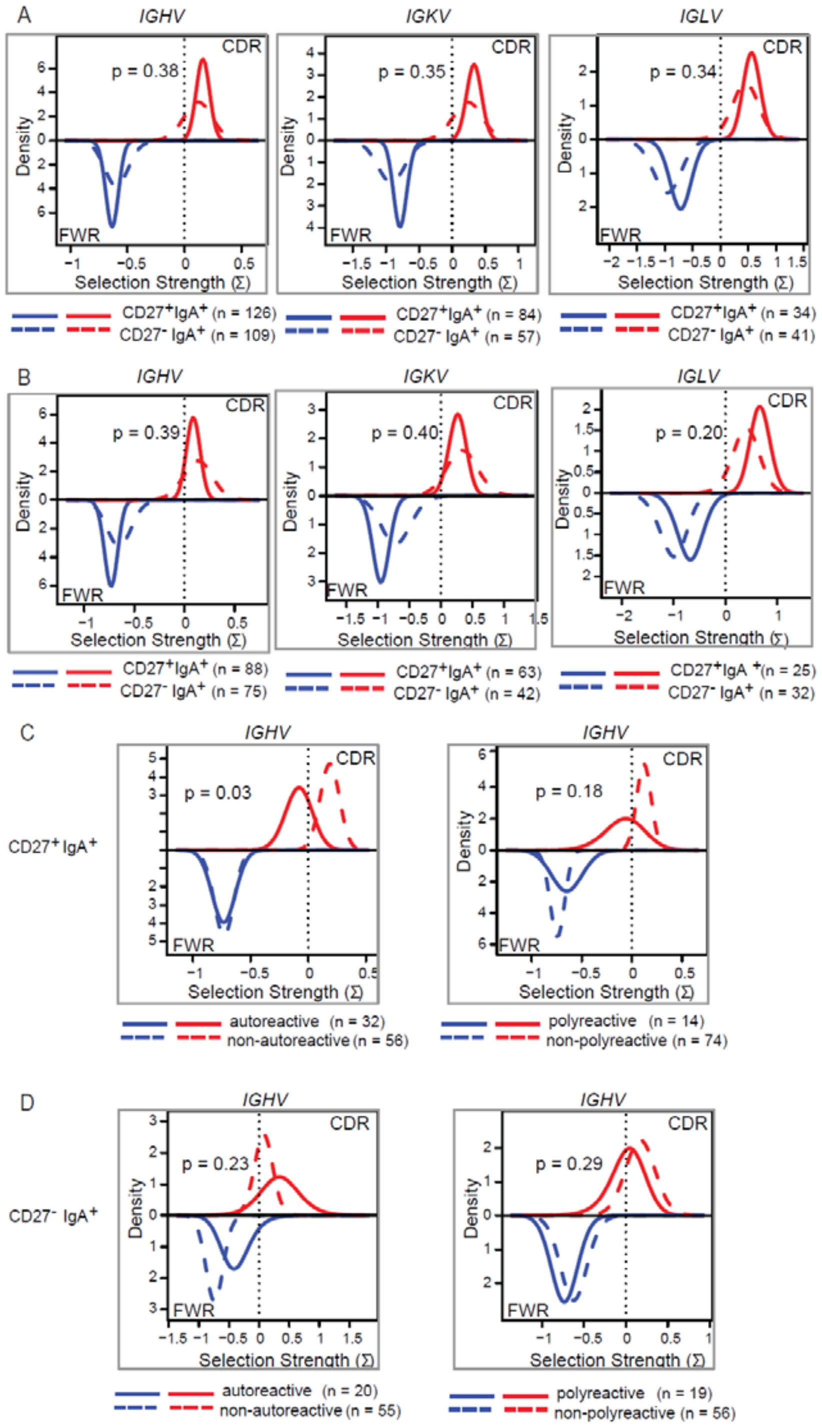

SUPPLEMENTAL FIGURE 1. Selection for replacement mutations. (**A**) Selection strengths in amplified rearrangements, and (**B**) selection strengths in cloned rearrangements as determined with the Bayesian estimation of Antigen-driven SELectIoN program (https://selection.med.yale.edu/baseline) (32). (**C**) Selection strengths in autoreactive (left panel) and polyreactive (right panel) antibodies derived from CD27+IgA+ B cells. (**D**) Selection strengths in autoreactive (left panel) and polyreactive (right panel) antibodies derived from CD27-IgA+ B cells. In all panels, red lines represent CDRs, blue lines represent FRs.

SUPPLEMENTAL TABLE I. Expression levels of selected genes in naive and memory-B-cell subsets.

												fold change		
	Gene symbol	Probe set	trans.	pre-naive	mat. naive	natural effector	IgM-only	CD27+ IgG+	CD27+ IgA+	CD27- IgG+	CD27- IgA+	CD27^{-}IgA^{+} vs CD27+IgA+	CD27^{-}IgA+ vs CD27-IgG+	CD27-IgA+ vs naive mat.
pan B	CD19	206398_s_at	1356.9	1521.8	1912.9	930.6	774.1	1226.8	1360.2	1272.3	1131.0	-1.2	-1.1	-1.7
	MS4A1 (CD20)	228592_at	5809.8	4802.1	6516.7	4603.6	4550.8	10107.4	10008.6	9587.5	7915.4	-1.3	-1.2	1.2
	CR2 (CD21)	205544_s_at	101.20	76.64	105.0	50.5	66.5	82.0	117.9	79.6	88.9	-1.3	1.1	-1.2
	CD40	35150_at	203.0	212.3	265.1	206.5	184.2	213.5	207.4	220.1	176.6	-1.2	-1.2	-1.5
	CD79A	205049_s_at	1889.1	2318.7	1878.6	1676.8	1577.1	897.7	929.1	1104.9	795.1	-1.2	-1.4	-2.4
	CD79B	205297_s_at	2062.18	1520.96	1458.40	1161.46	862.22	722.05	745.00	1066.61	961.20	1.3	-1.1	-1.5
	CD81	200675_at	1990.3	1391.2	1272.1	1513.4	1340.4	1381.0	1304.0	1560.8	1167.5	-1.1	-1.3	-1.1
	TNFRSF13C (BAFFR)	1552892_at	239.8	276.8	336.4	298.8	327.7	255.4	235.6	331.0	288.6	1.2	-1.1	-1.2
B cell subset	CD5	230489_at	133.0	100.2	35.7	51.0	51.2	37.6	32.8	37.5	36.9	1.1	1.0	1.0
	CD38	205692_s_at	150.3	77.2	42.0	39.6	40.5	29.5	39.3	41.4	36.8	-1.1	-1.1	-1.1
	IGHM	212827_at	9930.3	9629.5	10453.4	7616.8	6668.8	550.6	488.7	863.4	657.7	1.3	-1.3	**-15.9**
	IGHD	213674_x_at	4212.8	4559.7	4419.2	2340.6	541.2	57.3	72.5	144.5	93.2	1.3	-1.5	**-47.5**
	IGHA	217022_s_at	57.2	51.0	93.1	554.7	865.2	1922.5	6175.6	917.5	4632.9	-1.3	**5.0**	**49.8**
	IGHG	211430_s_at	79.5	197.3	397.3	1008.3	902.0	3356.3	1011.4	3791.6	841.0	-1.2	**-4.5**	**2.1**
	IGKC	205544_s_at	14485.2	13709.4	13117.2	14284.0	13377.4	12043.9	12019.7	11990.8	9414.2	-1.3	-1.3	-1.4
	IGLC	209139_s_at	318.4	263.1	329.0	445.8	501.7	542.6	527.4	473.3	414.0	-1.3	-1.1	1.3
	CD23	206760_s_at	383.2	738.4	721.6	164.1	100.1	90.5	94.7	139.8	81.3	-1.2	-1.7	**-8.9**
activation/ memory	CD27	206150_at	49.0	53.8	47.6	425.9	368.8	363.8	344.9	107.1	128.6	**-2.7**	1.2	**2.7**
	CD80	207176_s_at	32.8	42.9	31.7	64.6	66.3	133.3	97.8	104.8	81.9	-1.2	-1.3	**2.6**
	CD86	210895_s_at	166.5	105.0	171.2	334.3	276.6	442.7	359.7	357.2	365.5	1.0	1.0	2.1
	CD180	206206_at	224.6	221.8	199.7	291.6	236.1	176.5	184.4	203.3	177.1	1.0	-1.1	-1.1
	FAS	204781_s_at	31.0	24.7	36.9	91.3	119.8	268.0	186.8	149.8	314.9	**1.7**	**2.1**	**8.5**
	TNFRSF13B (TACI)	207641_at	72.3	58.9	70.4	194.9	177.1	214.6	187.2	138.1	207.9	1.1	**1.5**	3.0
	CD58	205173_x_at	21.8	26.4	31.9	93.5	105.8	148.8	136.4	126.5	198.3	1.5	1.6	**6.2**
BCR-signaling	DAPP1 (BAM32)	222858_s_at	562.9	427.0	550.6	657.6	467.8	642.3	598.6	600.1	461.7	-1.3	-1.3	-1.2
	PIK3AP1 (BCAP)	226459_at	778.9	700.1	925.0	789.9	789.0	1053.7	1045.3	1039.3	988.2	-1.1	-1.1	1.1
	BCL10	205263_at	1263.2	859.6	603.7	893.6	644.9	592.2	580.0	725.3	711.8	1.2	1.0	1.2
	BLNK	207655_s_at	939.1	737.0	931.8	671.5	645.0	967.9	1141.1	926.8	819.2	-1.4	-1.1	-1.1
	BTK	205504_at	582.1	484.4	496.4	379.0	360.1	453.9	435.1	406.5	414.9	1.0	1.0	-1.2
	CARD11	223514_at	485.5	399.6	626.8	557.8	742.8	631.0	616.8	525.5	576.5	-1.1	1.1	-1.1
	CDC42	206398_s_at	1400.4	1112.6	1105.6	1497.4	1410.4	1309.0	1223.8	1455.6	1658.2	**1.4**	1.1	1.5
	GAB1	212587_s_at	96.8	46.7	28.0	24.6	26.3	17.5	22.4	14.3	18.6	-1.2	1.3	1.5
	GAB2	205049_s_at	324.7	145.7	112.0	275.2	447.5	257.0	258.9	208.6	316.9	1.2	1.5	**2.8**
	GRB2	205297_s_at	1719.1	1295.9	1387.7	2523.6	2707.2	1628.3	1802.4	1800.8	1915.1	1.1	1.1	**1.4**
	LYN	208728_s_at	4985.1	3770.2	4259.0	3704.4	4436.6	2642.6	2763.1	3345.5	2872.1	1.0	-1.2	**-1.5**
	MALT1	202723_s_at	339.4	282.0	367.4	445.5	399.6	326.9	300.7	361.4	334.7	1.1	-1.1	-1.1
	PTEN	1557030_at	1127.4	972.0	916.9	1226.0	1035.6	930.4	1012.9	914.4	1044.0	1.0	1.1	1.1

