Supplementary Table S5. Resequencing of a subset of focal mutations. For each mutation shown, the total number of reads covering each position and the number of reads confirming the alteration are shown. Also shown are the locus-specific sequences of the primer pairs for each alteration. Loci that failed to amplify during verification are omitted from this list. The boldface read depth indicates the focus with the mutated allele. 23 of 28 loci (82%) verified successfully.

Case	Clonality	Chr	Position	Gene Symbol	Ref	Alt	Effect	Norm Cov	Gp3 Cov	Gp4 Focus 1 Cov	Gp4 Focus 2 Cov	Norm Alt Reads	Gp3 Alt Reads	Gp4 Focus 1 Alt Read	Gp4 Focus 2 Alt Reads	Forward Seq	Reverse Seq
10-01	Focal	3	39374844	*CCR8*	G	A	Coding	642	1234	3010	N/A	0	2	**646**	N/A	CTCACTGCTGTGTGAACCCTGTTAT	ATGTAGTCTACGCTGGAGGAACG
10-01	Focal	4	70359441	*UGT2B4*	G	A	Non-coding	8125	6055	11184	N/A	4	**3**	8	N/A	TCGTACTGAAACTTCAAAGCAGACA	TGAGACAATGGCAAAAGCTGACA
11-01	Focal	3	52404493	*DNAH1*	G	A	Non-coding	2378	31065	1157	N/A	54	581	**21**	N/A	CAAAGCTGTGTAGCAGAGGTCA	CGCTCCAGATCAGGGAGAAGATG
11-01	Focal	5	137762882	*KDM3B*	G	T	Coding	28757	223928	49769	N/A	103	**216714**	153	N/A	GTGTCATCTTCAGAAGCCATCACAA	GCTAGGTAGCCTAGAGGCCAGATT
11-01	Focal	22	36205898	*RBFOX2*	G	A	Coding	8051	646	6069	N/A	3	0	**1114**	N/A	TGATTGCCATGCATCCTTCCATT	CGCAGAATGGAATTCCCACAGA
11-02	Focal	16	71807237	*AP1G1*	G	A	Coding	965	5295	10743	19701	1	**4095**	10	19	AAGAGTTGGAGGTTTTCAGGAGCTT	TCTTGGGGAGCACCAGGCT
11-02	Focal	X	154348368	*BRCC3*	G	A	Silent	1183	252	22370	106	27	16	**17917**	6	ATGTCGGCAGTCAGCGGG	GCTGTGTGCATTTTCAGACTGTGT
11-02	Focal	5	1278807	*TERT*	G	A	Silent	1454	11070	5798	1011	0	**7928**	6	11	ATCCTGGACACGACTATCACACG	TCACACAGGTGGATGTGACGG

11-03	Focal	16	84158313	*HSDL1*	C	T	Coding	128154	91788	264807	N/A	66	55	**57465**	N/A	AGGTTCCCAGGAGTTGGCAAAA	TCCTTCAGTGTTGATTTTGGGTTCT
11-03	Focal	5	65466776	*SREK1*	G	A	Non-coding	127	719	375	N/A	0	1	**205**	N/A	ACAGGACAAAGAAAAAGGAACGAGAA	CCAATTGTCATCAGCAAATCCCTT
11-03	Focal	22	37603492	*SSTR3*	G	A	Silent	14797	97847	35791	N/A	12	**23313**	14	N/A	GCGGTCCACGCTCATGACA	GCCCTTCAGTCACCAACGTCT
11-03	Focal	1	118483775	*WDR3*	C	T	Coding	25601	64346	94281	N/A	144	90	**84290**	N/A	TCTGCTCTTGCTTCTTCTGTAGC	TGAGTGTTTGGAAGGAACAGCCTA
11-10	Focal	4	143393616	*INPP4B*	T	C	Non-coding	4818	12664	9931	N/A	9	**3722**	19	N/A	TCAGTGATACCGAACCCAGTAAGT	TCTGAGGCACTGGTATTGGGGA
11-10	Focal	7	77740060	*MAGI2*	A	G	Non-coding	125	278	877	N/A	0	**102**	0	N/A	TTCTCCCTTTGTATGGGCTCTACTT	TGTCAGACCCTGTCCCCTTCTT
11-10	Focal	11	4615225	*OR52I1*	T	C	Coding	1520	1968	4919	N/A	2	0	**1114**	N/A	TTTTCTGATCCTGCCATACCACC	CCACAAGGAGGAAGGAGGCA
11-10	Focal	4	142152631	*ZNF330*	C	T	Coding	6096	7124	7858	N/A	6	119	**3083**	N/A	TTCCATTGCAAGCTTTTAGTGATTT	CCAAGGACTGGTGGAGGGGTA
11-12	Focal	9	124408123	*DAB2IP*	G	A	Non-coding	51375	201033	115602	N/A	208	**71899**	67	N/A	AGCTTCCCCCGTTCATCAGTTT	GCTCACCTCCCAGAGATTCCATC
11-12	Focal	2	48018181	*MSH6*	T	C	Coding	1596	332	46	N/A	3	**170**	0	N/A	GGTTACCCCTGGTGGCCTTG	TGGCAGTAGTGACTCTTACCTGT
11-12	Focal	9	115759765	*ZNF883*	G	A	Non-coding	80097	563053	46350	N/A	36	123	**17262**	N/A	AGGTGTGTACTTCGACTGAAGGTT	GCTTTCAGCCATACCCCAGC

11-13	Focal	4	25005261	*LGI2*	A	G	Coding	22011	78380	388991	N/A	9	**12977**	341	N/A	GACAGCTGTGAATGAACGAGGC	AGCAGTTTGTGGAGATCCAAGCTC
