chr9	16563226	C	A	19	13	6	0.32	intron	OUT	\	\	\
LT26	LT-offspring-7	Bomo Chr7	12061125	A	G	22	15	7	0.32	intron	OUT	\	\	\
LT27	LT-offspring-8	Bomo Chr9	12498027	C	T	22	15	7	0.32	intergenic	OUT	\	\	\
LT28	LT-offspring-7	Bomo Chr2	6725532	A	T	25	17	8	0.32	intergenic	OUT	\	\	\
LT29	LT-offspring-4	Bomo Chr6	4398465	G	T	23	15	8	0.35	intergenic	OUT	\	\	\
LT30	LT-offspring-8	Bomo Chr4	7688387	C	T	11	7	4	0.36	intergenic	OUT	\	\	\
LT31	LT-offspring-2	Bomo Chr4	3879418	T	C	15	9	6	0.40	intergenic	OUT	\	\	\
LT32	LT-offspring-9	Bomo Chr9	9965125	A	G	22	13	9	0.41	intergenic	OUT	\	\	\
LT33	LT-offspring-10	Bomo Chr25	4214457	A	C	12	7	5	0.42	intergenic	OUT	\	\	\
LT34	LT-offspring-4	Bomo Chr12	12910891	C	A	24	14	10	0.42	intergenic	OUT	\	\	\

Supplementary table S2 continue

LT35	LT-offspring-3	Bomo Chr12	10113395	C	A	28	16	12	0.43	intergenic	OUT	\	\	\
LT36	LT-offspring-2	Bomo Chr28	8398364	G	A	25	14	11	0.44	intron	OUT	\	\	\
LT37	LT-offspring-6	Bomo Chr5	16870856	G	A	18	10	8	0.44	intergenic	IN	\	\	\
LT38	LT-offspring-1	Bomo Chr7	2632017	A	T	29	16	13	0.45	intergenic	IN	\	\	\
LT39	LT-offspring-9	Bomo Chr4	8346938	T	C	11	6	5	0.45	intron	OUT	\	\	\
LT40	LT-offspring-10	Bomo Chr16	9404338	T	C	22	11	11	0.50	intron	OUT	\	\	\
LT41	LT-offspring-6	Bomo Chr25	11619771	T	C	14	7	7	0.50	exon	OUT	\	\	\
LT42	LT-offspring-5	Bomo Chr10	12061810	A	G	18	9	9	0.50	intergenic	OUT	\	\	\
LT43	LT-offspring-6	Bomo Chr25	13991804	T	A	18	9	9	0.50	intergenic	OUT	\	\	\
LT44	LT-offspring-8	Bomo Chr22	3454265	C	T	26	12	14	0.54	intergenic	OUT	\	\	\
LT45	LT-offspring-7	Bomo Chr16	2634170	C	T	23	10	13	0.57	intergenic	OUT	\	\	\
LT46	LT-offspring-6	Bomo Chr27	9736194	T	C	19	8	11	0.58	intergenic	OUT	\	\	\
LT47	LT-offspring-7	Bomo Chr4	2457498	T	C	11	4	7	0.64	intron	OUT	\	\	\

Supplementary table S3. The callable sites, *de novo* mutations and mutation rate of A/T bases and C/G bases of each genome.

Normal condition				
Samples	Type	Callable sites	DNMs	Mutation rate
NC-offspring-1	A/T	268958939	3	5.58E-09
	C/G	174789627	2	5.72E-09
NC-offspring-2	A/T	269200386	2	3.71E-09
	C/G	174963584	3	8.57E-09
NC-offspring-3	A/T	268978318	1	1.86E-09
	C/G	174805058	1	2.86E-09
NC-offspring-4	A/T	268993707	2	3.72E-09
	C/G	174814567	4	1.14E-08
NC-offspring-5	A/T	269084915	0	0.00E+00
	C/G	174878885	0	0.00E+00
NC-offspring-6	A/T	269114062	2	3.72E-09
	C/G	174898390	0	0.00E+00
NC-offspring-7	A/T	269030733	0	0.00E+00
	C/G	174844270	1	2.86E-09
NC-offspring-8	A/T	268625491	1	1.86E-09
	C/G	174556031	2	5.73E-09
NC-offspring-9	A/T	269124370	3	5.57E-09
	C/G	174907598	0	0.00E+00
NC-offspring-10	A/T	268780770	3	5.58E-09
	C/G	174662354	1	2.86E-09
NC-offspring-11	A/T	269141698	1	1.86E-09
	C/G	174920238	4	1.14E-08
NC-offspring-12	A/T	269005495	3	5.58E-09
	C/G	174823757	1	2.86E-09
NC-offspring-13	A/T	268407932	4	7.45E-09
	C/G	174404284	4	1.15E-08
NC-offspring-14	A/T	269145423	2	3.72E-09
	C/G	174921096	2	5.72E-09
NC-offspring-15	A/T	268979652	3	5.58E-09
	C/G	174805945	1	2.86E-09
NC-offspring-16	A/T	268752876	3	5.58E-09
	C/G	174681921	0	0.00E+00
NC-offspring-17	A/T	268345513	2	3.73E-09
	C/G	174427833	1	2.87E-09
NC-offspring-18	A/T	268921117	4	7.44E-09
	C/G	174788996	3	8.58E-09
NC-offspring-19	A/T	268929646	1	1.86E-09
	C/G	174794804	3	8.58E-09
NC-offspring-20	A/T	268687451	1	1.86E-09
	C/G	174641563	0	0.00E+00
NC-offspring-21	A/T	269022366	3	5.58E-09
	C/G	174854186	2	5.72E-09
NC-offspring-22	A/T	268650981	2	3.72E-09
	C/G	174620880	0	0.00E+00
NC-offspring-23	A/T	269108936	3	5.57E-09
	C/G	174909819	3	8.58E-09
NC-offspring-24	A/T	268556123	1	1.86E-09
	C/G	174557512	2	5.73E-09
NC-offspring-25	A/T	268054890	1	1.87E-09
	C/G	174247081	0	0.00E+00
NC-offspring-26	A/T	268933941	1	1.86E-09
	C/G	174798600	1	2.86E-09

