# GATK BaseRecalibration report

Argument	Value
binary_tag_name	None
covariate	ReadGroup,QualityScore,Context,Cycle
default_platform	None
deletions_default_quality	45
force_platform	None
indels_context_size	3
insertions_default_quality	45
low_quality_tail	2
maximum_cycle_value	500
mismatches_context_size	2
mismatches_default_quality	−1
no_standard_covs	false
quantizing_levels	16
run_without_dbsnp	false
solid_nocall_strategy	THROW_EXCEPTION
solid_recal_mode	SET_Q_ZERO
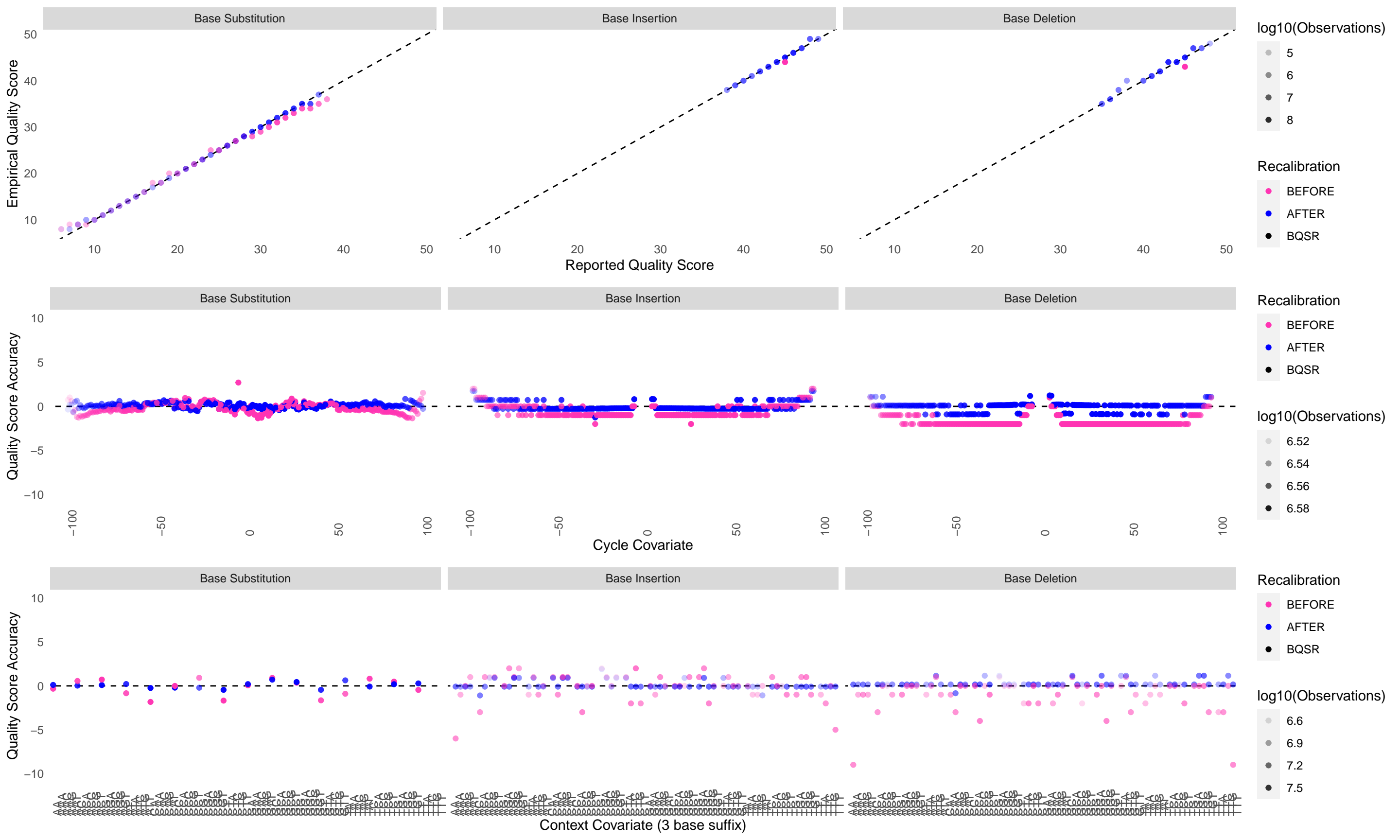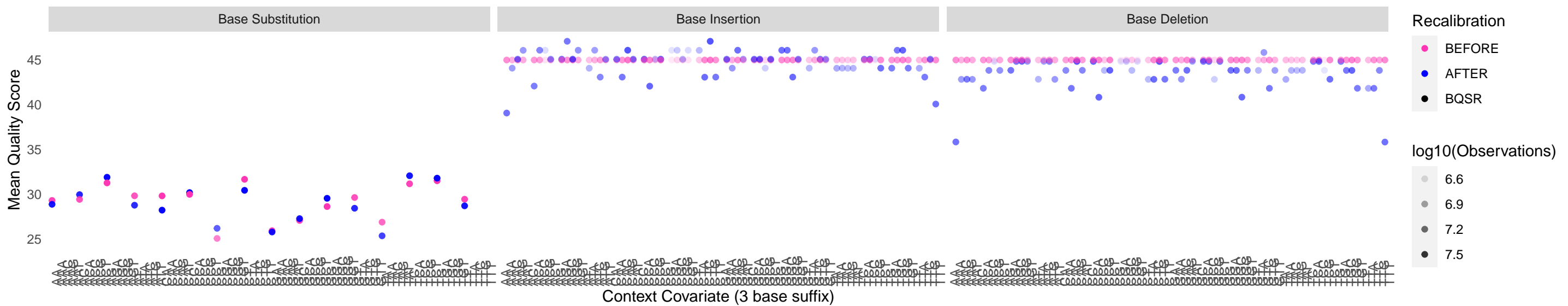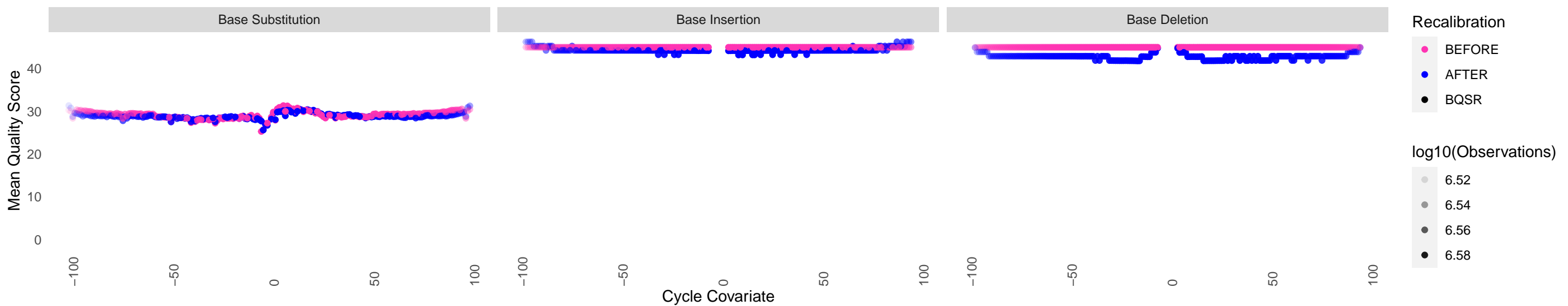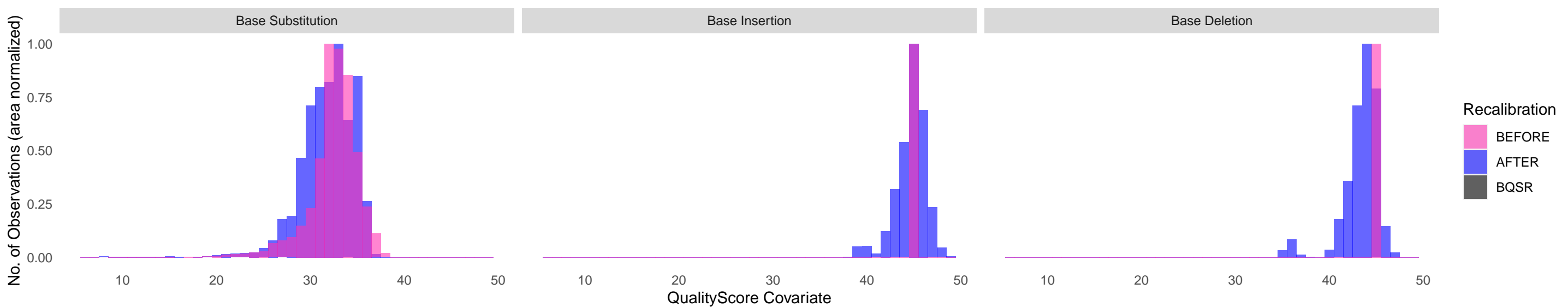
Overall error rates by event type

ReadGroup	TCGA–A7–A4SE–Tumor	TCGA–A7–A4SE–Tumor	TCGA–A7–A4SE–Tumor
EventType	M	I	D
EmpiricalQuality	29.0	44.0	43.0
EstimatedQReported	29.1	45.0	45.0
Observations	7.51e+08	7.51e+08	7.51e+08