	RAC1	203853_s_at	1625.5	1499.3	1586.7	1665.3	1570.5	1122.7	1283.1	1424.1	1374.4	1.1	1.0	-1.2
	PTPN6 (SHP1)	223049_at	598.3	911.9	667.6	464.7	479.2	735.3	626.3	675.0	581.9	-1.1	-1.2	-1.1
	PTPN11 (SHP2)	202626_s_at	404.4	333.1	374.2	426.9	468.5	435.6	443.5	529.9	523.0	1.2	1.0	1.4
	SYK	208309_s_at	1262.5	1005.2	1091.8	1836.2	1384.4	900.9	1062.1	877.5	746.8	-1.4	-1.2	-1.5
	INPP5D (SHIP1)	225363_at	714.8	600.7	876.8	625.9	826.9	1001.4	1088.0	942.7	907.8	-1.2	1.0	1.0
BCR-signaling inhibition	CD22	38521_at	921.1	1123.1	1365.1	568.0	560.4	516.5	570.8	620.0	591.6	1.0	1.0	**-2.3**
	CD72	215925_s_at	602.7	463.9	469.0	238.6	140.9	71.5	159.3	177.8	172.7	1.1	1.0	**-2.7**
	PTPRC (CD45)	212587_s_at	2878.7	2230.4	4002.0	3616.1	3147.2	3686.9	3588.3	2899.2	2431.0	-1.5	-1.2	-1.6
	SIGLEC10	1552807_a_at	335.7	216.6	272.8	545.0	495.2	382.7	394.5	424.1	450.3	1.1	1.1	1.6
	FCGRB	210889_s_at	377.2	384.1	490.8	544.2	493.6	384.1	449.2	431.7	513.3	1.1	1.2	1.0
	PDCD1	207634_at	52.7	67.1	61.2	60.3	57.4	53.6	52.1	55.3	58.7	1.1	1.1	1.0
	CEACAM1 (CD66A)	211881_x_at	316.4	343.5	382.1	248.7	179.0	131.8	129.8	172.6	129.5	1.0	-1.3	**-3.0**
	LAIR1	210644_s_at	124.6	160.5	120.6	68.6	45.1	61.2	66.9	81.0	46.9	-1.4	-1.7	**-2.6**
	LILRB3 (PIRB)	210225_x_at	61.7	65.5	68.4	76.8	62.5	56.8	64.9	69.6	77.3	1.2	1.1	1.1
	LILRB1 (ILT2)	229937_x_at	140.4	133.1	237.9	253.0	225.7	311.3	390.0	419.0	380.4	1.0	-1.1	1.6
CD40 signaling	A20	202644_s_at	1467.8	1022.2	953.3	1750.1	1961.5	2522.5	2133.4	1061.3	1375.4	-1.6	1.3	1.4
	TRAF3IP2 (ACT1)	215411_s_at	227.0	237.5	310.2	266.1	329.2	229.3	259.0	285.5	242.4	-1.1	-1.2	-1.3
	TANK	207616_s_at	529.4	422.6	715.7	584.4	616.1	668.7	579.2	656.9	519.8	-1.1	-1.3	**-1.4**
	TRAF1	205599_at	55.7	64.4	49.0	52.1	56.2	83.6	69.3	71.8	67.4	1.0	-1.1	1.4
	TRAF2	204413_at	54.2	49.0	52.6	52.6	51.3	52.1	58.8	48.4	55.8	-1.1	1.2	1.1
	TRAF3	208315_x_at	145.2	89.9	124.6	175.2	198.5	175.4	160.2	193.8	215.6	1.3	1.1	1.7
	TRAF5	204352_at	755.6	638.0	851.7	598.2	635.6	999.7	1109.2	1072.6	1118.1	1.0	1.0	1.3
	TRAF6	1569861_at	14.0	19.8	15.3	14.1	12.1	12.7	13.3	15.5	13.8	1.0	-1.1	-1.1
TLRs	TLR1	210176_at	190.0	253.8	308.0	132.2	119.1	124.1	111.5	124.5	79.2	-1.4	**-1.6**	**-3.9**
	TLR2	204924_at	34.3	45.6	36.3	44.4	41.6	41.6	38.4	47.5	36.5	-1.1	-1.3	1.0
	TLR3	206271_at	15.4	24.1	13.6	12.0	12.4	14.5	10.5	12.7	13.8	1.3	1.1	1.0
	TLR4	1552798_s_at	27.2	28.7	25.1	27.7	25.9	23.0	22.0	22.2	24.1	1.1	1.1	1.0
	TLR5	210166_at	26.2	46.6	23.8	27.6	25.8	23.1	20.7	24.3	25.1	1.2	1.0	1.1
	TLR6	239021_at	50.6	61.5	71.4	75.9	72.7	84.3	87.2	68.2	63.6	-1.4	-1.1	-1.1
	TLR7	220146_at	64.0	57.0	51.1	66.1	52.9	59.1	50.0	44.6	40.5	-1.2	-1.1	-1.3
	TLR8	220832_at	19.3	19.3	19.2	17.6	19.2	13.5	16.1	18.1	18.2	1.1	1.0	1.1
	TLR9	223903_at	45.6	51.4	44.9	48.1	48.5	39.5	43.0	40.8	49.5	-1.2	-1.2	-1.1
	TLR10	223750_s_at	82.5	83.7	92.2	211.4	146.7	157.8	154.2	158.0	205.3	1.3	1.3	2.2
TLR signaling	MYD88	209124_at	691.9	544.0	552.4	620.6	684.3	569.8	616.8	715.0	769.3	1.2	1.1	1.4
	IRAK1	201587_s_at	1469.8	1158.1	1377.0	1661.2	1663.1	1464.4	1490.8	1345.8	1721.5	1.2	1.3	1.3
	IRAK2	231779_at	46.5	71.6	104.5	163.9	233.4	170.3	139.1	276.7	265.8	**1.9**	1.0	**2.5**
	IRAK4	219618_at	106.1	85.3	97.2	86.7	85.9	105.5	99.9	95.5	95.2	1.0	1.0	1.0
	IKBKG (NEMO)	209929_s_at	149.5	131.1	155.6	124.8	123.1	147.2	160.2	184.4	165.2	1.0	-1.1	1.1
	TIRAP	1554091_a_at	51.1	47.0	39.9	47.5	49.8	49.5	44.1	58.1	45.4	1.0	-1.1	1.1
	TRAF6	205558_at	132.7	116.8	117.9	141.4	141.2	119.5	126.4	126.9	120.6	1.0	-1.0	1.0
	TBK1	218520_at	146.2	93.8	151.2	181.8	229.4	326.9	310.0	309.7	341.4	1.1	1.1	**2.3**

