

Table S1. Details of the NGS assay. For each gene, two pairs of complementary sequences over the ligation joints were determined *in silico* containing 10-11 nucleotides of the gene (flanked with [start](#) and [stop](#) codon) and plasmid specific sequences. The joints are named with V, vector; G, gene fragment; F, forward; and R, reverse, indicating the directions. The joint-read totals for each gene and their percentages of total joint-reads were calculated. These were then used to calculate the plasmid DNA ligation mixture abundance ratios.

Pool	Gene	Joint	Joint Sequence	Pooled ligation mixture			Pooled plasmid DNA			Plasmid/ligation ratio
				N joint-reads	Gene total	Gene %	N joint-reads	Gene total	Gene %	
1	g002	VGF	ATGCCTGCAGGCGGCCGCATGATAATAA	0			0			
		VGR	TTATTATCATGCGGCCGCCTGCAGGCAT	0			23			
		GVF	AATTCTTAGGCTAGCTCTAGAGGATC	0			0			
		GVR	GATCCTCTAGAGCTAGCCTATAAGAATT	0	0	0.0000	0	23	0.0036	-
	g003	VGF	ATGCCTGCAGGCGGCCGCATGATTGATA	1730			18305			
		VGR	TATCAATCATGCGGCCGCCTGCAGGCAT	16			14114			
		GVF	AGATATTTTAAAGCTAGCTCTAGAGGATC	118			16608			
		GVR	GATCCTCTAGAGCTAGCTTAAAAATATCT	2206	4070	9.7964	16031	65058	10.0636	1.0273
	g005	VGF	ATGCCTGCAGGCGGCCGCATGATAGAAA	2011			13464			
		VGR	TTTCTATCATGCGGCCGCCTGCAGGCAT	24			10057			
		GVF	TAGATTATTAGGCTAGCTCTAGAGGATC	88			11375			
		GVR	GATCCTCTAGAGCTAGCCTAATAATCTA	2170	4293	10.3331	12502	47398	7.3318	0.7095
	g006	VGF	ATGCCTGCAGGCGGCCGCATGATAGAGA	1443			14081			
		VGR	TCTCTATCATGCGGCCGCCTGCAGGCAT	9			11108			
		GVF	AGGAGATGTAAAGCTAGCTCTAGAGGATC	153			13754			
		GVR	GATCCTCTAGAGCTAGCTTACATCTCCT	1969	3574	8.6025	14576	53519	8.2787	0.9624
	g008	VGF	ATGCCTGCAGGCGGCCGCATGGTTACTT	342			1058			
		VGR	AAGTAACCATGCGGCCGCCTGCAGGCAT	380			948			
		GVF	ACGTAGGATAGGGTACCGAGCTCGAATT	1619			1205			
		GVR	AATTCGAGCTCGGTACCTATCCTACGT	2805	5146	12.3863	1014	4225	0.6535	0.0528
	g009	VGF	ATGCCTGCAGGCGGCCGCATGATAGTTA	1984			19842			
		VGR	TAACTATCATGCGGCCGCCTGCAGGCAT	12			15330			
		GVF	GCGGGGATTGAAGCTAGCTCTAGAGGATC	117			16929			
		GVR	GATCCTCTAGAGCTAGCTCAATCCCCGC	2452	4565	10.9878	20046	72147	11.1601	1.0157
	g010c	VGF	ATGCCTGCAGGCGGCCGCATGAAAATAA	1380			17371			
		VGR	TTATTTTCATGCGGCCGCCTGCAGGCAT	5			13694			
		GVF	ATATTCTATAAGCTAGCTCTAGAGGATC	52	2864	6.8936	15546	62033	9.5957	1.3920

	GVR	GATCCTCTAGAGCTAGC TTA TAGAATAT	1427			15422			
<i>g012</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GACAAACA	1994			18602			
	VGR	TGTTTGT CAT GCGGCCGCCTGCAGGCAT	11			10041			
	GVF	TTAAGAAT TAA GCTAGCTCTAGAGGATC	125			16569			
	GVR	GATCCTCTAGAGCTAGC TTA ATTCTTAA	2100	4230	10.1815	15189	60401	9.3432	0.9177
<i>g013</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GATATTAG	893			14591			
	VGR	CTAATAT CAT GCGGCCGCCTGCAGGCAT	8			11736			
	GVF	AAACTAA TAA GCTAGCTCTAGAGGATC	91			12334			
	GVR	GATCCTCTAGAGCTAGC TTA TTTAGTTT	1043	2035	4.8982	12546	51207	7.9210	1.6171
<i>g017</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GAAAAATGT	1640			11934			
	VGR	ACATTTT CAT GCGGCCGCCTGCAGGCAT	11			8705			
