

Table S1. Samples with single duplications at the *PLP1* locus.

Single duplication		
No	Individual	Size of duplication (kb)
1	BAB8921	666*
2	BAB8922	475
3	BAB8925	429*
4	BAB8926	534
5	BAB8929	513
6	BAB8930	555
7	BAB8932	221*
8	BAB8933	551
9	BAB8935	340
10	BAB8939	705*
11	BAB8942	389
12	BAB8943	516
13	BAB8944	562
14	BAB8945	440
15	BAB8946	362
16	BAB8947	367
17	BAB8948	423

Single duplication		
No	Individual	Size of duplication (kb)
18	BAB8949	998
19	BAB8950	429
20	BAB8951	488
21	BAB8952	427
22	BAB8953	425
23	BAB8954	4,484
24	BAB8956	758
25	BAB8957	949
26	BAB8958	257*
27	BAB8961	841
28	BAB8963	611
29	BAB8966	397
30	BAB8967	683
31	BAB8968	122*
32	BAB8969	404
33	BAB8971	366*

*Estimated size based on aCGH

Table S2. A summary of genomic rearrangements, coordinates and breakpoint junctions in the cohort of 50 PMD patients

Individual	Array pattern	Segment size (kb)	Coordinates based on sequences junction, if not achieve they are estimated based aCGH and marked by *	Rearrangement pattern based on Jct sequencing	Coordinates Based on the sequenced Jct (if achieved)	Features of JPs (nucleotides with microhomology /microhomeology are shown as upper case letters and two surrounding Nts by lower case). Gaps in microhomeologies are shown by dash	Inserted sequence () Deleted sequence <> Point mutation [] at join-points	Chimeric element	Junction in repetitive elements/LCRs
8920	DUP1	368	102739577 103107466	DUP NML INV/DUP	(+)103107466 (-)111181107	74bp Nt identity at Jct	No	Yes (93% identity)	LIPA5/LIPA3
	DUP2	211	110969769 111181107		(-)102739577 (+)110969769	caCTGAcc	No	No	AluSq2/-
8921	DUP	666	*102476739 103143213	DUP; Insertional translocation	Y(+)23730469 X(+)103143213	No	ca(T)gt	No	-/ LCR Y
8922	DUP	475	102713559 103188774	Tandem DUP	(+)102713559 (+)103188774	gaTCtt	No	No	LIPA4/LCRC
8923	DUP1	642	98855903 99498194	DUP NML DUP	(+)98855903 (+)103366577	No	at(GAA)tc	No	LIMC4/(TA)n
	DUP2	785	102581871 103366577		(+)99498194 (+)102581871	cgACAgA	No	Yes (90% identity)	AluY/AluY
8924	DUP1	112	*102240280 *102352764	DUP NML DUP NML DUP or DUP NML DUP on H2 background	NA	NA	NA	NA	NA
	DUP2	866	102356657 *103224075		JP1 (-)103295890 (-)102660402	ttACaAgCAATat	at(ATGGAGGTTAGA GTAATGTGAGGGC AT)ga	No	LTR (ERV1)/LTR (ERV1-MaLR)/Chain (ID: 1065)
	DUP3	9	102356655 *103305265		JP2 (-)102660369 (+)102356657	atGAGgaAAGtc	The insertion is the result of two microhomeology- mediated TS (JP1 & JP2)		
8925	DUP	429	*102716349 *103145619	Tandem DUP	NA	NA	NA	NA	NA
8926	DUP	534	102793976 103322069	Tandem DUP	(+)102793974 (+)103322069	ccGAgc	No	No	Chain (ID: 84669)/LCRA1b
8928	DUP	78	102138188 102215833	DUP NML DUP	(+)102215833 (+)102411921	ggATCTTCTGAta	No	No	-/LIPA15
	DUP	712	102411921 103123574		(+)102138188 (+)103123574	gaAGGtt	No	No	Chain (ID: 17282) /LIPA3
8929	DUP	513	102651193 103164455	Tandem DUP	(+)102651193 (+)103164455	No	ctG(gcattgg)ag Rep errors in Jct flanking regions: (-)102651263-74 ag<AAAAA>ac (-)102651247-54 aa<A>gg (-)102651206-19 ga<CTACAAA>tg	No	Chain (ID:95091)/ Chain (ID: 231647)