11-13	Focal	1	36755226	*THRAP3*	C	A	Coding	12386	1116	28	N/A	14	**508**	0	N/A	AAGAGAAGCGAAGGTGGGCA	CGGACATTGACCTGTGCCTC
11-14	Focal	2	27306488	*EMILIN1*	C	T	Silent	41996	338349	73739	N/A	44	171	**70010**	N/A	TGAGGTTATTCTCAGCTTCAGCTCC	CTCGGAAGCGCTCTTCACTCTCT
11-14	Focal	1	9777144	*PIK3CD*	C	T	Coding	129467	48363	100199	N/A	85	26	**60380**	N/A	GTCCATTCCTCCTCCATCCTCG	CATGGCCAGTAGCACATGGAGT
12-01	Focal	9	138709867	*CAMSAP1*	C	T	Silent	180353	149670	185219	N/A	291	200	**59035**	N/A	TAATCAGGAAGTCCCACCCTGC	GTTTCTGTCTCTGGCAGCTGATAA
12-02	Focal	7	82579281	*PCLO*	T	A	Silent	124065	59811	8533	N/A	33	13	**1**	N/A	TGAGGACTTTGTGTGTCTGAATCTG	CCAGCATAGCAGTTCAAACGGT
12-02	Focal	9	125760971	*RABGAP1*	T	C	Coding	25404	2232	5994	N/A	9	2	**0**	N/A	AGGAGCCTGTTCGATTTCTCCTG	TCAGCCTCAGACGTGATTTCTCC
12-02	Focal	12	122404860	*WDR66*	G	A	Non-coding	7388	1472	7461	N/A	24	3	**7**	N/A	CCCGACCAAAGAATCTTAAAACCT	AGCGCTGTTACCTTGTCTCTGT
12-03	Focal	7	129350236	*NRF1*	G	A	Coding	121841	15082	39024	8709	389	**14638**	80	22	AGCTGCTTATTGCATATTGGGACTA	GTGGCTGTGGCCTGTGTTTG

Supplementary Table S6. Subclonal mutations shared by two foci of Gp4 but not Gp3. For each focus with three foci of tumor sequenced, all somatic mutations shared by both foci of Gp4 tumor (but not shared by a clonal focus of Gp3 tumor) are shown. Mutations were considered shared between foci of Gp4 if found in at least one focus of Gp4 at high confidence and present at any frequency in the second focus, as well as not detected in the Gp3 and benign foci. To avoid misclassifying truncal mutations or undercovered germline SNP as Gp4-only, mutations were considered absent from the benign and Gp3 only if the other foci were covered at comparable coverage. Also shown is the reference and alternative allele depth, frequencies, and computed cancer cell fraction (CCF) for each focus and the matched benign control.

Case	**Genomic Coordinate**	**Classification**	**Gene Symbol**	**Effect**	**Description**	**Normal coverage (freq.)**	**Gp4 Focus 1 tumor coverage (freq.)**	**Gp4 Focus 2 tumor coverage (freq.)**	**Gp4 Focus 1 tumor CCF**	**Gp4 Focus 2 tumor CCF**
11-02	g.chr3:1425032G>A	Missense Mutation	CNTN6	p.M819I	contactin 6	73 (0.01)	47 (0.15)	23 (0.26)	0.40	0.70
11-02	g.chr2:160698852G>A	Silent	LY75-CD302	p.L1062L	LY75-CD302 readthrough	23 (0.00)	29 (0.14)	22 (0.23)	0.37	0.61
11-02	g.chr7:78263867G>A	Intron	MAGI2		membrane associated guanylate kinase, WW and PDZ domain containing 2	65 (0.00)	64 (0.09)	56 (0.14)	0.25	0.38
12-03	g.chr21:39975901G>A	Intron	ERG		v-ets avian erythroblastosis virus E26 oncogene homolog	19 (0.00)	11 (0.82)	18 (0.67)	2.18	1.78
12-03	g.chr1:42049343C>T	Missense Mutation	HIVEP3	p.D376N	human immunodeficiency virus type I enhancer binding protein 3	73 (0.00)	64 (0.27)	6 (0.50)	0.88	1.33
12-03	g.chr12:108917408C>A	Missense Mutation	SART3	p.R906S	squamous cell carcinoma antigen recognized by T cells 3	18 (0.00)	24 (0.25)	15 (0.27)	0.67	0.71

Supplementary Table S7. Genes with at least two-fold change between Gp4 and Gp3. Linear values for each gene were transformed into fold change values (Gp4 divided by Gp3) and fold change values were averaged. Average fold change values greater than 2 or less than -2 are shown. Student's paired *t*-test was performed; data is sorted by *P* value.