	GVF	TCAGACAT TGA GCTAGCTCTAGAGGATC	58			10723			
	GVR	GATCCTCTAGAGCTAGC TCA ATGTCTGA	1797	3506	8.4388	11823	43185	6.6801	0.7916
<i>g018</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GAACAGAT	0			0			
	VGR	ATCTGTT CAT GCGGCCGCCTGCAGGCAT	0			0			
	GVF	AATACGCA TAA GCTAGCTCTAGAGGATC	0			0			
	GVR	GATCCTCTAGAGCTAGC TTA TGCGTATT	0	0	0.0000	0	0	0.0000	-
<i>g020</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GATTACAA	183			13515			
	VGR	TTGTAAT CAT GCGGCCGCCTGCAGGCAT	15			11481			
	GVF	AAACTGTT TAA GCTAGCTCTAGAGGATC	48			14301			
	GVR	GATCCTCTAGAGCTAGC TTA AACAGTTT	307	553	1.3311	12171	51468	7.9614	5.9813
<i>g021</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GACAAATA	1264			7618			
	VGR	TATTTGT CAT GCGGCCGCCTGCAGGCAT	7			4485			
	GVF	TGGCACTG TAG GCTAGCTCTAGAGGATC	143			5766			
	GVR	GATCCTCTAGAGCTAGC CTA CAGTGCCA	895	2309	5.5577	6800	24669	3.8160	0.6866
<i>g022</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GTTGAAGA	170			13327			
	VGR	TCTTCAA CAT GCGGCCGCCTGCAGGCAT	9			12253			
	GVF	AAGAAATG TAA GCTAGCTCTAGAGGATC	120			14251			
	GVR	GATCCTCTAGAGCTAGC TTA CATTCTT	473	772	1.8582	13093	52924	8.1866	4.4057
<i>g024</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GAACATTA	1510			5473			
	VGR	TAATGTT CAT GCGGCCGCCTGCAGGCAT	9			4309			
	GVF	TAGGGAGG TAG GCTAGCTCTAGAGGATC	63			5354			
	GVR	GATCCTCTAGAGCTAGC CTA CTCCCTA	1491	3073	7.3966	5106	20242	3.1312	0.4233
<i>g026</i>	VGF	ATGCCTGCAGGCGGCCGC CAT GATGAACA	144			9578			
	VGR	TGTT CAT GCGGCCGCCTGCAGGCAT	2	556	1.3383	8994	37971	5.8736	4.3889

		GVF	GAATATTTTAA GCTAGCTCTAGAGGATC	97				11175			
		GVR	GATCCTCTAGAGCTAGCTTAAAAATATTC	313				8224			
	Total			41546				646470			
2		VGF	ATGCCTGCAGGCGGCCGCGCATGAAACTAT	299				5930			
	g027c	VGR	ATAGTTTCATGCGGCCGCGCTGCAGGCAT	2				6819			
		GVF	ATAATACC TAA GCTAGCTCTAGAGGATC	357				7588			
		GVR	GATCCTCTAGAGCTAGCTTA GGTATTAT	845	1503	5.3108		5288	25625	5.4160	1.0198
		VGF	ATGCCTGCAGGCGGCCGCGCATGAACAAAAG	921				8265			
	g028c	VGR	CTTTGTT CATGCGGCCGCGCTGCAGGCAT	2				9143			
		GVF	AGAATAAG TAA GCTAGCTCTAGAGGATC	122				10759			
		GVR	GATCCTCTAGAGCTAGCTTA CTTATTCT	1032	2077	7.3390		8548	36715	7.7599	1.0574
		VGF	ATGCCTGCAGGCGGCCGCGATGGGATTAG	747				4673			
	g029c	VGR	CTAATCC CATGCGGCCGCGCTGCAGGCAT	3				5114			
		GVF	TAAATGTA TAA GCTAGCTCTAGAGGATC	89				5773			
		GVR	GATCCTCTAGAGCTAGCTTA TATACATTTA	981	1820	6.4309		4046	19606	4.1438	0.6444
		VGF	ATGCCTGCAGGCGGCCGCGATGGAAAATT	867				4584			
	g030c	VGR	AATTTTC CATGCGGCCGCGCTGCAGGCAT	7				5282			
		GVF	AGGAAAAA TAA GCTAGCTCTAGAGGATC	85				6289			
		GVR	GATCCTCTAGAGCTAGCTTA TTTTTCCT	975	1934	6.8337		4678	20833	4.4032	0.6443
		VGF	ATGCCTGCAGGCGGCCGCGATGAGATATG	568				3391			
	g031c	VGR	CATATCT CATGCGGCCGCGCTGCAGGCAT	3				3936			
		GVF	AATCACAA TGA GCTAGCTCTAGAGGATC	103				4924			
		GVR	GATCCTCTAGAGCTAGCTCA TTGTGATT	1170	1844	6.5157		3363	15614	3.3001	0.5065
		VGF	ATGCCTGCAGGCGGCCGCGATGAATATCA	878				11930			