Supplementary table S3 continue

NC-offspring-27	A/T	268994300	3	5.58E-09
	C/G	174835925	1	2.86E-09
NC-offspring-28	A/T	269050711	2	3.72E-09
	C/G	174868715	1	2.86E-09
NC-offspring-29	A/T	268513143	1	1.86E-09
	C/G	174528449	2	5.73E-09
NC-offspring-30	A/T	269015363	0	0.00E+00
	C/G	174848604	3	8.58E-09
High temperature				
Samples	Type	Callable sites	DNMs	Mutation rate
HT-offspring-1	A/T	265048089	1	1.89E-09
	C/G	172554609	2	5.80E-09
HT-offspring-2	A/T	261746005	1	1.91E-09
	C/G	170466498	3	8.80E-09
HT-offspring-3	A/T	261772711	4	7.64E-09
	C/G	170486422	5	1.47E-08
HT-offspring-4	A/T	263335186	2	3.80E-09
	C/G	171469721	3	8.75E-09
HT-offspring-5	A/T	252798370	2	3.96E-09
	C/G	164779421	1	3.03E-09
HT-offspring-6	A/T	267105816	3	5.62E-09
	C/G	173746991	1	2.88E-09
HT-offspring-7	A/T	265101785	2	3.77E-09
	C/G	172443584	2	5.80E-09
HT-offspring-8	A/T	267483994	2	3.74E-09
	C/G	173971981	6	1.72E-08
HT-offspring-9	A/T	267169550	1	1.87E-09
	C/G	173811460	1	2.88E-09
HT-offspring-10	A/T	265606109	2	3.76E-09
	C/G	172811499	4	1.16E-08
Low temperature				
Samples	Type	Callable sites	DNMs	Mutation rate
LT-offspring-1	A/T	265699268	3	5.65E-09
	C/G	172958036	2	5.78E-09
LT-offspring-2	A/T	262779672	1	1.90E-09
	C/G	171127905	3	8.77E-09
LT-offspring-3	A/T	257273764	0	0.00E+00
	C/G	167625386	2	5.97E-09
LT-offspring-4	A/T	263784094	1	1.90E-09
	C/G	171776500	2	5.82E-09
LT-offspring-5	A/T	267046686	3	5.62E-09
	C/G	173815896	1	2.88E-09
LT-offspring-6	A/T	265184276	4	7.54E-09
	C/G	172440811	5	1.45E-08
LT-offspring-7	A/T	266902471	3	5.62E-09
	C/G	173667506	3	8.64E-09
LT-offspring-8	A/T	264431329	0	0.00E+00
	C/G	172033565	8	2.33E-08
LT-offspring-9	A/T	267312758	3	5.61E-09
	C/G	173883212	0	0.00E+00
LT-offspring-10	A/T	265638240	2	3.76E-09
	C/G	172788578	1	2.89E-09

Supplementary table S4. The callable sites, *de novo* mutations and mutation rate of each mutation type of each genome.

