Patient	Seq-NO.	Days Post-Transplant	PB Cells	Genomic Length	LAM Amplicon Length	Integrant-Host-Junction Sequence	Identity [%]	Chromosome	Sequence Orientation	Integration Locus	Genomic Locus / RefSeq Gene
1	80852 H02	12	WBC	54	147	TCCATTTAATACAGTtgaaagaccc	100	4	plus	48114519	1777bp upstream of TEC
1	78933 B06	12	WBC	177	270	GACCAGATGTGGGAAtgaaagaccc	98.4	5	plus	94448967	6025bp upstream of MCTP1
1	78933 C06	12	WBC	139	232	TGCTATAGTTACCGCtgaaagaccc	100	10	minus	121145584	187767bp in Intron 3 of GRK5
1	80852 F01	12	WBC	26	119	ATAAAAGGGAAGCCTtgaaagaccc	100	11	plus	128037827	31372bp upstream of FLI1
1	78933 A06	12	WBC	8	101	AATTAAAAtgaaagaccc					too short
1	80852 A02	12	WBC	13	106	AATTACTGCCGGTtgaaagaccc					too short
1	80852 B02	12	WBC	14	107	AATTATTTTAGCATtgaaagaccc					too short
1	78933 B07	13	WBC	38	131	CACACACACTCATAAtgaaagaccc	100	1	minus	155874598	14878bp upstream of AIM2
1	78933 F07	13	WBC	77	170	GACCTCAGGTGATCCtgaaagaccc	100	1	plus	164251126	3588bp in Intron1 of CREG1
1	78933 D07	13	WBC	52	145	TTGCTTACCCCACTGtgaaagaccc	100	2	minus	136728494	19044bp upstream of CXCR4
1	79697 C08	13	WBC	130	223	ATGTCACAGACAAAGtgaaagaccc	100	2	plus	17225602	41799bp upstream of VSNL1
1	78933 H06	13	WBC	28	121	AACAAATGAGGTTAGtgaaagaccc	100	6	plus	2935514	1582bp in Exon 1 of DKFZp686I15217
1	78933 E07	13	WBC	125	218	CTTGAAGGGTGGGTGtgaaagaccc	100	7	minus	94707759	1187bp in Intron 1 of PON2
1	80852 G03	13	WBC	289	382	CTCCCTATATGATTGtgaaagaccc	100	7	plus	43647712	27533bp downstream of BLVRA
1	80852 C04	13	WBC	79	172	CCAATAGCCTACCTTtgaaagaccc	100	8	plus	62757554	32002bp in Intron2 of ASPH
1	80852 G04	13	WBC	80	173	ATCGCTTGAACCCGGtgaaagaccc	98.8	9	minus	129009529	8983bp downstream of IER5L

1	80852 E04	13	WBC	51	144	TTTAAGTGAAACATCtgaaagaccc	96.1	11	minus	104041347	no Refseq gene within next 100kb
1	78933 F06	13	WBC	27	120	TCTGTCTTCAAGTTCtgaaagaccc	100	12	minus	107639068	11307bp upstream of CORO1C
1	80852 E03	13	WBC	278	371	TCCAGTAAGAGCTATtgaaagaccc	99.7	12	minus	92744212	170593bp in Intron2 of CRADD
1	80852 A04	13	WBC	26	119	GCCGTGCAATACCTTtgaaagaccc	100	12	plus	15927381	768bp in Intron 1 of STRAP
1	80852 C03	13	WBC	118	211	TTTTGAGTACATCACtgaaagaccc	100	14	plus	89156823	no Refseq gene within next 100kb
1	78933 A07	13	WBC	17	110	TTAAAATATTAAGAGtgaaagaccc					too short
1	80852 A05	13	WBC	13	106	GATTTTGTGCTAGtgaaagaccc					too short
1	80852 D04	13	WBC	3	96	AATtaaaagaccc					too short
1	80852 F03	13	WBC	8	101	AATTAGGCtgaaagaccc					too short
1	80852 H04	13	WBC	9	102	AATTACCCTtgaaagaccc					too short
1	78933 C08	14	WBC	62	155	CCCTTGTTTCATCAGtgaaagaccc	100	2			multiple hits
1	80852 A07	14	WBC	33	126	ATAGAATAAAGGAAAtgaaagaccc	100	3	plus	31122332	no Refseq gene within next 100kb
1	79697 C09	14	WBC	26	119	GGAACTACTTTTTCCtgaaagaccc	100	4	plus	185981905	35854bp in Exon 9 of FLJ33167
1	80852 A06	14	WBC	60	153	CATAGTTTCAAATAAtgaaaggccc	100	5	minus	59965457	66256bp in Intron 7 of DEPDC1B
1	79697 E09	14	WBC	93	186	GTGGGAGGATCGCTTtgaaagaccc	100	6	minus	109393783	117465bp in Intron 17 of ARMC2
1	78933 D08	14	WBC	29	122	ACTTTTAGGTCACTTtgaaagaccc	100	7	plus	7671363	no Refseq gene within next 100kb
1	78933 A09	14	WBC	49	142	GAAAGTTATTTAGTTtgaaagaccc	100	8	plus	124166005	11904bp in Intron 4 of MGC21654
1	80852 G07	14	WBC	24	117	GAACGGTCCTCTGACtgaaagaccc	100	15	plus	48215414	16703bp upstream of ATP8B4

