

Supplemental Figure 1: Representative gates used to identify and sort peritoneal B lineage cell populations.

Supplemental Figure 2: Distribution of CDR-H3 length of VH7183DJC μ transcripts isolated from sorted 1-day liver, peritoneal cavity and bone marrow mature B cells.

Distribution of CDR-H3 lengths of the sequenced population from neonatal liver fraction F (NL F - mature); peritoneal cavity (PerC) B-1a, B-1b and B-2; and adult bone marrow fraction F (BM F - mature, recirculating) from TdT sufficient and deficient mice (BM F TdT^{-/-}). (left) all V_H7183 transcripts; V_H7183 transcripts without N nucleotide addition (N-); (right) V_H7183 transcripts containing N nucleotide addition (N+). Prevalence is reported as the percent of the sequenced population of unique, in-frame, open transcripts from each B cell subset. To facilitate visualization of the change in variance of the distribution, the vertical lines mark the preferred range of lengths in the bone marrow fraction F.

Supplemental Figure 3: Distribution of average CDR-H3 hydrophobicity of VH7183DJC μ transcripts isolated from sorted 1-day liver, peritoneal cavity and bone marrow mature B cells.

Distribution of CDR-H3 loops hydrophobicity as assessed by a normalized Kyte-Doolittle scale (39, 40) from neonatal liver fraction F (NL F - mature); peritoneal cavity (PerC) B1a, B1b and B2; and adult bone marrow fraction F (BM F - mature, recirculating) from TdT sufficient and deficient mice (BM F TdT^{-/-}). (left) all V_H7183 transcripts; V_H7183 transcripts CDR-H3 without N nucleotide addition (N-); (right) V_H7183 transcripts containing N nucleotide addition (N+). Prevalence is reported as the percent of the sequenced population of unique, in-frame, open transcripts from each B cell subset. To facilitate visualization of the change in variance of the distribution, the vertical lines mark the preferred range of average hydrophobicity in the bone marrow fraction F.

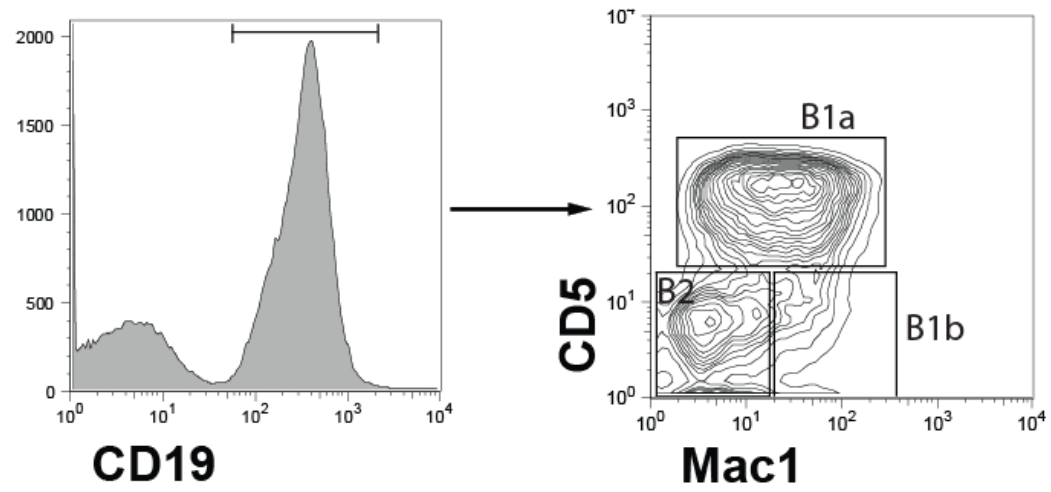
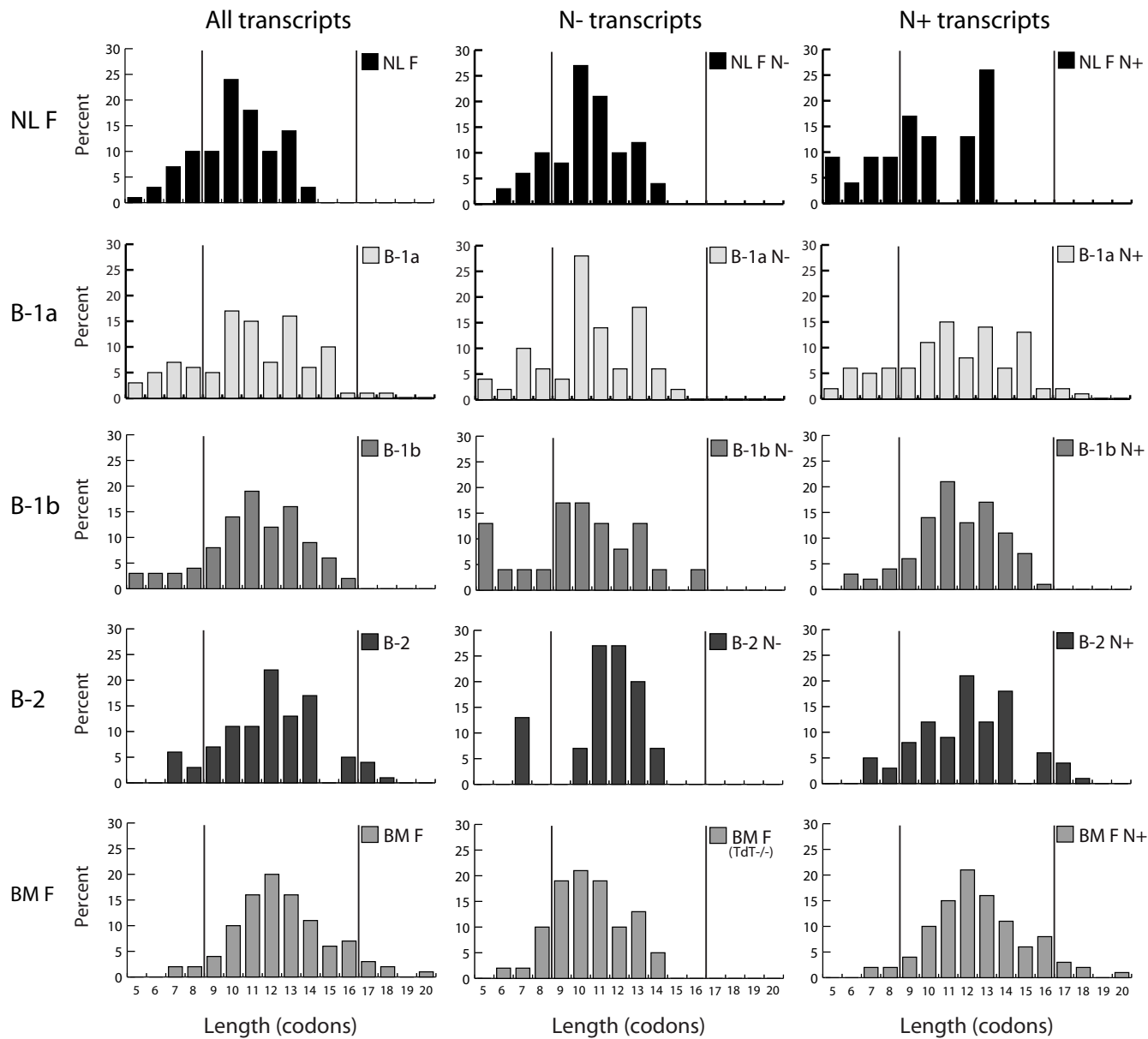
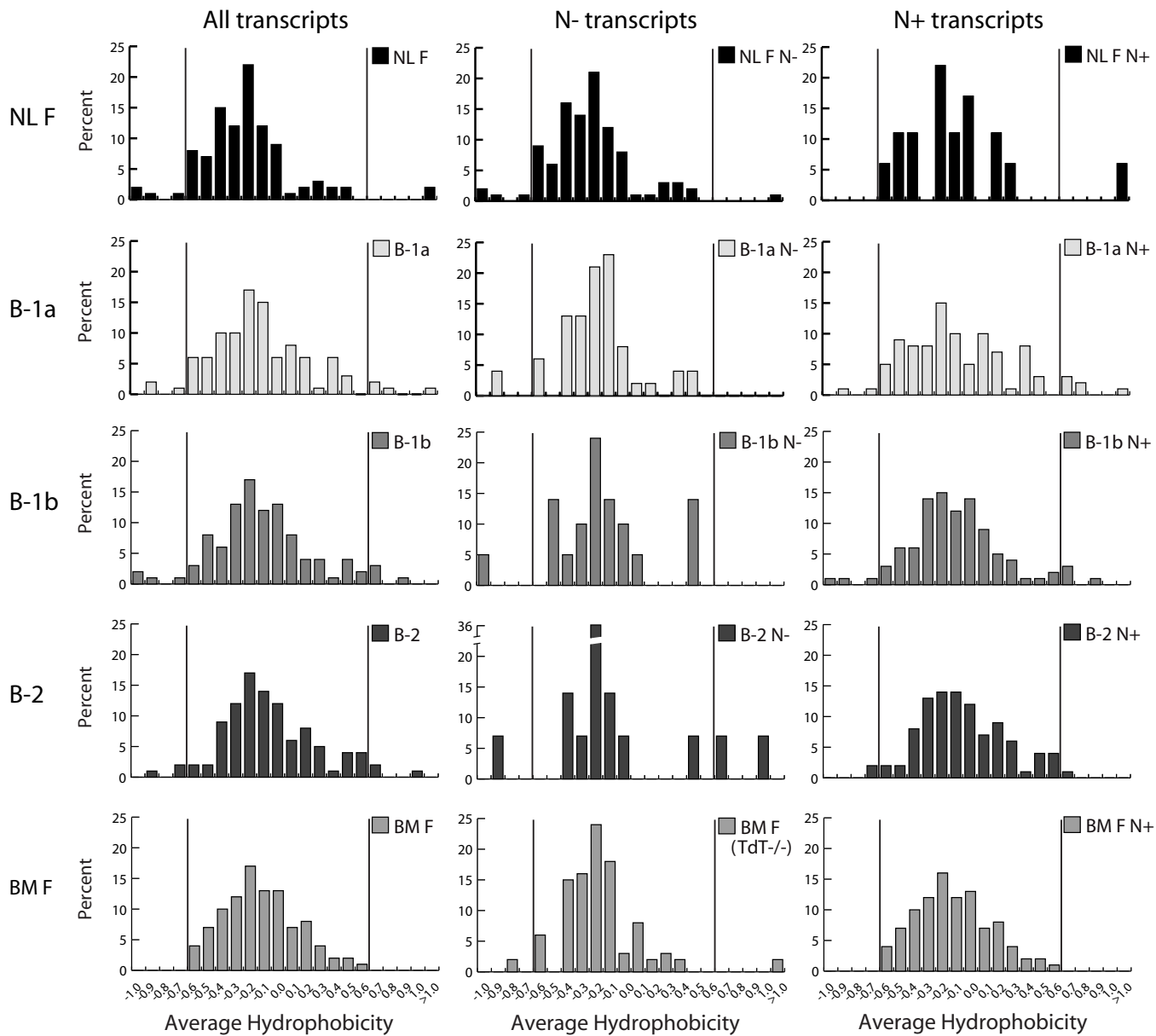


Figure 1





Supplementary Table (S1)

ID	FXN	VH	DH	DH Fam	D/I	JR	RF	VH	VP	V/D	No D	N	5'OP	DH	3' DP	D/J	N'	JP	JR	Amino acids	CDR-H3	Loop	Ave hydrophobicity
RLS40839	B-1a	13	DSF2.08	DSF	D	2	3	GCAGAG						CTAGTATGGT		A			JR	10	ASLWVTFYDF	LWVY	0.464
RLS40840	B-1a	15	No D	No D				GCAGAGA											JR	5	ARDVY		
RLS40841	B-1a	6	DQ52	DQ52	D	2	3	GCAGAG				GGGGGTCT		AACTGGGAC			CAA		JR	11	ARGRNWDQDY	RGRND	-0.585
RLS40842	B-1a	18	DSF2.05	DSF	D	4	1	GCAGG				GGGAAAC		GTAAAC			CCCTCTAGG		JR	13	ARGKRRFRAMNY	QRKRFRA	-0.546
RLS40843	B-1a	16	DFL16.1	DFL	D	2	1	GCAGG						TACTACGGTAGTAG		CTAC			JR	11	ARYGSSVYDF	YVGSY	-0.163
RLS40844	B-1a	18	DFL16.1	DFL	D	2	1	GCAGAG						TACGGTAGTAG			A		JR	10	ARGVSSVYDF	GVGR	-0.322
RLS40847	B-1a	9	DSF2.02	DSF	D	4	1	GCAGG				G		TACG		AC			JR	9	ARYYAMDY	YDYA	-0.193
RLS40848	B-1a	18	DFL16.1	DFL	D	2	1	GCAGAG				GAQCGGGATC		CTACGGTAGTAG			CC		JR	14	ARGAGVSSPFYDF	GAGVSSPF	-0.009
RLS40849	B-1a	12	No D	No D				GCAGAGA			GG								JR	8	AREGAMDY	EDA	-0.410