	g033c	VGR	TGATATT CATGCGGCCGCGCTGCAGGCAT	3				11898			
		GVF	AAGATGAA TAA GCTAGCTCTAGAGGATC	76				16237			
		GVR	GATCCTCTAGAGCTAGCTTA TTCATCTT	794	1751	6.1871		9566	49631	10.4898	1.6954
		VGF	ATGCCTGCAGGCGGCCGCGATGGATAAGA	703				6452			
	g034c	VGR	TCTTATCCATGCGGCCGCGCTGCAGGCAT	3				6920			
		GVF	TATTAATA TAA GCTAGCTCTAGAGGATC	441				8702			
		GVR	GATCCTCTAGAGCTAGCTTA TATTAATA	891	2038	7.2012		5370	27444	5.8005	0.8055
		VGF	ATGCCTGCAGGCGGCCGCGATGGAAAAAA	1086				9984			
	g039c	VGR	TTTTTTC CATGCGGCCGCGCTGCAGGCAT	5				11647			
		GVF	AATTAAC TGA GCTAGCTCTAGAGGATC	55				15136			
		GVR	GATCCTCTAGAGCTAGCTCA AGTTAATT	1104	2250	7.9502		8761	45528	9.6226	1.2104

g040c	VGF	ATGCCTGCAGGCGGCCGCATGAAAAATA	296				7810			
	VGR	TATTTTTT CAT GCGGCCGCCTGCAGGCAT	1				10260			
	GVF	TTTGGGAG TAA GCTAGCTCTAGAGGATC	99				12182			
	GVR	GATCCTCTAGAGCTAGC TTA CTCCCAA	653	1049	3.7066		7974	38226	8.0793	2.1797
g042c	VGF	ATGCCTGCAGGCGGCCGCATGAACTTAG	1160				7959			
	VGR	CTAAGTT CAT GCGGCCGCCTGCAGGCAT	3				9039			
	GVF	ATGAGAGA TAA GCTAGCTCTAGAGGATC	43				11325			
	GVR	GATCCTCTAGAGCTAGC TTA TCTCTCAT	1901	3107	10.9784		8065	36388	7.6908	0.7005
g043c	VGF	ATGCCTGCAGGCGGCCGCATGGACTTTT	353				5639			
	VGR	AAAAGTC CAT GCGGCCGCCTGCAGGCAT	3				6674			
	GVF	ATGGTTAT TAA GCTAGCTCTAGAGGATC	117				8861			
	GVR	GATCCTCTAGAGCTAGC TTA AATAACCAT	926	1399	4.9433		4945	26119	5.5204	1.1167
g044c	VGF	ATGCCTGCAGGCGGCCGCATGTTTAAAA	761				4666			
	VGR	TTTTTAA CAT GCGGCCGCCTGCAGGCAT	4				5404			
	GVF	AGGATGAG TAA GCTAGCTCTAGAGGATC	100				6231			
	GVR	GATCCTCTAGAGCTAGC TTA CTCATCCT	1044	1909	6.7453		5080	21381	4.5190	0.6699
g045c	VGF	ATGCCTGCAGGCGGCCGCATGGAAAAAG	79				7532			
	VGR	CTTTTT CAT GCGGCCGCCTGCAGGCAT	3				8772			
	GVF	ATGCTAA TAA GCTAGCTCTAGAGGATC	71				10313			
	GVR	GATCCTCTAGAGCTAGC TTA TTTAGCAT	323	476	1.6819		7217	33834	7.1510	4.2517
g046c	VGF	ATGCCTGCAGGCGGCCGCATGGCAAATG	619				4333			
	VGR	CATTTGCC CAT GCGGCCGCCTGCAGGCAT	3				5196			
	GVF	AAGACCTA TGA GCTAGCTCTAGAGGATC	716				5626			
	GVR	GATCCTCTAGAGCTAGC TCA TAGGTCTT	728	2066	7.3001		4359	19514	4.1244	0.5650
g053c	VGF	ATGCCTGCAGGCGGCCGC GTG TCTAAAA	864				5144			
	VGR	TTTTAGAC CAC GCGGCCGCCTGCAGGCAT	5				6568			
	GVF	TGTATTTT TAA GCTAGCTCTAGAGGATC	84				6527			
	GVR	GATCCTCTAGAGCTAGC TTA AAAAATACA	1399	2352	8.3107		4628	22867	4.8331	0.5816
g056c	VGF	ATGCCTGCAGGCGGCCGCATGGAAAAAT	150				7190			
	VGR	ATTTTT CAT GCGGCCGCCTGCAGGCAT	2				9591			
	GVF	ATATAGAA TAA GCTAGCTCTAGAGGATC	174				10619			
	GVR	GATCCTCTAGAGCTAGC TTA TTCTATAT	400	726	2.5653		6410	33810	7.1460	2.7856
Total			28301				473135			
3	g061c	VGF	ATGCCTGCAGGCGGCCGCATGGATAAATT	1559			14144			
VGR		AATTAT CCAT GCGGCCGCCTGCAGGCAT	16	3121	14.0371		10584	48959	9.5298	0.6789

	GVF	CAAGGAGG TAGGCTAGC TCTAGAGGATC	208			12048			
	GVR	GATCCTCTAGAG GCTAGCCTA CCTCCTTG	1338			12183			
<i>g062c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGGTAAATA	779			5			
	VGR	TATTTAC CATGCGGCCGC CTGCAGGCAT	1000			0			
	GVF	AAGATGGA TAA GGTACCAGCTCGAATT	0			2			
