

Quality Value	> 35	20 - 35	< 20
LOR Value	> 600bp	301-600bp	< 300bp

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
1	1G	G_F	7 %	260 bp	41
2	2G	G_F	4 %	256 bp	52
3	3G	G_F	5 %	257 bp	50
4	4G	G_F	3 %	258 bp	50
5	5G	G_F	3 %	257 bp	51
6	6G	G_F	4 %	259 bp	50
7	7G	G_F	4 %	260 bp	51

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
8	8G	G_F	3 %	259 bp	52
9	9G	G_F	5 %	259 bp	50
10	10G	G_F	5 %	259 bp	51
11	11G	G_F	5 %	260 bp	50
12	12G	G_F	4 %	258 bp	51
13	13G	G_F	6 %	260 bp	48
14	14G	G_F	3 %	257 bp	50
15	1G	G_R	2 %	259 bp	51
16	2G	G_R	2 %	262 bp	50

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
17	3G	G_R	15 %	634 bp	14
18	4G	G_R	3 %	261 bp	50
19	5G	G_R	1 %	262 bp	50
20	6G	G_R	4 %	259 bp	50
21	7G	G_R	2 %	261 bp	49
22	8G	G_R	4 %	259 bp	51
23	9G	G_R	1 %	260 bp	52
24	10G	G_R	2 %	262 bp	49
25	11G	G_R	2 %	260 bp	50

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
26	12G	G_R	22 %	635 bp	14
27	13G	G_R	7 %	296 bp	23
28	14G	G_R	3 %	261 bp	50
29	1S	S_F	7 %	678 bp	38
30	2S	S_F	7 %	677 bp	38
31	3S	S_F	10 %	624 bp	21
32	4S	S_F	6 %	677 bp	38
33	5S	S_F	9 %	678 bp	37
34	6S	S_F	7 %	677 bp	38

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
35	7S	S_F	12 %	730 bp	37
36	8S	S_F	14 %	729 bp	39
37	9S	S_F	16 %	728 bp	34
38	10S	S_F	7 %	674 bp	37
39	11S	S_F	7 %	678 bp	37
40	12S	S_F	7 %	678 bp	38
41	13S	S_F	8 %	678 bp	36
42	14S	S_F	7 %	676 bp	37
43	1S	S_R	29 %	660 bp	18

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
44	2S	S_R	38 %	649 bp	18
45	3S	S_R	10 %	485 bp	23
46	4S	S_R	38 %	648 bp	18
47	5S	S_R	25 %	668 bp	20
48	6S	S_R	33 %	655 bp	18
49	7S	S_R	26 %	647 bp	19
50	8S	S_R	30 %	353 bp	11
51	9S	S_R	11 %	760 bp	14
52	10S	S_R	12 %	671 bp	22

Reaction	Template Name	Primer Name	N-Base Calls	Length of Read	Quality Value
53	11S	S_R	34 %	647 bp	18
54	12S	S_R	34 %	660 bp	17
55	13S	S_R	29 %	663 bp	19
56	14S	S_R	33 %	630 bp	19

This report isn't a detailed analysis of the data, it displays a summary of performance regarding the read length and base-call quality of the reactions. Please check the data thoroughly before continuing with your research. If you wish to discuss your data further please contact [sequencing@sourcebioscience.com](mailto:sequencing@sourcebioscience.com)