	RIPK1	209941_at	119.9	74.2	103.6	110.2	130.4	127.2	121.8	137.9	117.4	1.0	-1.1	1.1
interleukins	IL1B	39402_at	37.4	36.4	40.0	37.0	38.1	35.3	28.3	33.8	32.4	1.1	1.0	-1.2
	IL2	209849_s_at	39.3	36.0	41.1	34.9	27.9	42.2	40.0	38.9	39.4	1.0	1.0	1.0
	IL3	207906_at	11.4	15.2	13.0	16.4	11.9	11.5	12.3	13.1	14.0	1.1	1.1	1.1
	IL4	207539_s_at	10.8	14.7	14.2	12.7	13.3	11.7	10.8	12.7	12.5	1.2	1.0	-1.1
	IL5	207952_at	16.9	20.2	17.9	20.3	17.2	17.0	15.9	13.9	19.0	1.2	1.3	1.1
	IL6	205207_at	93.8	234.7	475.0	517.8	561.2	130.4	174.6	101.3	95.5	-1.8	-1.1	**-5.0**
	IL7	206693_at	46.3	50.2	46.4	110.7	95.1	130.5	134.8	155.1	142.9	1.1	-1.1	3.1
	IL8	211506_s_at	17.5	27.7	21.1	18.0	18.2	13.9	15.3	15.3	18.9	1.2	1.2	-1.1
	IL9	208193_a	14.1	17.4	13.0	14.2	11.4	11.7	10.3	12.1	10.4	1.0	-1.2	-1.2
	IL10	207433_at	20.7	16.8	12.7	23.9	23.7	14.6	13.0	13.5	14.9	1.1	1.1	1.2
	IL11	206926_s_at	37.0	33.9	34.4	33.7	36.6	34.8	38.4	37.6	40.5	1.1	1.1	1.2
	IL13	207844_at	39.0	51.8	41.2	41.2	41.2	44.9	43.6	39.6	46.6	1.1	1.2	1.1
	IL15	205992_s_at	72.3	90.7	245.0	205.5	170.3	328.9	400.7	223.1	284.9	**-1.4**	1.3	1.2
	IL16	209827_s_at	364.7	387.6	421.7	343.4	331.7	261.1	378.1	426.2	447.8	1.2	1.0	1.1
	IL17A	208402_at	23.7	28.1	23.7	19.9	20.5	20.3	19.1	21.0	23.0	1.2	1.1	1.0
	IL17B	220273_at	21.4	23.9	25.2	21.2	19.8	17.6	19.1	20.5	19.1	1.0	-1.1	-1.3
	IL17D	227401_at	24.8	30.6	25.2	28.4	25.5	22.8	21.2	25.1	22.4	-1.1	-1.1	-1.1
	IL17F	234408_at	17.9	29.6	20.4	24.4	20.6	16.2	16.1	16.7	16.6	1.0	1.0	-1.2
	IL18	206295_at	20.0	16.7	20.1	23.9	17.8	20.5	16.6	15.6	17.6	-1.1	-1.1	-1.1
	IL19	220745_at	37.9	45.9	40.9	40.9	36.0	33.1	35.9	39.7	38.8	1.1	1.0	-1.1
	IL20	224071_at	20.2	22.8	18.5	19.2	19.8	18.6	20.0	17.3	19.3	1.0	1.1	1.0
	IL21	221271_at	19.3	22.9	19.2	16.8	17.5	17.6	17.6	19.2	20.2	1.1	1.1	1.1
	IL22	220056_at	37.8	44.2	40.9	34.3	37.7	33.7	32.9	34.3	39.4	1.2	1.1	1.0
	IL23A	220054_at	52.4	48.4	76.5	79.9	78.1	107.0	92.3	91.8	108.5	1.2	1.2	1.4
	IL24	206569_at	29.3	34.1	36.7	42.7	30.9	24.4	26.5	33.6	29.6	-1.1	1.1	-1.2
	IL25	220971_at	37.5	39.8	26.7	33.1	34.6	31.4	33.4	29.9	36.9	1.1	1.2	1.4
	IL26	221111_at	12.2	15.1	13.7	13.3	11.3	12.6	14.2	12.9	13.6	1.0	1.0	1.0
	IL27	1552995_at	54.1	50.6	56.7	57.6	58.5	43.4	46.1	51.1	50.3	1.1	1.0	1.0
	IL29	1552917_at	30.4	44.4	33.2	30.5	33.1	23.7	25.7	29.9	33.7	1.3	1.1	1.0
	IL32	203828_s_at	27.8	29.2	30.3	29.0	27.6	23.3	22.4	28.0	24.4	1.1	-1.1	-1.2
	IL33	209821_at	8.4	12.8	9.5	8.4	9.9	7.7	7.0	8.3	8.2	1.2	1.0	-1.1
	IL34	237046_x_at	64.5	63.1	65.1	67.2	65.7	62.0	59.9	59.8	71.4	1.2	1.2	1.1
	TNF	207113_s_at	28.7	36.9	33.4	46.0	55.0	38.3	48.8	35.5	36.0	-1.4	1.0	-1.1
interleukin receptors	IL1R1	215561_s_at	18.2	19.9	20.9	18.4	21.3	17.7	18.6	18.2	16.6	-1.1	-1.1	-1.3
	IL1R2	211372_s_at	23.4	31.4	24.4	22.7	24.3	22.7	19.9	23.5	24.7	1.2	1.0	1.0
	IL1RB	39402_at	37.4	36.4	40.0	37.0	38.1	35.3	28.3	33.8	32.4	1.1	1.0	-1.2
	IL2RA	206341_at	27.1	30.4	30.3	33.6	39.0	47.6	43.4	38.4	33.5	-1.3	-1.1	1.1
	IL2RB	205291_at	34.0	45.0	33.9	49.4	46.4	59.2	56.6	55.1	77.9	1.4	1.4	2.3
	IL2RG	204116_at	129.8	255.1	180.2	158.5	116.8	144.6	130.5	147.0	128.0	-1.0	-1.1	-1.4
	IL3RA	206148_at	81.9	59.4	46.4	43.5	48.2	39.7	38.9	37.4	48.9	1.3	1.3	1.1
	IL3R	207906_at	11.4	15.2	13.0	16.4	11.9	11.5	12.3	13.1	14.0	1.1	1.1	1.1
	IL4R	203233_at	1800.4	2788.7	3255.0	316.8	261.6	219.3	161.5	529.4	282.3	1.7	-1.9	**-11.5**
	IL5RA	211517_s_at	26.2	39.2	47.0	28.0	30.4	54.8	47.5	40.1	41.0	-1.2	1.0	-1.1

	IL5R	207952_at	16.9	20.2	17.9	20.3	17.2	17.0	15.9	13.9	19.0	1.2	1.4	1.1
	IL6R	226333_at	24.7	34.3	29.7	51.0	49.2	105.4	73.1	48.4	79.5	1.1	1.6	**2.7**
	IL7R	205798_at	24.7	35.6	26.1	26.2	26.5	25.2	22.9	29.7	25.3	1.1	-1.2	1.0
	IL9R	217212_s_at	38.2	32.1	34.3	33.8	31.8	34.7	33.9	29.2	33.8	1.0	1.2	1.0
	IL10RA	204912_at	466.7	870.8	908.8	1392.7	1639.9	1321.2	1379.3	1544.4	1454.3	1.1	-1.1	**1.6**
	IL10RB	209575_at	226.1	179.4	150.2	270.1	212.9	163.4	173.3	198.7	166.3	1.0	-1.2	1.1
	IL11RA	204773_at	62.9	54.0	94.7	57.9	86.0	109.5	119.3	88.8	84.4	-1.4	1.0	-1.1
	IL12RB1	206890_at	43.4	48.4	39.9	40.9	39.2	31.9	39.9	36.6	40.5	1.0	1.1	1.0
	IL12RB2	206999_at	17.7	21.0	16.4	15.1	15.2	16.3	14.9	16.4	14.4	1.0	-1.1	-1.1
	IL13RA1	201887_at	39.4	106.7	147.9	93.3	87.7	397.2	258.1	407.5	213.5	-1.2	**-1.9**	1.4
	IL15RA	207375_s_at	49.2	55.6	47.1	53.3	59.8	82.4	77.1	72.9	70.5	-1.1	1.0	1.5
	IL17RC	221926_s_at	64.5	63.3	46.2	48.4	48.2	42.2	43.6	43.1	39.8	-1.1	-1.1	-1.2
	IL17RB	224361_s_at	34.3	47.2	35.0	35.7	44.2	30.8	33.2	32.9	31.3	-1.1	-1.1	-1.1
	IL17RA	205707_at	180.9	142.1	149.2	144.1	146.8	145.2	148.9	145.6	143.5	1.0	1.0	1.0
	IL21R	221658_s_at	245.6	154.1	98.0	40.9	28.3	22.0	19.4	33.3	42.4	2.2	1.3	-2.3
	IL22RA1	220056_at	37.8	44.2	40.9	34.3	37.7	33.7	32.9	34.3	39.4	1.2	1.1	1.0
	IL23R	1561853_a_at	20.0	27.1	22.2	20.8	19.4	16.8	15.9	18.9	18.0	1.1	1.0	-1.2
	TGFBR1	224793_s_at	243.4	237.6	271.5	677.6	710.3	208.4	284.8	345.4	426.6	1.5	1.2	1.6
	TGFBR2	208944_at	1296.5	1168.9	1535.6	1358.0	1467.1	675.7	843.2	914.0	881.7	1.0	1.0	-1.7
	RARA	201605_x_at	756.4	720.7	558.6	640.1	612.5	488.1	490.4	532.2	551.6	1.1	1.0	1.0
trancription factors	PRDM1 (BLIMP1)	217192_s_at	50.8	55.7	55.5	58.3	56.4	74.9	72.0	68.8	63.2	-1.1	-1.1	-1.1
	FOXO1	202723_s_at	1119.5	1120.3	1458.5	558.7	536.1	371.7	393.7	446.2	324.8	-1.2	-1.4	**-4.5**
	IRF4	204562_at	175.3	126.5	120.7	166.4	212.6	167.6	234.2	180.9	219.6	-1.1	1.2	1.8
	KLF2	219371_s_at	4581.5	6246.3	6085.8	5168.3	4143.3	5815.8	4573.6	5177.5	3506.9	-1.3	**-1.5**	**-1.7**
	KLF4	221841_s_at	1052.4	1579.9	1343.9	572.3	217.2	620.3	442.6	189.9	176.8	-2.5	-1.1	**-7.6**
	KLF9	203542_s_at	969.8	1216.6	1640.5	1825.1	1318.6	869.2	928.8	1009.8	879.6	-1.1	-1.1	-1.9
	NOTCH2	202443_x_at	791.3	743.8	745.5	887.4	821.0	827.4	945.0	943.5	873.0	-1.1	-1.1	1.2
	PAK2 (p21)	208877_at	524.1	457.2	503.8	767.3	779.0	644.3	596.0	706.7	740.1	1.2	1.0	1.5
	PAX5	221969_at	4639.4	3919.2	5064.9	3251.1	3161.1	3160.1	3450.2	3462.2	2899.5	-1.2	-1.2	**-1.7**
	ZBTB16 (PZLF)	205883_at	29.6	56.9	177.4	41.1	30.9	25.2	31.2	43.8	39.4	1.3	-1.1	**-4.5**
	RORA	210426_x_at	17.2	17.9	21.4	188.0	206.0	354.8	339.8	165.1	283.2	-1.2	1.7	**13.2**
	RUNX1	209360_s_at	214.8	161.8	184.5	164.7	143.5	135.2	136.0	172.3	137.4	1.0	-1.3	-1.3
	RUNX2	232231_at	12.9	15.4	15.2	22.3	78.1	44.2	204.2	60.1	483.2	**2.4**	**8.0**	**31.9**
	RUNX3	204198_s_at	1188.5	1153.5	1444.0	1821.8	2343.7	2212.5	2005.9	1880.6	1948.0	1.0	1.0	1.3
	SOX5	207336_at	64.7	33.9	33.6	150.1	76.6	47.3	48.2	74.6	68.2	1.4	-1.1	2.0
	SPIB	205861_at	333.8	207.0	168.9	262.3	253.6	237.2	266.6	211.0	218.5	-1.2	-1.0	1.3
	TBX21(Tbet)	220684_at	33.6	52.9	45.6	79.8	65.4	92.1	91.7	110.4	75.6	-1.2	-1.5	1.7
chemokine receptors	CXCR1	207094_at	59.5	74.5	49.1	57.5	62.3	44.5	46.0	50.5	46.1	1.0	-1.1	-1.1
	CXCR2	207008_at	18.7	22.7	21.5	18.2	19.3	21.4	19.9	18.1	22.4	1.1	1.2	1.0
	CXCR3	217199_s_at	37.2	33.8	36.2	33.0	32.6	38.6	34.8	39.4	34.7	1.0	-1.1	1.0
	CXCR4	209201_x_at	4233.9	5514.2	3675.7	3376.7	3564.5	1772.1	2327.8	2614.2	1614.5	-1.4	-1.6	-2.3
	CXCR5	206126_at	429.7	367.1	459.7	788.3	952.2	370.0	510.4	429.8	436.7	-1.2	1.0	-1.1

