

## pTurboRFP-B vector

## Table of restriction sites

Enzyme Name	Sequence	Count	Cutting Position				
AatI	AGG!CCT	0					
AatII	GACGT!C	1	4034				
AccI	GT!MKAC	1	1991				
AccII	CG!CG	9	546	1820	1822	1925	2266
			2847	3177	3670	4002	
AccIII	T!CCGGA	1	1197				
AcyI	GR!CGYC	2	3649	4031			
AflI	G!GWCC	3	718	3250	3472		
AflII	C!TTAAG	0					
AflIII	A!CRYGT	1	2219				
AhaI	CC!SGG	7	702	921	1865	1900	2599
			3295	3646			
AhaII	GR!CGYC	2	3649	4031			
AhaIII	TTT!AAA	5	1121	1460	2978	2997	3689
AluI	AG!CT	26	142	169	315	459	622
			831	840	845	949	953
			973	982	1101	1230	1701
			1812	1861	1880	2161	2387
			2523	2780	3100	3301	3401
			3464				
AlwI	GGATCNNNN!	5	130	136	2868	2965	3745
AlwI	!NNNNNGATCC	8	123	663	858	2780	2866
			2964	3428	3749		
AlwNI	CAGNNN!CTG	1	2635				
AocI	CC!TNAGG	1	387				
AocII	GDGCH!C	9	185	212	245	822	1672
			2039	2537	3698	3783	
AosI	TGC!GCA	1	3334				
AosII	GR!CGYC	2	3649	4031			
ApaI	GGGCC!C	0					
ApaLI	G!TGCAC	4	208	2035	2533	3779	
ApyI	CC!WGG	9	305	353	449	1378	1434
			1682	2247	2368	2381	
AquI	C!YCGRG	1	2				
AseI	AT!TAAT	1	3284				
Asp700I	GAANN!NNTTC	1	3711				
Asp718I	G!GTACC	0					
AspI	GACN!NNGTC	1	1966				
AsuI	G!GNCC	10	278	521	613	718	1743
			3154	3233	3250	3472	4088
AsuII	TT!CGAA	0					
AvaI	C!YCGRG	1	2				
AvaII	G!GWCC	3	718	3250	3472		
AvaIII	ATGCA!T	0					
AvrI	!CYCGRG	1	1				
AvrII	C!CTAGG	0					
AxyI	CC!TNAGG	1	387				
BalI	TGG!CCA	2	788	1468			
BamHI	G!GATCC	1	128				
BanI	G!GYRCC	4	182	242	1667	3060	
BanII	GRGCY!C	0					
BanIII	AT!CGAT	0					
BbeI	GGCGC!C	0					
BbiII/AcyI	GR!CGYC	2	3649	4031			
BbvI	GCAGCNNNNNNN!	8	339	781	1870	1967	2638
			2641	2847	3541		

BbvI	!NNNNNNNNNNNGCTGC	7	458 3087	1799 3150	2111	2129	2548
BbvII	GAAGACNN!	1	429				
BbvII	!NNNNNNGTCTTC	1	4090				
BcefI	ACGGCNNNNNNNNNN!	6	340 2721	484	535	601	1127
BcefI	!NNNNNNNNNNNGCCGT	1	1553				
BclI	T!GATCA	1	144				
BcnI	CC!SGG	7	702 3295	921 3646	1865	1900	2599
BglI	GCCNNNN!NGGC	2	597	3232			
BglII	A!GATCT	0					
BinI	!NNNNNGATCC	8	123 2964	663 3428	858 3749	2780	2866
BinI	GGATCNNNN!	5	130	136	2868	2965	3745
BsePI	!GCGCGC	0					
BsmAI	!GTCTC	2	1419	3943			
BsmAI	!GAGAC	3	754	1867	3178		
BsmI	GAATGCN!	2	1194	1601			
BsmI	G!CATTC	0					
Bsp1286I	GDGCH!C	9	185 2039	212 2537	245 3698	822 3783	1672
BspHI	T!CATGA	3	2939	3947	4052		
BspMI	ACCTGCNNNN!	1	648				
BspMI	!NNNNNNNNGCAGGT	0					
BspMII	T!CCGGA	1	1197				
BsrI	ACTGGN!	8	732 2627	819 2640	1008 3588	1745	1999
BsrI	C!CAGT	8	867 3276	1448 3319	1966 3758	2752	3158
BssHII	G!CGCGC	0					
BstBI	TT!CGAA	0					
BstEII	G!GTNACC	0					
BstI	G!GATCC	1	128				
BstNI	CC!WGG	9	305 1682	353 2247	449 2368	1378 2381	1434
BstPI	G!GTNACC	0					
BstUI	CG!CG	9	546 2847	1820 3177	1822 3670	1925 4002	2266
BstXI	CCANNNNN!NTGG	0					
BstYI	R!GATCY	9	128 2957	668 2969	863 3737	2860 3754	2871
Bsu36I	CC!TNAGG	1	387				
CcrI	C!TCGAG	1	2				
CfoI	GCG!C	14	1822 2399 3242	1925 2466 3335	1955 2566 3672	2096 2740 4004	2129 2849
Cfr10I	R!CCGGY	1	3192				
Cfr13I	G!GNCC	10	278 3154	521 3233	613 3250	718 3472	1743 4088
CfrI	Y!GGCCR	3	786	1466	3500		
ClaI	AT!CGAT	0					
CviJI	RG!CY	75	142 315 522 606 746 845 1101	169 335 549 614 782 949 1114	232 393 557 622 788 953 1159	279 459 591 636 831 973 1230	308 471 600 705 840 982 1381