mRNA ID	Gene Symbol	Average Fold Change (Gp4 vs Gp3)	*P* Value
NR_037962	RHOU	3.863098279	0.0014
NM_004522	KIF5C	2.170975394	0.0017
NM_001040113	MYH11	-2.875613766	0.0040
NR_034105	CRNDE	2.054563765	0.0082
NM_001012977	PABPC1L2A	-2.250521295	0.0097
NM_001040665	STEAP2	2.044580245	0.0097
NM_001256410	RAB18	2.302530358	0.0159
NM_000414	HSD17B4	2.677735667	0.0193
NM_030939	C6orf62	2.390670598	0.0212
NR_002576	SNORA21	-2.236589128	0.0224
NM_016192	TMEFF2	5.010114016	0.0230
NM_002628	PFN2	2.015491998	0.0267
NM_213674	TPM2	-2.812618784	0.0288
NM_001205315	STEAP4	2.068694755	0.0291
NM_004569	PIGH	2.103350172	0.0297
NM_001141945	ACTA2	-2.072392092	0.0299
NM_001634	AMD1	3.317847997	0.0313
NM_001154	ANXA5	2.309493215	0.0418
NM_001014986	FOLH1	4.806463722	0.0437
NM_153826	CD46	2.190651077	0.0467
NM_006708	GLO1	3.612848414	0.0480
NR_045562	GULP1	2.483435589	0.0521
NM_001203	BMPR1B	2.070588472	0.0527
NM_004521	KIF5B	2.12810031	0.0528
NM_015076	CDK19	2.290294025	0.0546
NM_005013	NUCB2	2.2880836	0.0576
NM_000905	NPY	5.976453258	0.0577
NM_006198	PCP4	-5.162221863	0.0631
NM_001257391	CD63	2.129084745	0.0717
NM_000240	MAOA	3.53583713	0.0820
NM_001242915	ZFAND6	3.239059016	0.0827
NM_016497	MRPL51	10.46164199	0.0899
NM_004374	COX6C	2.121945085	0.1042
NM_001277198	CNIH4	2.051503886	0.1064
NM_003676	DEGS1	3.765565708	0.1101
NM_003299	HSP90B1	2.060209166	0.1109
NM_001220473	PPFIA2	3.320098095	0.1122
NM_007008	RTN4	4.435015606	0.1123
NR_104319	SCHLAP1	2.784417015	0.1155
NM_004766	COPB2	2.202044039	0.1187
NM_024312	GNPTAB	5.854525403	0.1395
NM_030774	OR51E2	4.391844706	0.1547
NM_015243	VPS13B	2.961494585	0.1559
NM_006267	RANBP2	2.901920817	0.1709
NM_001243797	TSC22D1	2.390604371	0.1717
NR_001575	RNF138P1	2.839981992	0.1759
NM_000214	JAG1	2.82802586	0.1783

NM_001005474	NFKBIZ	4.278067537	0.1797
NM_001024629	NRP1	2.011674456	0.1950
NM_020188	CMC2	3.321581506	0.1983
NM_025087	CWH43	2.09590401	0.1993
NM_004654	USP9Y	2.584481045	0.1997
NM_001037495	DYNLL1	2.271146646	0.2049
NR_015401	LINC00957	2.732038306	0.2089
NM_001271594	SESN3	2.46005016	0.2090
NM_003711	PPAP2A	2.855377388	0.2138
NM_002923	RGS2	2.779722772	0.2243
NR_015342	PCA3	-13.74152767	0.2297
NR_000009	SNORD4B	-2.459011511	0.2317
NM_001677	ATP1B1	2.001961571	0.2406
NR_002440	SNORD16	-2.204282113	0.2467
NM_018584	CAMK2N1	4.60631125	0.2485
NM_001003712	OSBPL8	2.119553286	0.2705
NM_001015038	PAGE2B	-2.349273947	0.2765
NM_001195100	PTP4A2	2.691204005	0.2783
NR_000017	SNORD36B	-4.380495431	0.2834
NM_000300	PLA2G2A	3.68168087	0.3021
NR_038400	LINC00308	5.615114468	0.3113
NM_181617	KRTAP21-2	-2.628813445	0.3114
NR_002559	SNORD29	-10.94592177	0.3144
NM_002298	LCP1	3.507951401	0.3219
NM_022170	EIF4H	-2.948698618	0.3261
NR_046944	RNU6-78P	-4.117813566	0.3379
NM_001282480	PRKG2	3.393207252	0.3387
NM_000110	DPYD	5.21862161	0.3405
NR_002959	SNORA18	-10.97243149	0.3423
