Sample2	Illlumina pool name	Sample	i5	i5 sequence	i7	i7 sequence	Conc ng/uL	Total uL	ng	% of pool		uL of library
aff_50	pool_1	50	517	GCGTAAGA	701	TAAGGCGA	4.95	17	84.15	0.82	16	3.23
aff_pool_m25	pool_2	pool_m25	502	CTCTCTAT	701	TAAGGCGA	15.3	17	260.1	0.82	16	1.05
aff_130530_M11	pool_3	130530_M11	503	TATCCTCT	701	TAAGGCGA	17	17	289	0.82	16	0.94
aff_140515_M5	pool_4	140515_M5	504	AGAGTAGA	701	TAAGGCGA	11.7	17	198.9	0.82	16	1.37
aff_180425_M38	pool_5	180425_M38	505	GTAAGGAG	701	TAAGGCGA	10.8	17	183.6	0.82	16	1.48
aff_148	pool_6	148	506	ACTGCATA	701	TAAGGCGA	3.8	17	64.6	0.82	16	4.21
aff_126	pool_7	126	507	AAGGAGTA	701	TAAGGCGA	4.6	17	78.2	0.82	16	3.48
aff_130516_M3	pool_8	130516_M3	508	CTAAGCCT	701	TAAGGCGA	3.95	17	67.15	0.82	16	4.05
aff_161	pool_9	161	517	GCGTAAGA	702	CGTACTAG	7.16	18	128.88	0.82	16	2.23
aff_180421_M7	pool_10	180421_M7	502	CTCTCTAT	702	CGTACTAG	11.3	17	192.1	0.82	16	1.42
aff_SM15_M71	pool_11	SM15_M71	503	TATCCTCT	702	CGTACTAG	10.2	18	183.6	0.82	16	1.57
aff_SM15_M168	pool_12	SM15_M168	504	AGAGTAGA	702	CGTACTAG	10.6	18	190.8	0.82	16	1.51
aff_SM15_M159	pool_13	SM15_M159	505	GTAAGGAG	702	CGTACTAG	6.97	18	125.46	0.82	16	2.30
aff_167	pool_14	167	506	ACTGCATA	702	CGTACTAG	8.74	18	157.32	0.82	16	1.83
aff_130530_M6	pool_15	130530_M6	507	AAGGAGTA	702	CGTACTAG	11.3	18	203.4	0.82	16	1.42
aff_SM15_M202	pool_16	SM15_M202	508	CTAAGCCT	702	CGTACTAG	5.33	17	90.61	0.82	16	3.00
aff_149	pool_17	149	517	GCGTAAGA	703	AGGCAGAA	7.63	17	129.71	0.82	16	2.10
aff_L+_SM15_M76	pool_18	L+_SM15_M76	502	CTCTCTAT	703	AGGCAGAA	15	18	270	0.82	16	1.07
aff_130516_M7	pool_19	130516_M7	503	TATCCTCT	703	AGGCAGAA	14.6	18	262.8	0.82	16	1.10
aff_L+_SM_M11	pool_20	L+_SM_M11	504	AGAGTAGA	703	AGGCAGAA	12.8	18	230.4	0.82	16	1.25
aff_170927_M9	pool_21	170927_M9	505	GTAAGGAG	703	AGGCAGAA	11.1	18	199.8	0.82	16	1.44
aff SM15 M201	pool_22	SM15_M201	506	ACTGCATA	703	AGGCAGAA	15.1	17	256.7	0.82	16	1.06
aff_180508_M66	pool_23	180508_M66	507	AAGGAGTA	703	AGGCAGAA	18.2	18	327.6	0.82	16	0.88
aff_180430_M13	pool_24	180430_M13	508	CTAAGCCT	703	AGGCAGAA	5.53	18	99.54	0.82	16	2.89
Wb	pool_25	Dinnu_Wb+	517	GCGTAAGA	704	TCCTGAGC	5.52	17	93.84	2.46	16	2.90
aff_SM15_M164	pool_26	SM15_M164	502	CTCTCTAT	704	TCCTGAGC	7.32	17	124.44	0.82	16	2.19
aff SM15 M208	pool_27	SM15_M208	503	TATCCTCT	704	TCCTGAGC	4.5	18	81	0.82	16	3.56
aff_SM15_M98	pool_28	SM15_M98	504	AGAGTAGA	704	TCCTGAGC	4.13	18	74.34	0.82	16	3.87
aff L+ SM15 M60	pool_29	L+_SM15_M60	505	GTAAGGAG	704	TCCTGAGC	1.36	18	24.48	0.82	16	11.76
