

Additional File S3:

Concordance with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® (n=17)

a) Non-reference sensitivity (NRS) for single nucleotide variants identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard (BTA1-BTA29)

Single sampe variant identification													Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
Animal	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
50K_1	0.779	0.800	0.800	0.806	0.827	0.827	0.846	0.856	0.855	0.813	0.848	0.848	0.914	0.891	0.899	0.906	0.915
50K_2	0.806	0.826	0.826	0.831	0.851	0.851	0.867	0.877	0.877	0.842	0.870	0.870	0.916	0.896	0.904	0.910	0.916
50K_3	0.820	0.835	0.835	0.847	0.863	0.863	0.895	0.903	0.903	0.868	0.891	0.891	0.920	0.894	0.902	0.916	0.922
50K_4	0.798	0.817	0.817	0.826	0.844	0.845	0.877	0.884	0.884	0.843	0.875	0.875	0.921	0.893	0.901	0.914	0.922
50K_5	0.797	0.822	0.822	0.823	0.848	0.848	0.883	0.893	0.893	0.849	0.875	0.875	0.922	0.894	0.902	0.917	0.923
50K_6	0.838	0.860	0.860	0.867	0.888	0.888	0.897	0.907	0.907	0.874	0.901	0.901	0.922	0.900	0.908	0.919	0.923
50K_7	0.820	0.840	0.840	0.846	0.866	0.866	0.878	0.888	0.888	0.857	0.883	0.883	0.920	0.896	0.904	0.913	0.921
50K_8	0.834	0.851	0.851	0.863	0.880	0.880	0.895	0.905	0.905	0.875	0.899	0.899	0.922	0.897	0.905	0.918	0.924
50K_9	0.839	0.849	0.849	0.865	0.875	0.875	0.889	0.893	0.893	0.875	0.888	0.888	0.906	0.879	0.887	0.900	0.906
50K_10	0.790	0.814	0.814	0.816	0.840	0.840	0.867	0.874	0.874	0.834	0.867	0.867	0.917	0.894	0.902	0.910	0.918
50K_11	0.800	0.823	0.823	0.828	0.851	0.851	0.873	0.879	0.879	0.837	0.874	0.874	0.916	0.894	0.901	0.910	0.917
50K_12	0.823	0.837	0.837	0.851	0.865	0.865	0.891	0.896	0.897	0.867	0.888	0.888	0.919	0.895	0.903	0.916	0.920
50K_13	0.814	0.833	0.833	0.840	0.859	0.859	0.883	0.892	0.892	0.859	0.883	0.883	0.919	0.894	0.902	0.911	0.919
50K_14	0.808	0.828	0.828	0.835	0.855	0.855	0.876	0.884	0.884	0.845	0.877	0.877	0.922	0.900	0.909	0.915	0.923
50K_15	0.834	0.850	0.850	0.861	0.876	0.876	0.894	0.900	0.900	0.869	0.892	0.893	0.921	0.899	0.907	0.916	0.923
50K_16	0.765	0.789	0.789	0.792	0.816	0.816	0.846	0.855	0.855	0.802	0.846	0.846	0.902	0.878	0.886	0.897	0.903
50K_17	0.797	0.814	0.813	0.823	0.840	0.840	0.861	0.868	0.868	0.838	0.864	0.864	0.918	0.898	0.907	0.912	0.920
Average	0.810	0.829	0.829	0.836	0.856	0.856	0.877	0.886	0.886	0.850	0.878	0.878	0.918	0.894	0.902	0.912	0.919

b) Non-reference discrepancy (NRD) for single nucleotide variants identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard (BTA1-BTA29)