NM_001003799	TARP	3.128707867	0.3465
NM_001033019	DEFB134	-3.358009359	0.3544
NR_004403	SNORD97	-2.845224212	0.3555
NM_003725	HSD17B6	-2.034220518	0.3588
NM_001012456	SEC61G	2.523303307	0.3632
NM_001190986	CRISP3	13.69443938	0.3662
NR_002564	SNORD26	-6.350675905	0.3756
NR_003140	SNORD117	-2.28378835	0.3804
NR_002561	SNORD30	-7.992724794	0.3859
NR_002956	SNORA14B	-25.5027109	0.3908
NR_038903	RAB30-AS1	-2.440090795	0.3946
NM_001136154	ERG	2.348746503	0.4108
NR_003033	SNORD5	2.729914108	0.4391
NM_001254718	MYBPC1	-2.164278745	0.4541
NM_005345	HSPA1A	3.752231853	0.4547
NM_003528	HIST2H2BE	4.914879194	0.4582
NM_022132	MCCC2	3.04405036	0.5491
NR_002447	SNORD24	-20.22256652	0.5907
NR_024387	CXADRP2	-2.624408588	0.6742
NM_001008	RPS4Y1	2.36943954	0.7224
NR_002962	SNORA23	-2.050110027	0.7878
NM_014917	NTNG1	-2.15483043	0.8797
NR_002572	SNORD58B	3.011467142	0.9559
NM_058186	FAM3B	-2.78083161	0.9936

Supplementary Table S8. Gene Expression Omnibus (GEO) and Sequence Read Archive (SRA) accession identification numbers. For each case and tumor/normal tissue reported in this paper, the GEO and SRA accession identification numbers for each case is reported.

Study ID	Focus	GEO	SRA
10-01	N		SRX290885
10-01	Gp3		SRX290886
10-01	Gp4		SRX290887
11-01	N		SRX290528
11-01	Gp3		SRX290531
11-01	Gp4		SRX290532
11-02	N		SRX288309
11-02	Gp3		SRX288310
11-02	Gp4 Focus 1		SRX288447
11-02	Gp4 Focus 2		SRX288448
11-03	N		SRX295000
11-03	Gp3	GSM1269835	SRX295001
11-03	Gp4	GSM1269836	SRX295002
11-04	Gp3	GSM1269837	
11-04	Gp4	GSM1269838	
11-05	Gp3	GSM1269839	
11-05	Gp4	GSM1269840	
11-06	Gp3	GSM1269841	
11-06	Gp4	GSM1269842	
11-07 Area 1	Gp3	GSM1269843	
11-07 Area 1	Gp4	GSM1269844	
11-07 Area 2	Gp3	GSM1269845	
11-07 Area 2	Gp4	GSM1269846	
11-09	Gp3	GSM1269847	
11-09	Gp4	GSM1269848	
11-10	N		SRX315064
11-10 Area 1	Gp3		SRX315065
11-10 Area 1	Gp4		SRX315067
11-10 Area 2	Gp3		SRX315068
11-10 Area 2	Gp4		SRX315069
11-12	N		SRX297101
11-12	Gp3	GSM1269849	SRX297102
11-12	Gp4	GSM1269850	SRX297103
11-13	N		SRX298673
11-13	Gp3	GSM1269853	SRX298674
11-13	Gp4	GSM1269854	SRX298675
11-14	N		SRX298261
11-14	Gp3	GSM1269851	SRX298262
11-14	Gp4	GSM1269852	SRX298263
12-01	N		SRX300927
12-01	Gp3	GSM1269859	SRX300942
12-01	Gp4	GSM1269860	SRX300943
12-02	N		SRX304896
12-02	Gp3	GSM1269857	SRX304897
12-02	Gp4	GSM1269858	SRX304898
12-03	N		SRX309628
12-03	Gp3	GSM1269855	SRX309630
12-03	Gp4 Focus 1	GSM1269856	SRX309631
12-03	Gp4 Focus 2		SRX309633

Supplementary Table S9. Exome sequencing metrics for each library. For each library, the version of the Agilent SureSelect Exome library is shown. Also shown: the size of the custom bait library (in bases), the number of pass-filter reads for each library (in reads), the percentage of targets covered at 2×, 10×, 20×, 30×, 40×, 50x and 100× coverage, and the total number of unique library molecules.