Normal condition				
Sample	Mutation type	Callable sites	DNMs	Mutation rate
NC-offspring-1	A:T→C:G	268958939	0	0.00E+00
	A:T→G:C	268958939	2	3.72E-09
	A:T→T:A	268958939	1	1.86E-09
	G:C→A:T	174789627	1	2.86E-09
	G:C→C:G	174789627	0	0.00E+00
	G:C→T:A	174789627	1	2.86E-09
NC-offspring-2	A:T→C:G	269200386	1	1.86E-09
	A:T→G:C	269200386	0	0.00E+00
	A:T→T:A	269200386	1	1.86E-09
	G:C→A:T	174963584	3	8.57E-09
	G:C→C:G	174963584	0	0.00E+00
	G:C→T:A	174963584	0	0.00E+00
NC-offspring-3	A:T→C:G	268978318	0	0.00E+00
	A:T→G:C	268978318	0	0.00E+00
	A:T→T:A	268978318	1	1.86E-09
	G:C→A:T	174805058	1	2.86E-09
	G:C→C:G	174805058	0	0.00E+00
	G:C→T:A	174805058	0	0.00E+00
NC-offspring-4	A:T→C:G	268993707	0	0.00E+00
	A:T→G:C	268993707	2	3.72E-09
	A:T→T:A	268993707	0	0.00E+00
	G:C→A:T	174814567	3	8.58E-09
	G:C→C:G	174814567	0	0.00E+00
	G:C→T:A	174814567	1	2.86E-09
NC-offspring-5	A:T→C:G	269084915	0	0.00E+00
	A:T→G:C	269084915	0	0.00E+00
	A:T→T:A	269084915	0	0.00E+00
	G:C→A:T	174878885	0	0.00E+00
	G:C→C:G	174878885	0	0.00E+00
	G:C→T:A	174878885	0	0.00E+00
NC-offspring-6	A:T→C:G	269114062	1	1.86E-09
	A:T→G:C	269114062	1	1.86E-09
	A:T→T:A	269114062	0	0.00E+00
	G:C→A:T	174898390	0	0.00E+00
	G:C→C:G	174898390	0	0.00E+00
	G:C→T:A	174898390	0	0.00E+00
NC-offspring-7	A:T→C:G	269030733	0	0.00E+00
	A:T→G:C	269030733	0	0.00E+00
	A:T→T:A	269030733	0	0.00E+00
	G:C→A:T	174844270	1	2.86E-09
	G:C→C:G	174844270	0	0.00E+00
	G:C→T:A	174844270	0	0.00E+00
NC-offspring-8	A:T→C:G	268625491	0	0.00E+00
	A:T→G:C	268625491	1	1.86E-09
	A:T→T:A	268625491	0	0.00E+00
	G:C→A:T	174556031	1	2.86E-09
	G:C→C:G	174556031	0	0.00E+00
	G:C→T:A	174556031	1	2.86E-09
NC-offspring-9	A:T→C:G	269124370	1	1.86E-09
	A:T→G:C	269124370	0	0.00E+00
	A:T→T:A	269124370	2	3.72E-09
	G:C→A:T	174907598	0	0.00E+00

Supplementary table S4 continue

	G:C→C:G	174907598	0	0.00E+00
	G:C→T:A	174907598	0	0.00E+00
NC-offspring-10	A:T→C:G	268780770	0	0.00E+00
	A:T→G:C	268780770	1	1.86E-09
	A:T→T:A	268780770	2	3.72E-09
	G:C→A:T	174662354	0	0.00E+00
	G:C→C:G	174662354	0	0.00E+00
	G:C→T:A	174662354	1	2.86E-09
NC-offspring-11	A:T→C:G	269141698	1	1.86E-09
	A:T→G:C	269141698	0	0.00E+00
	A:T→T:A	269141698	0	0.00E+00
	G:C→A:T	174920238	3	8.58E-09
	G:C→C:G	174920238	0	0.00E+00
	G:C→T:A	174920238	1	2.86E-09
NC-offspring-12	A:T→C:G	269005495	0	0.00E+00
	A:T→G:C	269005495	1	1.86E-09
	A:T→T:A	269005495	2	3.72E-09
	G:C→A:T	174823757	1	2.86E-09
	G:C→C:G	174823757	0	0.00E+00
	G:C→T:A	174823757	0	0.00E+00
NC-offspring-13	A:T→C:G	268407932	0	0.00E+00
	A:T→G:C	268407932	3	5.59E-09
	A:T→T:A	268407932	1	1.86E-09
	G:C→A:T	174404284	4	1.15E-08
	G:C→C:G	174404284	0	0.00E+00
	G:C→T:A	174404284	0	0.00E+00
NC-offspring-14	A:T→C:G	269145423	0	0.00E+00
	A:T→G:C	269145423	0	0.00E+00
	A:T→T:A	269145423	2	3.72E-09
	G:C→A:T	174921096	1	2.86E-09
	G:C→C:G	174921096	1	2.86E-09
	G:C→T:A	174921096	0	0.00E+00
NC-offspring-15	A:T→C:G	268979652	2	3.72E-09
	A:T→G:C	268979652	0	0.00E+00
	A:T→T:A	268979652	1	1.86E-09
	G:C→A:T	174805945	1	2.86E-09
	G:C→C:G	174805945	0	0.00E+00
	G:C→T:A	174805945	0	0.00E+00
NC-offspring-16	A:T→C:G	268752876	0	0.00E+00
	A:T→G:C	268752876	2	3.72E-09
	A:T→T:A	268752876	1	1.86E-09
	G:C→A:T	174681921	0	0.00E+00
	G:C→C:G	174681921	0	0.00E+00
	G:C→T:A	174681921	0	0.00E+00
NC-offspring-17	A:T→C:G	268345513	0	0.00E+00
	A:T→G:C	268345513	1	1.86E-09
	A:T→T:A	268345513	1	1.86E-09
	G:C→A:T	174427833	1	2.87E-09
	G:C→C:G	174427833	0	0.00E+00
	G:C→T:A	174427833	0	0.00E+00
NC-offspring-18	A:T→C:G	268921117	0	0.00E+00
	A:T→G:C	268921117	3	5.58E-09
	A:T→T:A	268921117	1	1.86E-09
	G:C→A:T	174788996	2	5.72E-09
	G:C→C:G	174788996	1	2.86E-09
	G:C→T:A	174788996	0	0.00E+00
	A:T→C:G	268929646	0	0.00E+00
	A:T→G:C	268929646	0	0.00E+00

