

Table S1 Forward, reverse, and single base extension primer used for SNP genotyping

SNP ID	Forward primer ID	Forward primer sequence	Reverse primer ID	Reverse primer sequence	Extended primer ID	Extended primer sequence
rs833061_W1	rs833061_W1_F	ACGTTGGATGAGTGAGGACGTGTGTGTCTG	rs833061_W1_R	ACGTTGGATGGGGACACACAGATCTATTGG	rs833061_W1_E	CTTCTCCCCGCTCCAAC
rs1805015_W1	rs1805015_W1_F	ACGTTGGATGAACCCTGCTTACCGCAGCTT	rs1805015_W1_R	ACGTTGGATGATCTCGGGTCTACTTCCTC	rs1805015_W1_E	ACCGCAGCTTCAGCAAC
rs3814055_W1	rs3814055_W1_F	ACGTTGGATGTCACCTGAAGACAACACTGTGG	rs3814055_W1_R	ACGTTGGATGGAGACCACGATTGAGCAAAC	rs3814055_W1_E	TTTGGCAATCCCAGGTT
rs2231142_W1	rs2231142_W1_F	ACGTTGGATGGTCATAGTTGTTGCAAGCCG	rs2231142_W1_R	ACGTTGGATGTGATGTTGTGATGGGCACTC	rs2231142_W1_E	AAGAGCTGCTGAGAACT
rs12721627_W1	rs12721627_W1_F	ACGTTGGATGTTGGTGTTCACAAAAGGGGT	rs12721627_W1_R	ACGTTGGATGCTGATGGAGTGTGATAGAAGGTGAT	rs12721627_W1_E	ACTCCAAATGATGTGCTA
rs2242480_W1	rs2242480_W1_F	ACGTTGGATGTGCTAAGGTTTCACCTCCTC	rs2242480_W1_R	ACGTTGGATGGCAGGAGGAAATTGATGCAG	rs2242480_W1_E	CTCCCTCCTTCTCCATGTA
rs9561765_W1	rs9561765_W1_F	ACGTTGGATGTTGAGAAAACAACCTCCGTG	rs9561765_W1_R	ACGTTGGATGAGGAAAACCAACATCTGGG	rs9561765_W1_E	AAAAGGTACTTCCAAGTCA
rs2235040_W1	rs2235040_W1_F	ACGTTGGATGTAACAAACCCGTAAGGAG	rs2235040_W1_R	ACGTTGGATGGATGCTGCTCAAGTTAAAGG	rs2235040_W1_E	AATGGCCAATTAAGACAAA
rs776746_W1	rs776746_W1_F	ACGTTGGATGGTAATGTGGTCCAAACAGGG	rs776746_W1_R	ACGTTGGATGATGTACCACCCAGCTTAACG	rs776746_W1_E	GTCCAAACAGGGAAGAGATA
rs2725250_W1	rs2725250_W1_F	ACGTTGGATGAAAAGTAGCCGAGTATGCTG	rs2725250_W1_R	ACGTTGGATGAATCTCTGCCTCCTGGGCT	rs2725250_W1_E	CTGGTGCACACCCATGGTTTC
rs28371759_W1	rs28371759_W1_F	ACGTTGGATGAGATAATTGATTGGGCCACG	rs28371759_W1_R	ACGTTGGATGTGATGCCCTACATTGATCTG	rs28371759_W1_E	ATTGATTGGGCCACGAGCTCC
rs1057868_W1	rs1057868_W1_F	ACGTTGGATGTGTGGAGTACGAGACCAAGG	rs1057868_W1_R	ACGTTGGATGGACTTGCGCACGAACATGG	rs1057868_W1_E	CGCACGGCCCGCTTCTCCCCG
rs683369_W1	rs683369_W1_F	ACGTTGGATGTCAGTCCTGTTGAATGCGG	rs683369_W1_R	ACGTTGGATGGACTGGCCTTACATACCTG	rs683369_W1_E	AGCCAACACCGAGAGAGCCAAA
rs1045642_W1	rs1045642_W1_F	ACGTTGGATGAAGGCATGTATGTTGGCCTC	rs1045642_W1_R	ACGTTGGATGGCTGAGAACATTGCCTATGG	rs1045642_W1_E	GTTGGCCTCCTTTGCTGCCCTCAC
rs3025039_W1	rs3025039_W1_F	ACGTTGGATGACTCTGCGCAGAGCACTTTG	rs3025039_W1_R	ACGTTGGATGATGGCGAATCCAATTCCAAG	rs3025039_W1_E	GCGAATCCAATCCAAGAGGGACC