			1426	1468	1580	1701	1727
			1745	1812	1861	1880	1913
			1958	1998	2142	2161	2234
			2245	2263	2289	2387	2523
			2528	2553	2632	2697	2708
			2751	2780	3100	3143	3155
			3196	3222	3226	3235	3301
			3391	3401	3464	3502	4089
CvnI	CC!TNAGG	1	387				
DdeI	C!TNAG	15	387	593	684	841	878
			974	1422	1728	1784	2029
			2494	2903	3069	3609	4035
DpnI	GA!TC	20	124	130	146	260	494
			670	865	2787	2862	2873
			2881	2959	2971	3076	3417
			3435	3481	3739	3756	3792
DraI	TTT!AAA	5	1121	1460	2978	2997	3689
DraII	RG!GNCCY	1	4088				
DraIII	CACNNN!GTG	1	715				
DsaI	C!CRYGG	1	1502				
EaeI	Y!GGCCR	3	786	1466	3500		
EagI	C!GGCCG	0					
EarI	!CTCTTC	2	2096	3900			
EarI	!GAAGAG	0					
EclXI	C!GGCCG	0					
Eco105I	TAC!GTA	0					
Eco31I	GGTCTCN!	0					
Eco31I	!NNNNNGAGACC	2	749	3173			
Eco47I	G!GWCC	3	718	3250	3472		
Eco47III	AGC!GCT	0					
Eco52I	C!GGCCG	0					
Eco57I	!CTGAAG	2	616	2745			
Eco57I	!CTTCAG	1	3793				
Eco81I	CC!TNAGG	1	387				
EcoNI	CCTNN!NNNAGG	0					
EcoO109I	RG!GNCCY	1	4088				
EcoRI	G!AATTC	0					
EcoRII	!CCWGG	9	303	351	447	1376	1432
			1680	2245	2366	2379	
EcoRV	GAT!ATC	0					
EcoT14I	C!CWGGG	1	1502				
EcoT22I	ATGCA!T	0					
EcoT38I	GRGCY!C	0					
EheI	GGC!GCC	0					
EspI	GC!TNAGC	1	841				
FinI	!GTCCC	0					
FinI	!GGGAC	0					
Fnu4HI	GC!NGC	28	277	328	472	547	589
			770	917	1543	1802	1813
			1859	1956	2009	2125	2143
			2146	2264	2419	2562	2627
			2630	2836	3101	3164	3503
			3530	3625	3854		
FokI	GGATGNNNNNNNNN!	1	1907				
FokI	!NNNNNNNNNNNNNCATCC	8	199	287	344	499	1181
			3078	3259	3546		
FspI	TGC!GCA	1	3334				
GdiII	!NNNNNYGGCCG	1	3494				
GdiII	CGGCCRN!	0					