Single sampe variant identification													Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
Animal	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
50K_1	0.046	0.045	0.045	0.049	0.048	0.047	0.047	0.046	0.046	0.049	0.048	0.048	0.048	0.096	0.090	0.090	0.104
50K_2	0.047	0.046	0.046	0.048	0.048	0.048	0.047	0.047	0.047	0.048	0.048	0.048	0.048	0.092	0.087	0.087	0.098
50K_3	0.042	0.041	0.041	0.043	0.042	0.042	0.039	0.038	0.038	0.039	0.038	0.039	0.038	0.039	0.084	0.083	0.084
50K_4	0.043	0.043	0.043	0.045	0.045	0.045	0.041	0.040	0.040	0.042	0.042	0.043	0.043	0.085	0.083	0.083	0.089
50K_5	0.045	0.044	0.044	0.047	0.046	0.046	0.042	0.041	0.041	0.043	0.043	0.043	0.043	0.082	0.092	0.091	0.084
50K_6	0.035	0.034	0.034	0.037	0.035	0.035	0.035	0.034	0.034	0.036	0.035	0.035	0.035	0.078	0.077	0.077	0.080
50K_7	0.043	0.041	0.041	0.045	0.043	0.043	0.043	0.042	0.042	0.044	0.043	0.043	0.043	0.085	0.085	0.085	0.090
50K_8	0.040	0.039	0.039	0.041	0.040	0.040	0.040	0.038	0.038	0.041	0.040	0.040	0.040	0.081	0.080	0.080	0.081
50K_9	0.051	0.050	0.050	0.052	0.051	0.051	0.049	0.049	0.049	0.049	0.049	0.050	0.099	0.100	0.101	0.102	0.099
50K_10	0.045	0.044	0.044	0.047	0.045	0.045	0.045	0.044	0.044	0.046	0.045	0.046	0.088	0.085	0.086	0.093	0.087
50K_11	0.047	0.046	0.046	0.048	0.046	0.046	0.047	0.047	0.047	0.048	0.048	0.048	0.048	0.090	0.087	0.087	0.092
50K_12	0.049	0.049	0.049	0.051	0.050	0.050	0.048	0.048	0.048	0.049	0.048	0.049	0.049	0.090	0.089	0.090	0.091
50K_13	0.049	0.048	0.048	0.051	0.050	0.050	0.048	0.048	0.048	0.050	0.049	0.049	0.049	0.093	0.092	0.091	0.094
50K_14	0.046	0.045	0.045	0.047	0.046	0.046	0.045	0.044	0.044	0.046	0.044	0.045	0.081	0.078	0.078	0.090	0.081
50K_15	0.040	0.041	0.041	0.042	0.042	0.042	0.039	0.039	0.039	0.040	0.040	0.040	0.040	0.085	0.084	0.084	0.086
50K_16	0.055	0.054	0.054	0.057	0.056	0.056	0.054	0.052	0.052	0.057	0.054	0.054	0.100	0.099	0.099	0.105	0.099
50K_17	0.046	0.046	0.046	0.048	0.048	0.048	0.045	0.044	0.044	0.047	0.048	0.048	0.088	0.082	0.082	0.098	0.087
Average	0.045	0.044	0.044	0.047	0.046	0.046	0.044	0.044	0.044	0.046	0.045	0.045	0.088	0.087	0.087	0.092	0.087

c) Single nucleotide variant concordance identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single vs. multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard. (BTA1-BTA29)