Supplementary table S4 continue

NC-offspring-19	A:T→T:A	268929646	1	1.86E-09
	G:C→A:T	174794804	3	8.58E-09
	G:C→C:G	174794804	0	0.00E+00
	G:C→T:A	174794804	0	0.00E+00
NC-offspring-20	A:T→C:G	268687451	0	0.00E+00
	A:T→G:C	268687451	0	0.00E+00
	A:T→T:A	268687451	1	1.86E-09
	G:C→A:T	174641563	0	0.00E+00
	G:C→C:G	174641563	0	0.00E+00
	G:C→T:A	174641563	0	0.00E+00
NC-offspring-21	A:T→C:G	269022366	0	0.00E+00
	A:T→G:C	269022366	1	1.86E-09
	A:T→T:A	269022366	2	3.72E-09
	G:C→A:T	174854186	0	0.00E+00
	G:C→C:G	174854186	0	0.00E+00
	G:C→T:A	174854186	2	5.72E-09
NC-offspring-22	A:T→C:G	268650981	0	0.00E+00
	A:T→G:C	268650981	1	1.86E-09
	A:T→T:A	268650981	1	1.86E-09
	G:C→A:T	174620880	0	0.00E+00
	G:C→C:G	174620880	0	0.00E+00
	G:C→T:A	174620880	0	0.00E+00
NC-offspring-23	A:T→C:G	269108936	0	0.00E+00
	A:T→G:C	269108936	3	5.57E-09
	A:T→T:A	269108936	0	0.00E+00
	G:C→A:T	174909819	3	8.58E-09
	G:C→C:G	174909819	0	0.00E+00
	G:C→T:A	174909819	0	0.00E+00
NC-offspring-24	A:T→C:G	268556123	0	0.00E+00
	A:T→G:C	268556123	0	0.00E+00
	A:T→T:A	268556123	1	1.86E-09
	G:C→A:T	174557512	1	2.86E-09
	G:C→C:G	174557512	0	0.00E+00
	G:C→T:A	174557512	1	2.86E-09
NC-offspring-25	A:T→C:G	268054890	0	0.00E+00
	A:T→G:C	268054890	1	1.87E-09
	A:T→T:A	268054890	0	0.00E+00
	G:C→A:T	174247081	0	0.00E+00
	G:C→C:G	174247081	0	0.00E+00
	G:C→T:A	174247081	0	0.00E+00
NC-offspring-26	A:T→C:G	268933941	0	0.00E+00
	A:T→G:C	268933941	0	0.00E+00
	A:T→T:A	268933941	1	1.86E-09
	G:C→A:T	174798600	1	2.86E-09
	G:C→C:G	174798600	0	0.00E+00
	G:C→T:A	174798600	0	0.00E+00
NC-offspring-27	A:T→C:G	268994300	1	1.86E-09
	A:T→G:C	268994300	2	3.72E-09
	A:T→T:A	268994300	0	0.00E+00
	G:C→A:T	174835925	1	2.86E-09
	G:C→C:G	174835925	0	0.00E+00
	G:C→T:A	174835925	0	0.00E+00
NC-offspring-28	A:T→C:G	269050711	0	0.00E+00
	A:T→G:C	269050711	1	1.86E-09
	A:T→T:A	269050711	1	1.86E-09
	G:C→A:T	174868715	0	0.00E+00
	G:C→C:G	174868715	0	0.00E+00
	G:C→T:A	174868715	1	2.86E-09

