# **Supplementary 1.**

Multiple alignments of *S. capitis sodA* gene (A) and percent identity matrix between sequences (B) generated by Clustal Omega. Red arrows show the SNPs.

A CLUSTAL O(1.2.4) multiple sequence alignment



	* *	
A3343939.1	CACATTGATAAACAAACTATIGGAAATTCATCATGACAAACACCATAACACATATGTAACT	600
A3M3941.1	CACATTGATAAACAAACTATIGGAAATTCACCATGACAAACACCATAACACATATGTAACT	6.60
A3343896.1	CACATTGATAAACAAACTATGGAAATTCACCATGACAAAGACCATAACACATATGTAACT	60
A3343949.1	CACATTGATAAACAAACTATGGAAATTCACCACGACAAACACCATAACACATATGTAACT	6.0
A3343897.1	CACATTRA TARACAARCTA TINGARATTCACCACGACARACACCA TARCACATA TINTA ACT	60
Mark American Print and		100000
A3343939.1	AAATTAAACTCAGCAGTTGAAGGAACAGATTTAGAAGCTAAATCAATC	120
AJ343941.1	AAATTAAACTCAGCAGTTGAAGGAACAGATTTAGAAGCTAAATCAATC	129
A3343896.1	ANALTDANCTCAGCAGTTGAAGGAACAGATTTAGAAGCTAAATCAATC	120
A3343940.1	AAATTAAACTCAGCAGTTGAAGGAACAGATTTAGAAGCTAAATCAATC	1.29
A3343897.1	AAATTAAACTCAGCAGTTGAAGGAACAGATTTAGAAGCTAAATCAATC	129
AND RESIDENCE OF		4.000
A3343939.1	GCTAATTTAGATAGCGTACCTTCAGATATTCAAACTGCAGTACGTAATAATGGTGGCGGT	180
AJ343941.1	GCTAATTTASATASCSTACCTTCASATATTCAAACTSCAGTACSTAATAATSGTGGCSGT	139
A3343896.1	GCTAATTTAGATAGCGTACCTTCAGATATTCAAACTGCAGTACGTAATAATGGTGGCGGT	1,000
A3343940.1	GCTAATTTAGATAGCGTACCTTCAGATATTCAAACTGCAGTACGTAATAATGGTGGCGGT	1,899
A3343897.1	GCTAATTTAGATAGCGTACCTTCAGATATTCAAACTGCAGTACGTAATAATGGTGGCGGT	1,000
	***************************************	
A3343939.1	CACTTAAACCACTCATTATTCTGGGAATTATTATCACCAAATTCTGAAGAAAAAGGTGAA	240
A3343941.1	CACTTAAACCACTCATTATTCTGGGAATTATTATCACCAAATTCTGAAGAAAAAGGTGAA	2,400
A3343896.1	CACTTAAACCACTCATTATTCTGGGAATTATTATCACCAAATTCTGAAGAAAAGGTGAA	249
A3343949.1	CACTTANACEACTCATTATTCTGGGAATTATTATCACCAAATTCTGAAGAAAAAGGTGAA	3,499
A3343897.1	CACTTAAACEACTCATTATTCTGGGAATTATTATCACCAAATTCTGAAGAAAAAGGTGAA	240
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A3343939.1	GTAGTAGACAAAATTAAAGAACAATGGGGTTCTTTAGATGAATTCAAAAAAGAATTTGCA	31000
A3343941.1	GTAGTAGACAAAATTAAAGAACAATGGGGTTCTTTAGATGAATTCAAAAAAGAATTTGCA	3400
A3343896-1	GTAGTAGACAAAATTAAAGAACAATGGGGTTCTTTAGATGAATTCAAAAAAGAATTTGCA	300
A3343949.1	GTAGTAGACAAAATTAAAGAACAATGGGGTTCTTTAGATGAATTCAAAAAAGAATTTGCA	3490
A3343897.1	GTAGTAGACAAAATTAAAGAACAAT96666TTCTTTAGATGAATTCAAAAAAGAATTT9CA	3499
A3343939.1	GATAMAGC 16CTGCACGCTTTGGATCTGGTTGGGCATGGTTAGTAGTAMATAACGGTCAA	34540
A3343941.1	GATAAAGC TGCTGCACGCTTTTGGATCTGGTTGGGCATGGTTAGTAGTAAATAACGGTCAA	350
A3343896.1	GATAMAGC 16CTGCACGCTTTGGATCTGGTTGGGCATGGTTAGTAGTAMATAACGGTCAA	3660
A3343940.1	GATAMAGC TOCTOCACGCTTTGGATCTGGTTGGGCATGGTTAGTAGTAAATAACGGTCAA	360
A3343897.1	GAT AAAGC 16CTGCACGCTTTGGATCTGGT1GGGCATGGTTAGTAGTAAATAACGGTCAA	3660
A3343939.1	TTAGAGATCOTTACTACTOCAGAGCAAGATAACCCATTAACTGAGGGTAGAACTCCAATC	420
A3343941.1	T TAGAMA DOGITACIAN TOCAMO CAMPA TAACCO ATTAMO I GAMGGI AAAAC TOCAA TO	420
A3343896.1	TTAGANATICSTTACTIC TCCAAACCAAGATAACCCATTAACTGAAGGTAAACTCCAATC	420
A3343949.1	TTAGAMATICGTTACTIC TOCAMACCAMGATAACCCATTAACTGAAGGTAAAACTCCAATC	420
A3343897.1	TTAGAGATOSTTACTACTOCAMACCAAGATAACCCATTAACTGAAGGTAAAACTCCAATC	420
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A3M3941.1	TIAGGTTIA 629	
A3343896.1	TIAGGITIA 429	
A3343949.1	TIAGGITIA 429	
A1848887.1	TIAGGTTIA 429	
and attended P 1 A.	THEORITIES NAME OF THE PARTY OF	