8930	DUP	555	102712023 103267065	Tandem DUP	(+)102712024 (+)103267065	ggTTCTgTTgAtt	No	No	LIPA4/Chain (ID: 1065)
8931	DUP	283	*102940231 *103223662	DUP NML DEL	NA	NA	NA	NA	Probable LCRA1a/LCRA1b chimera
	DEL	17	*103328530 *103345510		NA	NA	NA	NA	NA
8932	DUP	221	*102842768 *103064114	NA	NA	NA	NA	NA	NA
8933	DUP	551	102681876 103315029	Tandem DUP	(+)102681876 (+)103315029	No	gg(GATCCCAA)tg	No	LTR37A/LCRA1b
8934	DUP1	313	96605093 96917885	DUP NML INV/DUP	JP1 (+)96917885 (-)103158716	ggCATatGAGAAca	at(ATGAGAATCATG AAATTAGCAATCAA ACTTGTC)ga	No	-/ NA
					JP2 (-)103158754 (-)103163269	tcGACacATCaTAGta	The insertion is the result of microhomeology- mediated TSs at JP1 & JP2	No	NA/ LIMeg
	DUP2	398	102764968 103163269		(-)96605093 (+)102764968	56bp Nt identity at Jct	No	Yes (89% identity)	AluSx1/AluSg
8935	DUP	340	102708892 103048730	Tandem DUP	(+)102708892 (+)103048730	ccTgc	ccT<TTTT>gc	No	LIMC4/-
8936	DUP1	218	*102746676 *102965077	NA	NA	NA	NA	NA	NA
	DUP2	20	*102967589 *102988069						
	DUP3	325	*102993721 *103319046						
8937	DUP	341	102826552 *103258804	DUP QUAD TRP	(+)102826552 (+)103281547	tcATCag	No	No	No
	QUAD	22	*103258804 103281547		NA	NA	NA	NA	Presumed LCR2/LCRA1b chimera
	TRP	17	103281547 *103305096		NA	NA	NA	NA	Presumed LCR2/LCRA1b chimera
8938	DUP1	63	*101039766 *101103096	DUP TRP/INV DUP	(-)103048340 (+)101420448	No	84bp insertion from different templates	No	LTR (HERV16-int)/-
	TRP	317	*101103096 101420448		NA	NA	NA	NA	NA
	DUP2	1,628	101420448 103048340						
8939	DUP	705	*102570985 *103275726	NA	NA	NA	NA	NA	NA

8940	DUP1 & DUP2	602 70	102637533 *103224075 103256194 *103305742	DUP NML INV/DUP or a tandem DUP on H2 background	(+)102637533 (-)103256177	caGCTCAG-GCagg	tc<TAGTGTG>[c]a	No	<i>AluY/LTR (ERV1)</i>
8942	DUP	389	102798929 103187725	Tandem DUP	(+)102798929 (+)103187725	agACAcA	ag<t>ACAcA	No	-/LCRC
8943	DUP	516	102591617 103107622	Tandem DUP	(+)102591617 (+)103107622	ggTACct	No	No	MER74A/LIPA5
8944	DUP	562	102511210 103073638	Tandem DUP	(+)102511210 (+)103073638	gtAAaAAagATTgACAt g	No	No	-/LIME4a
8945	DUP	440	102942249 103382339	Tandem DUP	(+)102942249 (+)103382339	gaGCTgt	No	No	-/LTR (MER101)
8946	DUP	362	102801949 103163822	Tandem DUP	(+)102801949 (+)103163822	No	aa(TTG)at	No	LIMA9/-
8947	DUP	367	102875648 103243088	Tandem DUP	(+)102875648 (+)103243088	ttAAgAAcATgGtg	No	No	(LTR) MLT1A0/LCRA1a
8948	DUP	423	102845365 103268344	Tandem DUP	(+)102845365 (+)103268344	gtGGCAtag	No	No	L1MC3/Chain (ID: 1065)
8949	DUP	998	102304420 103280891	Tandem DUP with insertions	JP1 (+)103280891 (+)102308763 JP2 (+)102308855 (-)102303992 JP3 (-)102303224 (+)102304420	No cgAgGGGAT-TAtt ctGGGCgt	No tt(CCCCTC)aa No	No No Yes (88% identity)	-/LTR (MLT1L) LTR (MLT1L)/ LIMA3 <i>AluY/AluY</i>
8950	DUP	429	102757828 103186867	Tandem DUP with an insertion	(+)103186867 (-)103026494 (-)103026479 (+)102757828	gtGGGaT-ATat caGCCct	at(ATCCCCCTCA)g c is the result of TS	No No	LCR (Item: chrX:102190370)/LCRC No
8951	DUP	488	102812954 103301556	Tandem DUP	(+)102812954 (+)103301556	No	tt(GT)ct	No	-/LTR49-int & Chain (ID: 7704)
8952	DUP	427	102682377 103109731	Tandem DUP	(+)102682377 (+)103109731	gcCCctt	g[c]CCCt ; T>C	No	-/SINE (MIRb)
8953	DUP	425	102773657 103199137	Tandem DUP	(+)102773657 (+)103199137	gcTGggTTTGGaGAacc	No	No	L1MC5/LCRC
8954	DUP	4,484	99762680 104246638	Tandem DUP	(+)99762680 (+)104246638	ctAGct	No	No	<i>AluY/-</i>