Supplementary table S4 continue

NC-offspring-29	A:T→C:G	268513143	0	0.00E+00
	A:T→G:C	268513143	1	1.86E-09
	A:T→T:A	268513143	0	0.00E+00
	G:C→A:T	174528449	1	2.86E-09
	G:C→C:G	174528449	0	0.00E+00
	G:C→T:A	174528449	1	2.86E-09
NC-offspring-30	A:T→C:G	269015363	0	0.00E+00
	A:T→G:C	269015363	0	0.00E+00
	A:T→T:A	269015363	0	0.00E+00
	G:C→A:T	174848604	1	2.86E-09
	G:C→C:G	174848604	2	5.72E-09
	G:C→T:A	174848604	0	0.00E+00

High temperature				
Sample	Mutation types	Callable sites	DNMs	Mutation rate
HT-offspring-1	A:T→C:G	265048089	0	0.00E+00
	A:T→G:C	265048089	1	1.89E-09
	A:T→T:A	265048089	0	0.00E+00
	G:C→A:T	172554609	1	2.90E-09
	G:C→C:G	172554609	1	2.90E-09
	G:C→T:A	172554609	0	0.00E+00
HT-offspring-2	A:T→C:G	261746005	0	0.00E+00
	A:T→G:C	261746005	0	0.00E+00
	A:T→T:A	261746005	1	1.91E-09
	G:C→A:T	170466498	3	8.80E-09
	G:C→C:G	170466498	0	0.00E+00
	G:C→T:A	170466498	0	0.00E+00
HT-offspring-3	A:T→C:G	261772711	0	0.00E+00
	A:T→G:C	261772711	3	5.73E-09
	A:T→T:A	261772711	1	1.91E-09
	G:C→A:T	170486422	3	8.80E-09
	G:C→C:G	170486422	0	0.00E+00
	G:C→T:A	170486422	2	5.87E-09
HT-offspring-4	A:T→C:G	263335186	1	1.90E-09
	A:T→G:C	263335186	1	1.90E-09
	A:T→T:A	263335186	0	0.00E+00
	G:C→A:T	171469721	1	2.92E-09
	G:C→C:G	171469721	1	2.92E-09
	G:C→T:A	171469721	1	2.92E-09
HT-offspring-5	A:T→C:G	252798370	1	1.98E-09
	A:T→G:C	252798370	1	1.98E-09
	A:T→T:A	252798370	0	0.00E+00
	G:C→A:T	164779421	1	3.03E-09
	G:C→C:G	164779421	0	0.00E+00
	G:C→T:A	164779421	0	0.00E+00
HT-offspring-6	A:T→C:G	267105816	2	3.74E-09
	A:T→G:C	267105816	1	1.87E-09
	A:T→T:A	267105816	0	0.00E+00
	G:C→A:T	173746991	0	0.00E+00
	G:C→C:G	173746991	1	2.88E-09
	G:C→T:A	173746991	0	0.00E+00
HT-offspring-7	A:T→C:G	265101785	0	0.00E+00
	A:T→G:C	265101785	1	1.89E-09
	A:T→T:A	265101785	1	1.89E-09
	G:C→A:T	172443584	2	5.80E-09
	G:C→C:G	172443584	0	0.00E+00
	G:C→T:A	172443584	0	0.00E+00
	A:T→C:G	267483994	0	0.00E+00

Supplementary table S4 continue

HT-offspring-8	A:T→G:C	267483994	2	3.74E-09
	A:T→T:A	267483994	0	0.00E+00
	G:C→A:T	173971981	5	1.44E-08
	G:C→C:G	173971981	0	0.00E+00
	G:C→T:A	173971981	1	2.87E-09
HT-offspring-9	A:T→C:G	267169550	0	0.00E+00
	A:T→G:C	267169550	1	1.87E-09
	A:T→T:A	267169550	0	0.00E+00
	G:C→A:T	173811460	1	2.88E-09
	G:C→C:G	173811460	0	0.00E+00
	G:C→T:A	173811460	0	0.00E+00
HT-offspring-10	A:T→C:G	265606109	0	0.00E+00
	A:T→G:C	265606109	1	1.88E-09
	A:T→T:A	265606109	1	1.88E-09
	G:C→A:T	172811499	0	0.00E+00
	G:C→C:G	172811499	2	5.79E-09
	G:C→T:A	172811499	2	5.79E-09