rs4149117_W1	rs4149117_W1_F	ACGTTGGATGGGTTGTCTCCTTATGGGAAC	rs4149117_W1_R	ACGTTGGATGGGCTCAGAGCTGTTTAAACAC	rs4149117_W1_E	ATCCCATGAAGAAATGTGGTAAAG
rs12505410_W1	rs12505410_W1_F	ACGTTGGATGCCTTGGCACCTTAAATGAAC	rs12505410_W1_R	ACGTTGGATGCATGATTCAAACCTTGGCCTC	rs12505410_W1_E	GATTCAAACCTTGGCCTCTGATAATGC
rs10258429_W1	rs10258429_W1_F	ACGTTGGATGCAAAGTAATGATGGCAGCG	rs10258429_W1_R	ACGTTGGATGAGAAGGGATCCATCCTAAGC	rs10258429_W1_E	ACTCCTGAGCAGCTGGGCTCCCGCTCTG
rs2725252_W2	rs2725252_W2_F	ACGTTGGATGTTAGCCAAGCAGTCAGGAAC	rs2725252_W2_R	ACGTTGGATGGCTGATTGAAGGTGCATAAC	rs2725252_W2_E	GGTGCATAACAACCTCC
rs1051266_W2	rs1051266_W2_F	ACGTTGGATGTGAAGCCGTAGAAGCAAAGG	rs1051266_W2_R	ACGTTGGATGAGAAGCAGGTGCCCGTGGAA	rs1051266_W2_E	AAAGGTAGCACACGAGG
rs1050152_W2	rs1050152_W2_F	ACGTTGGATGCTACATCGTCATGGGTAGTC	rs1050152_W2_R	ACGTTGGATGTGGAAGAGTCATTCCCAAAC	rs1050152_W2_E	AGGGAAAAAAGGGTGA
rs3745274#1_W2	rs3745274#1_W2_F	ACGTTGGATGTTCTTCTTAGGGGCCCTCAT	rs3745274#1_W2_R	ACGTTGGATGTGATCTTGGTAGTGAATCG	rs3745274#1_W2_E	ACCCACCTTCTCTTCCA
rs274558_W2	rs274558_W2_F	ACGTTGGATGTTACTTCATCCGAGACTGGC	rs274558_W2_R	ACGTTGGATGACACTCACCACCAGAGTGC	rs274558_W2_E	ACCACCAGAGTGCCACGCA
rs2631372_W2	rs2631372_W2_F	ACGTTGGATGTGCTGAAGGTATAACCATCC	rs2631372_W2_R	ACGTTGGATGAGATGTTATCACAGGACTTG	rs2631372_W2_E	GGTATAACCATCCATCTTCA
rs1805010_W2	rs1805010_W2_F	ACGTTGGATGCTACAGGTGACCAGCCTAAC	rs1805010_W2_R	ACGTTGGATGACCACGTCATCCATGAGCAG	rs1805010_W2_E	GCCTCCGTTGTTCTCAGGGA
rs1870377_W2	rs1870377_W2_F	ACGTTGGATGCCATTCTTACAAGGGTATG	rs1870377_W2_R	ACGTTGGATGTATGCGCTGTTATCTCTTTC	rs1870377_W2_E	TGTTATCTCTTCTTATAGCCA
rs1801275_W2	rs1801275_W2_F	ACGTTGGATGAGATCCTCCGCCGAAATGTC	rs1801275_W2_R	ACGTTGGATGACCCTGCTCCACCGCATGTA	rs1801275_W2_E	TGCTCCACCGCATGTACAACTCC
rs1128503_W2	rs1128503_W2_F	ACGTTGGATGAGCCACTGTTTCCAACCAGG	rs1128503_W2_R	ACGTTGGATGTTTCTCACTCGTCTGGTAG	rs1128503_W2_E	TGCCACTCTGCACCTCAGGTTTCCAG
rs2631370_W2	rs2631370_W2_F	ACGTTGGATGGTTAGGTTCCCTTTCTGTAG	rs2631370_W2_R	ACGTTGGATGAGTGGCTTAGTGATAGAAAC	rs2631370_W2_E	TGTATATTTTACAATATAATGTGTTG
rs4986910_W2	rs4986910_W2_F	ACGTTGGATGTGAAGGACTCTGATTAGAGC	rs4986910_W2_R	ACGTTGGATGTTGGAAGTGGACCCAGAAAC	rs4986910_W2_E	TTCATGTTTCATGAGAGCAAACCTC
rs35599367_W2	rs35599367_W2_F	ACGTTGGATGTTATCAGGTGCCAGTGATG	rs35599367_W2_R	ACGTTGGATGCTCCTTGATCTCAGAGGTAG	rs35599367_W2_E	GTCTCCATCACACCCAG