- Percent Identity Matrix - created by Clustal2.1

1.7	AJ343939.1	100.00	99.77	99.77	99.53	99.53
211	AJ343941.1	99.77	100.00	100.00	99.77	99.77
345	A3343896.1	99.77	100.00	100.00	99.77	99.77
43	A3343940.1	99.53	99.77	99.77	100.00	100.00
80 m	A TRACKSON TO	0.00 (0.0)	49-01 78-78	4940 777	3 (200) AND	THE RESERVE AND ADDRESS.

## Supplementary 2A.

Multiple alignments of S. capitis gap gene generated by Clustal Omega. Red arrows show the SNPs.

▲ CLESTAL O(1.2.4) multiple sequence alignment

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MP45998773	WCACTATISCANSITICOCTTICACTISMISANGITTSANGTICATICS/FISSTISSATTICCOTISTTA	350	89409481.1	ETECTTCTTSTHICACTANCTCHTMSCACCASTTSCTAMETTTTMH/TIGHTMSTTTS	400
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MY4.28468.1		40	PROBABLE	#TECTTETTETHICALCTANCTCHTTMECACCAETTECTALMETTTTAMATEATRACTTTE	349
MY4.28463-1		40	W4034463.1	ETECTTETTETWCAACTAACTCATTAGCACCAGTTGCTAAAGTTTTAAATGATGAGTTTG	340
903-2009-1	ACACTA/ISCAAGITOSCTTCACTIGAGAGAGTTSAAGTCATGGATGGTGGATTCCSTSTTA	300	00000474-1	ENGCTTOTTERNICALCTUACTEMPHAGCACCASTTECTALAGTTTTTAMTCATGASTTTE	480
000-51789-1	HOACTATECAHEETOOCTTICACTEEAGAASTTIGAHETTATIGGATESTEEGATTICOOFISTTA	110	80081789.1	ETECTTCATED ACTACTA ACTICATIVA CACASITI ICAA A ASTITTA AATICATIGASITTII	439
\$100 SW100 N. D.	ACACTATECAABETCCCTTGACTEBAGAASTTGAABTTATEGATGCTBGATTCCCTGTTA	334	DUCCH905-1	ETECTTEXTENUCIACTA ACTEMITIA OCA DO A OTTE CAA A A STITTA AA TIGATIGA OTTE	434
min 52366-1	HOACTAFBCAHSETOSCTTGACTSSAGAASTTSAHETTAFIOSATSSTSSATTOOSTSTTA	157	H-0502004-1	@TOCTTOXTOTACTACTACTENTHOCACCAGTTISCAAANGTTTTANATICATISAGTTTS	457
MY 28404 1		49	H1528405-1	@TOCTTCATUSTACTACTEACTEACTACCACCACTTECAAAAGTTTTaaaTicaTGAGTTTE	349
MH-08-69-1		48	10000489-1	ETECTTO/TEN/CTACTA/ACTO/TTAGCACGASTTECAAAAGTTTT/W/TGATGASTTTS	349
MH-20436-1		48	MIGGRANG. 1	ETECTTO/TETHICTACT/ACTO/ITTAGCACGAGITTECAAA/AGTTTTAHI/TEA/TEAGTTTE	349
MAC DECISION 1.		49	W-628194.1	STOCTTCH TOTACTACTCHTTAGCACCACTTGCAAAACTTTTAHATICATGACTTTS	340
MM-200303.1		- 69	MINORAL SECTION AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON ADDR	ERECTTEX TERMETACTA ACTE ATT AGE ACCAST TRECASA ACT TITT ANA TIGATE ACT THE	349
medical property.		49	W600110-1	ETECTTOX TETWORACTARCTOX/TIMEGACGASTTEGAAAASTTTTAHATIGATGASTTTS	249
609 60736-1	ROACTA/TICAAGE/COCTTCACTEBAGAAGT/GAAGT/A/TOBATGG/TIBATTCCGTG/T/A	239	90901730.1	BTSCTTCXTSTNCTACTARCTCXTNSCACCAGTTSCAAAABTTTTARXTSATSAGTTTS	430
REGISTED.			PROBERT, 1	BTBCTTCXTSTNCTACTARCTCXTTMCACACOACTTSCAAAABTTTTMATSAAAABTTTS	349
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UP489487.1	IDMITAL GALLTALITATTE TO TAKE CARRIED AND THE CONTROL OF THE CONTR	349	anageagy, p	ститистичностичнителетичнослеентили тестелесии и тигоме	5.00