Single sampe variant identification													Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
Animal	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
50K_1	0.388	0.398	0.398	0.402	0.412	0.412	0.422	0.426	0.426	0.405	0.422	0.422	0.422	0.834	0.813	0.821	0.834
50K_2	0.393	0.402	0.403	0.405	0.415	0.415	0.422	0.427	0.427	0.411	0.424	0.424	0.424	0.835	0.815	0.823	0.834
50K_3	0.396	0.403	0.403	0.409	0.416	0.416	0.432	0.436	0.436	0.419	0.430	0.430	0.430	0.837	0.819	0.826	0.834
50K_4	0.400	0.409	0.409	0.414	0.423	0.423	0.440	0.443	0.443	0.423	0.438	0.438	0.438	0.836	0.817	0.825	0.834
50K_5	0.398	0.411	0.411	0.411	0.424	0.424	0.441	0.446	0.446	0.425	0.437	0.437	0.437	0.837	0.818	0.826	0.834
50K_6	0.414	0.424	0.424	0.428	0.438	0.438	0.443	0.447	0.447	0.432	0.445	0.445	0.445	0.837	0.819	0.826	0.834
50K_7	0.409	0.419	0.419	0.423	0.432	0.432	0.438	0.443	0.443	0.428	0.441	0.441	0.441	0.836	0.817	0.825	0.834
50K_8	0.414	0.422	0.422	0.428	0.437	0.437	0.444	0.449	0.449	0.435	0.446	0.446	0.446	0.837	0.819	0.826	0.834
50K_9	0.403	0.408	0.408	0.416	0.421	0.421	0.428	0.430	0.430	0.421	0.427	0.427	0.427	0.835	0.817	0.825	0.833
50K_10	0.391	0.403	0.403	0.404	0.416	0.416	0.429	0.432	0.432	0.414	0.429	0.429	0.429	0.836	0.817	0.825	0.834
50K_11	0.392	0.403	0.403	0.406	0.417	0.417	0.427	0.430	0.430	0.410	0.428	0.428	0.428	0.836	0.817	0.825	0.834
50K_12	0.409	0.416	0.416	0.423	0.430	0.430	0.442	0.445	0.445	0.431	0.441	0.441	0.441	0.836	0.818	0.825	0.834
50K_13	0.397	0.405	0.405	0.410	0.419	0.419	0.430	0.434	0.434	0.419	0.430	0.430	0.430	0.836	0.818	0.826	0.834
50K_14	0.414	0.424	0.424	0.427	0.438	0.438	0.448	0.452	0.452	0.433	0.449	0.449	0.449	0.836	0.816	0.824	0.834
50K_15	0.434	0.442	0.442	0.449	0.456	0.456	0.465	0.468	0.468	0.452	0.464	0.465	0.465	0.837	0.819	0.827	0.834
50K_16	0.388	0.400	0.400	0.402	0.413	0.413	0.429	0.433	0.433	0.407	0.429	0.429	0.429	0.832	0.814	0.821	0.831
50K_17	0.410	0.418	0.418	0.423	0.432	0.432	0.443	0.446	0.446	0.431	0.444	0.444	0.444	0.835	0.814	0.822	0.834
Average	0.403	0.412	0.412	0.416	0.426	0.426	0.437	0.441	0.441	0.423	0.437	0.437	0.437	0.836	0.817	0.825	0.834

d) Single nucleotide variant concordance by genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single vs. multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard (BTA1-BTA29)