	CXCR6	211469_s_at	28.9	42.0	39.6	33.7	31.5	34.8	28.8	34.6	34.2	1.2	1.0	-1.2
	CCR1	205099_s_at	19.4	18.5	21.0	22.9	22.2	20.8	21.6	19.8	23.4	1.1	1.2	1.1
	CCR2	207794_at	19.0	25.8	22.8	19.1	15.6	19.2	23.6	22.2	21.1	-1.1	1.0	-1.1
	CCR3	208304_at	18.5	28.1	18.2	17.6	19.8	17.5	17.4	20.6	21.7	1.2	1.1	1.2
	CCR4	208376_at	40.7	49.3	35.2	41.0	36.6	37.1	37.4	42.4	43.4	1.2	1.0	1.2
	CCR5	206991_s_at	27.8	36.5	28.2	30.2	32.4	27.4	26.2	30.0	27.9	1.1	-1.1	1.0
	CCR6	206983_at	50.7	62.0	101.7	162.7	121.8	67.8	97.1	112.8	86.8	-1.1	-1.3	1.2
	CCR7	206337_at	132.6	356.3	660.6	305.2	296.1	250.1	334.9	402.3	250.0	-1.3	-1.6	**-2.6**
	CCR8	208059_at	19.4	32.8	18.0	17.9	19.7	19.5	21.5	19.5	20.8	1.0	1.1	1.2
	CCR9	207445_s_at	45.7	29.7	20.1	29.8	44.8	17.4	35.6	20.5	87.3	**2.5**	**4.3**	**4.4**
	CCR10	220565_at	27.4	34.0	30.6	28.6	31.2	34.8	34.9	26.9	26.1	-1.3	1.0	-1.2
	CX3CR1	205898_at	27.2	31.5	27.1	18.3	20.8	24.7	29.0	27.6	42.4	1.5	1.5	1.6
	XCR1	1561226_at	29.0	32.0	28.4	28.6	26.8	24.5	24.3	24.6	25.4	1.0	1.0	-1.1
adhesion molecules	ITGAL (CD11A)	213475_s_at	130.1	110.7	166.3	217.4	201.0	360.9	326.4	229.9	274.0	-1.2	1.2	1.6
	ITGA4 (CD49D)	213416_at	639.8	497.5	692.7	527.4	388.4	960.5	712.7	866.7	812.6	1.1	-1.1	1.2
	ITGB1 (CD29)	211945_s_at	379.6	189.0	292.3	1075.1	1000.0	2920.9	2067.4	1560.3	1467.9	-1.4	-1.1	**5.0**
	ITGB2 (CD18)	202803_s_at	546.6	557.5	598.7	604.5	408.5	534.3	493.6	739.1	591.8	1.2	-1.2	1.0
	ITGB7	205718_at	261.7	171.0	170.0	174.7	193.2	157.3	147.5	152.5	149.6	1.0	1.0	-1.1
	SELL (CD62L)	204563_at	778.4	1347.5	1240.4	823.7	780.0	918.5	892.2	964.3	666.0	-1.3	-1.4	-1.9

Statistically significant differences between CD27-IgA+, and mat. naive, CD27+IgA+ and CD27-IgG+ memory-B cells are depicted in bold. Fold change was calculated by determining the absolute value of the ratio of transcript expression between the indicated populations. Values were assigned a negative value if gene expression was lower in CD27-IgA+ as compared to the indicated control population.

SUPPLEMENTAL TABLE II. Repertoire and reactivity of antibodies from CD27+IgA+ and CD27-IgA+ B cells of 5donors.

Ig		HEAVY									LIGHT					REACTIVITY									
		V_H	D_H	RF	J_H	(-)	CDR3 (aa)	(+)	Length	No of SHM	V_κ	J_κ	CDR3 (aa)	Length	No of SHM	Poly	Hep2	IFA	flagellin	*B.fragilis*	*C.difficile*	*E.cloacae*	*E.faecalis*	*S.aureus*	*E.coli*
CD27+IgA+	donor1-01	3-66	6-19	3	4	1	VLPFSPSGGWTPFDR	0	15	19	1-5	1	QQYDTYPWT	9	9										
	donor1-04	4-59	3-3	1	5	2	TVLLEWFFFEP	0	11	26	3-20	3	QQYGSSPFT	9	11	-	-	-	-	-	-	-	-	-	-
	donor1-05	3-9	5-24	2	6	2	DGRYSYMDV	1	9	29	3-15	5	QQYNYWPLT	9	22										
	donor1-06	5-51	3-10	2	4	1	RSGYSASDF	1	9	41	1-5	4	QEYDSYSGS	9	24										
	donor1-07	3-13	5-12	2	4	2	VRYDHGYDL	2	9	22	1-39	2	QQSYSTLLYN	10	1	-	+	-	-	-	-	-	-	-	-
	donor1-08	3-23	3-10	1	5	3	DRGVGEILNNWFDP	0	14	20	3-15	4	QQHSDWPLT	9	14	-	-	-	-	-	-	-	+	-	-
	donor1-09	3-15	/	/	4	1	TTGSVEGY	0	8	20															
	donor1-11	4-4	3-9	1	5	2	GDTYDWFFNS	0	10	31	3-20	4	QHYATSPLT	9	21										
	donor1-12	4-31	/	/	4	1	RPGNRTFYLGVCDY	2	14	27	3-20	2	QYYGRSPYS	9	12	-	-	-	-	+	+	+	+	+	+
	donor1-14	1-2	2-2	2	4	2	DHCSGTSCYAVD	0	12	28	1-33	4	QQYDDLRLT	9	12	-	-	-	-	-	-	-	-	-	-
	donor1-17	3-7	5-24	2	4	0	GFGPGY	0	6	4	4-1	1	QQYYNTPPWT	10	9	-	-	-	-	+	+	+	+	-	-
	donor1-19	3-30	3-16	1	4	4	DLGDDYPSLGVIDY	0	14	9	1-39	2	QQSYSTPPVFT	11	13	-	+	-	-	+	+	-	+	-	+
	donor1-20	3-74	1-26	3	4	1	LRVGAAIPHGFDL	2	13	36	3-20	2	QQYDGSPYT	9	2	-	+	-	-	-	-	-	-	-	-
	donor1-21	4-39	/	/	1	1	HFYAETFQN	1	9	21	3-20	4	QHYATSPLT	9	24										
	donor1-26	3-30	/	/	6	2	DRISPSGPKIVYVYYYMDV	2	19	39	3-11	3	QLGRTWPPA	9	18	-	-	-	-	-	-	+	+	-	+
	donor1-27	3-9	/	/	6	2	GKDISRGGMDV	1	9	32															
	donor1-29	3-23	/	/	4	3	AKDRTGGADTLDY	2	11	8	1-6	4	LQDYNYPRT	9	4	-	-	-	-	-	-	-	-	-	-
	donor1-30	5-51	2-21	2	6	1	SYCASTSCQTRGYFGMDV	1	18	14															
	donor1-31	3-24	/	/	4	1	SLRGAVTVRDY	2	11	12	3-20	3	QQFGSSRFT	9	6	-	+	-	-	-	+	-	+	+	+
	donor1-34	3-15	3-10	3	5	0	QTRNTVVRGVPINGGLAP	2	18	16	4-1	4	QQYYSSPLT	9	10	+	-	-	-	-	-	-	-	-	-
	donor1-37	3-7	5-5	2	4	0	VRGYGNGHWVF	2	11	21	3-20	1	HQYVGSPWT	9	13	-	+	-	-	-	-	-	-	-	-
	donor1-38										1-39	3	QQSYNFPRT	9	17										
	donor1-39	3-7	/	/	4	1	IFSGLTFDY	0	9	28	1-8	3	QQYSSYPFT	9	14	-	-	-	-	-	-	-	-	-	-
	donor1-41	3-15	3-10	3	3	2	VREGVIAAFDI	1	11	17	1-33	5	QQYDNLLRIT	10	4	-	-	-	-	-	-	+	-	-	-
CD27-IgA+	donor1-49	1-2	/	/	5	2	RKGDLLGEG	2	9	4	1-12	4	QQANSFPLT	9	4	+	-	c	-	-	-	-	-	-	-
	donor1-52	4-59	3-16	3	4	1	GFGGVIADY	0	9	0	3-11	2	QQRSNWPPEYT	11	0										
	donor1-59	4-59	2-2	2	4	1	VREGYCSSTSCYTGN	1	15	1	3-15	3	QQYNNWPL	8	0	-	-	-	-	-	-	-	-	-	-
	donor1-60	3-33	5-24	2	3	2	DGGGGHFDI	1	8	0	1-39	1	QQSYSTTWT	9	0	-	-	-	-	-	-	-	-	-	-
	donor1-62	3-23	6-19	2	4	1	FSGWYRGSLDY	1	11	11	1-27	3	QKYNSAPFT	9	2	+	-	c	+	+	+	+	+	+	+
	donor1-65	4-59	3-16	3	4	1	GFGGVIADY	0	9	0	3-20	3	QQHGSSPMT	9	12										
	donor1-71	1-2	6-19	3	5	2	DQVGRAVAGWFDP	1	13	9	3-15	2	QQHNNWPYS	9	4	-	+	-	-	-	+	+	+	-	+
	donor1-72	3-21	6-13	1	6	4	DREQQLDHLVTGYYSYGMDV	1	20	18	1-5	1	QQYNGYSRT	9	5	+	-	N	-	+	+	+	+	-	-
	donor1-73	3-48	1-7	2	4	2	DWWNWNSDN	0	9	10	4-1	2	QQYYSTPSYT	10	2										
	donor1-74	3-15	2-21	3	4	1	APAVTARPGLDY	1	12	22	1-5	2	QQYSDYPMYS	10	10										