	GVR	AATTCGAGCTC GGTACC TTATCCATCTT	0	1779	8.0013	0	7	0.0014	0.0002
<i>g065c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGAATTATT	412			14899			
	VGR	AATAATT CATGCGGCCGC CTGCAGGCAT	4			14530			
	GVF	AGGATAAT TAA GCTAGCTCTAGAGGATC	81			15130			
	GVR	GATCCTCTAGAG GCTAGC TTAATTATCCT	654	1151	5.1768	13964	58523	11.3914	2.2005
<i>g069c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGAAAAAAG	126			10685			
	VGR	CTTTTTT CATGCGGCCGC CTGCAGGCAT	12			11462			
	GVF	ATGCAGGA TAGGCTAGC TCTAGAGGATC	60			12853			
	GVR	GATCCTCTAGAG GCTAGC CTATCCTGCAT	334	532	2.3927	10922	45922	8.9386	3.7357
<i>g072c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGAATAAAT	400			9677			
	VGR	ATTTATT CATGCGGCCGC CTGCAGGCAT	15			9153			
	GVF	AGGAGAAA TAA GCTAGCTCTAGAGGATC	611			10772			
	GVR	GATCCTCTAGAG GCTAGC TTATTTCTCCT	440	1466	6.5935	9529	39131	7.6168	1.1552
<i>g075c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGGCACTAC	494			7644			
	VGR	GTAGTG CATGCGGCCGC CTGCAGGCAT	5			6296			
	GVF	GAGAAAT GTAAGCTAGC TCTAGAGGATC	226	27		7114			
	GVR	GATCCTCTAGAG GCTAGC TTACATTCTC	1984		12.1840	6379	27433	5.3398	0.4383
<i>g078c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGGCATCAG	45			2562			
	VGR	CTGATGC CATGCGGCCGC CTGCAGGCAT	0			2299			
	GVF	TTAATGAG TAA GCTAGCTCTAGAGGATC	160	4		2929			
	GVR	GATCCTCTAGAG GCTAGC TTACTCATTAA	276		2.1634	2319	10109	1.9677	0.9096
<i>g079c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGAAAAGAC	128			3063			
	VGR	GTCTTTT CATGCGGCCGC CTGCAGGCAT	2			2689			
	GVF	AAGATAAC TAA GCTAGCTCTAGAGGATC	60			3836			
	GVR	GATCCTCTAGAG GCTAGC TTAGTTATCTT	572	2	3.4272	3156	12744	2.4806	0.7238
<i>g080c</i>	VGF	ATGCCTGCAG GCGGCCGC ATGTCAAAAC	64			4665			
	VGR	GTTTTGA CATGCGGCCGC CTGCAGGCAT	2			4205			
	GVF	TAGTATT C TAA GCTAGC TCTAGAGGATC	48			4954			
	GVR	GATCCTCTAGAG GCTAGC TTAGAATACTA	358	72	2.1229	4167	17991	3.5019	1.6496
<i>g081c</i>	VGF	ATGCCTGCAG GCGGCCGC TTTGATAAGG	349	1324	5.9548	42	152	0.0296	0.0050

	VGR	CCTTATC CAA GCGGCCGCCTGCAGGCAT	2				35			
	GVF	AATTTGCA TAG GCTAGCTCTAGAGGATC	45				40			
	GVR	GATCCTCTAGAG GCTAGCCTA TGCAAATT	928				35			
<i>g083c</i>	VGF	ATGCCTGCAG GCGGCCGCATG ATTATCG	196				5441			
	VGR	CGATAAT CAT GCGGCCGCCTGCAGGCAT	2				4797			
	GVF	AAAATAAG TAA GCTAGCTCTAGAGGATC	48				4993			
	GVR	GATCCTCTAGAG GCTAGCTTA CTTATTTT	1088	1334	5.9998		4839	20070	3.9066	0.6511
<i>g085</i>	VGF	ATGCCTGCAG GCGGCCGCATG AAAACAA	320				1			
	VGR	TTGTTTT CAT GCGGCCGCCTGCAGGCAT	39				1			
	GVF	AAATGGAT TGA GGTACCGAGCTCGAATT	0				0			
	GVR	AATTCGAGCT CGGTACCTCA ATCCATTT	0	359	1.6146		0	2	0.0004	0.0002
<i>g086</i>	VGF	ATGCCTGCAG GCGGCCGCTTG AGTGCAG	787				15794			
	VGR	CTGCACT CAA GCGGCCGCCTGCAGGCAT	20				11996			
	GVF	AAACATT CTAA GCTAGCTCTAGAGGATC	107				16324			
	GVR	GATCCTCTAGAG GCTAGCTTA GAAATGTTT	1068	1982	8.9143		16931	61045	11.8823	1.3329
<i>g089</i>	VGF	ATGCCTGCAG GCGGCCGCGTG ATTTTAT	91				16926			
	VGR	ATAAAAT CAC GCGGCCGCCTGCAGGCAT	2				16141			
	GVF	GAAATAAA TGA GCTAGCTCTAGAGGATC	118				19076			