RLS40851	B-1a	6	DFL16.2	DFL	D	3	1	GCAGAC				CCCTTC		TTCTACTACGG		CT			JR	13	ARFLAYVWFAY	FLAYVWF	0.109
RLS40852	B-1a	9	DSF2.03	DSF	D	4	1	GCAGA				TC		TGTTTAC			CC		JR	11	ARSGYFAMDY	SGFYA	-0.035
RLS40853	B-1a	13	DSF2.09	DSF	D	4	1	GCAGAC			A			TGATGGTT			A		JR	12	ARHDYFAMDY	HDYFYA	-0.274
RLS40864	B-1a	4	DFL16.2	DFL	D	2	2	GCAGAGA	T			AGA		ACTACGGC					JR	10	ARRHTAFDY	HRTA	-0.314
RLS40865	B-1a	15	DFL16.1	DFL	D	2	1	GCAGAGA	TC			G		CGGTAGTAG		GAQCTT	T		JR	14	ARRKSTVYDF	RSSTVY	-0.487
RLS40866	B-1a	15	DFL16.1	DFL	D	1	1	GCAGAG		A				TTACTACGGTAGTAG		CT			JR	13	ARDYTSVYDF	YTSVY	-0.265
RLS40868	B-1a	13	DSF2.07	DSF	D	3	1	GCAGAG				GAGG		GGTAC			G		JR	11	ARQGNAMFAY	QGNAM	-0.460
RLS40869	B-1a	10	No D	No D				GCAA			C								JR	7	ATWYFV	WY	-0.205
RLS40870	B-1a	18	DQ52	DQ52	D	4	2	GCAGA				A		AACTGGGAC		CCGGCA			JR	14	ARRKGNVYAMDY	KGPNVYA	-0.087
RLS40871	B-1a	9T	DFL16.1	DFL	D	1	1	GCAGAC		A				TTACTACGGTAGTAG		CT			JR	13	ARHYGSSVYDF	HYGSSVY	-0.234
RLS40872	B-1a	5	DQ52	DQ52	D	2	1	GCAGA						ACTGGG					JR	7	ARTGYDF	TG	-0.020
RLS40874	B-1a	10	DFL16.1	DFL	D	2	1	GCAGA						TATTACTACGGTAGTAGT		AC			JR	13	ARVYGSVYDF	VYGSVY	-0.190
RLS40876	B-1a	6	DFL16.1	DFL	D	2	1	GCAGAGA				AAG		CTACGGTAGT		CTT			JR	11	ARQVGLDFY	VGLDFY	-0.007
RLS40877	B-1a	1	DSF2.02	DSF	D	2	1	GCAGAC		A				TGAT		TA			JR	7	ARDYDF	RD	-0.955
RLS40879	B-1a	15	DSF2.02	DSF	D	4	1	GCAGAGA				GG		ACTATGATTAC			TTC	T	JR	15	AREDYVFFYAMDY	EDVFFY	-0.248
RLS40880	B-1a	6	No D	No D				GCAGA			GG								JR	6	ARGFVY	G	0.030
RLS40881	B-1a	6	No D	No D				GCAGA			GGG								JR	6	ARGFVY	G	0.030
RLS40889	B-1a	13	DSF2.08	DSF	D	4	1	GCAGAGA				GA		AGTATGGTAAAC		CCC	T		JR	15	ARQVGNVYAMDY	QVGNVYA	-0.375
RLS40892	B-1a	9	DFL16.1	DFL	D	4	1	GCAGAC				TGG		TTTACTACGGTAGTAG					JR	17	ARLVYGSVYAMDY	LVYGSVYA	0.165
RLS40896	B-1a	18	DQ52	DQ52	D	2	2	GCAGG		A				ACTGGGAC		GT			JR	10	ARVYTFYDF	TGYT	-0.130
RLS40899	B-1a	12	DSF2.02	DSF	D	3	3	GCAGAG				GGGAGGG		TCTAC					JR	10	ARGGLNFAY	GLNFAY	-0.168
RLS40900	B-1a	9	DFL16.1	DFL	D	1	3	GCAGA				G		ATTACTACGGTAGTAG		CT			JR	13	TRDYGSVYDF	YDYSVY	-0.265
RLS40902	B-1a	6	No D	No D				GCAGAGA	T			AAGTCCCC							JR	6	ARRKSF	H	-0.910
RLS40903	B-1a	18	DFL16.1	DFL	D	4	2	GCAGA				TGGG		TACTACGGTAGTA		GCTA			JR	12	ARNDVYAMDY	NDVY	0.384
RLS40906	B-1a	10	DSF2.10	DSF	D	4	1	GCAGA						TATAGTACGAC					JR	10	ARVYAMDY	VYDA	-0.414
RLS40907	B-1a	13	DSF2.05	DSF	D	4	1	GCAGAGA				CG		ATGGTAACT		TA			JR	13	ARHGFLYAMDY	HGFLYA	0.015
RLS40908	B-1a	13	DSF2.05	DSF	D	1	2	GCAGAC		A				TGATA		ACT			JR	10	ARRHNVDFY	HNVY	-0.458
RLS40912	B-1a	9T	DSF2.09	DSF	D	4	1	GCAGAC		A				TGATGG		TTAC	TA		JR	11	ARRDGYAMDY	RDGYA	-0.275
RLS40914	B-1a	10	No D	No D				GCAGAGA				AAGGGGACGG							JR	10	ARRQGTGAY	RGGTG	-0.462
RLS40915	B-1a	6	DFL16.1	DFL	D	2	2	GCAGAC				GCTTGT		TTACTACGGTAG		C			JR	12	ARLPTVAFVY	PTVAFVY	0.490
RLS40917	B-1a	5	DQ52	DQ52	D	1	1	GCAGG						TGGAC					JR	8	ASGYFVY	GY	-0.103
RLS40918	B-1a	9T	DSF2.05	DSF	D	2	2	GCAGAC		A				TGTAATAC					JR	8	ARRNVYDF	RNVY	-0.627
RLS40920	B-1a	6	DQ52	DQ52	D	3	1	GCAGAC				T		AACTG		GG			JR	8	ARLTFAY	TFAY	0.453