Low temperature				
Samples	Mutation types	Callable sites	DNMs	Mutation rate
LT-offspring-1	A:T→C:G	265699268	1	1.88E-09
	A:T→G:C	265699268	0	0.00E+00
	A:T→T:A	265699268	2	3.76E-09
	G:C→A:T	172958036	2	5.78E-09
	G:C→C:G	172958036	0	0.00E+00
	G:C→T:A	172958036	0	0.00E+00
LT-offspring-2	A:T→C:G	262779672	0	0.00E+00
	A:T→G:C	262779672	1	1.90E-09
	A:T→T:A	262779672	0	0.00E+00
	G:C→A:T	171127905	1	2.92E-09
	G:C→C:G	171127905	0	0.00E+00
	G:C→T:A	171127905	2	5.84E-09
LT-offspring-3	A:T→C:G	257273764	0	0.00E+00
	A:T→G:C	257273764	0	0.00E+00
	A:T→T:A	257273764	0	0.00E+00
	G:C→A:T	167625386	0	0.00E+00
	G:C→C:G	167625386	0	0.00E+00
	G:C→T:A	167625386	2	5.97E-09
LT-offspring-4	A:T→C:G	263784094	0	0.00E+00
	A:T→G:C	263784094	1	1.90E-09
	A:T→T:A	263784094	0	0.00E+00
	G:C→A:T	171776500	0	0.00E+00
	G:C→C:G	171776500	0	0.00E+00
	G:C→T:A	171776500	2	5.82E-09
LT-offspring-5	A:T→C:G	267046686	1	1.87E-09
	A:T→G:C	267046686	1	1.87E-09
	A:T→T:A	267046686	1	1.87E-09
	G:C→A:T	173815896	1	2.88E-09
	G:C→C:G	173815896	0	0.00E+00
	G:C→T:A	173815896	0	0.00E+00
LT-offspring-6	A:T→C:G	265184276	0	0.00E+00
	A:T→G:C	265184276	2	3.77E-09
	A:T→T:A	265184276	2	3.77E-09
	G:C→A:T	172440811	4	1.16E-08
	G:C→C:G	172440811	0	0.00E+00
	G:C→T:A	172440811	1	2.90E-09
	A:T→C:G	266902471	0	0.00E+00
	A:T→G:C	266902471	2	3.75E-09

Supplementary table S4 continue

LT-offspring-7	A:T→T:A	266902471	1	1.87E-09
	G:C→A:T	173667506	3	8.64E-09
	G:C→C:G	173667506	0	0.00E+00
	G:C→T:A	173667506	0	0.00E+00
LT-offspring-8	A:T→C:G	264431329	0	0.00E+00
	A:T→G:C	264431329	0	0.00E+00
	A:T→T:A	264431329	0	0.00E+00
	G:C→A:T	172033565	4	1.16E-08
	G:C→C:G	172033565	1	2.91E-09
	G:C→T:A	172033565	3	8.72E-09
LT-offspring-9	A:T→C:G	267312758	0	0.00E+00
	A:T→G:C	267312758	3	5.61E-09
	A:T→T:A	267312758	0	0.00E+00
	G:C→A:T	173883212	0	0.00E+00
	G:C→C:G	173883212	0	0.00E+00
	G:C→T:A	173883212	0	0.00E+00
LT-offspring-10	A:T→C:G	265638240	1	1.88E-09
	A:T→G:C	265638240	1	1.88E-09
	A:T→T:A	265638240	0	0.00E+00
	G:C→A:T	172788578	1	2.89E-09
	G:C→C:G	172788578	0	0.00E+00
	G:C→T:A	172788578	0	0.00E+00

Supplementary table S5. The callable sites, *de novo* mutations and mutation rate of each genome in the silkworms under different conditions.

Normal conditions				
Samples	Callable sites	DNMs	Mutation rate	corrected mutation rate
NC-offspring-1	443748566	5	5.63E-09	5.78E-09
NC-offspring-2	444163970	5	5.63E-09	5.77E-09
NC-offspring-3	443783376	2	2.25E-09	2.31E-09
NC-offspring-4	443808274	6	6.76E-09	6.94E-09
NC-offspring-5	443963800	0	0.00E+00	0.00E+00
NC-offspring-6	444012452	2	2.25E-09	2.31E-09
NC-offspring-7	443875003	1	1.13E-09	1.16E-09
NC-offspring-8	443181522	3	3.38E-09	3.47E-09
NC-offspring-9	444031968	3	3.38E-09	3.47E-09
NC-offspring-10	443443124	4	4.51E-09	4.63E-09
NC-offspring-11	444061936	5	5.63E-09	5.78E-09
NC-offspring-12	443829252	4	4.51E-09	4.62E-09
NC-offspring-13	442812216	8	9.03E-09	9.27E-09
NC-offspring-14	444066519	4	4.50E-09	4.62E-09
NC-offspring-15	443785597	4	4.51E-09	4.62E-09
NC-offspring-16	443434797	3	3.38E-09	3.47E-09
NC-offspring-17	442773346	3	3.39E-09	3.48E-09
NC-offspring-18	443710113	7	7.89E-09	8.09E-09
NC-offspring-19	443724450	4	4.51E-09	4.62E-09
NC-offspring-20	443329014	1	1.13E-09	1.16E-09
NC-offspring-21	443876552	5	5.63E-09	5.78E-09
NC-offspring-22	443271861	2	2.26E-09	2.31E-09
NC-offspring-23	444018755	6	6.76E-09	6.93E-09
NC-offspring-24	443113635	3	3.39E-09	3.47E-09
NC-offspring-25	442301971	1	1.13E-09	1.16E-09
NC-offspring-26	443732541	2	2.25E-09	2.31E-09
NC-offspring-27	443830225	4	4.51E-09	4.62E-09
NC-offspring-28	443919426	3	3.38E-09	3.47E-09
NC-offspring-29	443041592	3	3.39E-09	3.47E-09
NC-offspring-30	443863967	3	3.38E-09	3.47E-09