Sample	Exome Version	Size of Custom Content	Genome Size	Number of bases in bait library	Number of bases in target regions	Pass Filter Reads	Unique Pass Filter Reads	Percent Unique Reads	Unique Aligned Pass Filter Reads	Percent of Unique Pass Filter Reads Aligned	Bases aligned in pass filter reads	Pass filter aligned bases	Bases Mapped Near Baits	Based Mapped Far From Baits
10-01 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	96855342	72120797	0.744624	65106647	0.902744	6298730912	2354133090	826258073	3118339749
10-01 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	108183314	79630565	0.736071	71704287	0.900462	6921799623	2607936925	939168602	3374694096
10-01 N	3	5998080	3137161264	57635363	57633968	106016624	74597322	0.703638	67015059	0.898357	6460939014	2410803700	843500621	3206634693
11-01 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	84999748	47860015	0.563061	42182021	0.881362	3919835064	1505856050	356310237	2057668777
11-01 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	133362450	96086844	0.720494	85276377	0.887493	7994292336	3148444882	912086763	3933760691
11-01 N	3	5998080	3137161264	57635363	57633968	88339758	64213475	0.726892	57632702	0.897517	5412483554	2179317915	611044489	2622121150
11-02 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	126569422	64434030	0.509081	57023378	0.884989	5479724157	1648752996	508147189	3322823972
11-02 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	105816302	60876503	0.575304	53321731	0.8759	5013694108	1602513492	519382660	2891797956
11-02 Gp4 Focus 2	5	3901294	3137161264	54413025	56496747	81239684	39297519	0.483723	31008668	0.789074	2858970143	608885919	282035763	1968048461
11-02 N	3	5998080	3137161264	57635363	57633968	75039912	47427374	0.632029	42408690	0.894182	4061324237	1455319343	485537466	2120467428
11-03 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	63239466	51520002	0.814681	43173311	0.837991	4036699998	785655536	318045888	2932998574
11-03 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	35923872	27013101	0.751954	23136672	0.856498	2160228375	667164098	239063277	1254001000
11-03 N	3	5998080	3137161264	57635363	57633968	53232944	36491534	0.685507	32300289	0.885145	3085926182	898133174	370530551	1817262457
11-10 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	96568478	72904012	0.754946	62007703	0.850539	5829322028	1813298385	559882403	3456141240
11-10 Gp3 Focus 2	3	5998080	3137161264	57635363	57633968	73830878	30751756	0.416516	21477581	0.698418	1809295652	657977352	221367010	929951290
11-10 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	80954012	55331259	0.68349	47186299	0.852796	4408368248	1355503684	420501897	2632362667
11-10 Gp4 Focus 2	3	5998080	3137161264	57635363	57633968	71924476	38915918	0.541066	29597594	0.760552	2432078924	738047268	255056129	1438975527
11-10 N	3	5998080	3137161264	57635363	57633968	110170342	70102706	0.636312	62586617	0.892785	6027896201	2003440974	587277749	3437177478
11-12 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	99934318	48187408	0.482191	37590667	0.780093	3303153535	955103158	309104455	2038945922
11-12 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	82933722	43948990	0.529929	38910841	0.885364	3664311061	1237376360	464439686	1962495015
11-12 N	3	5998080	3137161264	57635363	57633968	104911674	65883552	0.627991	59710877	0.906309	5654586156	1705109906	689629018	3259847232
11-13 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	69516728	33424647	0.480814	21108921	0.631538	1833306284	447104859	142063791	1244137634
11-13 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	87193886	40709535	0.466885	27000270	0.663242	2322566210	607400808	192004574	1523160828