RLS40924	B-1a	1	No D	No D				GCAGAGA	TG										JR	10	ARRDYAMDY	RDYA	-0.336
RLS40925	B-1a	18	No D	No D				GCAGAG				CGGATCTAGACC							JR	9	ARAGRFYDF	AGRFY	-0.150
RLS40926	B-1a	12	DSF2.03	DSF	D	4	1	GCAGAG				GGG		ATGGTACG		AC			JR	12	ARGGVYAMDY	GGVYA	-0.244
RLS40927	B-1a	1	DSF2.05	DSF	D	4	2	GCAGAC		A				TGGTACTAC					JR	10	ARRNVYAMDY	RNVYA	-0.276
RLS40930	B-1a	10	No D	No D				GCAGAC				GTA							JR	10	ARRNVYAMDY	RNVYA	-0.414
RLS40931	B-1a	18	DFL16.1	DFL	D	2	1	GCAGG				GGGT		TACGGTAGTAGTAC		AG			JR	13	ARGVSSVYDF	VSSVY	-0.131
RLS40932	B-1a	3	DSF2.02	DSF	D	2	1	GCAGA						TATGATACG		AC			JR	9	ARYDYDFY	YDY	-0.635
RLS41265	B-1a	18	DSF4	DSF4	D	2	1	GCAGA				T		CAGCTGGGG		T			JR	8	ARRADY	SAR	-0.210
RLS43230	B-1a	6	DFL16.1	DFL	D	2	2	GCAGAGA				AAGGGGGTGGGTA		TTATTAC		GGTCCGA			JR	17	ARQQGMLITVYVYDF	QGMILTVY	0.109
RLS43231	B-1a	10	DSF2.02	DSF	D	4	2	GCAGAC				GGAT	A	TCTACTATGATTACGAC		G			JR	15	ARRISMTTGAMDY	RISMTTGA	0.338
RLS43233	B-1a	18	DQ52	DQ52	D	2	3	GCAGA				TGGC		GGG		AC			JR	9	ARRDFFVY	RDFFVY	-0.678
RLS43234	B-1a	18	DSF2.08	DSF	D	4	1	GCAGA				TGGGCTA		AGTATGGTAACTAC		G	AAG		JR	15	ARRMYGNTEDAMDY	MYGNTEDA	-0.321
RLS43235	B-1a	10	DFL16.1	DFL	D	4	2	GCAGAC						ATTACTACGGTAGTAGTA		G	AGA		JR	15	ARLITTVATRAMDY	LITTVATRA	0.633
RLS43237	B-1a	5	No D	No D				GCAGG				TATAAGG							JR	8	ARRAMDY	IRA	0.390
RLS43238	B-1a	13	DFL16.2	DFL	D	2	1	GCAGAGA				AG		ACGGCT		AC			JR	10	ARRDQVYDF	QDY	-0.502
RLS43240	B-1a	18	DFL16.2	DFL	D	2	2	GCAA				TG		ACTACGGCTAC		G	GG	CT	JR	12	ARRTATDYDFY	TATDY	0.007
RLS43243	B-1a	10	DFL16.1	DFL	D	4	2	GCAGAGA	TG			GG		ACTACGGCTAC		AT			JR	15	ARRHTVIVYAMDY	HTVIVYA	0.411
RLS43244	B-1a	10	DSF2.08	DSF	D	1	1	GCAGG						GTAATGTA		CC	G		JR	13	ARRGRVYDF	GRVY	-0.415
RLS43246	B-1a	5	DSF2.03	DSF	D	3	1	GCAGAGA	T			C		ATGGT		C			JR	8	ARRRGLAY	RGLAY	-0.597
RLS43247	B-1a	4	DFL16.1	DFL	D	3	1	GCAGAC				CCA		ATTACTACGGTAGTAGTA		T			JR	13	ARRNYGSSVYDF	VYSSVY	-0.294
RLS43248	B-1a	15	DSF2.03	DSF	D	2	3	GCAGA				CCAGACTGG		CTACTATGTTACGAC		G	AGGGGTCTA		JR	18	ARQWMLLRSGVYDF	QMLLRSGVY	0.045
RLS43249	B-1a	6	DSF2.05	DSF	D	2	1	GCAGAGA	T			AATCT		TATGTA		C			JR	11	ARRNYGNDY	NYGNDY	-0.587
RLS43250	B-1a	9	DSF2.08	DSF	D	4	1	GCAGA															

RLS41960	B-1b	6	DFL16.1	DFL	D	4	1	GCAGACA	T		CCCC	ATTACTACGGTAGTAC	TAC		TATCTATGGACTAC	16	ARPHYGSSTYAMDY	HPHYGSSTYA	-0.243
RLS41956	B-1b	97	No D	No D			3	GCAGACA	T	AGGA					CTTAC	6	ARERTY	H	-0.910
RLS41619	B-1b	9	DFL16.1	DFL	D	2	2	GCAGG			GC	TTACTACGGTAGTAC	CCC		CTTGGACTAC	13	ARLTTVATFFDY	LTTVATFP	0.599
RLS41946	B-1b	9	DSF2.03	DSF	D	2	1	GCAGG			CCTT	TATGGTAC	C		ACTTGGACTAC	10	ASLYGVDFY	LYGVH	-0.004
RLS41941	B-1b	18	DFL16.1	DFL	D	1	2	GCAGG			GAAT	TTACTACGGTAG			ACTGGTACTGGATGC	13	ARHTTYVWFYDY	HFTVWFY	0.006
RLS41675	B-1b	18	DFL16.1	DFL	D	3	1	GCAGG			GGACC	ATTACTACGGTAGTA			CTTGGTGGTAC	13	ARHNYGTSWFAY	DHYGTSWF	-0.341
RLS41654	B-1b	18	DSF2.05	DSF	D	2	1	GCAGG			GGGA	GGTAACACT	G	G	CTTGGACTAC	10	ARGNYGVDFY	GGNYG	-0.236
RLS41897	B-1b	10	DSF2.08	DSF	D	4	1	GCAGGA			GAGCT	GTATGGTAACACT			TACTATGCTATGGACTAC	14	ARELYGNYTYAMDY	ELYGNYTYA	-0.098