8955	DUP1 & DUP2	314 55	102925509 *103224075 103271708 *103305742	DUP NM INV/DUP or a tandem DUP on H2 background	(-)103271708 (+)102925509	acCTGtActCaa	No	No	<i>Alu/L1PA12</i>	
8956	DUP	758	102612197 103369941	Tandem DUP	(+)102612197 (+)103369941	taTCTcc	No	No	Low complexity (C-rich)/NA	
8957	DUP	949	102150854 103099891	Tandem DUP	(+)102150854 (+)103099891	tcAGTTAaaAaTct	No	No	-DNA (MER102a)	
8958	DUP	257	*102846600 *103104194	NA	NA	NA	NA	NA	NA	
8959	DUP1	9	102671667 102680633	DUP NML DUP NML DUP Or a tandem DUP with inherited deletions	(+)102680633 (+)102682913	gtAaATGaCat	No	No	LTR(MLT1F2)/L1MD3	
	DUP2	96	102682913 102779006		(+)102779006 (+)102809177	29bp sequence identity at JP	No	No	Chain (ID: 17283)/ Chain (ID: 84669)	
	DUP3	546	102809177 103175979		(+)102671667 (+)103175979	tcAta	No	No	DNA(Tigger3b)/LCRC	
8960	DUP1 & DUP2	694 68	*102546322 *103224075 *103258805 *103305742	DUP NML INV/DUP or a tandem DUP on H2 background	NA	NA	NA	NA	NA	
8961	DUP	841	102341097 103181893	Tandem DUP	(+)102341097 (+)103181893	ctCCAgc	No	No	<i>AluV/LCRC</i>	
8962	DUP	63	102765476 102801040	Two Tandem DUPs	(+)102801040 (+)102765476	No	170bp insertion from two known region and small insertions of unknown origin	No	-/L1PB2/-/ LIMA9	
	DUP	177	102929346 103106237		(+)103106237 (+)102929346	ccAtt	No	No	-/LIME3A	
8963	DUP	611	102678485 103289950	Tandem DUP	(+)102678485 (+)103289950	No	tc(CCAA)gc	No	L1M1/L1PA8 and Chain (ID: 118438)	
8964	DUP	533	102560352 103093169	DUP TRP/INV DUP	(+)102560352 (-)103093169	tgCTGA-AAAtTta	No	No	LIMEc/SINE(MIRc)	
	TRP	130	103093169 *103224075							
	DUP	82	*103224075 *103305742				NA	NA	NA	Presumed LCRA1a/LCRA1b chimera

8965	DUP1	456	102319763 102775516	DUP NML DUP With two insertions at each junction	JP1 (+)102775516 (+)103352834	No	No	Yes	Chain (ID: 17283)/ LCRD	
					JP2 (+)103352851 (+)103281343	atGTAfTTTCtGTgc	No	No	No	LCRD/-
					JP3 (+)103281363 (+)102836592	tgGAa-cAGga	GAa[c]AG(g)aa; T>C	No	No	-/L1PA11
	DUP2	557	102836592 103352823		JP4 (+)103352823 (-)102775559	No	ga(GTAA)gt	No	-/Chain (ID: 17283)	
					JP5 (-)102775516 (-)102775657	No	ct(GTG)aa	No	Chain (ID:17283)/Chain (ID: 17283)	
					JP6 (-)102775578 (+)102319763	aaGtTGTCAGat	at(ACAT)tt	No	Chain (ID: 17283)/LCRD	
8966	DUP	397	103175456 102778246	Tandem DUP	(+)103175456 (+)102778246	NA	gg(GGGACTG)ct	No	LIME1/LCRC	
8967	DUP	683	102364351 103057067	Tandem DUP	(+)102364351 (+)103057067	tgGATCgAagTGct	No	No	LTR(MER11A)/-	
8968	DUP	122	*102943944 *103066669	NA	NA	NA	NA	NA	NA	
8969	DUP	404	102839729 103243779	Tandem DUP	(+)102839729 (+)103243779	No	cg(TA)tg	No	LTR (MER89)/LCRA1a	
8970	DUP	93	*102899075 *103050977	DUP TRP/INV DUP	NA	NA	NA	NA	NA	
	TRP	59	*103050977 *103224075							
	DUP	82	*103224075 *103305742			NA	NA	NA	NA	Presumed LCRA1a/LCRA1b chimera
8971	DUP	366	*102938912 *103305265	NA	NA	NA	NA	NA	(Based on aCGH) NA/LCRA1a	