	GVR	GATCCTCTAGAG GCTAGCTCAT TTTATTTT	232	443	1.9924		15550	67693	13.1763	6.6131
<i>g092</i>	VGF	ATGCCTGCAG GCGGCCGCATG AATATTA	1042				15222			
	VGR	TAATATT CAT GCGGCCGCCTGCAGGCAT	8				11823			
	GVF	ATAAAAA TAA GCTAGCTCTAGAGGATC	120				12184			
	GVR	GATCCTCTAGAG GCTAGCTTA TTTTTTTAT	1648	2818	12.6743		11679	50908	9.9091	0.7818
<i>g093</i>	VGF	ATGCCTGCAG GCGGCCGCTTG ATATTCT	575				13067			
	VGR	AGAATAT CAA GCGGCCGCCTGCAGGCAT	0				11160			
	GVF	GAGGTGAC TAG GCTAGCTCTAGAGGATC	50				14443			
	GVR	GATCCTCTAGAG GCTAGCTA GTACCTC	876	1501	6.7509		14390	53060	10.3280	1.5299
<i>Total</i>			22234				513749			
4	VGF	ATGCCTGCAG GCGGCCGCATG GCTAGAA	295				14649			
	VGR	TTCTAG CCAT GCGGCCGCCTGCAGGCAT	3				14742			
	GVF	TAGATATA TAA GCTAGCTCTAGAGGATC	136				14589			
	GVR	GATCCTCTAGAG GCTAGCTTA TATATCTA	578	1012	2.5216		13232	57212	6.7445	2.6747
<i>g107</i>	VGF	ATGCCTGCAG GCGGCCGCATG AGTACAT	423				5214			
	VGR	ATGTACT CAT GCGGCCGCCTGCAGGCAT	6				4472			
	GVF	CAATTCAA TAA GCTAGCTCTAGAGGATC	25	1185	2.9527		4733	19181	2.2612	0.7658

	GVR	GATCCTCTAGAGCTAGC TTA TTGAATTG	731			4762			
g108	VGF	ATGCCTGCAGGCGGCCGC ATG GGTATAA	196			10591			
	VGR	TTATACC CAT GCGGCCGCCTGCAGGCAT	1			11567			
	GVF	AATTTATG TAG GCTAGCTCTAGAGGATC	37			12880			
	GVR	GATCCTCTAGAGCTAGC CTA CATAAATT	282	516	1.2857	10029	45067	5.3128	4.1321
g109	VGF	ATGCCTGCAGGCGGCCGC ATG TCACAAG	1462			11628			
	VGR	CTTGTGA CAT GCGGCCGCCTGCAGGCAT	8			9564			
	GVF	ATGTAAAG TAA GCTAGCTCTAGAGGATC	70			12109			
	GVR	GATCCTCTAGAGCTAGC TTA CTTTACAT	1883	3423	8.5291	10600	43901	5.1753	0.6068
g131	VGF	ATGCCTGCAGGCGGCCGC ATG AAAAAAT	2010			19918			
	VGR	ATTTTTT CAT GCGGCCGCCTGCAGGCAT	19			17931			
	GVF	GGGATAAG TAA GCTAGCTCTAGAGGATC	88			20080			
	GVR	GATCCTCTAGAGCTAGC TTA CTTATCCC	1687	3804	9.4785	19345	77274	9.1095	0.9611
g135	VGF	ATGCCTGCAGGCGGCCGC ATG TCAAAATA	2214			21754			
	VGR	TATTTGA CAT GCGGCCGCCTGCAGGCAT	9			17892			
	GVF	AACAAGAA TAA GCTAGCTCTAGAGGATC	211			23892			
	GVR	GATCCTCTAGAGCTAGC TTA TTCTTGTT	2045	4479	11.1604	17129	80667	9.5095	0.8521
g136	VGF	ATGCCTGCAGGCGGCCGC ATG GAAAAAA	1044			10515			
	VGR	TTTTTTC CAT GCGGCCGCCTGCAGGCAT	2			8105			
	GVF	ACGAACAG TAA GCTAGCTCTAGAGGATC	114			11642			
	GVR	GATCCTCTAGAGCTAGC TTA CTGTTCGT	1294	2454	6.1147	9623	39885	4.7019	0.7690
g141	VGF	ATGCCTGCAGGCGGCCGC ATG GATAGAA	1840			17450			
	VGR	TTCTATC CAT GCGGCCGCCTGCAGGCAT	9			16618			
	GVF	AAAATGAA TAG GCTAGCTCTAGAGGATC	81			18377			
	GVR	GATCCTCTAGAGCTAGC CTA TTCATTTT	1621	3551	8.8481	16339	68784	8.1087	0.9164
g146	VGF	ATGCCTGCAGGCGGCCGC GTG AATACGG	764			22415			
	VGR	CCGTATT CAC GCGGCCGCCTGCAGGCAT	7			21605			
	GVF	TTAATATT TAA GCTAGCTCTAGAGGATC	75			22639			
	GVR	GATCCTCTAGAGCTAGC TTA AATATTAA	877	1723	4.2932	19599	86258	10.1686	2.3685
g150	VGF	ATGCCTGCAGGCGGCCGC ATG GATAAATT	2145			16698			
	VGR	AATTATC CAT GCGGCCGCCTGCAGGCAT	4			14616			
	GVF	AAGAAAGC TAA GCTAGCTCTAGAGGATC	56			18003			
	GVR	GATCCTCTAGAGCTAGC TTA GCTTTCTT	2049	4254	10.5998	15909	65226	7.6893	0.7254
