Supplemental data:

Table 1S: Candidate single nucleotide polymorphism in pharmacogenes involved in Cy pharmacodynamics and pharmacokinetics. Frequency in 93 non-Hodgkin lymphoma patients treated with high dose Cy with hazard ratio for relapse with 95% confidence intervals and raw p-value is shown.

	Reference Single Nucleotide Polymorphism (SNP) ID *number*	Gene abbreviation (position of polymorphism)	Gene name	Genotype	Frequency of SNP in cohort of 93 NHL patients	Relapse Hazard Ratio (95% CI)	Raw p-value
1	rs3211371	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	CT	23%	3.3 (1.6 - 6.5)	0.001
2	rs7483	GSTM3	glutathione S-transferase mu 3 (brain)	GA	51%	2.3 (1.0 - 4.9)	0.038
3	rs2740574	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	AG	16%	2.2 (1.1 - 4.8)	0.037
4	rs7483	GSTM3	glutathione S-transferase mu 3 (brain)	AA	12%	1.9 (0.6 - 6.3)	0.295
5	rs1805087	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	AG	33%	1.8 (0.9 - 3.5)	0.083
6	rs1128503	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	CT	46%	1.8 (0.8 - 4.2)	0.153
7	rs11615	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1	CC	15%	1.6 (0.7 - 3.8)	0.243
8	rs776746	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	GA	21%	1.5 (0.7 - 3.3)	0.275
9	rs2228100	ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	GG	11%	1.5 (0.5 - 4.0)	0.446
10	rs1042522	TP53	tumor protein p53	GC/CC	52%	1.4 (0.7 - 2.7)	0.345
11	rs3212986	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1	TT	8%	1.4 (0.5 - 4.0)	0.584
12	rs1800566	NQO1	NAD(P)H dehydrogenase, quinone 1	CT	36%	1.4 (0.4 - 4.8)	0.588
13	rs4726	SLC3A2	solute carrier family 3 member 2	CT	36%	1.3 (0.7 - 2.7)	0.430
14	rs1051266	SLC19A1	solute carrier family 19 (folate transporter), member 1	GA	49%	1.3 (0.6 - 2.9)	0.482

15	rs1128503	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	TT	24%	1.3 (0.5 - 3.5)	0.561
16	rs723685	SLC22A16	solute carrier family 22 (organic cation/carnitine transporter), member 16	TC	19%	1.2 (0.6 - 2.7)	0.605
17	rs1800566	NQO1	NAD(P)H dehydrogenase, quinone 1	TT	7%	1.2 (0.6 - 2.5)	0.589
18	rs1045642	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	TC	44%	1.2 (0.6 - 2.5)	0.680
19	rs9561778	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	GT/TT	36%	1.2 (0.6 - 2.4)	0.657
20	rs17367504	MTHFR	5,10-methylenetetrahydrofolate reductase	AG/GG	17%	1.2 (0.5 - 2.8)	0.624
21	rs4726	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	TT	8%	1.2 (0.3 - 4.0)	0.794
22	rs4880	SOD2	superoxide dismutase 2, mitochondrial	CT	41%	1.1 (0.5 - 2.3)	0.890
23	rs2070676	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	CG	12%	1.1 (0.4 - 3.3)	0.794
24	rs13181	ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2	GG	11%	1.1 (0.4 - 3.0)	0.887
25	rs1138272	GSTP1	glutathione S-transferase pi 1	CT/TT	14%	1.1 (0.4 - 2.9)	0.798
26	rs8192709	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	CT	11%	1.1 (0.4 - 2.8)	0.904
27	rs25487	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	AA	15%	1.1 (0.4 - 2.7)	0.846
28	rs1805087	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	GG	7%	1.1 (0.2 - 4.5)	0.944
29	rs2228100	ALDH3A1	aldehyde dehydrogenase 3 family, memberA1	CG	35%	1.0 (0.5 - 2.1)	0.929
30	rs1695	GSTP1	glutathione S-transferase pi 1	AG	46%	0.9 (0.5 - 1.9)	0.850
31	rs25487	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	GA	46%	0.9 (0.5 - 1.9)	0.863