	donor1-77	3-33	5-5	3	6	3	RDLDTATFYYYYGMDVW	1	15	6	3-20	2	QQYGSSQYS	9	2	-	-	-	-	-	-	-	-	-	-
	donor1-79	4-39	6-19	3	4	1	HPIAVAGWGGFDY	1	13	19	1-33	4	QQYDNLPLS	9	6	-	-	-	-	-	-	-	-	-	-
	donor1-80	4-39	3-3	2	5	2	PQGQRDYDFWSGHL	1	14	0															
	donor1-84	3-9	5-12	3	4	1	ARIVATITGVNYYFDS	1	16	16															
	donor1-85	3-9	/	/	3	2	DMSRGLGMFAFDM	1	13	30	3-20	4	QQRGS	5	15	-	-	-	-	-	-	-	-	-	-
	donor1-86	3-9	5-5	2	4	3	GSTSYGPDHELEN	0	13	20	3-15	4	QQYNKLPLT	9	8										
	donor1-87	1-18	2-21	2	3	1	GNGLSHCGGDCL	1	12	23	3-15	1	HQYTNWPT	8	10										
	donor1-91	3-74	4-4	2	6	2	MDYSNYVGHSGFDV	1	14	29															
	donor1-94	1-46	5-24	2	6	2	DSFANWGVMDV	0	11	20	3-20	2	QQYGSSMYS	9	9	-	-	-	-	-	-	-	-	-	-
CD27+IgA+	donor2-03	4-59	4-17	2	3	3	GKGDLSGTDAFDI	1	13	13	1-5	1	QQYNTYWT	8	8	-	-	-	-	-	-	-	-	-	-
	donor2-07	3-7	4-4	2	5	3	EWSNYADNWFDS	0	12	21	1-39	2	QQSYSTPT	8	23	-	+	-	-	-	-	-	-	-	-
	donor2-13	3-7	3-16	2	4	2	PTYFDYIWGRPPFGSFDY	1	18	12	4-1	4	QQYYETPLT	9	10	-	+	-	-	-	+	-	+	-	-
	donor2-17	4-31	6-13	2	5	2	DASSSPGWLDP	0	11	21	3-15	4	QQYNNWPPLT	10	7	-	+	-	-	-	-	-	-	-	-
	donor2-19	3-21	1-26	2	6	2	SDYIGASYYFYMDV	0	14	31	1-5	2	QQYSTYPYT	9	14							-			
	donor2-23	3-30	2-8	2	3	1	PCTGGVCYSSGLDV	0	14	9	1-39	4	QQSYSTPALS	8	7	-	+	-	-	-	-	-	+	+	-
	donor2-24	3-30	6-13	2	4	2	ETTGYSSRSFDY	1	12	7	1-39	3	QQSFTSSTT	9	12	-	-	-	-	-	-	-	-	+	-
	donor2-29	4-59	3-3	3	4	1	ERIGAATDY	1	9	26	1-39	1	QQSYITPRT	9	15	-	-	-	-	-	-	-	-	-	-
	donor2-30	1-69	3-10	3	6	3	DSNYHGSGSDYNSCCYMDV	1	19	9	1-5	1	QQYNRYST	8	5	-	-	-	-	-	-	-	-	-	-
	donor2-37	1-24	3-3	2	4	2	HNRFWRDYSRFFDY	3	14	27	3-15	4	QQYNSWPPLT	10	18	+	-	-	-	+	+	+	+	+	+
	donor2-38	1-46	4-4	2	5	1	GLSNYGWFDP	0	10	10	3-15	4	QHYNNWPLT	9	7	-	-	-	-	-	-	-	-	-	-
	donor2-39	4-15	4-17	2	4	3	DWANGDSFSPFDY	0	13	23	1-33	4	QQYDTLPT	8	17	-	-	-	-	-	-	-	-	-	-
	donor2-42	4-34	3-10	1	6	2	RAWFRESPYYYYYMDV	2	16	21	1-39	1	QQSYTTLWT	9	10	-	+	-	-	-	-	-	-	-	-
	donor2-44	3-23	3-16	1	4	2	DVARSQLGKFDC	2	12	15	1-8	1	QQYYNYPWT	9	6	-	-	-	-	-	-	-	-	-	-
	donor2-46	3-15	3-3	2	4	2	HGGYDFWSGYYDY	1	13	16	3-15	4	QQYNYWLT	8	9	-	+	c	-	+	-	-	-	-	-
CD27-IgA+	donor2-60	3-23	6-6	3	5	1	SSIAARPTWFDP	1	12	12	1-39	2	QQFYTTLPERS	11	9	-	-	-	-	-	+	-	-	-	-
	donor2-65	1-69	6-13	3	6	2	DRIAAATYLGYYYYYMDV	1	18	1	3-11	4	QQRSNWLT	8	0										
	donor2-68	4-30-4	/	/	2	1	RVSRHVYWFFDV	3	12	25	3-7	1	QQDYNLPWT	9	16										
	donor2-90	3-30	6-19	3	4	2	DVAGIAFDY	0	9	6	1-6	1	LQDYNYPWT	7	4										
	donor2-92	3-11	4-17	2	3	5	LADYGDYGDDAFDI	0	14	7															
	donor2-95	3-48	3-3	2	4	1	RHDFWGGYTY	1	10	20	3-20	1	QHYSLQT	7	10	+	-	-	+	+	+	+	+	+	+
CD27+IgA+	donor3-10	3-48	4-17	2	4	3	PDYGDYVGGLD	0	11	14	3-20	2	QQYGTSPPYT	10	6										
	donor3-12	3-23	2-15	2	4	1	GTQNYCSGATCYSLDY	0	16	20															
	donor3-18	3-23	3-22	2	4	1	RGDGASYY	1	8	21	1-27	1	QKYNGAPWT	9	11	-	-	-	-	-	-	-	-	-	-
	donor3-23	4-34	4-17	2	4	3	RLGVETTTDYFDY	1	13	9															
	donor3-25	3-30	3-9	2	2	3	AWGLLTGDYWDDWYFHF	1	17	39															
	donor3-28	3-53	2-15	2	4	1	GSGGYCSGSTCYSAFDC	0	17	42	3-15	1	QQYNNWLWT	9	25										
	donor3-32	3-30	6-13	3	4	1	VPAGTRSYIDY	1	11	21	1-37	5	QRTDSVLIS	9	17										
	donor3-35	3-23	1-26	2	2	1	GHKYCPSGSCYPYWYLDV	1	18	36	3-15	1	QQYNTWPGT	9	16	+	+	N	-	+	+	-	-	-	+
	donor3-37	4-61	5-12	1	5	3	GKIFMEWLEGFDP	0	13	8	4-1	4	QQYYGTPLT	9	5	-	-	-	+	-	-	-	+	-	+
	donor3-39	3-23	2-15	2	4	1	GTQNYCSGATCYSLDY	0	16	21	3-15	5	QQYNYFIT	8	7	-	-	-	-	-	-	-	-	-	-
	donor3-41	3-30	5-5	2	4	1	DRWGYRNGPTY	2	11	17	3-11	3	QLRTNWPPMLT	11	19										
	donor3-42	3-30	5-5	2	4	1	DRWGYRNGPTY	2	11	12	1-33	5	QHYDNFPIT	9	12										