596 500 RELL	HODGERAMICAMITTAAAFDAFTEISKTGAACGAGATISCAACGAAAFTHCCTTG886GAGACC	384	DISCOURSE, L	CTTTECTTCASCCTTTALTCACTSCTSTOTCCACCCTTTSTSCTCCTCSCCAAAATSCTCAAC	100.0
FF6.28468-1	HOSETHANGANITTANATEATTEN TEACCAGATHOMSCAAATTHOCTTORSSAGACC	300	PF028408.1	CTTTUCTTQAACCTTTAATCACTACTETOCACCCTTETACTCCCCCCAAAATACTCCACC	400
MY4.28463. 6	HOSSENHIGHAMTTANATEATTER/TSAADCASIATSCAASCAAATTHOCTTSSSSAGEC	1866	WYGORGOD, E	CTTTUCTTCASCOTTTASTCACTACTETOCACCETTETACTCCTCACCASASTACTCASC	400
10(3-21)(24-1)	HOSSTANDSANTTANATCATTOS/TSAADCASATSCAASCAAATTAOCTT9998SASACC	340	1001 State No. 6	CTTTECTTCASCCTTTALTCSCTSCTSCTSCCSCCTTSTSCTCCTCSCCSASSTSCTSCSSC	200
0.952789-1	HOSETHANGAMITHANATEATTOS/TIGAAEGASATISCAASGAAATTHOCTTISSSGASACC	389	CONTRACTOR IN	CTTTACTTCAACCTTTAATCACTACTACTACTACACCTTTATACTCCTC	487
Dog-589811-1	MODEL THREE CHARLES THE PROPERTY OF THE CHARLES OF THE CARLES OF THE CHARLES OF T	394	De4-58944 L	CTTTACTICALCOTTRACTCACTACTACTACTACTACTACTCACCAAAATACTCAAC	484
HIS-52866-1	#000TAHACAHATTAHATTAHTTISHTISHADOAGATSCHODAHATTHOCTTISSOSAGAD	317	HELCORE 1	CTTTECTTCASCCTTTAATCACTSCTSCTSCTSCTSTSTSCTCCCCCAAAATSCTCASC	587
MIN-20404-1	WOODTHANGARWITHANATEATTEGETGAACGAGATIIGGAAGGAAATTHOCTTIIGGGGAGACC	300	W428404.1	GTTTWGTTGAAGGTTTAATGACTACTACTATGCATGCTTWTACTGGTGACCAAAATACTCAAG	400
MN-20409-1	HOSETHANGANITHANTEATTES/TSAACGASATSCAGGAATTHCCTTSSSGAGACC	309	WYGORADO, E	CTTTUCTAGEAGGTTTMACTGACTECTACTGCATGCTTMATACTGCTCACCAAAATTACTGAAG	400
MM-20436-1	HOSETAHIGAHITTAAATCATTOSI TSAACGASATISCAASCAAATTHCCTTGSSGASACC	209	97428434. E	CTTTICTAGAGGTTTAATGAGTACTATGCATGCTTATACTGGTGGGGAAAATACTGAAG	-
NEW CHESIA . I.	HOSETAHIGANITTAAATEATTEIHTISAECAGATEDAGGAAATTHECTTGISGAGKEE	309	90°4-287884, 8	CTTTSCTAGAGGTTMATCACTSCTATSCATSCTMATACTSCTGGCGGGAAATSCTGGGG	4000
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00990730-1	IDMITALMANUT MANUTANTE PRANCIONATE AND MANUTANCE PROMINENT.	798	01951719.1	CTITICIACAGOCTINATCACTICIATOCATOCTIATACTOCTCACCAAATINETICAG	40.6
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	¥			<b>₩</b>	
87485487.1	THE ARMY DESIGNATIVE THE THE PROPERTY OF THE P	300	WASSAST, N	ATSCTOCTOACAAMMASSOLACIMICOTOOTSCTOTSCIASCAGGAGAAAAGATWITSC	100
D04-599001.0	TWGACHTOGACTTACTACTACTACTACTTCTACACTGACAWGATAAAGCACWG	344	Dod-Street, 1	ATSETOCTICACAGAMAGGOGACAMAGGTCGTGCTGCTGCAGCAGCAGAAAACACTATATCC	544
MIN. 200400-1	THIS ACKNOWLED THAT THE WHITE THE TEST THE THE CASE THE ACKNOWLED THE ACKNOWLED THE	300	876-28468, S	ATTECTOCICACACAMIAGGOCACIAMICCICCICETOCICCACCACACACACACACACACACACACACACACACAC	400
PRO-009465-1	THIS ACATOGRAD STREET AGAINST TACTISS TITTCH HOACTIS ACAHIS AT AMASO ACAHIS	200	W6-28463, E	#TEXTOCTC#CACAGAMAGGCGACAMACCTCGTGCTGCTGC#GCAGGAGAAAGAFTWTGC	400
100 F 200 F 24 - 1	THEACHT DIRECTION THAT AGAINST TACTOR TITTLE MOACHING AT A ANGOLOGIS	300	10120676.1	ATEXTOCTEACACAMMAGGOGAE MINOSTEGROETOCTGEAGGAGAGAGAAAACATTATOS	600