JP: Join-point, Nt: Nucleotide, Jct: Junction, NA: Not available, join-points are not resolved by Sanger sequencing, Dash (-): No repeat or repetitive element, Rep: replication.

Table S3. Original data from 7 studies on genomic rearrangements at the *PLP1* locus.

								Meta-analysis without re-interpretation of published data			This study only	
	Woodward <i>et al.</i> 2005 ^a	Lee <i>et al.</i> 2007 ^b	Carvalho <i>et al.</i> 2012	Bilir <i>et al.</i> 2013	Beck <i>et al.</i> 2015	Zhang <i>et al.</i> 2017	This study 2017	Total	% D ^c	%	% D	%

A) Nature and pattern of CNV events based on array results^d

Single DUP events		NA	7	-	4	-	29	33	73	134	54.5	50	66.0
Complex genomic rearrangement (CGR) event	Total DUP-NML-DUP (disregarding directionality)	NA	3	1	-	-	7	9	20	134	14.9	50	18.0
	Total DUP-TRP-DUP (disregarding directionality)	NA	1	-	-	15	8	3	27	134	20.1	50	6.0
	Other complexities	NA	3	-	-	1	5	5	14	134	10.4	50	10.0
	Total CGR events	NA	7	1	-	16	20	17	61	134	45.5	50	34.0
Total unique CNV events		NA	14	1	4	16	49	50	134	134	100.0	50	100.0

B) Features of sequenced junctions^e

Microhomology (>1 bp)	9	4	-	NA	11	27	15	60	159	37.7	57	26.3
One bp sequence match	1	-	-	NA	3	5	3	12	159	7.5	57	5.3
Microhomeology	NA	NA	NA	NA	NA	NA	19	25	NE	NE	57	33.3
All insertions (>= 1bp)	1	2	1	NA	4	23	13	44	159	27.7	57	22.8
Blunt end	2	-	-	NA	2	2	2	6	159	3.8	57	3.5
Chimeric <i>Alu</i> ^f	1	NA	-	NA	3	5	3	12	142	8.5	57	5.3
Chimeric LINE ^f	0	NA	-	NA	-	2	1	3	142	2.1	57	1.8
NAHR ^g	0	NA	NA	NA	NA	-	1	1	NE	NE	57	
Total number of sequenced junctions	12	5	2	0	21	62	57	159	Variable	100.0	57	100.0

							Meta-analysis without re-interpretation of published data			This study only	
Woodward <i>et al.</i> 2005 ^b	Lee <i>et al.</i> 2007 ^a	Carvalho <i>et al.</i> 2012	Bilir <i>et al.</i> 2013	Beck <i>et al.</i> 2015	Zhang <i>et al.</i> 2017	This study 2017	Total	% D ^c	%	% D	%

C) Genomic architectures overlapping sequenced join-points^d

PMD-LCR	LCRA1a	1	-	-	NA	-	-	2	3	308	1.0	114	1.8
	LCRA1b	-	-	-	NA	-	-	2	2	308	0.6	114	1.8
	LCRC	-	1	-	NA	-	-	7	8	308	2.6	114	6.1
	LCRD	-	-	-	NA	-	-	3	3	308	1.0	114	2.6
	LCR2	-	-	-	NA	-	-	3	3	308	1.0	114	2.6
	LCR3	-	-	-	NA	-	-	1	1	300	0.3	114	0.9
	Total PMD-LCR	1	1	0	NA	0	0	18	20	308	6.5	114	15.8
Segmental Duplications		1	-	-	NA	1	2	2	6	300	2.0	114	1.8
SelfChain^h		-	NA	2	NA	NA	NA	8	2	116	1.7	114	7.9
Repetitive elements	LINE	7	NA	1	NA	19	4	22	53	282	18.8	114	19.3
	<i>Alu</i>	7	NA	-	NA	7	8	8	30	282	10.6	114	7.0
	LTR	3	NA	1	NA	1	NA	13	18	158	11.4	114	11.4
Observed/Examined architectures: LCR, SelfChain, LINE, <i>Alu</i>, LTR, Purine/Pyrimidine tracts, Palindromes, Topoisomerase Consensus Cleavage sites, GAG seqs		8/8	1/1	3/5	NA	4/4	3/3	5/5	-	-	-	-	-
None		5	12	1	NA	14	110	25	167	308	54.2	114	21.9
Total number of sequenced breakpoint junctions		12	14	2	0	42	124	114	308	310	100	114	100.0