GsuI	!CTCCAG	1	3196					
GsuI	!CTGGAG	1	1301					
HaeI	WGG!CCW	8	557	600	788	1381	1468	
			2234	2245	2697			
HaeII	RGCGC!Y	2	2097	2467				
HaeIII	GG!CC	21	279	522	557	591	600	
			614	746	788	1114	1159	
			1381	1468	1745	2234	2245	
			2263	2697	3155	3235	3502	
			4089					
HapII	C!CGG	16	702	920	1156	1198	1326	
			1865	1899	2426	2573	2599	
			2789	3193	3227	3294	3404	
			3646					
HgaI	GACGCNNNNN!	2	2330	2908				
HgaI	!NNNNNNNNNGCGTC	2	1914	3638				
HgiAI	GWGCW!C	5	212	2039	2537	3698	3783	
HgiEII	!ACCNNNNNNGGT	2	2038	2799				
HhaI	GCG!C	14	1822	1925	1955	2096	2129	
			2399	2466	2566	2740	2849	
			3242	3335	3672	4004		
Hin1I	GR!CGYC	2	3649	4031				
HinP1I	G!CGC	14	1820	1923	1953	2094	2127	
			2397	2464	2564	2738	2847	
			3240	3333	3670	4002		
HincII	GTY!RAC	0						
HindIII	A!AGCTT	1	829					
HinfI	G!ANTC	11	56	408	735	850	941	
			1551	1692	2119	2194	2590	
			3107					
HpaI	GTT!AAC	0						
HpaII	C!CGG	16	702	920	1156	1198	1326	
			1865	1899	2426	2573	2599	
			2789	3193	3227	3294	3404	
			3646					
HphI	GGTGANNNNNNN!	11	514	948	1237	1245	1381	
			1449	1783	1841	1850	3598	
			3839					
HphI	!NNNNNNNTCACC	7	403	1243	1437	1491	2955	
			3182	3804				
KpnI	GGTAC!C	0						
Ksp632I	CTCTTCN!	2	2103	3907				
Ksp632I	!NNNNGAAGAG	0						
MaeI	C!TAG	7	807	950	1698	1807	2714	
			2967	3302				
MaeII	A!CGT	9	486	762	1288	1463	1972	
			2922	3338	3711	4031		
MaeIII	!GTNAC	12	1258	1363	1873	1968	2575	
			2638	2754	3037	3368	3426	
			3579	3767				
MboI	!GATC	20	122	128	144	258	492	
			668	863	2785	2860	2871	
			2879	2957	2969	3074	3415	
			3433	3479	3737	3754	3790	
MboII	GAAGANNNNNNN!	4	268	434	547	2881		
MboII	!NNNNNNNTCTTC	7	1476	2090	2952	3707	3785	
			3894	4090				
MfeI	!CAATTG	1	59					
MflI	R!GATCY	9	128	668	863	2860	2871	

			2957	2969	3737	3754	
MluI	A!CGCGT	0					
MmeI	!TCCRAC	3	514	2408	2592		
MmeI	!GTYGGA	0					
MnlI	CCTCNNNNNNN!	10	291	701	812	887	1826
			1856	2118	2401	3279	3485
MnlI	!NNNNNNNGAGG	17	93	112	171	210	231
			264	381	546	589	735
			1046	1697	2326	2650	3050
			3131	4078			
MroI	T!CCGGA	1	1197				
MseI	T!TAA	19	96	110	372	833	1120
			1459	1601	1653	1674	2000
			2925	2977	2982	2996	3049
			3284	3323	3688	4060	
MspI	C!CGG	16	702	920	1156	1198	1326
			1865	1899	2426	2573	2599
			2789	3193	3227	3294	3404
			3646				
MstI	TGC!GCA	1	3334				
MstII	CC!TNAGG	1	387				
MvaI	CC!WGG	9	305	353	449	1378	1434
			1682	2247	2368	2381	
NaeI	GCC!GGC	0					
NarI	GG!CGCC	0					
NciI	CC!SGG	7	702	921	1865	1900	2599
			3295	3646			
NcoI	C!CATGG	1	1502				
NdeI	CA!TATG	1	2042				
NdeII	!GATC	20	122	128	144	258	492
			668	863	2785	2860	2871
			2879	2957	2969	3074	3415
			3433	3479	3737	3754	3790
NheI	G!CTAGC	1	949				
NlaIII	CATG!	21	136	160	166	178	256
			322	402	1276	1506	1567
			1588	1858	1963	2223	2943
			3434	3444	3522	3558	3951
			4056				
NlaIV	GGN!NCC	11	130	184	244	1669	2251
			2290	3062	3156	3197	3408
			3998				
NotI	GC!GGCCGC	0					
NruI	TCG!CGA	0					
NsiI	ATGCA!T	0					
Nsp(7524)I	RCATG!Y	3	160	1858	2223		
Nsp(7524)V	TT!CGAA	0					
NspBII	CMG!CKG	7	581	1101	1545	1931	2561
			2806	3747			
NspII	GDGCH!C	9	185	212	245	822	1672
			2039	2537	3698	3783	
NspIII	C!YCGRG	1	2				
NspIV	G!GNCC	10	278	521	613	718	1743
			3154	3233	3250	3472	4088
NunII	GG!CGCC	0					
Paer71	C!TCGAG	1	2				
PalI	GG!CC	21	279	522	557	591	600
			614	746	788	1114	1159
			1381	1468	1745	2234	2245