RLS41609	B-1b	10	DSF2.08	DSF	D	4	1	GCAGGA			GAGCT	GTATGGTAACACT			TACTATGCTATGGACTAC	14	ARELYGNYTYAMEN	ELYGNYTYA	-0.098
RLS41927	B-1b	18	DSF2.09	DSF	D	4	1	GCAGGA			T	TCTATGATGGTACTAC	GT	TGGG	TATCTATGGACTAC	15	ARFYDGYVGYAMDY	FYDGYVGYA	0.145
RLS41890	B-1b	10	DFL16.1	DFL	D	4	2	GCAGGAC			TC	ATTACTACGGTAGTACTA	C	AGA	GCTATGGACTAC	15	AGLTTVATRAMDY	LTTVATRA	0.633
RLS41627	B-1b	10	DFL16.1	DFL	D	4	2	GCAGGAC			TC	ATTACTACGGTAGTACTA	C	AGA	GCTATGGACTAC	15	AGLTTVATRAMDY	LTTVATRA	0.633
RLS41948	B-1b	13	DSF2.03	DSF	D	4	3	GCAGGAC			GGGG	ARGGTAGCA	G	G	ACTATGCTATGGACTAC	13	ARHGLRZYAMDY	HGLRZYA	-0.226
RLS41621	B-1b	15	DQ52	DQ52	D	1	3	GCAGGAC			GTGGG	AACTGGGAC	G		GGTACTGGATGTC	12	ARHGGYGVDFY	GGHGGYD	-0.331
RLS41921	B-1b	1	No D	No D			3	GCAGGACA		CCCCG					GGTTTGGTAC	8	ARHGFAY	HFG	-0.417
RLS41907	B-1b	10	DSF4	DSF4	D	2	1	GCAGGACA			GGGGG	CAGCTGGGGTAC	GT		ACTACTTTGACTAC	14	ARQGAATYFFDY	QGAATYF	-0.063
RLS41916	B-1b	11	DSF4	DSF4	D	4	1	GCAGGGA			GG	CCTCGGG	GAT		CTATGCTATGGACTAC	12	ARESSGYAMDY	ESSGYA	0.166
RLS41640	B-1b	13	DFL16.1	DFL	D	1	1	GCAGGACA			AAC	TTACTACTAGCTY	TC		CTACTGGTACTGGATGTC	15	ARQFFYGVWFYDY	QFFYGVWFY	-0.263
RLS41912	B-1b	13	DSF2.05	DSF	D	1	1	GCAGGACA			GG	ATGGTAACACT	G	GGG	GGTACTGGATGTC	13	ARQGGNYGVDFY	QGGNYGV	-0.431
RLS41887	B-1b	15	DSF2.02	DSF	D	2	2	GCAGGAGA	T		G	CTATGATTAGCAC	G	GGGA	ACTACTTTGACTAC	14	ARDAMITGMFFDY	DAMITGM	0.099
RLS41870	B-1b	18	No D	No D			3	GCA		GAAGT					TTTGGCT	6	ARCFAY	G	0.030
RLS41678	B-1b	18	DSF2.08	DSF	D	4	1	GCAGGA			TCGGT	GTATGGTACT	T		CTATGCTATGGACTAC	13	ARHYGVYAMDY	YGVYFA	0.233
RLS41883	B-1b	6	No D	No D			4	GCAGGAC		CCGGAC					ATTACTATGCTATGGACTAC	11	ARPHYAMDY	PHYA	-0.170
RLS41652	B-1b	97	No D	No D			4	GCAGGAC		GAGGG					ATTACTATGCTATGGACTAC	11	ARHGGYAMDY	RGDYA	-0.340
RLS41653	B-1b	10	DSF2.02	DSF	D	4	1	GCAGGACA			AGGGGG	CTATG	AT		GCTATGGACTAC	11	ARQGYAMDY	QGYA	-0.462
RLS41918	B-1b	10	DSF2.11	DSF	D	2	1	GCAGGACA			AGGG	AGGTAGCAC	G	GG	TTTGGACTAC	13	ARQGYGVDFY	QGYGV	-0.585
RLS41666	B-1b	10	DSF2.05	DSF	D	3	2	GCAGGACA	TG		AGGGC	ATGGTAC	C	G	CTGGTGGTGGTAC	13	ARHMYVAFAY	HMYVAF	0.228
RLS41882	B-1b	15	DSF2.03	DSF	D	3	1	GCAGGA			AGGGGAA	ATGGTAC			TTTGGTAC	10	ARHGGYAMDY	RGGYD	-0.502
RLS41933	B-1b	18	DFL16.1	DFL	D	4	1	GCAGGA			AAGG	ACTATGGACTAC	CGT		TACTATGCTATGGACTAC	13	ARHGYGVDFY	HGYGVDFY	-0.043
RLS41623	B-1b	18	DSF4	DSF4	D	2	3	GCAGGA			CCGGGA	AGGCT	T		TACTTGGACTAC	10	ARHGSYAMDY	HGSY	-0.162
RLS41618	B-1b	18	DSF4	DSF4	D	4	3	GCAGGA			CCGAA	GGGCT	GG		GCTATGGACTAC	10	ARHGMAMDY	HGMAMDY	-0.162
RLS41962	B-1b	10	No D	No D			2	GCAGGACA		CCGGCT					TACTTGGACTAC	9	ARHFFYDY	HFFY	-0.713
RLS41649	B-1b	13	DSF2.02	DSF	D	3	1	GCAGGA			GGCT	CTATGATTAC	CGG	G	CTGGTGGTGGTAC	13	ARAVDYVAFAY	AVDYVAF	0.136
RLS41684	B-1b	18	No D	No D			2	GCAGGA		TCGGTAG					CTTGGACTAC	8	ARHFFYDY	HFFY	-0.500
RLS41685	B-1b	18	No D	No D			4	GCAGGA		AGGGATC					TTACTATGCTATGGACTAC	11	ARHSSYAMDY	HSSYAMDY	-0.262
RLS41961	B-1b	4	DFL16.1	DFL	D	4	1	GCAGGAC			GGGAA	ACTACGG	CC		ATGCTATGGACTAC	12	ARHRYGMAMDY	HRYGMAMDY	-0.526
RLS41608	B-1b	12	DFL16.2	DFL	D	4	1	GCAGGAC			CCGCC	TACTAGGG	CTC		TACTATGCTATGGACTAC	14	ARHGYLYAMDY	GYLYAMDY	0.213