Errors	9.57e+05	2.72e+04	3.78e+04

Error rates by event type and initial quality score

ReadGroup	QualityScore	EventType	EmpiricalQuality	Observations	Errors
TCGA–A7–A4SE–Tumor	6	M	8	140068	23032.22
TCGA–A7–A4SE–Tumor	7	M	9	212180	25207.87
TCGA–A7–A4SE–Tumor	8	M	9	284740	34598.72
TCGA–A7–A4SE–Tumor	9	M	9	454747	53893.48
TCGA–A7–A4SE–Tumor	10	M	10	512971	50234.88
TCGA–A7–A4SE–Tumor	11	M	11	503605	41350.80
TCGA–A7–A4SE–Tumor	12	M	12	397990	22639.80
TCGA–A7–A4SE–Tumor	13	M	13	547565	26362.55
TCGA–A7–A4SE–Tumor	14	M	14	439390	17645.74
TCGA–A7–A4SE–Tumor	15	M	15	432647	13482.46
TCGA–A7–A4SE–Tumor	16	M	16	325045	8234.98
TCGA–A7–A4SE–Tumor	17	M	18	491308	8120.82
TCGA–A7–A4SE–Tumor	18	M	18	637270	9342.15
TCGA–A7–A4SE–Tumor	19	M	20	746152	8304.46
TCGA–A7–A4SE–Tumor	20	M	20	1237257	11827.99
TCGA–A7–A4SE–Tumor	21	M	21	1841444	13254.16