32	rs714368	SLC22A16	solute carrier family 22 (organic cation/carnitine transporter), member 16	AG/GG	39%	0.9 (0.5 - 1.8)	0.826
33	rs2230054	CXCR2	interleukin 8 receptor, beta	TT	24%	0.9 (0.4 - 2.3)	0.867
34	rs1045642	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	CC	24%	0.9 (0.3 - 2.2)	0.766
35	rs13181	ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2	TG	50%	0.8 (0.4 - 1.8)	0.659
36	rs4073	IL8	interleukin 8	AA	24%	0.8 (0.4 - 1.6)	0.462
37	rs12248560	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	CT/TT	34%	0.8 (0.4 - 1.6)	0.519
38	rs1143684	NQO2	NAD(P)H dehydrogenase, quinone 2	TC/CC	41%	0.8 (0.4 - 1.6)	0.602
39	rs3745274	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	GT	39%	0.8 (0.4 - 1.5)	0.442
40	rs2279343	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	AG	40%	0.8 (0.4 - 1.5)	0.446
41	rs1695	GSTP1	glutathione S-transferase pi 1	GG	14%	0.8 (0.3 - 2.6)	0.741
42	rs4880	SOD2	superoxide dismutase 2, mitochondrial	TT	28%	0.8 (0.3 - 1.9)	0.537
43	rs4793665	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	CC	25%	0.8 (0.3 - 1.8)	0.555
44	rs3957357	GSTA1	glutathione S-transferase alpha 1	AA	15%	0.7 (0.4 - 1.5)	0.398
45	rs2230054	CXCR2	interleukin 8 receptor, beta	CT	51%	0.7 (0.3 - 1.7)	0.488
46	rs4793665	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	TC	41%	0.7 (0.3 - 1.5)	0.330
47	rs747199	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	CG/GG	24%	0.7 (0.3 - 1.5)	0.373
48	rs11615	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1	TC	45%	0.7 (0.3 - 1.4)	0.317
49	rs17997935	GSTM3	glutathione S-transferase mu 3 (brain)	AA	11%	0.7 (0.2 - 2.1)	0.529

50	rs4244285	CYP2C19	cytochrome P450, family 2, subfamily C, polypeptide 19	GA/AA	25%	0.6 (0.3 - 1.3)	0.197
51	rs12210538	SLC22A1	solute carrier family 22 (organic cation transporter), member 1	AG/GG	33%	0.6 (0.3 - 1.3)	0.198
52	rs3212986	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1	GT	32%	0.6 (0.3 - 1.3)	0.229
53	rs17997935	GSTM3	glutathione S-transferase mu 3	GA	44%	0.6 (0.3 - 1.2)	0.127
54	rs1051266	SLC19A1	solute carrier family 19 (folate transporter), member 1	AA	19%	0.6 (0.2 - 2.0)	0.435
55	rs3957357	GSTA1	glutathione S-transferase alpha 1	GA	49%	0.6 (0.2 - 1.7)	0.314
56	rs4073	IL8	interleukin 8	TA	46%	0.6 (0.2 - 1.4)	0.223
	CYP2B6 alleles based on CYP allele nomenclature website: (http://www.cypalleles.ki.se)						
	rs2279343 and rs3745274	CYP2B6*6	cytochrome P450, family 2, subfamily B, polypeptide 6		13%	0.2 (0.1 - 1.0)	0.051
	rs3211371	CYP2B6*5	cytochrome P450, family 2, subfamily B, polypeptide 6		23%	3.3 (1.6 - 6.5)	0.001
	rs2279343 and absence of rs 3745274	CYP2B6*4	cytochrome P450, family 2, subfamily B, polypeptide 6		1%	N/A	