11-13 N	3	5998080	3137161264	57635363	57633968	88648174	68463170	0.772302	60145510	0.878509	5569849788	2029786366	754383344	2785680078
11-14 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	93496090	39639907	0.423974	32647596	0.823604	3035581859	1286895966	404895911	1343789982
11-14 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	98293854	35909497	0.365328	30289272	0.843489	2805045035	1078750509	358034784	1368259742
11-14 N	3	5998080	3137161264	57635363	57633968	85543076	53622306	0.626846	47952521	0.894264	4621444607	1646624028	624241224	2350579355
12-01 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	98588890	53021655	0.537806	47469844	0.895292	4563236629	1960174461	656414480	1946647688
12-01 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	103418684	54442241	0.526426	46114403	0.847034	4208818825	1640518595	543173089	2025127141
12-01 N	3	5998080	3137161264	57635363	57633968	170637090	89536340	0.524718	80396743	0.897923	7747921347	2915918887	1.016E+09	3815710393
12-02 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	98962504	53054087	0.536103	46768698	0.881529	4476891863	1504803751	548518958	2423569154
12-02 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	81207320	47984633	0.59089	42427281	0.884185	4078690326	1215467036	508267406	2354955884
12-02 N	3	5998080	3137161264	57635363	57633968	64933654	43474071	0.669515	39682788	0.912792	3804440182	1170783114	454821800	2178835268
12-03 Gp3 Focus 1	3	5998080	3137161264	57635363	57633968	162459520	65502483	0.403193	57555837	0.878682	5429654546	2280941652	722927695	2425785199
12-03 Gp4 Focus 1	3	5998080	3137161264	57635363	57633968	117608098	48827856	0.415174	43025298	0.881163	4069261042	1752389364	531571092	1785300586
12-03 Gp4 Focus 2	5	3901294	3137161264	54413025	56496747	109639462	64814324	0.591159	55261918	0.852619	5173587408	1324943019	721794773	3126849616
12-03 N	3	5998080	3137161264	57635363	57633968	64159742	37539001	0.585087	34269128	0.912894	3317140570	1179252482	410020993	1727867095
Mean			3137161264	57461183	57572497	93901446.22	54528660.41	0.59015459	47093893	0.8539819	4429489082	1523798084	521832322	2383858676
Median			3137161264	57635363	57633968	93496090	53021655	0.585087	46114403	0.881362	4208818825	1504803751	508267406	2350579355

Sample	Bases Mapped to Bait Intervals	Percent On + Near Bases	Percent Off Target	Mean Bait Coverage (Fold)	Mean Target Coverage (fold)	Percent Unique On-Bait Bases	Percent Unique On-Target Bases	Fold Enrichment	Percent Targets without Coverage	Percent On Target Bases Coveraged at 2x	Percent On Target Bases Coveraged at 10x	Percent On Target Bases Coveraged at 20x	Percent On Target Bases Coveraged at 30x	Percent On Target Bases Coveraged at 40x
10-01 Gp3 Focus 1	2.354E+09	0.504926	0.495074	40.84529	43.152662	0.243057	0.243054	20.343504	0.074115	0.887552	0.713089	0.562823	0.449168	0.361247
10-01 Gp4 Focus 1	2.608E+09	0.512454	0.487546	45.248903	47.552748	0.241066	0.241064	20.508121	0.066828	0.901306	0.74226	0.597684	0.485551	0.396612
10-01 N	2.411E+09	0.503689	0.496311	41.828551	44.598637	0.227399	0.227396	20.310192	0.084645	0.875203	0.70326	0.55448	0.444707	0.36067
11-01 Gp3 Focus 1	1.506E+09	0.475062	0.524938	26.127294	27.696429	0.17716	0.177158	20.910455	0.082358	0.85391	0.589511	0.402961	0.286625	0.209107
11-01 Gp4 Focus 1	3.148E+09	0.507929	0.492071	54.626964	56.787964	0.236082	0.23608	21.436994	0.05116	0.932876	0.813294	0.674199	0.558394	0.463241
11-01 N	2.179E+09	0.515542	0.484458	37.812166	39.854156	0.246697	0.246694	21.916531	0.070403	0.896868	0.726179	0.557515	0.430252	0.334525