RLS41674	B-1b	15	DSF2.11	DSF	D	2	1	GCAGGAC			GGGGGATA	TACTAGGG	AC		TACTTGGACTAC	12	ARHGYRYAMDY	GYRYAMDY	-0.050
RLS41640	B-1b	10	DSF4	DSF4	D	2	1	GCAGGACA	T		T	GGGTAC	TGGGGGA		TTTGGACTAC	13	ARHMGDYDY	HMGDYDY	-0.048
RLS41680	B-1b	13	DSF2.02	DSF	D	3	2	GCAGGACA	T		AGGGGACG	TACTATGATTAC	G		TTTGGTAC	11	ARHGRMGTFAY	HGRMGTFAY	-0.140
RLS41906	B-1b	5	No D	No D			4	GCA		CTACCGGG					GCTATGGACTAC	8	ALPAMDY	PA	-0.300
RLS41683	B-1b	15	DSF2.02	DSF	D	2	1	GCAGGA			GATCGGGT	TATGAT	TAC		TTTGGACTAC	11	ARHGGYDYDY	GGYDYDY	-0.635
RLS41677	B-1b	18	DSF2.05	DSF	D	2	1	GCAGGA			TTTGGCT	CTATGGTAC	T		TACTTGGACTAC	12	ARHGYGVDFY	GYGVDFY	-0.069
RLS41679	B-1b	9	DSF2.05	DSF	D	4	1	GCAGGAC			CAGGGGT	TATGGTAC	C		CTATGGACTAC	12	ARHGYGVDFY	GYGVDFY	-0.050
RLS41920	B-1b	10	No D	No D			4	GCAGGAC		CGGGATCG					ATTACTATGCTATGGACTAC	12	ARHGGYAMDY	HGGYAMDY	-0.173
RLS41899	B-1b	6	DSF2.11	DSF	D	4	1	GCAGGAC			GGGG	CTATAG	GTCCGG		TTACTATGCTATGGACTAC	14	ARHGYRYAMDY	GYRYAMDY	-0.298
RLS41904	B-1b	15	DFL16.1	DFL	D	2	1	GCAGGAC			GGG	ACTACGGTAGTA	CCGGGGG		CTAC	11	ARHGGYGVDFY	GGYGVDFY	-0.230
RLS41616	B-1b	2	DFL16.1	DFL	D	4	1	GCAGGAGA	T		AGG	GGTAGTAGC	CAGAGAG		ACTATGCTATGGACTAC	15	ARHGGSSGYAMDY	HGGSSGYAMDY	-0.527
RLS41868	B-1b	15	No D	No D			2	GCA		AGGGGGTTTTAA					ACTAC	7	ARHGLYD	GLYD	0.815
RLS41672	B-1b	18	No D	No D			2	GCAGGA		TTTTTCCCGGGGG				GT	ACTACTTTGACTAC	12	ARHFFGGYFFDY	FFGGYFFDY	0.193
RLS41910	B-1b	13	DFL16.1	DFL	D	3	1	GCAGGAC			CCCTCCCTTAG	CGGTACT	GGGG		GGTTCCTTAC	13	ARHLLGGGGFAY	LLGGGGFAY	0.290
RLS41950	B-1b	11	DQ52	DQ52	D	3	1	GCAGGGA	T		GGCCC	AACTGGGAC		AGTCTCTCG	TAC	12	ARHGGPTVDFY	HGGPTVDFY	0.021
MS6w205	B-2	9	DFL16.2	DFL	D	1	1	GCAGGA	CA			TTACTACGG	CTAC		TGGTACTGGATGTC	12	ARHGYGVDFY	HGYGVDFY	-0.300
RLS41219	B-2	14	DFL16.1	DFL	D	2	2	GCAGGA				ATTACTACGGTAGT			CTTGGACTAC	10	ARLTTVFFDY	ITTVF	0.952
RLS41696	B-2	18	DFL16.1	DFL	D	2	1	GCAGGA				TATTACTACGGTAGT	CT		TGGACTAC	11	ARHYYGVDFY	YGVDFY	-0.163
RLS41254	B-2	18	DSF2.02	DSF	D	1	1	GCAGGA				TAGTATFAGAC	GTGG		GGTACTGGATGTC	12	ARHYGVGVDFY	VGVDFY	-0.169
MS6w210	B-2	9	DSF2.09	DSF	D	4	1	GCAGGAC	A			TGATGG			TTACTATGCTATGGACTAC	11	ARHGGYAMDY	HGGYAMDY	-0.275
MS6w201	B-2	11	DFL16.1	DFL	D	1	1	GCAGGG				ATTACTACGGTAGT	CT		GGTACTGGATGTC	13	ARHYSWYFFDY	YSWYFFDY	-0.265
RLS41224	B-2	14	DFL16.1	DFL	D	2	2	GCAGGAC				TTACTAG	G		ACTAC	7	ARLTTDY	LT	0.665
RLS41186	B-2	14	DSF2.02	DSF	D	3	1	GCAGGAC	A			TGATTAC	G		CTTAC	7	ARHAYD	HD	-0.955
MS12w209	B-2	6	DFL16.1	DFL	D	2	1	GCAGGAGA				CTACGGTACTAGTAC	GT		CTACTTGGACTAC	13	ARHYSYVFFDY	HYSYVFFDY	-0.048
RLS41231	B-2	10	DFL16.1	DFL	D	2	1	GCAGGACA				CTACGGTAGT	CTAC		TTTGGACTAC	11	ARHYSYFFDY	HYSYFFDY	-0.270
MS6w208	B-2	10	DSF4	DSF4	D	2	3	GCAGGACA				AGACAGCTCGGGTAC	G		ACTACTTTGACTAC	13	ARHGGSSYFFDY	HGGSSYFFDY	-0.464
RLS41171	B-2	18	DFL16.1	DFL	D	2	2	GCAGGAGA				TACTACGGTAGTAC			CTTGGACTAC	11	ARHDTVAFDY	DTVAFDY	0.472
RLS41173	B-2	14	DSF2.05	DSF	D	4	1	GCAGGACA	T			TATGGTAC	TAC		TATGCTATGGACTAC	12	ARHGYTYAMDY	HGYTYAMDY	-0.274
MS12w214	B-2	1	DSF2.11	DSF	D	3	1	GCAGGACA	TG			ACTATAGGTA	G		CTGGTGGTGGTAC	12	ARHDTYAFAY	HDTYAFAY	-0.446
RLS41230	B-2	11	DFL16.1	DFL	D	4	1	GCAGGGA	TC			ATTACTACGGTAGT	CTA		TGCTATGGACTAC	14	ARHYSYVAMDY	HYSYVAMDY	-0.236