1	79697 F09	14	WBC	23	116	CAGGATAGGATGCAGtgaaagaccc	100	18	minus	40593847	58380bp in Intron 1 of SETBP1
1	78933 H07	14	WBC	119	212	TTAAGAGCTTGAGGCtgaaagaccc	99.2	20	minus	30763159	31877bp in Intron 3 of COMMD7
1	78933 A08	14	WBC	207	300	ATACAGGTTCCAGGGtgaaagaccc	99.1	20	plus	237848	8887bp downstream of ZCCHC3
1	80852 C06	14	WBC	21	114	ACAAACAATGGAAGCtgaaagactc					multiple hits
1	78933 G08	14	WBC	28	121	CCAACGACCTTGATCtgaaagaccc					no hit
1	80852 B07	14	WBC	3	96	AATtgaaagaccc					too short
1	80852 A08	15	WBC	76	169	GTGTGGCCTAATAAtgaaagaccc	98.7	2	plus	36543852	48804bp in Intron 2 of CRIM1
1	80852 H08	15	WBC	159	252	ATCTTAACAAACAGGtgaaagaccc	100	3	plus	15815709	2372bp upstream of ANKRD28
1	80852 A09	15	WBC	89	182	GTTAAGATATTTCATtgaaagaccc	100	3	minus	159553012	242418bp in Intron 5 of MGC12197
1	80852 G08	15	WBC	21	114	TTTCATTCAAGAATCtgaaagaccc	100	13	plus	77171831	41659bp upstream of FLJ30046
1	78933 C09	15	WBC	9	102	AATTGTGATtgaaagaccc					too short
1	80852 G09	15	WBC	3	96	AATtgaaagaccc					too short
1	78933 G10	21	WBC	68	161	TTTGATTCTTTGAGGtgaaagaccc	98.6	2	minus	106249125	no Refseq gene within next 100kb
1	79697 A10	21	WBC	68	151	TTTGATTCTTTGAGCtgaaagaccc	100	2	minus	2658697	no Refseq gene within next 100kb
1	80852 B11	21	WBC	128	221	TACAAGGGTTATTTTtgaaagaccc	99.3	3	plus	103277943	no Refseq gene within next 100kb
1	79697 H10	21	WBC	137	230	AATATGACTGACATCtgaaagaccc	100	5	minus	10558333	40196bp downstream of ROPN1L
1	78933 E11	21	WBC	167	260	TGCTTTGTGTCGCAGtgaaagaccc	98.3	7	minus	23111987	193bp upstream of C7orf30
1	80852 H10	21	WBC	129	222	AACCCAGTAATGGCTtgaaagaccc	99.3	7	plus	130154856	no Refseq gene within next 100kb

1	78933 E02	21	WBC	22	115	AGGTGCCATTCCTTTtgaaagaccc	100	12	minus	121193424	16278bp in Intron 1 of MGC35140
1	80852 A10	21	WBC	75	168	AACCTCTCAAGTGATtgaaagaccc	100	16	minus	12406575	no Refseq gene within next 100kb
1	78933 H10	21	WBC	176	269	CCCCCACCCACCTACtgaaagaccc	99.5	17	minus	7181218	612bp in Intron 1 / Exon 1 of CENTB1
1	78933 A11	21	WBC	86	179	TGCAAAGATTGTTTCtgaaagaccc	100	18	plus	27468862	49764bp in Intron 5 of B4GALT6
1	78933 D10	21	WBC	115	208	GTCTGGGGTTCAAACtgaaagaccc	97.4	19	plus	44428610	1159bp upstream of IL28B
1	80852 F12	21	WBC	101	194	TCCCCTCAGTCCTCAtgaaagaccc	100	20	plus	5573746	34074bp upstream of KIAA1434
1	78933 B11	21	WBC	20	113	AAAGGCCAATGAAGGtgaaagaccc					no hit
2	78933 A01	11	WBC	3	96	AATtgaaagaccc					too short
2	78933 A02	21	WBC	54	147	CTGAATACTTACTATtgaaagaccc	100	16	minus	28531941	3791bp upstream of SULT1A1
2	78933 D03	30	WBC	68	161	ACCCAAAGCAAAGACtgaaagaccc					no hit
3	9084	13	WBC	79	172	GTCTTTGTTTCATAGtgaaagaccc	100	2	minus	136732882	23434bp upstream of CXCR4
3	9085	13	WBC	285	378	ACTCTTTCACATGAAtgaaagaccc					multiple hits
3	9086	14	WBC	110	203	GAGCTGAGATCGCGCtgaaagaccc	99.1	12	minus	120560220	10060bp in Intron 1 of LOC283385
3	9088	15	WBC	89	182	ACATTGGCACATCGCtgaaagaccc	100	12	plus	18867724	84336bp upstream of CAPZA3
3	9087	15	WBC	233	326	AAAAAAGAAAGAAGCtgaaagaccc	99.2	13	minus	70133789	no Refseq gene within next 100kb
3	4065	152	WBC	212	305	GGGGAAGGAAAAAACtgaaagaccc	99.6	1	plus	181568775	106526bp in Intron 5 of C1orf24
3	9706	335	G	93	186	CAAGGAGAGTTTGATtgaaagaccc	94.6	2	plus	128781865	10617bp in Intron 1 of HS6ST1