aff SM15 M157	pool_30	SM15_M157	506	ACTGCATA	704	TCCTGAGC	2.86	18	51.48	0.82	16	5.59
aff_SM15_M204	pool_31	SM15_M204	507	AAGGAGTA	704	TCCTGAGC	4.49	18	80.82	0.82	16	3.56
aff Pool M23	pool_32	Pool M23	508	CTAAGCCT	704	TCCTGAGC	2.89	18	52.02	0.82	16	5.54
aff_SM15_M160	pool_33	SM15_M160	517	GCGTAAGA	705	GGACTCCT	3.54	17	60.18	0.82	16	4.52
aff Pool M47	pool_34	Pool_M47	502	CTCTCTAT	705	GGACTCCT	5.26	18	94.68	0.82	16	3.04
aff_191	pool_35	191	503	TATCCTCT	705	GGACTCCT	3.7	18	66.6	0.82	16	4.32
aff 86	pool_36	86	504	AGAGTAGA	705	GGACTCCT	4.02	18	72.36	0.82	16	3.98
aff_SM15_M124	pool_37	SM15 M124	505	GTAAGGAG	705	GGACTCCT	3.85	18	69.3	0.82	16	4.16
aff_180508_M68_male	pool_38	30508_M68_ma	506	ACTGCATA	705	GGACTCCT	5.84	17	99.28	0.82	16	2.74
aff SM15 M22	pool_39	SM15 M22	507	AAGGAGTA	705	GGACTCCT	3.13	18	56.34	0.82	16	5.11
aff_180430_M7	pool_40	180430_M7	508	CTAAGCCT	705	GGACTCCT	5.63	18	101.34	0.82	16	2.84
aff 130539 M7	pool_41	130539_M7	517	GCGTAAGA	706	TAGGCATG	2.21	17	37.57	0.82	16	7.24
aff_192	pool_42	192	502	CTCTCTAT	706	TAGGCATG	2.14	18	38.52	0.82	16	7.48
aff 180423 M1	pool_43	180423 M1	503	TATCCTCT	706	TAGGCATG	11.6	17	197.2	0.82	16	1.38
aff_180508_M95_male	pool_44	30508 M95 ma	504	AGAGTAGA	706	TAGGCATG	3.89	18	70.02	0.82	16	4.11
aff_140515_M19	pool_45	140515 M19	505	GTAAGGAG	706	TAGGCATG	8.23	18	148.14	0.82	16	1.94
aff L+ SM15 M2	pool_46	L+ SM15 M2	506	ACTGCATA	712	GTAGAGGA	2.47	18	44.46	0.82	16	6.48
aff_180508_M21_male	pool_47	30508_M21_ma	507	AAGGAGTA	706	TAGGCATG	3.92	18	70.56	0.82	16	4.08
aff 180421 M9	pool_48	180421 M9	508	CTAAGCCT	706	TAGGCATG	4.36	18	78.48	0.82	16	3.67

		donat famala	F.17	00074404	707	07070740	2.44	40	42.02	2.46	1.0	6.56
a .	pool_49	_dunni_female_	517	GCGTAAGA	707	CTCTCTAC	2.44	18	43.92	2.46	16	6.56
b	pool_50	a_hana_female_	502	CTCTCTAT	707	CTCTCTAC	2.18	17	37.06	2.46	16	7.34
C	pool_51	milis_female_to	503	TATCCTCT	707	CTCTCTAC	3.02	18	54.36	2.46	16	5.30
d	pool_52	unni_female_tor	504	AGAGTAGA	707	CTCTCTAC	3.93	18	70.74	2.46	16	4.07
e	pool_53	Dpt_1bpdel_sar	505	GTAAGGAG	707	CTCTCTAC	6.71	18	120.78	2.46	16	2.38
f	pool_54	N_Dpt_SS_saral	506	ACTGCATA	707	CTCTCTAC	8.71	18	156.78	2.46	16	1.84
g	pool_55	14_Dpt_RR2_sai	507	AAGGAGTA	707	CTCTCTAC	10.8	17	183.6	2.46	16	1.48
h	pool_56	4_Dpt_RR_saral	508	CTAAGCCT	707	CTCTCTAC	3.06	18	55.08	2.46	16	5.23
aff_SR141	pool_57	SR141	517	GCGTAAGA	708	CAGAGAGG	3.23	18	58.14	2.46	16	4.95
aff_SM15_M210	pool_58	SM15_M210	502	CTCTCTAT	708	CAGAGAGG	3.08	18	55.44	0.82	16	5.19
aff_180508_M58_male	pool_59	30508_M58_ma	503	TATCCTCT	708	CAGAGAGG	7.91	17	134.47	0.82	16	2.02