RLS41248	B-2	2	DSF2.02	DSF	D	3	2	GCA		G		CTATGATTAGCAC	G	G	CTGGTGGTGGTAC	11	AAMITAMFAY	MITAMFAY	0.498
RLS41233	B-2	12	DFL16.1	DFL	D	4	1	GCA				TATTACTACGGTAGT	G		TGCTATGGACTAC	12	AYTYGSSCAMDY	YGSSCAMDY	0.191
RLS41244	B-2	2	DFL16.1	DFL	D	1	1	GCAGG				TACGGTAGT	CTAC		TGGTACTGGATGTC	12	ARHYSYVFFDY	YSYVFFDY	-0.160
RLS4																			

RLS41199	B-2	12	No D	No D	4	GCAGAG	G			TTACTATGCTATGGACTAC	9	ARGTYAMDY	GYFA	0.065			
RLS41256	B-2	15	DQ52	DQ52	D 2 1	GCAGAGA	T			CTGGAC	9	ARDGGTFDY	DSGT	-0.285			
RLS41249	B-2	15	DSF2.06	DSF	D 2 1	GCA				ACTAC	7	ASYVGY	YY	-0.270			
RLS41214	B-2	13	DFL16.1	DFL	D 1 1	GCAGAG				TTACTATGCTATGGACTAC	13	ARFYGSSWYFFV	FYGGSNV	-0.002			
RLS51692	B-2	18	DFL16.1	DFL	D 2 1	GCAGAG				CTACGGTAGT	10	ARLYGTYFDY	LYGY	0.158			
RLS41243	B-2	18	DSF2.03	DSF	D 2 1	GCAGAG				TTGGTAG	AC	TACTTGACTAC	YGXY	-0.356			
RLS41189	B-2	18	DFL16.1	DFL	D 1 1	GCAGAG				CGGTAGTAG	CTAC	TGGTACTCGATGTC	PGSSBYV	-0.174			
RLS41193	B-2	16	DSF2.03	DSF	D 4 1	GCAGGG				ATGGTAGGAC	CC	TTACTATGCTATGGACTAC	DGYDFYA	-0.298			
RLS41240	B-2	9	DSF4	DSF4	D 2 2	GCAGAGA				GGCT	G	TTTGACTAC	QSL	0.143			
RLS41185	B-2	18	DFL16.1	DFL	D 2 1	GCAGAGA				TAGTAG	CC	CTTGGACTAC	GGDF	-0.393			
M12w216	B-2	14	DSF2.03	DSF	D 4 3	GCA	A			TCTACTATGGTTA	GAG	TATGCTATGGACTAC	LLMLEYA	0.509			
RLS41243	B-2	10	DSF2.08	DSF	D 2 1	GCAG				GTATGGTA	G	GGC	YGNYG	-0.296			
RLS41207	B-2	10	DFL16.1	DFL	D 1 1	GCAG				ACTACGGTAGTAG	C	ACTGGTACTCGATGTC	DYGGSNV	-0.345			
M12w205	B-2	2	DSF2.09	DSF	D 1 3	GCAGAG				TACTAC	GAG	GGTACTCGATGTC	GVLY	0.292			
RLS41190	B-2	2	DQ52	DQ52	D 4 1	GCAGAG				TGGGAC	G	ACTATGCTATGGACTAC	GGHYA	-0.070			
RLS41252	B-2	2	DSF4	DSF4	D 4 3	GCAGAG				CAGCTGGGACTAC	GT	ACTATGCTATGGACTAC	ASSGVVYA	0.159			
RLS51699	B-2	5	DSF2.09	DSF	D 3 1	GCAGAC				GATGG	G	GTTAC	FD	-0.685			
M6w220	B-2	12	DFL16.1	DFL	D 2 2	GCAGAG				TATTACTACGGTAGTAGT	AC	ACTACTTGGACTAC	GITTVATMY	0.523			
RLS41172	B-2	2	DSF2.02	DSF	D 4 2	GCAGAGA				TATGAT	T	GCTATGGACTAC	EGMIA	0.460			
RLS41208	B-2	6	DFL16.1	DFL	D 2 2	GCAGAGA				TACGGTAGTAGTAC	G	GACTAC	HTVAT	0.487			
RLS41223	B-2	9T	DSF2.08	DSF	D 1 1	GCAGAGA				GTATGTA	GAG	GGTACTCGATGTC	QGVNRY	-0.374			
RLS41234	B-2	9T	No D	No D	2	GCAGAGA	T	CCC				ACTACTTGGACTAC	ARHYFY	-0.455			
M6w209	B-2	12	DSF2.05	DSF	D 4 1	GCAGAGA	TG			GGTATAC	G	CTATGCTATGGACTAC	HGGNYVA	-0.199			
M12w206	B-2	6	DFL16.2	DFL	D 4 3	GCAG				ATFAGTACGGTAC	GT	TGGACTAC	LLRLIA	0.500			
RLS41242	B-2	14	DSF2.02	DSF	D 3 1	GCAG				GATAGAC	GGTG	CGGTGTTGCTAC	VVDAN	-0.007			
RLS41225	B-2	18	DSF4	DSF4	D 3 3	GCAG				AGACAGCTGGGACTAC	C	TGCTAC	LDSSGY	-0.007			
RLS51697	B-2	18	DFL16.1	DFL	D 2 1	GCAGAG				ACTACGGTAGTAGTAC	GT	CTACTTGGACTAC	NVGSVYV	-0.083			
RLS41188	B-2	12	DFL16.1	DFL	D 1 2	GCAGAG				ACTACGGTAGTAGTAC	CC	ACTGGTACTCGATGTC	GTVVARNY	0.292			
RLS41222	B-2	13	DFL16.1	DFL	D 2 1	GCAGAC	A			TTACTACGG	ACGG	GACTAC	HYTG	-0.355			
M12w220	B-2	15	DSF2.07	DSF	D 3 1	GCAGAG				CTATACGG	GACC	GGTAC	ATYG	0.065			
RLS41210	B-2	15	DSF4	DSF4	D 4 2	GCAGAG				TGGGACTAC	CCTT	CTATGCTATGGACTAC	VGLPFYA	0.409			