009402309.0	THE ACATE SHICK THE TATTACH THE TACTOR THE THE TACHOL THAT THE BEST AND ACADES.	249	Guri Sabbin, N	ATSETOCTEACAGAMAAGGGACAMOCETEGESETOCTSCAGCAGGAGAAAAGAFTWTGE	540
004.09901.1	TABLECT CONCURRENT AGAINST TACTOCT THE THE TOTAL TOTAL TRANSPORT AGAINST TAKEN TO THE	366	European, L	AT SET TOO TO A CANADAMA DISCORDE MANDO TO CITADE TO CITADE AND AND ANAMADEM THAT DE	544
MISS 52966-1	TABLECATE SPECIFICAL TRANSPORT AND THE TITLE CASE THAT THE SPECIFICAL SPECIFICATION S	311	HR15(2900, 1	ATSCTOCTCACAGAMAGGCGAC MINOSTCGTGCTGCTGCMGCAGCAGCAGAAAACMTWTGC	5077
FF9-20406-1	THE AGAIN CHARLET HE TATTAGAIN THE TACT SHETTIC THICAG THE TANKING TAKKING ACKNOW	200	W6-28466, 1	ATSZTOCTOROACHUMAGGOGACHUMOGTOCTGCTGCTGCTGCMGCMGCMGAAACHTTWTGC	400
PER CHARGES . 3	THE ACT IT SEED THE TATTACHET BY THE THE THE TALL THE THE HEAD CACHES	200	W4-28459.1	#TRETTOCTICACACACAMINAGEOGAC MINICESTECTICE FOR MODERACAACACTISTICE	400
HY6.28436. 1	TABLEST CONCERNIES ATTACHED ESTAC PROTECTION CACADOS SAMURAS SAMURAS AND CACADOS	200	876-2043-6-1	ATSCTOCTOACAGHINAGGOGACHHIOGTOGTSGTSGTSGAGGAGGAGAAAAGATTIATOG	400
HF6-28-864	TAGACATOGACOTAGEATTAGACOGEACTOGETTTCTACACTGAETAAAGEAAAAGCACAAG	340	BY6-00384-1	AT SCTOCT CACAGAMARGGGGAC MANOST COTOS TOST SCIAGOAGAAAAACATTIKTOS	400
MATSON 1-1	TAGACATOGAO(TAGTATTAGAATICTACTECTTTCTACACTGATAAAGCACAAG	300	MACAGERS, D	ATSCTOCTCACAGAMAGGOGACAMOSTCGTGCTGCTGCAGCAGCAGCAGAAAAACATTATCC	-
HV4-28111-1	NGACATOGACITAGTATTAGAATIETACTBETTTETACACTIGATAAAIGATAAAIGACACAAIG	309	W0-20110.1	A FOLT COTO ACADAMA ROQUO ACAMINO POR PORTO POR POCADO ACADAMA CANTA POR	100.78
689-50736-1	TARGACAT DISCONSISTATI AGAINST ACT TO STATE ACT	256	009 027 10.1	ATSETTOCT CACACIMINA OGO CACIMINO CE CONCETTO CO CACCACIMICA CAMAMACATTRATO C	554
696-28377 / E	NOACHTOGROPHETATTAGAMTETACTBETTTCTACACTGATAMIGATAMIGACACHIG	309	WASSELLY, D	after not reach annual occure support of the treatment accurate annual culturation	-
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APR 00401.1	CTCACATEGATECAGGEGCTACTAAAAAAGEAT TAATETICTGCTCCAGETWCAGGTGAFTTWA	300	BY 4 KINDS T. U.	CTIACTCTROSCOPICTOCTAMACHITTSCHMACTMETOCKSIMITOCATSCHAMIT	100
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MA-24466 . 1	CTICACATOGATECHOSTSCTAMINANSTATTAMTCTICTOCTOCASCTIACASCTOCASCTTAM	339	WY628468.1	CTABLE TO THE ACCOUNT OF TAXABLE HAT TOO TAXABLE THE PROCESSING TO THE TAXABLE	128
MARKS 1.1	CTCACATEGATSCHOOTSC TANHAHAGTAT TAATCTICTGC TQCAGCTHCAGG TGATTTHA	- 117	MF4-28-24-5, 1	CTAMETIC ENCASORSE TOC TAMASS MET TOCKHOLD TOCKHOLD TOCKHOLD TOCKHOLD TO THE T	5.00
operation.	CTCACATEGATECHOOFSC TAAHHAAGTAT TAATETICTSC TOCASETHICASS TGATTTHA	300	tiga aperto, a	CTANCTIC TROUGOPTIC TOCTANA SENETTI GOT MANOTTAL TOCK SHART COATESTANAT	60.0