D) PMD-LCRs overlapping breakpoints at the level of aCGH for which sequencing was not possible

PMD-LCR	LCRA1a/ LCRA1b	NA	NA	-	NA	17	12	8	37
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*Denominator used for calculating percentages.

^a Number of unique samples. Samples that were studied further in more recent publications were excluded from the original publication count.

^b Only samples with *PLP1* copy number gain were examined.

^c Variable numbers due to variability of features examined in each of the published. A feature percentage was calculated based on the total number of samples obtained from studies that examined the corresponding feature. Studies that did not examine the corresponding feature were excluded from the total number.

^d As observed at the level of aCGH or other high resolution CNV detection method

^e As reported by authors for previously published cases (Without re-interpreting the data according to proposed parameters, some samples are reported in more than one study)

^f Chimeric element: DNA rearrangement that occurs through homologous recombination between two *Alu* or LINE elements and generates a single chimeric, *Alu* or LINE element.

^g NAHR: Homologous recombination between two highly similar non-allelic DNA sequences mediated by a pair of LCRs

^h Alignments of the human genome with itself found in self-chain track on UCSC

NA: HD-aCGH data not available or specific parameter not evaluated by original authors

NE: Not examined in the majority of previous publications

Dash (-): none

Table S4. Microhomeologous sequences at the join-points found in this study.

No	Sample	Total No. of Nucleotides	No. of matching Nucleotides	Identity Matching (%)	Putative priming sequence (Top) & Putative target annealing sequence (Bottom) NA indicates no putative priming/target annealing available
1	BAB8924-1	9	7	78%	ACAAGCAAT ACCA-CAAT
2	BAB8924-2	8	6	75%	GAGGAAAG GAGCCAAG
3	BAB8930	10	8	80%	TTTCTGTTTA TTTCTATTGA
4	BAB8934-1	10	8	80%	CATATGAGAA CATGGGAGAA
5	BAB8934-2	12	9	75%	GACACATCATAG GACTTATCTTAG
6	BAB8940	10	9	90%	GCTCAG-GCA GCTCAGAGCA
7	BAB8944	14	10	71%	AAAAAAGATT-ACA NA AAGAACTATTGACA
8	BAB8947	10	7	70%	AAGAACATGG NA AAAAATATAG
9	BAB8949-2	10	8	80%	AGGGGAT-TA AAGGGATGTA
10	BAB8950-1	8	6	75%	GGGAT-AT GGGTTCAT
11	BAB8953	13	10	77%	TGGGTTTGG-GAA NA TGCCTTTGGAGAA
12	BAB8955	8	6	75%	CTGFACTC CTGGACCC
13	BAB8957	10	7	70%	AGTTAAAAAT AGTTACCAGT
14	BAB8959	7	5	71%	A-ATG-C AAATGAC
15	BAB8964	9	7	78%	CTGA-AATT NA CTGACAACT

16	BAB8965-2	11	9	82%	GTATTTTCTGT GTAATTTTCAGT
17	BAB8965-3	7	5	71%	GAA-TAG GATGTAG
18	BAB8965-6	8	7	87%	GTTGTCAG GCTGTCAG
19	BAB8967	10	7	70%	GATCGAAGTG GATC-ACATG

Table S5. Other features at the join-points found in this study.