11-02 Gp3 Focus 1	1.649E+09	0.393615	0.606385	28.606621	30.21211	0.130265	0.130263	16.377391	0.074242	0.882056	0.659229	0.469211	0.339033	0.247669
11-02 Gp4 Focus 1	1.602E+09	0.42322	0.57678	27.804345	29.440781	0.151443	0.151441	17.397693	0.077202	0.885419	0.657781	0.460441	0.327116	0.235515
11-02 Gp4 Focus 2	633913476	0.311623	0.688377	11.190077	12.520817	0.074949	0.07803	12.278923	0.141115	0.750967	0.388334	0.183161	0.091492	0.048574
11-02 N	1.455E+09	0.477888	0.522112	25.250459	27.183251	0.193939	0.193937	19.504663	0.09708	0.853021	0.615281	0.424265	0.299329	0.214131
11-03 Gp3 Focus 1	785645828	0.273417	0.726583	13.631484	14.728587	0.124235	0.124233	10.593842	0.109364	0.814864	0.437562	0.222384	0.122621	0.071474
11-03 Gp4 Focus 1	667154456	0.419505	0.580495	11.575603	12.973597	0.185716	0.185713	16.810507	0.158784	0.727902	0.352322	0.183798	0.106239	0.064443
11-03 N	898121784	0.411113	0.588887	15.583023	17.080529	0.168718	0.168715	15.841745	0.124791	0.804806	0.476499	0.269803	0.160609	0.098801
11-10 Gp3 Focus 1	1.813E+09	0.407111	0.592889	31.461559	33.091735	0.187773	0.187771	16.93164	0.068879	0.895743	0.686248	0.49696	0.365638	0.272369
11-10 Gp3 Focus 2	657956037	0.486015	0.513985	11.416209	20.72764	0.08912	0.089117	19.794713	0.596433	0.201279	0.123776	0.102024	0.087306	0.075854
11-10 Gp4 Focus 1	1.355E+09	0.402871	0.597129	23.518611	25.074348	0.167441	0.167439	16.736731	0.088682	0.852591	0.57449	0.379353	0.262499	0.186627
11-10 Gp4 Focus 2	738039093	0.408335	0.591665	12.805459	18.597452	0.102614	0.102613	16.517881	0.429218	0.32582	0.198599	0.15189	0.121862	0.099705
11-10 N	2.003E+09	0.429788	0.570212	34.76062	36.893111	0.181849	0.181847	18.090834	0.080095	0.871417	0.662424	0.494922	0.381045	0.298458
11-12 Gp3 Focus 1	955095510	0.382727	0.617273	16.571478	26.501284	0.095573	0.095572	15.738717	0.513049	0.308876	0.169551	0.126347	0.103901	0.089004
11-12 Gp4 Focus 1	1.237E+09	0.46443	0.53557	21.469048	24.485946	0.149201	0.149199	18.380499	0.186072	0.696916	0.401027	0.267655	0.196713	0.151656
11-12 N	1.705E+09	0.423504	0.576496	29.584439	31.523104	0.162528	0.162526	16.413431	0.084974	0.878652	0.657115	0.468287	0.339877	0.25133
11-13 Gp3 Focus 1	447103372	0.321369	0.678631	7.757475	21.626267	0.064316	0.064316	13.274622	0.805469	0.077227	0.031952	0.026867	0.024404	0.022678
11-13 Gp4 Focus 1	607396800	0.344191	0.655809	10.538683	18.387602	0.069661	0.06966	14.234921	0.56986	0.241523	0.094378	0.063603	0.050249	0.042463
11-13 N	2.03E+09	0.499864	0.500136	35.217725	37.758536	0.228971	0.228968	19.836026	0.092718	0.86546	0.655421	0.489321	0.376423	0.295561
11-14 Gp3 Focus 1	1.287E+09	0.55732	0.44268	22.328236	32.756034	0.137642	0.137641	23.075403	0.445756	0.403619	0.247637	0.19139	0.159501	0.137205
11-14 Gp4 Focus 1	1.079E+09	0.512215	0.487785	18.716816	29.479019	0.109748	0.109746	20.93288	0.503423	0.347634	0.22168	0.172922	0.14348	0.122723
11-14 N	1.647E+09	0.491376	0.508624	28.569683	30.39136	0.192491	0.192488	19.393871	0.083059	0.880618	0.660979	0.465335	0.333238	0.242189
12-01 Gp3 Focus 1	1.96E+09	0.573406	0.426594	34.009927	36.090085	0.198823	0.198821	23.381348	0.087289	0.848771	0.543849	0.384633	0.298506	0.241404
12-01 Gp4 Focus 1	1.641E+09	0.518837	0.481163	28.463751	35.92585	0.158629	0.158628	21.216256	0.301275	0.54197	0.324264	0.247329	0.204527	0.174955
12-01 N	2.916E+09	0.507518	0.492482	50.592531	52.753587	0.170884	0.170883	20.485098	0.057615	0.917389	0.732652	0.577166	0.470277	0.391106
12-02 Gp3 Focus 1	1.505E+09	0.458649	0.541351	26.109036	27.390449	0.152058	0.152056	18.295786	0.067604	0.884028	0.568124	0.357956	0.247097	0.181298