Low temperature				
Samples	Callable sites	DNMs	Mutation rate	corrected mutation rate
LT-offspring-1	438657304	5	5.70E-09	6.02E-09
LT-offspring-2	433907577	4	4.61E-09	4.87E-09
LT-offspring-3	424899150	2	2.35E-09	2.49E-09
LT-offspring-4	435560594	3	3.44E-09	3.64E-09
LT-offspring-5	440862582	4	4.54E-09	4.79E-09
LT-offspring-6	437625087	9	1.03E-08	1.09E-08
LT-offspring-7	440569977	6	6.81E-09	7.19E-09
LT-offspring-8	436464894	8	9.16E-09	9.68E-09
LT-offspring-9	441195970	3	3.40E-09	3.59E-09
LT-offspring-10	438426818	3	3.42E-09	3.61E-09

High temperature				
Samples	Callable sites	DNMs	Mutation rate	corrected mutation rate
HT-offspring-1	437602698	3	3.43E-09	3.61E-09
HT-offspring-2	432212503	4	4.63E-09	4.87E-09
HT-offspring-3	432259133	9	1.04E-08	1.10E-08
HT-offspring-4	434804907	5	5.75E-09	6.05E-09
HT-offspring-5	417577791	3	3.59E-09	3.78E-09
HT-offspring-6	440852807	4	4.54E-09	4.78E-09
HT-offspring-7	437545369	4	4.57E-09	4.81E-09
HT-offspring-8	441455975	8	9.06E-09	9.54E-09
HT-offspring-9	440981010	2	2.27E-09	2.39E-09
HT-offspring-10	438417608	6	6.84E-09	7.21E-09

Supplementary table S6. The callable sites, *de novo* mutations and mutation rate in gene region and intergenic regions of each genome.

Normal condition								
Samples	Gene region				Intergenic region			
	DNMs	Callable sites	mutation rate	Corrected mutation rate	DNMs	Callable sites	mutation rate	Corrected mutation rate
NC-offspring-1	2	159045881	6.29E-09	6.45E-09	3	284702685	5.27E-09	5.41E-09
NC-offspring-2	0	159132594	0.00E+00	0.00E+00	5	285031376	8.77E-09	9.00E-09
NC-offspring-3	2	159048414	6.29E-09	6.45E-09	0	284734962	0.00E+00	0.00E+00
NC-offspring-4	0	159046059	0.00E+00	0.00E+00	6	284762215	1.05E-08	1.08E-08
NC-offspring-5	0	159078554	0.00E+00	0.00E+00	0	284885246	0.00E+00	0.00E+00
NC-offspring-6	1	159105079	3.14E-09	3.22E-09	1	284907373	1.75E-09	1.80E-09
NC-offspring-7	0	159079636	0.00E+00	0.00E+00	1	284795367	1.76E-09	1.80E-09
NC-offspring-8	1	158934688	3.15E-09	3.23E-09	2	284246834	3.52E-09	3.61E-09
NC-offspring-9	0	159114353	0.00E+00	0.00E+00	3	284917615	5.26E-09	5.40E-09
NC-offspring-10	2	158989674	6.29E-09	6.45E-09	2	284453450	3.52E-09	3.61E-09
NC-offspring-11	2	159120494	6.28E-09	6.45E-09	3	284941442	5.26E-09	5.40E-09
NC-offspring-12	1	159068964	3.14E-09	3.23E-09	3	284760288	5.27E-09	5.40E-09
NC-offspring-13	5	158821391	1.57E-08	1.62E-08	3	283990825	5.28E-09	5.42E-09
NC-offspring-14	2	159121383	6.28E-09	6.45E-09	2	284945136	3.51E-09	3.60E-09
NC-offspring-15	3	159063137	9.43E-09	9.68E-09	1	284722460	1.76E-09	1.80E-09
NC-offspring-16	1	158866158	3.15E-09	3.23E-09	2	284568639	3.51E-09	3.61E-09
NC-offspring-17	1	158643557	3.15E-09	3.23E-09	2	284129789	3.52E-09	3.61E-09
NC-offspring-18	2	158978312	6.29E-09	6.45E-09	5	284731801	8.78E-09	9.01E-09
NC-offspring-19	0	158989264	0.00E+00	0.00E+00	4	284735186	7.02E-09	7.21E-09
NC-offspring-20	0	158829931	0.00E+00	0.00E+00	1	284499083	1.76E-09	1.80E-09
NC-offspring-21	2	159033742	6.29E-09	6.45E-09	3	284842810	5.27E-09	5.40E-09
NC-offspring-22	2	158811220	6.30E-09	6.46E-09	0	284460641	0.00E+00	0.00E+00
NC-offspring-23	4	159081674	1.26E-08	1.29E-08	2	284937081	3.51E-09	3.60E-09
NC-offspring-24	1	158752340	3.15E-09	3.23E-09	2	284361295	3.52E-09	3.61E-09
NC-offspring-25	0	158436319	0.00E+00	0.00E+00	1	283865652	1.76E-09	1.81E-09
NC-offspring-26	1	158980824	3.15E-09	3.23E-09	1	284751717	1.76E-09	1.80E-09
NC-offspring-27	1	159021187	3.14E-09	3.23E-09	3	284809038	5.27E-09	5.40E-09
NC-offspring-28	2	159053369	6.29E-09	6.45E-09	1	284866057	1.76E-09	1.80E-09
NC-offspring-29	2	158735819	6.30E-09	6.46E-09	1	284305773	1.76E-09	1.80E-09
NC-offspring-30	2	159031623	6.29E-09	6.45E-09	1	284832344	1.76E-09	1.80E-09