	donor3-43	4-59	3-10	2	3	2	GSDVFDM	0	7	24															
	donor3-46	3-15	1-7	3	4	1	VQLITGTPTNYFDY	0	14	0	1-39	5	QQSYSTPLIT	10	3	-	-	-	-	-	-	-	-	-	-
	donor3-48	3-23	4-17	3	4	2	VFYADFVFIFDH	1	12	37	3-20	1	HQYFESPWT	9	32	-	-	-	-	-	-	-	-	-	-
CD27-IgA+	donor3-54	3-23	6-19	3	4	2	DRIAVAGIFDY	1	11	0	0	1	QQRSNWPPWT	10	0	-	-	-	-	-	-	-	-	+	+
	donor3-58	3-30	5-24	3	4	1	VVATVNSPFDY	0	11	10	10	3	QQYNIWPS	8	2	-	-	-	-	-	-	-	-	-	-
	donor3-59	5-51	6-19	3	4	1	HKPAVGTCFDY	1	11	11	11	4	QQYYSSPQD	9	7										
	donor3-68	4-31	3-22	2	5	3	GLYDSSGYYYEGRYFDP	1	17	13	13	5	QQRSNWIT	8	9										
	donor3-73	3-15	3-10	1	5	1	HTTLNVGLWFDS	1	12	33	33	3	QQAHTTPFT	9	18	+	-	-	+	-	+	+	+	+	+
	donor3-74	3-30	3-22	1	6	2	DRSGKSYYYYGMDV	2	14	18	18	4	QQYDYLPSFT	10	21	-	-	-	-	-	-	-	-	-	-
	donor3-78	3-7	1-26	2	5	2	DLTSGRYFGWFDS	1	13	9	9	3	QQYYSSPRT	9	9	-	-	-	-	-	-	-	-	-	-
	donor3-83	3-23	3-10	1	4	3	DKGALLWFEGFDQ	1	13	15	15	2	QQYNSYLYT	9	18	-	-	-	-	-	-	-	+	-	+
	donor3-84	1-58	2-21	2	5	1	AYCGGDCYFAS	0	11	11															
	donor3-92	4-59	3-10	2	5	2	GLYYYGDTGYPHWCFDP	1	17	21	21	1	HQYGNSPWT	9	16	+	+	-	+	-	-	+	+	+	+
	donor3-95	3-7	6-13	2	4	3	DGGSRWYGDFDY	1	12	11	11	4	QQNYNTPLT	9	11										
CD27+IgA+	donor4-01	1-69	6-6	2	4	1	DSTRGGSSSSYILGY	1	15	14	1-39	3	QQSYTIPVT	9	8	-	+	-	-	-	-	-	-	-	-
	donor4-02	3-30	2-15	3	5	4	DRAEDTILVIAVGWFDP	1	17	25	1-5	1	QQYNTYSKT	9	10	-	-	-	-	-	-	-	-	-	-
	donor4-05	1-18	3-22	2	4	1	SLGSSGYHSVNFDY	1	16	16	1-37	1	QRTYNAPPWT	10	12										
	donor4-08	3-21	3-9	2	4	2	AVGFSGYDLLTGYYDY	0	16	30	3-20	5	QQYGRSVT	4	10	-	-	-	-	-	+	-	-	-	-
	donor4-10	3-11	4-23	2	3	2	GGLWSREGWDI	1	11	20	4-1	4	QQYYETSLT	9	9	-	-	-	-	+	-	+	-	+	+
	donor4-17	3-48	4-23	2	3	3	DARDYGGKPLAFDV	2	14	9	2-28	1	MQVLQDSSNV	10	6	-	-	-	-	-	-	-	-	-	-
	donor4-18	3-48	3-3	3	3	2	DFIISGVTRPLDI	1	13	17	1D-17	1	LQHHSFPRT	9	13	+	+	c	-	-	-		-	-	-
	donor4-19	3-30-3	3-16	2	4	1	IWGTYLDY	0	8	8	3-15	3	QQYSNWRVT	9	13	-	+	-	-	-	-	-	-	-	-
	donor4-20	1-46	1-26	3	3	2	RRGGSYYRDAFDI	3	13	27	3-20	3	QQYGSSPT	8	16	-	-	-	-	-	-	-	-	-	-
	donor4-22	3-9	3-22	2	4	2	DMGRGGGSGSYYYNYFDS	1	18	24	3-11	4	QHRSNWPALS	10	14	-	+	-	-	-	-	-	-	-	-
	donor4-23	3-49	2-2	3	6	1	VPAANPNFYSGMDV	0	14	15	1-39	3	QQSYSNLFT	9	10										
	donor4-24	3-53	4-17	3	4	1	DRGPTTVTPPGVFGF	1	15	22	1-5	4	QQYNNYLLS	9	23										
	donor4-28	3-30	6-13	2	5	2	ETIIAATGLYNWFDP	0	15	13	3-20	4	QQYASYPLT	9	8	-	-	-	-	-	-	-	-	-	-
	donor4-30	3-33	2-15	2	6	2	GGYCSGTSCQYYDGMDV	0	17	13	2-28	1	MQALQTPGT	9	2	-	-	-	-	-	-	-	-	-	-
	donor4-31	4-34	3-3	1	5	4	VRRFLEWMALEENWFDP	2	17	21	3-11	2	LQRKYWPPYT	10	2	-	-	c	-	-	-	-	-	-	-
	donor4-33	1-18	2-2	2	4	1	NRGFCSSTSCYSDY	1	14	23	1-9	4	QHLNTYPP	8	12	+	+	c N	+	-	+	+	+	+	+
	donor4-35	1-18	5-5	3	5	2	GVRFHSDMVDGRGNRLDP	4	18	18	3-11	4	QQRSSWPPTT	10	13										
	donor4-36	3-48	3-3	2	6	3	GMYYDFETGMDV	0	12	17	1-39	1	QQTYNVPRT	9	24	-	-	-	-	-	-	-	-	-	-
	donor4-41	3-30	4-23	2	4	5	DLEVDGPESDYGY	0	13	31	2-30	2	MQGTHWPPLYT	11	17										
	donor4-46	4-30-4	6-19	2	5	1	TRGGGWFDP	1	9	18	4-1	2	QQYYSTPYT	9	9	-	-	-	-	-	+	-	-	-	-
	donor4-47	5a	2-15	2	4	1	GYCGGGSCYLAFDS	0	14	11	1D-12	4	QQANSFPLT	10	17	-	+	c	-	-	-	-	-	-	+
	donor4-48	3-23	/	/	6	1	HILTVGPSLVVPFGMDV	1	17	21	1-12	4	QQAYEFPVT	9	21										
IgA+	donor4-49	1-69	2-21	2	6	2	APPSRDSFYYYYAMDV	1	16	3															
	donor4-51	4-34	6-6	3	4	2	DRPFVPYYFDY	1	13	1															
	donor4-54	3-23	1-26	3	4	1	QKSGSYDY	1	8	3	1-17	1	LQHNSYPRT	9	1	-	+	-	-	-	-	-	-	-	-

	donor4-64	3-48	1-16	3	2	3	EYMITFGGVRDANWYFDL	1	18	0	1-5	1	QQYNSYPGT	9	1	-	-	-	-	-	-	-	-	-	-
	donor4-70	1-69	2-2	3	6	1	GISVVVPAAIVLGYYYYGMDV	0	21	0	2-28	2	MQALQTPGT	9	0	+	+	-	-	+	+	+	+	-	+
	donor4-71	3-72	3-16	3	3	2	EHRSQGGGGAFDI	1	13	2															
	donor4-76	3-21	5-18	1	3	4	DPGVDTGTGSTHDAFDI	1	17	18	1-39	4	QQSYSGGT	8	14	-	-	-	-	-	-	-	-	-	-
	donor4-79	1-18	2-2	2	4	2	DGFCSSASCYMPFDY	0	15	9	3-11	4	QQRTNWPPVT	10	9	-	+	-	-	-	-	-	-	-	-
	donor4-80	5-51	6-13	2	4	1	RLLAAVGRSLGPTFDY	2	16	2	1-5	1	QQYNSYST	8	1	-	-	-	-	-	-	-	-	-	-
	donor4-81	1-3	3-3	3	4	1	TRITIYGVPPAAD	1	14	19	3-11	4	HHRSDWPLT	9	19	+	+	-	+	+	+	+	+	+	+
	donor4-82	3-7	6-19	1	3	6	DGDSSGWEDYDAFDI	0	15	2	1-39	2	QQGFSTPPTT	10	6	-	-	-	-	-	-	-	-	-	-
	donor4-83										3-20	2	QQYGSSPPYT	10	7										
	donor4-87	4-4	/	/	4	1	RAPSGPFDF	1	9	29	1-39	2	QQSFSRPPT	9	21	-	-	-	-	+	-	+	-	-	-
	donor4-89	3-21	6-13	1	4	1	GGTSWSIDS	0	9	20	4-1	1	QQYYNTPRT	9	7										
	donor4-91	3-30	2-15	2	5	2	GGGYCGGESCYESGP	0	15	23	1-39	1	QQTYSTPRT	9	15	-	-	-	-	-	-	-	-	-	-
	donor4-95	1-18	4-17	2	4	4	DRTDYREPAWIDY	2	13	2	4-1	1	QQYYNTPRT	9	7										
CD27+IgA+	donor5-02	1-2	1-14	3	4	3	DLDNRVFDY	1	9	23	3-11	1	QHVTNWPPGTWT	12	13										
	donor5-03	3-33	1-26	1	4	1	GGRTVVGATTLTNFDY	1	16	23	3-20	4	QQFLISPPT	9	22	-	+	-	-	-	-	-	-	-	-
	donor5-04	3-49	3-9	2	5	3	EGEGFYEILTGYPSLTK	0	17	12	3-11	1	QQRSNRPPWT	10	7	-	-	-	-	-	-	-	-	-	-
	donor5-05	4-59	1-26	2	4	2	DRGGSFRGFDY	2	11	30	4-1	4	QQYLSAPLT	9	16	-	-	-	-	-	-	-	-	-	-
	donor5-09	3-33	6-19	2	3	2	EASLAGRPRAFDI	2	13	11	1-9	2	QHLNSYFNT	9	2	-	+	-	-	-	-	-	-	-	-
	donor5-10	3-33	3-22	3	4	1	RGITMMKNPFDY	1	12	15	1-39	1	QQSHSYPLA	9	12				-						
	donor5-14	3-15	4-23	2	4	0	RGGKTWGPY	1	9	42	3-20	2	QQYGSAPYT	9	11	+	+	-	-	-	+	-	-	-	-
	donor5-15	4-61	5-24	2	6	1	GGVAGPSTTSYNYYGLDV	0	18	11	1-9	1	QPLNSF	6	4	-	-	-	-	-	-	-	-	-	-
	donor5-19	5-51	/	/	4	2	QGDLGFQPFDY	0	11	7	1-39	1	QQSYYLPRT	9	4										
	donor5-21	3-49	4-17	2	4	2	RWGSYGDHIFDY	2	12	9	1-27	1	QKYNTAPE	8	4	-	+	c	-	-	-	-	-	-	-
	donor5-22	3-21	5-24	3	4	3	EGDYGYNSPFDL	0	12	19	3-11	2	QQRTNWPPYT	10	5	-	-	-	-	-	-	-	-	-	-
	donor5-33	3-53	3-16	2	3	3	ARDIYPGYDAFDI	1	13	6	3-11	2	LQRSTWPQYT	10	26	-	-	-	-	-	-	-	-	-	-
	donor5-34	3-23	3-22	2	4	3	ERCYYDNGGCFGVDY	1	15	7															
	donor5-35	3-23	1-26	2	4	1	KIGGQYPFDY	1	10	31	3-15	2	QHYNWWPYT	9	17	-	-	-	-	-	-	-	-	-	-
	donor5-44	1-46	3-16	3	4	2	EARGGAATLDF	1	11	11	1-39	2	QQSYSSPRT	9	10	+	+	c	+	+	+	+	+	+	+
	donor5-48	1-46	3-16	3	4	2	EARGGAATLDF	1	11	17	1-39	2	QQSYSSPRT	9	10	+	+	N	+	+	+	+	+	+	+
	donor5-49	3-21	3-22	2	4	1	HSSGYLFDY	1	9	2	3-11	2	QQRSNWPPMYT	11	2	-	+	c	-	+	+	-	-	-	+
	donor5-53	3-74	2-2	2	5	1	QKYISCYE	0	8	2	3-20	4	QQYGSSPPGLT	11	1	-	+	-	-	-	-	-	-	-	-
	donor5-60	4-39	/	/	4	2	RKHDGGGHHYFDN	4	15	37	3-20	4	HQYDNSPLT	9	33	-	+	-	-	-	-	-	-	-	-
CD27-IgA+	donor5-62	1-2	3-16	2	6	4	GDISSGYLDYDWGNYRLNYYGMDV	1	24	3	2-28	4	MQALQTPST	10	1	-	-	-	-	nd	nd	-	-	-	-
	donor5-63	3-23	5-5	2	4	4	GDEYSDYFDY	0	10	3	1-13	2	QQFNSYPYT	9	10	+	+	-	-	-	-	-	-	+	+
	donor5-66	1-69	5-24	3	4	1	DGVY	0	4	24	1-5	2	QQYSSFYT	10	14	+	+	-	+	+	+	+	+	+	+
	donor5-67	3-7	3-3	2	4	1	DSFWSGLH	1	8	5	1-5	2	QQYNSYPYT	9	0	+	-	-	+	+	+	+	+	+	+
	donor5-69	3-11	/	/	4	1	VNSSDVLFHY	1	10	7	3-11	2	QQRSNWPLYT	10	2	-	-	-	-			-	-	-	-
	donor5-71	3-15	3-22	2	4	3	AWEYYDSSGYYYEPLPY	0	17	5	3-20	4	QQYGSSPLT	9	4	-	-	-	-	-	-	-	-	-	+
	donor5-72	3-33	6-19	2	3	3	DHASGWYAEAFDI	1	13	12															
	donor5-75	3-48	6-13	1	3	1	GRSGYSSSFFDI	1	12	7	3-20	4	QQYGSSPGLS	10	2	-	-	-	-	-	-	-	-	-	-