RLS41241	B-2	18	DFL16.2	DFL	D 4 2	GCAGAG				TTACTACGGTAC	CGAG	GCTATGGACTAC	VTTATEA	0.276			
RLS41212	B-2	9T	DFL16.1	DFL	D 4 1	GCAGAG				CGGTAGTAG	GGG	GCTATGGACTAC	RGSSA	-0.112			
RLS41239	B-2	2	DFL16.2	DFL	D 4 3	GCAGAGA				ACTACGGTAC	G	GCTATGGACTAC	EGLLRA	0.000			
RLS41235	B-2	6	DQ52	DQ52	D 2 3	GCAGAGA				AACGGG	AC	TTTGACTAC	HWND	-0.684			
RLS41216	B-2	12	DFL16.2	DFL	D 1 3	GCAGAGA				ACTACGGGCTAC	C	GCTATGGACTAC	EGLLRY	-0.016			
RLS41177	B-2	6	DSF2.09	DSF	D 4 1	GCAGAGA	T			GATGG	A	ACTATGCTATGGACTAC	HDSNYA	-0.360			
RLS41197	B-2	14	DFL16.1	DFL	D 2 1	GCAGAGA	TG			ATTACTACGGTAGTAG	G	ACTTGGACTAC	HGVYSSD	-0.399			
RLS41259	B-2	13	DSF2.02	DSF	D 2 3	GCAG				GATAGAC	CC	ACTTGGACTAC	GLRFY	-0.230			
RLS41220	B-2	11	DSF2.11	DSF	D 4 2	GCAGGG				CTATAG	AGGAG	GCTATGGACTAC	ALEEA	0.248			
RLS41206	B-2	11	DSF2.05	DSF	D 4 1	GCAGGG				TGGTACTAC	G	GGACTAC	GGNYD	-0.442			
M6w213	B-2	12	DFL16.2	DFL	D 4 2	GCAGAG				TACTACGGC	C	T	ATTACTATGCTATGGACTAC	GRVYYA	-0.076		
RLS51690	B-2	4	DSF2.02	DSF	D 4 1	GCAGAGA				GATAGC	G	CTATGCTATGGACTAC	QRVAYA	-0.329			
RLS41253	B-2	6	DQ52	DQ52	D 2 3	GCAGAGA				GGAC	TGG	TACTTGGACTAC	QGVY	-0.476			
RLS41215	B-2	11	DFL16.1	DFL	D 2 1	GCAGGG				ACTACGGTAGTAC	GGCTA	GACTAC	ENYGS	-0.239			
M12w219	B-2	18	No D	No D	2	GCAGAGA		GGAC				TGGACTAC	DC	-0.485			
RLS41218	B-2	18	DSF2.02	DSF	D 4 1	GCAGAGA				ATGATAGAC	G	ATGCTATGGACTAC	ERNYDA	-0.725			
M6w203	B-2	10	DFL16.1	DFL	D 3 1	GCAGAGA	TG			GGTATGCTAC	AA	GGTTCCTGTC	HGSSSG	-0.307			
RLS41244	B-2	10	DSF2.02	DSF	D 3 1	GCAGAGA	TG			TATGATAGAC	G	GGTTCCTGTC	HGLYDYG	-0.249			
RLS41240	B-2	10	DSF2.02	DSF	D 4 3	GCAGAGA	TG			GATAC	GG	TACTATGCTATGGACTAC	HRLPYA	-0.115			
M6w204	B-2	18	DFL16.1	DFL	D 3 2	GC				GTAGTA	ACTGG	GTTAC	AN	-0.115			
M12w203	B-2	10	DFL16.1	DFL	D 4 3	GCAGAG				TACTACGG	GAAC	CTATGCTATGGACTAC	ELLSYA	0.129			
M12w217	B-2	18	DFL16.2	DFL	D 4 2	GCAGAG				ACGGCTA	TGC	ACTATGCTATGGACTAC	STARVA	-0.171			
M6w218	B-2	14	DSF2.07	DSF	D 4 1	GCAGAC				CGTGG		TATGCTATGGACTAC	FWNYVA	-0.280			
RLS41222	B-2	13	No D	No D	4	GCAGAGA		AAGGG				TGCTATGGACTAC	QGA	-0.375			
RLS12w224	B-2	15	DFL16.1	DFL	D 2 1	GCAGAGA	T			TTATTACTACGGTAGTAG	T	ACTACTTGGACTAC	DGTYGSSBY	-0.222			
RLS41237	B-2	10	DSF2.03	DSF	D 3 1	GCAG				TGGTAGAC	G	ACGC	GG	CGTGGTCTGCTAC	HGYDAN	-0.219	
RLS51686	B-2	5	DFL16.1	DFL	D 4 1	GCAGAG				TATTACTACGGTAGTAG	G	GAGG		GCTATGGACTAC	VYGGRRR	-0.123	
RLS51687	B-2	18	DFL16.1	DFL	D 1 1	GCAGAG				TACGGTAGTAGTAC	GTA	A		ACTTGGACTAC	SGYSSVN	-0.020	
RLS41217	B-2	18	DSF2.09	DSF	D 4 3	GCAGAG				TGGTACTAC	GT	GGGA		ACTATGCTATGGACTAC	RMLRNYA	-0.046	
RLS41206	B-2	2	No D	No D	2	GCAGAG		GGGGGG					CTTGGACTAC	GG	0.030		
RLS41250	B-2	2	No D	No D	4	GCAGAG		GAGGGT					CTATGCTATGGACTAC	GPVA	0.352		
RLS41258	B-2	10	DFL16.1	DFL	D 4 1	GCAGAC		GGGATTA		TTATTACTACGGTAGTAG	CTA	TGCTATGGACTAC	RDYVSSYA	-0.277			
RLS51698	B-2	13	DFL16.1	DFL	D 2 2	GCAGAC				TACGGTAGTAGTAC	G	CGG		TACTTGGACTAC	RTVATRY	0.110	
RLS41176	B-2	1	DSF2.05	DSF	D 1 1	GCAGAGA				ATGGTA	G	GG		TGGTACTCGATGTC	GDGNYVY	-0.399	
RLS41204	B-2	13	DFL16.1	DFL	D 1 2	GCAGAGA	T			TATTACTACGGTAGTAGT	CCGTA	GA		GCTACTCGATGTC	HPYITVVAEY	0.246	