Table S2 Association of *CYP* polymorphisms with the steady-state IM plasma trough concentrations in 192 Chinese GIST patient

SNP_ID	Gene	Genotype	n	IM trough plasma concentration (ng/mL)	
				Mean ± SD	P
rs12721627	<i>CYP3A4</i>	GG	192	1,253.10±301.14	NA
rs2242480	<i>CYP3A4</i>	CC	106	1,224.16±301.60	0.07
rs2242480	<i>CYP3A4</i>	CT + TT	86	1,302.28±301.15	0.52
		TT	16	1,295.19±251.31	
rs28371759	<i>CYP3A4</i>	CT + CC	176	1,256.58±307.79	NA
		TT	191	1,260.58±303.72	
rs35599367	<i>CYP3A4*22</i>	CT	1	1,106.93	NA
		GG	192	1,253.10±301.14	
rs4986910	<i>CYP3A4*3</i>	TT	192	1,253.10±301.14	NA
rs776746	<i>CYP3A5</i>	GG	95	1,251.96±320.31	0.68
		AG + AA	97	1,268.13±288.93	
rs776746	<i>CYP3A5</i>	AA	20	1,266.85±323.26	0.88
		AG + GG	172	1,259.53±302.48	
rs3745274	<i>CYP2B6</i>	TT	6	1,359.38±354.47	0.38
		GT + GG	186	1,251.69±299.51	
rs3745274	<i>CYP2B6</i>	GG	111	1,236.49±297.17	0.35
		GT + TT	81	1,280.85±305.98	

IM, imatinib mesylate; GIST, gastrointestinal stromal tumor; SNP, single nucleotide polymorphism; n, the numbers of patients; SD, standard deviation; NA, not applicable.

Table S3 Association of *SLC* polymorphisms with the steady-state IM plasma trough concentrations in 192 Chinese GIST patient