g155	VGF	ATGCCTGCAGGCGGCCGC ATG GATATTC	806			12255			
	VGR	GAATATC CAT GCGGCCGCCTGCAGGCAT	8	1889	4.7068	11693	48382	5.7036	1.2118

	GVF	TAGGTGAGTAGGCTAGCTCTAGAGGATC	122				12197			
	GVR	GATCCTCTAGAGCTAGCCTACTCACCTA	953				12237			
<i>g¹⁵⁶</i>	VGF	ATGCCTGCAGGCGGCCGCGCATGGGAATTA	1958				5361			
	VGR	TAATTCCCATGCGGCCGCGCTGCAGGCAT	6				4467			
	GVF	GTTATGAGTAAGCTAGCTCTAGAGGATC	78				5644			
	GVR	GATCCTCTAGAGCTAGCTTACTCATAAC	2134	4176	10.4054		4467	19939	2.3505	0.2259
<i>g¹⁵⁹</i>	VGF	ATGCCTGCAGGCGGCCGCGCATGAAGTTCA	1799				5820			
	VGR	TGAACTTCATGCGGCCGCGCTGCAGGCAT	10				5161			
	GVF	ATTTCTTATAGGCTAGCTCTAGAGGATC	49				5817			
	GVR	GATCCTCTAGAGCTAGCCTATAAGAAAT	1609	3467	8.6388		5529	22327	2.6320	0.3047
<i>g¹⁶⁶</i>	VGF	ATGCCTGCAGGCGGCCGCGCATGTTTATTT	1205				14716			
	VGR	AAATAAACATGCGGCCGCGCTGCAGGCAT	3				13389			
	GVF	TCATTGAGTAAAGCTAGCTCTAGAGGATC	68				16807			
	GVR	GATCCTCTAGAGCTAGCTTACTCAATGA	1201	2477	6.1720		13822	58734	6.9239	1.1218
<i>g¹⁶⁹</i>	VGF	ATGCCTGCAGGCGGCCGCGCATGGAAATGG	522				13832			
	VGR	CCATTTCCATGCGGCCGCGCTGCAGGCAT	8				12031			
	GVF	AAAGGAGGTAGGCTAGCTCTAGAGGATC	85				15266			
	GVR	GATCCTCTAGAGCTAGCCTACCTCCTTT	545	1160	2.8904		12422	53551	6.3129	2.1841
<i>g¹⁷¹</i>	VGF	ATGCCTGCAGGCGGCCGCGCATGTTATAC	141				14296			
	VGR	GTATAACCATGCGGCCGCGCTGCAGGCAT	7				15531			
	GVF	ATGGTGAGTAAAGCTAGCTCTAGAGGATC	127				18288			
	GVR	GATCCTCTAGAGCTAGCTTACTCACCAT	288	563	1.4028		13772	61887	7.2956	5.2006
<i>Total</i>			40133				848275			
5	VGF	ATGCCTGCAGGCGGCCGCGCATGGTGAGTA	2563				3951			
	VGR	TACTCACCATGCGGCCGCGCTGCAGGCAT	1953				3861			
	GVF	AAAATGAATAAGGTACCGAGCTCGAATT	1872				4162			
	GVR	AATTCGAGCTCGGTACCTATTTCATTTT	1876	8264	15.4612		3654	15628	2.4312	0.1572
	VGF	ATGCCTGCAGGCGGCCGCGCATGAATAAAG	430				9036			
	VGR	CTTTATTTCATGCGGCCGCGCTGCAGGCAT	3				9107			
	GVF	AACCAGGCTAAGCTAGCTCTAGAGGATC	108				10610			
	GVR	GATCCTCTAGAGCTAGCTTAGCCTGGTT	791	1332	2.4920		9070	37823	5.8840	2.3611
	VGF	ATGCCTGCAGGCGGCCGCGCATGATAAGCT	2655				1577			
	VGR	AGCTTATCATGCGGCCGCGCTGCAGGCAT	1501				1506			
	GVF	TTTTACTATAGGGTACCGAGCTCGAATT	1504				1581			
	GVR	AATTCGAGCTCGGTACCTATAGTAAAA	1505	7165	13.4051		1287	5951	0.9258	0.0691

<i>g</i> ¹⁷⁶	VGF	ATGCCTGCAGGCGGCCGCATGGATTTTA	203			13572			
	VGR	TAAAATCCATGCGGCCGCCTGCAGGCAT	13			13653			
	GVF	GAAATGACTAAGCTAGCTCTAGAGGATC	142			19780			
	GVR	GATCCTCTAGAGCTAGCTTAATCATTTTC	310	668	1.2498	11411	58416	9.0876	7.2714
<i>g</i> ¹⁷⁷	VGF	ATGCCTGCAGGCGGCCGCATGACTAAAG	939			5024			
	VGR	CTTTAGTCATGCGGCCGCCTGCAGGCAT	3			4536			
	GVF	AAGCATTTTAAAGCTAGCTCTAGAGGATC	48			4907			
	GVR	GATCCTCTAGAGCTAGCTTAATAATGCTT	1486	2476	4.6324	4815	19282	2.9996	0.6475
<i>g</i> ¹⁷⁹	VGF	ATGCCTGCAGGCGGCCGCATGGATATAC	2048			16889			
	VGR	GTATATCCATGCGGCCGCCTGCAGGCAT	7			13147			
	GVF	TAATGTTATAAGCTAGCTCTAGAGGATC	75			15998			
	GVR	GATCCTCTAGAGCTAGCTTAATAACATTA	1832	3962	7.4125	14793	60827	9.4626	1.2766
<i>g</i> ¹⁸¹	VGF	ATGCCTGCAGGCGGCCGCATGCTATGG	972			8760			
	VGR	CCATAGGCATGCGGCCGCCTGCAGGCAT	7			7904			
	GVF	CATTTTCTTAAAGCTAGCTCTAGAGGATC	52			8649			