12-02 Gp4 Focus 1	1.215E+09	0.42262	0.57738	21.088911	22.142399	0.149675	0.149673	16.220725	0.069349	0.880762	0.524342	0.294692	0.189962	0.134015
12-02 N	1.171E+09	0.427291	0.572709	20.313624	22.66386	0.180305	0.180302	16.750721	0.138769	0.795248	0.525007	0.342683	0.232312	0.161081
12-03 Gp3 Focus 1	2.281E+09	0.553234	0.446766	39.575385	43.683025	0.140401	0.140399	22.865978	0.142641	0.7454	0.456438	0.338172	0.274996	0.23302
12-03 Gp4 Focus 1	1.752E+09	0.561272	0.438728	30.40476	32.997801	0.149002	0.149001	23.440284	0.117306	0.775521	0.437683	0.291969	0.222961	0.180966
12-03 Gp4 Focus 2	1.394E+09	0.395613	0.604387	24.34974	26.843468	0.120845	0.127178	14.765202	0.10218	0.847206	0.643807	0.461555	0.320627	0.216466
12-03 N	1.179E+09	0.479109	0.520891	20.460572	22.070116	0.183799	0.183797	19.350435	0.104368	0.837811	0.549855	0.347599	0.229275	0.155163
Mean	1.526E+09	0.4529364	0.54706357	26.492299	30.09828	0.160650676	0.160903216	18.3879612	0.1877884	0.7294116	0.50178105	0.35414473	0.2631841	0.201710946
Median	1.505E+09	0.46443	0.53557	26.109036	29.440781	0.162528	0.162526	18.380499	0.09708	0.848771	0.549855	0.357956	0.262499	0.186627

Sample	Percent On Target Bases Coveraged at 50x	Percent On Target Bases Coveraged at 100x	Unique Library Molecules	% Under Covered AT regions	% Under Covered GC Regions
10-01 Gp3 Focus 1	0.291391	0.103567	27131421	2.571488	18.043049
10-01 Gp4 Focus 1	0.325268	0.124014	30550244	2.783109	17.93582
10-01 N	0.29473	0.112987	25056624	1.267461	22.734788
11-01 Gp3 Focus 1	0.1559	0.044196	12464057	3.91791	8.551229
11-01 Gp4 Focus 1	0.385419	0.160596	34322079	4.199153	9.66224
11-01 N	0.261819	0.083192	24087567	2.746272	15.514336
11-02 Gp3 Focus 1	0.182206	0.043339	12915249	2.783361	14.35033
11-02 Gp4 Focus 1	0.171405	0.039818	14151751	3.903233	14.213213
11-02 Gp4 Focus 2	0.027127	0.002651	5024312	7.306844	6.541224
11-02 N	0.154675	0.032886	13599985	1.747904	21.312466
11-03 Gp3 Focus 1	0.043797	0.006025	10056115	3.388409	15.020479
11-03 Gp4 Focus 1	0.040624	0.005499	7569665	2.187367	17.359724
11-03 N	0.062211	0.008306	9553012	3.206655	16.656886
11-10 Gp3 Focus 1	0.205073	0.054978	20245671	3.273632	15.689328
11-10 Gp3 Focus 2	0.066595	0.03779	5513199	2.597397	8.36857
11-10 Gp4 Focus 1	0.13551	0.032587	13473136	4.478897	16.514127
11-10 Gp4 Focus 2	0.082613	0.035372	6513160	1.741161	9.862863
11-10 N	0.235998	0.079225	17825283	3.484452	18.147618
11-12 Gp3 Focus 1	0.07808	0.047419	8521212	18.828768	4.276563
11-12 Gp4 Focus 1	0.120729	0.049056	11096815	28.90725	3.408482
11-12 N	0.188138	0.050901	17128191	2.077016	15.047545
11-13 Gp3 Focus 1	0.021334	0.017015	3863167	5.534232	8.348112
11-13 Gp4 Focus 1	0.037197	0.023896	5271994	2.104619	12.109629
11-13 N	0.234841	0.083359	27195751	2.564102	18.173925
11-14 Gp3 Focus 1	0.120254	0.069601	10387188	28.608067	4.782018
11-14 Gp4 Focus 1	0.106623	0.058708	8787688	30.998783	3.571985
11-14 N	0.178704	0.044864	16222890	2.047872	13.408678
12-01 Gp3 Focus 1	0.200371	0.093551	16977634	31.255815	3.381309
12-01 Gp4 Focus 1	0.152456	0.086027	14790596	32.497526	3.333902
12-01 N	0.329422	0.153487	25070246	15.534268	6.335949
12-02 Gp3 Focus 1	0.138657	0.04975	13396695	18.615858	2.897681
12-02 Gp4 Focus 1	0.100099	0.033165	11582122	20.348277	3.240493
12-02 N	0.113477	0.022241	11857638	1.221552	25.553171
12-03 Gp3 Focus 1	0.201781	0.113895	18023350	32.697887	5.145077
12-03 Gp4 Focus 1	0.151909	0.078831	13813082	32.910659	4.985944
12-03 Gp4 Focus 2	0.143639	0.018999	12887348	0.510163	23.063813
12-03 N	0.107337	0.020492	10379587	2.797521	13.185417
Mean	0.1580381	0.0573591	14792046.6	9.9363497	11.911567
Median	0.151909	0.047419	13396695	3.388409	13.185417