No	Join-points with microhomology	Microhomology
1	BAB8920-2	CTGA
2	BAB8922	TC
3	BAB8926	GA
4	BAB8928-1	ATCTTCTGA
5	BAB8928-2	AGG
6	BAB8937	ATC
7	BAB8942	ACA
8	BAB8943	TAC
9	BAB8945	GCT
10	BAB8948	GGCAT
11	BAB8950-2	GCC
12	BAB8952	CCC
13	BAB8954	AG
14	BAB8956	TCT
15	BAB8961	CCA

No	Join-points with Insertions
1	BAB8921
2	BAB8923
3	BAB8929
4	BAB8933
5	BAB8938
6	BAB8946
7	BAB8951
8	BAB8962-1
9	BAB8963
10	BAB8965-4
11	BAB8965-5
12	BAB8966
13	BAB8969

No	Join-points with chimeric <i>Alus</i> , LINEs, Self-Chains
1	BAB8923-1 (<i>Alu</i>)
2	BAB8934-3 (<i>Alu</i>)
3	BAB8942-3 (<i>Alu</i>)
4	BAB8920-1 (LINE)
5	BAB8959-3 (Self-Chain)

No	Join-points with blunt end
1	BAB8949-1
2	BAB8965-1

No	Join-points with 1 bp sequence match
1	BAB8935
2	BAB8959-1
3	BAB8962-2

Table S6. Microhomeologous sequences at the join-points found by re-analyzing breakpoint sequences from previous studies.

No	Sample	Total No. of Nucleotides	No. of matching Nucleotides	Identity Matching (%)	Putative priming sequence (Top) & Putative target annealing sequence (Bottom) NA indicates no putative priming/target annealing available	Previously reported microhomology	Reference
1	P026	11	8	73%	CTGACACCTCA CTCAGTCCTCA	CCTCA CCTCA	1
2	P083	5	4	80%	ACA-A ACATA	ACA ACA	1
3	P116	6	5	83%	CAATGA CAGTGA	TGA TGA	1
4	P176 (PMD7)	8	7	87%	ATAA-TAT ATAACTAT	TAT TAT	1
5	P224	6	5	83%	AAGGTC AA-GTC	GTC GTC	1
6	PMD9	7	5	71%	CTGCCTG CT--CTG	CTG CTG	1
7	BAB2448	13	10	77%	TGGGTTGG-GAA NA TGCCTTGGAGAA	TTTGG TTTGG	2
8	1264-2	14	11	79%	AGTCCAGTTAGCCC AGTTCAGTG-GCCC	AGT AGT	2
9	BAB2867	7	5	71%	TTCATCA TCCATGA	CAT CAT	3
10	P250	10	8	80%	TTGACTGGCC TTGA--GGCC	-	4
11	P255	7	5	71%	AATGCTC AAAGCCC	AA AA	4
12	P820	12	9	75%	ATT-AGGAGAAA ATTGATGAGCAA	AA AA	4
13	P1150-1	7	5	71%	AGG-AAG AGTCAAG	AG AG	4
14	P1407	7	5	71%	TGCTCAT TG-TCCT	TG TG	4
15	J003-1	6	5	83%	AGAGCC AGATCC	CC CC	5
16	J003-2	13	10	77%	AGAAATGCAG-CA AGAAAAG-AGACA	AGAAA AGAAA	5

17	J016	10	7	70%	TTTTGATACA NA TTTAGAAAAA	GA GA	5
18	J029-2	6	5	83%	GGTATG GGGATG	ATG ATG	5
19	J035	9	7	78%	GCTAGAGTA GCT-GAGGA	GCT GCT	5
20	J038	7	5	71%	GTAAAC NA GCTATAC	TA TA	5
21	J041	8	6	75%	ATCCTCCA ATC--CCA	CCA CCA	5
22	J050-2	8	7	87%	AATACTGT AAGACTGT	ACTGT ACTGT	5
23	J065	10	7	70%	ATTGCATCAC ATTA-ATAAC	ATT ATT	5
24	J068-1	7	5	71%	CAAGAAC C-AGACC	C C	5
25	J068-2	8	6	75%	TTCTCCGT TTCT--GT	TTCT TTCT	5
26	J079-1	15	11	73%	ATGAATGAAATTGTA ATGAA--AA--TGTA	ATGAA ATGAA	5
27	J080	8	7	87%	CAGGCCCA CAGGCACA	CAGGC CAGGC	5
28	J082	15	12	80%	TGC-CCAGGCTGGAC TGCACCAGGCA-GAC	TGC TGC	5
29	J083	8	6	75%	CTTC-ACT CTGCAACT	ACT ACT	5
30	J102	14	11	79%	TTG--CTATACAAG TTGAGC-AGACAAG	TTG TTG	5
31	J103	7	6	86%	ATATGTC ATATCTC	ATAT ATAT	5
32	J108	15	11	73%	AAAATTATGAGATTT AAAATC-TCAGACTT	AAAAT AAAAT	5

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