aff_180508_M75_male	pool_60	30508_M75_ma	504	AGAGTAGA	708	CAGAGAGG	1.32	17	22.44	0.82	16	12.12
aff_pool_M41	pool_61	pool_M41	505	GTAAGGAG	708	CAGAGAGG	2.47	18	44.46	0.82	16	6.48
aff_180425_M58B	pool_62	180425_M58B	506	ACTGCATA	708	CAGAGAGG	2.78	18	50.04	0.82	16	5.76
aff_140515_M14	pool_63	140515_M14	507	AAGGAGTA	708	CAGAGAGG	2.83	18	50.94	0.82	16	5.65
aff_154	pool_64	154	508	CTAAGCCT	708	CAGAGAGG	2.04	18	36.72	0.82	16	7.84
aff_SM_M8	pool_65	SM_M8	517	GCGTAAGA	709	GCTACGCT	1.06	17	18.02	0.82	16	15.09
aff_180508_M82_male	pool_66	30508_M82_ma	502	CTCTCTAT	709	GCTACGCT	3.69	17	62.73	0.82	16	4.34
aff_SM15_M207	pool_67	SM15_M207	503	TATCCTCT	709	GCTACGCT	1.07	18	19.26	0.82	16	14.95
aff pool M43	pool_68	pool M43	504	AGAGTAGA	709	GCTACGCT	2.68	18	48.24	0.82	16	5.97
aff_SM_M4	pool_69	SM_M4	505	GTAAGGAG	709	GCTACGCT	1.06	18	19.08	0.82	16	15.09
aff pool M6	pool_70	pool_M6	506	ACTGCATA	709	GCTACGCT	1.34	18	24.12	0.82	16	11.94
aff 170425 M3	pool_71	170425_M3	507	AAGGAGTA	709	GCTACGCT	3.02	18	54.36	0.82	16	5.30
aff 128	pool_72	128	508	CTAAGCCT	709	GCTACGCT	1.06	18	19.08	0.82	16	15.09
 aff_102	pool_74	102	502	CTCTCTAT	710	CGAGGCTG	1.68	18	30.24	0.82	16	9.52
aff 180508 M10 male	pool_75	30508 M10 ma	503	TATCCTCT	710	CGAGGCTG	2.72	18	48.96	0.82	16	5.88
aff 180423 M8	pool_76	180423 M8	504	AGAGTAGA	710	CGAGGCTG	1.58	18	28.44	0.82	16	10.13
aff_170427_M5	pool_77	170427_M5	505	GTAAGGAG	710	CGAGGCTG	1.83	18	32.94	0.82	16	8.74
aff_SM15_M185	pool_78	SM15_M185	506	ACTGCATA	710	CGAGGCTG	2.5	18	45	0.82	16	6.40
aff SM M13	pool_79	SM_M13	507	AAGGAGTA	710	CGAGGCTG	1.02	17	17.34	0.82	16	15.69
aff_140	pool_80	140	508	CTAAGCCT	710	CGAGGCTG	2.51	18	45.18	0.82	16	6.37
i	pool_81	FA andrea	517	GCGTAAGA	711	AAGAGGCA	3.58	18	64.44	2.46	16	4.47
k	pool_82	FB andrea	502	CTCTCTAT	711	AAGAGGCA	2.04	17	34.68	2.46	16	7.84
I I	pool_83	FC_andrea	503	TATCCTCT	711	AAGAGGCA	4.37	18	78.66	2.46	16	3.66
m	pool_84	DA_andrea	504	AGAGTAGA	711	AAGAGGCA	5.45	18	98.1	2.46	16	2.94
n	pool_85	DB andrea	505	GTAAGGAG	711	AAGAGGCA	5.56	18	100.08	2.46	16	2.88
0	pool_86	DC andrea	506	ACTGCATA	711	AAGAGGCA	6.11	18	100.08	2.46	16	2.62
	pool_87	yaf_170	517	GCGTAAGA	711	GTAGAGGA	4.26	17	72.42	0.82	16	3.76
aff_yaf_170			502				6.32	17	107.44	0.82	16	2.53
aff_yaf_141	pool_88	yaf_141		CTCTCTAT	712	GTAGAGGA		17				
aff_yaf_194	pool_89	yaf_194	503	TATCCTCT	712	GTAGAGGA	8.6		146.2	0.82	16	1.86
aff_yaf_144	pool_90	yaf_144	504	AGAGTAGA	712	GTAGAGGA	3.62	17	61.54	0.82	16	4.42
aff_yaf_54	pool_91	yaf_54	505	GTAAGGAG	712	GTAGAGGA	4.2	17	71.4	0.82	16	3.81