Single sampe variant identification													Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
Animal	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
50K_1	0.954	0.955	0.955	0.951	0.952	0.953	0.953	0.954	0.954	0.951	0.952	0.952	0.952	0.945	0.949	0.949	0.940
50K_2	0.953	0.954	0.954	0.952	0.952	0.952	0.953	0.953	0.953	0.952	0.952	0.952	0.952	0.948	0.952	0.952	0.945
50K_3	0.958	0.959	0.959	0.957	0.958	0.958	0.961	0.962	0.962	0.961	0.962	0.961	0.954	0.955	0.955	0.953	0.945
50K_4	0.957	0.957	0.957	0.955	0.955	0.955	0.959	0.960	0.960	0.958	0.958	0.957	0.951	0.953	0.953	0.948	0.952
50K_5	0.955	0.956	0.956	0.953	0.954	0.954	0.958	0.959	0.959	0.957	0.957	0.957	0.953	0.952	0.952	0.952	0.953
50K_6	0.965	0.966	0.966	0.963	0.965	0.965	0.965	0.966	0.966	0.964	0.965	0.965	0.955	0.957	0.957	0.955	0.957
50K_7	0.957	0.959	0.959	0.955	0.957	0.957	0.957	0.958	0.958	0.956	0.957	0.957	0.951	0.952	0.952	0.948	0.951
50K_8	0.960	0.961	0.961	0.959	0.960	0.960	0.960	0.962	0.962	0.959	0.960	0.960	0.954	0.955	0.955	0.954	0.955
50K_9	0.949	0.950	0.950	0.948	0.949	0.949	0.951	0.951	0.951	0.951	0.951	0.950	0.945	0.946	0.945	0.944	0.946
50K_10	0.955	0.956	0.956	0.953	0.955	0.955	0.955	0.956	0.956	0.954	0.955	0.954	0.950	0.952	0.952	0.947	0.951
50K_11	0.953	0.954	0.954	0.952	0.954	0.954	0.953	0.953	0.953	0.952	0.952	0.952	0.950	0.952	0.952	0.948	0.951
50K_12	0.951	0.951	0.951	0.949	0.950	0.950	0.952	0.952	0.952	0.951	0.952	0.951	0.949	0.950	0.950	0.948	0.950
50K_13	0.951	0.952	0.952	0.949	0.950	0.950	0.952	0.952	0.952	0.950	0.951	0.951	0.948	0.949	0.949	0.947	0.948
50K_14	0.954	0.955	0.955	0.953	0.954	0.954	0.955	0.956	0.956	0.954	0.956	0.955	0.952	0.954	0.954	0.947	0.953
50K_15	0.960	0.959	0.959	0.958	0.958	0.958	0.961	0.961	0.961	0.960	0.960	0.960	0.949	0.950	0.950	0.949	0.950
50K_16	0.945	0.946	0.946	0.943	0.944	0.944	0.946	0.948	0.948	0.943	0.946	0.946	0.942	0.944	0.944	0.939	0.943
50K_17	0.954	0.954	0.954	0.952	0.952	0.952	0.955	0.956	0.956	0.953	0.952	0.952	0.948	0.952	0.952	0.942	0.949
Average	0.955	0.956	0.956	0.953	0.954	0.954	0.956	0.956	0.956	0.954	0.955	0.955	0.950	0.951	0.951	0.947	0.950

e) Concordance for homozygous reference genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard (BTA1-BTA29)

Single sampe variant identification														Multi sample variant identification				
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper	
Animal	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	
50K_1	0.023	0.023	0.023	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.710	0.697	0.704	0.713	
50K_2	0.024	0.024	0.024	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.026	0.026	0.026	0.719	0.705	0.712	0.718	
50K_3	0.022	0.023	0.023	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.023	0.024	0.024	0.720	0.711	0.718	0.717	
50K_4	0.022	0.022	0.022	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.710	0.703	0.709	0.709	
50K_5	0.025	0.025	0.025	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.714	0.705	0.712	0.711	
50K_6	0.022	0.022	0.022	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.024	0.715	0.705	0.712	0.712	
50K_7	0.025	0.025	0.025	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.712	0.702	0.708	0.713	
50K_8	0.025	0.025	0.025	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.714	0.706	0.713	0.718	
50K_9	0.027	0.027	0.027	0.028	0.029	0.029	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.725	0.717	0.724	0.725	
50K_10	0.023	0.023	0.023	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.025	0.026	0.026	0.715	0.704	0.711	0.714	
50K_11	0.025	0.026	0.026	0.026	0.026	0.027	0.027	0.027	0.027	0.027	0.026	0.027	0.027	0.716	0.705	0.713	0.716	
50K_12	0.026	0.026	0.026	0.027	0.027	0.028	0.027	0.027	0.027	0.027	0.028	0.028	0.028	0.716	0.705	0.712	0.719	
50K_13	0.026	0.026	0.026	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.720	0.709	0.717	0.719	
50K_14	0.026	0.026	0.026	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.706	0.695	0.700	0.710	
50K_15	0.026	0.026	0.026	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.027	0.027	0.028	0.702	0.691	0.698	0.705	
50K_16	0.026	0.026	0.026	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.027	0.709	0.700	0.707	0.708	
50K_17	0.025	0.025	0.025	0.027	0.027	0.027	0.027	0.027	0.026	0.026	0.026	0.027	0.027	0.704	0.690	0.697	0.703	
Average	0.025	0.025	0.025	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.026	0.713	0.703	0.710	0.712	

f) Concordance for heterozygous genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller (single and multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard (BTA1-BTA29)