BUT BUT BUT L	CTCACAFDGAFIICAGGFGCTAAAAAAGEAFTAAFETICTGCTGCAGGTGCAGGTGAFTTIAA	300	CONTRACTOR L	CTEMETIC THICHOGENEETIC THANAGEMETIC GOTTEMENT THE TOCKNING TO CHOOSE THAN I	100
ELS. STREET, 3.	CTCACATOCATEGAGGESCTANAMAGEATTANTCTCCTCCTCCACCTGCTGCTGAFTTMA	300	DISCOURSE OF THE	CTAMETIC REGISSIFIC TO CTAMAGE BETT SOTTAMEST TATTOCH SHART TO CASSAST TO ACCOUNT AME	484
HP3.82966.1	CTCACATOGRATISCHOOFISC TAAAAAAGEAF TAATCTICTOCTOCTOCTOCTOCTOGTOATTTIAA	337	HRS 529661, U	CTEACTC INCASOFIC TOCTAMAGE SETTING TAMAGETTE POCCHOMATOCH CONTRACT	600
HP4-28464-1	CICACITOR/TROSCRETE TAXABLE PER TAXATCC TOCTOCARTIC TO TRAFFITM	330	WYGORGOS, E	CTEACTCTECACCTCCTCCTALAGEMETTGCTALAGTTETTGCAGGMETGGAGGMTAAL-	128
HP4-28499-1	CTCACATOGATECAGGEGCTAAAAAAGTAFTAATCTICTGCTGCAGCTGCTGGTGATTTML CTCACATOGATECAGGTGCTAAAAAAGTAFTAATCTICTGCTGCAGCTGCTGGTGATTTML	110	WY4.28406. E	CTIMETIC TREASEST CONTRACTOR AND ADDRESS TO	100
876-28436-1 874-28364-1			901028436, U	CTEACTC RODOCTIC TOCTALLACTE FOOCTAMENTAL TOCKGOOD TOOLS CONTINUE.	100
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MA-20113-1	CICACATOGATOCAGGTOCTAAAAAGTAFTAAATCTCTGCTGCGGGTACTGGTGAFTTWA	110		CTAILTCTRESCOTECTOCTARRESETTOCCTRANSTTRETTOCRESSATIONSCOTTARA- CTAILTCTRESCOTECTOCTARRESETTOCCTRANSTTRETTOCRESSATIONSCOTTARA-	528
60953730-1	CTCACATOGATGCAGGTSCTAAAAAAGTAFTAATCTCTGCTGCAGCTACTGGTGAFTTAA	316		CTANCEC INCOME TO THAN IN PROPERTY AND THE PROPERTY AND T	100
894-28177-1	CTCACATOGATGCAGCTECTAAAAACTACTAATOTCTGCTGCAGCTACTGCTGATTTAA		MONAGETY, N	CTARTOTECHNOCOCCULARIOM CONTRACTOR TOCHNATOR CONTRACTOR	524
				ACCORDING TO SELECTION AND ADDRESS OF THE PARTY OF THE PA	-
M1405487.1 89459981.1	MACAPOSTATICACACTARCORDATGATTAGATGCTCTGARACGCTTGTATCAG MACAPOSTATICACACTARCORDATGARTTAGATGCTCTGARACGCTTGTATCAG	400 064			
NFG 200409 . 1	HIS ALTOCOME TO CONTRACT THE PROPERTY OF THE P	300			
Mrs 20063 . 1	MICARDENTOACACTACONS/SAFTIGING PC15AACGETTS/1/CIG				
2023-020-03-1	MACAPISEM TO ACACT ACCUMUNISM TRIGHTS THE TOWARD STREAM OF	400			
909 902309 . 1	MACANTOETHTCACACTAACD/T04TQA4TT10HT0ETTCT0AACD/ETTETATCA0	200			
100 (0000) -1	BUCKSTREETERS CONTROL TO A THROUGH THE TRANSPORT THE TOTAL OF T	204			
HER \$2566.1	BACAMINETATICACIC TARGUTERIO AUTTROPRETTIC TRANSCRITTERATICA	100			
HM 2004 1	BACKETS CHARGE TANGETS AND THE PROPERTY OF THE PARTY OF T	20			
894.20299.1	INCOMPRESENTANCE SANCERS SANTESONS INCOME TO SANCER TREATED	200			
89428436-1	MACANTOETHTCARCACTARCOMBATGARTTREMT0ETTCT9AACAETTIETATCR0	200			
MANAGEMENT TO	MACAMPORTATION CACTAGO DI MATTIONI DE L'ACCIONA CALTERNATION DE	300			
MM-20083-1	ANCHITOSTATIONCIC TARGUTOLISMITTEN POSTTICISMI CHETTETATICHE	200			
MP4.20033-1	BUCHFORTHTCACKTAKCOTGATGAATTAGATGETTCTGAAACAFTTIPATCAG	200			
685736-1	HACHTOCTATICACACTARCOTOATSARTHOUTOCTTCTSARCACTTISTATCAS	376			
MW-20037 .1	MACAPDETATTCACACTAAECATIGATEGATTAGATGETTICTIGAGACHETTIETATCAG	100			