SNP_ID	Gene	Genotype	n	IM trough plasma concentration (ng/mL)	
				Mean ± SD	P
rs683369	<i>SLC22A1</i>	CC	141	1,260.65±310.63	0.76
		CG + GG	51	1,257.35±284.14	
rs683369	<i>SLC22A1</i>	GG	3	1,240.91±353.56	0.93
		CG + CC	189	1,260.08±303.34	
rs1050152	<i>SLC22A4</i>	CC	191	1,252.89±302.13	NA
		CT	1	1,292.58	
rs2631370	<i>SLC22A5</i>	CC	78	1,254.17±291.20	0.79
		CT + TT	114	1,258.73±308.22	
rs2631370	<i>SLC22A5</i>	TT	32	1,205.21±285.86	0.23
		CT + CC	160	1,267.38±303.52	
rs2631372	<i>SLC22A5</i>	CC	21	1,291.74±288.90	0.67
		CG + GG	171	1,252.96±302.68	
rs2631372	<i>SLC22A5</i>	GG	97	1,238.20±292.59	0.47
		CG + CC	95	1,276.41±309.48	
rs274558	<i>SLC22A5</i>	AA	32	1,205.21±285.86	0.23
		AG + GG	160	1,267.38±303.52	
rs274558	<i>SLC22A5</i>	GG	78	1,254.17±291.20	0.79
		AG + AA	114	1,258.73±308.22	
rs4149117	<i>SLCO1B3</i>	GG	113	1,263.76±292.42	0.66
		GT + TT	79	1,254.04±319.77	
rs4149117	<i>SLCO1B3</i>	TT	8	1,180.48±291.11	0.38
		GT + GG	184	1,263.66±303.94	
rs1051266	<i>SLC19A1</i>	GG	37	1,260.38±275.23	0.73
		AG + AA	155	1,251.36±308.07	
rs1051266	<i>SLC19A1</i>	AA	50	1,234.73±285.16	0.62
		AG + GG	142	1,259.57±307.56	

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Table S4 Association of *VEGFA*, *NR1I2*, *KDR*, *POR*, *IL4R*, and *EGFR* polymorphisms with the steady-state IM plasma trough concentrations in 192 Chinese GIST patients

SNP_ID	Gene	Genotype	n	IM trough plasma concentration (ng/mL)	
				Mean ± SD	P
rs3025039	<i>VEGFA</i>	CC	116	1,244.79±287.21	0.91
		CT + TT	76	1,282.36±326.27	
rs3025039	<i>VEGFA</i>	TT	12	1,347.06±404.04	0.36
		CT + CC	180	1,253.99±295.80	
rs833061	<i>VEGFA</i>	CC	15	1,325.19±301.12	0.43
		CT + TT	177	1,255.05±303.56	
rs833061	<i>VEGFA</i>	TT	109	1,271.38±308.75	0.44
		CT + CC	83	1,244.08±296.51	
rs3814055	<i>NR1I2</i>	CC	113	1,233.28±293.37	0.14
		CT + TT	79	1,298.02±314.63	
rs3814055	<i>NR1I2</i>	TT	12	1,226.31±305.74	0.88
		CT + CC	180	1,262.00±303.68	
rs1870377	<i>KDR</i>	AA	46	1,285.81±309.90	0.52
		AT + TT	146	1,247.80±298.37	
rs1870377	<i>KDR</i>	TT	63	1,216.16±286.00	0.21
		AT + AA	129	1,276.68±306.85	
rs1057868	<i>POR</i>	CC	73	1,234.20±257.17	0.78
		CT + TT	119	1,256.46±326.01	
rs1057868	<i>POR</i>	TT	33	1,294.46±327.72	0.52
		CT + CC	159	1,244.52±295.96	
rs1801275	<i>IL4R</i>	AA	143	1,254.69±309.83	0.90
		AG + GG	49	1,264.83±280.11	
rs1801275	<i>IL4R</i>	GG	8	1,246.85±187.62	0.89
		AG + AA	184	1,257.90±306.28	
rs1805010	<i>IL4R</i>	AA	55	1,260.77±277.88	0.87
		AG + GG	137	1,255.41±310.23	
rs1805010	<i>IL4R</i>	GG	41	1,277.86±309.39	0.60
		AG + AA	151	1,250.85±299.05	
rs1805015	<i>IL4R</i>	CC	2	1,430.48±327.80	0.38
		CT + TT	190	1,257.99±303.28	
rs1805015	<i>IL4R</i>	TT	169	1,243.18±302.87	0.20
		CT + CC	23	1,325.97±285.63	
rs10258429	<i>EGFR</i>	CC	165	1,261.82±295.88	0.15
		CT + TT	27	1,199.82±333.87	
rs10258429	<i>EGFR</i>	TT	1	1,246.62	NA
		CT + CC	191	1,253.14±302.14	

IM, imatinib mesylate; GIST, gastrointestinal stromal tumor; SNP, single nucleotide polymorphism; n, the numbers of patients; SD, standard deviation; NA, not applicable.