Animal	Single sampe variant identification												Multi sample variant identification					
	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper	
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW						
50K_1	0.810	0.811	0.811	0.839	0.839	0.839	0.851	0.850	0.850	0.851	0.854	0.854	0.981	0.957	0.965	0.971	0.983	
50K_2	0.815	0.817	0.817	0.844	0.846	0.846	0.861	0.860	0.860	0.860	0.864	0.864	0.980	0.960	0.967	0.973	0.981	
50K_3	0.838	0.838	0.838	0.869	0.868	0.868	0.879	0.877	0.878	0.878	0.878	0.878	0.981	0.958	0.967	0.974	0.983	
50K_4	0.821	0.821	0.821	0.851	0.850	0.850	0.865	0.863	0.862	0.864	0.866	0.867	0.982	0.953	0.962	0.974	0.983	
50K_5	0.833	0.833	0.833	0.860	0.859	0.859	0.871	0.870	0.871	0.869	0.870	0.870	0.980	0.956	0.966	0.976	0.981	
50K_6	0.833	0.834	0.834	0.864	0.864	0.864	0.872	0.870	0.870	0.870	0.872	0.872	0.980	0.959	0.968	0.975	0.981	
50K_7	0.832	0.834	0.834	0.861	0.862	0.862	0.871	0.870	0.870	0.869	0.872	0.872	0.980	0.956	0.965	0.972	0.983	
50K_8	0.834	0.836	0.836	0.868	0.869	0.869	0.876	0.875	0.875	0.878	0.879	0.879	0.981	0.956	0.966	0.972	0.981	
50K_9	0.839	0.841	0.841	0.869	0.871	0.871	0.879	0.877	0.877	0.876	0.879	0.879	0.967	0.947	0.955	0.963	0.968	
50K_10	0.819	0.820	0.820	0.846	0.847	0.847	0.863	0.860	0.860	0.865	0.867	0.867	0.978	0.956	0.966	0.974	0.979	
50K_11	0.824	0.826	0.826	0.855	0.857	0.857	0.869	0.866	0.866	0.867	0.870	0.870	0.981	0.956	0.964	0.975	0.983	
50K_12	0.832	0.832	0.833	0.859	0.860	0.860	0.874	0.874	0.874	0.870	0.873	0.874	0.979	0.954	0.964	0.973	0.980	
50K_13	0.830	0.830	0.830	0.859	0.859	0.859	0.871	0.871	0.871	0.873	0.875	0.875	0.981	0.956	0.966	0.974	0.982	
50K_14	0.820	0.821	0.821	0.850	0.851	0.851	0.863	0.861	0.861	0.862	0.866	0.866	0.978	0.956	0.967	0.971	0.979	
50K_15	0.841	0.841	0.841	0.870	0.870	0.870	0.879	0.877	0.877	0.878	0.880	0.881	0.979	0.957	0.966	0.975	0.981	
50K_16	0.825	0.827	0.827	0.852	0.854	0.854	0.864	0.863	0.863	0.866	0.868	0.868	0.968	0.945	0.955	0.967	0.969	
50K_17	0.804	0.807	0.807	0.835	0.837	0.837	0.852	0.852	0.852	0.855	0.857	0.857	0.978	0.955	0.963	0.977	0.979	
Average	0.827	0.827	0.828	0.856	0.857	0.857	0.868	0.867	0.867	0.868	0.870	0.870	0.979	0.955	0.964	0.973	0.980	

g) Concordance for homozygous alternative genotypes identified using Platypus, Samtools, UnifiedGenotyper and Haplotype Caller
(single and multi sample variant identification) using variants identified with the Illumina BovineSNP50 v1 DNA Analysis BeadChip® as a gold standard (BTA1-BTA29)