#### Supplementary 2B.

Percent identity matrix between sequences of S. capitis gap gene generated by Clustal Omega.

Percent Identity Matrix - created by Clustal2.1 1: AF495487.1 100.00 99.88 100.00 100.00 99.46 98.68 97.79 97.96 98.48 98.11 98.11 98.11 98.11 98.11 97.31 2: EU659982.1 99.88 100.00 100.00 100.00 100.00 98.77 97.91 97.91 98.48 98.11 98.11 98.11 98.11 98.11 97.54 97.92 3: MF620468.1 100.00 100.00 100.00 100.00 100.00 98.67 98.48 98.48 98.48 98.11 98.11 98.11 98.11 98.11 98.11 97.92 4: MF620463.1 100.00 100.00 100.00 100.00 100.00 98.67 98.48 98.48 98.48 98.11 98.11 98.11 98.11 98.11 98.11 97.92 5: DQ321676.1 97.91 97.73 99.46 100.00 100.00 100.00 98.88 98.48 98.11 98.11 98.11 98.11 98.11 6: GU951789.1 98.68 98.77 98.67 98.67 98.88 100.00 98.89 98.92 99.43 99.43 99.43 99.43 99.43 99.43 98.68 99.63 7: EU659903.1 97.79 97.91 98.48 98.48 97.91 98.89 100.00 100.00 100.00 99.62 99.62 99.62 99.62 99.62 8: HM352966.1 97.96 97.91 98.48 98.48 97.73 98.92 100.00 100.00 100.00 99.62 99.62 99.62 99.62 99.62 99.42 99.43 98.48 9: MF628466.1 98.48 98.48 98.48 98,48 99.43 100.00 100.00 100.00 99.62 99.62 99.62 99.62 99.62 99,43 99.62 10: ME630450.1 98.11 98.11 98.11 98.11 98.11 99.43 99.62 99.62 99.62 100.00 100.00 100.00 100.00 100.00 100.00 99.81 11: ME638436.1 98.11 98.11 98.11 98.11 98.11 99.43 99.62 99.62 99.62 188.88 188.88 188.88 160.66 188.88 100.00 99.81 12: MF620384.1 98.11 98.11 98.11 98.11 98.11 99.43 99.62 99.62 99.62 188.88 100.00 100.00 100.00 100.00 100.00 99.81 13: MF620383.1 98.11 98.11 98.11 98.11 98.11 99.43 99.62 99.62 99.62 180.00 100.00 100.00 100.00 100.00 100.00 99.81 14: MF620333.1 98.11 98.11 98.11 98.11 98.11 99.43 99.62 99.62 99.62 100.00 100.00 100.00 100.00 100.00 100.00 99.81 15: GU951710.1 97.31 97.54 98.11 98.11 97.43 98.68 99.63 99.42 99.62 100.00 100.00 100.00 100.00 100.00 100.00 99.81 16: MF620377.1 97.92 97.92 97.92 97.92 97.92 99.24 99.43 99.43 99.43 99.81 99.81 99.81