	GVR	GATCCTCTAGAGCTAGCTTAAGAAAATG	1386	2417	4.5220	7246	32559	5.0651	1.1201
<i>g</i> ¹⁸²	VGF	ATGCCTGCAGGCGGCCGCATGATTAATA	1575			11392			
	VGR	TATTAATCATGCGGCCGCCTGCAGGCAT	10			8969			
	GVF	TACAATTATAGGCTAGCTCTAGAGGATC	54			12104			
	GVR	GATCCTCTAGAGCTAGCCTATAATTGTA	1691	3330	6.2301	9725	42190	6.5633	1.0535
<i>g</i> ¹⁸³	VGF	ATGCCTGCAGGCGGCCGCATGAGAGAAG	2133			16463			
	VGR	CTTCTCTCATGCGGCCGCCTGCAGGCAT	11			14642			
	GVF	AGGAAAAATAAAGCTAGCTCTAGAGGATC	187			16520			
	GVR	GATCCTCTAGAGCTAGCTTATTTTTCCT	2114	4445	8.3162	15280	62905	9.7859	1.1767
<i>g</i> ¹⁸⁵	VGF	ATGCCTGCAGGCGGCCGCATGAATGAGT	161			12612			
	VGR	ACTCATTTCATGCGGCCGCCTGCAGGCAT	7			13467			
	GVF	AGGAGAGATAAGCTAGCTCTAGAGGATC	205			18012			
	GVR	GATCCTCTAGAGCTAGCTTATCTCTCCT	344	717	1.3414	11823	55914	8.6983	6.4843
<i>g</i> ¹⁸⁷	VGF	ATGCCTGCAGGCGGCCGCATGAAGCAGA	1979			2574			
	VGR	TCTGCTTCATGCGGCCGCCTGCAGGCAT	27			1955			
	GVF	TAGATATTTAAAGCTAGCTCTAGAGGATC	130			2518			
	GVR	GATCCTCTAGAGCTAGCTTAATAATCTA	2000	4136	7.7381	1748	8795	1.3682	0.1768
<i>g</i> ¹⁸⁸	VGF	ATGCCTGCAGGCGGCCGCATGAACAAAG	1783			14223			
	VGR	CTTTGTTTCATGCGGCCGCCTGCAGGCAT	11			11812			
	GVF	TTATAAAGTAGGCTAGCTCTAGAGGATC	77	3433	6.4228	12860	50504	7.8567	1.2232

	GVR	GATCCTCTAGAGCTAGCCTACTTTATAA	1562			11609			
g^{190}	VGF	ATGCCTGCAGGCGGCCGCATGAATGGTA	1893			8627			
	VGR	TACCATTGCGGCCGCCTGCAGGCAT	14			7671			
	GVF	TGAGTCAATAGCTAGCTCTAGAGGATC	144			8981			
	GVR	GATCCTCTAGAGCTAGCTTATTGACTCA	1927	3978	7.4425	8067	33346	5.1875	0.6970
	VGF	ATGCCTGCAGGCGGCCGCATGGTAATTG	1389			15268			
g^{191}	VGR	CAATTACGCGGCCGCCTGCAGGCAT	11			13432			
	GVF	ATAAGGAGTAGCTAGCTCTAGAGGATC	64			15746			
	GVR	GATCCTCTAGAGCTAGCTCACTCCTTAT	1271	2735	5.1169	14498	58944	9.1697	1.7920
	VGF	ATGCCTGCAGGCGGCCGCATGGAATTTA	649			10453			
g^{192}	VGR	TAAATTCCGCGGCCGCCTGCAGGCAT	11			10588			
	GVF	ACATACTATGAGCTAGCTCTAGAGGATC	66			12407			
	GVR	GATCCTCTAGAGCTAGCTCATAGTATGT	756	1482	2.7727	10773	44221	6.8793	2.4811
	VGF	ATGCCTGCAGGCGGCCGCCTGGAGAAAT	1498			14979			
g^{194}	VGR	ATTTCTCCACGCGGCCGCCTGCAGGCAT	4			12749			
	GVF	GAGGGAAAAGCTAGCTCTAGAGGATC	112			16970			
	GVR	GATCCTCTAGAGCTAGCTTATTTCCCTC	1296	2910	5.4443	10810	55508	8.6352	1.5861
	Total		53450			642813			
g^{195}	VGF	ATGCCTGCAGGCGGCCGCATGGAATATT	576			21518			
	VGR	AATATTCCGCGGCCGCCTGCAGGCAT	3			21476			
	GVF	TATTCTTTAGCTAGCTCTAGAGGATC	55			24508			
	GVR	GATCCTCTAGAGCTAGCTTAAAGAATA	634	1268	4.7775	20210	87712	13.9325	2.9163
g^{196}	VGF	ATGCCTGCAGGCGGCCGCATGAAACATT	113			22625			
	VGR	AATGTTTCGCGGCCGCCTGCAGGCAT	2			26451			
	GVF	GTAGAAATAGCTAGCTCTAGAGGATC	84			28687			
	GVR	GATCCTCTAGAGCTAGCTTAAATTTCTAC	297	496	1.8688	22396	100159	15.9096	8.5133
g^{198}	VGF	ATGCCTGCAGGCGGCCGCATGAAAGTAG	1272			16580			
	VGR	CTACTTTGCGGCCGCCTGCAGGCAT	9			14317			
	GVF	AGGAAAAATAGCTAGCTCTAGAGGATC	34			15988			
	GVR	GATCCTCTAGAGCTAGCTTATTTTTCCT	918	2233	8.4134	14888	61773	9.8123	1.1663
g^{199}	VGF	ATGCCTGCAGGCGGCCGCCTGCTAATA	1585			31107			
	VGR	TATTAGACGCGGCCGCCTGCAGGCAT	3			27280			