RLS41198	B-2	10	DFL16.1	DFL	D 2 1	GCAGAG				TTACTACGGTAG	CGG	GT		ACTACTTGGACTAC	GDYSSPY	-0.054	
RLS41226	B-2	18	DFL16.1	DFL	D 2 1	GCAGAG				TTACTACGGTAGTAGT	TCCC	CCA		GACTAC	ARPYGSSDY	SPYGS	-0.169
RLS41211	B-2	18	DQ52	DQ52	D 4 3	GCAGAG				ACGGGAC	GT	GAG		GCTATGGACTAC	ARNDVVA	-0.310	
M6w207	B-2	6	DSF2.07	DSF	D 3 1	GCAGAC		GGGGGG		ACTATGCTATGGACTAC	TG	G		CGTGGTCTGCTAC	RGDYNVAY	-0.198	
RLS41255	B-2	10	DSF2.02	DSF	D 4 2	GCAGAG				GATAGC	GGGG			ACTATGCTATGGACTAC	RETDVA	-0.143	
RLS41202	B-2	6	DFL16.1	DFL	D 4 2	GCAGAGA				TATTACTACGGTAGTAGT	AC	TGGG		ATGCTATGGACTAC	ARQITVATRDY	0.247	

RLS41247	B-2	6	DSF2.11	DSF	D	2	1	GCAGACA	TG		AAG	ACTATAGGTACGAC	G	ACGGG	TTTGGACTAC	14	ARREDPRYDGGFVY	REDPRYDDG	-0.747
MS6w212	B-2	10	DSF2.05	DSF	D	4	1	GCAAGA			GGGAT	TGGTAAGTAC	GT	GAGA	GCTATGGACTAC	13	ARGIGNYVRAMDY	GIGNYVRA	0.195
RLS41246	B-2	18	No D	No D		2	2	GCAAGA			TCCCACACT			T	TACTTTGACTAC	9	ARSQLYFVY	SQLY	0.007
RLS51688	B-2	9	DFL16.1	DFL	D	4	2	GCAAGAC			TAAATTCTC	TTATTACTACGGTAGTAG			ATGCTATGGACTAC	17	ARLSLITTVYANAMY	LSLITTVYANA	0.583
MS6w219	B-2	10	No D	No D		1		GCAAGACA	T		TCTGGGAGG				TGCTACTTCGATGTC	11	ARRHSGWYFVY	HSGWY	-0.448
MS6w224	B-2	10	No D	No D		1		GCAAGACA	TG		CCGGCTCCG				ACTGGTACTTCGATGTC	12	ARHAGISWYFVY	HAGISWY	-0.231
RLS41245	B-2	18	No D	No D		4		GCAAGA			AAGAAGAGGG				ATGCTATGGACTAC	10	ARREKSDANDY	REKSDA	-0.506
RLS41187	B-2	18	DSF2.02	DSF	D	1	2	GCAAGA			CGGGGG	TCTACTATGAT		GGAG	TGCTACTTCGATGTC	14	ARRGSTMWYFVY	RGSTMWY	-0.139
RLS41238	B-2	6	DSF2.02	DSF	D	4	2	GCAAGAC			TGATGACC	ACGAC	G	GT	TATGGACTAC	11	ARLMTTVYANDY	LMTTV	0.598
RLS41242	B-2	18	DFL16.1	DFL	D	4	1	GCAAG			CCCTGC	TTATTACTACGGTAGTAG		AGGGA	ATGCTATGGACTAC	16	ASPAYTSGSGNAMDY	PAYTSGSNA	-0.180
RLS41203	B-2	6	DSF2.02	DSF	D	4	1	GCAAGAC			GGGGG	TACCAC		AGGGCT	TATGCTATGGACTAC	13	ARRGYDRAVAMDY	GYDRAVA	-0.321
RLS41182	B-2	13	DFL16.1	DFL	D	2	1	GCAAGACA	T		TGGA	ACTACGGTAGTAGCTAC	GT	CGGGGT	TACTTTGACTAC	17	ARRHWYSSVYGGYFVY	HWYSSVYGGY	-0.114
RLS41175	B-2	10	No D	No D		4		GCAAG			GGACCCCTACCCC			T	ATTACTATGCTATGGACTAC	13	ARDPFPYYTAMDY	DFPYYTA	-0.256
RLS41200	B-2	18	DFL16.1	DFL	D	2	2	GCAAGA			ATG	GTAGTAC	GT	CGGGGAGTGC	CTACTTTGACTAC	14	ARHWATSGRSYFVY	WATSGRSY	0.151
RLS41194	B-2	6	DFL16.1	DFL	D	1	1	GCAAGACA			GGGGAA	GGTAGTAGTAC		CTGGGG	TGCTACTTCGATGTC	16	ARQGGESYLWYFVY	GGESYLWY	-0.247
RLS41196	B-2	2	DFL16.1	DFL	D	4	1	GCAAG			GAGGAAGCCT	TACGGTAGTAGTAC	GT	GGGG	GCTATGGACTAC	16	ARRKPYGSSVYCAMDY	RPYGSSVYCA	-0.098
RLS41209	B-2	18	DFL16.1	DFL	D	2	1	GCAAGA			TCCCTAGGTGG	TTATT		CCCC	CTTTGACTAC	12	ARSLGGYSFFVY	SLGGYSP	0.089
MS6w217	B-2	18	DQ52	DQ52	D	3	3	GCAA				CTAAGTGG		AGAAGTAACT GGAGAA	CCGCTTTCCTAC	14	ATMWRDWRWTFAY	WRDWRWTFAY	-0.573
RLS41205	B-2	2	No D	No D		1		GCAAGAC			CTCTGACTAGGAGCTA				GTAAGTTCGATGTC	12	ARFSTBSQVFFVY	FSTBSQV	-0.459
RLS41228	B-2	5	No D	No D		4		GCAAGAC			CCCTCTCCCTCCACAG				GCTATGGACTAC	12	ARPLSPQAMDY	PLSPQA	0.033
RLS41236	B-2	5	DSF2.11	DSF	D	4	1	GCAAGA			GGGAA	CTACTAT		TGGTCTCTCT ATGC	TATGGACTAC	14	ARGNYSLYAMDY	NYSLYAMA	0.017
RLS41229	B-2	6	DFL16.1	DFL	D	1	1	GCAAGACA			AGGAATTCGGCCTAATCA	TAGTAG		AAGCTTCC	GGTACTTCGATGTC	18	ARQCIRRRHSRFRVY	QIRRRHSRFRY	-0.442