			2263 4089	2697	3155	3235	3502
PflMI	CCANNNN!NTGG	3	715	727	1433		
PleI	GAGTCNNNN!	1	2598				
PleI	!NNNNNGACTC	4	844	1686	2113	3101	
PmaCI	CAC!GTG	0					
PpuMI	RG!GWCCY	0					
PstI	CTGCA!G	0					
PvuI	CGAT!CG	1	3482				
PvuII	CAG!CTG	1	1101				
RsaI	GT!AC	8	173	323	575	794	1080
			1618	2027	3592		
RsrI	G!AATTC	0					
RsrII	CG!GWCCG	0					
SacI	GAGCT!C	0					
SacII	CCGC!GG	0					
SalI	G!TCGAC	0					
Sau3AI	!GATC	20	122	128	144	258	492
			668	863	2785	2860	2871
			2879	2957	2969	3074	3415
			3433	3479	3737	3754	3790
Sau96I	G!GNCC	10	278	521	613	718	1743
			3154	3233	3250	3472	4088
SauI	CC!TNAGG	1	387				
ScaI	AGT!ACT	3	794	1618	3592		
ScrFI	CC!NGG	16	305	353	449	702	921
			1378	1434	1682	1865	1900
			2247	2368	2381	2599	3295
			3646				
SduI	GDGCH!C	9	185	212	245	822	1672
			2039	2537	3698	3783	
SecI	C!CNNGG	9	216	351	352	447	1432
			1433	1502	1681	2379	
SexI	!CTCGAG	1	1				
SfaNI	GCATCNNNNN!	9	366	483	1044	1717	2020
			2096	2316	3368	3808	
SfaNI	!NNNNNNNNNGATGC	7	519	558	687	1529	1885
			2056	3559			
SfiI	GGCCNNNN!NGGCC	1	597				
SinI	G!GWCC	3	718	3250	3472		
SmaI	CCC!GGG	0					
SnaBI	TAC!GTA	0					
SnaI	!GTATAC	1	1989				
SpeI	A!CTAGT	0					
SphI	GCATG!C	0					
SplI	C!GTACG	0					
SspI	AAT!ATT	2	1513	3916			
SstI	GAGCT!C	0					
SstII	CCGC!GG	0					
SstIII	!ACGT	9	485	761	1287	1462	1971
			2921	3337	3710	4030	
StuI	AGG!CCT	0					
StyI	C!CWGG	1	1502				
StySJI	!GAGNNNNNNGTRC	1	2016				
StySJI	!GYACNNNNNNCTC	1	792				
TaqI	T!CGA	7	3	270	297	765	1733
			2319	3763			
TaqII	GACCGANNNNNNNNNN!	1	3645				
TaqII	!NNNNNNNNNTCGGTC	2	2121	3460			

TaqII	CACCCANNNNNNNNNNN!	3	260	365	3798			
TaqII	!NNNNNNNNNTGGGTG	2	1425	3815				
ThaI	CG!CG	9	546	1820	1822	1925	2266	
			2847	3177	3670	4002		
Tsp45I	!GTSAC	4	1873	1968	3368	3579		
TspEI	!AATT	13	18	45	60	77	89	
			107	834	1201	1606	1645	
			2979	3285	3540			
Tth111I	GACN!NNGTC	1	1966					
Tth111II	CAARCANNNNNNNNNN!	2	2809	2848				
Tth111II	!NNNNNNNNNTGYTTG	2	1753	2816				
TthHB8I	T!CGA	7	3	270	297	765	1733	
			2319	3763				
VspI	AT!TAAT	1	3284					
XbaI	T!CTAGA	1	1806					
XcyI	C!CCGGG	0						
XhoI	C!TCGAG	1	2					
XhoII	R!GATCY	9	128	668	863	2860	2871	
			2957	2969	3737	3754		
XmaI	C!CCGGG	0						
XmaIII	C!GGCCG	0						
XmnI	GAANN!NNTTC	1	3711					
XorII	CGAT!CG	1	3482					