	GVF	TTAAAAATAGCTAGCTCTAGAGGATC	51			28325			
	GVR	GATCCTCTAGAGCTAGCTTAAATTTTAA	2520	4159	15.6701	30016	116728	18.5415	1.1832
g^{201}	VGF	ATGCCTGCAGGCGGCCGCATGAATTATG	129	570	2.1476	5882	24692	3.9222	1.8263

	VGR	CATAATT CAT GCGGCCGCCTGCAGGCAT	1				5945			
	GVF	TTTTATTT TAA GCTAGCTCTAGAGGATC	40				7118			
	GVR	GATCCTCTAGAG GCTAGCTTA AAAAATAAAA	400				5747			
g ²⁰²	VGF	ATGCCTGCAGG GCGGCCGCAT GAATTATA	98				2961			
	VGR	TATAATT CAT GCGGCCGCCTGCAGGCAT	1				3102			
	GVF	AGGGGT TAA GCTAGCTCTAGAGGATC	119				3790			
	GVR	GATCCTCTAGAG GCTAGCTTA TAACCCCT	574	792	2.9841		2962	12815	2.0356	0.6822
g ²⁰⁴	VGF	ATGCCTGCAGG GCGGCCGCAT GTATCCTG	608				9444			
	VGR	CAGGATA CAT GCGGCCGCCTGCAGGCAT	1				7892			
	GVF	CAACAAA TGA GCTAGCTCTAGAGGATC	78				9925			
	GVR	GATCCTCTAGAG GCTAGCTCA TTTTGTG	1376	2063	7.7729		8468	35729	5.6753	0.7301
g ²⁰⁶	VGF	ATGCCTGCAGG GCGGCCGCAT GTAAAAAT	797				13275			
	VGR	ATTTTAC CAT GCGGCCGCCTGCAGGCAT	5				11383			
	GVF	GAGAATAC TAA GCTAGCTCTAGAGGATC	137				13683			
	GVR	GATCCTCTAGAG GCTAGCTTA GTATTCTC	1403	2342	8.8241		12359	50700	8.0534	0.9127
g ²⁰⁸	VGF	ATGCCTGCAGG GCGGCCGCAT GATTTATA	157				4288			
	VGR	TATAAAT CAT GCGGCCGCCTGCAGGCAT	1				4228			
	GVF	TACAGCCA TAG GCTAGCTCTAGAGGATC	48				5572			
	GVR	GATCCTCTAGAG GCTAGCTTA TGGCTGTA	523	729	2.7467		4290	18378	2.9192	1.0628
g ²⁰⁹	VGF	ATGCCTGCAGG GCGGCCGCAT GATTATAG	269				3734			
	VGR	CTATAAT CAT GCGGCCGCCTGCAGGCAT	4				2978			
	GVF	GAGAGAAA TAG GCTAGCTCTAGAGGATC	652				4115			
	GVR	GATCCTCTAGAG GCTAGCTTA TTTCTCTC	620	1545	5.8212		3646	14473	2.2989	0.3949
g ²¹⁰	VGF	ATGCCTGCAGG GCGGCCGCAT GAGTAATA	56				5881			
	VGR	TATTACT CAT GCGGCCGCCTGCAGGCAT	0				5983			
	GVF	CAGATAAA TAA GCTAGCTCTAGAGGATC	183				6909			
	GVR	GATCCTCTAGAG GCTAGCTTA TTTATCTG	388	627	2.3624		5843	24616	3.9101	1.6552
g ²¹¹	VGF	ATGCCTGCAGG GCGGCCGCAT GATGAATG	493				7520			
	VGR	CATTCAT CAT GCGGCCGCCTGCAGGCAT	0				6642			
	GVF	AAGGTATG TAA GCTAGCTCTAGAGGATC	87				8579			
	GVR	GATCCTCTAGAG GCTAGCTTA CATACCTT	1219	1799	6.7782		7327	30068	4.7761	0.7046
g ²¹²	VGF	ATGCCTGCAGG GCGGCCGCAT GAAAAAAC	509				2261			
	VGR	GTTTTTT CAT GCGGCCGCCTGCAGGCAT	62				1753			
	GVF	AAGGAGAT TAA GCTAGCTCTAGAGGATC	221				2100			
	GVR	GATCCTCTAGAG GCTAGCTTA ATCTCCTT	996	1788	6.7367		1831	7945	1.2620	0.1873

g^{213}	VGF	ATGCCTGCAGGCGGCCGCATGTATATAT	974			6394			
	VGR	ATATATACATGCGGCCGCCTGCAGGCAT	179			6264			
	GVF	ATGACTTATGAGCTAGCTCTAGAGGATC	254			8408			
	GVR	GATCCTCTAGAGCTAGCTCATTAAGTCAT	1562	2969	11.1865	6269	27335	4.3420	0.3881
g^{215}	VGF	ATGCCTGCAGGCGGCCGCATGATAAATA	216			2012			
	VGR	TATTTATCATGCGGCCGCCTGCAGGCAT	68			1869			
	GVF	AACGATGGTAACTAGCTCTAGAGGATC	125			2756			
	GVR	GATCCTCTAGAGCTAGCTTACCATCGTT	755	1164	4.3857	1857	8494	1.3492	0.3076
g^{216}	VGF	ATGCCTGCAGGCGGCCGCATGAATGCTA	589			2226			
	VGR	TAGCATTTCATGCGGCCGCCTGCAGGCAT	64			1729			
	GVF	TTAGTTGGTAACTAGCTCTAGAGGATC	265			2040			
	GVR	GATCCTCTAGAGCTAGCTTACCCTAA	1079	1997	7.5242	1937	7932	1.2599	0.1675
Total			26541			629549			