Supplementary table S6 continue

High temperature								
Samples	Gene region				Intergenic region			
	DNMs	Callable sites	Mutation rate	Corrected mutation rate	DNMs	Callable sites	Mutation rate	Corrected mutation rate
HT-offspring-1	2	156396731	6.39E-09	6.56E-09	1	281205967	1.78E-09	1.82E-09
HT-offspring-2	0	154725845	0.00E+00	0.00E+00	4	277486658	7.21E-09	7.39E-09
HT-offspring-3	3	154612026	9.70E-09	9.95E-09	6	277647107	1.08E-08	1.11E-08
HT-offspring-4	2	155458074	6.43E-09	6.60E-09	3	279346833	5.37E-09	5.51E-09
HT-offspring-5	2	149686949	6.68E-09	6.85E-09	1	267890842	1.87E-09	1.91E-09
HT-offspring-6	2	157960066	6.33E-09	6.50E-09	2	282892741	3.53E-09	3.63E-09
HT-offspring-7	1	156968771	3.19E-09	3.27E-09	3	280576598	5.35E-09	5.49E-09
HT-offspring-8	3	158111213	9.49E-09	9.73E-09	5	283344762	8.82E-09	9.05E-09
HT-offspring-9	0	157969221	0.00E+00	0.00E+00	2	283011789	3.53E-09	3.63E-09
HT-offspring-10	0	157192671	0.00E+00	0.00E+00	6	281224937	1.07E-08	1.09E-08

Low temperature								
Samples	Gene region				Intergenic region			
	DNMs	Callable sites	Mutation rate	Corrected mutation rate	DNMs	Callable sites	Mutation rate	Corrected mutation rate
LT-offspring-1	2	156764126	6.38E-09	6.54E-09	3	281893178	5.32E-09	5.46E-09
LT-offspring-2	2	155122214	6.45E-09	6.61E-09	2	278785363	3.59E-09	3.68E-09
LT-offspring-3	1	152302751	3.28E-09	3.37E-09	1	272596399	1.83E-09	1.88E-09
LT-offspring-4	1	155687414	3.21E-09	3.30E-09	2	279873180	3.57E-09	3.67E-09
LT-offspring-5	1	157606647	3.17E-09	3.25E-09	3	283255935	5.30E-09	5.43E-09
LT-offspring-6	2	157034368	6.37E-09	6.53E-09	7	280590719	1.25E-08	1.28E-08
LT-offspring-7	2	157898935	6.33E-09	6.50E-09	4	282671042	7.08E-09	7.26E-09
LT-offspring-8	2	156641725	6.38E-09	6.55E-09	6	279823169	1.07E-08	1.10E-08
LT-offspring-9	1	158122658	3.16E-09	3.24E-09	2	283073312	3.53E-09	3.62E-09
LT-offspring-10	1	157272803	3.18E-09	3.26E-09	2	281154015	3.56E-09	3.65E-09