	donor5-76	1-2	1-14	3	4	3	DLDNRVFDY	1	9	21															
	donor5-77	4-4	2-15	2	6	1	CGGSGGSCLHYGMDV	1	15	0	1-39	1	QQSYSTPRT	9	1	-	-	-	-	-	-	-	-	-	-
	donor5-81	3-23	5-24	3	4	3	GRDRYAFFDD	2	10	10	3-20	1	QQYGSSLWT	9	3	-	-	-	-	-	-	-	-	-	-
	donor5-86	4-39	6-19	1	5	2	TPESSGWHPAGSGWFDP	1	17	18	1-16	4	QQYNSYPLT	9	12	-	-	-	-	-	-	-	-	-	-

		VH	DH	RF	JH	(-)	CDR3 (aa)	(+)	Length	No of SHM	Vλ	Jλ	CDR3 (aa)	Length	No of SHM	Poly	Hep2	IFA	flagellin	*B.fragilis*	*C.difficile*	*E.cloacae*	*E.faecalis*	*S.aureus*	*E.coli*
CD27+IgA+	donor1-02	3-53	/	/	6	1	KGRTSCPYGMDV	2	12	31	2-14	1	SSYTSRNTFV	10	21	+	+	N	-	-	-	-	-	+	-
	donor1-03	4-4	3-3	1	5	1	SSTFLGVTGWSDP	0	13	24	1-40	1	QSYDSGLSGYV	11	14	-	-	-	-	-	-	-	-	-	-
	donor1-07	3-13	5-12	2	4	2	VRYDHGYDL	2	9	22	3-25	2	QSGDSETTV	9	36	-	-	-	-	-	-	-	-	-	-
	donor1-20	3-74	1-26	3	3	1	LRVGAAIPHGFDL	2	13	31	2-23	1	CSYTGDTNIYV	11	22										
	donor1-23	4-39	2-8	2	4	2	NIEGYCSNGVCYAADY	0	16	25															
	donor1-24	3-74	2-8	2	3	2	ARDFGAVGSTNAFDI	1	13	16	2-8	1	SSYAGSYIYV	10	13	+	-	-	-	-	-	-	-	-	-
	donor1-26	3-30	/	/	6	2	DRISPSGPKIVYVYYYMDV	2	19	37															
	donor1-30	5-51	2-21	2	6	1	SYCASTSCQTRGYFGMDV	1	18	14	1-40	2	QSFDSSLNAVV	11	8	-	-	-	-	-	-	-	-	-	-
	donor1-32	3-30	2-15	3	4	2	EPIVVVGVPTFYFDY	0	15	23	2-23	1	CSYATGNRYV	10	14	-	-	-	-	-	-	-	-	-	-
	donor1-36										1-51	7	ATWDSSLNIVV	11	27										
	donor1-40	3-23	4-17	3	4	1	HSSTMTTNFDS	1	11	14	3-21	3	QVWDTSSNHPL	9	15										
	donor1-44	4-39	3-22	3	5	0	QPITMMVVV	0	9	10	2-14	1	SSYTSSSTL	9	8	-	+	-	-	-	-	-	-	-	-
CD27-IgA+	donor1-53	3-33	3-10	3	6	2	SGDVVRGGPPGYYYPMDV	1	18	16															
	donor1-56	3-48	4-17	2	3	4	DVQKYNDGDAFDV	1	13	34	1-40	1	QSYDGSLNIYV	11	18	-	-	-	-	-	-	-	-	-	-
	donor1-66	3-33	/	/	5	2	EALGFDP	0	7	0	3-1	2	QAWDSSFVV	9	0	-	+	-	-	-	-	-	-	-	-
	donor1-68	1-2	4-4	3	4	3	DSRDMTTLDY	1	10	0	3-1	2	QAWDSSFVV	9	0	-	+	-	-	-	-	-	-	-	-
	donor1-69	1-46	2-21	1	2	2	DRNILWWQGSFDL	1	13	17	2-14	2	SSYTSSSTVV	10	2	+	+	-	+	+	+	+	+	+	+
	donor1-73	3-48	1-7	2	4	2	DWWNWNSDN	0	9	10	1-51	3	GTWDSSLSAGV	11	6	-	-	-	-	-	-	-	-	-	-
	donor1-76	1-46	2-2	2	4	3	YCSSTSCYKGYSDSNDPFDQ	1	20	32	2-14	2	SSFTNRNPPLGE	12	33										
	donor1-84	3-9	5-12	3	4	1	ARIVATITGVNYYFDS	1	16	16	1-51	2	GTWDDSLSVVV	11	17	-	-	-	-	nd	nd	-	-	-	-
	donor1-88	3-23	2-21	2	4	2	DLLAYWTNPDY	0	11	24	1-44	1	GTRDDSGRYF	10	16	-	-	-	-	-	-	-	-	-	-
	donor1-90	3-23	/	/	4	2	SGVLGPETVATIFVDY	0	16	0	3-1	2	QAWDSSTVV	9	0	-	-	-	-	-	-	-	-	-	-
	donor1-92	4-4	3-10	2	4	2	DHRGSGACDY	1	10	0	1-44	1	AWDDSLNGPY	10	0	-	+	-	-	+	-	-	-	-	-
	donor1-96	3-23	/	/	4	2	IPDRAGYFDS	1	10	0	3-1	3	QAWDSSTWV	9	0										
CD27+IgA+	donor2-08	3-74	6-6	2	4	1	SSYPYYFDH	1	9	23	2-8	2	SSNAGSDNFVV	11	10										
	donor2-10	3-64	3-3	3	4	1	FGVYYFDY	0	8	14	2-11	1	CSYAGSYTYV	10	6	+	+	-	+	+	+	+	+	+	+
	donor2-11	4-34	4-17	2	3	5	ITWDGEMSDDFDV	0	13	31	7-46	3	LLSFGGARV	9	15	-	-	-	-	-	-	+	-	-	-
	donor2-16	3-21	5-24	3	6	1	PSTIHYFYHMDV	2	12	15	2-8	3	SSYAGSNNLV	10	7	-	-	-	-	+	+	+	+	-	-
	donor2-20	3-33	5-24	2	4	2	DDGITVPAH	1	9	36	2-14	1	SSYTISSTSI	10	19	-	-	-	-	-	-	-	-	-	-
	donor2-22	3-33	2-15	2	4	2	DCSGGSCYSADY	0	12	16	2-23	3	CSYAGSEAFWI	11	21	-	+	-	-	-	+	-	+	-	+
	donor2-43	3-23	1-26	3	6	2	VGAVVLTYPPMEYMDV	0	16	19	1-47	2	ATWDDSLRGVV	11	16										
	donor2-45	3-33	3-3	2	5	2	ERSGNGGNWFDP	1	12	20	1-40	2	QSYDSRLRGVV	11	19	+	-	-	-	-	-	-	-	-	-
+	donor2-49	1-2	4-17	2	4	2	YYCARGGAGDFDF	1	13	32	1-44	2	ATWDDSLNGVV	11	21	-	-	-	-	-	+	-	-	-	-