Single sampe variant identification													Multi sample variant identification				
Animal	Platypus			Platypus (Primitives)			Samtools			UnifiedGenotyper			Haplotype Caller	Platypus	Platypus (Primitives)	Samtools	Unified Genotyper
	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR	RAW	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR	IR+BQSR
50K_1	0.810	0.811	0.811	0.851	0.850	0.850	0.851	0.854	0.854	0.981	0.957	0.971	0.956	0.922	0.931	0.957	0.957
50K_2	0.815	0.817	0.817	0.861	0.860	0.860	0.860	0.864	0.864	0.980	0.960	0.973	0.955	0.926	0.935	0.957	0.956
50K_3	0.838	0.838	0.838	0.879	0.877	0.878	0.878	0.878	0.878	0.981	0.958	0.974	0.959	0.927	0.935	0.960	0.959
50K_4	0.821	0.821	0.821	0.865	0.863	0.862	0.864	0.866	0.867	0.982	0.953	0.974	0.957	0.925	0.934	0.958	0.958
50K_5	0.833	0.833	0.833	0.871	0.870	0.871	0.869	0.870	0.870	0.980	0.956	0.976	0.955	0.931	0.939	0.956	0.957
50K_6	0.833	0.834	0.834	0.872	0.870	0.870	0.870	0.872	0.872	0.980	0.959	0.975	0.957	0.930	0.938	0.958	0.957
50K_7	0.832	0.834	0.834	0.871	0.870	0.870	0.869	0.872	0.872	0.980	0.956	0.972	0.958	0.930	0.938	0.957	0.958
50K_8	0.834	0.836	0.836	0.876	0.875	0.875	0.878	0.879	0.879	0.981	0.956	0.972	0.956	0.927	0.934	0.958	0.958
50K_9	0.839	0.841	0.841	0.879	0.877	0.877	0.876	0.879	0.879	0.967	0.947	0.963	0.960	0.926	0.935	0.957	0.960
50K_10	0.819	0.820	0.820	0.863	0.860	0.860	0.865	0.867	0.867	0.978	0.956	0.974	0.956	0.929	0.936	0.954	0.958
50K_11	0.824	0.826	0.826	0.869	0.866	0.866	0.867	0.870	0.870	0.981	0.956	0.975	0.956	0.929	0.937	0.955	0.957
50K_12	0.832	0.832	0.833	0.874	0.874	0.874	0.870	0.873	0.874	0.979	0.954	0.973	0.956	0.931	0.939	0.960	0.958
50K_13	0.830	0.830	0.830	0.871	0.871	0.871	0.873	0.875	0.875	0.981	0.956	0.974	0.958	0.932	0.938	0.956	0.959
50K_14	0.820	0.821	0.821	0.863	0.861	0.861	0.862	0.866	0.866	0.978	0.956	0.971	0.958	0.926	0.935	0.959	0.959
50K_15	0.841	0.841	0.841	0.879	0.877	0.877	0.878	0.880	0.881	0.979	0.957	0.975	0.958	0.932	0.940	0.957	0.959
50K_16	0.825	0.827	0.827	0.864	0.863	0.863	0.866	0.868	0.868	0.968	0.945	0.967	0.955	0.925	0.932	0.952	0.956
50K_17	0.804	0.807	0.807	0.852	0.852	0.852	0.855	0.857	0.857	0.978	0.955	0.977	0.958	0.926	0.936	0.954	0.959
Average	0.827	0.827	0.828	0.868	0.867	0.867	0.868	0.870	0.870	0.979	0.955	0.973	0.957	0.928	0.936	0.957	0.958

Raw= no InDel realignment or base quality score recalibration

IR= InDel realignment

IR+BQSR= InDel realignment followed by base quality score recalibration