## Supplementary 3.

Multiple alignment of sodA sequences among Staphylococcus species performed by BLAST. The red square shows the region of sodA specific for S. capitis.

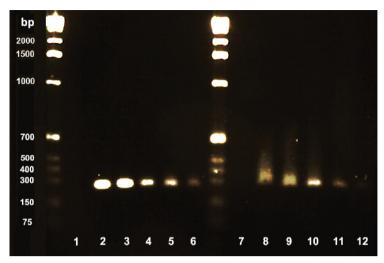
Species	Accession No.		Sequence	
S. capitis	AJ343896.1	273	TTTAGATGAATTCAAAAAAGAATTTGCAGATAAAGCTGCTGCACGCTTTGGATCTGGTTG	332
S. capitis	AJ343897.1	273	TTTAGATGAATTCAAAAAAGAATTTGCAGATAAAGCTGCTGCACGCTTTG <mark>GA</mark> TCTGGTTG	332
S. capitis	AJ343939.1	273	TTTAGATGAATTCAAAAAAGAATTTGCAGATAAAGCTGCTGCACGCTTTG <mark>G</mark> A <mark>T</mark> CTGGTTG	332
S. pasteuri	AJ343898.1	273	TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCAGCAGCTCGTTTCGGTTCAGGTTG	332
S. warneri	JX436495.1	300	TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCTGCAGCTCGCTTTGGCTCAGGTTG	359
S. epiderimidis	EU652774.1	276	TTTAGATGAATTTAAAAAAGAATTTGCAGATAAAGCTGCAGCACGCTTTGGTTCAGGATG	335
S. saccharolyticus	AJ343932.1	273	TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCTGCAGCTCGTTTTGGTTCAGGTTG	332
S. succinus	AY845222.1	273	TTTAGACGCATTCAAAGAAGAATTTGCGAATAAAGCTGCAGCACGTTTCGGTTCAGGTTG	332
S. hominis	AJ343911.1	273	TTTAGATGAGTTTAAAAAAGAATTCGCTGATAAAGCTGCAGCACGTTTTGGTTCAGGTTG	332
S. gallinarum	AJ343909.1	273	TTTAGATGCATTTAAAGAAGAATTTGCAGATAAAGCTGCAGCACGCTTTGGTTCAGGTTG	332
<ol><li>chromogenes</li></ol>	AJ343944.1	273	TTTAGATGATTTCAAAAAAGAATTTGCAGACAAAGCAGCAGCTCGTTTTGGTTCTGGTTG	332
S. haemolyticus	AJ343950.1	273	TTTAGATGAATTCAAAAAAGAATTCGCTGACAAAGCAGCAGCTCGTTTCGGTTCAGGTTG	332
S. arlettae	AJ343894.1	273	TTTAGATGCATTTAAAGAAGAATTTGCAAATAAAGCTGCAGCACGTTTTGGTTCAGGTTG	332
S. nepalensis	AY878698.1	273	TTTAGATGCGTTTAAAGAAGAATTTGCTGATAAAGCTGCAGCTCGCTTTGGTTCAGGTTG	332
S. equorum	AY818177.1	274	TTTAGATGCATTCAAAGAAGAGTTTGCTAACCAAGCTGCAGCACGTTTCGGTTCAGGTTG	333
5. xylosus	AY571691.1	340	TTTAGATGCATTTAAAGAAGAATTTGCAGATAAAGCAGCAGCACGTTTCGGTTCAGGTTG	399