	donor2-58	3-30	3-10	3	4	1	AQGITIVQPFDC	0	12	12	2-14	2	SSYTSSSTMI	10	9	-	+	-	-	-	-	+	+	-	+
	donor2-64	3-30-3	3-3	2	4	2	QGIVFDFWSRFFVDH	2	15	32	1-51	3	GTWDSSLSAGM	11	17	+	+	-	+	+	+	+	+	+	+
	donor2-65	1-69	6-13	3	6	2	DRIAAATYLGYYYYYMDV	1	18	1	3-1	2	QAWDSSVVV	9	0	+	+	-	-	+	+	+	+	+	+
	donor2-70	1-2	4-17	2	5	2	ADYGDYPNF	0	9	7															
	donor2-82	3-33	/	/	4	1	RSRIGGTFYFDY	2	12	9	1-40	3	QSYDSSLSGWV	11	4	-	-	-	-	-	-	-	-	-	-
	donor2-88	3-30-3	4-23	3	4	3	VGEPTVDPLFDY	0	12	1	3-1	2	QAWDSGTVV	9	5	-	-	-	-	-	-	-	-	-	-
	donor2-91										2-11	1	CSYAGSYYV	9	5										
	donor2-92	3-11	4-17	2	3	5	LADYGDYGDDAFDI	0	14	7	1-40	1	QSYDSSLSGYV	11	9	-	-	-	-	-	-	-	-	-	-
CD27+IgA+	donor3-14	3-23	3-9	1	4	2	VGPYFDILTAYDY	0	13	14															
	donor3-23	4-34	4-17	2	4	3	RLGVETTTDYFDY	1	13	9	1-51	3	GAWDSSLSAGV	11	12	-	-	-	-	-	-	+	-	+	+
	donor3-32	3-30	6-13	3	4	1	VPAGTRSYIDY	1	11	21	1-40	2	QSFDSSLSGHVL	12	8	-	-	-	-	-	-	-	-	-	-
	donor3-33	5-51	6-19	2	6	2	QGNSYWYLGADFGLDV	0	16	17	2-8	1	SSYAGSYTYV	10	13	+	+	-	+	+	+	+	+	+	+
	donor3-44	1-46	3-10	2	4	2	ARETTMVTWDY	1	11	12	2-14	1	SSYTSSNSYV	10	10	-	-	-	-	-	-	-	-	-	-
CD27-IgA+	donor3-66	5-51	5-24	2	5	1	WGGYPVAPMKNFFDL	1	15	15	2-14	2	TSYSSSYTHVV	11	12	-	-	-	-	-	-	-	-	-	-
	donor3-67	4-59	4-17	1	5	2	HSTYREVRFDP	2	11	6	2-8	2	SSYAGSKNLV	10	9	-	-	-	-	-	-	-	-	-	-
	donor3-71	1-46	6-19	2	5	3	DAPRSSAWYTLPEHSPWLDT	2	20	23	2-11	2	ISYAGGYIFV	10	31	+	-	-	+	+	+	+	+	+	+
CD27+IgA+	donor4-13	3-48	4-23	2	4	1	SSPLAGNSYQVDY	0	13	23	1-51	2	GAWDSLLSAGA	11	25										
	donor4-14	3-23	1-26	2	4	1	GRYSGSYYLQTDS	1	13	31	1-44	2	AAWDNRPNAAV	11	10	-	-	-	-	-	-	-	-	-	-
	donor4-34	3-74	2-21	2	4	3	DLEQCTGDCLLF	0	12	27	2-8	1	SSYVGSSKNYV	11	17	-	-	-	-	-	-	-	-	-	-
	donor4-44	3-30	3-22	2	4	2	ALYYYDSSGYPPDY	0	14	18	2-18	1	SSYTASGTNV	10	19	+	+	-	-	+	-	-	+	-	-
	donor4-50	3-7	5-18	3	4	2	VRGYSFGDVVDY	1	12	15	3-21	1	QVWDISNAHATV	12	6										
CD27-IgA+	donor4-59	3-21	2-8	2	4	2	DQGWLWPKPDY	1	11	0	1-44	2	AAWDDSLNGLE	11	0	+	+	-	+	+	-	+	+	-	-
	donor4-60	3-33	3-10	2	4	2	DQYFSGSGYNFDY	0	13	19	2-11	3	CSYAGSYTLL	10	13	-	-	-	-	-	-	-	-	-	-
	donor4-67	3-21	3-10	2	3	1	INYNAFDI	0	8	6	2-23	3	CSYAGSSTLGV	11	7	-	-	-	-	-	-	-	-	-	-
	donor4-71	3-72	3-16	3	3	2	EHRSQGGGGAFDI	2	13	2	3-1	1	QAWDSSTYYV	10	3	-	-	-	-	-	-	-	-	-	-
	donor4-73	3-30	3-16	3	4	1	GMLTFGGVLTPQVYYFDF	0	18	15	1-44	2	ATWDGSLNGPV	11	7	+	-	-	-	-	-	-	-	-	+
	donor4-74	3-15	1-26	3	4	1	SGSYFFRLDS	1	10	17	2-14	2	SSYTSSSTLV	10	5	+	-	-	-	-	+	+	+	-	+
	donor4-75	3-7	2-8	3	4	2	DMGLHGVSDY	1	10	15	3-21	3	HVWDGSSEHRV	11	16	-	-	-	-	-	-	-	-	-	-
	donor4-76	3-21	5-18	1	3	4	DPGVDTGTGSTHDAFDI	1	17	18	3-27	3	YSAADNSLGV	10	2										
	donor4-77	4-4	4-17	2	6	3	RLDGDYYYGMDV	1	12	4	3-1	2	QAWDSSTVV	9	4	-	-	-	-	-	-	-	-	-	-
	donor4-85	5-51	3-22	2	4	3	LGDYDSSGTLRD	1	12	3	2-14	2	SSYTSSSTLVV	11	6										
	donor4-86	4-59	4-17	3	4	1	ASTFTVTGDY	0	10	15	2-14	3	NSYTSTSSLV	10	8	-	-	-	-	+	-	-	-	-	-
	donor4-89	3-21	6-13	1	4	1	GGTSWSIDS	0	9	20	6-57	3	QSYDSRVRV	9	24	+	-	-	+	+	-	-	-	-	+
	donor4-92	3-49	3-10	3	4	3	DLMGEGFDY	0	9	10	1-47	3	AAWYDSLSGW	11	3	-	-	-	-	-	-	-	-	-	-

													V												
	donor4-93	4-61	1-7	1	6	2	DRVITGTTVAMDV	1	13	7	1-44	3	AAWDDSLNGHWV	12	4	-	+	-	-	-	-	-	-	-	-
CD27+IgA+	donor5-12	4b	3-22	2	4	2	GATYDSSGFRYLPIEY	1	16	15	2-14	2	SSYTGASTLHVV	12	17	-	-	-	-	-	-	-	-	-	-
	donor5-17	3-7	6-19	1	5	1	LGGSGWSLDH	1	10	13	2-14	2	NSFSSSSTLLV	11	11										
	donor5-24	3-53	6-13	2	6	1	HGIATAGTPFYYGMDV	1	16	7	3-21	2	CQVWDINSEAVF	10	18	-	-	-	-	-	-	-	-	-	-
	donor5-27	3-33	3-22	2	3	1	DPPYSGYAFHI	1	11	16	1-44	2	AAWDESLNVVA	11	15	-	+	-	-	-	-	-	-	-	-
	donor5-32										2-8	1	CSYAGTNSFV	10	19										
	donor5-34	3-23	3-22	2	4	3	ERCYYDNGGCFGVDY	1	15	7	7-46	3	LLSYSGVWV	10	11	-	-	-	-	-	-	-	-	-	-
	donor5-40	5-51	1-26	3	5	2	QRVELRYSGTYVVLPQFDP	2	19	32	2-14	2	TSSTRDTVPVVV	12	19										
	donor5-42	3-15	7-27	2	6	0	KYLGV	1	5	0	2-14	2	SSYTSSSTLV	10	2	-	+	-	-	-	-	-	-	-	-
	donor5-47	3-48	5-5	3	4	2	GGRTSVDNTDY	1	11	20															
CD27-IgA+	donor5-50	3-11	6-19	1	4	2	GEGGPSSGWYPFPFDY	0	16	6	1-47	3	AAWDDSLSGLRV	12	3										
	donor5-61	3-23	/	/	4	0	FPY	0	3	2	1-40	2	QSYDSSLSGYVV	12	5	-	-	-	-	-	-	-	-	-	-
	donor5-64	3-48	6-19	3	4	1	VQWLVLGPFDY	0	11	0						-	-	-	-	-	-	-	-	-	-
	donor5-65	1-8	5-5	2	4	1	SRRGYSYVDF	0	10	5	1-51	3	GTWDSRLTAGWV	12	11										
	donor5-87	3-73	2-2	3	6	1	VVPATILSGMDV	0	12	7	3-25	3	QSADGSGPWV	10	8										

RF, reading frame; -, non-reactive; +, reactive; c, cytoplasmic staining; nd, not determined

SUPPLEMENTAL TABLE III. Targeting and selection of individual mutations in rearranged *IGHV*.

	total sequences		cloned antibodies					
	CD27$^+$IgA$^+$ (126)	CD27$^-$IgA$^+$ (109)	CD27$^+$IgA$^+$ (88)	CD27$^-$IgA$^+$ (75)	polyreactive (33)	non-polyreactive (130)	autoreactive (52)	non-autoreactive (111)
RGYW (%)	564.2/2647 (21.3)	**339.5/1399 (24.3)***	363.8/1691 (21.5)	234.2/955 (24.5)	137.8/611 (22.6)	455.5/2039 (22.3)	186.4/851 (21.9)	406.9/1799 (22.6)
WRCY (%)	379.1/2647 (14.3)	191.2/1399 (13.7)	235.4/1691 (13.9)	131.4/955 (13.8)	82.2/611 (13.4)	287.0/2039 (14.1)	125.6/851 (14.8)	243.6/1799 (13.5)
WA (%)	355.3/2647 (13.4)	199.7/1399 (14.3)	232.5/1691 (13.7)	135.4/955 (14.2)	76.4/611 (12.5)	298.8/2039 (14.7)	109.6/851 (12.9)	265.7/1799 (14.8)
TW (%)	216.3/2647 (8.2)	94.7/1399 (6.8)	142.3/1691 (8.4)	67.9/955 (7.1)	55.6/611 (9.1)	155.7/2039 (7.6)	64.4/851 (7.6)	145.8/1799 (8.1)
Transitions (%)	1339/2647 (50.6)	744/1399 (53.2)	856/1691 (50.6)	520/955 (54.5)	329/611 (53.8)	1050/2039 (51.5)	431/851 (50.6)	948/1799 (52.7)
Transversions (%)	1308/2647 (49.4)	655/1399 (46.8)	835/1691 (49.4)	435/955 (45.5)	282/611 (46.2)	989/2039 (48.5)	420/851 (49.4)	851/1799 (47.3)
FR R/S (ratio)	1109/649 (1.7)	585/349 (1.7)	684/421 (1.6)	390/245 (1.6)	227/170 (1.3)	**845/503 (1.7)***	357/215 (1.7)	715/458 (1.6)
CDR R/S (ratio)	683/206 (3.3)	360/103 (3.5)	445/141 (3.2)	246/72 (3.4)	159/55 (2.9)	532/157 (3.4)	200/77 (2.6)	**491/135 (3.6)***

FR indicates framework region; CDR, complementarity determining region; R/S is the ratio between replacement (R) and silent mutations (S); The number of analyzed sequences is indicated in the brackets next to the population name.

All analyses were performed with the JoinSolver program and the differences between each analyzed population as compared with centrocytes were statistically analyzed with the X^2 test. Significant differences between CD27$^+$IgA$^+$ and CD27$^-$IgA$^+$ B cells, polyreactive and non-polyreactive B cells and autoreactive and non-autoreactive B cells are depicted in bold. *, $p<0.05$