

Table 5. Pattern of resistant mutations isolated from the resistant clones of AP23464 and PD166326

		AP23464	PD166326	
		200 nM	50 nM	100 nM
KINASE DOMAIN	Number of colonies per 10 ⁷ cells	33	78	3
	CAP	<i>A34T</i>	5	21
	SH2	<i>E138K</i>		3
	3	L248R	1	3
	4	G250E		3
	5	Y253H		17
	6	E255K	8	16
	7	<i>E258K</i>	1	2
	8	<i>V260G</i>		1
	9	<i>W261G</i>		2
	10	<i>L266R</i>		1
	11	<i>V268G</i>		1
	12	A269V	1	
	13	<i>V270G</i>		1
	14	E275K		4
	15	E279K		1
	16	E281K		2
	17	<i>E282K</i>	1	1
	18	<i>L284L</i> [TTG=CTG]	15	
	19	E286K	1	
	20	<i>E292K</i>	1	2
	21	T315I	2	1
	22	<i>F317C</i>		1
	23	<i>F317V</i>		1
	24	<i>S349L</i>		1
	25	F359C		2
	26	<i>L451V</i>	1	
	27	<i>P465K</i>		3
		<i>S481C</i>	1	
TOTAL MUTATIONS		38	89	3

Screening was performed against 10 million BAF3-BCR/ABL cells generated by transformation with native, non-mutagenised BCR/ABL. Resistant variants that are unique to AP23464 and PD166326 are indicated in bold italics.