TCGA–A7–A4SE–Tumor	22	M	22	2276928	12897.53
TCGA–A7–A4SE–Tumor	23	M	23	2595186	11618.48
TCGA–A7–A4SE–Tumor	24	M	25	3713840	11996.33
TCGA–A7–A4SE–Tumor	25	M	25	4767098	13733.53
TCGA–A7–A4SE–Tumor	26	M	26	10118145	24069.72
TCGA–A7–A4SE–Tumor	27	M	27	12065971	25758.96
TCGA–A7–A4SE–Tumor	28	M	28	14308241	25113.45
TCGA–A7–A4SE–Tumor	29	M	28	22592297	33606.65
TCGA–A7–A4SE–Tumor	30	M	29	35258296	42911.11
TCGA–A7–A4SE–Tumor	31	M	30	70710364	70686.23
TCGA–A7–A4SE–Tumor	32	M	31	152311962	111729.48
TCGA–A7–A4SE–Tumor	33	M	32	148772225	91885.21
TCGA–A7–A4SE–Tumor	34	M	33	130260958	63199.29
TCGA–A7–A4SE–Tumor	35	M	34	75289861	30009.80
TCGA–A7–A4SE–Tumor	36	M	34	36340597	13785.05
TCGA–A7–A4SE–Tumor	37	M	35	17070302	5347.06
TCGA–A7–A4SE–Tumor	38	M	36	3028548	743.37
TCGA–A7–A4SE–Tumor	45	I	44	750685198	27241.52
TCGA–A7–A4SE–Tumor	45	D	43	750685198	37795.49