#### Supplementary 4.

Multiple alignment of gap sequences among Staphylococcus species performed by BLAST. The red square shows the region of gap specific for S. capitis.

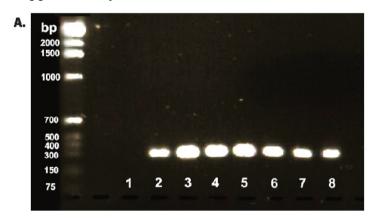
Species	Accession No.		Sequence	
S. capitis	MF620468.1	50	ACGGTAAAGA A TAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620466.1	50	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620463.1	50	ACGGTAAAGA A TAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620459.1	50	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620436.1	50	ACGGTAAAGA A TAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620384.1	50	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620383.1	50	ACGGTAAAGA A TAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620377.1	50	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	MF620333.1	50	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	109
S. capitis	HM352966.1	158	ACGGTAAAGA A TAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	217
S. capitis	GU951710.1	137	ACGGTAAAGA A TAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	196
S. capitis	GU951709.1	130	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	189
S. capitis	EU659903.1	125	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	184
S. capitis	EU659902.1	125	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	184
S. capitis	AF495487.1	181	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	240
S. capitis	DQ321676.1	181	ACGGTAAAGA ATTAAATCATTCGATGAACCAGATGCAAGCAAATTACCTTGGGGAGACC	240
5. warneri	MG874730.1	115	ACGGTAAAGAAGTTAAATCATTCGATGAACCAGATGCAAGCAA	167
S. epidermidis	AF495479.1	181	ACGGTAAAGAAGTTAAATCATTCGATGAACCAGATGCAAGCAA	233
S. aureus	MH092070.1	76	GGTAAAGAAGTTAAATCATTCAATGAACCAGATGCAAGCAA	126
S. haemolyticus	MF620444.1	52	GGTAAAGAAGTTAAATCATACGAAGAACCAGATGCAAGCAA	104

## **Supplementary 5.**



**Agarose gel image of PCR products from optimisation of DNA-template dilution.** Lane 1-6 show the products of *gap*, while lane 7-11 show the products of *sodA*. The DNA template used for the optimisation was extracted from clinical isolate of *S. capitis* no. 58. Lane 1 and 7: negative control (ddH<sub>2</sub>O); Lane 2 and 8: undiluted DNA template; Lane 3 and 9: diluted template 1:10; Lane 4 and 10: diluted template 1:100; Lane 5 and 11: diluted template 1:1,000; Lane 6 and 12: diluted template 1:10,000.

#### Supplementary 6.





**Agarose gel image of PCR products of** *gap* **(A) and** *sodA* **(B) from optimisation of annealing temperature.** DNA template used for the optimisation was extracted from clinical isolate of *S. capitis* no. 58 and diluted 1:10. Lane 1: negative control (ddH<sub>2</sub>O); Lane 2: annealing temperature of 50°C; Lane 3: annealing temperature of 52°C; Lane 4: annealing temperature of 55°C; Lane 5: annealing temperature of 57°C; Lane 6: annealing temperature of 59°C; Lane 7: annealing temperature of 61°C, Lane 8: annealing temperature of 62°C.